STATUS GO FOR PRECLINICAL IMAGING

EDITED BY: Claudia Kuntner, Bernhard Baumann, Adriana Tavares and Andreas Hess

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STATUS GO FOR PRECLINICAL IMAGING

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Editorial: Status Go for Preclinical Imaging

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Keywords: preclinical imaging, PET, SPECT, MRI, ultrasound, microscopy, quantification

Editorial on the Research Topic

Status Go for Preclinical Imaging

This special Research Topic includes a collection of reviews and original articles on preclinical imaging. Preclinical imaging encompasses the use of imaging methods to study animal models, tissue samples, and other unique specimens, such as eggs (*in ovo*). Preclinical imaging is driven by advances in medical physics and instrumentation as well as by active research in biology and medicine. Given the multi-disciplinary nature of preclinical imaging, some articles from this collection appear in the journal Frontiers in Physics whereas others appear in the journal Frontiers in Physiology.

Over time, preclinical imaging has evolved from a technique perceived to be niche and of limited value to an established workhorse in medical research, supporting drug discovery programs, mechanistic studies focused on understanding (patho-)physiology and disease development as well as progression, and aiding the development of paradigms for clinical imaging. Preclinical imaging also encompasses scales of different orders of magnitude, from molecular/microscopic to structural/macroscopic as well as organismic scale, thus providing not only superb anatomical detail but also excellent quantitative functional information. Despite the tremendous and everexpanding role of preclinical imaging in medical research, its full potential can only be delivered if preclinical researchers apply the same amount of effort and rigor to their preclinical protocols as is used in clinical settings. This means that thoughtful study planning and use of established standardized protocols, accompanied by careful handling of the subjects (e.g., animals, eggs, or tissue samples) is of paramount importance to generate preclinical imaging datasets with translational value. Furthermore, there is a need to implement robust image analysis approaches, including reliable and reproducible methods to obtain quantitative data. Finally, state-of-the-art statistical testing and controlling must be applied.

In the present Research Topic, 13 articles are divided into 6 reviews, 1 mini-review, 4 original research articles, 1 perspective, and 1 brief research report, covering some of the latest research activities on diverse topics including microscopy, positron emission tomography (PET) quantification, single photon emission computed tomography (SPECT) for neuroimaging, small animal magnetic resonance imaging (MRI), ultrasound, *in ovo* imaging, *in vivo* cell tracking using multiple imaging methods and correlated multimodal imaging (CMI).

The review article by Walter et al. provides a comprehensive overview of the challenges of CMI, where information from the same specimen with two or more modalities is combined to create a composite view of the sample. In this review paper, the different imaging techniques available for CMI, including correlated light microscopy, electron microscopy, and biological hybrid imaging, are described alongside the advantages and disadvantages of each modality.

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Kuntner C, Baumann B, Tavares AAS and Hess A (2020) Editorial: Status Go for Preclinical Imaging. Front. Phys. 8:344. doi: 10.3389/fphy.2020.00344 Kuntner et al. Editorial: Preclinical Imaging

In this Frontiers special issue, five papers discuss the latest research in nuclear imaging techniques. The paper by He et al. describes strategies for the extraction of an arterial or imagederived input function for quantification of the adenosine type 1 receptors (A1) with PET. The impact of attenuation correction on [18F]FDG PET imaging is described by Wanek et al. using data from phantom and rat studies. Oelschlegel and Goldschmidt's paper focuses on describing the use of cerebral blood flow SPECT imaging to study brain-wide activation patterns in awake rodents. Dual tracer PET/SPECT studies are reported by Blower et al. using phantoms to investigate the crosscontamination of PET signal on SPECT measurements and viceversa. Finally, a perspective article by Jones et al. provides an outlook at the possibilities of how preclinical imaging might be instrumental to deliver the full potential of the clinical total-body PET technology.

Traditionally, hybrid radionuclide imaging has been used to study the physiology and pathophysiology in humans and rodents. However, it can also be used to examine tumoral uptake of radiotracers together with anatomical information in the Hen's Egg Test Chorioallantoic-Membrane (HET-CAM) model by so-called *in ovo* imaging (Winter et al.). This is an emerging new application for preclinical imaging. Another more routine application of preclinical imaging involves the use of imaging technology to track cells *in vivo* and consequently help with the development of novel cancer immunotherapies. Imaging methods used to track cells are applied as summarized in the review by Iafrate and Fruhwirth.

This special issue on preclinical imaging also covers the utility of preclinical MRI as a promising diagnostic tool to monitor disease progression and response to therapy in preclinical models. Technical aspects of *in vivo* small animal cardiovascular

MRI are summarized in the review by Li et al. whereas Anderson et al. describe the development of MR diffusion imaging protocols for structural connectomics analysis in mouse models of human disease.

Finally, the Research Topic is further complemented by a review on preclinical ultrasound imaging techniques and applications (Moran and Thomson) and a mini-review on recent technological and methodological advances in the field of multiphoton microscopy (Pozzi et al.).

The Research Topic editors greatly appreciate the amount of work from contributors, reviewers, and Frontiers staff. We believe that the articles published in this Research Topic provide further evidence that preclinical imaging is an invaluable tool in medical and biological research and will continue to supply the field with new critical knowledge on the causes, consequences, and treatment options of multiple diseases. This is a moment when the preclinical imaging community needs to go further, continuing to push the limits of this tool.

AUTHOR CONTRIBUTIONS

All authors listed have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Image-Derived Input Functions for Quantification of A₁ Adenosine Receptors Availability in Mice Brains Using PET and [¹⁸F]CPFPX

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Purpose: *In vivo* imaging for the A_1 adenosine receptors (A_1ARs) with positron emission tomography (PET) using 8-cyclopentyl-3-(3-[^{18}F]fluoropropyl)-1-propylxanthine ([^{18}F]CPFPX) has become an important tool for studying physiological processes quantitatively in mice. However, the measurement of arterial input functions (AIFs) on mice is a method with restricted applicability because of the small total blood volume and the related difficulties in withdrawing blood. Therefore, the aim of this study was to extract an appropriate [^{18}F]CPFPX image-derived input function (IDIF) from dynamic PET images of mice.

Procedures: In this study, five mice were scanned with [18 F]CPFPX for 60 min. Arterial blood samples (n=7 per animal) were collected from the femoral artery and corrected for metabolites. To generate IDIFs, three different approaches were selected: (A) volume of interest (VOI) placed over the heart (cube, 10 mm); (B) VOI set over abdominal vena cava/aorta region with a cuboid ($5 \times 5 \times 15$ mm); and (C) with $1 \times 1 \times 1$ mm voxels on five consecutive slices. A calculated scaling factor (α) was used to correct for partial volume effect; the method of obtaining the total metabolite correction of [18 F]CPFPX for IDIFs was developed. Three IDIFs were validated by comparison with AIF. Validation included the following: visual performance; computing area under the curve (AUC) ratios (IDIF/AIF) of whole-blood curves and parent curves; and the mean distribution volume (V_T) ratios (IDIF/AIF) of A₁ARs calculated by Logan plot and two-tissue compartment model.

Results: Compared with the AIF, the IDIF with VOI over heart showed the best performance among the three IDIFs after scaling by 1.77 (α) in terms of visual analysis, AUC ratios (IDIF/AIF; whole-blood AUC ratio, 1.03 \pm 0.06; parent curve AUC ratio, 1.01 \pm 0.10) and $V_{\rm T}$ ratios (IDIF/AIF; Logan $V_{\rm T}$ ratio, 1.00 \pm 0.17; two-tissue compartment model $V_{\rm T}$ ratio, 1.00 \pm 0.13) evaluation. The A₁ARs

distribution of average parametric images was in good accordance to autoradiography of the mouse brain.

Conclusion: The proposed study provides evidence that IDIF with VOI over heart can replace AIF effectively for quantification of A_1ARs using PET and $I^{18}FICPFPX$ in mice brains.

Keywords: image-derived input function, positron emission tomography, A₁ adenosine receptors, [¹⁸F]CPFPX, mice brains

INTRODUCTION

The A₁ adenosine receptors (A₁ARs) are involved in various neurological as well as psychiatric disorders (Paul et al., 2011), and play significant role in processes such as sleepwake regulation (Porkka-Heiskanen and Kalinchuk, 2011) and memory consolidation (Gessi et al., 2011; Paul et al., 2011). At present, multiple antagonists, agonists, and allosteric modulators are under development to explore the therapeutic effect of adenosine receptors (Kiesman et al., 2009). Small animal imaging could simplify the evaluation process of these compounds; moreover, various mice models of adenosine-related diseases might help to identify potential applications (Elmenhorst et al., 2013). Therefore, there is a high interest in in vivo imaging techniques for the A₁AR with positron emission tomography (PET) in mice to visualize molecular processes quantitatively. PET with the radiotracer 8-cyclopentyl-3-(3-[¹⁸F]fluoropropyl)-1-propylxanthine ([18F]CPFPX) can be used to quantify the in vivo concentration of A₁ARs in the brain (Bauer et al., 2003). For this quantification, the concentration of parent radiotracer in plasma is necessary as the input function to the brain. The arterial input function (AIF) is still the gold standard (Meyer et al., 2006; Chen et al., 2007; Zanotti-Fregonara et al., 2009a) for quantification of target receptors via the invasive procedure of arterial cannulation. However, in mice, the total blood volume is small, and continuous blood sampling during the whole experiment is relatively difficult and technically challenging (Laforest et al., 2005; Yee et al., 2005). In addition, measuring the AIF might affect the physiological function of the small animal. Multiple blood samplings in mice have often conducted as a terminal procedure preventing longitudinal studies within individual (Kim et al., 2006; Ferl et al., 2007; Wu et al., 2007).

Several methods have therefore been developed to overcome the difficulties of arterial blood sampling including image-derived input functions (IDIFs) (Chen et al., 1998; Naganawa et al., 2005; Su et al., 2005; Fang and Muzic, 2008; Mourik et al., 2008), which became an attractive non-invasive alternative compared to AIF. The high spatial resolution of modern small-animal PET scanners (Lecomte et al., 1994; Cherry et al., 1997; Chatziioannou et al., 1999) allows to acquire IDIFs even from small anatomical regions. In brain PET studies from mice, only a few organs such as heart and abdominal vena cava/aorta are expected to be directly visible from initial time frames after injection. Accordingly, IDIFs were successfully established in "large" (~2 mm diameter) blood vessels in mice (Lanz et al., 2014).

Most studies, however, reported the extraction of the IDIFs from rodent hearts because outlining blood vessels

was challenging (Parker and Feng, 2005; Zanotti-Fregonara et al., 2009b; Croteau et al., 2010). When using heart muscle cells or liver, however, the spill-over effects have to be considered. Compared with heart, IDIFs from "large" blood vessel are less influenced by spill-in effects from surrounding tissues (Lanz et al., 2014), while partial volume effects caused by limited resolution and difficult delineation have to be considered carefully.

According to the previous results and the specific distribution pattern of A_1AR , we extracted IDIFs over both heart as well as abdominal vena cava/aorta in mice scanned with PET and [^{18}F]CPFPX. For quantification of A_1AR availability in mice brains, three different approaches for volume of interest (VOI) definition for respective IDIFs were selected.

Since the radioligand we used in this study showed fast metabolization, namely, the parent radioligand accounted for only \sim 18% of total radioactivity in whole blood 60 min after radiotracer injection, data were corrected for metabolites.

To evaluate the accuracy and precision of the different imagederived input approaches, AIFs from the same animals were used as reference standard.

Thus, the aim of this present study was to define appropriate IDIFs for dynamic [¹⁸F]CPFPX PET in mice.

MATERIALS AND METHODS

Animal Preparation

All procedures were approved by German regional authorities (Landesamt für Natur, Umwelt und Verbraucherschutz) and performed on the basis of the German Animal Welfare Act. The animal experimental data reported in this study are in compliance with the Animal Research: Reporting *in vivo* Experiments guidelines. Five healthy male C57BL/6 mice (28 weeks; 37.80 \pm 5.42 g, mean \pm SD) with free access to standard mouse food and water were housed in a 12 h light/dark cycle at 22°C.

Anesthesia was introduced with 5% isoflurane in 2 L/min oxygen and maintained at 1.5–2% isoflurane in 1 L/min oxygen. The surgical cannulation (PE10, Becton Dickinson, Sparks, MD, United States) of the femoral artery and heparin-coated microtubes served for blood sampling; another catheter placed in the tail vein was used for a bolus injection of [^{18}F]CPFPX. The dead volume of the catheter was $14.17 \pm 2.09 \,\mu l$.

Breathing rate (pressure pad, 41 \pm 10 bpm) and body temperature (rectal probe) were used to continuously monitor

all animals throughout the PET scans (BioVet System, m2m Imaging, Salisbury, QLD, Australia). A constant body temperature (37.17 \pm 0.58°C) was maintained by a heating lamp.

[¹⁸F]CPFPX PET Scan and Image-Derived Input Function Extraction Methods

Radiosynthesis and formulation of [18 F]CPFPX were performed as described earlier (Holschbach et al., 2002). [18 F]CPFPX was routinely obtained ready for injection with a radiochemical yield of 20 \pm 5%, a radiochemical purity of 99.5 \pm 0.3%, and a molar activity of 396 \pm 114 GBq/mol.

All PET data were acquired on a Siemens Inveon Multimodality PET scanner (Siemens, Knoxville, TN, United States) with Inveon Acquisition Workplace 1.5 (Siemens). The mice were positioned supine (to allow blood sampling) with their heads fixed by the nose cone of the anesthesia system.

A dual-source 57 Co transmission scan was processed for 10 min to correct attenuation before emission scans. Directly afterward, a bolus of [18 F]CPFPX (0.83 \pm 0.18 MBq) was injected over 1 min via a syringe pump (model 44, Harvard Apparatus, Holliston, MA, United States) at time of scan start.

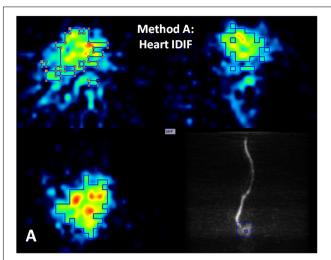
List-mode PET data were acquired for 60 min after tracer application and framed into a dynamic sequence of 12×10 , 3×20 , 3×30 , 3×60 , 3×150 , and 9×300 s frames. One hundred fifty-nine slices were reconstructed by filtered back projection (Ramp filter, cutoff = 0.5) after Fourier rebinning into 2D sinograms. All PET images were corrected for attenuation and scatter radiation.

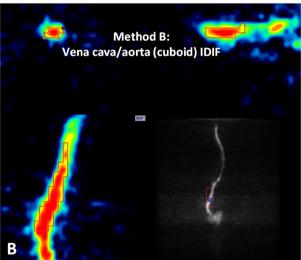
Postprocessing of PET images and activity extraction from the VOIs were performed with PMOD 3.408 software (version 3.408, PMOD Group, Zurich, Switzerland). To explore an appropriate image-derived input, three different approaches were selected (**Figure 1**) using the first time frames after [18 F]CPFPX injection (image of the first 10 s) as a guide. For method A (**Figure 1A**), a large VOI covering the whole organ was placed over the heart (cube, 10 mm), and for method B (**Figure 1B**), over the abdominal vena cava/aorta region (cuboid, $5 \times 5 \times 15$ mm). In a second step, an automatic algorithm from PMOD was utilized to identify only those voxels, within these volumes exceeding 50% of the total activity inside the VOI for subsequent read out. For method C (**Figure 1C**), $1 \times 1 \times 1$ mm voxels on five consecutive slices (Lanz et al., 2014) were manually placed over the abdominal vena cava/aorta region (also centered on highest activity spot).

In this study, an optimal calculated scaling factor (α) was calculated to correct the partial volume effects of regions for IDIF effectively using the equation below:

$$Sum = \sum_{i=1}^{7} \left[C_{AIF}(t_i) - C_{raw_IDIF}(t_i) \times \alpha \right]^2$$
 (1)

where α is the scaling factor used in this study for the three different approaches, $C_{\rm AIF}$ is the radioactivity concentration (kBq/cc) of AIF at any time point (t_i), and $C_{\rm raw_IDIF}$ is the raw radioactivity concentration of the three different IDIFs used in this study at the same time points. The optimal scaling factor α





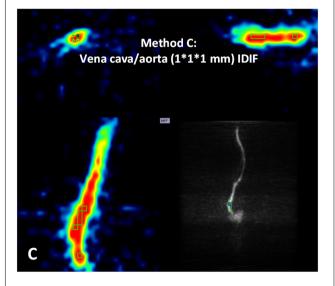


FIGURE 1 | Positron emission tomography images of heart and abdominal vena cava/aorta in a representative mouse during the first 10 s after [18F]CPFPX bolus injection were used to define different volumes of interest (Continued)

FIGURE 1 | Continued

(VOIs) with image-derived input functions (IDIFs). Each image has three planes: coronal plane (upper left), sagittal plane (upper right), and horizontal plane (lower left). The lower right of each image shows a maximum-intensity-projection (MIP) map on the coronal plane. (A) VOI placed over the heart (cube, 10 mm). (B) VOI placed over abdominal vena cava/aorta region (cuboid, $5\times5\times15$ mm). (C) VOI ($1\times1\times1$ mm voxels with five consecutive slices) delineated on abdominal vena cava/aorta region (centered on the highest activity spot).

is obtained by minimizing Sum, namely, the difference between arterial inputs and corrected image-inputs is lowest with the optimized α . More detailed information about Eq. (1) is discussed in section "Discussion."

Arterial Blood Sampling and Metabolite Correction

During PET acquisition, blood samples (20.51 \pm 5.78 μl per time point) were taken from the femoral artery at 1, 10, 20, 30, 40, 50, and 60 min after tracer injection. After blood sampling, heparinized saline solution was used to prevent coagulation inside of the catheter by flushing. All whole-blood and plasma samples were weighed in preweighted tubes, then measured in a high-sensitivity γ -counter (ISOMED 2100; Medizintechnik Dresden, Germany) to calibrate the activity concentration with radioactive decay correction (relative to the start of the acquisition). The fraction of unchanged radioligand in total plasma activity (parent curve) was determined using a previously published approach (Meyer et al., 2004) using thin layer chromatography.

Since the radiometabolite fraction of [¹⁸F]CPFPX is high (Bier et al., 2006; Matusch et al., 2006), data were corrected for metabolism, and the extraction of the parent radioligand was corrected for residual activity in the precipitate after protein extraction (extraction correction). The following equation was used for data interpolation:

Total metabolite correction
$$(t) = \frac{1}{(1 + a \times (t - d)^b)^c} \times \frac{1}{(1 + e \times t^2)^f}$$
 (2)

where a, b, c, and d are fitted to describe the metabolite fraction; e and f are fitted to describe the extraction fraction. More detailed information about Eq. (2) is discussed in section "Discussion."

Accuracy of Image-Derived Input Functions

The accuracy and precision of the different image-derived extraction methods of input functions were evaluated by comparison with AIF.

Visual Comparison

After using the scaling factor on image inputs, time-activity curves of whole-blood and parent tracer obtained with each method were compared with standard arterial whole-blood and parent time-activity curves. The comparison considered overall shape of the curves, the height of the peaks, as well as the slope of the tails.

Area Under Curve Ratios

In addition to the visual comparison, a quantitative analysis was performed using area under curve (AUC) ratios between the image- and arterial-derived curves (Zanotti-Fregonara et al., 2011). The image/arterial ratios of both whole-blood time-activity curves and metabolite-corrected parent time-activity curves were calculated. The image-derived parent curve of each mouse was estimated by multiplying the image-derived whole-blood time-activity curve with group average parent/whole blood ratios at the same time points.

Kinetic Modeling

After postprocessing with scaling factor α , PET data were analyzed with both the Logan plot model (Logan et al., 1990) and the two-tissue compartment model (2TCM) (Leenders et al., 1990; Koeppe et al., 1991). Logan analysis was implemented with $t^*=20$ min and with no weighting. 2TCM analysis used "prescribed weighting" (standard deviation of the pixel values in the VOI is used for the calculation of the weights) in all IDIF methods. For AIF, the three-term exponentials function was applied in the configuration of blood activity fitting and interpolation.

All distribution volumes $(V_{\rm T})$ with different input functions were obtained for brain regions, such as cortex, hippocampus, and thalamus for each mouse. The mean $V_{\rm T}$ ratios (image-derived input/arterial input) based on three different IDIFs were calculated and compared. The linear regression was used to show the correlation between image-derived input and arterial input, while the Bland-Altman plot was introduced to describe agreement between image-derived input and arterial input.

Parametric Images and Autoradiography

Average parametric images (n=5) of $V_{\rm T}$ in mice brains were calculated by application of Logan plot for both AIF and IDIF over heart (method A). Logan plot was set up with $t^*=20$ min, and with no masking.

The results of in vivo binding by different PET input functions were further verified by in vitro autoradiography. After decapitation, the mouse brain was removed, frozen in 2-methylbutane (-40° C) and stored at -80° C. Brain sections (20-µm thickness) were mounted on slides. Preincubation was conducted in 170 mM Tris-HCl buffer (pH 7.4) and 2 U/L adenosine deaminase for 15 min at 4°C. Later on, main incubation lasted for 2 h at room temperature with the same buffer including [3H]CPFPX (0.99 nM; molar activity, 2,009 GBq/mmol) (Holschbach et al., 2003), 100 µM Gpp(NH)p and 2 U/L adenosine deaminase. After washing with preincubation buffer and a rapid rinse in ice-cold water, sections were dried with a stream of air (room temperature) and exposed against phosphor-imaging plates (BAS2025; Fuji, Japan) with tritium activity standards (Amersham Biosciences, Piscataway, United States). For further processing of digital autoradiography, an image plate reader (spatial resolution of 50 µm; BAS 5000;

Fuji, Japan) and image analysis software (Image Gauge 4.0; Fuji, Japan) were used. To get less background noise image in Image Gauge 4.0, 32-color type (displays in 32 pseudo-colors) was used with linear method (adjusts contrast with a linear curve).

RESULTS

Blood Sample Analysis

The whole-blood activity curves reached at highest value at \sim 60 s among the seven blood sampling time points, followed by a rapid drop (**Supplementary Figure 1A**). Plasma activity showed a stable percentage of whole-blood activity with a mean plasma/whole blood ratio of 1.67 \pm 0.04. Metabolite correction of [¹⁸F]CPFPX was done (Eq. 2) with parameters set to a (0.18), b (1.84), c (0.34), d (0.30), e (0.19), and f (0.02). Group mean parent/whole blood ratio [(plasma/whole blood ratio) \times total metabolite correction] over time was calculated (**Supplementary Figure 1B**) based on Eq. (2).

Visual Analysis

After extraction of IDIFs with different methods, a calculated scaling factor ($\alpha = 1.77$) was used to correct for partial volume effects in whole-blood curves (**Figure 2A**).

The tails of whole-blood curves obtained by three different IDIF approaches generally matched closely with the reference arterial inputs. The image-derived whole-blood curve with the VOI over the heart performed best.

Compared with the arterial parent compound curves (**Figure 2B**), the image-derived parent compound curves performed equally well. The shape of the image-derived input over heart (method A) was smoother than vena cava/aorta (cuboid) VOI (method B) and $1 \times 1 \times 1$ mm VOI (method C).

Ratios of Area Under Curves

After scaling, the mean AUC ratio between image-derived and arterial inputs of both whole-blood and corrected parent curves were estimated. As given in **Table 1**, the mean AUC ratio was smaller for heart (method A) and aorta $(1 \times 1 \times 1 \text{ mm})$

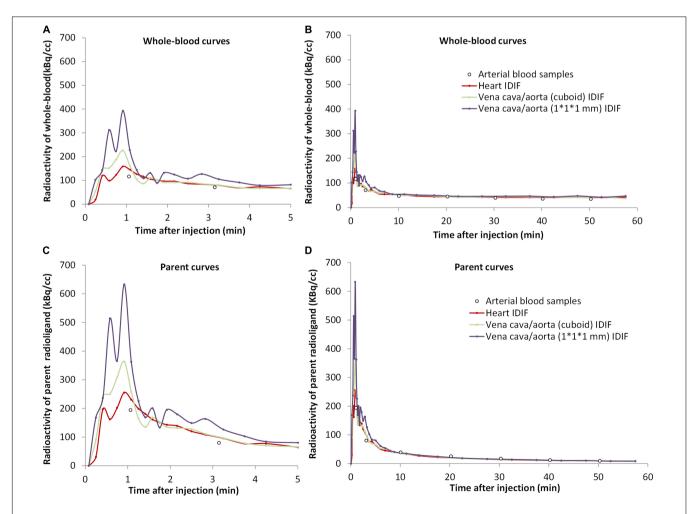


FIGURE 2 | The concentrations over time of [18F]CPFPX in whole-blood (A,B) and parent radioligand (C,D) (with metabolite correction) curves from the arterial input function (white dots) and from the three image-derived input functions (IDIFs) with different volumes of interest (VOIs) (colored lines) in a representative animal. The left curves (A,C) are excerpts of the first 5 min of the total curves (B,D).

TABLE 1 | Mean AUC ratios (IDIF/AIF) for each VOI related IDIF in both whole-blood and parent curves.

	Method A Heart (mean ± SD)	Method B Vena cava/aorta (cuboid) (mean ± SD)	Method C Vena cava/aorta (1 \times 1 \times 1 mm) (mean \pm SD)
Whole-blood AUC ratio	1.03 ± 0.06	1.11 ± 0.14	1.08 ± 0.10
Parent curve AUC ratio	1.01 ± 0.10	1.04 ± 0.14	1.06 ± 0.23

n = 5. AUC, area under curve; VOI, volume of interest; IDIF, image-derived input function; AIF, arterial input function.

(method C) VOIs than for aorta (cuboid) VOI (method B). Specifically, the difference in the whole-blood arterial AUC and image-derived AUC was \leq 10% for both methods A and C. Moreover, method A had a whole-blood AUC ratio (1.03) that was closest to identity with a low standard deviation (SD) of 0.06.

On the other hand, the AUC ratio of parent curve in the aorta (1 \times 1 \times 1 mm; method C) was worse than in the heart (method A) and cuboid aorta (method B) VOIs (**Table 1**). The high ratio and SD in method C (1.06 \pm 0.23) indicated that the results from this image-derived approach were inconstant and not fitted

ideally among all tested mice, while method A performed best with an AUC ratio close to 1 and a low SD value (1.01 \pm 0.10).

Kinetic Modeling (Logan and 2TCM Analysis)

In Figure 3, the $V_{\rm T}$ values of image-derived and arterial inputs generated by both Logan graphical and 2TCM analysis are presented for the following brain regions: striatum (STR), cortex (CTX), hippocampus (HIP), thalamus (THA), cerebellum (CB), hypothalamus (HYP), amygdala (AMY), olfactory bulb (OLF), and midbrain (MID).

The $V_{\rm T}$ values of each mouse obtained by the Logan graphical analysis (**Figures 3A–C**) show better correlations between arterial and image-derived inputs $V_{\rm T}$ in all three IDIF extraction methods, while the $V_{\rm T}$ values with the 2TCM model were more dispersed around the identity line (**Figures 3D–F**).

As seen in Bland-Altman plots (**Figure 4**), according to the comparison between AIF and IDIF over heart (method A) (**Figures 4A,D**), 0% (0/45) and 4.44% (2/45) difference dots were located outside of the 95% limits of agreement by Logan and 2TCM analysis, respectively; in comparison between AIF and method B, 2.22% (1/45) difference dots (**Figures 4B,E**) were located out of the 95% limits of agreement with both

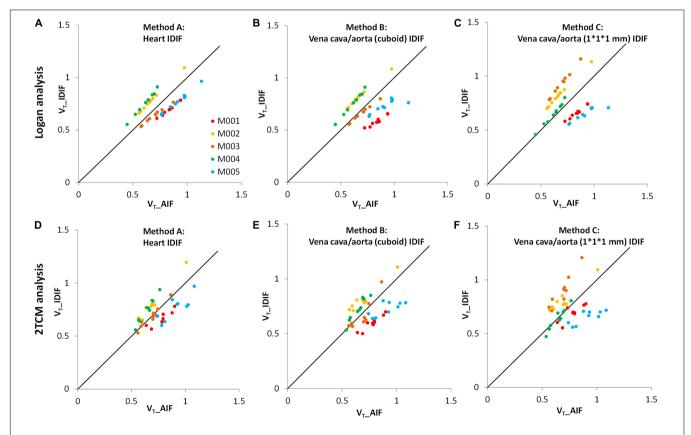


FIGURE 3 Comparison of distribution volumes (V_T) values between image-derived input function (IDIF) and arterial input function (AIF). All V_T values of different input functions in various brain regions were generated by two kinetic models: the Logan graphical model (upper) and the 2TCM model (lower). **(A,D)** The IDIF with the volume of interest (VOI) placed over the heart (method A); **(B,E)** the IDIF with the VOI set over abdominal vena cava/aorta region with a cuboid (method B); **(C,F)** the IDIF with the VOI delineated with 1 × 1 × 1 mm voxels on five consecutive slices over the abdominal vena cava/aorta region (method C). Different dots represent different brain regions (n = 9). Different colors represent different mice (n = 5). The solid line is the line of identity.

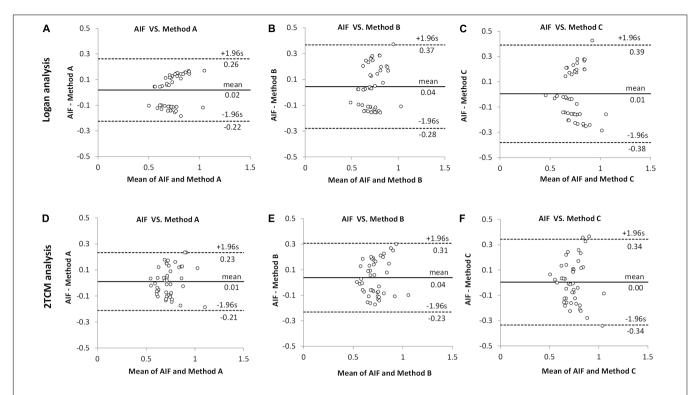


FIGURE 4 | Comparison between arterial input function (AIF) and image-derived input function (IDIF) of distribution volumes (V_T) by Bland–Altman analysis. All V_T values obtained by Logan and 2TCM kinetic modeling were the same as the data in **Figure 3**. **(A,D)** The IDIF with the volume of interest (VOI) placed over the heart (method A) compared with AIF. **(B,E)** The IDIF with the VOI set over abdominal vena cava/aorta region with a cuboid (method B) compared with AIF. **(C,F)** the IDIF with the VOI delineated with 1 \times 1 \times 1 mm voxels on five consecutive slices over the abdominal vena cava/aorta region (method C) compared with AIF. Different dots represent different brain regions (n = 9) in all mice (n = 5).

Logan and 2TCM analysis; as for method C, 2.22% (1/45) and 6.67% (3/45) difference dots (**Figures 4C,F**) were located out of the limits by Logan and 2TCM analysis, respectively. Moreover, based on the comparison between AIF and method A (**Figures 4A,D**), the ratios of the maximum difference to the mean within the 95% limits of agreement were 25.01% (0.1849/0.7390) and 25.26% (0.1860/0.7363) by Logan and 2TCM analysis, respectively. However, ratios were higher in comparison between AIF and other input functions (methods B and C): 39.33% (0.2856/0.7261), 37.27% (0.2694/0.7227), 38.42% (0.2865/0.7457), and 44.21% (0.3270/0.7396) in **Figures 4B,C,E,F**, respectively.

Therefore, irrespective of Logan or 2TCM analysis, the best $V_{\rm T}$ performance of the IDIFs were found qualitatively with the heart (method A) VOI (**Figure 3A**).

In detail, the mean $V_{\rm T}$ ratios between image-derived and arterial inputs for method A (**Table 2**) were 1.00 ± 0.17 by Logan and 1.00 ± 0.13 by 2TCM analysis, respectively. Both modeling results were approaching unity. Specific $V_{\rm T}$ values of different brain regions obtained with method A by Logan and 2TCM models are given in **Supplementary Table 1**.

Figure 5 shows the average parametric images (n = 5) of $V_{\rm T}$ with Logan plot for both AIF and IDIF over heart (method A). **Figures 5A,D** present the typical distribution of A₁AR in mice brains, which is in good accordance to the distribution pattern in autoradiography (**Figure 5G**).

DISCUSSION

The main goal of the present study was to establish an optimal [18 F]CPFPX IDIF which can replace AIF requiring blood sampling in mice. Three non-invasive IDIFs were tested using different VOI-based approaches: (A) VOI placed over the heart (cube, 10 mm); (B) VOI set over abdominal vena cava/aorta region with a cuboid ($5 \times 5 \times 15$ mm); and (C) VOI delineated with $1 \times 1 \times 1$ mm voxels on five consecutive slices, also over the abdominal vena cava/aorta region (centered on highest activity spot). We evaluated all the image-derived input results by

TABLE 2 | Mean $V_{\rm T}$ ratios (IDIF/AIF) obtained from striatum, cortex, hippocampus, thalamus, cerebellum, hypothalamus, amygdala, olfactory bulb, and midbrain for each VOI related image-derived approach in both Logan graphical and 2TCM analysis.

		Method B	Method C
	Method A	Vena cava/aorta	Vena cava/aorta
	Heart	(cuboid)	(1 × 1 × 1 mm)
	(mean ± SD)	(mean ± SD)	(mean ± SD)
Logan $V_{\rm T}$ ratio 2TCM $V_{\rm T}$ ratio	1.00 ± 0.17	0.97 ± 0.21	1.02 ± 0.25
	1.00 ± 0.13	0.97 ± 0.16	1.02 ± 0.21

n = 5. V_T, total distribution volume; VOI, volume of interest; 2TCM, two-tissue compartment model; IDIF, image-derived input function; AIF, arterial input function.

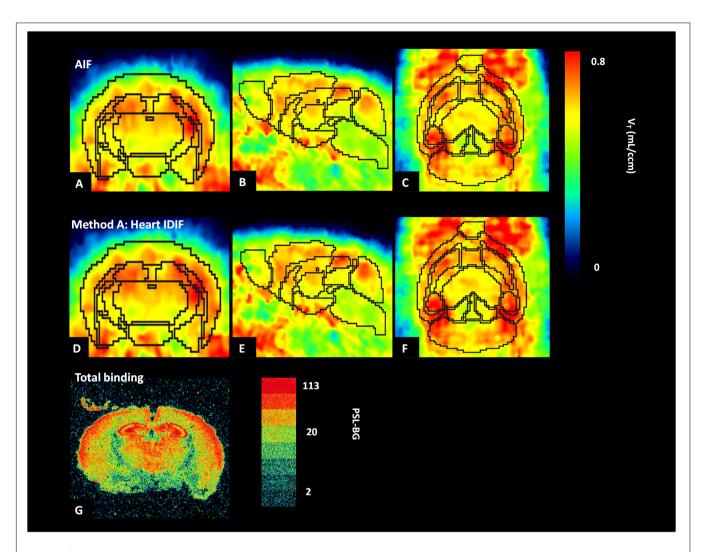


FIGURE 5 | Average parametric images (n = 5) of A₁ adenosine receptors (A₁ARs) distribution in mice brains calculated by application of Logan plot in PET: coronal plane (left column), sagittal plane (middle column), and horizontal plane (right column) images representing cerebral A₁AR using the arterial input function (AIF) (**A-C**) and the image-derived input function over the heart (heart IDIF) (**D-F**). Mouse brain autoradiograph (at 0.99 nM concentration of [3 H]CPFPX) shows receptor total binding (**G**).

comparison with standard AIF. We found that method A (VOI placed over the heart) closely follows the AIF. It also showed more accurate, stable and more reliable results than methods B and C in terms of AUC ratios and kinetic modeling of both Logan plot and 2TCM analysis.

As shown in **Figures 3**, **4**, **Table 2**, and **Supplementary Table 1**, all results of kinetic modeling analysis with all three image-derived approaches were calculated with both Logan plot and 2TCM. Considering the three different image-derived and the AIFs applied in this study, the Logan-derived $V_{\rm T}$ values of a 60-min scan were very similar to those obtained with 2TCM analysis, with a difference of <5% (**Supplementary Figure 2**). Therefore, in further studies, we propose to directly select Logan analysis for kinetic modeling not only because it is more robust regarding the modeling parameters but also because it is less sensitive than 2TCM modeling analysis toward extraction of the first part of the input curve. Logan analysis based on the

AUC of the input function is less sensitive than 2TCM analysis to the initial shape of the input function. The radioactivity concentration of the initial part of whole-blood curve changes rapidly, and consequently, it is difficult to acquire a correct curve from the image data (Zanotti-Fregonara et al., 2011). Under these circumstances, $V_{\rm T}$ values are sometimes poorly obtained with 2TCM.

Except from the gold-standard approach of arterial plasma input function and IDIF, the input function for kinetic models can also be acquired by applying a reference region method. When studying brain receptors, cerebellum is used as reference region for some neuroreceptor quantifications. Unfortunately, there often is no reference region for other neuroreceptors, for example, the studies for nicotinic receptors with tracer: (2-[¹⁸F]fluoro-A-85380) (Zanotti-Fregonara et al., 2012) and mGluR1 with ([¹¹C]ITDM) (Bertoglio et al., 2019) in mice.

Different suggestions have been put forward to deal with partial volume as well as spill-out and spill-in effects, respectively. According to Chen et al. (2007) and Kang et al. (2018), the activity $C_{\rm measured}$ from VOIs can be considered as a combination of two components: the true radioactivity in the blood vessel and the radioactivity from surrounding regions:

$$C_{\text{measured}}(t) = \text{PV} \times C_{\text{vessel}}(t) + \text{SO} \times C_{\text{surrounding}}(t)$$
 (3)

where C_{measured} (t) is the measured radioactivity in the blood obtained from PET, $C_{\text{vessel}}(t)$ is the true radioactivity in the blood vessel, and C_{surrounding} (t) is radioactivity from surrounding tissues; PV is the determined partial volume correction coefficient, and SO represents the experimental spill-over correction coefficient required to consider the spatial resolution of the small-animal PET scanner and the reconstruction methodology. Lanz et al. (2014) proposed another method for the "spill-out effect" correction of the imaged-derived inputs by a double-exponential function. However, instead of one scaling factor (α), this convolution operation needs four parameter optimizations and a modified Levenberg-Marquardt non-linear regression method. Compared with the above-mentioned studies, we simplified the equations and functions to correct the radioactivity concentration of IDIFs. The main reason for that is that [18F]CPFPX rarely showed obvious affinity for myocardium, so that the spill-over effect could be ignored. In our study, because of spill-out and related partial volume effects, the raw image-derived activity of whole blood was always lower than the measured AIF (p < 0.05, by t test). To correct the abovementioned effects in IDIFs, an optimal scaling factor ($\alpha = 1.77$) was calculated (see Eq. 1) and subsequently used for scaling of different IDIFs.

Metabolite correction for IDIF is another important aspect for tracers with high radiometabolite fractions. So far, the majority of studies about the IDIFs prefer to use tracers with negligible metabolism, such as Sari et al. (2017) who discussed image-derived methods for [18F]FDG only focusing on partial volume effects and not metabolite correction. For radiotracers with fast metabolism, such as [18F]CPFPX, one key part of obtaining IDIFs is the total metabolite correction. In the present study, we not only explored how to solve partial volume effects with a scaling factor (a) but also developed a method of obtaining the total metabolite correction (Eq. 2) of [18F]CPFPX for image-derived input approaches. Specifically, after scaling with factor α , the parent curve (IDIF) was obtained by following formulas: parent curve(IDIF) = wholeblood curve(IDIF) × (mean parent/whole-blood ratio), mean parent/whole-blood ratio = plasma curve(IDIF) × total metabolite correction (t)/whole-blood curve(IDIF), plasma $curve_{(IDIF)} = 1.67 \times whole-blood curve_{(IDIF)}$.

Although this study required a small amount of blood samples for calculating the scaling factor (α) and the parameters (a–f) of total metabolite correction equation (Eq. 2), there are still opportunities to achieve completely blood-free IDIFs for acquiring parent curves for future [18 F]CPFPX or other tracer studies in mice. On the other hand, we can use blood-based methods to optimize the accuracy of the IDIFs. For example,

Lanz et al. (2014) tried to decrease the effect of tracer dispersion in blood during the first minute after the [¹⁸F]FDG bolus injection. They estimated the average scaling parameter using a single blood sample at 1.5 min, which resulted in higher accuracy for the extraction of IDIFs in animals.

There is a potential drawback of the evaluation regarding the AUC ratio. Since the first blood sample was collected 1-2 min after tracer injection, it is possible that the peaks of the arterial blood curves were lower than the peaks of image-derived curves (Figure 2). Taking this into account when using the AUC ratios between image-derived and arterial curves, resulting values would be bigger. This may explain why all AUC ratios in **Table 1** were >1. Another limitation of the present study is the relatively low number of mice. However, even though we used only five animals and there were individual differences, we strongly believe in the representativeness of our results. For instance, in Figures 3A-C, although every mouse performed significant correlations (R^2) between arterial and image-derived inputs $V_{\rm T}$ values by Logan analysis, there was still no perfect overlay with the line of identity because of the individual slopes and intercepts. However, when we did the average of all five mice, the $V_{\rm T}$ values of image-derived inputs got much closer to arterial inputs (Table 2). Notwithstanding these findings, an increased study power will undoubtedly help optimizing the data in further non-invasive input function studies.

In the present study, autoradiography was used for qualitative analysis of A_1AR with $[^3H]CPFPX$. Compared with parametric PET images from $[^{18}F]CPFPX$ of arterial and IDIF (**Figures 5A,D**), the distribution of A_1AR in autoradiography (**Figure 5G**) showed the same binding patterns. For example, high concentrations of A_1AR in cortex, hippocampus, and thalamus were detected by both PET and autoradiography, and the qualitative distribution of A_1AR labeled with $[^3H]CPFPX$ (0.99 nM) in coronal sections was similar to previous data of Bailey et al. (2003).

A potential improvement of our image-derived input approach might derive from a closer look at heartbeat affects. Previously, only the left ventricle was used as the region of interest to reduce the motion of heart and improve the precision. Recently, Herraiz et al. (2016) and Verhaeghe et al. (2018) showed that the left ventricle volume can be estimated by means of cardiac gating during PET acquisition. For this purpose, PET raw data were divided into time subsets according to the different phases of the heart activity. Thus, a more accurate measurement and verification of whole-heart image-derived inputs might be obtained in future studies when gated PET imaging will be applied (Locke et al., 2011; Mabrouk et al., 2012).

CONCLUSION

The present study provides evidence that a non-invasive IDIF can validly replace the standard AIF in quantification of A_1AR PET using the fast metabolizing radioligand [^{18}F]CPFPX in mice. Furthermore, a VOI over the heart is the best choice to extract the IDIF after comparing different VOI placements regarding image-derived curves, AUC ratios, and kinetic modeling results (V_T).

DATA AVAILABILITY STATEMENT

The datasets analyzed during the current study are available from the corresponding author on reasonable request.

ETHICS STATEMENT

The animal study was reviewed and approved by the German regional authorities (Landesamt für Natur, Umwelt und Verbraucherschutz) and performed on the basis of the German Animal Welfare Act.

AUTHOR CONTRIBUTIONS

DE, AB, and TK designed the study. FW, TK, AO, and DE were responsible for experiments and data collection. XH did analysis and interpretation of data, and drafted and revised the manuscript. DE, TK, SB, and AD made contribution to the

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data interpretation. JE and BN contributed with tracer synthesis. All authors critically revised the manuscript and approved the final version.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphys. 2019.01617/full#supplementary-material

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Study of the Cumulative Dose Between Fractions of Lung Cancer Radiotherapy Based on CT and CBCT Image Deformable Registration Technology

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Luo J, Ma C, Yu S, Li Z and Ma C (2020) Study of the Cumulative Dose Between Fractions of Lung Cancer Radiotherapy Based on CT and CBCT Image Deformable Registration Technology. Front. Phys. 8:21. doi: 10.3389/fphy.2020.00021 **Objective:** To analyze the difference between planned dose and delivered dose by accumulating the dose based on CT and CBCT image deformable registration.

Methods: The clinical data of 24 NSCLC (non-small cell lung cancer) patients receiving conformal radiotherapy or intensity-modulated radiotherapy (IMRT) were retrospectively analyzed. With the CBCT image of each week as the target image, we performed the deformation registration for CBCT images and planning CT images in RayStation. The delivered dose of CBCT images compared to the planning CT images was accumulated with the use of mapping relationships in registration. The differences in planned dose and accumulative dose of target and at-risk organs were compared.

Results: The average planned and accumulative doses of GTV in 24 patients were 5832.45 ± 645.42 and 5750.65 ± 630.27 cGy, respectively (P < 0.05). The average planning target volume (PTV) in CT plans and accumulation plans reaching the prescription dose was 95.59 and 81.47% of the PTV (P > 0.05). At the stage of treatment, the volumes of the at-risk organs in CBCT images were not significantly different. There were no statistically significant differences in the probability of complications in the right lung, left lung, heart, total lung, or spinal cord (P > 0.05).

Conclusion: With the dose deformable registration method, the dose caused by changes in the target anatomical structure of NSCLC patients was found. The dose to organs did not change much. However, in some patients, the received radiation in the target organ was less than the prescribed dose.

Keywords: non-small cell lung cancer, dose-volume histogram, fraction delivered dose, deformable registration, accumulative dose

INTRODUCTION

In current radiotherapy practice IMRT technology can significantly improve the rate of tumor control and reduce complications. Therefore, IMRT is widely used in some complex target radiotherapies [1]. Multiple factors can affect the precise implementation of radiotherapy. There will be changes in the location of the target for each radiotherapy fraction, which can lead to difference between the planned dose and cumulative dose. For example, a target volume reduction will lead to bad dose distribution, and the surrounding normal tissue into the high dose area can increase the normal tissue radiation dose [2]. Therefore, it is necessary to analyze these changes during the process of fraction radiotherapy.

Adaptive radiation therapy (ART) is based on image data, cumulative dose, and other dose information to understand the various changes in patients, make timely adjustments to the planning target volume (PTV) and clinical target volume (CTV), and modify the prescribed dose and treatment plan to improve follow-up treatment and more accurately apply radiation therapy. Generally speaking, image-guided radiotherapy, volume-guided radiotherapy, and dose-guided radiotherapy are part of ART [3]. In this study, we analyzed the difference between planned dose and delivered dose by calculating the accumulated dose based on deformable registration, and we analyzed the changes in the volume and dose of targets and organs-at-risk by comparing cone beam CT (CBCT) images and planning CT images of patients with non-small cell lung cancer (NSCLC). We initially studied the actual dose volume histogram of target and OARs in NSCLC radiotherapy.

MATERIALS AND METHODS

Plan CT Acquisition and Target Contour

A total of 24 patients with NSCLC who underwent CRT or IMRT (24 sets of CT images and CBCT images) were retrospectively analyzed from January 2014 to January 2015 in Shandong Tumor Hospital. 18 patients were male, and the others were female. The median age was 58 years (range, 47-65 years). General clinical data of patients were as shown in Table 1. The pCT was obtained with a fan-beam helical CT scanner (Philips Brilliance Big Bore 16 slice CT, Philips Medical Systems, Eindhoven, The Netherlands) with 3 mm slice thickness and 512×512 pixels. The pCT was imported into the RayStation radiotherapy planning system via the network. The target and OARs were contoured on pCT. The target of radiotherapy included the gross tumor target (GTV), the clinical target (CTV) with the small lesion, the inner target (ITV) edge of the target movement, and the margin of the PTV. When the lung cancer target was outlined, the width and window position of the CT window were 1,600 and −600 HU, respectively, and the window width and window position of the Mediastinum window were 400 and 20 HU, respectively. Unless, there was evidence of invasion, CTV should not have exceeded the anatomical range. The lung cancer primary tumor was GTV + $(6 \sim 8)$ mm + respiratory mobility + setup error. The mediastinal lymph node was PTV for GTV + $(3 \sim 5)$ mm + respiratory mobility + setup error. The doctor could base the

TABLE 1 | General clinical data of patients.

Characteristics	Value	
Gender		
Male	18	
Female	6	
Age	47-65 y, median 58	
Stage		
IIIA	14	
IIIB	10	
Squamous	16	
Adenocarcinoma	8	
GTV/cm ³	$17.6 \pm 8.1 \text{ cm}^3 \text{ Range (8.69–36.58)}$	
PTV/cm ³	$98.59 \pm 30.27 \mathrm{cm^3} \mathrm{Range} (744.65 – 2197.43)$	
Left lung/cm ³	1355.52 \pm 744.65 cm ³ Range (744.65–2197.43)	
Right lung/cm3	$1738.77 \pm 890.12 \text{ cm}^3 \text{ Range } (1047.76-2424.55)$	

dose on the normal structure around the target to modify it as appropriate. The OARs included the lungs, spinal cord, heart, and esophagus.

The Radiotherapy Plan Design

The physicians used the RayStation treatment planning system, and the conformal plans generally included a 6 MV X-ray and 4–6 fixed conformal fields. The lateral angle was adjusted as far as possible to make its long axis parallel to the target, reducing the volume through the lung tissue, to ensure that at least one field completely avoided the spinal cord, and all the field angle intervals should have been as high as 40° . It was common to have 5 fields for lung tumors. Conventional IMRTs typically consisted of 5–7 fields, and the separation angles were the same. When IMRT was applied to lung cancer, the number of fields and the angle separation tended to be adjusted according to the actual situation. The prescription dose was $2.0~\rm Gy \times 30~fractions$; V30 < 20% or average lung dose (Dmean) $\leq 20~\rm Gy$; heart V30 $\leq 46\%$ or Dmean $<26~\rm Gy$; esophageal V50 $\leq 30\%$ or Dmean $\leq (34\sim40)~\rm Gy$, maximum dose (Dmax) $\leq (58\sim74)~\rm Gy$.

CBCT Image Acquisition

Twenty-four patients underwent CBCT scanning before treatment. According to the scanning range, the reference center level was selected. In the three-dimensional laser light, the front and the left and right sides of the center of the body were marked. The Elekta Synergy (Elekta Oncology Systems, Crawley, UK) accelerator XVI system acquired the CBCT images. The system consists of a high-level X-ray tube and a large, amorphous silicon X-ray detection board through the telescopic robot arm installed on both sides of the linear accelerator rack. The scan mode was half-phan mode, and the rotation angle was 200°. The scanning parameters were as follows: tube voltage 120 kV, tube current 25 mA, acquisition rate 5.5 frames/s, plus bowtie filter, and S20 collimator. The process of XVI acquisition was issued by the tube pulsed X-ray (frequency fixed to 5.75 Hz). The radiation went through the scanning object, and then the signal was read and stored by the plate detector. The above process was repeated to collect data. The image reconstruction matrix was 512 \times 512, the

reconstructed layer thickness was 3 mm, and the CBCT image was 88 layers. The CBCT scan was done once every time the patient was treated, and the image registration and the setup error were corrected. Finally, all CT and CBCT images were imported into the RayStation treatment planning system.

CT and CBCT Image Deformable Registration

CBCT image targets and OARs were outlined by the function of automatic profiling in the RayStation treatment planning system. The outlines were then manually corrected by the clinicians. The CT image was used as the reference image, and the daily CBCT image was used as the target image. The rigid registration was based on the outer contour of the body, and then the deformation registration was applied based on the gray-value information. If necessary, we manually modified the result of the rigid registration. We applied the target mapping to the planned CT target and OAR to the CBCT image.

CBCT Fractional Dose Calculation and Accumulation

Using dose tracking and cumulative doses in the Adaptive Radiation module in the RayStation treatment planning system, the individual CBCT electronic density tables obtained from each patient's CT image map were selected for CBCT images. Based on the CBCT image, the fractional dose was calculated, and the fractional dose was added to the planned CT image to obtain the cumulative dose.

Normal Tissue Complication Probability (NTCP)

Normal tissue complication probability (NTCP) values were also calculated for each OAR with the Lyman-Kutcher-Burman (LKB) model. The three parameters were derived according to Burman identification: several parameters, including mean hepatic dose, percentage volume of normal lung with a radiation dose more than 20 Gy (V20 Gy), and normal tissue complication probability (NTCP), were calculated from DVH. The NTCP model of Lyman was used. In the NTCP model,

$$NTCP = 1/\sqrt{2\pi} \int_{-\infty}^{t} \exp(-t^2/2) dt$$
 (1)

$$t = (D - TD_{50}(v))/(m \times TD_{50}(v))$$
 (2)

$$v = V/V_{ref} \tag{3}$$

$$TD(2) = TD(v) \times v^{n}$$
(4)

where TD50(v) is the 50% tolerance dose for uniform irradiation of the partial volume V. The partial- and whole-lung radiation tolerance doses were related by a power law relationship:

Where Vref is the volume of normal lung. The parameter n is the volume effect parameter, for which the value of 0.87 from the literature was applied. The parameter m is the steepness of the dose-complication curve for a fixed partial volume, and an estimate of 0.18 was used. The TD50 of 24.5 Gy was applied in the calculation. The effective-volume method of Kutcher

and Burman was used to provide estimates of equivalent doses and volume pairs for uniform partial organ irradiation from the DVHs summarizing the non-uniform irradiation. The three parameters were derived according to Burman's identification: lung (TD50 = $24.5 \,\text{Gy}$, n = 0.87, m = 0.18), heart (TD50 = $48.0 \,\text{Gy}$, n = 0.35, m = 0.10) and spinal cord (TD50 = $66.5 \,\text{Gy}$, n = 0.05, m = 0.175).

Statistical Analysis

Statistical analysis was carried out using the statistical software SPSS version 19.0. Data are expressed as mean \pm standard deviation and were compared using the *t*-test. P < 0.05 was statistically significant.

RESULTS

Target and OAR Volume Changes

The mean volume change of the tumor target in 24 patients was 88.26% of the original volume on the CBCT image. CBCT automatically outlined the results, and the CT automatically outlined results were not very different. The results of the CBCT in the third patient showed an increase in volume, while the CBCT in the fifth patient showed a reduction in volume. Due to respiratory movement caused by the tumor target and the surrounding tissue movement, there was an error in the target of the radiotherapy and the plan target, resulting in changes in the dose.

The CBCT showed that the volume of the lungs changed relative to the fraction of treatment, and the volume of the lungs in most patients changed greatly with the fraction of treatment. The treated left and right lung were reduced to 93.39 and 96.79% of the original volume, respectively. At the end of treatment, the mean volume of the left and right lungs in 24 patients with CBCT images was 88.95 and 80.32% of the original volume, respectively. Comparison of CT and CBCT images showed the same changes in the left and right lung volumes. Besides the first case of a patient with a larger left lung volume, the remaining volumes were reduced. This shows that CBCT to analyze the pulmonary deformation of the registration was still more accurate and automatically showed that the method could better reflect the changes in lung volume.

Target and OAR Dose Changes

Figure 1 shows little change in CT and CBCT images with the fraction dose of the target. Most of the target volumes on the CT images and CBCT were not very different, and the impact on the dose was not large. The dose of PTV was not significantly different in any of the 24 patients, and the error was within 5%, indicating that the target was in a high-dose area during each fraction.

Figure 2 shows the change in CT and CBCT images with the fraction of dose to the OARs. The left and right lungs of 24 patients showed a substantially reduced lung volume and a mean increase in lung dose as a result of CT and CBCT calculation. The patient CBCT was used to sketch the results, and the left and right lung doses in the course of treatment were much greater than the CT image doses. The left and right lung CBCT

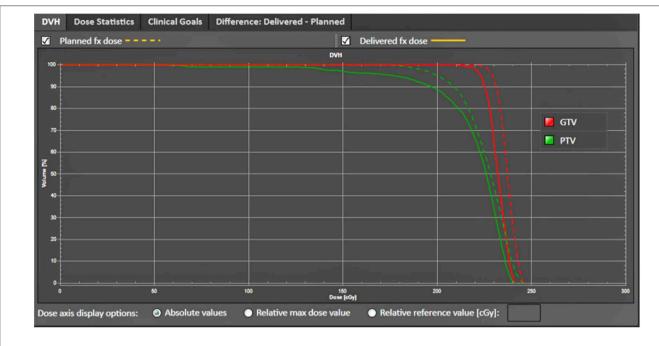


FIGURE 1 | DVH changes of the target area, the GTV and PTV.

of the 24 patients showed 167.31 \pm 165.75 and 79.33 \pm 54.11 cGy, respectively, and the cumulative dose was 164.63 \pm 164.96 and 77.63 \pm 53.36 cGy, respectively. Most of the 24 patients showed the same dose treatment progress, gradually decreased lung volume, and gradually increased lung dose, indicating that the reduction in lung volume and its dose increase have a certain relevance to whether the treatment at the original dose will cause excessive exposure.

Figure 3 shows the change in atelectasis on CT images with the fraction dose. There were four plans: Plan0327, Plan0403, Plan0410, and Plan0417. This patient had cT4N2M0 NSCLC and was treated with 30 fraction \times 2.0 Gy. Two IGRT specialists, independent of each other, visually evaluated every MVCT. For each MVCT, the observed changes in atelectasis were scored. This result shows that it is very important to use image-guided radiotherapy (IGRT).

The Cumulative Dose Changes of Targets and OARs

Table 2 shows the cumulative dose of GTV D99. In addition to the first and fifth cases of patients with GTV, the cumulative dose was lower than the planned dose, but it was still within the clinical requirements to achieve the lowest dose. The other target did not show significant changes. No dose to the target showed any significant changes, indicating that the target had been under high dose coverage. In addition, there was no significant difference between CT and CBCT cumulative doses. When the target was reduced, we had to give the original target a sufficient dose to ensure the control rate of the tumor, indicating that the target was in the high-dose area.

The basic clinical information of the order, age, sex, and staging of 24 patients is shown in **Table 2**, and the volumes of GTV, PTV, left lung, and right lung as measured by CT images before treatment are listed.

Table 2 shows the results of GTV D95, D50, average, and PTV planned dose and cumulative dose changes and some evaluation parameters of the paired t-test analysis. The average dose changes yielded t values of 1.919, 2.299, 2.372, 2.197 in the course of treatment. The respective P values were 0.096, 0.055, 0.049, and 0.064. The CT plan and cumulative plan of the target PTV V100 reached the prescription dose of average volumes 95.59 and 81.47%. For GTV, the difference between planned dose and cumulative dose was statistically significant (P < 0.05).

Table 3 shows some of the differences in the assessment parameters of the lungs and the spinal cord and the difference between the planned dose and the applied cumulative dose. The cumulative dose to the lung and spinal cord in 24 patients decreased compared with the planned dose, and the cardiac Dmean accumulation showed an increase. Paired t-test analysis showed that the mean values of Dmean, left lung Dmean, heart Dmean, whole lung Dmean and spinal Dmax were 1.222, 0.480, -0.291, 0.786, and 1.683, respectively, and the P values were 0.261, 0.646, 0.780, 0.457, and 0.136, which were not statistically significant.

DISCUSSION

There are many important organs around a radiotherapy target. The control rate of lung cancer and the radiation therapy dose is related to the surrounding normal tissue dose limit and has become the biggest obstacle for conventional radiotherapy to

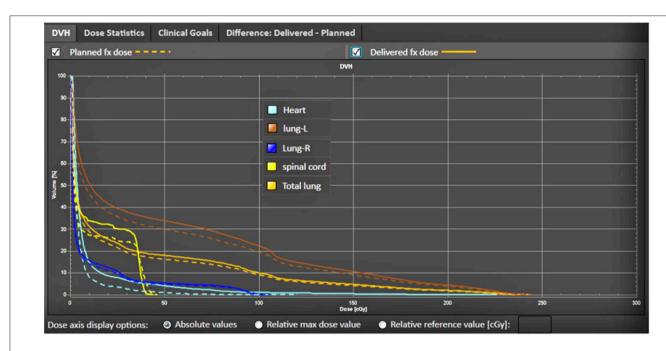


FIGURE 2 | DVH changes of the OARs, including the heart, spinal cord, and lungs.

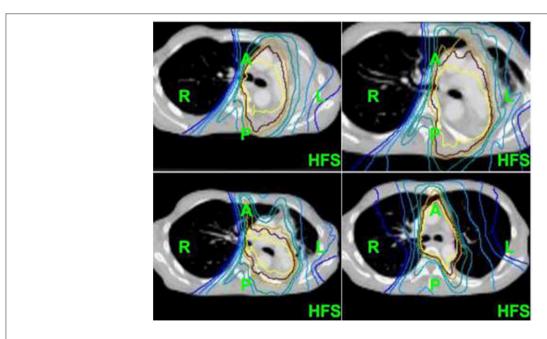


FIGURE 3 | The change in atelectasis on CT images with the fraction dose.

improve the tumor dose. CRT or IMRT radiotherapy can produce a dose distribution that is highly suitable for the shape of the target, reducing the surrounding normal tissue exposure and limiting the organ's dose, but from the pretreatment planning through the entire course of treatment [4], the dose distribution of the initial treatment plan changes during the actual treatment, and the difference between the administered dose and the

planned dose is conducive to adjusting the radiotherapy plan for better and more accurate radiotherapy.

In this study, GTV Dmean decreased significantly during the course of treatment, indicating that the experience of the outgoing boundary may not have met the requirements. Kwong et al. [5] indicated that the results of the lung cancer GTV center for the displacement of the head and foot direction were

TABLE 2 | Differences in exposure dose between CT plan and accumulation plan.

GTV	CT plan	Accumulation plan	t-value	P-value
D ₉₅	6179.00 ± 616.24	6156.35 ± 614.94	1.935	0.086
D ₅₀	6308.90 ± 656.02	6662.25 ± 629.93	2.467	0.067
Average	6307.45 ± 624.22	5753.90 ± 630.27	2.254	0.039
PTV (V ₁₀₀)	$96.59 \pm 2.29\%$	$89.67 \pm 18.71\%$	2.456	0.067

TABLE 3 | Differences in organs-at-risk dose between CT plan and accumulation plan.

Organs (Gy)	CT plan	Accumulation plan	t value	P value
Right lung D _{mean}	793.30 ± 54.11	776.3 ± 53.36	1.222	0.261
Left lung D _{mean}	1673.10 ± 165.75	1646.3 ± 164.96	0.480	0.646
Heart D _{mean}	618.80 ± 66.70	683.8 ± 60.91	-0.291	0.780
Total lung D _{mean}	1181.40 ± 67.22	1158.7 ± 66.19	0.786	0.457
Spinal cord D _{max}	3726.20 ± 185.91	3600.0 ± 173.14	1.683	0.136
NTCP of right lung (%)	1.60 ± 0.74	1.33 ± 0.86	1.702	0.085
NTCP of left lung (%)	6.00 ± 1.94	5.34 ± 1.76	0.897	0.124
NTCP of heart (%)	4.77 ± 2.15	4.55 ± 2.37	-0.532	0.112
NTCP of total lung (%)	2.53 ± 1.32	1.95 ± 1.22	1.023	0.075
NTCP of spinal-cord (%)	2.03 ± 0.72	1.81 ± 0.94	1.224	0.090

significantly smaller than those of the corresponding direction of the diaphragm. Therefore, the expansion of the safety boundary according to experience may cause excessive exposure of normal tissue. PTV reached as low as 81.47% of the prescribed dose volume. In three selected middle esophageal cancer patients with three-dimensional conformal radiotherapy, Brown et al. [6] illustrated the need to replan during the course of treatment.

Replanning should be done only at the right time. Ding et al. [7] studied 87 patients with IMRT and three-dimensional adaptive radiotherapy, followed by 18F-FDG PET/CT scans after 40 Gy irradiation, and mapped the target. Zhang et al. [8] studied 40 cases of NSCLC radiotherapy target volume changes. Comparing the number of irradiations \leq 20 times the reset and 20 times after the reduction of the GTV reduction ratio and Dmean decline ratio in the ipsilateral lung and whole lung, they concluded that 40 Gy/20 replanning is the most reasonable, but different individuals should be differentially planned using PET and CT fusion images. The tumors subsided significantly in their patients.

Because the soft-tissue contrast of CT images is high, the soft-tissue contrast of CBCT is poor. In a previous study, we used CT scanning to repeat the changes that doctors made in target and normal tissues. In this study, we used CT and multiple CBCT to outline the results. The lungs and target changed as the treatment progressed, and to varying degrees. CBCT images were used to outline the tumors. The lungs and spinal cord permitted a better sketch effect, and for targets with a low surrounding tissue contrast, the algorithm still needs to continue to be improved

[9]. The image algorithm mainly includes the frequency domain Contourlet transform, wavelet transform and spatial domain non-local mean filtering [10–12]. These algorithms have much room for development.

By the use of deformation registration, we can outline the CT image profile to the kilovolt-like CBCT image, decomposed into multiple CBCT calculations, and the CBCT dose is added each time. The total dose will be transplanted to the planning CT image. The obtained results will reduce the patient position changes, organ volume changes, and other uncertain factors. The results of dose uptake using CBCT showed that there was some difference between the delivered dose and the planned dose during the treatment of the lungs, while the dose to the heart increased and the dose to the spinal cord decreased slightly. More cases are needed to supplement the data and confirm the conclusions of this study.

Since we need to superimpose each dose on the original CT and compare it with the planning CT, we need to calibrate the CBCT's HU-RED table accurately to obtain a more accurate cumulative dose [13]. In this study, we used RayStation software to automatically divide the HU values by the different tissue densities. The accuracy of the method was improved compared to the traditional method of calibration. Another method is to map the ROIs between CT and CBCT, but due to positioning errors and CBCT image quality, these two methods cannot completely eliminate the error [14–19], but they can meet the current clinical requirements.

In summary, this NSCLC radiotherapy target and an OAR real DVH preliminary study was based on the offline artificial correction method, and the process took much more time. In addition, whether the accuracy of the two image target regions and normal tissue deformation registration affects the calculation of DVH parameters remains to be verified. By improving the speed and accuracy of deformation registration, we can achieve rapid online correction of radiotherapy targets and adaptive radiotherapy.

CONCLUSION

The doses to the lung and to other normal organs did not change much, and there was no statistically significant difference in the probability of complications in normal tissues. However, in some patients, the radiation dose in the target area was reduced, which may have led to missed targets.

DATA AVAILABILITY STATEMENT

The datasets generated for this study are available on request to the corresponding author.

ETHICS STATEMENT

This study was carried out in accordance with the recommendations of Ethics Committee Approval at Shandong Cancer Hospital and Institute. The protocol was approved by Ethics Committee of the Shandong Cancer Hospital and

Institute. As the study is retrospective, the need for written informed consent from participants was waived.

AUTHOR CONTRIBUTIONS

JL and CdM drafted conception and design and draft the manuscript. ZL and CsM contributed to acquire, analyze, and interpret data. SY contributed to acquire data and enhanced its intellectual content. All authors read and approved the final manuscript.

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Scattering Compensation for Deep Brain Microscopy: The Long Road to Get Proper Images

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Multiphoton microscopy is the most widespread method for preclinical brain imaging when sub-micrometer resolution is required. Nonetheless, even in the case of optimal experimental conditions, only a few hundred micrometers under the brain surface can be imaged by multiphoton microscopy. The main limitation preventing the acquisition of images from deep brain structures is the random light scattering which, until recently, was considered an unsurmountable obstacle. When in 2007 a breakthrough work by Vellekoop and Mosk [1] proved it is indeed possible to compensate for random scattering by using high resolution phase modulators, the neuro-photonics community started chasing the dream of a multiphoton microscopy capable of reaching arbitrary depths within the brain. Unfortunately, more than 10 years later, despite a massive improvement of technologies for scattering compensation in terms of speed, performances and reliability, clear images from deep layers of biological tissues are still lacking. In this work, we review recent technological and methodological advances in the field of multiphoton microscopy analyzing the big issue of scattering compensation. We will highlight the limits hampering image acquisition, and we will try to analyze the road scientists must tackle to target one of the most challenging issue in the field of biomedical imaging.

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INTRODUCTION

The analysis of brain function and dysfunction is inherently bound to the visualization of neuronal morphology in intact tissues and most importantly is tightly related to the investigation of synaptic and cellular activity in extended neuronal networks [2]. The first disruptive advancement in the field of neurophotonics arrived at the beginning of the 90's, when in the Webb laboratory [3] it was proven that the two-photon microscopy (2PM), only theoretically envisaged more than 50 years before [4], was indeed feasible. The advent of femtosecond-pulsed infrared laser sources and the development of advanced scanning methods opened new routes to researchers aiming to perform imaging of thick biological samples [5]. A deeper light penetration, a reduced photodamage together with the possibility to detect non-ballistic fluorescence photons because of the intrinsic confocality of multiphoton excitation, allowed 2PM to become the gold standard technique for *in vivo* brain imaging. Unfortunately, the strongly turbid media distorting incident light avoids clear

and fully resolved images from deeper layer in the brain to be obtained, even in small animals. The maximum imaging depth is in fact related to the ability of incident light to target the focal plane (ballistic photons) in a diffraction limited volume. In particular, the repeated scattering of the incident wavefront is, most of the time, so robust that the spatial coherence is completely lost beyond a small volume with a radius comparable to the wavelength of light [1, 6–8]. While purely morphological imaging of structures deep within a three-dimensional sample can easily be achieved by chemically fixing and optically clearing the tissue [9], functional imaging requires the preservation of physiological condition, and inevitably requires more complex solutions.

Two non-exclusive strategies are currently adopted to overcome the physical limitations preventing image formation in deep brain layers: (i) changing the laser source to increase the probability of the excitation process to occur; (ii) inserting Adaptive Optics (AO) in the light path to correct the incident wavefront after its determination [10]. In the first case, longer wavelengths, either in the form of two [8] or three photon excitation (3PM) can yield a substantial increase [11] in the penetration depth mainly taking advantage of the lower ratios between scattering and molecule absorption in the mid infrared (see below). In analogy to what was done with astronomy, the second approach proposes the adjustment of the incident wavefront based on the feedback coming from the sample, either through the aid of wavefront sensors or not.

MODULATING THE INCIDENT LIGHT TO IMPROVE MULTI-PHOTON PERFORMANCES

An extensive analysis of 2PM signal degradation by brain tissues has been conducted by Theer and Denk [12]. In this work, the authors showed that signal rapidly fades during the travel across tissues to disappear when the signal to background ratio (SBR) becomes unitary [12]. This condition typically occurs between 5 and 6 effective attenuation lengths (la) below the surface of the tissue. For instance, in the mouse cortex at 775nm excitation wavelength the 2PM l_a is about 130 μm and the resulting penetration depth is $700 \sim \mu m$ [13]. This means that, in adult mice, 2PM imaging is limited to cortical layers. The access to subcortical structures is thus restricted to technical approaches encompassing invasive optical probes or the removal of the overlying tissues. A few years after the work by Theer and Denk, in 2013 Horton and colleagues calculated the tradeoff between tissue scattering and molecule absorption [13], the two main determinants of signal degradation. This work allowed to determine the optimal spectral window for twophoton excitation. The minimal reduction of 2PE due to brain scattering was in fact registered at wavelengths centered on two narrow regions around 1,300 and 1,700 nm. In addition, the imaging depth scales linearly with the attenuation coefficient, but it scales logarithmically with the average power incident on the tissue surface and on the duty cycle [8]. In 2003 Theer et al. had tried to lower the repetition rate of the laser to increase the pulse power impinging on the sample and therefore limiting the attenuation coefficient [14]. This trick allowed researchers to image down to 1 mm in the mouse brain, with a significant improvement of 2PM performances. Despite the increase in the penetration depth, near infrared excitation wavelengths do not preserve from the strong attenuation due to brain scattering. To further improve the overall image quality, Kobat et al. [8] exploited the 1,300 nm window by performing long wavelength 2PM. The excitation of brain vasculatures filled with dextran molecules allowed researchers to collect signals down to 1.2 mm below the brain surface. The same authors [15], a couple of years later showed images at a depth of 1.6 mm with a relatively low power (120 mW) at the brain surface. Beside the effective increase in the penetration depth, these methods collectively suffer from a few limitations (see **Table 1**): (I) The phototoxicity scales with the incident average power; (II) long wavelengths coupled with 2PM strongly limit the number of excitable fluorophores, especially excluding the widely employed green fluorescent protein and most of its derivates; (III) the image resolution scales down with the excitation wavelength; (IV) longer wavelength sources are more expensive and sophisticated than a single mode-locked pulsed infrared laser.

Some of these constraints can be overcome by exploiting three-photon absorption at long wavelength (>1,300 nm). In the early 90's two separate demonstrations of the feasibility of 3PE were independently reported [11, 16]. Besides a better penetration depth due to the reduced scattering, 3PM also provides an improvement of image quality through an overall better excitation localization [16]. The emitted fluorescence of 3PE in fact fades off as $1/z^4$ compared to $1/z^2$ of 2PM (where z is the distance from the focal plane). This, in turn brings a tremendous increase of the signal to noise ratio. Moreover, the use of long wavelength (>1,500 nm) gives the possibility to employ a large spectrum of fluorescent molecules commonly used with single photon fluorescence imaging. Finally, long wavelength and high-pulse energy excitation at a low repetition rate significantly increases the amount of excited molecules. The main disadvantage of such technique is the light source needed to properly excite fluorophores with three photons [17] which necessarily has to be a high-power laser with an optical parametric amplifier (OPA). Furthermore, the low repetition rate most likely to be used for 3PE may require long scanning procedures to obtain at least one pulse per effective image pixel.

THE IMPACT OF ADAPTIVE OPTICS ON 2PM PERFORMANCES

From a physical standpoint, the effect of a turbid medium on the propagation of light can be described as a spatially dependent phase retardation of the wavefront. While an ideal spherical wavefront, such as that generated by the objective would focus in a diffraction limited spot, any distortion from a spherical form would subtract power from the intended focus and redirect it elsewhere in the sample, reducing excitation efficiency and increasing background noise. The techniques aimed at mitigating such problems are known as adaptive optics (AO). The

TABLE 1 | Strategies for improving 2PM deep brain imaging.

Strategy	Method	Advantage	Disadvantage	References
Laser source change	Long-wavelength 2PM	- >1 mm penetration depth	Increased phototoxicityFewer fluorophoresLower resolutionSophisticated laser sources	[8, 12, 14, 15]
	3PM	 >1 mm depth Large number of fluorophores Low energy incident light 	- Expensive laser source - Slow scanning procedures	[13, 16, 17]
Adaptive optics	Wavefront sensor	- Wide choice of adaptive elements	Exogenous guide starAnisoplanatism	[18–24]
	Sensorless	- Endogenous fluorescence	- Numerous iterations	[6, 7, 19, 25–28]
	OPC	Low cost adaptive elements	Requires coherent signals	[29-31]

principle at the basis of adaptive methods is that, by exploiting phase modulating optical components, the incident wavefront impinging onto the surface of a turbid medium, can be shaped until matches the wavefront in the focal plane affected by the medium itself [10]. This is particularly important because the precise focusing of light into the medium at a desired depth is fundamental not only for high-resolution imaging [32] but also for optogenetics [33], functional imaging [34] or photodependent therapies [35].

Traditional AO is performed with smooth phase modulators, such as deformable mirrors, capable of compensating relatively low-resolution aberrations defined as a continuous function in the optical system's pupil. The two main roads to get to wavefront determination and correction are with a wavefront sensor of any kind, or "sensorless." The first group draws inspiration from astronomy, the field which drove the development of AO, where a deformable mirror corrects the wave profile following the feedback given by a wavefront sensor. *In vivo* wavefront sensing AO must necessarily be guided by a point-like light source in the focal plane inside the sample itself, serving as a guide star for the wavefront sensor. The wavefront from the guide star is then measured by a sensor (e.g., Shack-Hartmann-SHWS) to implement the active correction performed by the adjustable optical components.

In this configuration, the incident wavefront is determined by the acquisition of a de-scanned guidestar that can have the form of exogenous fluorescence molecules [1], second-harmonic radiating nanoparticles [36], photo-acoustic feedback [37], focused ultrasonic waves [29] or kinematics targets to extrapolate intrinsic dynamics [38]. Recently [18], in the Kleinfeld laboratory has been developed a method to perform 2PM imaging 800 µm under the brain surface with the correction of optical aberration through signals coming from brain microvessels labeled with Cy5.5, a strongly red shifted molecule. The robust measurement of aberration is achieved through a descanned Shack Hartmann wavefront sensor (formed by a microlens array and an Electron-Multiplying CCD) producing a spot pattern that feeds the algorithm piloting the shape of a deformable mirror [18]. This method allowed researchers not only to generate high quality images deep inside mouse brain but also to collect functional signals (calcium and glutamate changes) during in vivo sensori-motor tasks. In a different approach, the two-photon emission of previously labeled fluorescent neurons is collected by a SHWS and used to implement an iterative correction of the wavefront through a Liquid Crystal Spatial Light Modulator (LC-SLM) over subsets of large brain volumes [19]. Alternatively, multiple laser lines have been added in the optical setup to excite fluorescent microspheres injected into brain tissue [20] while keeping similar adaptive schemes (SHWS and deformable mirror). Beside the use of SLM and DM, researchers have developed algorithms to control other optical components such as Micromirrors [21, 22], adaptive lenses [23] or ferroelectric SLM [24].

In the case of a sensorless approach, the modulation of the incident beam wavefront is performed through an optimization procedure of the two-photon emission (2PE) intensity as a function of the wavefront correction [25]. The 2PE signal can be also used to measure the quality of images degraded by a priori known trial aberrations [6]. This scheme requires a modelbased optimization describing the aberration effect on the chosen metric. Sensorless methods have the main advantage that it is not necessary to introduce neither additional optical components in the detection part of the microscope, nor guide star sources in the sample. On the contrary, these methods typically suffer from longer optimization times compared to wavefront sensing [19], requiring the acquisition of a minimum of N + 1 images in order to achieve optimal correction with an adaptive element with N actuators [6, 39, 40], small volumes of proper correction [26], the introduction of fluorescent beads in the scattering medium [27] and may require serial images acquisition [28]. Interestingly, to speed up the optimization process, Galwaduge et al. [7] iteratively determined the correction across the whole pupil instead of working on a subset of pixels. Furthermore, differently from previous approaches, the "whole pupil" scheme takes advantage only on the 2PE intensity to correct the wavefront without image acquisition.

A substantial problem in the application of adaptive optics in microscopy is given by the fact that when scanning, light directed to different areas of the field of view travels through different parts of the sample, and needs therefore a different correction, a phenomenon known as anisoplanatism [41]. Adaptive optics systems generally only correct an average aberration through

all the field of view and are effective only on relatively small regions. An approach to mitigate this problem is to conjugate the adaptive element to a plane between the objective and the sample, instead of the pupil of the system [30], or splitting the pupil in multiple subregions for different areas of the field of view [42]. These approaches however require high resolution correctors, which are either very expensive or slow in their correction.

DYNAMIC SCATTERING COMPENSATION

Traditionally, only correction of smooth wavefronts was considered possible with adaptive optics, and scattering was considered an unsolvable problem. The work by Vellekoop and Mosk proved [1] that scattering can indeed be compensated through the application of a high resolution, discontinuous phase modulation by means of a high resolution spatial light modulator. While groundbreaking in concept, scattering compensation has a number of technical difficulties which make application in multiphoton microscopy challenging. Due to the discontinuous nature of the correction pattern, Shack Hartmann wavefront sensors cannot be used, while sensorless approaches can require millions of measurements to iteratively adjust the wavefront due to the high number of degrees of freedom of the correction. This is incompatible with microscopy usage, as the brain tissue can rapidly change during measurement on a sub-second timescale [43]. An alternative strategy widely adopted is to measure the scattering response in a parallel manner by adopting the principle of time reversal or "optical phase conjugation" (OPC). The recording of propagating scattered light field both in phase and amplitude should in fact allow the reproduction of a backpropagating phase conjugated field. This field, in turn could retrace its trajectory through the medium and return to the original input light field [31]. The main disadvantage of this approach is that interferometry or alternatively coherent waves mixing is necessary. It is therefore difficult to implement with fluorescence signals which are incoherent unless coupled with ultrasound waves [29].

DISCUSSION

A massive technological effort by the photonics community has produced the development of sophisticated imaging tools. However, the holy grail of neurophotonics has yet to be discovered: it is still almost impossible to perform sub-cellular resolution imaging in deep brain structure without invasive approaches. A proper compensation of scattering in a three-dimensional turbid medium is in fact still an unresolved issue, despite most of the required technologies are available. It is our opinion that the ideal corrector should be a high resolution spatial light modulator, with enough speed to provide sensorless optimization on time scales compatible with experimental needs. While wavefront-sensing correction has long been considered the state of the art in adaptive optics for microscopy, its technical complexity, inability to effectively compensate for anisoplanatism, and its unreliability for high-order aberrations,

make it, in our opinion, unsuitable for the future challenges we described in this manuscript. Recent development in pixel overdrive technologies [44] have started reaching the commercial market, providing the scientific community with tools capable of hundreds of Hz modulation. Very fast SLMs would in turn require high performing optimization procedures. In addition, real-time optimization of scattering compensation in dynamically changing scattering media was recently proven possible through an FPGA implementation [45]. Finally, a conjugate adaptive optics configuration, such as the one reported by Park and colleagues [42], would need to be used in order to achieve the widest possible field of view.

Still, the extremely anisoplanatic nature of scattering correction would, in the end, require some form of parallelized correction in multiple, small fields of view. This would require focusing in multiple diffraction limited spots over an extensive field of view (which was already proven possible in the original Vellekoop publication in 2007) and, most importantly, a reliable method to independently collect the fluorescence signal from multiple foci. This last critical step is still an open question while promising initial results have been achieved by exploiting the temporal separation of excitation pulses [46] and, more recently, through speckle demixing [47]. An additional problem is due to the even more pronounced anisoplanatism of the correction, where the size of the corrected field of view can be as small as the resolution itself, if the correction is applied in the pupil.

To our knowledge, the most successful application of scattering compensation reported to date in multiphoton microscopy was performed by conjugating a high speed, high resolution deformable mirror with the highly scattering, but relatively thin intact skull of an adult mice, to image microglial cells underneath [42]. Unfortunately, while extremely impressive, the proposed method cannot be generalized to thicker scattering layers.

Acquiring high quality images with subcellular resolution of deep brain structure is a goal that has not yet been realized. However, the combination of incident scattering compensation with deconvolution algorithms widely adopted in conventional imaging to compensate isotropic emission can substantially improve the performances of 2P systems, giving hope that this dream can be converted into reality into the next few years.

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All authors contributed in the preparation and revision of the manuscript.

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Total Body PET Imaging From Mice to Humans

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The technology of Total Body PET scanning has been recently established. To advance its application for undertaking across body research in humans, small animal PET scanning is positioned to undertake programs of the pre-clinical development of paradigms and protocols that would be translatable to human total body studies.

Keywords: positron emission tomography, total body PET, small animal PET, systems biology, molecular imaging

INTRODUCTION

Positron emission tomography (PET) is the most specific and sensitive method for imaging regional tissue molecular interactions and pathways in humans [1]. The specificity comes from the range of imaging biomarkers that can be used labeled with positron emitting radionuclides. These range from the short lived of minutes radioactive half-life, to longer lived of hours to days half-life. The radiochemists have overcome the challenges of radiosyntheses labeling with radionuclides such as carbon-11 and fluorine-18 to chelation radio labeling with longer lived metals such as zirconium-89. The sensitivity for detecting low mass, i.e., truly tracer levels of biomarkers arises through:

- i) radiolabeling procedures that provide high specific activity of the tracer compound,
- ii) the use of imaging based upon coincident detection which offers highly efficient, electronic collimation for recording regional tissue concentrations of tracer.

Exploiting the electronic collimation through 3D PET by extending the axial length of PET scanners, evolved cautiously in the early years. This was initially restrained both by cost and ensuring the important need to record quantitative scan data that can be processed to derive meaningful quantitative parameters of regional tissue function. Initial clinical research and healthcare applications of PET focused on individual organs of the body e.g., brain or heart and oncology focused on static [¹⁸F]FDG imaging for tumor detection within the torso. Hence, there was little immediate incentive to embrace the cost of extending the axial length of PET scanners beyond a typical 24 cm axial length. For a review of the development of human PET scanners see Jones and Townsend [2].

SMALL ANIMAL PET SCANNERS

Preclinical small animal PET scanners arose both from the need to support the preclinical development of imaging biomarkers and the advances initially made to maximize the use of electronic collimation in humans. It was realized that the efficiency offered by wide axial coincidence detection resulted in the sensitivity needed to achieve high spatial resolution when scanning small laboratory animals. Since the early 1990's, small animal PET scanners have undergone a number of technical advances in order to improve the spatial resolution along with the accompanying sensitivity to support the statistical demands of increasing the spatial resolution see Miyaoka and Lehnert [3]. Total body imaging in mice is well-established as most of the preclinical scanners provide axial field

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of views covering the whole body of mice. As such in preclinical research it is common to examine radiotracer distribution at a whole-body level in mice. Moreover, in preclinical imaging, researchers have also profited from dynamic imaging to obtain quantitative results by kinetic modeling [4, 5]. However, in human imaging the first total body scanner became available in 2018 and total body based kinetic modeling still in its infancies.

HUMAN TOTAL BODY PET SCANNER (TBP)

A human total body PET scanner (TBP) of some near 2 meters axial length has been developed that is destined to become transformative for molecular imaging in humans [6–8]. The first human results have been obtained demonstrating; images of high statistical quality, total body regional kinetics which, when processed, produce total body quantitative parametric images of tissue function [8, 9] as shown in **Figures 1**, **2**. An alternative design of TBP scanner, using non-Anger logic detectors, is under construction with a projected overall length of 1.4 meters [10, 11].

The projected applications of TBP are in both clinical healthcare and research with iteration between both areas.

Clinical Healthcare Procedures With TBP

In standard clinical healthcare, TBP will enable current examinations to be undertaken much better with advantages in quality and practicability:

- A. The quality advantages of TBP are:
- i) Significantly improved image quality,
- ii) Quantitative imaging, based upon kinetic modeling is much more easily, and non-invasively undertaken using high quality image derived arterial input functions,
- iii) Widening the applications of PET—translating from the new clinical research areas developed with TBP,
- iv) Increased range of imaging bio-markers available in a given imaging center, from wider and further afield commercial distribution centers because of longer effective shelf lives.
 - B. The practical advantages of TBP in healthcare are:
- i) Scan times of minutes: more patient throughput per unit of time,
- ii) Scan times of minutes resulting in less movement induced blurring,
- iii) Remove the need for arterial blood sampling,
- iv) Could do the clinical load of 3-4 conventional scanners: space and staff saving,
- v) Prescribe scans with lower radiation dose to patients and staff, and offering opportunities for screening,

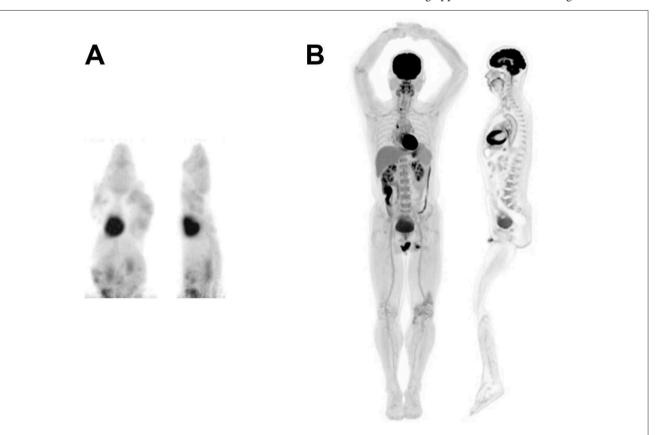


FIGURE 1 | Selected views from a (A) mouse and (B) human total-body scan showing total-body MIP and total-body sagittal view. Mouse image was acquired using the micro PET Focus 220 scanner whereas the human image was acquired using the EXPLORER total body PET scanner. This research was originally published in JNM [8]. © SNMMI.

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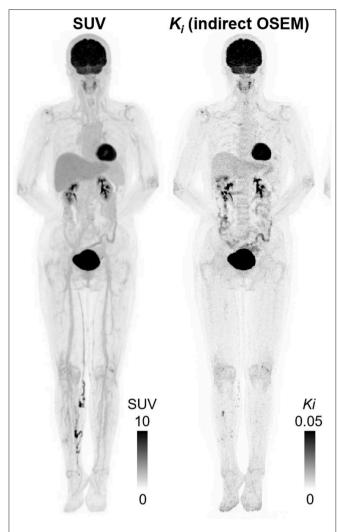


FIGURE 2 | Maximum intensity projection (MIP) using last 30 min of data (left to right): SUV; indirect OSEM Patlak slope K_i (3 iterations 10 subsets); This research was originally published in JNM [9]. © SNMMI.

vi) Longer shelf life of radiolabelled tracers from distribution centers-avoiding the cost of in-house GMP production of new tracers labeled with fluorine-18, and, across cities, carbon-11.

Clinical Research Applications With TBP

The clinical research applications with TBP rests to some extent on the underlying means to study lower levels of occult pathology e.g., in cancer, inflammation and infection but also the "Systems Biology" of human beings. Such studies are destined to cover: pharmacokinetics, pharmacodynamics, oncology, cardiovascular, endocrinology, immunology, maternal-fetal studies, and brain-body interactions e.g., in psychiatry, neurology, and inflammatory diseases.

OUTLOOK ON TBP IMAGING

From the outset, the take up of TBP is facing numbers of challenges. In the first instance this is the cost of such an instrument. However, "Since the 1970's, the technical

developments in PET instrumentation have resulted in major improvements in image quality for patient studies. These advances, although initially seen to be somewhat costly, have, by opening up new clinical applications, proved ultimately to be cost-effective" [2]. Never-the-less, funders at this time are asking for proof-of-concept pilot data that demonstrates that transformative studies will be made possible. Hence the pressure on the few operational TBP scanners to provide for early proofof-concept data. To advance the new investigative field of total body PET, it will be necessary to formulate, validate/characterize, suitable paradigms and corresponding protocols. TBP based "systems biology" research is in its infancy. Such research would cover for example measures of: The whole-body's functioning of the vascular system and regional variations and changes therein. Physiological and endocrinology interactions between different organs of the body. Movement of cells from within and across the body. Pharmacokinetics and pharmacodynamic effects throughout the body. Physiological and metabolic interaction and exchange within and between the mother and fetus.

While some pilot human studies are envisaged, in order, to address the broad scope for such investigations, there is clearly a need to explore and consolidate such pilots at the pre-clinical level. This is where small animal PET scanner technology, which is already in place for total body PET studies of mice and rats, is destined to play a significant role in establishing paradigms and protocols that are translatable to human TBP. It is estimated that there are \sim 400 small animal PET scanners worldwide. These already existing extensive preclinical small animal PET programs represent a major resource within the molecular imaging community. They are wellpositioned to develop, characterize and validate the paradigms and protocols for the more advanced total body PET scanning based "system biology" human studies. Inevitably there will be some reverse translation not least asking for more performance of the small animal PET technology and effecting quantitative parametric imaging.

ETHICS STATEMENT

The study protocol was approved by the Zhongshan Hospital Shanghai Ethics Committee. The patients/participants provided their written informed consent to participate in this study.

AUTHOR CONTRIBUTIONS

The author confirms being the sole contributor of this work and has approved it for publication.

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How Non-invasive in vivo Cell Tracking Supports the Development and Translation of Cancer Immunotherapies

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Immunotherapy is a relatively new treatment regimen for cancer, and it is based on the modulation of the immune system to battle cancer. Immunotherapies can be classified as either molecular or cell-based immunotherapies, and both types have demonstrated promising results in a growing number of cancers. Indeed, several immunotherapies representing both classes are already approved for clinical use in oncology. While spectacular treatment successes have been reported, particularly for so-called immune checkpoint inhibitors and certain cell-based immunotherapies, they have also been accompanied by a variety of severe, sometimes life-threatening side effects. Furthermore, not all patients respond to immunotherapy. Hence, there is the need for more research to render these promising therapeutics more efficacious, more widely applicable, and safer to use. Whole-body in vivo imaging technologies that can interrogate cancers and/or immunotherapies are highly beneficial tools for immunotherapy development and translation to the clinic. In this review, we explain how in vivo imaging can aid the development of molecular and cell-based anti-cancer immunotherapies. We describe the principles of imaging host T-cells and adoptively transferred therapeutic T-cells as well as the value of traceable cancer cell models in immunotherapy development. Our emphasis is on in vivo cell tracking methodology, including important aspects and caveats specific to immunotherapies. We discuss a variety of associated experimental design aspects including parameters such as cell type, observation times/intervals, and detection sensitivity. The focus is on non-invasive 3D cell tracking on the whole-body level including aspects relevant for both preclinical

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experimentation and clinical translatability of the underlying methodologies.

INTRODUCTION

Immunotherapy is a relatively new concept that is increasingly applied to a variety of conditions. Most of the currently approved or emerging immunotherapy approaches are in the oncology arena. In some cases, they were curative, which represents a major leap over most previous treatment concepts. Mechanistically, they modulate the immune system to better attack the cancer. There

are two types of anti-cancer immunotherapy, molecular and cell-based immunotherapy. Both approaches are already in clinical use, whereby molecular immunotherapies currently are further developed with more applications and more approved therapeutics.

Molecular immunotherapies usually modulate the immune system by targeting immune checkpoints using antibodies or antibody-derived molecules. Examples include ICIs targeted at CTLA-4 (e.g. ipilimumab) or the PD-1/PD-L1 axis (e.g. nivolumab, atezolizumab, and pembrolizumab) (Hodi et al., 2010; Topalian et al., 2012; Larkin et al., 2015; Darvin et al., 2018). These immunotherapeutics were largely developed using

Abbreviations: ATMP, advanced therapy medicinal products; BLI, bioluminescence imaging, a preclinical imaging technology; CAR, chimeric antigen receptor, an artificial molecule; CAR-T, chimeric antigen receptor T-cell therapy; CD2, cluster of differentiation 2, a cell adhesion molecule found on the surface of T-cells and natural killer cells; also known as T-cell surface antigen T11/Leu-5, LFA-2, LFA-3 receptor, erythrocyte receptor and rosette receptor; CD3, cluster of differentiation 3, a T-cell co-receptor; CD4, cluster of differentiation 4, a glycoprotein found on the surface of immune cells such as T helper cells, monocytes, macrophages, and dendritic cells; CD7, cluster of differentiation 7, found on thymocytes and mature T-cells; CD8, cluster of differentiation 8, a glycoprotein that serves as a co-receptor for the T-cell receptor; predominantly expressed on the surface of cytotoxic T-cells; CD19, cluster of differentiation 19, also known as B-Lymphocyte Surface Antigen B4, T-Cell Surface Antigen Leu-12 and CVID3 is a transmembrane protein; CD25, cluster of differentiation 25, also known as IL-2 receptor alpha chain, a part of the high-affinity IL receptor; CT, computed tomography, a whole-body imaging technology employing X-rays; CTLA-4, cytotoxic T-lymphocyte-associated protein 4, also known as cluster of differentiation 152; a molecule that is part of an immune checkpoint axis; DC, dendritic cell, a type of immune cell; DFO, desferrioxamine, a chelator for metal ions; FDA, U.S. Food and Drug Administration; [18F]FHBG, 9-(4-[18F]-Fluoro-3-[hydroxymethyl]butyl)guanine, a radiotracer for the reporter gene HSV1-tk; FMT, fluorescence mediated tomography, a fluorescence-based whole-body imaging technology; HMPAO, hexamethylene-propyleneamine oxime, an agent to label cells directly with ^{99m}Tc; HSV1-tk, Herpes Simplex Virus 1 thymidine kinase, an enzyme that can be exploited as a reporter gene; ICI, immune checkpoint inhibitor; IL, IL, immune mediators; specified by a number to identify the individual molecule (e.g. IL-2 and IL-12); IrAE, immune related adverse event; LAG-3, lymphocyte-activation gene 3, an immune checkpoint molecule; MRI, magnetic resonance imaging, an imaging technology; MSOT, multispectral optoacoustic tomography, an advanced form of PAT imaging; NET, norepinephrine transporter, a mammalian protein that can be used as a host reporter gene; NIS, sodium iodide symporter, a mammalian protein that can be used as a host reporter gene; NK, natural killer cell, a type of immune cell; OCT, optical coherence tomography, an optical imaging technology; OPT, optical projection tomography, a preclinical optical imaging technology; OVA, ovalbumin, main protein found in egg white; widely used as a model antigen in T-cell biology; Numerous mouse cancer models have been modified to express OVA to aid in enhancing and tracking tumor-specific T-cell responses; PAT, photoacoustic tomography, an imaging technology; PD-1, programed cell death protein 1, an immune checkpoint molecule; PD-L1, programed death ligand 1, also known as cluster of differentiation 274 or B7 homolog 1 (B7-H1); constitutes an immune checkpoint axis together with PD-1; PET, positron emission tomography, a whole-body imaging technology detecting γ-photons produced by the annihilation of positrons stemming from the decay of certain radioisotopes; PSMA, prostate-specific membrane antigen, a glutamate carboxypeptidase 2 also known as folate hydrolase 1; qPCR, quantitative polymerase chain reaction, an analysis technique to determine specific DNA amounts in biological samples; RSOM, raster-scanning optoacoustic mesoscopy, a preclinical imaging technology exploiting the photoacoustic effect; SPECT, single photon emission computed tomography, a whole-body imaging technology detecting radioisotope location in 3D; TCR, T-cell receptor, a multi-protein complex responsible for many T-cell activation mechanisms; TCR-T, T-cell receptor-modified T-cell therapy; TIL, tumor infiltrating lymphocyte; US, ultrasound imaging, a cheap standard imaging technology.

similar regulatory approval frameworks to other receptortargeting drugs. Although in several cases the whole-body distribution of these therapeutics would be accessible through imaging the molecular immunotherapy itself, this is not routinely performed. Only very recently did studies report the whole-body distribution of radiolabeled checkpoint inhibitors in man (e.g. atezolizumab, Bensch et al., 2018; Jauw et al., 2019) to assess whether imaging them might reveal prognostic information. Despite molecular immunotherapies changing the landscape of cancer treatment (Ledford et al., 2018), significant challenges remain. These include non-responding patients (Feng et al., 2013), severe immune-related adverse events (IrAE, i.e., ICI weakening the normal physiological barriers against autoimmunity resulting in various local and systemic autoimmune responses), and the development of resistance (Darvin et al., 2018).

Cell-based immunotherapies consist of live immune cells that are administered to patients. The anti-tumor properties are either intrinsic to these therapeutic cells or conferred to them through genetic engineering. The therapeutic immune cells are either taken from a different human donor (allogeneic) or are isolated from the patient (autologous) before undergoing manipulations that transform the cells into immunotherapeutic cells. A historic lack of clarity surrounding the regulatory aspect of live cell-based therapy resulted in debates on what constitutes manipulations requiring regulatory approval (Anon, 2014), but it is now accepted that any cells that have been cultured with any drugs are subject to regulatory approval. The new paradigm of cell-based immunotherapy has forced regulatory agencies to re-evaluate their approval processes to accommodate for living drugs and to avoid slowing progress; for example, the new ATMP framework accelerates the approval process if there is demonstrable clinical need (Marks and Gottlieb, 2018). The first ever clinically approved cell-based anti-cancer immunotherapies were the chimeric antigen receptor T-cell (CAR-T) therapies tisagenlecleucel and axicabtagene ciloleucel, both of which are autologous CD19targeted CAR-T immunotherapies for the treatment of certain hematological malignancies (B-cell lymphomas; U.S. Food and Drug Administration, 2017). While spectacular treatment successes have been reported for CAR-T immunotherapies, alike molecular immunotherapeutics, not all patients responded and sometimes the effects were only temporary (Neelapu et al., 2017; Schuster et al., 2017; Maude et al., 2018), and these therapeutics have also been associated with severe side-effects and fatalities during trials (Linette et al., 2013; Saudemont et al., 2018). In addition, CAR-T immunotherapy has generally yielded disappointing results in solid tumors (Martinez and Moon, 2019). Nonetheless, the portfolio of immune cells envisaged for cell-based anti-cancer immunotherapy is increasing and now includes T-cell receptor-modified T-cells (TCR-T), γδ T-cells, NK and dendritic cells (DC). Importantly, there are several unknowns including the *in vivo* distribution, persistence and survival of cell-based immunotherapies as well as their efficacy at target and non-target sites, and there is a need to investigate these aspects during their development and translation into the clinics.

THE NEED FOR IMAGING IN IMMUNOTHERAPY DEVELOPMENT

During the early stages of drug development, animal models are frequently employed to investigate the efficacies of drug candidates in defined disease settings. For instance, multiple animal tumor models have been used in the development of chemotherapeutics and targeted therapies (Cekanova and Rathore, 2014). Similar experimentation has also been necessary for the development of immunotherapies to establish targeting efficiencies, pharmacokinetics/pharmacodynamics, whether there is spatial heterogeneity to therapy delivery, and whether therapy presence is related to efficacy. Novel and accurate biomarkers are also essential to guide immunotherapy development to ensure optimal benefit for cancer patients. Notably, imaging biomarkers differ from conventional tissue/blood-based biomarkers in several important aspects (O'Connor et al., 2017). Foremost, imaging biomarkers are noninvasive, thus overcoming sampling limitations and associated tissue morbidities of conventional tissue/blood biomarkers, and they provide whole-body information albeit usually for only one target at the time. Furthermore, dynamic imaging can provide pharmacokinetic information. As with other biomarkers, imaging biomarkers should be standardized across multiple centers to unleash their full potential for diagnosis, patient stratification and treatment monitoring. Pathways for the development and standardization of dedicated imaging biomarkers have been structured and excellently described by a large team of cancer researchers (O'Connor et al., 2017), and we refer the reader to this publication for specific details.

Whole-body *in vivo* imaging technologies (**Figure 1**) that can interrogate cancers and therapeutics in preclinical models are very valuable tools in this context. They show great potential to provide answers to various challenges central to immunotherapy:

- (1) Which immune cell classes are present in tumors and are they critical for response?
- (2) What role do other components of the tumor microenvironment play?
- (3) What are the consequences of heterogeneity within tumors and between lesions?
- (4) What are biomarkers of true response and true progression?
- (5) What is the relationship between target expression levels, affinity, and response?
- (6) Can resistance be detected early or even be predicted?
- (7) How can the distribution, fate, persistence and efficacy of cell-based immunotherapies be tracked *in vivo*?
- (8) Can off-target effects and associated toxicities be detected early or be predicted?
- (9) How can combination treatments be designed in a rational and effective manner?

Given that metastasis is responsible for >90% of cancer mortality, novel immunotherapy treatments need also to be evaluated for their efficacies against secondary lesions. Metastases can significantly differ from the primary tumor because of tumor evolution, and consequently can show a different therapy

response compared to the primary lesion (Caswell and Swanton, 2017; Kim et al., 2019). While anti-metastatic endpoints have long been regarded impractical, it is noteworthy that an anti-metastatic prostate cancer drug, apalutamide, recently received FDA approval on the basis of metastasis-free survival as a new endpoint (measuring the length of time that tumors did not spread to other parts of the body or that death occurred after starting treatment, U.S. Food and Drug Administration, 2018). This raised the prospects for further such research, not least in the context of immunotherapy, and if immunotherapy were to be used as a treatment at earlier stages of cancer. Thus, preclinical models of metastasis employing *in vivo* traceable cancer cells have also a role to play in the development of immunotherapies (Gomez-Cuadrado et al., 2017).

IMAGING APPROACHES IN IMMUNOTHERAPY DEVELOPMENT

Brief Overview of Relevant Imaging Technologies

Medical imaging revolutionized the diagnosis and treatment of human disease by providing anatomical, physiological and molecular information (Mankoff, 2007). Imaging technologies differ in their capabilities and limitations. Figure 1 details the properties of those imaging technologies relevant to this review. Notably, several modalities are already in routine clinical use, for example US, magnetic resonance imaging (MRI), the radionuclide imaging modalities SPECT and PET, and X-ray computed tomography (CT). PAT and MSOT are two closely related relatively new modalities and have recently been translated into the clinical for special applications. PAT/MSOT delivers near infrared laser pulses into biological tissues with the latter absorbing and converting some of the laser pulse energy into heat, leading to transient thermoelastic expansion and thus wideband ultrasonic emission, which is used to compute an image (Ntziachristos et al., 2005; Wang and Yao, 2016). A purely optical imaging approach that is currently used in the clinical setting is OCT with applications in ophthalmology (Jung et al., 2011; Tao et al., 2013) and dermatology (Mogensen et al., 2009; Olsen et al., 2015). In general, the various imaging technologies can be categorized into modalities that subject the patient to a radiation dose (CT, PET, and SPECT) and modalities that are employing non-ionizing radiation (MRI, OCT, PAT/MSOT, and US). Depending on the research/clinical question, CT, MRI, PAT/MSOT, and US can be used with or without a contrast agent. In contrast, PET and SPECT strictly require contrast agents for image formation; these are often termed radiotracers, not least in reference to the very small concentrations required ("tracer levels;" picomolar concentration range) as both PET and SPECT are orders of magnitude more sensitive than the other clinically useable imaging technologies (Figure 1).

In preclinical settings, BLI can compete in sensitivity with radionuclide imaging modalities, but at much reduced experimental complexity and cost (instrument cost and running

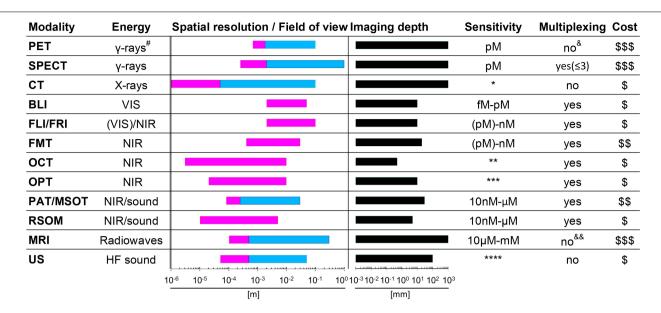


FIGURE 1 | Properties of various whole-body imaging modalities. Imaging modalities are ordered according to the electromagnetic spectrum they exploit for imaging (top, high energy; bottom, low energy). Routinely achievable spatial resolution (left end) and fields of view (right end) are shown in red. Where bars are blue, they overlap red bars and indicate the same parameters but achievable with instruments used routinely in the clinic. Imaging depth is shown in black alongside next to sensitivity ranges. Instrument cost estimations are classified as (\$) < 125,000 \$, (\$\$) 125-300,000 \$ and (\$\$\$) > 300,000 \$. #Generated by positron annihilation (511keV). *Contrast agents sometimes used to obtain different anatomical/functional information. **In "emission mode" comparable to other fluorescence modalities (~nM). ***Fluorophore detection can suffer from photobleaching by excitation light. ****Highly dependent on contrast agent. **Dual isotope PET is feasible but not routinely in use; it requires two tracers, one with a positron emitter (e.g. 18F and 89Zr) and the other with a positron-gamma emitter (e.g. 124 I, 76Br, and 89Y), and is based on recent reconstruction algorithms to differentiate the two isotopes based on the prompt-gamma emission (Andreyev and Celler, 2011; Cal-Gonzalez et al., 2015; Lage et al., 2015). **Multichannel MRI imaging has been shown to be feasible (Zabow et al., 2008). PET, positron emission tomography; SPECT, single photon emission computed tomography; CT, computed tomography; BLI, bioluminescence imaging; FLI, fluorescent lifetime imaging; FRI, fluorescent reflectance imaging; FMT, fluorescent moderaphy; OCT, optical coherence tomography; OPT, optical projection tomography; PAT, photoacoustic tomography; MSOT, multispectral optoacoustic tomography; RSOM, raster-scan optoacoustic mesoscopy; MRI, magnetic resonance imaging; US, ultrasound.

cost), which renders it a widely used tool. It relies on the presence of luciferase reporter proteins, which convert an administered chemical substrate into light that is then collected by highly sensitive cameras. As luciferase proteins are of non-mammalian origin, BLI is not translatable to the human setting. Another disadvantage is that BLI relies on light emitted within tissues which in turn is subject to absorption and scatter within the tissue matrix, thereby precluding reliable 3D quantification (Li et al., 2013; Dunlap, 2014; Jiang et al., 2016). Fluorescence-based whole-body imaging has also been developed (FLI/FRI), whereby fluorescence light is generated within a thick samples/small animal through excitation light; the approach has the same issues as BLI but is far less sensitive. To obtain true 3D data a tomographic design is required. Among the optical modalities listed in Figure 1, this is provided by optical projection tomography (OPT), which can be considered as the optical analog of CT. OPT operates on the micrometer to millimeter scales (Sharpe et al., 2002; Cheddad et al., 2012) thereby bridging the scale gap between classical whole-body imaging technologies and microscopy. It can either provide tomographic data on light absorption or fluorescence signals, and has been used in live zebrafish (Bassi et al., 2011; McGinty et al., 2011), fruit flies (Vinegoni et al., 2008; Arranz et al., 2014) and for whole organ imaging in mice (Alanentalo et al., 2008; Gleave et al., 2012; Gupta et al., 2013). An alternative approach offering larger fields

of view in the centimeter range is diffuse optical tomography or FMT, which exploits photon tissue propagation theory to allow for 3D reconstruction at centimeter depth but its resolution is affected by weak signals and high tissues scattering (**Figure 1**; Graves et al., 2004; Ntziachristos, 2006; Venugopal et al., 2010; Zacharakis et al., 2011; Wang et al., 2015; Lian et al., 2017). In this review we lay emphasize on methodologies that are providing reliable quantifiable 3D information and have the potential to be clinically translatable.

As imaging modalities differ in their capabilities and limitations (Figure 1), combination technologies have become particularly important. For example, PET offers excellent sensitivity and provides absolute quantitative data (Lajtos et al., 2014) but can only detect signals at millimeter resolution. Hence, PET imaging was combined with other modalities providing higher anatomical resolution, such as CT (Basu et al., 2014) or MRI (Catana, 2017). This resulted in multi-modal wholebody imaging approaches adding anatomical context (from CT, MRI) to molecular imaging information (e.g. from PET or SPECT). Very recently, ultrafast US was combined with PET technology to form a new hybrid technology with the potential to provide molecular, anatomical and functional imaging data (Provost et al., 2018). Multi-modal imaging technologies are extremely useful to obtain maximal information from imaging, whereby the recent work of Bensch et al. provides a very good example for its power in the context of immunotherapy (Bensch et al., 2018).

The Role of Anatomical Imaging

Anatomical imaging methods such as computed tomography (CT) or MRI provide excellent 3D resolution in vivo and enable quantification of tumor size and growth if the tumor differs sufficiently in contrast from surrounding tissues. Importantly, these techniques are non-specific and do not quantify tumor or immune cells specifically, but can account for the entirety of the tumor mass or reveal parameters such as texture (Lambin et al., 2012). This can cause issues for treatment monitoring if tumor size or radiomic features are not correlated to treatment response. If efficacy assessment is based on tumor shrinkage (cf. RECIST criteria in humans, Eisenhauer et al., 2009), then anatomical imaging is not appropriate for the assessment of immunotherapeutics, which initially can cause tumor sizes to increase or plateau before tumor regression occurs. This phenomenon is termed "pseudo-progression" and is evident in both molecular and cell-based immunotherapeutics (Nishino et al., 2017). It is caused by the very mechanisms of immunotherapy, which re-educates the immune system to detect and attack cancer cells, thereby resulting in immune cell infiltration/expansion, and tumors initially enlarging rather than regressing. Pseudo-progression has been recognized and is being accounted for in new criteria relevant for immunotherapy monitoring (Wolchok et al., 2009; Seymour et al., 2017).

Molecular Imaging and Immunotherapy

Molecular imaging differs from anatomical imaging in that it provides specific molecular information on the whole-body level. Molecular imaging can be exploited to visualize and quantify the presence of a target of interest at a given time on the wholebody level. This can be used to diagnose and guide patient stratification and treatment decisions. Via molecular imaging, the heterogeneity of target expression can be assessed, for example, between primary and secondary lesions or within individual tumors (Alizadeh et al., 2015; Kurland et al., 2017; Bensch et al., 2018). Importantly, molecular imaging can support treatment monitoring, for example, inform on target engagement, therapy efficacy, and in certain cases can be used to probe the activity of a therapeutic. Molecular imaging employs a broad variety of different contrast agent classes based on target-specific small molecules as well as a variety of biomolecules. The latter include full-length antibodies, bivalent F(ab')₂ fragments, minibodies, monovalent Fab fragments, diabodies, single-chain variable fragments (scFv), nanobodies, affibodies (listed in order of decreasing molecular weight). Strategies for developing and optimizing such targeted probes for non-invasive imaging using radioactive, optical, magnetic resonance, and ultrasound approaches have been recently summarized by Freise and Wu (Freise and Wu, 2015). The imaging of T-cell effector molecules such as the PD-L1/PD1 axis has been shown to be a successful approach to study T-cell in vivo distribution in preclinical models (Natarajan et al., 2015; Heskamp et al., 2019) and in humans (Jauw et al., 2019). However, a caveat of molecular imaging is its reliance on one chosen molecular target, because its

expression might change during tumor progression, and with these changes also the imaging read-outs would change. Recently, the predictive power of molecular imaging for treatment outcome was demonstrated through visualization of the radiolabeled ICI atezolizumab by multimodal PET/CT imaging (combined molecular and anatomical imaging, Bensch et al., 2018; Figure 2). In this study, clinical responses were better correlated with pretreatment [89Zr]Zr-desferrioxamine (DFO)-atezolizumab PET signals than with immunohistochemistry- or RNA-sequencingbased predictive biomarkers. [89Zr]Zr-DFO-pembrolizumab, which targets PD-1 on T-cells, is currently being tested in clinical trials involving non-small cell lung cancer or metastatic melanoma patients (NCT02760225, NCT03065764). Similarly, the T-cell expressed ICI target CTLA-4 has been imaged in preclinical mouse models of colon cancer to better understand target expression and therapy side effects (Higashikawa et al., 2014). Additionally, ⁸⁹Zr-labeled ipilimumab targeting CTLA-4 in humans is in phase II trials (NCT03313323) to better comprehend the pharmacodynamics/pharamacokinetics of this antibody-based immunotherapeutic and its IrAEs. Other imaging targets related to T-cell effector functions include interferon-y and granzyme B, which have both been studied in mice (Larimer et al., 2017, 2019; Gibson et al., 2018).

In preclinical models, the use of reporter genes to detect cancer cells in vivo (see Section "Non-invasive Whole-Body in vivo Cell Tracking") can overcome specificity issues of anatomical imaging. Cancer cell tracking by means of reporter gene imaging is frequently performed using bioluminescence technology which is cost-effective and fast but suffers from the limitations of optical imaging, which preclude accurate quantification (Figure 1, see Section "Brief Overview of Relevant Imaging Technologies"). A recent article comparing BLI alone with combined BLI and radionuclide imaging demonstrated such aspects providing real-life examples in the context of cancer cell tracking (Vandergaast et al., 2019). It is noteworthy that other imaging technologies can fare well in some specialized cases. For example, metastasis tracking of melanin-producing murine melanoma cells was achieved in mice at reasonable sensitivity and resolution compared to the study aims by using PAT (Lavaud et al., 2017). Alternatively, radionuclide cancer cell tracking methodologies have been developed but they are more expensive and lower throughput techniques but provide 3D tomographic and fully quantitative information (e.g. Fruhwirth et al., 2014; Diocou et al., 2017; Volpe et al., 2018). The latter is currently being tackled by the development of multi-animal radionuclide imaging beds (e.g. four-mouse hotels, Greenwood et al., 2019).

IN VIVO IMAGING OF T-CELL POPULATIONS

Specific cell surface markers on T-cells are attractive imaging targets as they enable the *in vivo* visualization of either all T-cells or distinct T-cell sub-populations. They can also be exploited for the quantification of therapeutic responses affecting T-cell presence (or absence) in cancerous tissues. For example, targeting T-cell receptors (TCR) is attractive

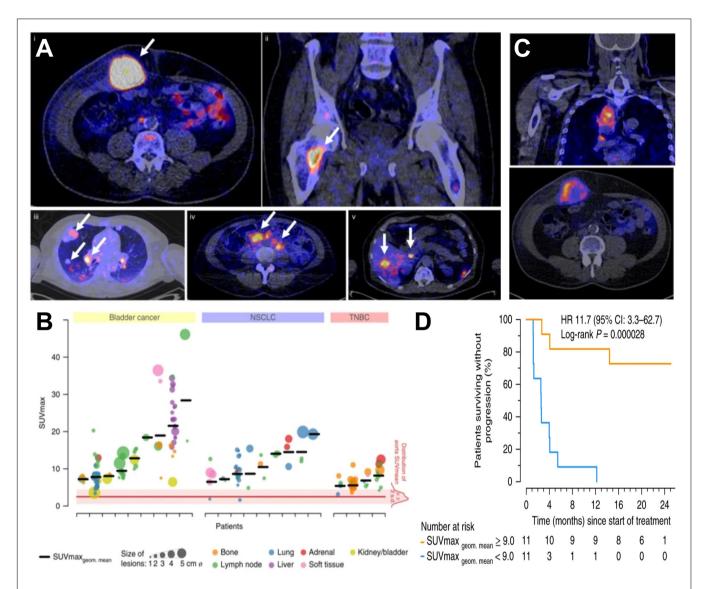


FIGURE 2 | Molecular imaging can be used as a non-invasive tool to predict clinical response of immunotherapy. **(A)** Examples of PET/CT images of four patients illustrating ⁸⁹Zr-atezolizumab tumor uptake in five different locations on day 7 post-contrast agent administration (white arrows indicate tumor lesions; PET scans were performed once per patient and time point). Images (i) and (ii) are from the same patient, whereas images (iii), (iv), and (v) are each from a separate patient. **(B)** Overview of ⁸⁹Zr-atezolizumab uptake as SUV_{max} at day 7 post-contrast agent administration in 196 tumor lesions with a diameter > 2 cm grouped per tumor type and ordered by increasing geometric mean SUVmax per patient, visualizing tumor size and site, and with the distribution of aorta for blood pool background uptake as reference. Horizontal bars indicate geometric mean SUVmax per patient. **(C)** PET/CT images of lesions of two patients with heterogeneous intralesional ⁸⁹Zr-atezolizumab uptake on day 7 post contrast agent administration. *(Top)* Mediastinal lesion of a NSCLC patient (SUV_{max} 19.9) and *(Bottom)* abdominal wall metastases of a bladder cancer patient (SUV_{max} 36.4). **(D)** Progression-free survival according to the geometric mean standard uptake value (SUV_{max}) per patient obtained by non-invasive PET imaging using ⁸⁹Zr-labeled atezolizumab (orange, above-median geometric mean uptake; blue, below-median geometric mean uptake; N = 22 patients; two-sided log-rank test). For comparison, Hazard Ratios (HR) were only 2.6 and 1.3 for two different PD-L1 antibodies used in histology. For details see Bensch et al. (2018). (Reproduced with modifications from the indicated reference).

because due to their high turnover on the plasma membrane, the bound radiotracers can gradually accumulate within the T-cells. In one preclinical study, TCRs were targeted using a ⁸⁹Zr-conjugated anti-murine TCR F(ab')2 fragment selective for the murine TCR beta domain. Using PET/CT imaging, this radiotracer was shown to track the location of adoptively transferred engineered T-cells *in vivo*; notably, imaging data and *ex vivo* quantification of transgenic T-cell

numbers in tumors correlated well (Yusufi et al., 2017). Additionally, using a ⁶⁴Cu-labeled anti-chicken OVA-TCR antibody, it was demonstrated that associated TCR internalization neither impaired antigen recognition *via* the TCR, nor did it diminish T-cell viability or function in mice (Griessinger et al., 2015).

Alternatively, targeting CD3, a T-cell surface glycoprotein and pan-T-cell marker, has been suggested. Therefore, a

radiometal-chelated antibody against CD3 ([89Zr]Zr-DFO-CD3) was designed to quantify T-cell infiltration during anti-CTLA-4 treatment in colon cancer xenograft models. As the host species were mice, a murine anti-CD3 antibody was required in this case, and large amounts of infiltrated T-cells were found in the tumor prior to regression (Larimer et al., 2016). The LAG-3 was similarly exploited to image T-cells in xenografts established in transgene mice expressing human LAG-3 as host strains (Kelly et al., 2018). The radiolabelling strategy also utilized the siderophore-based chelator DFO, and this ⁸⁹Zr-based radiotracer is now in clinical development. Moreover, ⁸⁹Zr-LAG-3 PET is currently investigated in patients suffering from head and neck cancer or non-small cell lung cancer (NCT03780725). Notably, both anti-CD4 and anti-CD8 cys-diabodies have been radiometal-labeled (89 Zr, 64 Cu) to track the corresponding T-cell sub-populations in preclinical models. Using these radiotracers, researchers imaged treatment responses of immunotherapies, for example response to checkpoint inhibitors such as anti-PD-1 (Seo et al., 2018) or anti-PD-L1 (alone or in combination with adoptive cell therapy) (Tavare et al., 2016; Freise et al., 2017; Zettlitz et al., 2017). The advantage of incorporating antibody fragments rather than full-length antibodies into the design of in vivo imaging agents is that the end product will reach its target more quickly, and it will be excreted faster (Bates et al., 2019). Such engineered antibody fragments targeting CD8 have already progressed into clinical trials (NCT03107663, NCT03802123, and NCT03610061). To increase specificity and reduce liver toxicity and Fc y receptor binding, bispecific antibodies targeting both T-cells (e.g. via 4-1BB) and either tumor antigens (e.g. CD19) or tumor stroma (e.g. FAP) have been developed. The bispecific antibodies have also been conjugated to radioisotopes to track their in vivo distribution in rodents by SPECT or PET imaging (Claus et al., 2019).

The mentioned approaches are applicable to the development of various molecular immunotherapies and cell-based immunotherapies. A general limitation is that the obtained imaging signals cannot be used to back-calculate precise T-cell numbers because the precise expression levels of T-cell surface marker molecules are unknown at the point of imaging. All above described methods probe T-cell presence but not their activities. As for cell-based immunotherapies, there is an additional limitation, namely the lack of discrimination between adoptively transferred and resident cells. To overcome this the adoptively transferred cells would need to be labeled to distinguish them from the resident ones (cf. Section "Non-invasive Whole-Body *in vivo* Cell Tracking").

IMAGING THE ACTIVATION OF T-CELLS

Upon antigen-recognition and co-stimulation, naïve T-cells become activated in secondary lymphoid organs, which results in the expression of various cell surface markers of T-cell activation. The latter can be imaged using specific antibodies or antibody-fragments. For example, OX40 (CD134/TNFRSF4) is such a cell surface-expressed marker of T-cell activation and it has been used to image the spatiotemporal dynamics of T-cell activation

following in situ vaccination with CpG oligodeoxynucleotide in a dual tumor-bearing mouse model (Alam et al., 2018). Moreover, it was shown that OX40 imaging using 64Cu-DOTA-AbOX40 as a contrast agent for PET predicted tumor responses with greater accuracy than both blood-based measurements for early response (i.e., Luminex analyses including interferon-y, tumor necrosis factor α, MCP1, MIP1B etc.) and anatomical measurements in this mouse model. Another example is the trimeric IL -2 receptor (CD25/IL-2Ra), which was exploited to visualize activated T-cells in immune-compromised mice by PET imaging using the contrast agent N-(4-[18F]fluorobenzoyl)- IL -2 (Di Gialleonardo et al., 2012). IL-12 has also been implicated as a specific target for T-cell activation. Consequently, 99mTc-labeled IL-12 has been used to detect T-cell activation in vivo in mice, albeit in colitis and not yet in tumor models (Annovazzi et al., 2006). Moreover, bioluminescence and radionuclide imaging tools to assess TCRspecific activation of T-cells have been developed (Ponomarev et al., 2001; Kleinovink et al., 2018), however, these approaches are still in preclinical development and are based on genetic engineering of T-cells and thus constitute specialized variants of cell tracking as described in Section "Non-invasive Whole-Body in vivo Cell Tracking".

Alternatively, it is possible to exploit the observation that T-cells undergo metabolic changes upon activation in tissues (van der Windt and Pearce, 2012; Buck et al., 2016) resulting in the influx of substrates not normally present in non-activated T-cells. While targeting metabolic pathways with imaging agents can distinguish activated from non-activated T-cells, this approach can suffer from competing signals generated by different cells in close vicinity. A very promising PET tracer in this context 2'-deoxy-2'-[¹⁸F]fluoro-9-β-D-arabinofuranosylguanine ([18F]F-AraG), which accumulates in activated T-cells predominantly via two salvage kinase pathways (Ronald et al., 2017). Notably, the unlabeled compound has previously been used as a T-cell depleting drug in refractory T-cell acute lymphoblastic leukemia. [18F]F-AraG PET imaging in a murine acute graft-vs.-host-disease (GvHD) model enabled visualization of secondary lymphoid organs harboring activated donor T-cells prior to clinical symptoms of GvHD. Notably, the biodistribution of [18F]F-AraG was favorable and it may be useful for imaging activated T-cells in the context of immunooncology, which is currently investigated in several clinical trials (NCT03311672, NCT03142204, and NCT03007719).

NON-INVASIVE WHOLE-BODY *IN VIVO* CELL TRACKING

The exploitation of molecular imaging has also enabled spatiotemporal whole-body *in vivo* tracking of administered cells (Kircher et al., 2011). One form of *in vivo* cell tracking has long been used to localize occult infections in patients (de Vries et al., 2010; Roca et al., 2010). Technological and methodological advances over the last decade led to a resurgence of cell tracking, this time in conjunction with the emergence of live cell therapeutics. For their development, several important questions remain largely elusive and require attention;

- (i) the whole-body distribution of therapeutic cells;
- (ii) their potential for re-location during treatment and the kinetics of this process;
- (iii) whether on-target off-site toxicities occur;
- (iv) how long the administered cells survive; and
- (v) which biomarkers are best suited to predict and monitor cell therapy efficacy.

Traditional approaches in preclinical cell therapy development relied on dose escalation with toxicity evaluation, tumorigenicity tests, and qPCR-based persistence determination. Whole-body imaging-based in vivo cell tracking can inform on questions (i)-(iv) of these aspects in a truly non-invasive manner. However, many clinical trials are still performed largely without knowledge of the in vivo distribution and fate of the administered therapeutic cells, making it impossible to adequately monitor and assess their safety, thereby raising ethical questions when considering complications in clinical trials that could have been averted or mitigated if whole-body imaging had been used (Linette et al., 2013; Saudemont et al., 2018). With cell-based anti-cancer immunotherapies currently centered on adoptively transferred T-cells, either subjected to genetic engineering or ex vivo expansion only, there was a need to develop corresponding imaging tools to quantify T-cells in vivo on the whole-body level.

Methods of in vivo Cell Tracking

In vivo cell tracking rests on the principles and mechanisms of molecular imaging to achieve contrast between cells of interest and the other cells of the organism. In some cases, there are intrinsic features of the cells of interest that can be exploited for generating contrast, for example, when cells produce targetable molecules that show low or no expression in other tissues. Under these circumstances, conventional molecular imaging offers cell tracking possibilities both preclinically and clinically. Examples demonstrating this are; tracking thyroid cancer metastases using the NIS (Kogai and Brent, 2012; Portulano et al., 2014), exploiting the PSMA to image prostate cancer and its spread (Perera et al., 2016; Oliveira et al., 2017), carcinoembryonic antigen (CEA) for colorectal cancer imaging (Tiernan et al., 2013), or melanin imaging in melanomas (Tsao et al., 2012). However, in most in vivo cell tracking scenarios, including all reported cases of cell-based immunotherapy, contrast agents or contrastgenerating features must be introduced to the cells of interest. Fundamentally, cell labels can be introduced to cells via two different methodologies, direct or indirect cell labeling.

Direct Cell Labeling for Cell-Based Immunotherapies

Direct cell labeling is performed upon cells *ex vivo*, and the subsequently labeled cells are re-administered into subjects, where they can be tracked using the relevant imaging technology (**Figure 3A**). Cells can either take up the contrast agents on their own (e.g. through phagocytosis, *via* internalizing receptors etc.) or are labeled through assisted contrast agent uptake (e.g. using cell permeant contrast agents, transfection etc.). There is a large variety of ready-to-use contrast agents available including chelated radiometals (for PET or SPECT),

¹⁹F-fluorinated nanoparticles and iron oxide nanoparticles (for various MRI types), as well as organic fluorophores and fluorescent nanoparticles (for optical imaging); for more details the reader is referred to a recent review by Kircher et al. (2011). One strength of MRI imaging is its excellent wholebody resolution. Consequently, various nanoparticles have been used to label and track adoptively transferred cells in preclinical models by MRI (Oiu et al., 2018). When applied to cellbased immunotherapy in humans, ¹⁹F-fluorinated nanoparticles have been proven effective cell-tracking contrast agents for MRI (Srinivas et al., 2013), as ¹⁹F is naturally almost absent in tissues. Unfortunately, the detection sensitivity of ¹⁹F is very low and requires specialized equipment. Attempts to improve detection sensitivities included the use of molecules and nanoparticles incorporating many ¹⁹F atoms (Srinivas et al., 2012). Longitudinal tracking of activated T-cells in vivo was reported for a period of nearly three weeks in mice (Srinivas et al., 2009), but others found only limited utility for in vivo tracking of similarly labeled CD4+/CD8+ T-cells (in a murine diabetes model, Saini et al., 2019). Despite multiple optical contrast agents available for cell labeling, whole-body in vivo cell tracking using optical methodologies is very limited. This is caused by the intrinsic shortcomings of optical imaging including high tissue absorption and scatter precluding accurate in vivo localization and quantification. This includes 3D fluorescence molecular tomography (FMT), which also suffers from poor resolution, limited depth penetration and low sensitivity compared to other modalities (Figure 1). In the following, we focus on direct cell labeling with radioisotopes, because radionuclide imaging is currently the most sensitive tool for in vivo tracking of directly labeled cells in mammals. When co-registered with CT or MRI for additional anatomical detail, SPECT/PET-MRI/CT images are most promising to aid clinical translation of cell-based immunotherapies. Radioisotope can be used for cell labeling by either (i) exposing cells to chelating agents such as radiometalcomplexed hydroxyquinolines (oxines) resulting in cellular uptake via diffusion or transport-mediated processes, or by (ii) linking radioisotopes onto cell surfaces, either electrostatically (e.g. using cell insertion peptides) or covalently.

In inflammatory conditions and infectious disease, the radiometal chelators [111In]In-oxine and [99mTc]Tc-HMPAO have been routinely used clinically for tracking ex vivo labeled cells, e.g. white blood cells (Roca et al., 2010; de Vries et al., 2010). This decades-old methodology has more recently been applied to clinical studies of CD4⁺ T-cells in Hodgkin's lymphoma (Grimfors et al., 1989), to assess penetrance of tumor-infiltrating lymphocytes in melanoma (Fisher et al., 1989; Griffith et al., 1989) or autologous CD8⁺ T-cells in early stage non-small cell lung cancer patients who receive anti-PD-L1 immunotherapy in a neo-adjuvant setting (NCT03853187). Both ¹¹¹In and ^{99m}Tc are compatible with SPECT imaging or scintigraphy, an imaging technology which has previously been shown to be insufficiently sensitive in clinical studies (James and Gambhir, 2012). Although technological advances in SPECT instrumentation are improving the situation somewhat, PET imaging remains the method of choice, since it offers absolute quantification and higher sensitivity on clinical instrumentation.

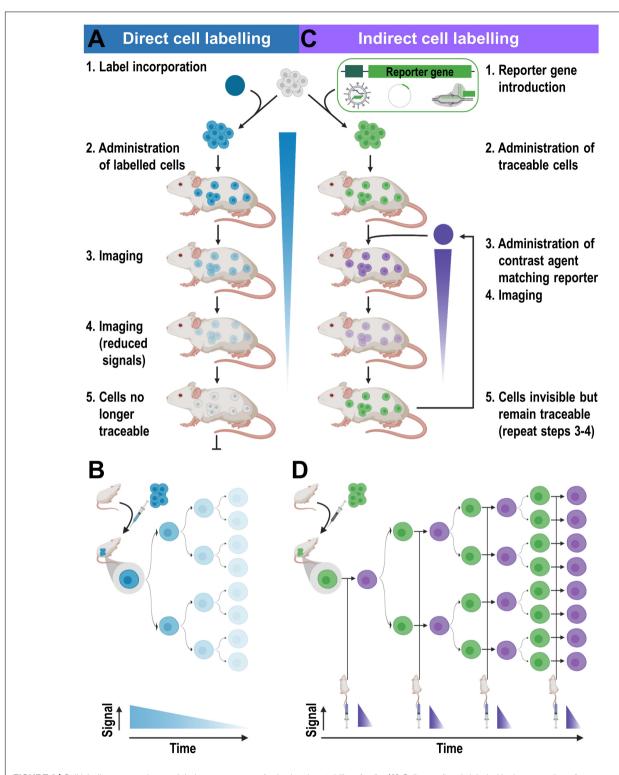


FIGURE 3 | Cell labeling approaches and their consequences for *in vivo* detectability of cells. **(A)** Cells are directly labeled by incorporation of a contrast agent (blue) matching the desired imaging technology. Cells can either take up the contrast agent on their own (e.g. through phagocytosis, *via* internalizing receptors etc.) or are labeled through assisted contrast agent uptake (e.g. cell permeant contrast agents, transfection etc.). The labeled cells (blue) are administered to animals and remain traceable until the contrast agent concentration per cell becomes too dilute to be detectable. Several processes including label efflux, label dilution through cell division, and in the case of radioisotopes also radioactive decay contribute and limit the maximum observation time *in vivo*. **(B)** Scheme depicting the effects of label dilution on cell detectability. **(C)** Indirect cell labeling requires the incorporation of a reporter gene (green) under the control of a suitable promoter (dark green). Reporter genes are frequently introduced using viruses but can also be incorporated *via* episomal plasmids or gene editing. Engineered cells (green) are administered to animals and can be visualized *in vivo via* administration of corresponding contrast agents (purple) followed by imaging, which can be repeated to enable long-term tracking. **(D)** Filial generations of reporter gene expressing cells remain traceable, hence indirectly labeled cells are *in vivo* traceable indefinitely.

The PET isotope equivalent of ¹¹¹In (τ = 2.8 days) is ⁸⁹Zr $(\tau = 3.3 \text{ days})$, which has a similar half-life but different decay properties (⁸⁹Zr: 23% positron emission, higher energy γ-rays than ¹¹¹In but lacking Auger electron emission). Like ¹¹¹In, cell labeling with 89 Zr became possible with oxine chelators (Charoenphun et al., 2015; Sato et al., 2015), and it was shown to be better retained inside cells than [111 In] In-oxine (Charoenphun et al., 2015). This is a major advantage because the images correspond to the locations of the radioisotope; if labels leak out of cells rapidly they are more likely to give unreliable results. [89Zr]Zr-oxine has been widely applied preclinically for immune cell labeling of cytotoxic T lymphocytes (CTL), γδ T-cells, DC and CAR-T (Sato et al., 2015; Weist et al., 2018; Man et al., 2019). With GMP-compatible protocols now available, [89Zr]Zr-oxine is on a trajectory toward clinical translation and ultimately it will replace [111 In] In-oxine, which has become increasingly scarce in the EU due to economic reasons (Dhawan and Peters, 2014). A limitation of PET is its restricted spatial resolution (Figure 1) which is fundamentally limited by the radioisotope-dependent average positron range in matter (Phelps et al., 1975; Cal-Gonzalez et al., 2013). A way to mitigate its low resolution is to combine it with anatomical imaging methods that feature higher resolution (PET/MRI and PET/CT). For cell tracking applications also nanoparticle-based, multimodal PET/MRI probes have been envisaged, for example iron oxide nanoparticles that are crosslinked to radioisotopes (Garcia et al., 2015).

An alternative direct cell labeling methodology is to link contrast agents to the cell surface of cells. For example, [89Zr]Zr-DFO-NCS was used to label human mesenchymal stem cells and while retained on the cell surface for about a week, cell viability appeared to be unaffected (Bansal et al., 2015). This approach is constrained by the availability of cell surface reactive groups that can be exploited, in this case primary amines, and it has the potential to interfere with cell surface proteins and impair cell function. This could restrict its use, particularly if tracerlevel concentrations are superseded to achieve high *ex vivo* cell labeling to expand the cell tracking time (cf. **Figures 3A,B**). However, no systematic comparative studies between cell uptake and cell surface linking of radiometals in lymphocytes have so far been reported.

Indirect Cell Labeling Applied to Immunotherapy Development

Indirect cell labeling is based on genetic engineering of cells to ectopically express a reporter, which serves as an imaging target (Figure 3C). This imaging target is then imaged *in vivo* after administration of suitable contrast agents, for example short half-life radiotracers, in a process that can be repeated to detect the traceable reporter-expressing cells over time (Figures 3C,D). Introduction of genetically encoded reporters is most frequently performed by viral transduction to ensure genomic integration and long-term expression. In some cases, episomal plasmids have been used (e.g. delivered by transfection or electroporation; Lufino et al., 2008; Ronald et al., 2013). Lately, gene editing approaches have been exploited for reporter insertion as they can be advantageous to viral transduction because they offer precise control over the genomic site of reporter insertion

(Bressan et al., 2017). With feasibility having been demonstrated, this approach is likely to receive greater attention in the cell therapy field in future. Contrast formation relies on one of several mechanisms (**Figure 4**): either

- (a) label uptake into cells by transporters,
- (b) label binding to cell surface-expressed reporters, or
- (c) expression of contrast-forming proteins, which either
 (i) produce a label through enzymatic action (e.g. luciferases, tyrosinase), or (ii) act as labels themselves (e.g. fluorescent proteins).

All these mechanisms can be useful for preclinical cell tracking and a variety of corresponding reporter genes are listed in Table 1. For clinical cell tracking, the emphasis must lies on the mechanisms (a) and (b), because the contrastforming proteins are either not of human origin or produce toxic products if expressed outside their original context (e.g. tyrosinase; Urabe et al., 1994) and thus not clinically translatable. Alongside improvements of imaging technologies, also the corresponding reporter genes have been developed and optimized. A fundamental drawback of indirect cell labeling is that it requires genetic engineering. However, this is neither a concern for preclinical experimentation nor for cell therapies already reliant on it (e.g. CAR-T) (Saudemont et al., 2018). Several factors require careful consideration when planning reporter gene-afforded in vivo cell tracking experiments, particularly in the context of immunotherapies (see Section "Experimental Design Considerations for in vivo Cell Tracking").

Multiplex Cell Tracking

It would be highly beneficial to track both primary tumors and metastases alongside the therapeutic in preclinical models. Combining preclinical whole-body cancer cell tracking with imaging of molecular or cell-based immunotherapeutics could enable image-based quantification of the extent a labeled/traceable immunotherapy reaches in vivo traceable cancers, and whether the immunotherapy is delivered to all primary/secondary lesions. Dual-modality approaches would be required for this, ideally both tomographic in nature to enable the 3D quantification of metastasis burden alongside the immunotherapy. While almost every well-performed preclinical immunotherapy imaging study cross-correlates tumor targeting of the traceable therapeutic with either anatomical or molecular imaging in the primary tumor, metastases have rarely been accounted for. One example of such a study evaluating also the metastatic sites involved was performed by Edmonds et al. (Edmonds et al., 2016) in a preclinical breast cancer model. The authors employed dual-radioisotope imaging to co-track cancer metastases and a liposomally encapsulated immunomodulatory drug with the aim to optimize the time between liposome administration and the subsequent adoptive transfer of γδ T-cell immunotherapy involving both primary and secondary lesions. In a subsequent preclinical study, the same authors co-tracked ⁸⁹Zr-oxine labeled γδ T-cells (direct labeling approach) to NIS reporter expressing breast cancer cells (indirect labeling approach

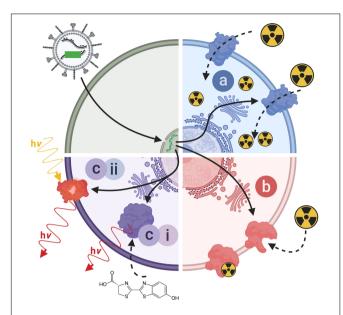


FIGURE 4 | Molecular imaging mechanisms relevant to reporter genes for indirect cell labeling. Cartoon showing the three main molecular imaging mechanism that are exploited for indirect cell labeling. (a) Transport (blue): these reporters are expressed at the plasma membrane of cells and each expressed reporter can transport several contrast agent molecules into the cell, which constitutes a signal amplification mechanism. The radionuclide transporters NIS and NET belong to this class of reporters. (b) Protein binding (red): these reporters are also normally expressed at the plasma membrane of cells and contrast agents bind directly to them; minor levels of signal amplification are theoretically possible if several contrast agents could bind to the reporter, or if several contrast agents could be fused to a reporter binding molecule; however, signal amplification is inferior compared to transporters. Examples for this reporter class are PSMA and SSTR2. (c) Contrast forming reporters (purple) can be sub-divided into two categories; enzymes that can generate contrast, and proteins that act as labels with intrinsic contrast. (ci) Enzymatic contrast formation: such reporters either entrap a molecular probe or generate a contrast agent from a precursor that needs to be either supplied externally or is available within the cell. Thymidine kinases such as HSV1-tk are examples for enzymes that entrap a radiotracer through its phosphorylation, and thereby generate contrast. Firefly luciferases are examples of reporters that convert an externally supplied substrate [shown: luciferin light ($h\nu$)]. Tyrosinase is an example of a reporter which converts cell-intrinsic precursors to the contrast agent melanin. (cii) Intrinsic contrast: these reporters produce a signal on their own, normally upon stimulation. Classical examples are all fluorescent proteins, which generate specific light emissions upon excitation with light matching their excitation spectra. For details and literature references to relevant reporter genes see Tables 1, 2. NIS, sodium/iodide symporter; NET, norepinephrine transporter; PSMA, prostate specific membrane antigen; SSTR2, somatostatin receptor 2.

using 99m TcO₄ $^-$ as a NIS radiotracer) employing sequential multi-modal PET-SPECT-CT imaging (Man et al., 2019).

EXPERIMENTAL DESIGN CONSIDERATIONS FOR in vivo CELL TRACKING

To ensure immunotherapy development benefits from cell tracking, it is imperative that the cell labeling approaches

for therapeutic and/or cancer cells are chosen with the experimental goals in mind. Considerations must include a variety of different aspects such as cell tracking time, cell tracking interval, experimental setting (preclinical or clinical), use of immunocompetent or immunocompromised host organisms, imaging technology, and contrast agent properties and availability. To detect cells, the employed cell label must match the envisaged imaging technology to be used. The choice of the imaging technology dictates the achievable spatial resolution and imaging depth (Figure 1), impacts on minimal temporal resolution through image acquisition speeds, and contributes majorly to detection sensitivity and cost. Availability of the imaging technology and the necessary label further impact on the feasibility of collaborative across different institutions, which is of particular importance for clinical translation of a methodology and the chances of its subsequent adoption in clinical practice.

Imaging Technology and Its Impact on Cell Detection Sensitivity

Considerations for the Selection of the Imaging Technology

Exquisite detection sensitivity is required for *in vivo* cell tracking applications. In practice, this means sensitivities should be within or below the picomolar concentration range (Figure 1), which can be achieved best with bioluminescence and radionuclide imaging modalities. Unlike radionuclide imaging technologies, BLI neither provides absolute quantitative data nor true 3D information and is applicable only preclinically. However, despite its shortcomings, BLI has so far been the most frequently used preclinical approach to measure the impact of immunotherapeutics on *in vivo* traceable bioluminescent tumors; most likely due to BLI being relatively cheap and fast. In special cases, BLI can currently provide unique information relevant to immunotherapy development on the preclinical level. For example, dual-luciferase reporter methodology enabled the quantification of in vivo T-cell activation in specifically engineered transgene mice (Mezzanotte et al., 2011; Kleinovink et al., 2018). While it is fundamentally possible to perform such preclinical experiments with more quantitative 3D radionuclide tomography, it has not been reported so far; most likely due to more complex logistics and higher costs associated with this approach (e.g. two different radiotracers with similar pharmacokinetics/pharmacodynamics would be needed for each individual imaging session).

In many cases, 3D tomographic whole-body imaging data is required in rodents or larger mammals, i.e., non-translucent organisms. This generally limits the use of optical imaging technologies due to their inherent limitations relating to tissue light absorption and scatter. Hence, radionuclide imaging modalities are preferred for such purposes, but they require dedicated reporter genes, which are scarce compared to the plethora of different fluorescent proteins or luciferases that have been developed (Thorn, 2017; Shcherbakova et al., 2018; Mezzanotte et al., 2017). If clinical translation is the main goal for cell tracking applications, then radionuclide imaging is the

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TABLE 1 | Reporter gene classes according to their molecular imaging mechanisms (cf. Figure 4) including selected examples.

Mechanism [cf. Figure 4]	Reporter	Properties	Matching imaging modality	References	
Transporter [a]	Mammalian transporters	Sodium iodide symporter (NIS, SLC5A5); Norepinephrin transporter (NET, SLC6A2); Dopamine transporter (DAT, SLC6A3).	Various radiotracers for PET and SPECT for all reporters listed.	(Dai et al., 1996; Moroz et al., 2007; Jauregui-Osoro et al., 2010; Khoshnevisan et al., 2016, 2017; UCL Business PLC, 2017; Jiang et al., 2018)	
	lon transporter from magnetotatic bacteria	MS-1 magA.	MRI (Endogenous or exogenous iron).	(Nakamura et al., 1995; Zurkiya et al., 2008; Cho et al., 2014)	
	Polypeptides	Sodium-Taurocholate Co-transporting Polypeptide (NTCP).	Fluorescence and MRI.	(Wu et al., 2019)	
Cell surface protein binding [b]	G-protein-coupled receptors	Somatostatin receptor type 2 (SSTR2); Dopamine receptor ($\mathrm{D_2R}$).	PET and SPECT radiotracers available; PET radiotracers available.	(Satyamurthy et al., 1990; MacLaren et al., 1999; Rogers et al., 1999, 2000; Zinn et al., 2000a; Chaudhuri et al., 2001; Liang et al., 2001; Hwang et al., 2007)	
	Recycling receptor	Transferrin receptor.	MRI (SPIO).	(Weissleder et al., 2000)	
	Cell-surface antigen-based reporter	Human carcino-embryonic antigen-based reporters are recombinant proteins based on CEA minigene (N-A3) fused to extracellular and transmembrane domains of human FcyRllb receptor, CD5 or TfR carboxyterminal domain.	PET and SPECT radiotracers available.	(Hammarstrom, 1999; Hong et al., 2008; Kenanova et al., 2009; Barat et al., 2011; Girgis et al., 2011)	
	Mammalian cell surface protein	PSMA and mutants; radiotracers bind to the protein using it as a cell surface protein and not exploiting its enzymatic properties.	PET and SPECT radiotracers available.	(Castanares et al., 2014; Minn et al., 2019)	
Enzymes [ci]	Bacterial enzymes	E. coli dihydrofolate reductase (eDHFR); E. coli β-galactosidase.	PET; Various including OPTICAL (chemiluminescence), MRI, PET and SPECT.	(Fowler and Zabin, 1977; Louie et al., 2000; Li et al., 2007; Liu and Mason, 2010; Green et al. 2017; Sellmyer et al., 2017, 2019; Guo et al., 2019; Krueger et al., 2019)	
	Mammalian and non-viral kinases	Pyruvate kinase M2, thymidine kinases (viral such as HSV1-tk and mammalian variants), deoxycytodine kinases.	Various PET tracers for the individual kinases.	(Tjuvajev et al., 1995; Ponomarev et al., 2007; Jang et al., 2010, 2012; Likar et al., 2010; Park et al., 2015; Lee et al., 2017; Haywood et al., 2019; Seo et al., 2019).	
	Other mammalian enzymes	Tyrosinase	PAT/MSOT, MRI, PET.	(Weissleder et al., 1997; Ponomarev et al., 2004; Krumholz et al., 2011)	
	Luciferases	Various luciferases including Firefly, Green Click Beetle; Gaussia, Renilla; and NanoLuc.	OPTICAL (bioluminescence): Firefly, Green Click Beetle: D-luciferin; Gaussia, Renilla: coeloenterazine; NanoLuc: imidazopyrazinone.	(Lorenz et al., 1991; Loening et al., 2006; Tannous, 2009; Inoue et al., 2011; Hall et al., 2012; Schaub et al., 2015; Germain-Genevois et al., 2016; La Barbera et al., 2017; Mezzanotte et al., 2014, 2017; Hunt et al., 2016; Aswendt et al., 2019; Weihs and Dacres 2019; Zhang et al., 2019)	
Fluorescent Proteins [cii]	Proteins with intrinsic fluorophores	Red fluorescent: E2-Crimson/mTagRFP/mPlum/mNeptune; Infrared fluorescent: iRFP 670/iRFP 720.	OPTICAL (fluorescence upon appropriate excitation): (emission λ_{max}): 543/584/649/650; (emission λ_{max}): 670/720.	(Merzlyak et al., 2007; Kremers et al., 2009; Lin et al., 2009; Filonov et al., 2011; Liu et al., 2013; Shcherbakova and Verkhusha, 2013; Deliolanis et al., 2014; Isomura et al., 2017; Zhou et al., 2018; Fukuda et al., 2019)	
Frequency-selective contrast/other	Artificial protein	Contrast based on transfer of radiofrequency labeling from the reporter's amide protons to water protons.	MRI (CEST).	(Gilad et al., 2007; Farrar et al., 2015)	
Formation of gas vesicles/other	Mammalian acoustic reporter gene (mARG)	Gas vesicles are produced which generate US contrast.	US (3.2 MPa insonation).	(Farhadi et al., 2019)	

most suitable approach to address the questions raised in Section "Non-invasive Whole-Body *in vivo* Cell Tracking."

Detection Sensitivity and the Duration of Cell Tracking

Detection sensitivity of labeled cells depends on the cellular label concentration and the matched imaging technology. The different labeling methodologies affect the cellular label concentration in different ways (see Section "Non-invasive Whole-Body in vivo Cell Tracking"). Label dilution, label efflux and in the case of radioactive labels dosimetry, can be severe limitations of direct cell labeling methodologies. The impact of label dilution has been discussed above (Section "Direct Cell Labeling for Cell-Based Immunotherapies"). Copper isotopes are the main example wherein label efflux causes issues. ⁶⁴Cu $(\tau = 12 \text{ h})$ had been suggested as a shorter half-life PET isotope (Adonai et al., 2002; Li et al., 2009; Bhargava et al., 2009) potentially competing with the SPECT isotope 99 mTc ($\tau = 6.0$ h). However, its unfavorably high cellular efflux (>50% per 4-5 h) paired with efficient liver uptake resulted in low signal-tobackground ratios in vivo (Adonai et al., 2002; Bhargava et al., 2009; Li et al., 2009; Griessinger et al., 2014). High label efflux also limited the use of the long half-life PET radiometal ⁵²Mn for cell tracking (Gawne et al., 2018). For considerations regarding dosimetry see Section "Impact of Cell Labeling Methodology on Cell Function."

For indirectly labeled cells, the molecular imaging mechanism of the used reporter gene and the cellular expression level of the reporter gene are crucial, while the label dilution aspect plays no significant role (Figure 3D). Reporter genes which enzymatically entrap radiotracers that are taken up into cells offer high cell detection sensitivities. Examples are thymidine kinases, which phosphorylate and thereby entrap radiotracers in the cells, e.g. HSV1-tk is detected through its corresponding PET radiotracer [18F]FHBG. Transporters (e.g. NET or NIS) provide signal amplification as each reporter protein can transport several radiotracer molecules into the cell. It is noteworthy that ectopic expression of reporters can affect the fate of their substrates. For example, NIS is normally expressed in thyroid follicular cells and its regular substrate, iodide, is metabolized into thyroid hormones after cell import. Upon ectopic expression in non-thyroidal cells, e.g. cancer cells or immune cells, this downstream mechanism affecting the equilibrium of the imported iodide is non-existent resulting in iodide not being accumulated to the same extent compared to thyroid tissues. To apply radioiodide for cell tracking in humans, it would be necessary to counteract high thyroid uptake and radioiodide metabolization there as this could lead to thyroid damage. The latter is possible by prior administration of non-radioactive iodide, but this also impacts on detection sensitivity of the traceable cells of interest. Noniodide NIS radiotracers, which are not metabolized and wash out of thyroid cells would thus be preferable. As NIS is not very selective regarding its anion substrates (Paroder-Belenitsky et al., 2011) anionic radiotracers that are roughly similar in size and shape were developed for NIS imaging; they include ^{99m}TcO₄⁻, [¹⁸F]BF₄⁻, [¹⁸F]SO₃⁻ or [¹⁸F]PF₆⁻ (Jauregui-Osoro

et al., 2010; Khoshnevisan et al., 2017; Jiang et al., 2018). They are not entrapped in cells, neither in thyroidal tissues nor in cells ectopically expressing NIS. Therefore, it would be advantageous to use non-iodide NIS radiotracers for clinical cell tracking. Another advantage of the new NIS PET radiotracers is that they are based on ¹⁸F, which has superior decay properties compared to 124 I. 18 F decays with a half-life of 109.8 min to $^{18}\mathrm{O}$ with 96.9% positrons (E_{mean} = 0.250 MeV and 0.6 mm average positron range), while 124I decays with a half-life of 4.18 days to 124 Te with only 22.7% positrons (11.7% β_2 ⁺ at E_{mean} = 975 MeV and 4.4 mm mean range, and 10.7% β_1^+ at $E_{mean} = 0.687$ MeV and mean 2.8 mm range, plus a minor 0.3% β_3 ⁺ at 0.367 MeV and 1.1 mm mean range) accompanied by several γ -rays and a high proportion of electron capture (Conti and Eriksson, 2016). Consequently, ¹⁸F produces more positrons per decay resulting in better detectability. It is noteworthy that ¹⁸F positrons also have a lower mean energy than those of 124I resulting in lower mean positron ranges (until annihilation and emission of detectable γ-rays) and therefore enabling better PET resolution. While free positron range considerations are currently irrelevant for clinical PET imaging (instrument resolution with 3-4 mm larger than most average free positron ranges of relevant PET isotopes), they are of concern for preclinical PET imaging (instruments can provide resolution even below 1 mm with the right isotope) (Deleve et al., 2013; Nagy et al., 2013). Notably, first-in-man clinical studies using [18F]BF₄⁻ to image NIS have already been completed (O'Doherty et al., 2017), thereby lowering the hurdles for NIS-afforded PET reporter gene imaging as a means of cell tracking in humans. Such considerations regarding the selection of radioisotopes as part of an individual reporter:contrast agent pair are transferable also to other reporters for which contrast agents with different radioisotopes are available (see Table 2). Selection of the best suited reporter:contrast agent pair is paramount.

The detection sensitivities of NIS-expressing extra-thyroidal cells have been reported preclinically to be as good as hundreds/thousands for cancer cells expressing NIS (Fruhwirth et al., 2014; Diocou et al., 2017) and CAR-T expressing PSMA in vitro (Minn et al., 2019), or tens of thousands for effector T-cells using various different reporter genes in vivo (Moroz et al., 2015) (Figure 5). Comparative studies aiming at the evaluation of how different reporter genes impact on T-cell detectability have been performed in the past (Moroz et al., 2015). Importantly, since this study new reporter gene:contrast agent pairs have become available, for example PSMA paired with its high-affinity PET ligand [18F]DCFPyL (Minn et al., 2019) or NIS paired with its PET radiotracer [18F]BF₄⁻ (see above). Consequently, new comparative studies are needed to conclude on relative reporter:contrast agent performance in relevant immune cells; ideally performed such that also reporter expression levels and their intracellular availabilities for interaction with their contrast agents are precisely controlled. As reporter expression levels are cell type-dependent, it is highly recommended to determine detection sensitivities of indirectly labeled cells in each case and also on the available instrumentation before designing in vivo cell tracking experiments.

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TABLE 2 | Promising host-compatible reporter genes and their corresponding imaging tracers.

Reporter				Reporter in vivo detection		
Class	Name	Properties	Imaging modality and contrast agent	Contrast agent properties	References	
Transporter	Sodium iodide symporter (NIS)	Symports Na ⁺ alongside various anions. Endogenous expression in thyroid, stomach, lacrimal, salivary and lactating mammary glands, small intestine, choroid plexus and testicles.	PET: ¹²⁴ -, [¹⁸ F]BF ₄ -, [¹⁸ F]SO ₃ F-, [¹⁸ F]PF ₆ SPECT: ^{99m} TcO ₄ -, ¹²³	Tracers do not cross BBB.	(Dai et al., 1996; Jauregui-Osoro et al., 2010; Khoshnevisan et al., 2016, 2017; Jiang et al., 2018)	
	Norepinephrine transporter (NET)	NaCl-dependent monoamine transporter. Endogenously expressed in organs with sympathetic innervation (heart, brain),	PET: [¹²⁴ I]MIBG**; [¹¹ C]hydroxyephedrine. SPECT: [¹²³ I]MIBG**.	Tracers do not cross BBB.	(Moroz et al., 2007)	
	Dopamine transporter (DAT)	NaCl-dependent.	PET: [¹¹ C]CFT, [¹¹ C]PE2I, [¹⁸ F]FP-CIT. SPECT: ¹²³ I-β-CIT**, ¹²³ I-FP-CIT**, ¹²³ I-loflupane**, ⁹⁹ mTRODAT.	Few data in public domain. Tracers cross BBB.	(UCL Business PLC, 2017)	
Enzyme	Pyruvate kinase M2	Expression during development, also in cancers.	PET: [¹⁸ F]DASA-23.	Background in organs of excretion route. Suggested for cell tracking within brain. Tracer crosses BBB.	(Haywood et al., 2019)	
	Thymicline kinase (hmtk2/h∆TK2)	Human kinase causing cellular tracer trapping.	PET: [¹²⁴] FIAU**, [¹⁸ F] FEAU, [¹⁸ F] FMAU (for hTK2-N93D/L109F).	Tracers do not cross the BBB; Endogenous signals in gall bladder, intestine and organs involved in clearance.	(Ponomarev et al., 2007)	
	Deoxycytidine kinase (hdCK)	Human kinase causing cellular tracer trapping.	PET: [¹²⁴ I]FIAU**, [¹⁸ F]FEAU.	Tracers do not cross the BBB; Endogenous signals in gall bladder, intestine and organs involved in clearance.	(Likar et al., 2010; Lee et al., 2017)	
Cell surface receptor	Somatostatin receptor type 2 (SSTr2)	G-protein-coupled receptor. Endogenous expression in brain, adrenal glands, kidneys, spleen, stomach and many tumors (i.e., SCLC, pituitary, endocrine, pancreatic, paraganglioma, medullary thyroid carcinoma, pheochromocytoma);	PET: ⁶⁸ Ga-DOTATOC, ⁶⁸ Ga-DOTATATE. SPECT: ¹¹¹ In-DOTA-BASS. (best tracers selected here).	Tracers may cause cell signaling, change proliferation and might inhibit impair cell function. Non-metal octreotide radiotracers can cross blood brain barrier (BBB).	(Rogers et al., 1999, 2000; Zinn et al., 2000a,b; Chaudhuri et al., 2001)	
	Dopamine receptor (D ₂ R)	G-protein-coupled receptor. High endogenous expression in pituitary gland and striatum.	PET: [¹⁸ F]FESP, [¹¹ C]Raclopride, [¹¹ C]N-methylspiperone.	Slow clearance of [¹⁸ F]FESP; Tracers cross BBB.	(Satyamurthy et al., 1990; MacLaren et al., 1999; Liang et al., 2001; Hwang et al., 2007)	
	Transferrin receptor (TfR)	Fast recycling receptor.	MRI: Transferrin-conjugated SPIO.	Transferrin-conjugated SPIOs are internalized by cells.	(Weissleder et al., 2000)	
Cell surface protein	Glutamate carboxy-peptidase 2 (PSMA) and variant tPSMA ^{N9del}	tPSMA ^{N9del} has higher plasma membrane concentration. High expression in prostate.	PET: [¹⁸ F]DCFPyL, [¹⁸ F]DCFBC. SPECT: [¹²⁵ I]DCFPyL**.anti-PSMA antibodies and ligands can be flexibly labeled*, e.g. J951-IR800.	Background signal in kidneys. Tracers do not cross BBB.	(Castanares et al., 2014; Minn et al., 2019)	
Cell surface antigen	Human carcino-embryonic antigen (hCEA)	Overexpressed in pancreatic, gastric, colorectal and medullary thyroid cancers.	PET: ¹²⁴ I-anti-CEA scFv-Fc H310A**, [¹⁸ F]FB-T84.66 diabody SPECT: ^{99m} Tc-anti-CEA Fab' (approved), ¹¹¹ In-ZCE-025, ¹¹¹ In-anti-CEA F023C5i.	Tracers do not cross BBB.	(Griffin et al., 1991; Hammarstrom, 1999; Hong et al., 2008; Kenanova et al., 2009)	

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	Reporter	16		Reporter in vivo detection	
Class	Name	Properties	Imaging modality and contrast agent	Contrast agent properties	References
Artificial cell surface molecule	Artificial cell surface DOTA antibody reporter 1 molecule (DAbR1)	ScFv of anti-DOTA antibody 2D12.5/G54C fused to human CD4 TM domain.	PET; ⁸⁶ Y-AABD.	Tracer is a DOTA complex that binds irreversibly to a cysteine residue in the 2D12.5/G54C antibody. Tracer does not cross BBB.	(Wei et al., 2008)
	Estrogen receptor α ligand binding domain	No reported physiological function.	PET: [¹⁸ F]FES.	Tracer is clinically used estrogen receptor imaging agent.	(Qin et al., 2013)
	Anti-PEG Fab fragment*	Some tracers cross BBB; PEG is non-toxic and approved by FDA.	PET: ¹²⁴ I-PEG-SHPP*,**. MRI: SPIO-PEG. Fluorescence: e.g. NIR797-PEG.	lodine tracers bear risk of deiodination. (Chuang et al., 2010) Some tracers cross BBB.	(Chuang et al., 2010)
Carrier protein	Ferritin		MRI: iron.	Iron is not equally distributed across the (Cohen et al., 2005; brain and therefore may cause local Genove et al., 2005) susceptibility shifts that are above the MRI detection limit.	(Cohen et al., 2005; Genove et al., 2005)

Promise was evaluated based on (i) host-compatibility of the reporter and (ii) availability of contrast agents. *Any other modality can be used provided a suitable contrast forming moiety will be attached to PEG and the CEA antibodies, respectively, **Radioiodinated tracers can become de-iodinated in vivo resulting in free iodide that is subsequently taken up into NIS expressing organs. "*Badioiodinated tracers can become de-iodinated in vivo resulting in free iodide that is subsequently taken up into NIS expressing organs.

Proliferation of Traceable Cells and in vivo Tracking Time

Paramount for choosing the cell labeling approach is how rapid the traceable cells divide and how long-term an observer wishes to track them *in vivo*. Tracking cancer cells in preclinical tumor models normally entails following them over multiple cell divisions, spreading over weeks if not months. To evaluate cell-based anti-cancer immunotherapies, cell engraftment, expansion and survival are of interest, whereby observation times, usually several days up to several weeks, are long-term compared to division/expansion events of therapeutic cells.

For direct cell labeling applications label efflux and label dilution are limiting (**Figures 3B,D**). If radioisotopes are used for direct cell labeling then their half-lives additionally limit achievable tracking times with 4-5 half-lives being realistic with existing small-animal PET instrumentation; e.g. about two weeks for ⁸⁹Zr (Khoshnevisan et al., 2017) depending on the amount of radiolabel loading and instrument sensitivity. As the continued presence of the radioisotope in direct cell labeling results in a radiation dose to the cell and consequently radiation damage accumulation, a compromise must be reached between the maximum label concentration, which should not impair cell function (see Section "Impact of Cell Labeling Methodology on Cell Function"), and the maximum achievable tracking time.

In contrast, indirect cell labeling does not suffer from label dilution as the genetically encoded reporter is passed on to filial generations, thereby rendering the observation time theoretically indefinite. Indirect cell labeling relies on repeat administration of contrast agents, if radioactive then short half-live radioisotopes. This adds complexity as for example radiotracers need to be freshly prepared for every imaging session (Figure 3D), but it is certainly advantageous that the overall received doses are smaller than in direct cell labeling when compared over the same tracking periods. Consequently, indirect cell labeling is the preferred method of choice for long-term cell tracking, including cancer cell tracking in spontaneous metastasis models or the long-term evaluation of cell-based immunotherapies.

In vivo Cell Tracking Interval

During tracking of directly labeled cells, the imaging interval is not linked to the imaging technology other than that animal welfare considerations must be considered (e.g. minimum interval of repeat-anesthesia). However, for indirect cell labeling approaches with radionuclide reporter gene and corresponding radiotracers, the choice of radioisotope affects the minimum imaging interval because the radiotracer from an earlier imaging session must have had time to sufficiently decay before a new batch can be administered to enable a subsequent imaging session (Figure 3D). For example, there are various radiotracers for the radionuclide reporter NIS, which have differing radioisotope half-lives; these include 99 mTcO₄⁻ ($\tau = 6.01$ h) and 123 I⁻ $(\tau = 13.2 \text{ h})$ for SPECT or $^{124}\text{I}^ (\tau = 101 \text{ h})$ and $[^{18}\text{F}]\text{BF}_4^ (\tau = 1.83 \text{ h})$ for PET. Again, \sim 4-5 half-lives are needed for sufficient radiotracer decay and this defines the minimum time interval acceptable between imaging sessions. It was previously shown that repeat-imaging of NIS-expressing cells is possible after four half-lives using 99 mTcO $_4$ ⁻, i.e., after 24 h (Diocou et al., 2017); however, this would not be possible for over two weeks when using 124 I⁻, while $[^{18}$ F]BF $_4$ ⁻ would allow \sim 8 h intervals.

As for radionuclide imaging-afforded cell tracking it is noteworthy that radiotracer concentrations are very low, generally below target saturation, hence presence of prior administered radiotracers is normally negligible for later imaging sessions due to very low picomolar radiotracer concentrations, even if they would stay intact and not be excreted. A special case in this context is 99mTc, which decays to long-lived 99Tc and consequently remains in the same chemical form after its decay. Thus, it could accumulate over repeat imaging sessions unless excreted. For example, in preclinical NIS imaging experiments in mice the radiotracer ^{99m}TcO₄⁻ is administered at 15 – 30 MBq per animal. This equates to about 0.5 - 1.0 pmol of the total pertechnetate species (sum of 99 mTcO₄⁻ and 99 TcO₄⁻) taking into account a typical ^{99m}TcO₄⁻ generator elution regimen and ⁹⁹TcO₄⁻ carrier presence (Lamson et al., 1975). Even in an unrealistic worst-case scenario excluding its renal excretion, each repeat NIS imaging session would add this amount to the animal. However, the overall pertechnetate concentration would still be far below NIS saturation as its Michaelis-Menten constant for pertechnetate is likely very similar to those reported for ReO₄ or ClO₄ (Paroder-Belenitsky et al., 2011) and hence in the low micromolar range. Others repeatedly imaged animals with NIS-expressing cancer cells by 99mTcO4 -- SPECT and found no impact of earlier imaging sessions on subsequent ones (Diocou et al., 2017). For radiotracers that decompose chemically following radioisotope decay this consideration is irrelevant. Such an example is the NIS PET radiotracer [18F]BF₄⁻, in which ¹⁸F decays to ¹⁸O resulting in a chemically instable product ultimately generating borate, which is no longer a substrate for NIS (Khoshnevisan et al., 2016). While presented using the example of NIS here, such considerations can also be relevant for other reporter gene:radiotracer pairs.

Cell Viability and Its Impact on Detected Cell Tracking Signals

Signals from directly labeled cells do not report on whether the cells are alive. Moreover, recorded signals might not even stem from the initially labeled cell population (e.g. due to label efflux or cell death and subsequent deposition or uptake into different cells). In contrast, indirect cell labeling is fundamentally linked to cell viability as the reporter is encoded in the DNA of the traceable cells. However, signal loss in reporter expressing cells is also a possibility, for example, when the reporter gene expression cassettes become epigenetically silenced. Notably, so-called 'safe harbor locations' have been discovered in mammalian genomes (Pellenz et al., 2019), and reporter genes can be inserted into such locations using gene editing methodologies. The latter has recently be demonstrated in different stem cell types even with large reporter genes such as NIS (Wolfs et al., 2017; Ashmore-Harris et al., 2019).

Stem cell tracking experiments conducted with cells that were both iron oxide nanoparticle-labeled ("direct" cell label) and expressing luciferase and the fluorescent protein

GFP ("indirect" reporter genes) elegantly demonstrated the differences between the two different cell labeling methodologies (Figure 6). Even though MRI signals from the iron oxide nanoparticle were detectable for four weeks, these signals were found through ex vivo validation by histology to stem from resident macrophages that had phagocytosed the nanoparticles, which were released from dying stem cells. In contrast, luciferase signals were recorded only from living cells and were validated ex vivo also by histology (Li et al., 2008). This study highlighted comprehensively that reporter gene imaging much better reflects cell viability and that great care must be taken to avoid ascribing signals from directly labeled cells to the wrong cell populations. Consequently, employing direct cell labeling necessitates independent crossvalidation, which could include e.g. in vivo co-tracking by reporter gene imaging and ex vivo validation by histology or flow cytometry.

Within indirect cell tracking, there can be variations in how reporter genes reflect cell viability. Differences can arise due to the steady-state concentrations of certain reporter proteins in cells, determined by the production and degradation rate of the reporter. These turnover parameters have not been systematically studied for most reporter genes except some fluorescent proteins (Khmelinskii et al., 2016). In certain conditions, turnover can be manipulated, for example through genetic modification with oxygen degradation domains to speed up reporter degradation in normoxic conditions (Goldman et al., 2011; Misra et al., 2017). In general, both fluorescent proteins and reporters relying on contrast agent binding are likely to produce signals if present. Dying traceable cells or cell debris from them will remain detectable until the reporter proteins are cleared or destroyed. In contrast, reporters with enzyme or transporter functions need to be active to generate contrast in cells, and this requires a form of cellular energy to drive the transport. For example in the case of NIS, the Na⁺/K⁺ gradient (Dohan et al., 2003) is critical and its breakdown results in loss of NIS transporter activity, which is the basis for the high sensitivity of NIS to cell death. Consequently, if cell viability is central to the goals of a study, an activity-dependent reporter may yield more reliable data than a reporter which signal relies merely on protein presence.

Impact of Cell Labeling Methodology on Cell Function

It is obvious that there should be no impact of the cell labeling methodology on the function and long-term fate of the labeled cell. Contrast agents for direct cell labeling that are compatible with highly sensitive *in vivo* detection of labeled cells are often radiotracers. While chemical/biological toxicity is mostly irrelevant due to very low tracer-level concentrations (picomolar), they have the potential to exert radio-damage to the cells depending on their cellular concentration and location, their half-life and type of radioactive decay. For example, despite their short range the Auger electrons emitted by ¹¹¹In and to a lesser extent by ^{99m}Tc have the potential to exert significant DNA damage if they come in close proximity with DNA within

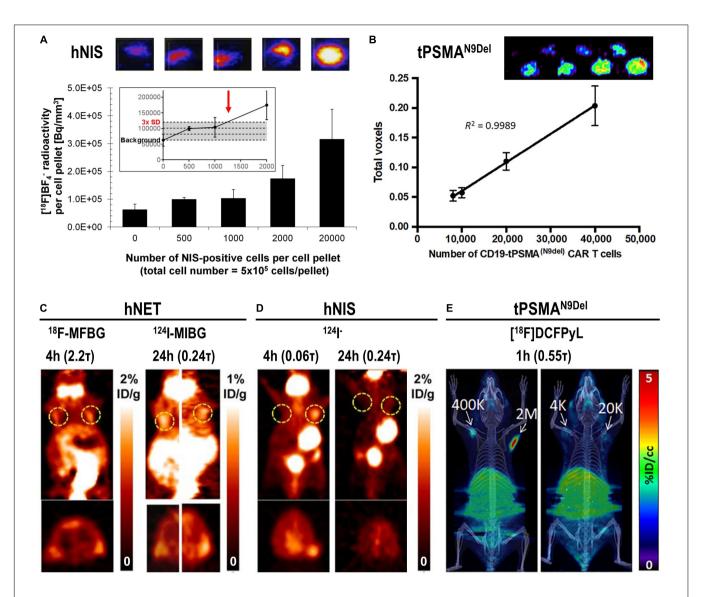


FIGURE 5 | In vitro and in vivo detection sensitivity of reporter gene expressing cells. (A) In vitro determination of the detection limit of NIS-positive cells within a cell pellet of NIS-negative cells for the NIS radio tracer [18F]BF₄ using nanoPET/CT equipment from Mediso. For experimental details see Diocou et al. (2017) (top) Typical results of nanoPET/CT imaging of cell pellets and (bottom) quantitative analysis of imaging experiments. The limit of detection was determined to be ~1,250 NIS-positive cells (inset, red arrow). (B) Standard curve demonstrating a linear relationship between the PET signal and the number of CD19-tPSMAN9del CAR-T. (top) In vitro phantom from which the standard curve was derived. The in vitro phantom used varying numbers of CD19-tPSMA(N9del) CAR T cells incubated with [18F]DCFPyL, a high affinity, positron-emitting ligand targeting PSMA; cell numbers were in the top row 103, 2 · 103, 4 · 103, and 6 · 103, and in the bottom row 8 · 103, 104, 2 · 104, and 4 · 104. Images were acquired using a SuperArgus small-animal PET/CT instrument from Sedecal. The data in the graph show results from the bottom row of images. The detection limit was determined to be around 2,000 cells. For experimental details see Minn et al. (2019). (C,D) PET in vivo imaging of human primary T-cells transduced with hNET (C) or hNIS (D) reporter genes. Different numbers of T-cells were injected subcutaneously, followed by systemic administration of indicated corresponding radiopharmaceuticals. PET imaging at indicated time points after radiotracer administration was performed using a Focus 120 microPET scanner from Siemens. Number of T-cells injected is (left dashed ring) 3 · 10⁵ and (right dashed ring) 10⁶. No potentially interfering signals were thresholded and data are expressed as percentage injected dose per gram (%ID/g). For experimental details see Moroz et al. (2015). (E) NSG mice injected with the indicated number of CD19-tPSMAN9del CAR-T in 50 µL (50% Matrigel) in the shoulders (white arrows). Mice were in vivo imaged on the Sedecal's SuperArgus small-animal PET/CT at 1 h after administration of the corresponding radiotracer [18F]DCFPyL. PET data are expressed in percentage of injected dose per cubic centimeter of tissue imaged (%ID/cc). To improve the display contrast of the in vivo images, relatively high renal radiotracer uptake was masked using a thresholding method. For experimental details see Minn et al. (2019). (Figure combined from the publications referenced in the legend above; permissions from corresponding publishers obtained).

the cell nucleus (Sahu et al., 1995). Consequently, cell labeling with agents directly releasing them into the cytosol such as [111In]In-oxine could be more harmful than agents linking

them to the cell surface. However, systematic comparative and quantitative studies on such radiobiological effects are not yet available in lymphocytes. Nevertheless, it can be safely assumed

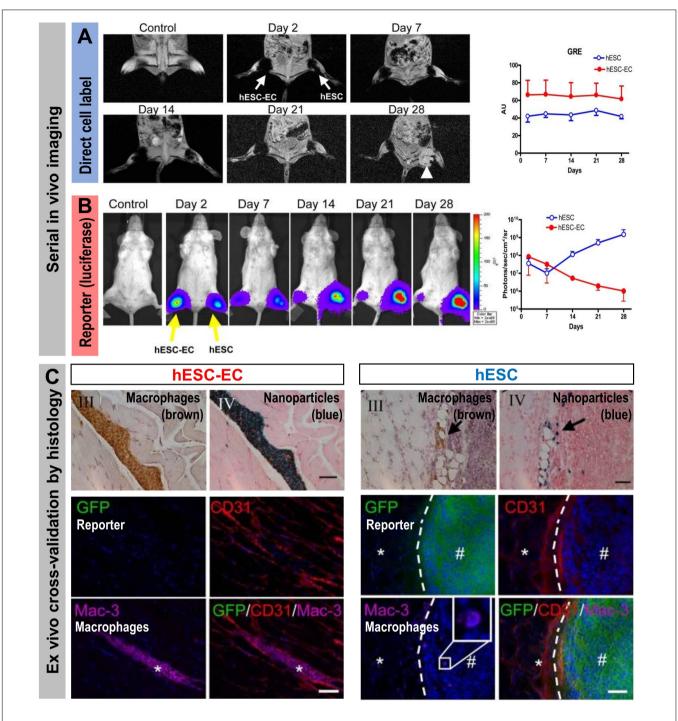


FIGURE 6 | How the type of cell labeling impacts on conclusions drawn from signals obtained from serial imaging. Cell viability can be assessed better from indirectly labeled cells than from directly labeled cells as shown by a cross-validation study using both direct and indirect cell labeling within the same cells. Reporter gene (luciferase and GFP)-expressing human embryonic stem cells (hES) or human embryonic stem cells differentiated to endothelial cells (hESC-EC) were directly labeled using iron oxide nanoparticles. (A) MRI imaging to track the directly loaded nanoparticle cell label (A/left) Serial in vivo MR [gradient-recalled echo (GRE]] images of iron oxide nanoparticles. No hypointense signal was found in control animals injected with unlabeled cells. MR signals showed no significant difference from day 2 to day 28 (the white arrow indicates teratoma formation in the hind limb injected with hES cells). (A/right) Quantitative analysis of GRE signals from all animals transplanted with hES cells and hESC-ECs [signal activity is expressed as authority unit (AU)]. (B) Tracking of the cells by virtue of reporter gene imaging (indirect cell labeling). (B/left) Planar bioluminescence imaging reveals differences in signals obtained from hind limbs that received either hES or hESC-EC cells. After initial similar signal decreases in both limbs, the signals from limbs with hES increased significantly over time, coinciding with teratoma formation in these limbs. (B/right) Quantification of 2D bioluminescence signals from each limb (photons/sec/cm²/sr; note the log10 scale). (C, top) Immunohistochemical (IHC) analysis of initially double labeled hES cells and hESC-ECs clearly reveals iron oxide (by Prussian Blue) co-localizing with a macrophage stain (by specific antibody Mac-3); IHC counterstains were Nuclear Fast Red and Hematoxylin, respectively. Note that macrophages loaded with iron particles can be found in between muscle bundles.

FIGURE 6 | Continued

(**C**, bottom) Immunofluorescence staining of GFP for transplanted luciferase co-expressing hESC-ECs (left) or hESC (right). Other panels show respective counterstains for microvasculature (CD31) or macrophages (Mac-3); nuclei were stained with DAPI (blue) in merged images. All images are from four weeks after transplantation. There were no transplanted GFP+ hESC-ECs found nearby macrophages. In tissues that received hES cells, GFP+ hESC were found to form teratoma (#) but no Prussian Blue-stained nanoparticles were found in corresponding IHC regions. The dashed line separates teratoma from normal muscle fibers (*). All scale bars are 20 μm. (Figure modified with permission from Li et al., 2008).

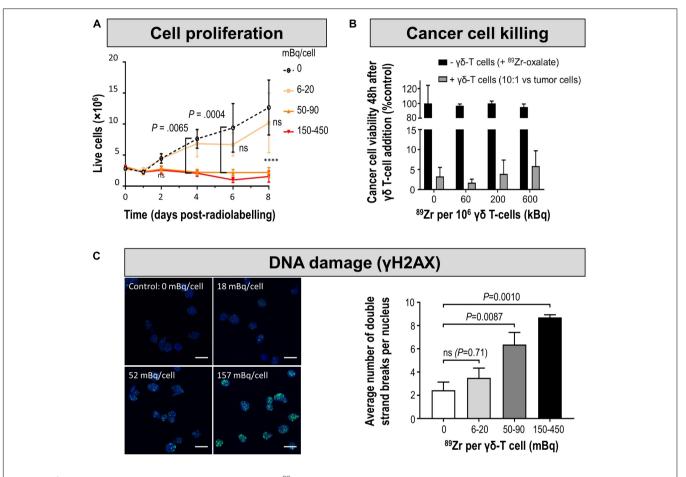


FIGURE 7 | Cell characterization after direct labeling of T-cells with $[^{89}\text{Zr}]\text{Zr}$ -oxine. (**A**) *In vitro* proliferation of differently radiolabeled human $\gamma\delta$ T-cells demonstrates that with higher amounts of cell label per cell, the capacity to proliferate diminishes. As expansion capacity is crucial for cell-based immunotherapy applications, it is paramount to perform such proliferation assays for sufficiently long times and quantify any differences even if they happen several days after cell labeling. (**B**) Tumor cell killing assay demonstrates that even $\gamma\delta$ T-cells containing radioactivity levels incompatible with further expansion still retain at least part of their tumor killing function if supplied in sufficiently high amounts. Here, the authors reported this using a triple negative breast cancer cell line *in vitro* by quantifying tumor cell viability 48 h after immune cell addition. Notably, unchelated ⁸⁹Zr supplied to tumor cells did not kill them and served as one of the controls. (**C**) (*left*) DNA damage analysis in radiolabeled human $\gamma\delta$ T-cells. Representative images of γ -H2AX foci (green) and nuclei (blue); scale bars are 10 μm. (*right*) Cumulative data from the quantification of γ -H2AX foci per nuclei after radiolabelling. For statistical analysis of all data see Man et al. (2019), from where this figure is reproduced with modification and permission.

that great care must be taken when radiolabelling e.g. T-cells with radiometals, because irradiation is a successful method to deplete the immune system of lymphocytes indicating their distinct sensitivity to radiation (Manda et al., 2012; Piotrowski et al., 2018). Generally, the longer the half-life the larger the dose the labeled cells receive; and this is also valid for their *in vivo* environment which experiences crossfire from the labeled cells. Consequently, careful consideration of dosimetry is required as well as biological evaluation of radiation effects in radiolabeled cells. For example, [89Zr]Zr-oxine labeled $\gamma\delta$

T-cells were tracked to NIS-reporter gene expressing tumors visualized by $^{99}\rm mTcO_4{}^-$ in breast xenograft murine models to determine if the immunostimulatory drug alendronate would result in enhanced tumor targeting by the administered $\gamma\delta$ T-cells (Man et al., 2019). To achieve this, the authors first titrated cellular radioactivity amounts delivered into $\gamma\delta$ T-cells and validated its impact on $\gamma\delta$ T-cell viability/proliferation, occurrence of DNA double strand breaks and retention of tumor cell killing function (**Figure 7**). This resulted in an optimized radiolabelling regimen that was then used for *in vivo* cell

tracking. Using a similar approach, others determined tumor targeting and tumor retention of [$^{89}\mathrm{Zr}$]Zr-oxine-labeled CAR-T in a glioblastoma and prostate cancer animal model (Weist et al., 2018). The reported tolerated radioactivity levels in labeled cells were 20 mBq/cell for $\gamma\delta$ T-cell and 70-80 mBq/cell for effector T-cells/CAR-T in these studies. Fundamentally, the tolerated radioactivity amounts limit the possible tracking time for such labeled cells.

As indirect cell tracking is based on repeat administration of short half-life radioisotopes (**Figure 3C**), total received doses are lower compared to direct cell labeling-afforded cell tracking over equivalent time spans. While radio damage is likely less of concern in this context, there are currently no systematic studies on radio damage of reporter-expressing lymphocytes incubated repeatedly with short half-life radiotracers available.

Another important aspect relates to the question of whether there is any impact of the typically very small administered radiotracer amounts ("tracer levels," "microdoses") on the corresponding target biology/physiology; in the context of this article for example whether imaging affects adoptively transferred immunotherapies. Generally accepted is the use of tracer level amounts, whereby a microdose is defined as "less than 1/100 of the dose of a test substance calculated (based on animal data) to yield a pharmacological effect of the test substance with a maximum dose of <100 µg or, in the case of biological agents, <30 nmol" (European Medicines Agency, 2004; VanBrocklin, 2008). However, there are studies available now, which should serve as a primer to investigate this matter more closely as molecules emerged that have biological effects at administered doses comparable to what is generally accepted as tracer level/microdose amounts. First, in a study aimed at radiotherapeutic evaluation of the human somatostatin receptor (hSSTr2) agonist [90Y]Y-DOTATOC, it was found that the agonist impaired immune function in humans (Barsegian et al., 2015). Hence, it cannot be ruled out at this point that other somatostatin-related imaging agents also have effects on the immune system, and consequently this imaging agent might not be suitable to in vivo track hSSTr2 reporter expressing adoptively transferred T-cells. Moreover, a recent study reported that immunoPET performed to in vivo track adoptively transferred T-cells in tumor-bearing mice impacted on immunotherapy outcome (Mayer et al., 2018). The authors used ⁸⁹Zr-DFO-conjugated anti-CD7 and anti-CD2 antibody fragments (F(ab')2), respectively, to quantify adoptively transferred T-cell populations in tumors. While they did not find any impact of both imaging tracers on T-cells in vitro, they found that the anti-CD2 radiotracer caused severe T-cell depletion and abrogated the effects of the adoptively transferred T-cell immunotherapy (the anti-CD7 radiotracer performed as expected and had no impact on adoptively transferred T-cells). The amounts of radiolabeled antibody fragment used in this study were \sim 9 µmol/kg [1 mg/kg F(ab')₂], which was, for example, about five times less compared to what was used in the seminal immunoPET study that originally developed the anti-CD8 cis-diabody (\sim 50 μ mol/kg \approx 3 mg/kg), which is now in clinical development (see Section "In vivo Imaging

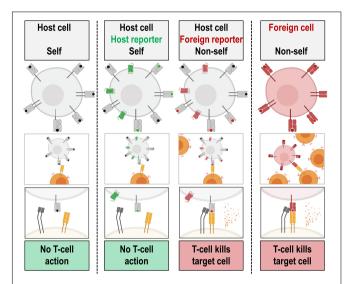


FIGURE 8 | Simplified cartoon illustrating one way of cytotoxic T-cells to recognize foreign reporter antigens. A variety of immune recognition mechanisms exist in mammals as part of their innate and adaptive immune system. Here, as a simplified example, recognition of antigen-presenting MHC class I molecules on target cells by a cytotoxic CD8+ T-cells is visualized. The TCR (orange) of the cytotoxic CD8+ T-cells recognizes foreign antigen presented on host MHC class I molecules (light gray with red foreign antigen) but not host antigen on host MHC class I molecules (green: antigen from host reporter; black: any other host antigen). Foreign MHC class I molecules are also recognized by CD8⁺ T-cells. The T-cell co-receptor CD8 (dark gray) binds to MHC class I molecules upon TCR binding and the overall process activates CD8⁺ T-cells. CD8⁺ T-cell action results in granzyme and perforin release, and consequent killing of the corresponding target cell. Several mechanisms ensure that host antigens are not recognized; they include deletion of self-recognizing T-cells and tolerance conferred by regulatory T-cells. This simplified scheme demonstrates the importance to employ host reporters in experiments involving species with intact adaptive immunity.

of T-Cell Populations"). From these two examples follows clearly that great care must be taken with imaging agents in the context of immunology even when used at amounts generally accepted to be in the range of what normally constitutes tracer levels/microdoses, because there can be effects on immune cells and their functions *in vivo*, depending on the chosen imaging target. Furthermore, this is strong evidence that *in vitro* experimentation might not be indicative of such effects. Moreover, this is also an argument for the need of careful comprehensive *in vivo* validation experiments in relevant animal models during the development of imaging agents, irrespective of whether envisaged to aid immunotherapy development or intended for future immunotherapy monitoring in the clinics.

Immunogenicity and Contrast Are Linked in Reporter Gene Applications

For *in vivo* tracking of cell-based immunotherapies using reporter genes, immunogenicity of the reporter represents another very important aspect. It is linked to the achievable contrast at different body locations, which we explain in the following. For best contrast, a foreign reporter would

appear ideal as it is expressed nowhere in the host organism guaranteeing good contrast. In animal disease models, such reporters are, for example, fluorescent proteins, luciferases (Mezzanotte et al., 2017) or the PET reporter herpes simplex virus 1 thymidine kinase (HSV1-tk) (Gambhir et al., 2000; Yaghoubi and Gambhir, 2006; Likar et al., 2009). All of them provide excellent contrast in vivo with varying sensitivities and spatial resolutions depending on the imaging modality used to probe them (cf. Figure 1). However, all of them are proteins foreign to mammals and consequently any cell expressing them in mammals can be detected and cleared by an intact host immune system (Figure 8). While this might represent only a minor issue if heavily immunocompromised animals are used, for example in human tumor xenograft models, it cannot be ignored in syngeneic models or the human clinical setting. While the foreign reporter (HSV1tk) was used in the first proof-of-principle clinical reporter gene imaging study (Keu et al., 2017), this was performed in the setting of late-stage glioblastoma in heavily pre-treated patients, all of whom died within a year of the study start. In fact, immunogenicity of HSV1-tk has been well documented (Berger et al., 2006) and consequently HSV1tk has been ruled out for reporter gene-afforded routine cell tracking of adoptive cell-based immunotherapies in humans; it should also not be considered for research in preclinical syngeneic models.

Immunogenicity issues can best be overcome by using host reporter proteins (**Table 2**) that are normally endogenously expressed in the organism of interest. Importantly, these host reporters should be endogenously expressed in only a very limited number of host tissues, only in tissues where signals do not interfere with the experimental goals, and ideally at low levels to ensure favorable contrast in adjacent organs (cf. different background patterns in **Figure 5**).

Mammalian NIS has been found to be useful as a radionuclide reporter if used together with non-iodine radiotracers, which results in better signal-to-background (Diocou et al., 2017). Generally in mammals, NIS is endogenously expressed at high levels in the thyroid gland and at lower levels in few extrathyroidal tissues (salivary glands, mammary glands, stomach and small intestine, testes) (Portulano et al., 2014). This means that for cell tracking applications in other organs the host reporter gene NIS provides excellent signal-to-background ratios when exogenously expressed in cells of interest. NIS has been used to track many different cell types preclinically (Sieger et al., 2003; Groot-Wassink et al., 2004; Che et al., 2005; Dingli et al., 2006; Merron et al., 2007; Terrovitis et al., 2008; Carlson et al., 2009; Higuchi et al., 2009; Fruhwirth et al., 2014; Diocou et al., 2017) including stem cell and CAR-T-cell therapies (Emami-Shahri et al., 2018; Kurtys et al., 2018; Ashmore-Harris et al., 2019). It has not yet been used in the clinic but due to its favorable properties and the readily available corresponding radiotracers for both PET and SPECT for its detection, it is a promising candidate for use in future clinical trials.

The human somatostatin receptor subtype 2 (hSSTr2) is another reporter with some potential for cell tracking using clinically approved PET tracers based on somatostatin

analogs [e.g. [68Ga]Ga-DOTATATE (antagonist) or [68Ga]Ga-DOTATOC (agonist)] and it has been used preclinically for CAR-T tracking (Zhang et al., 2011; Vedvyas et al., 2016). A significant pitfall of hSSTr2 use as a reporter for immunotherapies is that it is expressed endogenously on various immune cell types including T-cells, B-cells and macrophages (Elliott et al., 1999). This negatively affects imaging specificity in immunocompetent models and likely humans. It is also expressed in the cerebrum, kidneys and also the gastrointestinal tract (Yamada et al., 1992). Moreover, it was found that the hSSTr2 agonist [90Y]Y-DOTATOC impaired immune function in humans (Barsegian et al., 2015). Whilst radioactive contrast agent concentrations are very low, it cannot be ruled out without further studies that somatostatin analogs and their derivatives might also impair some immune system functions. Another important caveat of hSSTr2 use as a reporter is that it internalizes upon substrate binding (Oomen et al., 2001; Cescato et al., 2006) and this is likely to affect the detection sensitivity of hSSTr2-expressing cells through reduction of its steady-state concentration on the plasma membrane.

A very promising host reporter gene with very limited endogenous expression is PSMA (Castanares et al., 2014). It has been developed alongside PET radiotracers that were originally intended for molecular imaging of PSMA-expressing prostate cancer. PSMA is a type II plasma membrane protein that can be internalized upon ligand binding. It has a short cytoplasmic N-terminal tail, which is responsible for its internalization (Rajasekaran et al., 2003). N-terminally modified PSMA variants, PSMAW2G and tPSMAN9del, were recently designed to prevent receptor internalization and to increase PSMA surface expression with the authors hypothesizing that would increase PET radiotracer binding and overall imaging sensitivity (Minn et al., 2019). Moreover, the tPSMA^{N9del} variant lacks putative intracellular signaling motifs rendering it less likely to affect normal T-cell function. tPSMAN9del was used as a reporter to track CAR-T cells in a preclinical model of acute lymphoblastic leukemia by PET imaging with the radiotracer [18F]DCFPyL (Minn et al., 2019). [18F]DCFPyL is a radiotracer for PSMA, in fact a high-affinity PSMA ligand that can be produced in good quantities and with high specific activity (Ravert et al., 2016), and it has already been used in humans and is currently also in a phase II clinical trial for the detection of metastatic prostate cancer via PSMA (NCT03173924), another application that requires the detection of small amounts of cells.

Despite some notable advances in recent years, there is still significant room for improvement to optimize host reporter/tracer pairs, for example to improve signal-to-background, tailor them better to application in specific immune cells, and enhance the steady-state concentrations in traceable cells and thereby cell tracking sensitivity.

CONCLUSION AND OUTLOOK

The development of both molecular and cell-based immunotherapies can be greatly assisted by *in vivo* imaging, which provided valuable insight into spatiotemporal dynamics

of immune responses and the complex interactions of the tumor microenvironment. In vivo imaging has earned itself a place among the indispensable tools for immunotherapy development at preclinical stages, and many available molecular imaging technologies can be used for understanding the mechanisms governing immunotherapy function and to improve immunotherapy efficacy and safety. Newly identified relevant targets will require some degree of molecular imaging development to generate the relevant contrast agent, but multiple robust methodologies for turning target-specific biomolecules such as antibodies, antibody fragments/derivatives or peptides into contrast agents are already available. Various molecular imaging techniques aiding immunotherapy are currently at the brink of clinical application, mostly still in explorative studies, some in clinical trials, and they focus on early response monitoring with response prediction representing a major goal. Individual response monitoring at the patient level is particularly important as responses can be heterogeneous between lesions within the same individual and also between patients, rendering this a potential routine clinical application of molecular imaging in the future. A currently somewhat underexplored area is immunotherapy presence and action at secondary lesions. Preclinically, traceable cancer models would be very useful tools in this context, enabling in vivo quantification of therapy arrival and perhaps therapy action at the intended target sites. Clinically, molecular imaging will help inform on lesion heterogeneity as well as potential response heterogeneity in patients.

Cell-based immunotherapies represent an area in need of further development to unleash their full potential and render them more efficacious, safer to use, and more widely applicable. Therefore, it remains highly beneficial to better understand their *in vivo* distribution, behavior and fate, and to use such non-invasively acquired information to elucidate and tailor their mechanisms of action. Cell-based immunotherapies can be classified into two groups that (a) do not need genetic engineering for efficacy, and those that (b) fundamentally require genetic engineering (e.g. CAR-T, TCR-T).

The first group, which includes immunotherapies based on e.g. TILs and γδ T-cells, the choice between direct and indirect cell labeling depends on the precise research question, practicalities and of course whether clinical translation of the tracking methodology is envisaged and for what purpose. Implementing genetic engineering to enable indirect cell labeling to these therapies adds a significant regulatory burden and it is certainly difficult to justify the additional efforts required for the sole purpose of in vivo cell therapy tracking. Consequently, recently developed direct cell labeling approaches involving cell tracking by PET (e.g. γδ T-cell labeling with [89Zr]Zr-oxine) are promising tools despite their obvious limitations caused by the cell labeling methodology itself (label efflux, label dilution, complex dosimetry, limited observation times). However, the situation is likely to improve through the development of totalbody PET, which has been reported to be 40-times more sensitive than conventional PET (Cherry et al., 2018). This sensitivity advantage could either be invested into faster PET scanning or scanning with much less radioactivity. In vivo cell tracking studies

using this new technology will reveal to what extent the sensitivity advantage of total-body PET can be used to extend the tracking time of directly labeled cells.

For cell-based immunotherapies that require genetic engineering, an immunocompatible host reporter gene can be implemented without adding to the regulatory burden. Indirect cell labeling is clearly advantageous over direct cell labeling in such cases as it enables longer-term monitoring, reflects cell proliferation/survival, and avoids complex dosimetry considerations during cell labeling. Genetic engineering technologies have been steadily advanced and include now viral as well as non-viral delivery methods as well as site-specific integration via gene editing approaches (Figure 3C). Moreover, the reporter gene can be co-delivered with other relevant components during genetic engineering of the cells as was previously demonstrated rendering CAR-T traceable by SPECT or PET (Emami-Shahri et al., 2018; Kurtys et al., 2018; Minn et al., 2019). If contrast agents can be used that match the reporter and are already clinically approved, this is obviously beneficial. Importantly, it is unlikely that a one-fits-all approach across cancers involving only one immunocompatible host reporter gene is viable. More likely, various cancers at different body locations with varying endogenous host reporter expression levels will be targeted by genetically engineered cell-based immunotherapies in which the targeting moiety as well as the host reporter must be tailored. Undoubtedly, more research into host reporter/contrast agent pairs is warranted to provide the most flexible tools to render these immunotherapies in vivo traceable with best contrast in a quantitative manner.

In summary, we described how *in vivo* imaging can aid the development of molecular and cell-based anti-cancer immunotherapies and explained a variety of methodological and experimental design aspects. Notably, these concepts can also be extrapolated to immunotherapies intended to treat other conditions, for example, in the fields of regenerative medicine (Naumova et al., 2014), transplantation (Afzali et al., 2013; Safinia et al., 2016), diabetes type I (Alhadj Ali et al., 2017; Smith and Peakman, 2018), multiple sclerosis (Chataway et al., 2018), and infectious diseases (Hotchkiss and Moldawer, 2014).

AUTHOR CONTRIBUTIONS

GF contributed the article concept. Both authors compiled the figures, wrote the manuscript, and contributed to manuscript revision, read, and approved the submitted version.

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Correlated Multimodal Imaging in Life Sciences: Expanding the Biomedical Horizon

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The frontiers of bioimaging are currently being pushed toward the integration and correlation of several modalities to tackle biomedical research questions holistically and across multiple scales. Correlated Multimodal Imaging (CMI) gathers information about exactly the same specimen with two or more complementary modalities that -in combination—create a composite and complementary view of the sample (including insights into structure, function, dynamics and molecular composition). CMI allows to describe biomedical processes within their overall spatio-temporal context and gain a mechanistic understanding of cells, tissues, diseases or organisms by untangling their molecular mechanisms within their native environment. The two best-established CMI implementations for small animals and model organisms are hardware-fused platforms in preclinical imaging (Hybrid Imaging) and Correlated Light and Electron Microscopy (CLEM) in biological imaging. Although the merits of Preclinical Hybrid Imaging (PHI) and CLEM are well-established, both approaches would benefit from standardization of protocols, ontologies and data handling, and the development of optimized and advanced implementations. Specifically, CMI pipelines that aim at bridging preclinical and biological imaging beyond CLEM and PHI are rare but bear great potential to substantially advance both bioimaging and biomedical research. CMI faces three main challenges for its routine use in biomedical research: (1) Sample handling and preparation procedures that are compatible across modalities without compromising data quality, (2) soft- and hardware solutions to relocate the same region of interest (ROI) after transfer between imaging platforms including fiducial markers, and (3) automated software solutions to correlate complex, multiscale, multimodal and volumetric image data including reconstruction, segmentation and visualization. This review goes beyond preclinical imaging and puts accessible information into a broader imaging context. We present a comprehensive overview of the field of CMI from preclinical hybrid imaging to correlative microscopy, highlight requirements for optimization and standardization, present a synopsis of current solutions to challenges of the field and focus on current efforts to bridge the gap between preclinical and biological imaging (from small animals down to single cells and molecules). The review is in line with major European initiatives, such as COMULIS (CA17121), a COST Action to promote and foster Correlated Multimodal Imaging in Life Sciences.

Keywords: bioimaging, correlated multimodal imaging, CMI, COMULIS, CLEM, correlative microscopy, hybrid imaging, correlation software

INTRODUCTION

The ideal imaging setup would provide both (i) holistic and (ii) multiscale information about the same sample:

Holistic imaging refers to probing all relevant information spaces for the same sample, assessing both structural and functional information (Figure 1). Functional imaging allows to portray dynamic physiological, metabolic and biological processes within the sample, such as diffusion, perfusion or glucose uptake. This requires both sensitivity to low molecular concentrations and specificity, the number of potential molecules resolved per scan (Figure 2). Since these processes occur in a complex tissue environment, ideally, this information is acquired in-vivo or in a close-to-native context without damaging the sample by irradiation. This requires trade-offs in bioimaging using single modalities since usually either structural or functional information is gathered by a single modality, and high-resolution localization with protein or ultrastructural accuracy often requires sectioning the sample and prevents invivo studies.

Multiscale structural imaging visualizes the same sample across all relevant scales. Ideally, it combines high axial and

Abbreviations: AFM, Atomic Force Microscopy; CARS, Coherent Anti-Stokes Raman Spectroscopy; CLEM, Correlative Light and Electron Microscopy; CMI, Correlated Multimodal Imaging; CT, Computed Tomography; EM, Electron Microscopy; FIB, Focused Ion Beam; FM, Fluorescence Microscopy; HREM, High Resolution Episcopic Microscopy; LM, Light Microscopy;LSFM, Light Sheet Fluorescence Microscopy; MPI, Magnetic Particle Imaging; MPM, MultiPhoton Microscopy; MRI, Magnetic Resonance Imaging; MSI, Mass Spec Imaging; OCT, Optical Coherence Tomography; OI, Optical Imaging; PAI, Photoacoustic Imaging; PET, Positron Emission Tomography; PHI, Preclinical Hybrid Imaging; RS, Raman Spectroscopy; SEM, Scanning Electron Microscopy; SHG, Second Harmonic Generation Microscopy; SPECT, Single Photon Emission Computed Tomography; Superresolution, Superresolution Microscopy (such as STORM, PALM, STED); SXT, Soft X-ray Tomography; TEM, Transmission Electron Microscopy; TPEF, Two-Photon Excited Fluorescence Microscopy; US, Ultrasound.

lateral resolution with high penetration depths, and is able to image or scan a wide field of view in a reasonable time that allows the correlation of complementary parameters acquired across the entire sample. However, bioimaging is usually performed using single modalities, which restricts multiscale imaging: Either a large field of view is imaged at low magnification, which provides overview and tissue context but restricts localization, or the specimen is imaged at high resolution, which provides (sub)cellular insights but limits contextual information. Besides, penetration depth comes at the expense of lateral resolution (Figure 3) and is limited due to aberration and attenuation by scattering and absorption (with highly wavelength-dependent elastic (Rayleigh) scattering—the intensity of Rayleigh-scattered light is $I \propto 1/\lambda^4$), and hence restricts 3D *in-vivo* imaging. The achievable penetration depth is proportional to the scattering mean free path, and strongly depends on the composition of the biological tissue, such as the presence and organization of microvasculature or collagen [2].

No single modality can gain multiscale or holistic information and accurately and comprehensively decipher the inner working of cells or entire organisms. Only the combination and-importantly-the multimodal correlation of imaging technologies allow to overcome the limitations mentioned above by integrating the best features of the combined techniques (compare Tables 1, 2, 3). Correlated Multimodal Imaging (CMI) gathers information about the specimen with two or more complementary modalities that—in combination—create a composite view of the sample. It is a holistic multiscale approach that spans the entire resolution range from nano- to millimeters, and provides complementary information about structure, function, dynamics, and molecular composition of the sample. CMI can hence study biomedical processes within their overall spatio-temporal context, and mechanistically analyze pathologies, diseases and organisms down to the underlying molecular events. Correlative Light and Electron Microscopy (CLEM), as a well-established case of CMI, can for

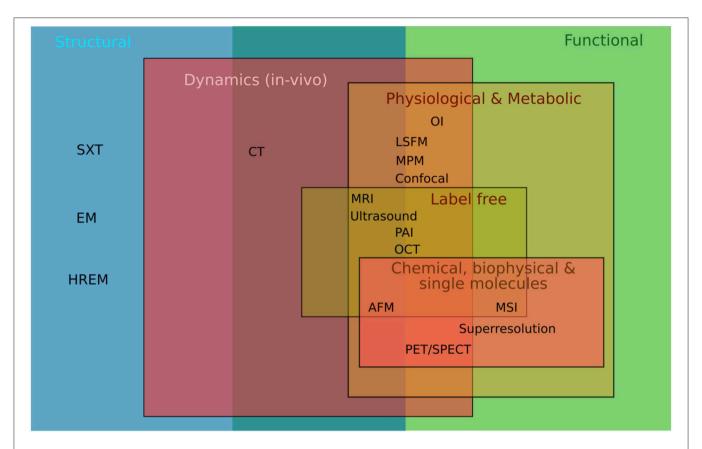


FIGURE 1 | Holistic imaging accessing all relevant information spaces from structural to functional imaging. Representation for the modalities mentioned in the text: SXT, Soft X-ray Tomography; HREM, High Resolution Episcopic Microscopy; EM, Electron Microscopy; CT, Computed Tomography; OI, Optical Imaging including bioluminescence and fluorescence imaging; LSFM, Light Sheet Fluorescence Microscopy; MPM, MultiPhoton Microscopy, Confocal, Confocal Microscopy; MRI, Magnetic Resonance Imaging; Ultrasound, PAI, Photoacoustic Imaging; OCT, Optical Coherence Tomography; AFM, Atomic Force Microscopy; MSI, Mass Spec Imaging; Superresolution, Microscopy such as STORM, PALM, STED; PET/SPECT, Positron Emission Tomography/Single Photon Emission Computed Tomography.

example gather both spatial (Electron Microscopy, EM) and functional information about a specific molecule (Fluorescence Microscopy, FM) within its subcellular context, and achieve nearatomic resolution (EM) within a relatively broad field of view (FM). Additionally, due to its complementarity and different contrast mechanisms, CMI allows to validate quantifications and conclusions drawn from any single modality.

For this review, we solely focus and distinguish between preclinical (imaging small animals and molecular processes *in-vivo*) and biological imaging (largely microscopy, *ex-vivo* visualization of subcellular processes and molecules, cells or tissues of model organisms). So far, CMI approaches in biological and preclinical research mainly focus on the correlation of two modalities [3]. There is one well-established example for each field: (1) Hardware-fused platforms for Hybrid Imaging [4] in preclinical research and diagnostics (which we refer to as **Preclinical Hybrid Imaging, PHI**), and (2) **Correlative Light and Electron Microscopy (CLEM**) in biological research [5]. The most prominent (and commercially available) implementations surely are micro-Positron Emission Tomography and micro-Computed Tomography (PET/CT) and Single Photon Emission Tomography (SPECT)/CT, but there is a large variety of other

CMI combinations both in preclinical research and correlative microscopy which will broaden the accessible biomedical information significantly. The field of CMI is highly dynamic and heading toward more complex integrated implementations of multimodal workflows that also include advanced non-commercial setups, such as Soft X-Ray Tomography in biological imaging. Currently, however, there are only very few strategies that aim at bridging biological and preclinical imaging—even though these **Novel CMI Pipelines** reap the full potential of this approach in tackling biomedical research questions mechanistically. In this context, data handling and **Correlation Software** for diverse imaging data sets play a crucial role in CMI.

While the benefits of PHI and CLEM are more and more recognized in biomedical research, they lack gold standards for protocols or data handling and limit quantification. This includes for example the quantification of the correlation accuracy in CLEM or biomedical imaging ontologies. Apart from standardization, both PHI and CLEM leave room for optimization and the integration of advanced setups, such volume or super-resolution CLEM [6, 7] or hybrid preclinical multimodal platforms for Optical Coherence Tomography (OCT), Photoacoustic Imaging (PAI), and non-linear *in-vivo*

microscopy [8]. For the routine implementation of CMI in biomedical research, several common bottlenecks need to be overcome, such as sample handling and preparation procedures that are compatible across modalities without compromising data quality, soft- and hardware solutions to relocate the same region of interest (ROI) after transfer between imaging platforms including fiducial markers, and automated software solutions to

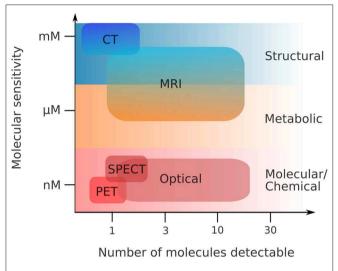


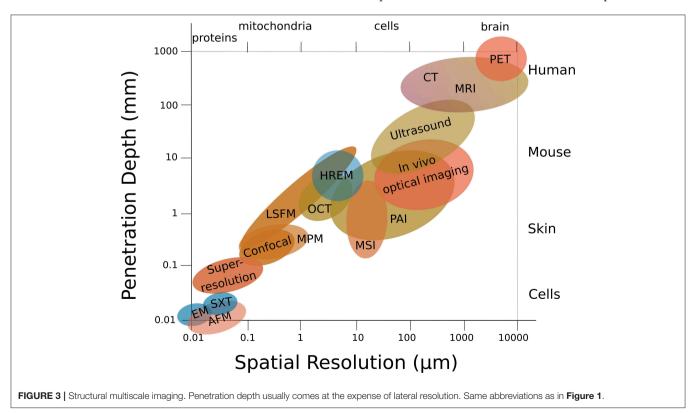
FIGURE 2 | Functional imaging—sensitivity vs. specificity. Same abbreviations as in **Figure 1**. Adapted from Pogue et al. [1], with permission from the American Journal of Roentgenology (copyright owner).

correlate complex, multiscale, multimodal and volumetric image data including reconstruction, segmentation and visualization. Due to these challenges and lack of gold standards, availability of CMI in routine biomedical research is limited. Specifically for novel CMI pipelines, the involved cutting-edge imaging technologies can be expensive and time-consuming—and simply not available to a single researcher. They require a broad range of interdisciplinary expertise across different imaging modalities from sample preparation to image processing. Besides, it is difficult for the user to keep track of the constantly expanding range of available modalities and their strengths and limitations. The use of CMI in biomedical research is also restricted by the lack of readily accessible commercial solutions that allow to address biomedical research questions without substantial technological R&D.

CMI will play a crucial role in the future of bioimaging and in life sciences, which is reflected by major European initiatives, such as the European Society for Hybrid Imaging or COMULIS, an EU-funded COST network that aims fostering CMI, disseminating its benefits, and accelerating its technological implementation as a versatile tool in biomedical research by addressing the mentioned challenges and bottlenecks.

STATE-OF-THE-ART CLEM and Correlative Microscopy

Ever since the first analysis of a biological sample using EM by Porter et al. [9], the light microscope was used first to target the cell of interest. This highlights one of the hallmarks of the power of CLEM: The identification of a specific event to



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TABLE 1 | Imaging parameters, advantages and limitations of the most used in-vivo preclinical imaging techniques.

Modality	СТ	MRI	US	PET	SPECT	MPI	OI
Contrast mechanism	X-ray attenuation of tissues	Emitted RF signal after nuclear spin excitation	Acoustic impedance between tissue interfaces	Photon emission after positron annihilation	Emitted gamma-ray photons	Non-linear superparamagnetic nanoparticle magnetization changes	Fluorescence or bioluminescence light emission
Penetration	>500 mm	>500 mm	10-150 mm	>500 mm	>500 mm	>500 mm	1–10 mm
Intrinsic contrast	High (bone) Low (soft tissues)	High	Low	None (Requires positron-emitting radioisotope labeled imaging agent)	None (Requires gamma-emitting radioisotope-labeled imaging agent)	None (Requires superparamagnetic nanoparticle contrast imaging agent)	Variable (autofluorescence) None (bioluminescence- requires imaging agent)
Spatial resolution	$\leq 100 \mu m$	\leq 100 μ m	30–800 μm	1–2 mm	0.5–2 mm	1 mm	1 mm
Sensitivity (Imaging agent)	mM	μМ-рМ	n.a.	рМ	pM-nM	Mq	nM
Typical acquisition time	10–25 min	5–60 min	5–15 min	10–90 min	30-90 min	1–2 min	2–10 min
Advantages	 excellent bone imaging 	 non-ionizing radiation very good soft tissue contrast biochemical information (spectroscopy) 	 high temporal and spatial resolution portable instrumentation cost efficient 	 high sensitivity fully quantitative data high range of applications (imaging agent dependent) dynamic measurements 	 high range of applications (imaging agent dependent) simultaneous radioisotope imaging possible 	 non-ionizing radiation high speed high sensitivity fully quantitative data high range of applications dynamic measurements 	 non-ionizing radiation high throughput cost effective
Limitations	 radiation dose low soft tissue contrast 	expensive equipmenthigh maintenance costslack of bone contrast	limited tissue penetrationpoor contrastdifficult to quantitate	 use of radioactive agents highly specialized equipment and staff required high costs 	use of radioactive agentssemi-quantitative datacosts	- limited commercially available contrast agents	limited tissue penetration depth low spatial resolution semi-quantitativedata
Main application	- anatomical (bone) - imaging	anatomical (soft tissue)imaging in vivo MR spectroscopy	- blood vessel imaging	 diagnostic imaging (oncology, neurology, cardiology) pharmacokinetic and pharmacodynamic imaging 	diagnostic imaging (oncology, neurology, cardiology) drug development	vascular imagingoncologycell tracking	cancer imagingcell traffickinggene expression

CT, Computed Tomography; MRI, Magnetic Resonance Imaging; US, Ultrasound; PET, Positron Emission Tomography; SPECT, Single Photon Emission Computed Tomography; MPI, Magnetic Particle Imaging; OI, Optical Imaging including bioluminescence and fluorescence imaging.

TABLE 2 | Imaging parameters, advantages and limitations of the most used in-vivo microscopy techniques in preclinical research.

Modality	ОСТ	RS	MPM (CARS, TPEF, SHG)	PAI	
Contrast mechanism	Optical scattering based on refractive index changes motion contrast (speckle and/or phase decorrelation)	Inelastic scattering of photons (Raman scattering)	 Molecular vibration (Raman scattering) Fluorescence Non-linear optical scattering 	Endogenous and/or exogenous optical absorption Photoacoustic effect	
Penetration	~1–2 mm	~0.5 mm	~0.5 mm	~10 mm	
Axial resolution	\geq 0.5 μ m (light source dependent)	${\geq}0.3\mu\text{m}$ (diffraction limited)	\geq 0.3 μ m (diffraction limited)	$\sim\!80\mu\text{m}$ (implementation dependent)	
Lateral resolution	\geq 1 μ m (diffraction limited)	\geq 1 μ m (diffraction limited)	\geq 1 μ m (diffraction limited)	\sim 40 μ m (photoacoustic wave)	
Frame rate	3D/1 Hz	2D/1-10 s/point	2D/<10 Hz	3D/<10 mHz	
ROI	$10 \times 10 \text{ mm}^2$	$1-100 \ \mu m^2$	$0.5 \times 0.5 \text{ mm}^2$	$10 \times 10 \text{ mm}^2$	
Advantages	 in vivo fast non-invasive label-free morphology quantitative blood flow 	Full molecular fingerprint	 in vivo endogenous contrast morphology -molecular fingerprint 	 in vivo penetration depth endogenous and exogenous contrast 	
Limitations	limited molecular informationreduced subcellular resolution	reduced penetration depthreduced FOVspeed	reduced penetration depthreduced field of view	resolutionspeedstructural contrast	

OCT, Optical Coherence Tomography; RS, Raman Spectroscopy; MPM, MultiPhoton Microscopy; CARS, Coherent Anti-Stokes Raman Spectroscopy; TPEF, Two-Photon Excited Fluorescence Microscopy; SHG, Second Harmonic Generation Imaging; PAI, Photoacoustic Imaging.

be analyzed at higher resolution in the electron microscope. Since then, CLEM has been applied to answer specific biological questions, most notably the seminal work by Rieder, using (live) Differential Interference Contrast (DIC) light microscopy to study microtubule organization during cell division [10]. CLEM took off shortly after the groundbreaking use of Green Fluorescent Protein (GFP) [11] that transformed life science research. The groups of Polishchuk et al. [12, 13] used the expression of GFP tagged to a viral protein (VSV-G) to first study the movement of post-Golgi transport carriers and subsequently analyze that exact same carrier at high resolution in EM. This workflow nicely exemplified that by combining the power of each technique, the sum is greater than its parts (1+1=3, [14]). Live imaging by FM provided the history of the carrier (originating from the Golgi) and EM not only showed the ultrastructure of the carrier but in addition provided information about its surrounding environment as a bonus, the so-called reference space. One of the great advantages of this workflow is its relative simplicity. It makes use of an imaging dish with a finder pattern embossed in it. The pattern can be recorded in the light microscope (LM) and as the finder pattern stands out from the rest of the glass coverslip, the pattern is also transferred to the resin block. This allows for trimming down the sample to only a very few cells around the cell of interest [15]. In principle, any lab with a light and an electron microscope will be able to perform this technique.

There are many different approaches to a CLEM experiment given the diversity of EM (TEM, SEM, electron tomography) and FM techniques (LSFM, MPM, super-resolution, confocal), which can be roughly classified in chemical fixation and

embedding (in-resin) approaches, and cryo approaches (see e.g. Table 3). We have compiled a large number of those in a series of three books in the Methods in Cell Biology series (Volume 111, 124, and 140). Of particular interest for routine use is the preservation of in-resin fluorescence. This method retains the fluorescence (of GFP) after high pressure freezing and freeze substitution to Lowicryl [16-18]. So, after sectioning first, the fluorescence can be recorded with high Zresolution because the section is only 70-100 nm thick and then can be mapped with high precision (50 nm) onto the underlying ultrastructure. An interesting development here is the integrated light and electron microscope that would allow for even better and more direct correlation as discussed later. It is important to highlight that the development of each of those techniques is driven by the need to answer a biological question and it should always be the case that this biological question is driving what kind of technology will be applied. As an example, we have been studying the formation of membrane tubules emanating from endosomes that transport and recycle cargo back to the plasma membrane. Chemical fixation as done by the pre-embedment approach described earlier [15] causes the tubules to fragment into smaller carriers, thus destroying the very object of study [19]. Hence a cryo-fixation method had to be developed that allows for capturing events observed live in the fluorescence light microscope on a time scale of seconds to be observed down the electron microscopy. This resulted in the development of the EMPACT2 + RTS with Leica Microsystems and allowed us and others to capture short-lived cellular events for study at the ultrastructural level [19-21]. Apart from CLEM, other well-established examples of correlative microscopy include the

Correlated Multimodal Imaging in Life Sciences

Walter et al.

 TABLE 3 | Imaging parameters, advantages, and limitations of the most used ex-vivo microscopy techniques in biological research.

Modality	AFM	TEM	Superresolution	Confocal	LSFM	Soft X-ray
Contrast mechanism/Working principle	Deflection of the cantilever is converted into force or lateral and vertical position. Contrast: e.g., spring constant of cantilever	Electrons interact with the sample. Heavy atoms deviate electrons more from their path and generate contrast. Heavy metals are generally used to enhance contrast in biological samples	Uses the physical properties of statistically photoactivatable fluorophores (PALM) and selective deactivation of fluorophores (STED) Contrast: e.g., quantum efficiency of fluorophore, labeling density	Fluorescent molecules are excited by lasers and emit at a longer wavelength Contrast: e.g., quantum efficiency of fluorophore	LSFM scans a thin slice of the sample—optical sectioning—using a plane of light instead of a point	The sample is illuminated with 'water window' X-rays (2.3–4.4 nm), which are absorbed 10 times more strongly by carbon-containing biomolecules than by water (Beer-Lambert Law)
Penetration	Not specified: Material and AFM tip dependent ($< 20 \mu m$)	<1 µm	Technology dependent: \sim 10 μm	<100 µm	≥1 cm	$<$ 20 μ m (material dependent)
Axial resolution	<1 nm	>2 nm	Technology dependent: >100 nm	≥0.4 µm	≥0.4 µm	∼ 50–20 nm
Lateral resolution	<1 nm	<1 nm	Technology dependent: >5 nm	\sim 150–200 nm (wavelength dependent)	≥500 nm (objective dependent)	∼ 50–20 nm
ROI	<100 × 100 μm ²	$<$ 10 \times 10 μ m ²	Technology dependent: \sim 50 \times 50 μ m ²	~0.2–1 mm ²	~0.2-1 mm ² (limitation is the production of a uniform, thin light sheet over the volume)	~15 × 15 μm²
Advantages	 very high lateral and axial information live imaging possible no label physical/ chemical material properties manipulation/pipetting molecules 	ultrastructural information reference space in relation to structure of interest very high resolution	 highest resolution light microscopy techniques co-localization of single molecules 	Live imagingmolecular interactionsfast data collection	 Live imaging less photo damage to sample (longer imaging) in vivo volumetric imaging 	 Close-to-native ultrastructural context in intact cells High throughput Niche technique between FM & EM
Limitations	acquires mainly near surface informationno real time imaging	 no live imaging usually elaborate processing (time consuming) 	 no real time imaging applicable to nearly immobile molecules mostly not very suited for live imaging 	missing cellular context (only labels visible)diffraction limited resolution	Special holders, limited specimen exchange	Access to synchrotron radiationMolecular context missingno live imaging

AFM, Atomic Force Microscopy; TEM, Transmission Electron Microscopy; Superresolution, Microscopy such as STORM, PALM, STED; Confocal, Microscopy; LSFM, Light Sheet Fluorescence Microscopy; SXT, Soft X-ray Tomography.

combination of FM and AFM. Besides, the combination of Soft X-ray Tomography (SXT) with FM and its super-resolution implementations allows to correlate two complementary contrast mechanisms at similar spatial resolution, and was used to study cell infections or the molecular distributions within the ultrastructural architecture [22, 23].

Advanced super-resolution FM circumvents the diffraction barrier with spatial resolution below 200 nm and has become a powerful tool for the observation of specific molecules in living cells, tissues, and even whole organisms. It is a valuable tool to study bio-molecular dynamics, interactions and co-localization via selective and specific labeling of certain components within cells and to provide biological information at the nanoscale by measuring forces of interacting objects. However, even with the recent implementation of high-speed AFM, the temporal resolution of fluorescence-based techniques cannot be reached. Likewise, the introduction of super-resolution microscopy cannot reach the spatial resolution of AFM. However, the combination of "Force-and-Light" allows to watch and simultaneously manipulate or control individual molecules. These two techniques in combination allow probing fundamental biological processes at a previously unrepresented level. In general, it is possible to combine all parameters gained from AFM techniques with those of FM ones (Figure 4). Nevertheless, it needs to be considered which combinations yield meaningful insights into the investigated system, and more importantly, which combinations do not influence each other-such as measuring of interaction forces and interaction kinetics as the kinetics will be directly altered by an applied force. Moreover, synchronized operations of both techniques instead of sequential ones are limited by the individual mechanical stability of each technique (e.g., thermal drift, acoustic disturbance, mechanical, and electronic noise/vibration).

To date, various combinations have been successfully confirmed to characterize previously inaccessible biological information. For example, the AFM tip was used as a nanopipette to supply targeted molecules to bio-membranes and its temporal interaction was described using FM [24, 25]. This approach allows for a so-called touch-and-watch experiment to study the uptake of foreign or active substances for example. Besides, there are a variety of correlative applications, which assessed combinations of the properties depicted in Figure 4: (i) Elasticity and diffusion using for example Förster Resonance Energy Transfer (FRET) between dye molecule [26-30]; (ii) interaction forces and diffusion using single molecule force spectroscopy and Total Internal Reflection Microscopy (TIRF), termed Single Molecule Cut and Paste, to assemble/split nucleotide-based aptamers individually [25, 31, 32]; (iii) interaction forces and localization using super-resolution FM to resolve the architecture of focal adhesion under physiological relevant conditions [33, 34]; and manipulation and localization to assemble single molecules patterns via the AFM to identify blinking parameters and maximal resolvable fluorophore density [35, 36].

Preclinical Hybrid Imaging

Preclinical imaging of small laboratory animals covers all clinically used methods for human *in-vivo* imaging and also

several methods that have not been implemented to humans yet. *In-vivo* imaging consists of **anatomical** (**structural**) **imaging** and **molecular** (**functional**) **imaging**.

Anatomical Imaging of body structures utilizes X-rays (CT-Computed Tomography), magnetic properties of tissues (MRI-Magnetic Resonance Imaging) or interacting of tissues with sound/pressure waves (US-ultrasonography or ultrasound imaging). CT images correspond to differential attenuation of X-rays depending on the density of interacting structures. CT images are characterized by very good spatial resolution but low contrast—so they are used preferentially for imaging of hard structures (bones). MRI imaging is based on nuclear magnetic resonance of hydrogen nuclei (protons) in oscillating magnetic fields. MRI provides inferior spatial resolution compared to CT but excellent soft tissue resolution [37]. Ultrasound waves penetrate soft tissues and form echoes on the boundary of tissues with different acoustic impedance. This allows for imaging of soft tissues such as muscle, tendon, veins, and inner organs. Higher frequency waves (40 to 70 MHz) penetrate little into the tissue (10-15 mm) but provide excellent spatial resolution down to 30 µm. US imaging is generally 2D but can be acquired and computed to form a 3D and 4D data set [38].

Molecular Imaging localizes a position of accumulated molecules (contrast agents). All three anatomical *in-vivo* techniques can be enhanced to molecular imaging by the use of contrast agents. Even without the use of contrast agents, MRI can track changes in blood flow and oxygenation of brain tissue connected to increased brain activity after stimulus and thus reveal the brain regions activated by such stimulus [39]. Ultrasound Doppler imaging can also detect functional changes in blood flow without contrast application.

Other pure molecular in-vivo imaging methods utilize radioisotopic, magnetic, optical or optoacoustic contrasts. The obtained images only show regions of contrast accumulation and must be co-registered with anatomical images to validate the exact position of the signal in the body, i.e. always require correlative or hybrid imaging approaches. Radioisotopic imaging methods include PET and SPECT. PET data acquisition is based on positron-emitting radioisotopes, in which the positron travels a short distance in the surrounding tissue, then annihilates with an electron forming a pair of high energy photons (511 keV), which travel in opposite directions and are detected by a ring of detectors surrounding the object of interest. The coincident signals are recorded and the position of radioisotopic contrast lays on the connecting line of the two detected photons. The mean distance of the emission and annihilation positions (positron range) is dependent on the energy of the PET isotope and the attenuation properties of the surrounding tissue [40]. In contrast to PET, SPECT imaging is based on single photon emitting isotopes that are detected by a gamma camera. To determine the direction from where the photon traveled, the collimator (typically made out of lead or tungsten) with single or multiple pinholes or slits must be placed between the imaged object and detector. Only photons that pass the collimator are detected. Based on the trajectory between the collimator and the detector, the position of annihilation can be reconstructed. SPECT isotope energies typically range between 30 and 300 keV

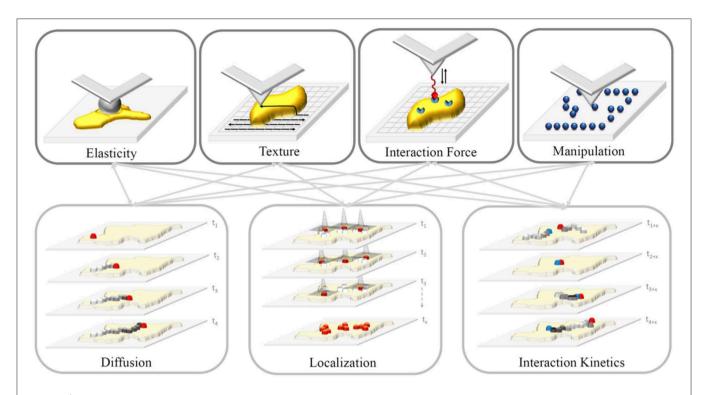


FIGURE 4 | Sketch of properties gained from AFM (upper row) and FM-based (lower row) techniques. Gray arrows depict possible combinations of properties. In general, we can differentiate acquired information premised on AFM, whether they are generated via force spectroscopy (measurement of interaction forces via functionalized tips or elasticity via ball-bearing tips) or by spatial scanning (sample texture or feature manipulation depending on the applied force) of the sample (yellow). In contrast, FM-based techniques study movement (e.g., diffusion) and interaction kinetics of molecules, and localize these particles down to an accuracy of a few nanometers depending on the number of detected photons.

and allow multi-isotope imaging when utilizing isotopes with no overlapping energy windows. SPECT and PET imaging have intrinsically different properties in terms of sensitivity and spatial resolution. While in SPECT, the collimator design vastly limits the number of detected photons and hence the sensitivity, PET imaging does not need a collimator and moreover, benefits from the ring design of detectors around the object of interest since the two photons are detected concomitantly by two detectors opposing the site of annihilation. Hence, sensitivity in PET is superior to SPECT sensitivity. Spatial resolution in PET, however, is limited by positron range and crystal size, whereas in SPECT, since the photon originates directly from the nucleus, spatial resolution is theoretically superior to PET resolution. However, spatial resolution and sensitivity are dependent on multiple factors, such as choice of isotope, crystal material, utilized detectors, etc. and especially in SPECT, collimator choice must be adapted based on the desired application. In order to diminish the effects of ionizing radiation, radioisotopes with short half-lives are used for PET and/or SPECT imaging. PET and SPECT scanners are usually constructed as hybrid devices (PET/CT, SPECT/CT, or PET/SPECT/CT). Recently, new PET detector materials compatible with magnetic resonance allowed the construction of PET/MRI hybrid scanners. The advantage of such scanners is excellent soft tissue contrast for precise localization of signal within organs, and the absence of CT imaging allows to diminish the radiation dose accumulated in imaged objects.

Magnetic properties of contrast agents are the basis for magnetic particle imaging (MPI) and electron paramagnetic resonance (EPR) imaging. MPI measures the position of superparamagnetic nanoparticles by detecting their non-linear magnetization response to oscillating magnetic fields [41]. The method ensures positive contrast localization with high spatial and temporal resolution. EPR imaging is similar to nuclear magnetic resonance; electron spins are affected instead of atomic nuclei spins. Different excitation frequencies are used compared to MRI (mostly in the microwave range). Absolute oxygen levels, reactive oxygen species (ROS), oxidative stress or spin probes can be determined *in vivo* by this method [42]. Magnetic molecular methods are usually co-registered with MRI or CT [43].

Optical imaging (OI) is fast and relatively cheap imaging of fluorescence and/or luminescence signals. Fluorescent probes are excited by matching wavelengths and emit fluorescent signal. The limitation of the method is the low light penetration through the tissues. The measured signal is thus not quantitative with more light loss for deeper probe localization. As hemoglobin (oxy- and deoxy-) absorbs the light in wavelengths below 650 nm, the optimal imaging window opens in the near-infrared (NIR) region (650–1,350 nm). Water absorbs at longer wavelengths [44]. Luminescence based on cellular expression of luciferase

enzymes converting substrates to visible light gives superior images because it avoids illumination and corresponding tissue autofluorescence [45]. Fluorescent images are co-registered to hybrid images using brightfield or X-ray anatomical imaging. While OI was initially limited to 2D imaging, several technologies have been developed in recent years which allow 3D tomographic imaging in combination with morphological imaging based on CT. For preclinical OI, firefly luciferase is the most commonly used transgene allowing longitudinal studies on e.g., promoter activity in transgenic mice, growth and dissemination of implanted tumors [46] or biodistribution and proliferation of organisms in infection models [47]. Kuo et al. published the first tomographic imaging setup for luciferase imaging, termed diffuse luminescence imaging tomography (DLIT) [48]. Such systems are now also available with built-in CT capability, where CT data are used to determine surface topology. When implanting luciferase labeled tumor cells, this technology allows proper signal allocation to organs when combined with CT contrast agents. NIR fluorescence imaging (NIR) is not only applied in preclinical but also in clinical applications, e.g., for image guided surgery [49]. For the absorption range of 700-900 nm, several fluorophores, nanoprobes and reporter genes have been developed. Another emerging area in OI is the use of the so-called second NIR window (NIR-II) ranging from 1,000 to 1,700 nm [50]. This wavelength range enables imaging with improved tissue penetration depth and spatial resolution, but also minimized tissue autofluorescence and reduced scattering. Correlative imaging of NIR fluorescence and CT is enabled by applying fluorescence molecular tomography imaging (FMT, [51]). Using a commercialized system, tomographic imaging is achieved by acquiring multiple fluorescence images from different positions in transmission mode.

Another molecular imaging method is photoacoustic imaging (PAI). The laser NIR pulses penetrate into the tissue and deliver energy to photoacoustic contrast molecules which undergo a thermoelastic expansion [52]. This expansion then generates ultrasound waves detected by the ultrasound probe. There are specific endogenous contrasts (oxyhemoglobin, deoxyhemoglobin, melanin) and exogenously delivered photoacoustic contrasts for labeling of cells, vasculature, tumors etc. The contrasts give specific positive signal on the ultrasonic background. While other preclinical molecular imaging methods have a spatial resolution around 1 mm, photoacoustic imaging can produce images with a resolution of 50 μ m or less. Nevertheless, the method is limited by the effective light penetration about 10 mm in soft tissues.

While CT has traditionally been used to assess morphologies in bone tissue, it holds more potential to the field of correlative imaging. Going beyond the depiction of mineralized tissues, it provides 3D reference volumes in integrated PET/CT, SPECT/CT or OI/CT devices that readily provide registered, multimodal data sets. Furthermore, CT can be used in a post-mortem, high-resolution, soft-tissue approach. Vascular structures can be visualized at high resolution in 3D via contrast agent perfusion [53], and contrast-enhanced microfocus CT (CE-CT) allows for simultaneous visualization of bone and soft tissues [54]. This makes CT a potent tool for both (a) integrated *in-vivo*

applications providing longitudinal, registered 3D volumes in limited resolution and contrast, and (b) high-resolution postmortem imaging with soft tissue contrast for 3D anatomical and pathological correlation.

Another important multimodal imaging approach that is gaining importance in preclinical settings as it preserves the tissue is label-free (optical) imaging and non-invasive, aseptic assessment of tissues and cells in-vivo at high resolution. While FM relies on specific contrast or the application of dyes or fluorescent proteins to highlight certain structures, most molecules do not exhibit intrinsic contrast and the application of dyes or fluorescent proteins might interfere with function and is typically limited to three to four colors due to spectral overlap, which makes it difficult to discriminate between the labeled structures or cells. Especially, optical coherence tomography (OCT) has matured over the last three decades to a potent non-invasive, high-resolution, label-free interferometric optical diagnostic imaging modality enabling video-rate in vivo cross-sectional tomographic visualization of structures with resolution comparable to histopathology, serving as in vivo optical biopsy [55, 56]. Despite the large potential of OCT, sensitivity and specificity to detect pathologic tissue is restricted and the correlation with other techniques is required. Raman spectroscopy (RS) complements OCT by giving a quantitative measure of the full molecular fingerprint of biomolecules such as lipids, proteins, carbohydrates, and nucleic acids, but is intrinsically slow. It relies on the effect of inelastic scattering of photons, stimulating molecular vibrations providing specific information on the chemical composition and molecular structure, and is an emerging technique in life sciences owing to its unique capability of generating spectroscopic fingerprints of cells and tissues in a nondestructive and label-free approach. It has been demonstrated that the combination OCT/RS on cancerous tissue can increase diagnostic sensitivity, specificity and accuracy compared to a single modality [57]. Two-photon excited fluorescence (TPEF) microscopy can be used to visualize endogenous fluorophores such as NADH and FAD giving information about redox states. Additionally, second harmonic generation (SHG) imaging is well-suited to image collagen fibers. Since SHG signals arise from induced polarization rather than from absorption, this leads to significantly reduced photobleaching and phototoxicity compared to fluorescence methods. SHG microscopy in combination with TPEF microscopy can monitor collagen structure changes and cellular metabolic activity in vivo during wound healing [58]. Hybrid multimodal multiphoton microscopy (MPM) [59] with single-photon sensitivity and submicron spatial resolution using the response of endogenous chemical biomarkers in skin, such as collagen or lipids acts as fast and label-free in vivo optical biopsy [60]. The synergistically combination of OCT with nonlinear optical imaging techniques such as TPEF, SHG, and CARS (Coherent Anti-Stokes Raman Spectroscopy) provides access to detailed information of tissue structure and molecular composition in a fast, label-free and non-invasive manner [61]. MPM offers high axial resolution with molecular contrast but limited speed and penetration depth. Combining MPM with OCT [62] adds wide-field morphologic information to the chemical fingerprint [63]. As described above, PAI can overcome penetration and scanning range limits of OCT, allowing imaging of deep vasculature [64, 65]. PAI can monitor angiogenesis, map blood oxygenation with sub-100 μm resolution and centimeter penetration depth. In combination with OCT it adds valuable vascular information in depth to the ultrahigh-resolution images [66, 67].

The combination of these optical modalities not only overcomes the limitations of isolated, standard imaging approaches, but also provides unique and complementary information (see **Tables 1**, 2) which is only achievable through the correlation of these data.

Novel CMI Pipelines

Since CMI allows to gain structural, functional, dynamical and chemical information about a single sample for a well-defined time point or even time lapse series across all relevant length scales and levels of biological organization, it is the most suitable approach to gain otherwise inaccessible insights into a huge variety of intricate biological processes and understand them within their complex (micro)environment. So far, common CMI approaches mainly focus on the combination of two modalities with two prevalent examples in biological imaging (CLEM) and preclinical research (PHI) that allow to combine functional with structural information from a singular event or within a single study (see Introduction). In PHI, two complementary imaging modalities are fused within a single setup, such as PET/CT or PET/MRI. PHI serves as a valuable diagnostic and research tool that can uncover molecular processes and biochemical pathways in living animals non-invasively within their anatomy, and has been used to study wide variety of biomedical questions, for example in cancer biology or brain research [68]. CLEM has become the method of choice to analyze rare and specific processes within tissues or cell lines, and has been used to study a wide variety of biological questions including membrane trafficking and viral pathways [17]. The maturity of the two fields is reflected in several commercial implementations for PHI (e.g., PET/CT or SPECT/CT), and a first commercially available integrated fluorescence and scanning electron microscope and commercial tools, ancillary equipment and software for CLEM to facilitate re-locating of the region of interest across modalities (see section State-of-the-Art). As illustrated in section Stateof-the-Art, the limits of CLEM and PHI are currently pushed towards developing advanced implementation. For CLEM, these efforts include for example advanced FM approaches, such as (cryo)super-resolution or FM of thick tissues [6, 7]. Apart from CLEM, more and more other dual-modality combinations of microscopy technologies have been established during the last decade. Examples of these setups include various combinations of AFM with (advanced) FM (cp. section CLEM and Correlative Microscopy); combinations of soft X-ray tomography (SXT) and FM, for example to localize proteins involved in mitochondrial fission within their close-to-native subcellular context [22, 34, 69]; the correlation of mass spectrometry-based imaging (MSI) with EM to combine the inherently lower-resolution chemical images obtained from secondary ion mass spectrometry

(SIMS) with the high-resolution ultrastructural images from EM [70]; and the combination of SIMS [71] and matrixassisted laser desorption/ionization MSI (MALDI MSI) [72] with fluorescence in-situ hybridization (FISH) to link microbial phylogeny to metabolic activity at the single-cell level. Also, the newly developing field of molecular histology has to be mentioned that incorporates findings from MADLI MSI or infrared spectroscopy (IR) in classical histomorphology [73]. Besides, an increasing interest has arisen in research focused on elemental and molecular information that play crucial roles in both physiological and pathological metabolic processes. MALDI MSI was combined with laser-ablation inductively coupled plasma MS (LAICP MS) to study lipid changes colocalized with platinum, sulfur or phosphor distributions [74], and SIMS data were combined with topographical information from AFM to record accurate chemical 3D maps [75]. Advanced PHI includes R&D setups and pipelines that showcase combinations of *in-vivo* OI, OCT/PAI, US, MRI, CT, or PET [8, 76]. Examples as outlined in section Preclinical Hybrid Imaging include label-free imaging using OCT and RS [57], or the combination of MRI and OI [77].

Novel CMI pipelines go beyond correlative microscopy and PHI setups and usually include more than two complementary modalities. They aim at (1) bridging (preclinical) in-vivo imaging with ex-vivo biological microscopy to zoom in from a living sample to individual cellular structures and/or (2) adding localized spectroscopic [biophysical (e.g., mechanical properties or vibrational modes) or chemical (e.g., molecular or elemental)] information to the acquired structural and functional parameters. With all the electromagnetic spectrum explored for imaging, only incremental improvements in contrast, resolution, or sensitivity are expected for the available spectrum of imaging technologies (see e.g. Tables 1-3). To explore the multiple spatial and temporal scales necessary for a holistic understanding of organisms and their biology, novel CMI pipelines will be the method of choice. However, novel CMI pipelines with more than two modalities are in their infancy due to lack of access to a single researcher, the broad expertise required to oversee several modalities and due to lacking workflows and software solutions to track ROIs across modalities from living 3D tissue down to high lateral molecular resolution. While there are several EUfunded initiatives that aim at improving accessibility of advanced imaging technologies and interdisciplinary imaging expertise (such as Euro-BioImaging or COMULIS), such novel CMI pipelines nevertheless require substantial method development. Due to the diverse plethora of potential combinations of imaging technologies, setting up universal correlation protocols for CMI pipelines is not feasible. Sample preparation procedures for exvivo microscopy differ substantially across the technologies and even within a modality; AFM images alone, for example, can be acquired under various conditions (vacuum, atmosphere, and liquid). Correlative imaging usually requires modality-specific preparation and setup trade-offs, such as between preservation of fluorescence and subcellular architecture for CLEM, between the AFM laser and excitation spectra of the used fluorophores to avoid bleaching for correlative AFM [78], or between preservation of fluorescence and X-ray contrast for correlative CT. Dependent on the used technology, the sample preparation needs to be adapted.

In respect to correlation strategies, universal protocols to assess correlation accuracy are not implemented and restrict finding the same ROI after relocation between imaging platforms or co-alignment of data sets. Strategies to improve correlation of different technologies include (1) resolution matching of the technologies and (2) correlative markers that can be visualized in different imaging technologies.

A common approach to improving correlation accuracy in correlative microscopy is to match the FM resolution to that of the microscopy technique with the highest resolution (EM, SXT, AFM) by integrating super-resolution FM. For CMI pipelines that bridge in-vivo with ex-vivo imaging, usually intermediate (mesoscopic) resolution steps need to be implemented—as for example mesoscopic ex-vivo MRI for the integration of macroscopic in-vivo MRI data and microscopic CT data [79]. A common example includes the emerging use of CT in a different context: As an intermediate imaging technology to create a 3D template of the sample after in-vivo imaging and before sectioning of the sample to probe the ROI. CT can visualize thick tissues in 3D at micrometer resolution, tracks distortions and morphological changes of the ROI after embedding and fixation, and allows ROI identification even without (preserving) fluorescence. CT is specifically suited as an intermediate technology between in-vivo optical microscopy and EM since it can also visualize the sample in resin blocks due to the heavy-metal stains used for EM sample preparation. It qualifies for other correlative microscopy approaches as well since it can reveal endogenous landmarks, such as the vasculature, after barium sulfate perfusion.

While there are a variety of fiducial markers that can be used and tracked in correlative microscopy (such as QDs or dyelabeled nanoparticles), there are currently no correlative markers that can be visualized with high accuracy both by microscopy and preclinical imaging technologies. Besides, robust fiducial markers that might withstand electron bombardment or high X-ray doses are also lacking. A common approach to facilitate correlation when using CT as an intermediate modality is near-infrared branding (NIRB). Prior to CT, a pulsed, near-infrared laser is used to create defined 3D marks in the fixed tissue that can be traced by both FM and EM, and hence facilitates dissecting the sample to assess the ROI in a biopsy. In Karreman et al. [80], the position of the ROI was predicted with an accuracy of below 5 μm .

A typical correlation workflow for a CMI pipeline including for example, *in-vivo* optical microscopy, CT and EM typically might include the following steps, and will need to be adapted for the specific biomedical research question: (1) *in-vivo* functional imaging of molecular dynamics using FM, such as spinning disk, light sheet or multi-photon microscopy, or *in-vivo* imaging of metabolic processes using advanced preclinical imaging technologies, such MRI or OCT; (2) (a) near-infrared branding, sample fixation, dissection, and further EM processing or (b) dissection, high pressure freezing, and freeze substitution; (3) resin embedding (lowicryl if fluorescence is to be preserved); (4) CT for identification of ROI; (5) volume EM. This workflow must be adapted according to the desired biomedical outcome. To

preserve the native ultrastructure, cryo-fixation (high-pressure freezing) might be desired. This might be followed either by freeze substitution or by a cryo-workflow with the aim to perform cryo-EM. Surely, preserving the fluorescence (either with LR-white or HM20 acrylic resins and adapted EM protocols or by keeping the sample under cryo-conditions) can be of advantage to re-locate ROIs. If considering serial section EM (or on-section CLEM), fiducial markers can be added, and a commercial CLEM system can be used to re-identify the ROI in the fluorescence channel and retrieve it in the EM using e.g., SerialEM.

Several workflows have so far been established that solved the above-mentioned challenges on sample preparation, relocalization of ROIs, and data correlation. Recent examples for multiscale combinations of in-vivo and ex-vivo imaging include the correlation of intravital microscopy, CT and EM to study single tumor cells in the cerebral vasculature [81]; correlation of X-ray holographic nano-tomography, EM and FM to disentangle dense neuronal circuitry in Drosophila melanogaster and mammalian central and peripheral nervous tissue [82]; correlation of local neuronal and capillary responses by two-photon microscopy with mesoscopic responses detected by ultrasound (US) and BOLD-fMRI [83]; or extended CMI pipelines that include the correlation of a variety of imaging technologies, such as non-invasive US, CT and highresolution episcopic microscopy (HREM) for phenotyping left/right asymmetries of all visceral organs in a mouse model of heterotaxy or combined OCT, PAI and HREM of chick embryos at multiple development stages [8, 84, 85]. Further examples of novel CMI pipelines that uncover biophysical or chemical information include the correlation of FM, molecular (MALDI MSI) and elemental imaging [X-ray fluorescence (XRF)] to analyze lipids and elements relevant to bone structures in the very same sample section of a chicken phalanx without tissue decalcification at the µm scales [86].

Correlation Software

In addition to the experimental elements helping to bridge the different modalities mentioned in the previous sections, analyzing automated software solutions to correlate complex, multiscale, multimodal and volumetric image data including reconstruction, segmentation, and visualization are an essential pillar of CMI. Image processing and image analysis in biomedical imaging is a wide field of research, having their own conferences (such as ISBI, MICCAI, or NEUBIAS) and specialized journals (IEEE TMI or Medical Image Analysis for example), with thousands of new methods published every year. One common aspect defining the field is the cross expertise needed to develop new algorithms and software: The physics of the imaging modality, and the knowledge of the biological model or of the disease and organs beyond studies are usually important elements to be considered when developing an image processing or analysis method, making this field highly pluridisciplinary. Methods tackle different problems such as restoration (denoising and enhancing the quality and resolution of the acquired images), segmentation (identifying and spatially localizing objects in images), registration (aligning different images of the same or similar objects), and visualization (generating a comprehensive, potentially interactive, representation of the acquired imaging data). In this review, we focus on the two latter, in the context of CMI. Other main elements are mostly specific to one modality and we refer the reader to existing reviews for general approaches, for example, for the use of deep learning for all of these main components of image analysis [87] or for specific components for a specific modality (such as for EM image data restoration [88]). Note that one exception can be made regarding segmentation, where aligned volume can be sometimes used for what is called multimodal segmentation where information gathered from the different modalities refine the segmentation of the ROI [89]. This last category is actually one example of the interest of CMI from the image analysis point of view, where CMI helps image analysis and quantification.

Image (2D or 3D) registration is the process of computing the transformation linking two images or volumes to overlay matching structures (**Figure 5**). It is a prerequisite for joint quantitative evaluation of the data across modalities and scales for any kind of multimodal visualization of imaging data.

The model of transformation, i.e., the number of degrees of freedom allowed between the two images, is an important choice, relying on the knowledge of the physical relationship between the sample or the organ from one modality to the other modality.

This transformation can be seen as a change of coordinate system if the organ or sample was not undergoing important deformation or deterioration between the two modalities. In that case, a rigid (rotations and translations), similarity (rigid plus uniform scaling), or affine (similarity plus shearing or reflection) may be sufficient. If there are deformations due to the sample evolution over time or due to the sample preparation step for the second modality, a more complex model allowing global and/or local deformation will have to be used (non-rigid or elastic models), according to the required accuracy. Currently, registration is often done in a semi-automated way in two steps: first, manual or automatic identification of landmarks or whole structures (segmentation) in the images to be correlated; second, manual definition of corresponding pairs of these features by the user. These landmarks serve then as an input to the registration process, that is computing an optimal transformation by maximizing the spatial matching of all defined features pairs.

In CLEM, mainly three software solutions are used to perform landmark- or segmentation-based registration: a plugin for FIJI [90] (distribution of ImageJ including many useful plugins) called BigWarp (initially developed to provide training and validation sets), a plugin for ICY called ec-CLEM [91], and the

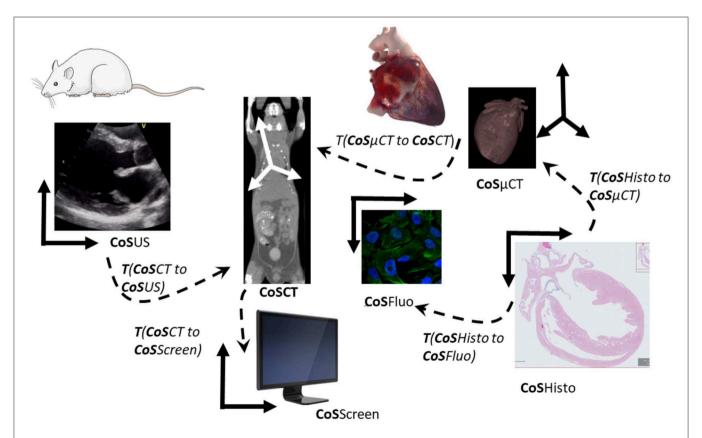


FIGURE 5 | Transformations and coordinate systems involved in the merging and visualization of multimodal data. All transformations between pair of images can be then combined to link all acquisitions and move between scales and modalities. CoS means Coordinate System. T (CoSUS to CoSCT) means the transformation spatially linking the two CoS, allowing for example to locate a US image in the CT volume. To compute the cell in the CT CoS, one can then combine transformations and apply it to the fluorescent cell images (CoSFluo) for example T (CoSFluo to CoSCT) = inverse [T (CoSHisto to CoSFluo)] \times T (CoSHisto to CoS μ CT) \times T (Cos μ CT) to CoSCT). Note that these changes of the coordinate system (or transformations) have to be computed in 3D to take into account possible changes of obliquity, and that they do not take into account deformations induced by sample preparation from one imaging modality to another one.

commercial software AMIRA (Thermofisher, Bordeaux France). Several structures have been used to correlate, including vessel, mitochondria, nuclei, added fiducials such as quantum dots (QDs) in the correlative microscopy field, or specific anatomical landmarks in the medical fields. Several other solutions exist in particular in the medical field, but are very dependent of the medical or biological question and of the workflow of imaging. One method will usually be composed based on a set of existing basic bricks performing one task to achieve the expected results [92].

The challenges in fully automated multimodal registration come from the discrepancy in the appearance of structures by different contrast mechanisms and resolution. While the specimen or sample undergoing imaging is usually kept the same size, imaging can focus on a very different field of view with a very different resolution. Algorithms then have to deal with what is called occlusion effect. The problem is usually tackled in a two-step process: first finding the coarse relationship between images, then doing a more accurate registration, that may take into account local deformation if any [93]. These local deformations are usually due to the sample preparation step (for instance, dehydration in histology, which makes the workflow of Figure 5 very challenging without the use of fiducials). Two main approaches can be considered [94]:

- (1) Considering the full content of the images and trying to find a common representation intensity space to be able to use monomodal approaches and metrics, or to define a metric that would take into account the possible discrepancy (a classical one is called mutual information, and is comparing joint histogram rather than intensity itself). These approaches are preferred when the different modalities present potentially similar content but with different aspects, for example, when matching bright field imaging with low magnification electronic images [95-97], when cell or nuclei edges are visible on both modalities, or CT with MRI where most of the anatomical structure will be appearing. An interesting approach in deep learning, rather than learning the common space between images, is to directly learn the transformation parameters linking two modalities by using pre-registered images undergoing a set of different parameters for one given transformation as a training set [98].
- (2) Considering elements of interest extracted from both modalities, for example anatomical landmarks (points or shape of interest) or multimodal markers visible in both modalities (such as fluorescent QDs in CLEM). These approaches, generally called feature-based registration, are of particular interest when the relation between content is unknown or cannot be taken as an assumption (for example for the validation of a new probe or a new imaging modality). The method to find the matching and compute the transformation can be done with two main paradigms: transforming the image data in localizations with potential additional features using point-based registration ([89, 91] for the AutoFINDER part of ec-clem) or shape-based registration, potentially with intensity-based

machine learning approaches [99]. Note that a plethora of variants exists for point-cloud registration, some of them sounding particularly promising for feature-based multimodal registration [100]. Interesting approaches mixed both feature-based and full registration by restraining the learning data set to registered features [101].

For both approaches one of the commonly used libraries for software implementation is ITK (https://itk.org) usually coupled with its visualization counterpart VTK (https://vtk.org).

Very powerful (command line) tools for landmark based or fully automatic image registration (rigid and deformable) are Elastix (http://elastix.isi.uu.nl), its derivative Simple Elastix (http://simpleelastix.github.io) and ANTs (http:// picsl.upenn.edu/software/ants/). They allow the definition of fully parameterizable complex registration pipelines. Both libraries support the creation of so-called templatesstandard reference spaces that enable the co-registration, comparison and joint analysis of images related to the same structure as represented on the template. These images can come either from the same or different subjects and, as long as there is enough joint information content to ensure registration, they can come from another modality. Multichannel imaging, where one channel enables easy registration to the template, can support the integration of imaging data with complementary information to the template, like the integration of anatomical and functional images or spatial gene expression data. One prominent example for such standard spaces are standard brain templates that are used to spatially integrate collections of multi-modal brain data e.g., of humans or rodents like the Allen Brain (https:// portal.brain-map.org/) or Human Brain Project (https:// ebrains.eu) atlases, or the brain of adult [102] and larval [103] drosophila melanogaster.

Visualizing multimodal data, also referred as image fusion, require the knowledge of the spatial transformation linking the images, obtained by registration as explained above. Once this spatial relationship is known, there are several ways to fuse the image information for its interpretation by the user (Figure 6). Visualization per se is mainly categorized in two areas: image and volume rendering (for example using ravcasting algorithms), and region of interest rendering, using for example surface representation with meshes of polygons to match the ROI outside, after segmentation. One simple surface representation without proper identification is isosurface rendering, where a surface shape is defined by an intensity threshold and a surface mesh generated from it. A third way is to use slicing from a 3D volume and come back to a 2D visualization problem. One of the difficulties in multimodal visualization is the difference of spatial resolution between images, calling for interpolation, e.g., upsampling the images of the modalities with lower resolution to the same resolution as the images with the highest resolution. Most registration algorithms automatically resample the moving image to the resolution of the images to which it is registered (the fixed or target image), meaning pixels not existing in the original image have been created by interpolation.

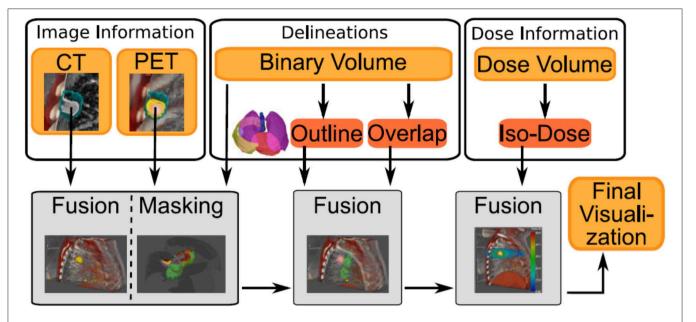


FIGURE 6 | Example of image sources (volume rendering or segmentation) from different modalities, where each type of modalities will be processed differently to provide the final visualization. Figure extracted from Schlachter et al. [104] under the Creative Commons Attribution License.

Efficient visualization of multimodal images will usually propose a combination of different visualization methods [104] and can add an additional channel of information related to the registration itself, such as the error in registration [105, 106]. One of the particular challenges is to deal with data that do not have the same dimensionality, such as time lapse vs. 3D or hyperspectral images, and heterogenous data [107]. To keep the full resolution of the biggest image, with data that can reach several terabytes in size for just one specimen, efforts are ongoing regarding efficient approaches of displaying and manipulating very big data, such as the big data viewer [108] as also used in the BigWarp Fiji Plugin.

For a more exhaustive list of software used in the field, the reader is invited to refer to a constantly updated list of software established in collaboration between the COST actions NEUBIAS (CA15124) and COMULIS (CA17121): www.comulis.eu & www.biii.eu.

CHALLENGES OF THE FIELD AND CURRENT SOLUTIONS

Standardization

CLEM and Correlative Microscopy

As highlighted earlier, every biological question demands its own technological approach. This makes standardization difficult. There will never be one workflow to tackle every single question. It is important however, to try to avoid re-inventing the wheel all over again. Dissemination of established protocols and training the next generation of scientists in these protocols is therefore of the utmost importance. COMULIS is actively promoting such training and standardization where possible.

In CLEM, one of the areas where standardization would be possible is on the correlation precision. Where correlation

down to around 50 nm is currently possible (e.g., [16]), for certain approaches an even more precise correlation would open up completely new possibilities. Can we map single fluorophores onto a single protein structure inside a crowded cellular environment? This is currently a dream scenario but will likely be possible in the future (see section CLEM and Correlative Microscopy).

For the moment we will have to do with internal or external added markers that can be used as fiducials for the alignment of the two datasets. If these dual-modality markers are used also to label specific proteins of interest, the first choice are quantum dots as they are fluorescent and their core, generally being made of Cadmium and Selenium, and is made of heavy metals for visualization in EM. Care must be taken however that the proteins coupled to such probes still fulfill its original function. We have shown that Transferrin coupled to QDs does not recycle anymore but, likely due to multiple receptors binding to one QD, is directed down the degradative pathway [109]. An alternative approach, using fluorescent moieties coupled next to a gold particle, has its own issues. It is well-known that fluorescent dyes can be quenched when in close proximity of gold particles [110]. We have recently shown that Alexafluor488 coupled to a 10 nm gold particle is quenched by 95% [111] rendering that particular probe useless as a true CLEM probe. One is probably better off using two individual probes, one tagged with fluorescence and one tagged with gold particles. In our experience a 1:10 ratio works well. Due to technical restraints we have not been able to measure the quenching effect of smaller gold particles yet. One can also add a fiducial marker from the outside. Kukulski et al. [16, 18] reported the use of 50 and 100 nm sized fluorescent beads that are added just before fixation and which are also readily identifiable in the electron microscope. The current methodology allows to correlate the LM and EM images from such experiments

down to approximately 50 nm and would at the moment be considered as the standard. With the increasing integration of super-resolution FM technologies into CLEM workflows, this precision is most likely to improve. This does however warrant a remark. Again, it is all down to the underlying question what kind of precision is required. When one is for instance searching for a rare transfected cell amongst a field of untransfected cells all that is required is a correlation precision in the range of micrometers rather than nanometers.

In correlative AFM, first combinations studied the sample first using FM and then transferred it to the AFM [112], which restricted correlation. Early efforts imaged the fluorescence of labeled molecules and topographically imaged the same area. This was misleadingly termed as synchronized operation. The two high-resolution techniques can hardly operate simultaneously due to their reciprocal disturbances. Apart from the mechanical instability of the construction, FM excitation laser(s) can induce disturbances by influencing the detection system of the AFM and/or by short-time heating of the cantilever. Additionally, the AFM laser can lead to photobleaching of fluorescently labeled molecules. In general, these problems can be solved by carefully planning the performed experiments and adequately assembling the correlative setup. The biological material itself and the molecule of interest has to be immobile or immobilized as otherwise we would not be able to benefit from the merge. Most immobile samples are studied in combination of AFM with superresolution as both techniques demand immobile samples. Optical microscopy allows studying molecules within transparent samples in contrast to AFM, which is exclusively applicable on surfaces. TIRF excites fluorophores only close to an interface between different optical densities. To limit the influence of the optical excitation to the AFM system, it is convenient to combine these two methods.

Preclinical Hybrid Imaging

Over the last decade, there has been an ongoing discussion about the ability to successfully translate preclinical findings into clinical practice [113-116]. Multiple studies have demonstrated that a bench-to-bedside translation from preclinical results into clinical practice is not as easy as anticipated [113, 115, 117]. Figure 7 illustrates multiple biological, methodologic and technical factors inherently linked to the reproducibility, reliability, and comparability of preclinical imaging data. Each of these factors has a significant impact on the validity of the acquired data and hence can influence reproducibility and reliability of results. Furthermore, it has been shown that replication of already published results is not as straightforward as the scientific community would hope [113, 119, 120]. Hence, standardization of preclinical imaging protocols and techniques to overcome the "replication crisis" has been stated to be of utmost interest [121, 122].

In sharp comparison to the preclinical research field, clinical standardization is much further advanced and accreditation programs of scanners have been implemented together with unified quality control protocols to ensure reliable, comparable and reproducible results. Furthermore, standardized protocols are in place, which allow multi-center comparison and pooling

of the data [123–125]. However, multi-center comparison is still not as easy as anticipated, but up to this point the efforts undertaken have clearly shown its benefit in clinical practice [126, 127].

It is important to emphasize that "over"- standardization in the preclinical environment is not the goal. The fast, dynamic pace of preclinical development is still a strength of one of its kind and should not be outmaneuvered. However, we have to ensure that preclinical findings can be translated more straightforward into clinical research and practice. Therefore, certain techniques, such as anesthesia protocols and animal handling, need to be unified. Furthermore, as has been stated multiple times, precise reporting of methods and techniques is of utmost importance to ensure feasible replication, as well as to facilitate findings from literature and build up based on the existing knowledge [128, 129]. Guidelines, such as the "Animals in Research: Reporting in vivo Experiments (ARRIVE)" guidelines help to improve the quality of reporting, and will consequently maximize the output and validity of published data [129]. In addition, multiple journals have updated their requirements for manuscript submission so that the respective authors either need to upload imaging data as well as all metadata, or to include a data availability statement during submission [130, 131]. An open access of the imaging data and respective metadata is certainly a huge step toward transparency and increased reproducibility and reliability of the data [132], as it has been demonstrated that image analysis is highly user- and software-dependent [133]. Randomized preclinical multi-center studies have been proposed to overcome the lack of reproducibility due to inadequate sample size, low significance, and low confidence of data [134-137]. However, the potential of multi-center studies cannot be fully accessed without proper standardization techniques in place in each participating institute. A recent study focusing on utilizing a basic [18F]fluorodeoxyglucose ([18F]FDG) imaging protocol in 4 different institutes demonstrated that the comparability among multiple institutes might be hampered due to, e.g., animal handling (each institute had different fasting protocols of animals in place; temperature regulation of animals during acquisition differed significantly), and animal facility environment or image analysis [133].

In regards to image analysis, the use of hybrid imaging technologies, with which anatomical co-registration data can be acquired using CT or MRI, significantly enhances the reliability of image analysis since this allows a precise definition of ROIs on the anatomical images that can be overlaid with functional imaging data (e.g., PET or OI data) to ensure the correct placement of ROIs, which is often difficult on functional data only [133]. Multimodal hybrid imaging can enhance reproducibility of results, but nevertheless precise standardized protocols to do so need to be implemented.

There is a huge demand for standardization in preclinical imaging and efforts to implement standardized protocols undertaken by initiatives, such as COMULIS, on a multi-center basis are certainly major steps toward more reproducibility and reliability of preclinical imaging data, as well as increased translation into clinical research and practice.

Correlation Software

As seen from section Correlation Software, different methods have already been proposed in the literature for image registration or multimodal visualization. However, a few of them are actually used by researchers in life sciences, and one of the main reasons for this is the lack of user-friendly implementation and availability as software. In addition, as underlined in the other sections, every biological or medical questions comes with its own image analysis workflow [92]. In order to help with these workflows, but also to help data sharing and open science, a standardization of the representation of the multimodal spatial relationship and content types will be important. In the medical imaging field, such standards are in place, using Digital imaging and communications in medicine (DICOM), which includes guidelines for the representation of spatial transformation between multimodal images [linear (C20.2 DICOM) or deformable (C 20.3 DICOM)]. However, the list of metadata proposed by DICOM is really exhaustive and may prevent users and constructors to actually fill in this information, which represents 15% of major errors as reported in Gueld et al. [138]. In particular, this effort will be important for imaging modalities for which this standard is not in use now and information is not automatically filled in, or for third-party software or home-made methods to compute the spatial transformation that link two images or volumes. For this reason, there is ongoing effort associated with the deployment of public image archive [139–141] to define some minimal metadata requirement, and the one associated with CMI have still to be defined by the community.

Computing the accuracy and assessing the quality of the registration is one of the central problems of correlative microscopies or more generally CMI, in particular because the structure of interest is usually not marked in both modalities, and so it is essential to confirm the correlation is correct and not biased by user assumptions. This is of particular importance when dealing with largely multiscale approaches, since one pixel can be matched with a structure of hundreds of pixels in another modality, and then an error of one pixel could lead to erroneous conclusions. In previous publications [16, 142], an iterative leave-one-out method was used to assess the accuracy of the registration, where the registration error was computed as the average error of localization of beads not used for the registration and was therefore empirical. Recent work tried to find a theoretical estimation of the error, using the Cramer

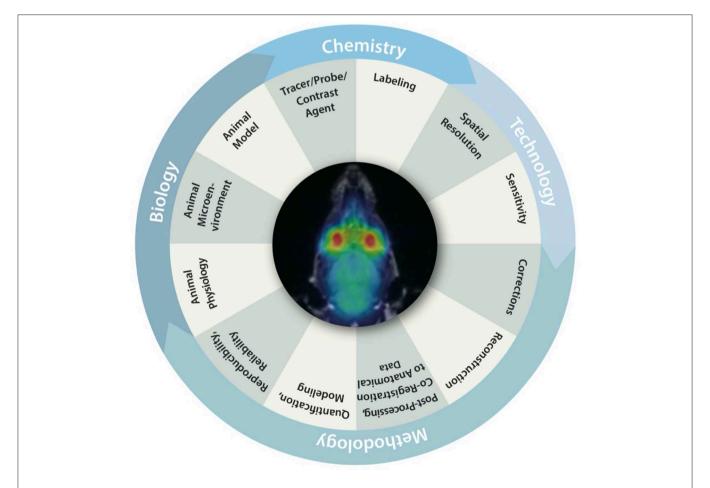


FIGURE 7 | Biological, chemical, methodological and technical factors inherently linked to the reproducibility, reliability and comparability of preclinical imaging data. Figure adapted from Figure 1 from Herfert et al. [118] with reprint permission from Springer according to their creative common license http://creativecommons.org/licenses/by/4.0/.

Rao limits [143] to estimate the transform error by taking into account the high resolution limit of accuracy. In ec-clem, the error is estimated using a formalism from the medical field for 2D and 3D rigid registration [144], originally developed for image guided surgery. It can be applied to correlative microscopy but is limited to a rigid-transformation point-based framework, and has the advantage of not requiring any ground truth matching in the images. In addition, this method may lack a proper mathematical formalism to demonstrate their usability in the fields. Note that metrics to compare images based on intensity may not be adapted in most of the case due to the discrepancy of image content (structures not present in both images). In the case of the absence of fiducials or anatomical landmarks to validate the registration, another currently used method to validate the accuracy of a registration is to use segmentation quality metrics, such as DICE metrics, to assess the overlap between known segmented structure.

Challenges are the competition of algorithms on a given dataset, where the ground truth is known in order to rank the algorithms according to a set of metrics designed for the challenge. Some challenges have been organized for the multimodal field, but usually focused on one particular problem (Anhir focused on multiplexed histological data or Curious for US to MRI brain images registration [145]). These challenges are of great interest since they provide a way to identify the actual level of accuracy state of the art and give direction for future research. They will also help define common and standard ways to assess the accuracy of the alignment of multimodal data, by defining community accepted stand error metrics.

Requirements for Optimization and Challenges to the Field

CLEM and Correlative Microscopy

In the recently published book "Correlative Imaging: Focusing on the Future," there was one over-arching theme that was highlighted in almost all chapters: Data. If handling data from a single modality can already create headaches for the data analysis and IT people, how about trying to combine datasets from different imaging modalities. Developments and possible solutions will be discussed in other parts of this review.

On the hardware side there are also clear trends visible and they almost seem to diverge from each other. On the one hand, there are the cryo-CLEM approaches trying to map protein structures in ultrastructural data, on the other, volume CLEM (a collection of techniques including FIB-SEM, SBF-SEM, array tomography, electron tomography) is more focused on large scale structures and mainly looks at connectivity between cells.

As with the integration of GFP in CLEM from 2000, the resolution revolution in cryoEM has now also been integrated into CLEM workflows, especially aided by the development of LM stages that can work under Liquid Nitrogen conditions [146–148]. These devices allow for the observation of fluorescent structures of plunge frozen samples and record their location for further studying in a cryo-TEM. Whereas, these stages

are now fairly commonly in use, the development of cryo-CLEM workflows is still improving; e.g., super-resolution cryo-fluorescence has been recently shown [149]. One of the issues that needs to be dealt with in cellular cryoEM is the thickness of the sample. In most cases, only the outer edges of a cell can be directly imaged. Anything more inside will be too thick to image directly. Cryo-FIB-milling is currently the only way to acquire thin slices of frozen material for cryo-electron tomography (ET) [150]. Targeting the correct area in Z-height, the depth of the sample, is still one of the bottlenecks but acquiring fluorescence data in 3D using confocal cryo-fluorescence will further aid with this targeting problem.

Life is 3D, so also techniques falling under the quiet revolution banner (FIB-SEM, SBF-SEM, Array tomography, electron tomography) are being integrated more and more into CLEM approaches. Especially in these cases, finding the structure of interest adds another dimension of complexity. Resolution in z is generally lower than in x, y so targeting is even more difficult. Also acquisition of z-stacks acquired before processing for EM can be useful and essential but the coordinates may change during the processing. The addition of fiducials or endogenous tissue-existing landmarks, such as blood vessels, can be useful. In addition, a bridging step with intermediate resolution such as CT are relatively new additions to the CLEM workflows [80].

Fully integrated light and electron microscopes should be able to provide the best correlation between the two modalities and both integrated LM-TEM [151] and LM-SEM [111, 152] have been developed and are still improving. Of note here is that all these systems can only work with fixed samples and one of the hallmarks of light microscopy, live imaging, is lost. As before, it is the biological question that will determine what workflow and technology fits best.

In correlative AFM, correlative challenges and opportunities are faced by recent technological advancements, improving temporal and spatial resolution of already established techniques. The combination of these highly sophisticated setups is far from trivial and highly challenging. High-Speed Atomic Force Microscope, for example, allows studying dynamic processes at sub-molecular and sub-second scale and can be combined with STED to track molecular movement at nanometer resolution and in the millisecond range.

To enable a precise and simultaneous superposition, disturbances in correlative AFM must be sufficiently shielded. An acoustically shielded chamber around the FM including the AFM measuring head is suitable for this purpose. All components that can cause electronic or acoustic interference must be removed from the isolation chamber. Typically, water-cooled EM-CCD cameras are used here to minimize interference from the outset. During simultaneous applications, the problem arises that the measuring tip of the AFM is heated by the excitation laser. This problem cannot be prevented; in this case, combinations with TIRF or confocal microscopy are usually used. It is important to keep the excitation energy at the position of the cantilever low. If both techniques are used at the same time, a real time superposition of the images is currently not possible. In most cases, the images have to be adapted to each other by mathematically forced imaging errors.

For this purpose, a fluorescent grid is suitable which is taken before the actual measurement with both techniques at the same position and subsequently adapted to each other. Currently, the AFM manufacturers already offer their own software for superimposing the images. The measuring tip is moved to several different positions, which are recorded simultaneously on the microscope and then superimposed directly. However, the measuring tip in the fluorescence image cannot be superimposed more precisely than the resolution of the microscope. Of course, the resolution can be increased by fitting techniques, known from super-resolution microscopy, but the resolution of the AFM itself can never be achieved.

Further challenges will be the combination and further development of additional microscopy technologies, such as correlative SXT. Since imaging under cryo-conditions preserves a close-to-native environment (as for cryoEM) and in certain cases (as for SXT due to its operation in the water window) is the only possible implementation, the development of cryo-FM will play a crucial role in correlative microscopy. For correlative SXT, superresolution FM is specifically appealing since it matches the achievable spatial resolution, and further efforts will focus on its cryo-implementation [23].

Preclinical Hybrid Imaging

One of the current bottlenecks for PHI lays in radiation doses for X-ray imaging together with radioisotopic imaging methods. CT, PET, and SPECT imaging delivers substantial radiation dose into the animal, and, of course, to the patient as well in clinics. The prolonged CT scanning times along with high doses of radioisotopes applied to the animal may interfere with the immune system, tumor growth and rapidly proliferating tissues (bone marrow, intestine) renewal. There are estimates that up to one percent of patients repeatedly scanned for possible metastases by whole body CT, PET/CT or SPECT/CT during a 5-years follow-up period may die because of new tumors induced by the imaging process [153, 154]. The significantly lower radiation load to the patient brings PET/MRI imaging; nevertheless, the high dose coming from high energy PET isotope injection cannot be avoided. Moreover, CT is excellent for hard tissue (bone) and contrast (e.g., angiography) imaging but soft tissue discrimination is rather poor. Several companies brought to the market so called spectral CT devices. They are usually based on dual energy X-ray sources, and the comparison of the energy-dependent attenuation of signal can improve the soft tissue recognition and distinguish contrasts and the bone, which is not possible in classical CT devices [155]. These CT machines can utilize slightly lower radiation dose compared to previous generation. Due to the recent progress in the development of novel radiation detectors, there occurred a possibility to introduce a completely new radiation detection approach. Under international collaboration in CERN, the photon counting TimePix detectors were developed. The current generation of TimePix3 detectors allows a simultaneous detection of the exact position, energy and time of the photon interaction. These properties can be used for true spectral CT detection. Novel detectors are much more sensitive and have a high spatial resolution of 55 µm. The CT image can be obtained very fast (in

seconds compared to 20 to 30 min for high-resolution standard scans), thus significantly reducing the absorbed radiation dose. The filtering of noise allows to increase the signal-to-noise ratio. According to different attenuation tissue patterns, soft tissue recognition is easier even without contrast [156]. The high speed of TimePix3 detectors (1,700 images per second) and energy resolution is suitable for coincident event registration also in PET imaging [157]. The proof-of-principle of the use of the TimePix3 detectors has been published [158]. Several groups are testing the use of Compton cameras for SPECT imaging instead of collimated SPECT detection [159, 160]. Compton cameras allow to calculate the trajectory of incoming photons from original hit position and Compton scattering detected by a second detector layer. This allows to increase the sensitivity of SPECT from <0.1 to 80% for the most used SPECT isotope ^{99m}Tc. SPECT imaging thus only requires a fraction of currently used radiation activity, and the absence of collimator facilitates the construction of combined CT/PET/SPECT devices with just one ring of detectors that can simultaneously record fast fully trimodal hybrid whole body imaging with very low radiation load. The main limitation is still the high price of detectors which could be in future substantially lowered by demand for production in large series.

Most of the optical imagers allow to detect fluorophores from visible light up to the NIR region with the longest wavelengths around 850 to 900 nm. This covers the close NIR region with relatively good light penetration. The signal loss in deeper tissues does not permit quantitative data nor fully tomographic imaging. Mouse tissues are much more transparent for shortwave infrared light (SWIR) with wavelengths between 1,000 and 2,000 m. No autofluorescence, reduced light scattering and lack of absorption by blood are the main advantages of imaging in the SWIR region [161]. The first commercial *in vivo* optical scanner allowing imaging of contrasts with longer excitation wavelengths than 1,000 nm appeared on the market in 2019. The method is still limited by the low availability of fluorescent contrast agents for use in the SWIR region.

Besides, there is the current challenge of correlating additional beneficial but not yet readily/commercially available imaging modalities (same challenge as faced by the biological microscopy community). For example, while fusion of optical tomography data (DLIT, FLIT, or FMT) with CT can be achieved using commercial imaging systems, co-registration of OI and MRI is still in the developmental state. As OI and MRI are recorded in separate systems, relocations of animals between the recording sessions have to be conducted with great diligence to avoid anatomical distortion and positional changes. Chehade developed a shuttle made of CT- and MRI- compatible material, which allowed the relocations of mice while keeping them properly in place [77].

These challenges hold also true for *in-vivo* microscopy—despite its impressive advances. It is still challenging to synergistically combine optical technologies in one platform since they do not match in imaging speed, size, resolution and contrast, and proper imaging pipelines have to be established. In this context, CMI platforms for label-free sample screening bear great potential, and working combinations of these

modalities (such as OCT, RS, MPM, SHG—STATE-OF-THE-ART/Preclinical Hybrid Imaging) will need to be identified on the basis of their added value in tackling specific biomedical research questions.

Novel CMI Pipelines

Novel CMI pipelines will continue to bridge *in-vivo* (preclinical) and *ex-vivo* (biological) imaging and allow to zoom in from physiological native tissue context to subcellular molecular resolution. This comes with several challenges to be tackled: (1) sample preparation that is compatible across imaging modalities without compromising data quality, (2) hard- and software solutions to relocate the same ROI after changing the imaging platform, (3) robust markers that can be detected in different imaging technologies, (4) lack of high throughput and automatization, (5) software solutions to correlate the imaging data and standards for data handling and storage, (6) availability of research infrastructure (i.e., cutting-edge imaging technologies from PET scanners down to cryo-EM).

(1) Sample preparation procedures are mainly an issue across ex-vivo imaging technologies since these require specific fixation and embedding that might be incompatible with other techniques. Typically, most in-vivo imaging protocols such as MRI, CT or US do not interfere with downstream processing for histologic and ultrastructural observation. This is true even when routine contrast agents are administered for in-vivo imaging. Typical example of incompatibility are the quenching of fluorophores by standard EM preparation protocols (compare section CLEM and Correlative Microscopy) or incompatibility of glutaraldehyde fixation or JB4 resin embedding with many protocols for immunohistochemistry. In general, fixation is a critical parameter in correlative workflows and requires optimization since it usually comes with sample-distorting artifacts, such as tissue shrinkage, swelling, hardening, and color change. Besides, it is of highest importance to fix the tissue or organism right after euthanasia to prevent autolysis and degradation of cellular structures [162]. To improve the penetration of fixatives, the tissue or sample might need to be incised. The sample should then be incubated in at least 20 times the sample volume, and, to facilitate correlation, be pre-embedded in 1% agarose using a casting mold prior to processing [163]. Ideally, both macroscopic and microscopic morphologies are preserved by the simultaneous stabilization of all cellular components as achieved by cryofixation. However, while preserving the close-to-native morphology, the drawback of cryofixation in comparison to chemical fixation is its limited depth to which samples can be well-frozen. High-pressure freezing allows to fix a thickness of maximally 0.6 mm. Continuing to work under cryo-conditions ensures close-to-native architecture, but poses additional challenges to potential follow-up microscopy technologies such as FM-since current cryoobjectives are limited in their optical performance (such as low numerical aperture) [164].

Importantly, all destructive staining needs to be avoided: An example is the perfusion of vasculature with heparin, formalin, NaCl and barium sulfate with gelatin to stain blood vessels via the ventricles after anesthesia in mice. Vasculature staining can be replaced in certain cases by post-mortem staining with Lugol's solution, a mixture of one part iodine and two parts potassium iodide in water [165].

Imaging thick tissues or entire organisms *in vivo* and subsequently zooming-in into the subcellular ultrastructure is facilitated by current advances in FM of non-transparent organisms, such as longer wavelengths for deeper penetrations depths [166], development of improved near-infrared probes [167], or photoacoustics [168]. While studying even thicker tissue—though *in-vitro*—will be facilitated by further advancements in clearing larger samples using lipid extraction to reduce light scattering, it is questionable whether this will also facilitate correlative microscopy approaches since clearance of larger samples might interfere with ultrastructural preservation.

(2) Identifying the same ROI across diverse in- and ex-vivo imaging platforms is currently an inherent bottleneck of novel CMI approaches. Specifically, the relocation of a ROI in thick living tissue at high subcellular or molecular resolution presents the biggest challenge faced by CMI when bridging in-vivo preclinical imaging and ex-vivo biological microscopy. As outlined in 2.3, current strategies focus on NIRB as an intermediate step for volume CLEM. If no additional processing step is foreseen between modalities (which might induce distortions or even require reduction of the volume by sectioning), the straightforward approach to correlate the ROI across modalities is to use a joint transferable coordinating system. A well-established example is the annotation of FM to define ROIs with a dedicated CLEM module and import and relocate these coordination lists into the cryo-EM microscope using SerialEM [169]. Other approaches focus on using the same holder for different imaging modalities. Examples include immobilization beds for preclinical imaging in mice using PET and CT (where additionally ²²Na fiducial markers can be placed into stationary pegs at defined depths to provide a 3D references to simplify image registration), or the combination of x-ray spectromicroscopy with electron tomography, where Allende meteorite grains were deposited on a TEM grid and transferred between the electron microscope and the COSMIC soft x-ray beamline [170]. First "plug-and-play" holder solutions are being described that are compatible and even commercially available, which can fit in a variety of microscopes for correlative imaging without changing the holder. While it facilitates relocation of ROIs tremendously, this approach cannot overcome the main limits or CMI pipelines: To assess a ROI in thick tissue, the tissue will still need to be cut due to the limited penetration depths of most high-resolution ex-vivo microscopy techniques.

To facilitate ROI relocation, CMI also aims at setting up hardware-fused hybrid setups that inherently co-localize the same ROI due to their joint coordination system. Apart from well-known commercially available PHI scanners (such as PET/CT, SPECT/CT, or PET/MRI), as described in section State-of-the-Art, examples include (i) a variety of hybrid AFM and FM setups [30, 171, 172], (ii) first implementations of integrated EM-FM setups [111, 173], (iii) several combined setups of OCT with photoacoustics or non-linear microscopy [174], and (iv) diverse hardware-based approaches to combine OI techniques with CT or MRI [175]. Nevertheless, in certain cases, relocation across single modality systems using cross-platform transport beds for CMI may provide superior performance compared to hybrid systems where compromises may have been made in the integration process.

If hybrid setups are not available (as is mostly the case), correlation can be facilitated by imaging the exact same sample without intermediate processing steps. For example, instead of performing FM before EM fixation and embedding, EM sections could be imaged directly with FM if preserving fluorescence or immunolabeling them.

(3) There is a plethora of multimodal probes for correlative microscopy and preclinical imaging, but there are hardly any robust markers that can be detected across modalities when combining various contrast mechanism with high microscopic accuracy. For correlative microscopy, most commonly used markers include QDs or polymer beads. Other examples include biocompatible nanosized, fluorescent and electron-dense intracellular nanodiamonds (internalized in living cells via endocytosis) as probes for 3D CLEM [176]. For the combination of preclinical imaging modalities, mainly CT, MRI, and optical approaches, there is a variety of CMI probes: (1) Lipid-based markers, such as liposomes or lipoproteins as carriers; (2) macromolecular carriers where different contrast agents are attached to a common macromolecule (and its reactive amines, thiols, or carboxyls); (3) nanoparticles, such as QDs, iron oxide nanoparticles or nanoparticle carriers; or (4) small molecules where two or more probes are directly fused together with minimal intervening bonds [177]. Further examples include high-contrast, non-radioactive tungsten-based fiducial markers for multimodal brain imaging with MRI, PET and CT that are attached outside of the sample in close proximity of the ROI, and numerous dual PET and NIR fluorescence imaging probes [178, 179], such as fluorescence-labeled monoclonal antibodies (mAbs) and systemic applications of both mAbs and peptides in PET/SPECT in-vivo. While ⁶⁴Cu the prevalent isotope for systemic mAb imaging, ¹⁸F and ⁶⁸Ga isotopes better match the targeting half-lives of peptides. Although dual agents for PET and NIR imaging are in its infancy and no agent has been approved by the FDA so far, several preclinical applications have been reported [179]. Examples for markers for advanced CMI pipelines include photo- or chemically-convertible tags (such as miniSOG or APEX) that can be detected in FM, CT and EM and were used to identify the ROI across multiple imaging modalities [180–182].

Most multimodal probes are exogenous. The ultimate goal is to have the organism or cells express their own probes

after transfection. Fusions of GFP for fluorescence imaging and herpes simplex virus thymidine kinase (HSV-TK) for PET have been reported in several studies. HSV-TK can also be fused to other optical reporters and constructs of luciferase. With QDs and (NIR) fluorophores being used across preclinical and biological imaging modalities, these two markers appear most promising for advanced CMI pipelines. While a single CMI marker will guarantee the same pharmacokinetics and colocalization of the signal for each modality and reduces the stress on the blood clearance mechanisms of small animals (as induced by multiple doses of agents), the variations of sensitivities of different imaging modalities need to be considered when aiming for the detection of a single probe correlatively. In certain cases, it may not be practical to simply add all functionalities to one molecule [177].

For a rough alignment of untreated samples between relocation of imaging platforms, registration marks such as gridded coverslips or finder grids [183], or deposition of metal structures or engraving of the surface are commonly used. To provide rough orientation when dissecting ROIs from living organisms for subsequent ex-vivo analysis, the margins of adjacent tissue are demarcated in their bodily orientation with surgical ink or notches on the skin. For advanced CMI pipelines from thick tissue to 2D sections, endogenous landmarks or NIRB can be used. In volume CLEM, blood vessels, nuclei or myelinated axons can be used as endogenous fiducials since they show sufficient contrast both in light and electron microscopy and are distinctive in size and shape—as demonstrated for mouse brain imaging using a CMI pipeline with in-vivo 2-photon microscopy and FIB/SEM [6].

- (4) Nanometer-resolution of the subcellular architecture of tissues usually requires time-intensive scanning of the sample (as for FIB/SEM or AFM) since lateral resolution often comes at the expense of penetration depth and field of view. The selection of a volume of interest several orders of magnitude smaller than the sample imaged by FM is hence both crucial and challenging. Solutions to studying big volumes at high resolution and with high throughput include the use of multi-beam setups (such as multi-beam SEM [184]) with parallelized data collection, or the automation of the identification of ROIs and image acquisition [185]. Since advanced CMI setups require tedious protocol optimization, time-intensive image acquisitions and intermediate processing steps, in general, novel CMI pipelines suffer from lack of throughput, which restricts reproducibility and statistics. Currently, the focus of CMI pipelines is rather on identifying working combinations to address previously inaccessible biomedical research than on fostering throughput. Once those correlations have been showcased and are proven feasible by substantial R&D efforts, CMI will enter further automatization and simplification to generate throughput.
- (5) Advances and current trends in correlation software are discussed in sections Correlation Software and Correlation Software. To expedite automated multimodal image

registrations and quantification, data handling specific to multimodality needs to be established, including universal imaging formats, ontologies, and data storage and repositories. While there is currently no universally established microscopy format with additional diversity between preclinical and biological imaging approaches, repositories and public archives for diverse imaging data are being implemented—from single molecules (EMPIAR) to tissues (Tissue-IDR). Correlative data sets (such as CLEM data to link functional information across spatial and temporal scales) will be included in the so-called addedvalue databases that are developed around the archive. They aim at gathering a greater understanding for specific biological areas through systematic integration of images [141]. Integration of such multimodal data sets and their interoperability will be facilitated by universal large-scale multi-granular imaging ontologies, whose need is being described in first publications [186, 187].

(6) Novel CMI pipelines require access to diverse imaging technologies. All these technologies and the necessary expertise are unlikely to be found in a single laboratory, which restricts the development and implementation of CMI. To facilitate access to complementary imaging technologies and exchange of knowledge, several initiatives have been established. Two prominent examples are (1) COMULIS (Correlated Multimodal Imaging in Life Sciences), a COST Action (CA17121) to foster CMI, and (2) Euro-BioImaging, a European Research Infrastructure Consortium providing open access to imaging technologies in biological and biomedical research.

Correlation Software

As already underlined, most of the automated methods are developed ad hoc for a particular multimodal problem. Machine learning and deep learning are definitely moving the image analysis field a step forward [87] since their main interest is to create an ideal method of processing based on training data sets, translating the effort of developing ad-hoc computer vision or signal processing methods to the effort of annotating data and formalizing the problem as input/output. Note that deep learning is still in progress and a lot of research is still going on to optimize these methods and reduce the number of training datasets required, as well as taking into account the errors in annotations in training data sets [87]. Based on these approaches, a universal solution without any user input is not envisioned per se, but rather a universal framework for multimodal registration, or the creation of a giant bank of pretrained models. It could be envisioned to be set up with minimal user input, i.e., by providing registered data sets or at least identifying on both modalities what should be used for matching. There are ongoing approaches for a universal segmenting tool, based on deep learning, trained on different data, for example, for nuclei segmentation [188]. Interestingly, it has been shown that some of the models trained could be applied in a new different modality (even if all at the same microscopic scale), for example, with different staining without the need of further training.

Another challenge in the field is the integration of very heterogeneous data, such as CMI with very different dimensions (multiplexing or spectral data with hundreds of outputs for one spatial localization, temporal vs. static) with non-imaging data such as -omics data. This effort could be facilitated by two approaches: the single cells approaches, and the development of spatially localized proteomics or genomics which are now starting to appear as commercial platform and would facilitate these links. But then the analysis of this largely heterogeneous data still requires to develop new statistical tools.

Another trend is to use multimodal aligned images as training sets to construct inference models to reduce the needs for one or the other modality. For example, Li et al. [189] used a deep learning approach to generate PET images from MRI and demonstrated similar classification results using the generated PET images than the true PET images for Alzheimer Disease and Mild Cognitive impairment. In this preliminary study, a 3D convolutional neural network was trained with MRI patches as input and matching PET patches as output using half of a database of patients having both exams. The parameters of the network capture a relationship between both modalities. This trained network was then used to generate the predicted PET images from MRI images, and validated against the remaining half of the database. The same principles have been applied also to microscopy images, where for example restoration based on deep learning have shown impressive results [190], and even predicting fluorescent labeling from transmitted light images [191].

These approaches in the long term could then reduce the number of modalities required to answer a particular question. To achieve such a goal, sharing well-annotated aligned multimodal data is of particular importance. Efforts are on-going in this direction to share repositories and public archives ([141], Empiar, IDR).

CONCLUSIONS AND OUTLOOK: FUTURE OF THE FIELD

To have an even bigger impact and to become a basic life science technology as FM is nowadays, it will be crucial for correlative microscopy to develop and disseminate automated workflows that can deal with huge amounts of data and seamlessly merge diverse data sets. This process will be facilitated by a number of factors: the improved capabilities of integrated systems, the adaption of standard file formats, and the deposition and sharing of these information-rich datasets.

For PHI, preclinical molecular *in-vivo* whole-body imaging is fully dependent on hybrid imaging and co-registration with anatomical images. Some devices are already multimodal in their hardware settings, but images from different techniques are taken sequentially and implemented automated co-registration often requires manual intervention to obtain the best results. Multimodal animal beds allow to scan the same anesthetized animal in different devices, co-register multiple imaging methods and obtain enhanced molecular information about the *in-vivo*

processes. The implementation of new methods and contrast agents broadens the spectrum of imaging possibilities, and simultaneously acquired multiple hybrid images facilitate proper visualization. Besides, OI has seen significant expansion in biomedical and diagnostic applications, which go beyond simple visualization of the sample. Novel modalities allow label-free mapping of biomolecules *in vivo* providing a way to determine a stage of disease progression or enable tomographic assessment of deep tissue layers. Nevertheless, current research efforts are indicating that in many biomedical applications, a single modality is inadequate to provide a comprehensive picture of a disease. Instead a targeted combination of modalities, which give access to a set of (label-free) parameters is necessary.

In summary, CMI is a field under construction, relying on broad expertise. In particular, data processing, analysis and management need to be incorporated in the initial reflections leading to a project, and a continuous and iterative dialog has to take place during the whole project with image data analysts such that the communities can understand the requirements and needs of each other. Setting up standard approaches and sharing protocols and generated data will definitely be the key elements for achieving a smooth communication. A real holistic view will be achieved when other type of data will be also correlated with imaging data, but to reach such a goal the CMI community needs to develop its own solid ground.

Ideally, CMI will lead to multimodal platforms that allow to functionally and morphologically characterize the entire sample *in-vivo*, fast and non-destructively at high axial and lateral resolution and high penetration to gain a mechanistic understanding of organisms and diseases. By synergistically fusing complementary imaging techniques, CMI platforms can give insights into a variety of tissue properties during a single image acquisition, and better tissue characterization can be achieved than by the separate imaging modalities alone. Complementary information provided by the fused

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imaging modalities and machine-learning-assisted data analysis will ultimately yield novel biomarkers by a multi-dimensional classification accelerating the discovery and translation of novel therapeutic strategies. Such hybrid platforms of high accuracy will correlate the modalities instantly without the need for post-processing correlation software. Surely, 3D cellular, ultrastructural and molecular tissue maps as acquired by CMI will substantially transform biomedical research and diagnostics in the future.

AUTHOR CONTRIBUTIONS

AW initiated, coordinated, and supervised the manuscript and wrote all CMI sections, Introduction, Conclusion, and Abstract. LS wrote main parts of the PHI sections. PP-G wrote all software sections. PV and BP main parts of the correlative microscopy sessions. JM, MO, BP, PS, AU, SH, DF, and MM-D contributed to each section. KB, SG, MG, TW, and WW provided feedback and edits.

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Optimizing Diffusion Imaging Protocols for Structural Connectomics in Mouse Models of Neurological Conditions

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Network approaches provide sensitive biomarkers for neurological conditions, such as Alzheimer's disease (AD). Mouse models can help advance our understanding of underlying pathologies, by dissecting vulnerable circuits. While the mouse brain contains less white matter compared to the human brain, axonal diameters compare relatively well (e.g., $\sim 0.6 \,\mu m$ in the mouse and $\sim 0.65-1.05 \,\mu m$ in the human corpus callosum). This makes the mouse an attractive test bed for novel diffusion models and imaging protocols. Remaining questions on the accuracy and uncertainty of connectomes have prompted us to evaluate diffusion imaging protocols with various spatial and angular resolutions. We have derived structural connectomes by extracting gradient subsets from a high-spatial, high-angular resolution diffusion acquisition (120 directions, 43-µm-size voxels). We have simulated protocols with 12, 15, 20, 30, 45, 60, 80, 100, and 120 angles and at 43, 86, or 172-μm voxel sizes. The rotational stability of these schemes increased with angular resolution. The minimum condition number was achieved for 120 directions, followed by 60 and 45 directions. The percentage of voxels containing one dyad was exceeded by those with two dyads after 45 directions, and for the highest spatial resolution protocols. For the 86- or 172-µm resolutions, these ratios converged toward 55% for one and 39% for two dyads, respectively, with <7% from voxels with three dyads. Tractography errors, estimated through dyad dispersion, decreased most with angular resolution. Spatial resolution effects became noticeable at 172 µm. Smaller tracts, e.g., the fornix, were affected more than larger ones, e.g., the fimbria. We observed an inflection point for 45 directions, and an asymptotic behavior after 60 directions, corresponding to similar projection density maps. Spatially downsampling to 86 μm, while maintaining the angular resolution, achieved a subgraph similarity of 96% relative to the reference. Using 60 directions with 86- or 172-µm voxels resulted in 94% similarity. Node similarity metrics indicated that major white matter tracts were more robust to downsampling relative to cortical regions. Our study provides guidelines for new protocols in mouse models of neurological conditions, so as to achieve similar connectomes, while increasing efficiency.

Keywords: diffusion imaging, MRI, connectivity (graph theory), mouse model, brain, neurodegenerative diseases

INTRODUCTION

A growing body of evidence suggests that altered brain connectivity is present in a variety of neurologic and psychiatric diseases. For example neurological conditions such as AD [1, 2], autism spectrum disorders [3], and psychiatric conditions such as schizophrenia [4] can be viewed as connectopathies. Multimodal network analyses can help identify early alterations associated with pathological processes both at the functional and structural levels. Structural connectomes based on diffusion MRI may produce sensitive biomarkers to monitor these conditions since they integrate the effects of multiple pathologies (atrophy, myelination, toxicity of the environment due to, e.g., oligomers, microstructural changes) [5].

While studies on diffusion imaging in the human brain have previously addressed the tradeoffs associated with spatial vs. angular resolution, the mouse brain provides insight into white matter connectivity at a vastly different scale and, thus, deserves special attention. We need to compare 2-mm linear dimension voxel sizes in humans (corresponding to 8-mm³ voxel volumes), vs. 0.2–0.043-mm linear dimension voxel sizes (corresponding to $\sim 8 \times 10^{-2}$ - 8×10^{-5} -mm³ voxel volumes) required to distinguish similar levels of anatomical detail in mouse brains [6–11]. This increased resolution enables the observation of brain architecture at the level of cellular layers, which, therefore, can help us gain insight into the mechanistic drivers behind the etiology and progression of disease, using animal models where axonal dimensions are relatively similar to humans [12, 13].

Yet, using sensitive methods for identifying pathways affected early on in animal models remains difficult. Difficulties in optimizing diffusion imaging protocols arise from the need for long acquisition times, to achieve sufficient signal to noise for smaller voxels. These are required for dissecting vulnerable pathways and networks, early on in the disease process, or subtle changes in time or following interventions. The mouse brain architecture, in contrast with the human brain, presents with thin, relatively sparse white matter tracts. The imaging protocols required for resolving small tract-based connections are, thus, demanding a high spatial resolution. In addition, increasing the angular sampling and the number of b values may reduce biases and produce more accurate models. This translates into long protocols, and subsequently costs in terms of time and money, which need to be balanced against the desired increases in spatial and angular resolution.

In this work, we have examined the balance between spatial and angular resolutions and inferred suggestions for recommended future protocols. In particular, we examined a set of nodes/brain regions that are relevant for neurodegenerative conditions such as AD. We used simulations based on downsampling a high-spatial, high-angular data set, and assessed the effect of relaxing these requirements/parameters on the accuracy of the reconstructed tracts and connectome, when compared against our reference protocol. We have focused our analyses on regions expected to be affected in AD, such as fimbria, fornix, and hippocampus, septum, hypothalamus, and also the lateral geniculate nucleus. We evaluated how different protocols led to increasingly more robust results and how fast errors change

with spatial and angular sampling resolution. Our results can inform future population studies, in particular, for models of neurodegenerative disease.

METHODS

Imaging was performed, as previously reported [14] on a 9.4-Tesla small-animal imaging system controlled by an Agilent VnmrJ 4 console. Diffusion imaging was accomplished using a 3D diffusion-weighted spin-echo pulse sequence with repetition time (TR) = 100 ms, echo time (TE) = 15 ms, and b value = $4,000~\text{s/mm}^2$. The acquisition matrix was $568 \times 284 \times 228$ over a $24.4 \times 12.2 \times 9.8~\text{mm}$ field of view, resulting in isotropic $43 \times 43 \times 43~\mu\text{m}$ voxels (referred from now on as $43-\mu\text{m}$ linear voxel dimension). The diffusion protocol included 120 diffusion directions [15, 16] and 11 non-diffusion-weighted (b0) measurements (i.e., one b0 every 12 diffusion measurements).

Angular downsampling of the original diffusion data set was performed by obtaining the optimal diffusion directions for each angular subset [15, 16] and extracting the closest gradient vector from the 120 unique diffusion directions. The closest gradient orientation was chosen by maximizing the dot product between the optimal gradient vector and the possible vectors found in the original gradient table.

Spatial downsampling of the original diffusion data set was performed by cropping the data in k space, resulting in three levels of isotropic spatial resolution: 43-, 86-, 172- μ m linear voxel dimension.

The condition numbers for the gradient subset matrices, defining angular sampling, were calculated in MATLAB (Natick, MA), based on the ratio between the largest and smallest singular values for each matrix. The stability of the condition numbers was evaluated for each of the gradient subsets following 50,000 simulated rotations of these matrices.

Diffusion data processing was done on a high-performance computing cluster with 96 physical cores and 1.5 TB of RAM. All 131 image volumes were registered to the first b0 image using advanced normalization tools (ANTs) affine transformation [17] to correct for eddy current distortions. Scalar image volumes were reconstructed using FSL's DTIFIT [18]. Fiber data for probabilistic tractography were reconstructed using FSL's BEDPOSTX [19] with a maximum of four fiber orientations per voxel. In-home written scripts and FSL were used to estimate the numbers of tracts with one, two, three, or four dyads and to estimate errors/uncertainty based on dyad dispersion.

Automated atlas-based segmentation was performed [20] using an atlas, which combines the Waxholm Space atlas [21] for subcortical labels, and the Ullmann atlas of the neocortex [22], with a total of 332 regions—symmetrized relative to the midsagittal plane. Connectomes were constructed using SAMBA [23], and DSI Studio [24] for a subset of brain regions. These include for simplicity, the connectivity matrices generated pertaining solely to left-sided seed regions connecting to left-sided targets. We next evaluated the similarity of connectomes based on global Spearman correlation coefficients among 12 representative acquisition schemes (four angular sampling

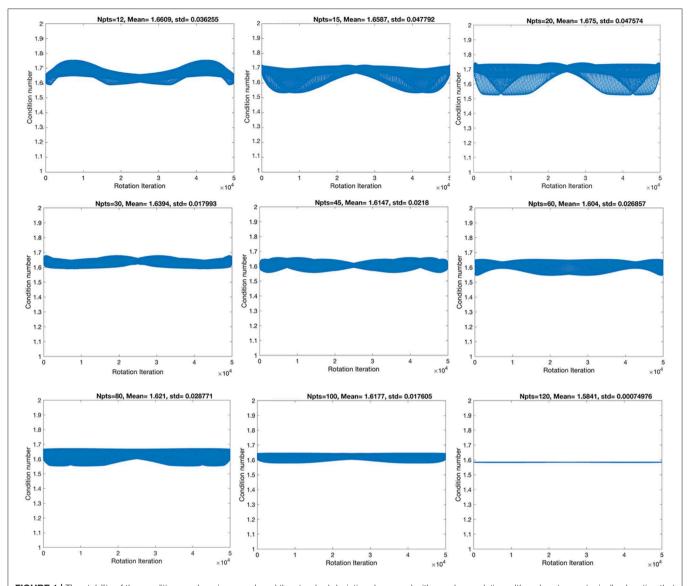


FIGURE 1 | The stability of the condition numbers increased, and the standard deviation decreased with angular resolution, although not monotonically, denoting that some sampling schemes are more robust to rotational variance, due to their geometrical symmetry properties.

TABLE 1 | The smallest mean condition numbers (CN) ranked the 120-direction scheme as optimal, followed by the 60, then 45-direction schemes.

Angles	CN	CN (mean)	STD	STD (CN)/SQRT (Angles)	Rank CN (mean)	Rank STD
12	1.647	1.661	3.626E-02	1.047E-02	8	7
15	1.709	1.659	4.779E-02	1.234E-02	7	9
20	1.696	1.675	4.758E-02	1.064E-02	9	8
30	1.633	1.639	1.799E-02	3.285E-03	6	3
45	1.610	1.615	2.180E-02	3.250E-03	3	4
60	1.561	1.604	2.685E-02	3.467E-03	2	5
80	1.645	1.621	2.877E-02	3.217E-03	5	6
100	1.643	1.618	1.761E-02	1.761E-03	4	2
120	1.585	1.584	7.494E-04	6.841E-05	1	1

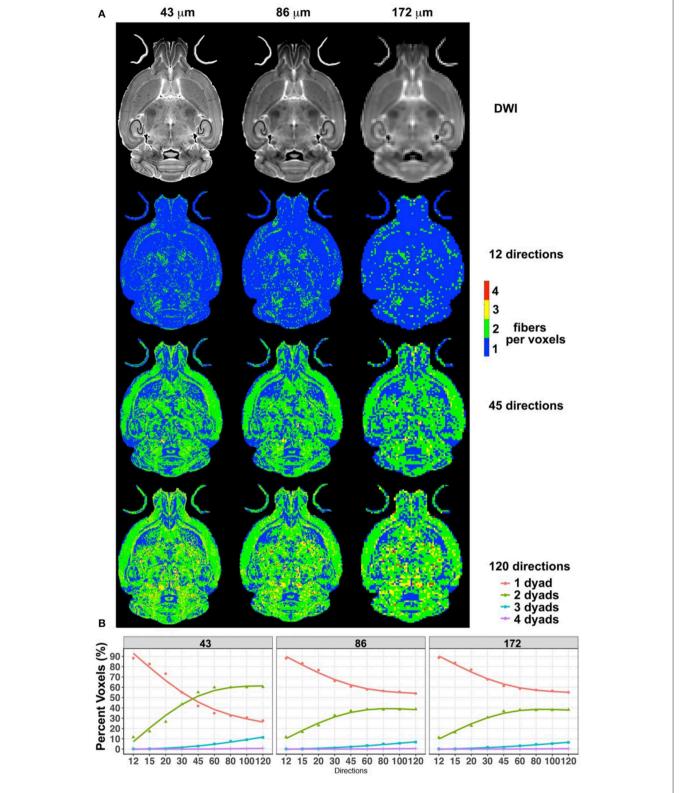


FIGURE 2 | The effect of spatial resolution (horizontal axis) and angular resolution (vertical axis) on the number of voxels with one, two, three, or four fibers (dyads) per voxels (A). (A) Effects for 12, 45, and 120 directions, chosen as examples for low-, medium-, and high-angular sampling. (B) Effects for sampling schemes between 12 and 120 at three spatial resolutions (43, 86, and 172 μm). These results illustrated the advantages of high-angular and spatial-resolution protocols in terms of sensitivity and stability.

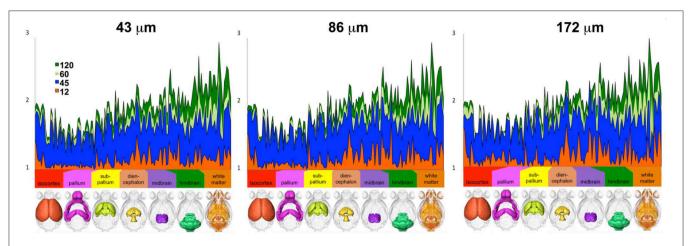


FIGURE 3 | The number of voxels with one, two, and three dyads varied per region, but differences relative to the reference protocol (high-spatial, high-angular resolution) consistently decreased with increasing number of angular directions (only 12, 45, 60, and 120 directions are shown for simplicity) and with increasing spatial resolution (i.e., smaller voxels; ranging from 43-μm linear dimension for the reference to 86 and 172 μm).

schemes and three spatial resolution levels). Node wise similarity was evaluated as in Blondel et al. [25]. Specifically, the similarity matrices were obtained as the limit of the normalized even iterates of $S_k + 1 = BS_kA^T + B^TS_kA$, where A and B are the two graph adjacency matrices, and S_0 is a matrix whose entries are equal to 1.

RESULTS

We have evaluated the effect of different angular diffusion sampling schemes and spatial resolutions on mouse brain connectivity, from the point of view of stability, with reference to a published data set, and with the aim to identify balanced acquisition schemes in terms of cost and accuracy.

First, we have evaluated nine angular sampling schemes from the point of view of their stability, through their condition numbers, as well as their standard deviations (**Figure 1**). The condition numbers define the asymptotic worst-case relative change in output for a relative change in input.

The highest spatial and angular resolution scheme had the smallest condition numbers (1.58) and standard deviation (7.5 \times 10⁻⁴). The ranking in terms of condition number was followed by the 60- and 45-direction angular sampling schemes, while the standard deviation followed the ranking 100, 45, and 60 (**Table 1**).

We focused the rest of our analyses on the 45- and 60-direction schemes and compared the results against the reference 120-direction scheme, at three different spatial resolution levels throughout.

Downsampled diffusion data sets were used to estimate the total number of fibers per voxel in each set (**Figure 2**). The total fiber count increased from 7.4×10^6 for 12 directions to 1.07×10^7 for 45 and 1.13×10^7 for 60 directions and 1.23×10^7 for 120 directions. The steepest changes occurred below 45 directions.

Interestingly, while the number of voxels detected to have one fiber direction was dominant for small angular sampling schemes, this number was exceeded by the number of voxels identified to have two fiber directions, if the sampling schemes had more than 45 angular directions and at a spatial resolution of 43 μm. The number of voxels with one dyad reached 42% for 45 directions, and 35% for 60 directions. The number of voxels with two dyads increased with increasing angular sampling, reaching 55% for 45 directions and 60% for 60 directions. Thus, these two curves intersected, and the ratio of one- to two-dyad voxels changed after ~45 directions. However, the two curves did not intersect for the 86- and 172-µm spatial resolution scenarios. The number of voxels with one fiber direction plateaued at ~55%, and the number of voxels with two fiber directions at \sim 38% for 86- and 172-μm spatial resolutions, with modest increases between 45 and 60 angular samples, and <7% contribution from voxels with three directions. These two data sets had very similar behaviors in terms of the number of voxels with one or two dvads.

These effects were found to be region dependent, although we noted a consistent trend in the ratios between one, two, and three dyads across all three resolution samples (**Figure 3**).

We next focused our analysis on the fimbria and fornix because these tracts have been reported to be relevant in neurodegenerative conditions such as Alzheimer's disease. Our qualitative evaluation showed that tract density maps reconstructed from 12 directions did not capture the cortical-cortical connectivity with the same sensitivity as the 45-, 60-, or 120-direction schemes (**Figure 4**). While less striking, the loss of spatial resolution also resulted in a change in the anatomical definition for the projections, and loss of connectivity through smaller regions (e.g., alveus).

The connectivity of the left hippocampus (**Figure 5**) illustrated a striking similarity between the 120- and 60-directions schemes and loss of similarity for lower angular resolution schemes. In particular, cortical projections occupied

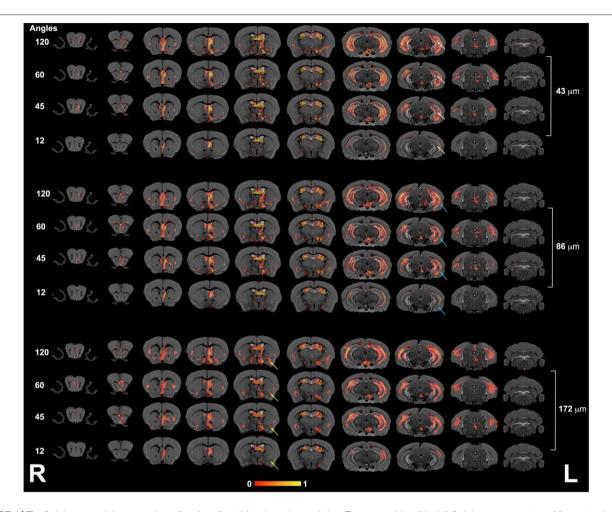


FIGURE 4 | The fimbria connectivity mapped as a function of spatial and angular resolution. The connectivity of the left fimbria was reconstructed for protocols with 12, 45, 60, and 120 directions, at the full 43- μ m resolution, clearly illustrating limitations of smaller angular sampling protocols at capturing projections though the hippocampus (white arrows) and amygdala (yellow arrows). Less clear were the effects of spatial resolution in the range 43–172 μ m where SNR and partial volume effects both played a role. However, the projections through the hippocampus covered reduced areas, and projections into the alveus were partially lost in the lower resolution protocol (blue arrows). L, left; R, right.

smaller areas, especially those requiring interhemispheric connections. The loss of spatial resolution resulted in some clusters appearing larger (e.g., in the amygdala), or conversely, some of the connections were lost (e.g., hindbrain, cerebellum).

We based our quantitative error analysis on the dyad dispersion for the first- (Figure 6A) and second-order dyads (Figure 6B). Our results showed that errors decayed as the number of angular samples increased both for white matter and for gray matter regions, and the errors increased as we relaxed the spatial resolution. This effect toward increased dispersion was particularly important for thin regions such as the fornix in dyad one (Figure 6A). An inflection point was noticed in particular for gray mater regions for 45 directions, and the curves tended to converge toward an asymptotic behavior starting with 60 directions. The dispersion values were larger for the second-order dyad (Figure 6B), but the trends were consistent with those observed for dyad one, with an asymptotic behavior

predominantly observed in gray matter regions for schemes with more than 60 directions.

Probabilistic tractography was used to generate connectivity matrices, based on the number of streamlines connecting selected regions that are likely to play a role in neurodegenerative disease models. In general, the connectivity differences between our reference and those of the 45- or 60-direction data sets were considerably smaller relative to those involving 12 directions (Figure 7). The sensitivity to capturing connectivity of smaller, and in particular, cortical gray matter regions was evident in the chord diagrams (Figure 7), which appeared sparser for 12 directions relative to 45, 60, and 120 directions. The sparsity was evident for gray matter-to-gray matter connections, in particular, for cortical domains. For small angular resolutions, the connectomes were dominated by wide bands involving myelinated white matter tract regions connecting to the hippocampus or septum. Gray matter-to-gray matter connections appeared more prominent with higher angular

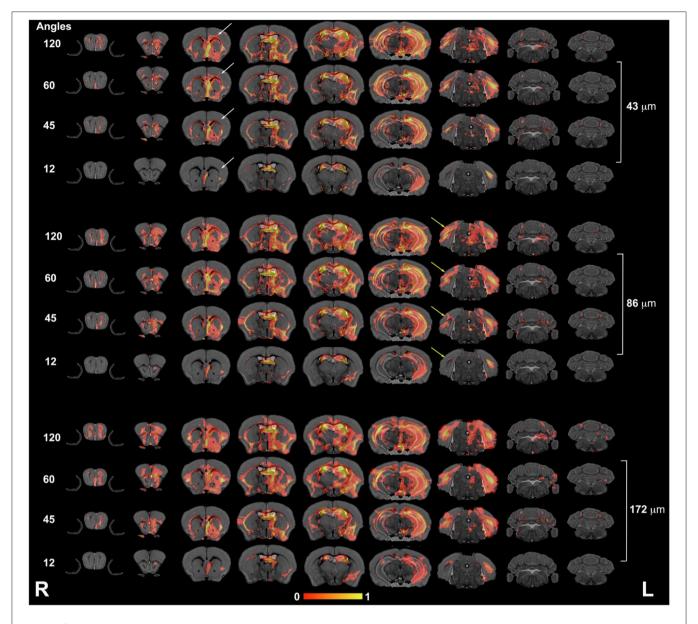


FIGURE 5 | The hippocampus connectivity mapped as a function of spatial and angular resolution. Hippocampal connectivity (the left hemisphere was seeded) was affected more by angular resolution, especially for cortical regions (white arrows), but also in the ability to retrieve cross hemispheric projections (yellow arrows). L, left; R, right.

sampling, in particular for schemes with more than 45 directions, with a noticeable qualitative similarity between 60 and 120 angles.

To quantify the similarity between connectomes, we used non-parametric correlation analysis. The Spearman correlation among the connectivity matrices was significant (p < 0.001) for all comparisons tested.

The highest global correlation overall was found among the 86- μ m spatial resolution connectomes acquired with 60 and 120 directions, 0.97, while the correlation between connectomes acquired at the same 86- μ m spatial resolution with 45 and 120 directions was 0.92. When compared against the reference high-spatial, high-angular resolution protocol (S1, A120), the highest

correlations were with (S2, A120) at 0.96, followed by (S1, A60) and (S2, A60) at 0.94, then (S4, A120) at 0.93 (**Figure 8,** left). When comparing the 45-direction protocols against the reference (high-spatial, high-angular resolution) protocol (S1, A120), the highest correlation was obtained with (S2, A45) at 0.91 followed by (S1, A45) at 0.90 (**Figure 8,** right).

In our experiments (S1, A120) was robust to downsampling, achieving a correlation of 0.96 with (S2, A120) and 0.93 with (S4, A120). The angular resolution had a strong effect, with the similarity dropping to 0.7 with (S1, A12), 0.9 with (S1, A45), and 0.94 with (S1, A60). The lowest similarity from our subgraph comparison was between (S2, A120) and (S2, A12) at 0.64,

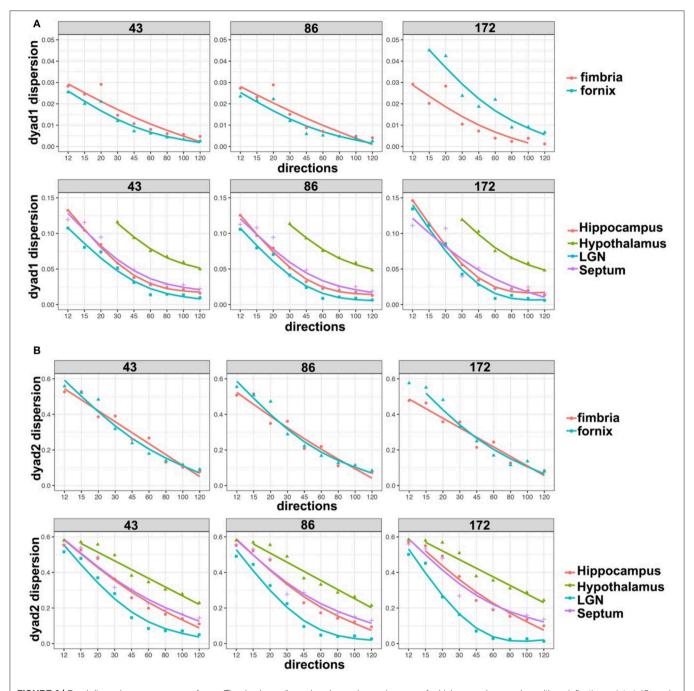


FIGURE 6 | Dyad dispersion as a measure of error. The dyad one dispersion shows decreasing errors for higher angular samples, with an inflection point at 45° and increasing stability after 60° (A). Similar errors were apparent for 43 and $86\,\mu\text{m}$, but the errors were larger for $172\,\mu\text{m}$. Dyad two showed a stronger effect of resolution, and larger errors, which also tapered off after more than 60 directions were acquired (B). LGN, lateral geniculate nucleus.

followed by (S2, A120) with (S1, A12) and (S2, A12) with (S4, A120) at 0.65. Our results suggest that higher-angular resolution schemes are generally more robust to detecting changes in animal models of neurological conditions.

Furthermore, we computed measures of similarity between individual graph vertices. The vertex-wise graph similarity pairwise for these subgraphs, shown in **Figure 9** after thresholding at a 0.1 level, illustrated differences in

sparsity. Graphs were less sparse as the numbers of angular samples/directions increased above 45 to 60 and 120 directions. Based on the vertex score, the robustness of some nodes relative to others became evident when undergoing downsampling, first for fimbria, followed by the fornix. The similarity between the hippocampus (Hc) and fimbria (fi) and fornix (fx) was 0.1 and 0.07. For the 45-direction scheme, the similarity between full resolution and 86-µm resolution for fimbria was 0.45, while for

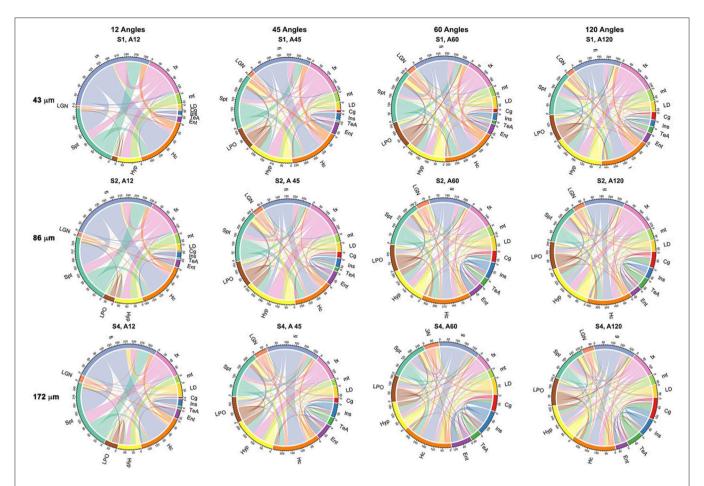


FIGURE 7 | Adjacency matrices shown as chord diagrams for a subset of 13 regions relevant to neurodegenerative diseases showed qualitatively greater similarity to the reference connectome of 120 directions (A120) for 45 (A45) and 60 directions (A60) when compared to the similarity between 120 (A120) and 12 directions (A12). Spatial resolution also had an effect on the chord diagrams, in particular, at the level four times downsampling (S4; 172 μ m), but this was less pronounced when comparing two times downsampling (S2; 86 μ m) with fully sampled (S1; 43 μ m) protocols. The chord diagrams showed that all protocols can capture the connectivity of the hippocampus (Hc) and its connecting fibers (fx, fornix; fi, fimbria), but shorter protocols have reduced sensitivity for smaller nuclei (LD, laterodorsal thalamic nuclei; LGN, lateral geniculate nuclei; LPO, lateral preoptic nucleus) and lack sensitivity required for cortical connectivity, e.g., for the cingulate (Cg) and entorhinal cortices (Ent).

the fx, it was 0.18, and for the hippocampus and septum, it was 0.16 indicating more robustness for larger regions. Hc with fi and fx was 0.21 and 0.11, respectively. The similarity for fi (0.27) and fx (0.24) decreased with downsampling spatial resolution for the 120-direction schemes; however, more regions picked up more similar connections across these two graphs. For example, the hippocampus score was 0.21, and for septum, 0.15, with Hc to fi and fx being 0.17 and 0.12, respectively. These results suggest that while major white matter tracts were robust with respect to changes in spatial and angular resolution, this needs to be balanced against the vulnerability of smaller white matter tracts and cortical domains to such changes, and sparsity of the connectome and graph similarity matrices are important factors to consider.

In conclusion, our results support that angular and spatial resolution need to be balanced with respect to time- and costimposed demands to enable population studies, and parameters for efficient protocols with minimum loss of sensitivity should

be recommended, suggesting that an acquisition with 60 angular samples provides a good compromise in terms of minimizing errors relative to a reference high-spatial, high-angular resolution protocol. Halving both spatial and angular resolutions yields an eight-time speed factor. When time is a constraint, compromises in terms of spatial resolution may need to be made. Importantly, more efficient acquisitions are amenable to future population studies.

DISCUSSION

Several studies using tractography-based connectomics have reported abnormal network organization associated with morphometric changes and AD pathologies [26, 27]. Still, to understand the etiology of human neurodegenerative diseases such as AD has proven difficult. This is due to AD's complex nature, multiple pathologies, and various associated comorbidities. In spite of their limitations and simplicity,

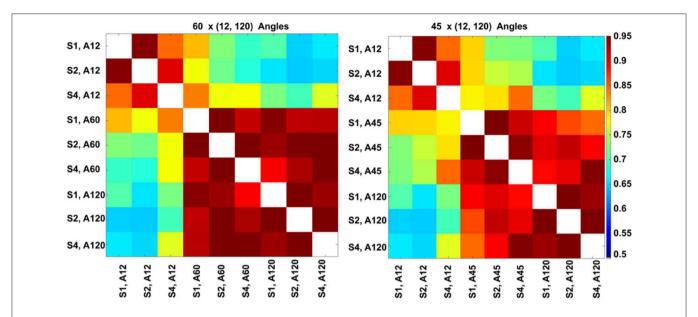


FIGURE 8 | Global connectome similarity. Spearman correlations among the connectomes obtained for three resolution levels (S1, fully sampled at 43-μm linear voxel dimension; S2, downsampled by a factor of 2–86 μm; S4, downsampled by a factor of 4–172 μm; and each of the 12, 45, 60, and 120 angular resolution schemes (A12, A45, A60, A120) indicated that the highest similarities were obtained between the 60 and 120 angular samples schemes for all spatial resolutions. While the patterns were similar, similarities were lower for the 45 and 120 angular sample schemes for all resolutions relative to 60- and 120-direction schemes. When comparing against the reference set, the median was 0.89 for sets with 45 directions, but 0.92 for sets with 60 directions; and the maximum for 45 directions was 0.91, but 0.94 for 60 directions. The global maximum 0.97 was obtained when comparing (S2, A60) vs. (S2, A120); or (S1, A45) vs. (S2, A45).

mouse models provide tools to examine the effect of singular pathologies, and the interaction of multiple factors in a well-controlled environment and, importantly, from early on.

Given the challenges in phenotyping mouse models of neurological conditions, imaging protocols are required to provide sensitive quantitative biomarkers with good spatial mapping abilities. In a previous study, we have defined a diffusion MRI data reference set with the highest reported resolution for the whole mouse brain [11]. This data set was acquired using 120 angular samples and 43-µm spatial resolution, requiring a scan time of 235 h. Replicating this acquisition for population studies is prohibitive in terms of both time and cost. To address this problem, we must define reduced protocols that ensure sufficient fidelity and compare well with the reference data set, but that can be acquired in a greatly reduced time. This will enable population studies and give insight into vulnerable networks that may provide early biomarkers and enable us to quantify disease progression or response to interventions. We, thus, performed a simulation study, examining subsets of angular samples from the reference set, and the effect of reducing spatial resolution.

We have focused on evaluating regions of interest in Alzheimer's research, from hippocampus, which represents 5% of the mouse brain volume, to fimbria and fornix, which represents only 0.05% of the mouse brain volume [13]. In our simulations, we have extracted nine gradient subsets to evaluate subsequent changes in several metrics. Our metrics evaluated the stability/noise of the diffusion schemes through the condition number; the relative number of detected voxels with one, two,

three, and four directions or dyads, globally and on a per-region basis; the extent of projections for the fimbria and hippocampus; the dyad dispersion and connectome similarity globally, and on a per-node basis. Our results corroborated to support that schemes with 45 angular samples started to approximate well the reference connectome and that errors were substantially reduced and started plateauing for 60 angular samples acquired with 43-or $86-\mu m$ spatial resolution.

The performance of the 60-direction protocols was very similar to the reference set, both qualitatively and quantitatively, and executing such protocols would lead to substantial reductions in acquisition time (eight times when combined with a downsampled spatial resolution), providing a connectome with 0.94 correlation with the reference set. Further reductions in acquisition times come from compressed sensing [28], which several groups have implemented for mouse MRI [29–31]. Such advances can help translate diffusion protocols into population studies [32] incorporating multiple biomarkers from morphometry [33], microstructural properties based on diffusion [13] or magnetic susceptibility [34], or network properties [35]. Such integrative studies may better predict changes in behaviors, modeling those observed in humans with neurodegenerative conditions [34].

Optimization studies are important when it comes to assess newly proposed diffusion models, acquisition schemes, various pathologies, and different animal models—to help understand the human brain [36, 37]. In this study, we were limited to a single specimen meta-analysis using extracted gradient subsets, but this approach provided useful information to help

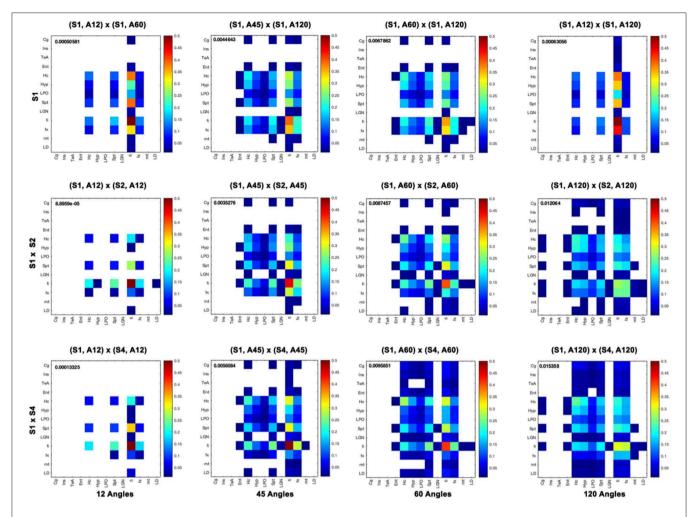


FIGURE 9 | Vertex-based graph similarity showed that white matter tracts were more robust to downsampling relative to nodes representing gray matter and, in particular, cortical domains. Our subgraph's regions of interest include the cingulate cortex (Cg), insular cortex (Ins), temporal association areas (TeA), entorhinal cortex (Ent), hippocampus (Hc), hypothalamus (Hyp), preoptic telencephalon (LPO), septum (Spt), lateral geniculate nucleus (LGN), fimbria (fi), fornix (fx), mamilothalamic tract (mt), and laterodorsal thalamic nuclei (LD). When comparing graphs for different spatial resolutions, the fi was most similar between 43- and 86-μm resolutions with a score of 0.85, and also relative to 172 μm with a score of 0.82, but most other graph nodes were not. Among angular sampling schemes, the fimbria was also robust, with a similarity score between the 12 and 120 directions of 0.5, followed by the fornix, hippocampus, and septum with 0.1. The cortical regions were most likely to be dissimilar when changing spatial or angular sampling schemes. Median similarity scores are shown for each graph comparison.

devise future group-based analyses. We have used the condition number for our acquisition schemes as a measure of noise performance [38], but better schemes may be designed in the future to increase rotational stability. Our recommendations are based on a finite set of metrics for a subgraph selected based on relevance to AD and a single b value acquisition. More regions would need to be included to generalize the recommendations; however, our results point to robustness of major white matter tracts, in contrast to thin, small white matter tracts and cortical–cortical connections, which are particularly vulnerable to reduced acquisition schemes. Moreover, future studies may be improved by the addition of multiple diffusion shells and more complex diffusion models. A reduction by a factor of eight in acquisition time for half the resolution and 60 directions provided an attractive avenue. However, the number

of voxels with more than one dyad could not be retrieved to the same extent at lower spatial resolution. Still the similarity of the subgraphs based on anatomical regions known to be involved in pathological aging approached 0.94. Our study benefitted from the use of high-performance computing, which enhances the speed of optimization and quality control studies required before establishing new protocols in both mice and humans [39].

Our methods are applicable to other DWI studies in rodent models, and we expect that the conclusions will remain valid in the same range of spatial resolutions and may change as we approach resolutions used in human brain imaging. Still, our results align with recommendations for human brain studies, where angular sampling schemes with more than 30 directions [40] are recommended for a robust estimation of the diffusion tensor orientations and mean diffusivity. More

than 45 directions are required for spherical deconvolution using spherical harmonics of order eight [41, 42]. Acquiring more than 45 directions helps with fitting and avoiding issues with imperfections in the uniformity of the diffusion gradient directions and meet signal-to-noise requirements. Therefore, 40 directions or more are widely used for the human brain [26, 27], and state of the art protocols employ multiple diffusion shells/b values, e.g., n=3, and with 60 directions per shell [43]. Harmonization efforts [44] are currently under way to establish diffusion imaging guidelines and/or translate among protocols, such as those used for ADNI3 [45].

While the field of mouse imaging is much smaller, and efforts for standardization are not yet widespread, we hope that our study can inform the design of future experiments using statistical connectomics in models of neurological conditions, such as Alzheimer's disease, and that network biomarkers will provide enhanced sensitivity to early and subtle changes arising due to multiple, interacting pathologies.

DATA AVAILABILITY STATEMENT

All datasets generated for this study are included in the article/supplementary material.

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AUTHOR CONTRIBUTIONS

RA, CL, GC, and AB designed simulation experiments and wrote code. SR and EC contributed code. GJ is the director of CIVM, oversees resources, and provided input in the initial phases of the project. RO'B contributed insight into the brain networks to be evaluated. RA, CL, and AB wrote the manuscript, which the other authors reviewed and edited.

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Impact of Attenuation Correction on Quantification Accuracy in Preclinical Whole-Body PET Images

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Background: Whole-body PET images can be obtained by using the "step-and-shoot" (SaS) method (using multiple bed positions) or continuous bed motion (CBM). As transmission scans are not always feasible, an alternative method where attenuation data can be generated via emission-based attenuation correction (AC) maps is of interest. The aim of this preclinical study was to investigate the influence of the acquisition method and AC on the quantitation accuracy of [¹⁸F]FDG-PET.

Methods: [¹⁸F]FDG-PET phantom images were acquired using either SaS or CBM. Transmission scans were recorded for the SaS method using a ⁵⁷Co-point source. Emission-based attenuation sinograms were obtained from the images after segmentation and inverse Fourier rebinning. PET images were reconstructed without AC, transmission based (TX-AC) and emission-based (EM-AC) attenuation correction. Moreover, [¹⁸F]FDG-PET scans of rats bearing mammary carcinomas acquired using either SaS or CBM were analyzed retrospectively and quantification in tissues was compared.

Results: Phantom recovery coefficients (R_C) varied greatly, ranging from 0.49 \pm 0.01 to 1.15 \pm 0.07, dependent on acquisition method, reconstruction algorithm and AC method. In CBM acquired images, EM-AC improved quantification accuracy when compared to no-AC images in the phantom studies (R_C 0.79 \pm 0.02 vs. 0.49 \pm 0.01, respectively) and in tumors of rats (DMBA model: 1.16 \pm 0.42 SUV vs. 0.86 \pm 0.28 SUV, respectively).

Conclusion: The method of AC has a strong influence on the quantification of [¹⁸F]FDG. Our data indicates that EM-AC improves quantification in images obtained by CBM and SaS. However, the obtained values were still underestimated when compared to TX-AC corrected images.

Keywords: positron emission tomography, attenuation correction, quantification, FDG, emission-based attenuation

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INTRODUCTION

Quantitative whole-body examinations are one of the key strengths of preclinical positron emission tomography (PET) and computed tomography (CT) systems. However, due to the restricted axial field of view (FOV) of several centimeters both in clinical and preclinical PET scanners, a whole-body scan in humans or larger animals such as rats or rabbits cannot be recorded in

one single scan acquisition. Therefore, for obtaining a whole-body scan, two different scanning methods are commonly applied.

In the first method, the "step-and-shoot" (SaS) method, several emission scans are recorded using multiple bed positions to cover the whole body [1]. For this, the subject is positioned on the bed, moved to the first bed position and coincidences are recorded for a predefined time (e.g., 10-15 min). Then the bed is moved to the next position and the procedure is repeated. Typically, the bed positions overlap each other for several cm in order to facilitate subsequent processing of the images. To correct for photon attenuation in the scanned subject, a separate attenuation correction (AC) scan is recorded for each single bed position in singles mode using either a transmission source such as ⁵⁷Co (TX-AC) or a CT-based attenuation map [2]. Finally, the reconstructed and TX-AC corrected images are stitched, and decay corrected using algorithms usually implemented in the scanner software. The advantage of this method is that it usually follows established laboratory procedures for emission scans as this type of scanning is routinely performed and it provides a higher slice sensitivity [3]. However, scanning time is increased for each scanned individual which significantly decreases the daily imaging throughput.

An alternative method to the SaS-method is the continuous bed motion (CBM) method. Here, the bed is continuously moved horizontally back and forth through the axial FOV between a specified start- and end-position and coincidences are recorded. The main advantage of this method is that it provides a more uniform sensitivity over the entire image and offers better image quality due to over sampling [4], which often aids in the identification of smaller tumors or affected lymph nodes. Preclinical PET systems have implemented CBM since 2009 [5, 6], whereas the clinical implementation just started more recently [7-10]. The main disadvantage of CBM in preclinical imaging is that it usually does not offer the possibility to perform a transmission scan required for AC. This is of special relevance for stand-alone preclinical PET scanners, which are not combined with a CT and can thus not use the CT image to generate a μ-map for attenuation correction. Consequently, the improved image quality provided by CBM comes at the cost of a decreased quantification accuracy. One way to overcome this issue is the generation of emission-based attenuation correction (EM-AC) factors or maps [11]. Here, image data is first segmented assuming a uniform attenuation in manually delineated regions and then forward projected to generate an attenuation sinogram, which is then used for attenuation correction during image reconstruction [12]. This method is relatively fast, easy to use and implemented in most preclinical PET systems. In addition, EM-AC eliminates the time required for an extra attenuation measurement, resulting in a significant reduction in overall scanning time.

In this study we compared No-AC, TX-AC, and EM-AC and their influence on image quantification by phantom measurements acquired using the SaS and CBM method. We furthermore investigated the biological relevance of our findings by performing a retrospective analysis of a dataset of [¹⁸F]FDG-PET scans in rats bearing chemically induced breast cancer

tumors. We first evaluated brain and liver uptake in whole-body scans of rats acquired using the SaS method and applied no-AC, TX-AC, or EM-AC during reconstruction of the images. Secondly, we assessed whole-body scans of rats acquired using the CBM method and compared the quantification in tumors in reconstructed images using either filtered back projection (FBP) or ordered subset expectation maximization (OSEM) with or without EM-AC.

METHODS

Phantom Study

A cylindrical hollow phantom made from polyethylene with a diameter of 7 cm, a length of 16.5 cm and a wall thickness of 0.2 cm was filled with 36.1 \pm 8.0 MBq aqueous [18 F]FDG solution and placed on the scanner bed of a preclinical PET scanner (micro PET Focus 220, Siemens Healthineers, Knoxville, TN, USA), which provides 7.6 cm axial and 22 cm transaxial FOV [13]. After moving the phantom to the center FOV, PET emission scans at 3 consecutive bed positions were acquired for 10 min/bed position with an energy window of 350-750 keV and a coincidence time window of 6 ns. The horizontal bed position was moved between the measurements in axial direction for ~6.6 cm to cover a total axial FOV of 20.8 cm. A horizontal overlap of 1 cm was applied to the images to facilitate further stitching of the images. Afterwards, a 10-min transmission scan using a rotating ⁵⁷Co point source (120–125 keV energy window) was recorded in singles mode for each bed position. CBM measurements were performed by placing the phantom on the scanner bed and a subsequent emission recording for a time of 20 min (350-750 keV energy window, 6 ns timing window). The phantom was moved through the field of view for four times back and forth (8 passes) to cover the same region of interest multiple times during data acquisition spanning an axial FOV of 27.1 cm.

Animal Studies

Chemicals

Radiosynthesis and quality control of [¹⁸F]FDG was performed using standard methods [14]. 1-Methyl-1-nitrosourea (MNU) and 1-methyl-1 nitrosourea (DMBA) were obtained by Sigma-Aldrich (Schnelldorf, Germany). For *in vivo* application, MNU was dissolved in sterile saline solution and acidified to pH 5.0 with acetic acid. DMBA was dissolved in sesame oil.

Research Animals and Tumor Induction

Female 5–6 weeks old Sprague-Dawley rats (Crl:CD, Charles River, Sulzfeld, Germany) were initially used in the study. Animals were housed in groups in a temperature and humidity-controlled facility on a 12 h light/ dark cycle and fed a standard laboratory diet. Food and water were available *ad libitum* and animals were weighed weekly during the experiment. Tumors were generated following published procedures by the administration of the carcinogens MNU [15, 16] or DMBA as follows [17, 18]. MNU was injected intraperitoneally at a dose of 50 mg/kg and a volume of 5 mL/kg body weight (n = 12). If animals did not exhibit tumors within 3 weeks, MNU injection was repeated on day 29 and day 57 after initiation of

the study. DMBA was administered by oral gavage at a dose of 20 mg/kg (n=8) or 50 mg/kg BW (n=12) at a volume of 5 mL/kg. Animals were observed regularly to determine the development and localization of tumors. All experiments involving laboratory animals were approved by the respective authorities and the study procedures were in full accordance with the European Communities Council Directive of September 22, 2010 (2010/63/EU). All procedures were in compliance with the institutional biosecurity and radiation safety regulations.

PET Imaging Procedure

At the time point of PET imaging, mean body weight of rats were 236 \pm 33 g. The following standardized imaging setup was applied for all [18F]FDG scans [19-21]. In brief, rats were deprived of food for $18 \pm 4 \,\mathrm{h}$ prior [18F]FDG administration. Rats had access to drinking water at all times. Body warming was achieved by placing the entire cage on a heating pad kept at 38°C. Warming was initiated ∼30 min before tracer injection and continued throughout the uptake and image acquisition period. Rats were pre-anesthetized by inhalation anesthesia (1-4% isoflurane in oxygen) in an induction box. Subsequently, 0.1 mL containing 30.0 \pm 12.5 MBq [18 F]FDG solution diluted with saline was administered intravenously via tail vein injection under isoflurane anesthesia. Rats were kept anesthetized throughout the whole uptake and imaging period and the isoflurane concentration level was adjusted to obtain a breathing rate of 20–60 breath/min during the PET acquisition, indicating a comparable level of anesthesia.

PET emission data with an energy window of 350–750 keV and a coincidence time window of 6 ns were acquired at 1 h after [18 F]FDG injection into rats (n=9) using the SaS method for 10 min/bed position with three bed positions to cover the whole body of the animal. The bed was moved from one position to the next by 6.6 cm covering in total an axial FOV of 20.8 cm. Overlap in the resulting images between the positions was 1 cm. Before the emission scan, an attenuation measurement was done with the rotating 57 Co point source for 10 min at each position. Total scan time per animal was 60 min.

In a second cohort of rats (n=20) a 20 min scan (350–750 keV energy window, 6 ns timing window) was acquired at 1 h after [18 F]FDG injection using the CBM tool to cover the whole body of the rats. Thereby, the bed was slowly moved through the FOV for four times back and forth (8 passes) covering an axial FOV of 27.1 cm.

Image Data Generation and Analysis

As the rat images were analyzed retrospectively, some of the original raw data (list mode files and sinograms) were no longer available. Thus, all emission sinograms used for comparing different AC methods were generated by inverse Fourier rebinning from the available image files, which were originally reconstructed using Fourier rebinning (FORE) followed by filtered back projection (FBP), using the forward projection tool implemented in the image analysis software ASIPro VM 6.0 (Siemens Healthineers). To be consistent, we applied the same procedure to the acquired phantom images. The thus generated emission sinograms were further used for image

reconstruction as described below. To validate this approach, we also compared image files reconstructed from the generated emission sinograms with image files from the original emission sinograms (when available).

The generated emission sinograms were reconstructed using FORE followed by FBP algorithm with ramp filter or OSEM at an image zoom of 3.163 and an image matrix of $128 \times 128 \times 95$ (SaS) or $128 \times 128 \times 351$ (CBM) resulting in a voxel size of $0.6 \times 0.6 \times 0.796$ mm³. The standard data correction protocol (normalization, decay correction, and injection decay correction) was applied to the data. Scatter correction was not applied to the emission data as the used reconstruction software does not permit scatter correction of non-AC data to allow for a comparable ratio between the AC and non-AC corrected images.

For calculation of the EM-AC file, the emission calibration and segmentation tool implemented in ASIPro VM 6.0 was used. PET emission images were segmented to obtain the outer border of the phantom or the rat. The area inside the segmented phantom or rat was assumed to be water and assigned an attenuation coefficient of 0.095 cm⁻¹ (511 keV), the area outside was assumed to be background and assigned an attenuation coefficient of 0 cm⁻¹. After segmentation was completed, a 2D sinogram was projected and inverse Fourier rebinning with a span of 47 and a ring difference of 23 was performed. The obtained sinogram was defined as emission-based sinogram (EM-AC sinogram) for attenuation correction. The flow chart of the processed image data, calculated sinograms and reconstructed image files is depicted in Figure 1. Images were reconstructed without (No-AC), with transmission-based (TX-AC) and with emissionbased (EM-AC) attenuation correction. Images obtained with the SaS technique were stitched together using the stitching tool implemented in ASIPro VM 6.0.

A calibration factor for converting units of PET images into absolute radioactivity concentration units was generated by imaging a phantom filled with a known concentration of [¹⁸F]FDG at identical measurements parameters and reconstructed using FBP including TX-AC. The activity concentration in the phantom was calculated from the activity measured in a dose calibrator (CRC-25R, Capintec Pittsburgh, PA, USA) and the fill volume of the phantom.

Three cylindrical volumes of interest (VOI) with a diameter of 55 mm and 10 mm height were outlined on multiple planes of the PET images from the phantom study using the image analysis software Amide [22]. For evaluation of the effects of different AC methods the recovery coefficients (R_C) as the ratio of measured activity concentration to known activity concentration for each AC method were calculated with the following equations:

$$R_C = \frac{C_T}{C_{known}}$$

where C_T is the radioactivity concentration derived from the target VOI in kBq/cc in the uncorrected image (No-AC), TX-AC, and the EM-AC corrected image, respectively. C_{known} is the known radioactivity concentration calculated from the administered radioactivity (kBq) measured in a dose calibrator

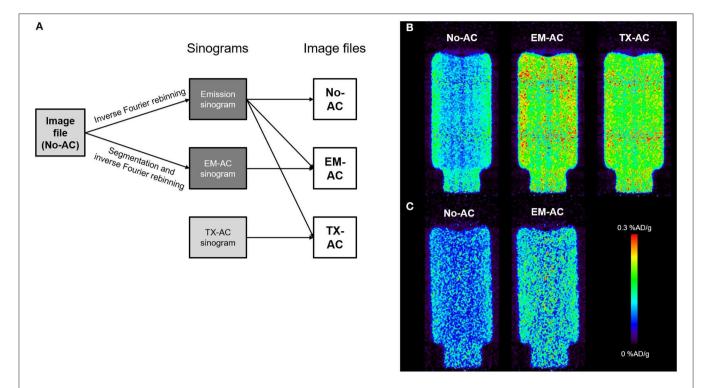


FIGURE 1 | (A) Flow chart of the steps involved in the emission-based (EM-AC) and transmission-based (TX-AC) attenuation correction in the current study. Data files in light gray are original data (images or sinograms), data files in dark gray were calculated from the image files and final image files reconstructed using the 3 different AC methods (No-AC, EM-AC and TX-AC). (B) Phantom FDG-PET images acquired using the SaS method with 3 bed positions and C) phantom FDG-PET images acquired using the CBM method. The applied AC method is indicated in the images and PET images are displayed in percent applied dose per gram (%AD/g).

and the fill volume of the phantom (mL) under the assumption of a density of water of 1 $g*mL^{-1}$.

In the animal studies, predefined ellipsoidal or spherical VOIs were applied for whole brain (12 \times 20 \times 8 mm³) and liver (10 mm diameter) whereas the tumor was manually delineated on multiple planes of the PET images. The derived [$^{18}\text{F}]\text{FDG}$ concentration values were calculated from the mean and max value of the VOI and quantified in terms of standardized uptake value (SUV $_{\text{mean}}$ and SUV $_{\text{max}}$) using the following equation:

$$SUV = \frac{C_T}{D_{Inj}} \times W_S$$

where C_T is the mean or maximum radioactivity concentration in the target VOI in kBq/cc, D_{Inj} the administered dose in kBq and W_S the body weight of the animal in gram.

For comparing the effect of the different AC methods on tumor quantification, individual tumor values are derived either from one animal with one or multiple tumors or from animals, which were scanned multiple times.

Statistics

All values are given as mean values (\pm standard deviation). The obtained AC-corrected values were compared to No-AC corrected values using a paired t-test in GraphPad Prism 8.3.0.; p < 0.05 was considered statistically significant.

RESULTS

As not all emission sinograms were available at the time of analysis, the emission sinograms used for all AC techniques (phantom and rats, No-AC, EM-AC, and TX-AC) were generated from the original images by applying inverse Fourier rebinning. In order to validate this approach images reconstructed from the generated sinograms were compared to images reconstructed from the original sinograms (phantom and rat SaS). Quantitative analysis of phantom images based on the generated or original sinograms were in good agreement (SUV $_{\rm mean}$ < 1%). In rats, similar differences of liver and brain activity (SUV $_{\rm mean}$ < 1%) between images based on the generated or original sinogram were observed. In contrast, maximum activity concentration (SUV $_{\rm max}$) were significantly lower using the inverse Fourier rebinning approach compared to the original sinograms on both, phantom and rat images.

The recovery coefficients (R_C) calculated from the set of reconstructed images, applying No-AC, TX-AC or EM-AC of the cylindrical phantom filled with [¹⁸F]FDG solution scanned with the SaS method and CBM are summarized in **Table 1**. Moreover, phantom images acquired using the SaS and the CBM method and reconstructed using No-AC, EM-AC, and TX-AC (only SaS method) are shown in **Figures 1B,C**. As shown in the phantom images, axial image uniformity is superior in the phantom images acquired using CBM as compared to phantom images acquired using SaS. In the later, the overlapping bed position are clearly

TABLE 1 | Recovery coefficients (R_C) for mean radioactivity concentrations of the phantom studies which were acquired either with the SaS method or continuous bed motion (CBM) and the images reconstructed using different method of attenuation correction (AC).

		SaS	СВМ
FBP		R _C	R _C
	No-AC	0.63 ± 0.01	0.49 ± 0.01
	TX-AC	1.02 ± 0.08	n.a.
	EM-AC	1.15 ± 0.07	0.79 ± 0.02
OSEM		R _C	R _C
	No-AC	0.63 ± 0.01	0.50 ± 0.01
	TX-AC	1.07 ± 0.01	n.a.
	EM-AC	1.15 ± 0.07	0.80 ± 0.02

For calculation of the R_C please refer to the materials and method section. n.a., not assessed.

visible in the images. Applying no attenuation correction during image reconstruction leads to an underestimation of mean radioactivity concentrations in the investigated VOI of 50 or 37% in CBM and SaS acquired emission scans, independent from the applied image reconstruction algorithm (FBP or OSEM). Implementing transmission-based attenuation correction (TX-AC) to the identical images acquired in SaS mode increased the quantification accuracy as assessed by the R_C value to 1.02 \pm 0.08 and 1.07 \pm 0.01 for FBP and OSEM reconstructed images, respectively. Emission-based AC showed comparable improvements in quantification accuracy in SAS acquired images (R_C of 1.15 \pm 0.07 and 1.15 \pm 0.07) for FBP and OSEM. In phantom images acquired with CBM, EM-AC increased the quantification accuracy in FBP (R_C of 0.79 \pm 0.02) and OSEM (R_C of 0.80 ± 0.02) reconstructed images compared to No-AC images.

The results from the retrospective analysis using No-AC, EMAC, or TX-AC for quantification of brain and liver [18 F]FDG uptake in rat images acquired with the SaS method (n=9) are shown in **Figures 2A,B**. Rat FDG images are shown in **Figure 2C**. Mean brain uptake (SUV $_{\rm mean}$) was increased by 40% (p < 0.0001) and 18% (p < 0.0001) when applying the TX-AC and EM-AC method, respectively, compared to No-AC (**Figure 2A**). In the liver VOI the effect of AC was even more pronounced with increases of 60% (p < 0.0001) and 32% (p = 0.008) in mean liver uptake (SUV $_{\rm mean}$) values after TX-AC and EM-AC, respectively (**Figure 2B**). Overall in both analyzed VOIs, [18 F]FDG uptake values (SUV $_{\rm mean}$) were significantly lower in the EM-AC images as compared to the TX-AC images.

Whole-body rat images acquired using the CBM method are shown in **Figure 3B**. The obtained uptake values in tumors, calculated from whole-body rat images acquired using CBM and reconstructed using either No-AC or EM-AC are shown in **Figure 3A**. In parallel to the phantom study, EM-AC generally increased the mean uptake values irrespective of the image reconstruction algorithm used. For example, [18 F]FDG SUV $_{\rm mean}$ tumor uptake values in FBP reconstructed images were increased by 33 \pm 10% (p=0.0034) in the DMBA group (n=14)

and by $36 \pm 8\%$ (p = 0.001) in the MNU group (n = 6) after EM-AC. When performing OSEM reconstruction, EM-AC led to an increase in SUV_{mean} tumor uptake values by 68% (p < 0.0001) and 78% (p = 0.001) in the DMBA and MNU group, respectively. Interestingly, EM-AC had an effect in the same order of magnitude on the SUV_{max} tumor values (\sim 38% increase) when using FBP reconstruction, whereas in the OSEM reconstructed images, SUV_{max} tumor values exhibited an increase of \sim 100% after applying EM-AC.

DISCUSSION

In contrast to human PET studies, where the CBM acquisition method was just recently introduced and is now used for diagnostic [18F]FDG-PET [9, 23], this method is rarely applied in preclinical whole-body imaging. The main reason for this is that in preclinical imaging either the transaxial FOV of the preclinical PET scanner is large enough for a whole-body scan of the scanned subject (e.g., mouse), the exact imaging region is known to the examiner (e.g., in subcutaneous tumor studies) or the quantitative properties of PET imaging are prioritized over data on whole-body distribution, which might be the case in imaging of larger animals such as rats or rabbits. However, CBM offers the opportunity to increase image throughput, as the total measurement time required for a CBM acquisition is significantly lower than the cumulative effort for emission and transmission acquisitions at multiple bed positions. Compared to SaS, imaging time in CBM could be reduced by a factor of two, therefore doubling the putative imaging output per day which consequently effects the study statistics and allows for higher group numbers—factors that are of high importance in oncology studies. Additionally, the anesthesia duration for the scanned subjects can be shortened in CBM, which decreases the overall burden for the laboratory animals under investigation, again an important factor in oncology studies where repeated measurements over study days (e.g., therapy monitoring studies) are required. Moreover, it has been reported and demonstrated in the phantom study that CBM offers the advantage of a more uniform sensitivity over the entire image and therefore results in a better image quality when compared to SaSacquired images.

In this study we investigated alternative approaches for AC to achieve accurate estimates of radiotracer concentration in different regions of interest in images acquired with CBM. Initially, phantom studies using a rat-sized hollow cylinder filled with a known activity concentration of [18F]FDG in aqueous solution were performed. PET emission images were recorded using both acquisition methods, SaS and CBM, and corresponding transmission scans were performed for the SaS images. Furthermore, the originally FBP-reconstructed images were segmented, and attenuation coefficients were manually assigned to the corresponding parts of the image which was subsequently inverse Fourier rebinned into an emission-based attenuation sinogram. This EM-AC sinogram was then used for AC in the reconstruction of the phantom images using FBP and OSEM algorithm.

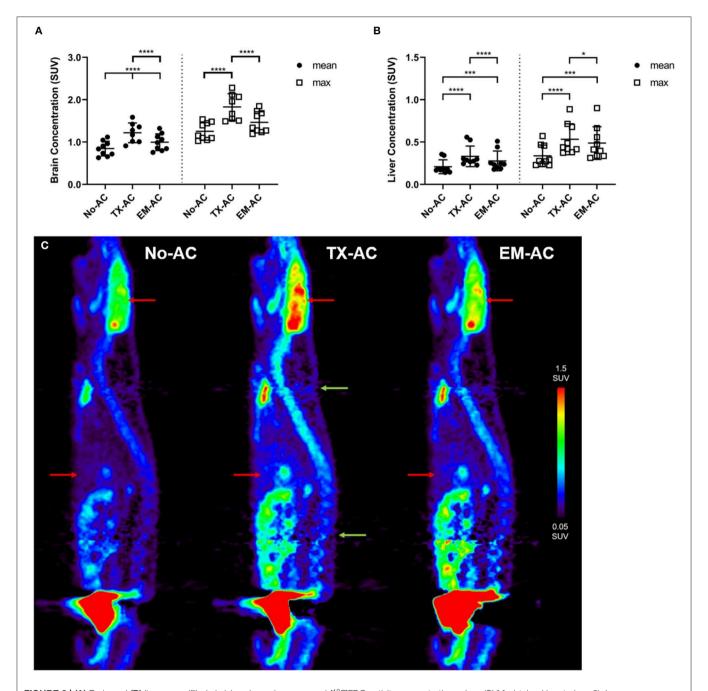


FIGURE 2 | (A) Brain and **(B)** liver mean (filled circle) and max (open square) [18 FJFDG activity concentration values (SUV) obtained in rats (n=9). Images were recorded using the SaS method and reconstructed with FBP without (No-AC), with transmission-based (TX-AC) and with emission-based (EM-AC) attenuation correction ($^*p < 0.05$, $^{***}p < 0.001$, $^{***}p < 0.001$). **(C)** Sagittal rat FDG-PET images acquired using the SaS method and reconstructed with FBP. Brain and liver are indicated with red arrows and overlapping bed positions are indicated with green arrows.

During data search for "real" rat imaging data to compare phantom data with, it was recognized that not all original raw data were still available for retrospective analysis. Therefore, the possibility to generate emission sinograms out of the original image files by inverse Fourier rebinning was investigated, initially in the phantom dataset, as well as subsequently in the rat images. Comparison of the quantification result of the inverse

Fourier rebinned sinograms (and further reconstructed images) with the original image files showed an excellent agreement. Consequently, the generation of the emission sinograms out of the image files can be a feasible approach if the original listmode or sinogram raw data is missing and images need to be reconstructed with a different reconstruction algorithm or parameters.

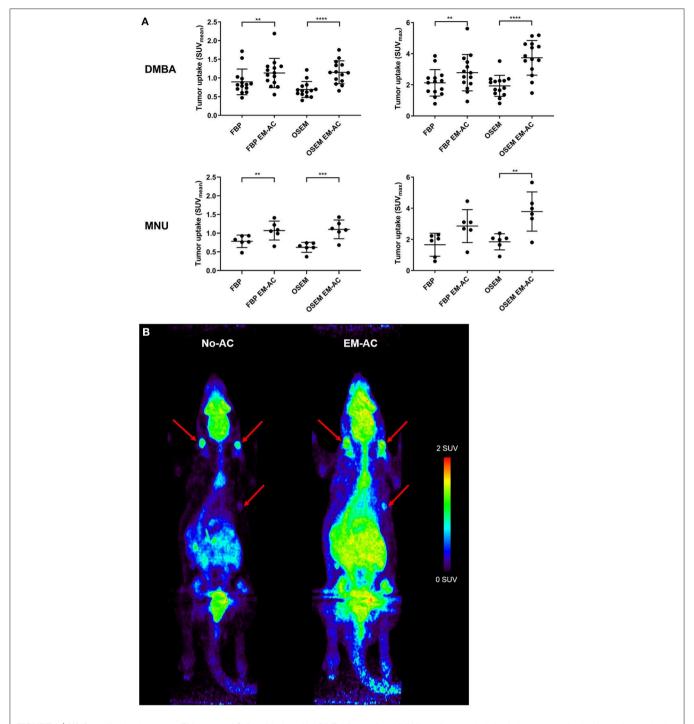


FIGURE 3 | **(A)** Quantification in tumors (SUV_{mean} and SUV_{max}) induced by DMBA (n = 14) or MNU (n = 6) in rat whole body images acquired with continuous bed motion (CBM). Images were reconstructed using FBP or OSEM without attenuation correction and with emission-based attenuation correction (EM-AC) (**p < 0.01, ****p < 0.001, ****p < 0.0001). **(B)** Maximum intensity projection of a whole-body PET image showing [n = 18]FDG distribution in a tumor bearing rat (MNU) acquired with CBM without AC (left side) and with EM-AC (right side). Tumors are indicated with red arrows. Images were reconstructed with OSEM.

Quantitative evaluation of the phantom data and comparison of the derived concentration values to the expected values revealed the influence of the acquisition mode (SAS vs. CBM) and attenuation correction on those data. Applying no

attenuation correction to the phantom data showed a reduction in quantitative accuracy by -37% in SaS acquired images reconstructed using FBP or OSEM. These values are quite in line with literature data where it was reported that the

accuracy of the activity concentration is reduced by -38% in the uncorrected vs. the attenuation corrected image [24]. Moreover, a simulation study using the Moby phantom with increasing diameters from 2.1 cm to 6.4 cm also showed a 30-40% error in soft tissue quantification starting from 4.7 cm diameter, which is roughly the diameter of a rat [25]. The reduction was even more pronounced in the phantom CBM data, were a decrease of -50% in quantitation accuracy was observed. Applying TX-AC to SaS acquired data increased quantification accuracy to acceptable levels of <10% for all reconstruction algorithms. Interestingly, EM-AC overestimated the activity concentration by 15% in SaS acquired images. However, the such derived values are well within the tolerance range for PET measurements keeping in mind that especially FDG-PET scans in rodents are heavily influenced by animal handling of up to a factor of 2 as shown in a recent study [21]. In CBM data, EM-AC greatly improved image quantitation for both reconstruction algorithms, even though these values are still below the expected concentrations or compared to TX-AC data.

As a next step, the effect of transmission-based (TX-AC) vs. emission-based (EM-AC) attenuation correction in SaS acquisitions of whole-body rat PET images were assessed. In brain and liver VOIs the activity concentration without AC and with TX-AC reflected the results of the phantom studies as such, that mean brain and liver [18F]FDG uptake values were increased by 40 and 60%, respectively, after applying TX-AC. Application of EM-AC to the same data increased the SUV_{mean} in brain and liver by 18 and 32%, respectively. This is in contrast to the phantom study were both AC methods achieved a comparable result in terms of quantification accuracy. A possible explanation for this observation might be an incorrect segmentation. As the skull itself was not visible in the FDG rat images, it was not feasible to include bone material into the segmented images and thus leading to an underestimation of brain FDG uptake. A previous study suggests a careful evaluation of EM-AC in applications where a uniform structure cannot be assumed [26].

When using CBM for tumor-bearing rats this study found that the [18F]FDG uptake after EM-AC was increased with respect to uncorrected images by 34% in the tumors VOI's. Similar results were also obtained by other groups in subcutaneous tumor mouse models [27], where they reported an attenuation recovery of \sim 13% in tumors. This value is slightly lower as the results from this study, but as mice were used in contrast to rats, a lower attenuation recovery might be expected. D'Ambrosio et al. [28] compared two attenuation correction methods based on CT and segmentation of emission images in phantom, mice and rat images. In line with this study, it was reported that EM-AC leads to lower uptake values (lower ROI counts) as compared to TX-AC. For example, differences between the EM-AC and CT-AC method of <9% for the myocardium and left ventricle VOI in rats were reported. This difference is much lower as the difference found in the liver and brain VOI in this study (\sim 17%). However, this might be due to the different position of the VOI inside the body and the attenuation effect of the surrounding tissue.

However, even with this underestimation in [¹⁸F]FDG organ and tumor uptake, EM-AC did improve tumor identification and tumor delineation in CBM acquired images. Especially small tumors with lower [¹⁸F]FDG uptake can be easily overlooked without AC (see **Figure 3B**). This is of special relevance in chemically induced tumor models, where tumors can develop spontaneously, and the exact tumor locations are unknown. More importantly, the EM-AC method could be an important alternative in preclinical PET/MR scanners where no attenuation correction is available.

CONCLUSION

Attenuation correction had a strong influence on the quantification accuracy of PET images. The present study revealed, that EM-AC can improve quantitative accuracy in PET scans acquired with continuous bed motion. Moreover, tumor identification and tumor delineation in the final images especially for small tumors could be improved by EM-AC in CBM and SaS acquired images even if the obtained values were still underestimated as compared to TX-AC reconstructed images.

DATA AVAILABILITY STATEMENT

The datasets generated for this study are available on request to the corresponding author.

ETHICS STATEMENT

All applicable institutional and/or national guidelines for the care and use of laboratory animals were followed and the study was reviewed and approved by the responsible national authorities (Amt der Niederösterreichischen Landesregierung).

AUTHOR CONTRIBUTIONS

TW initiated and designed the study, coordinated, and participated in the experiments. LS performed data reconstructions and image data analysis. TF was responsible for preparing the animal model. SM and MS performed the microPET measurements. TW, MB, and CK summarized the data and drafted the manuscript. All authors read and approved the final manuscript.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Preclinical Ultrasound Imaging—A Review of Techniques and Imaging Applications

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Ultrasound imaging is a well-established clinical imaging technique providing real-time, quantitative anatomical and physiological information in humans. The lack of ionizing radiation and relative low purchase and maintenance costs results in it being one of the most frequently used clinical imaging techniques with increasing use for guiding interventional clinical procedures. Until 20 years ago, translation of clinical ultrasound practices to preclinical applications proved a significant technological challenge due to the smaller size (25 g vs. 70 kg) and rapid conscious heart-rate (500-700 bpm vs. 60 bpm) of the mouse requiring an increase in both spatial and temporal resolution of 10-20-fold in order to achieve diagnostic information comparable to that achieved clinically. Since 2000 [1], these technological challenges have been overcome and commercial high frequency ultrasound scanners have enabled longitudinal studies of disease progression in small animal models to be undertaken. Adult, neonatal and embryonic rats, mice and zebrafish can now be scanned with resolutions down to 30 microns and with sufficient temporal resolution to enable cardiac abnormalities in all these species to be identified. In mice and rats, quantification of blood flow in cardiac chambers, renal, liver and uterine vessels, and intra-mural tissue movements can be obtained using the Doppler technique. Ultrasonic contrast microbubbles used routinely for clinical applications are now being further developed to include targeting mechanisms and drug-loading capabilities and the results in animal models bode well for translation for targeted drug delivery in humans.

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INTRODUCTION

Although ultrasound has been used extensively since its development to study preclinical animal models much of the early work in this field was undertaken using transducers designed for ultrasound scanning of clinical small-parts or intra-operative imaging and operating in the frequency range between 10 and 20 MHz. Such frequencies enable images with spatial resolutions of the order of hundreds of microns to be acquired thus limiting their effectiveness in detecting abnormalities in smaller preclinical models. Additionally, clinical scanners designed to image the human heart with 60–100 beats per minute (bpm) had insufficient temporal resolution to image the rapid heart movement of preclinical models (400–600 bpm). The technological challenges of designing and manufacturing a commercial ultrasound scanner capable of resolving structures smaller than 100 microns and with sufficient temporal resolution to resolve cardiac motion within a mouse heart was overcome with

the launch of the first commercially available preclinical ultrasound scanner in year 2000. Since then there has been a meteoric rise in the number of biology research publications using preclinical ultrasound imaging to assess adult, neonatal and embyronic rats, mice, and zebrafish with spatial resolutions approaching 30 micron and with frame-rates of up to 350 Hz achievable when imaging adult murine hearts enabling cardiac abnormalities to be identified. In addition, blood flow within cardiac chambers, renal, liver and uterine vessels can be measured in real-time using the Doppler function on the scanners and elastic properties of tissues can be measured using elastography techniques. New and exciting applications using ultrasonic contrast microbubbles designed to target specific biological markers and with drug-loading capabilities are being developed and tested in animal models. Technological advances in transducer manufacture has resulted in linear array transducers now replacing the first generation of mechanically-driven singleelement transducers.

In this manuscript we will review the different imaging modes available on preclinical ultrasound scanners and highlight their utility for imaging of preclinical models. For clarity, the words preclinical animal model are used to describe small noncompanion animals for which the genetic footprint can be modified and refers predominantly to mice, rats and zebrafish. All images and experiments described were performed under a UK Home Office Licence following ethical review by the University of Edinburgh.

TECHNIQUES OF ULTRASOUND IMAGING

Ultrasound waves are emitted from an ultrasound transducer. The choice of frequency of the transducer is important as higher frequencies give increased spatial resolution (i.e., smaller objects can be resolved) but the depth over which useful information can be obtained is reduced. For preclinical imaging, frequencies between 20 and 55 MHz are generally used with 15-20 MHz (image depth 3-4 cm) being used for adult rats, 30-40 MHz (image depth 10-20 mm) for adult mice and higher frequencies (up to 50 MHz, image depth 9 mm) used for neonatal mouse studies and embryonic and adult zebrafish imaging. When the transducer is coupled to the surface of the body using warmed ultrasound coupling gel, ultrasound images can be acquired in real-time. Ultrasound images are essentially two-dimensional (2D) cross-sectional slices through the body with the portion of anatomy closest to the transducer (generally the skin) displayed at the top of the screen and organs more distal displayed at depth. The depth at which organs are displayed on the screen is determined by the length of time the emitted ultrasound beam takes to return to the surface of transducer assuming a standard speed of sound in soft tissue of 1,540 ms⁻¹ and assuming no multiple scattering has taken place. Unlike clinical ultrasound imaging in which scans are undertaken with the sonographer moving the transducer in real-time over the skin surface, for preclinical ultrasound scanning, the transducer is mounted in a probe-holder with 3D versatile movement enabling the probe to be oriented to any desired angle whilst avoiding small, but at high resolution, significant human movement compromising the quality of image acquisition. For almost all ultrasound imaging of preclinical models, the models are anesthetized prior to ultrasound scanning. With rats and mice, prior to ultrasound scanning, thick animal hair can be removed using electric hair clippers followed by the application of a depilatory cream to the scanning area. The use of the cream ensures that air bubbles are not trapped under any remaining hair stubble. Once the hair is removed, warmed coupling gel is placed on the body of the animal. Meanwhile, the temperature of the animal is recorded continuously especially in experiments where large amounts of the mouse hair has been removed. The probe is then lowered into the coupling gel. Due to the small size of preclinical models and their physical fragility, when scanning most organs, the ultrasound transducer does not touch the animal but scans through a thin layer of gel between the transducer head and the animal skin.

2D B-Mode Imaging

B-mode imaging or brightness-mode is the most commonly used mode in ultrasound imaging. In B-mode imaging 2D cross-sectional images of the animal are displayed in real-time on the screen. Images are acquired in transmit-receive mode where the transducer emits an ultrasound pulse, then pauses to receive signals back at the transducer which have been reflected and scattered from organ boundaries and parenchyma. This received signal is rapidly processed to form the gray-scale image displayed on the screen with highly reflective structures such as organ boundaries giving brighter (whiter) echoes and structures which scatter less ultrasound (e.g., blood) being darker. The focal position (highlighted as a yellow arrow in Figure 1) is the depth of optimal spatial resolution within the image. Using array probes, multiple focal zones can be selected but this will have a detrimental effect on the maximum frame-rate obtained. This may not be important for the more static abdominal organs but for cardiac imaging generally only one focal zone is used.

Due to the rapid generation of ultrasound images, all scanners have the capability to freeze image acquisition and scroll (cine) through a pre-defined number of images in order to review the most recent acquisitions. Single images and short video clips can be saved on the scanner—the length of video clip is usually pre-set and tends to be longer for video clips acquired during echocardiographic studies and contrast imaging studies than for abdominal scans (see below).

M-Mode Imaging

M-mode imaging or motion-imaging is used principally to study fast moving structures such as heart-wall movement or valvular movement. A single line is selected in the B-mode image intersecting the chamber walls or valves of interest and ultrasound data is acquired only along the pre-selected M-mode line. Consequently data is acquired with high temporal resolution, as only one line of data is acquired rather than 128 lines of data in a full B-mode image. The M-mode data is displayed as a continuous function of time scrolling across the screen with depth on the y-axis and time on the x-axis (**Figure 2**).

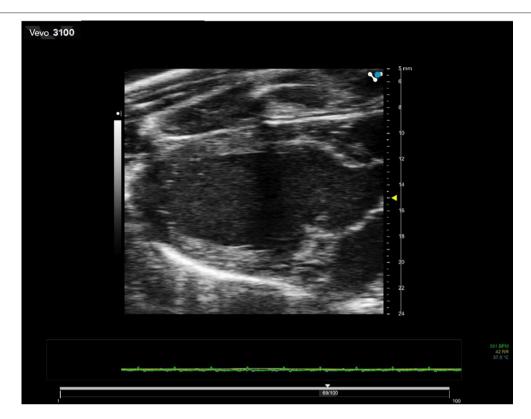


FIGURE 1 | 2D B-mode image of a rat heart in diastole. Transducer used is 21 MHz center-frequency and focus of the beam is set at 15 mm depth. The dark zone running through the center of the image is caused by shadowing from the ribs.

Three-Dimensional (3D) and 4-Dimensional (4D) Imaging

Currently, three-dimensional preclinical ultrasound images are generated by the acquisition of consecutive B-mode ultrasound images acquired at discrete step sizes along a pre-determined path. Commercial software then reconstructs the 3D volume with elevational resolution dependent on the step size between consecutive B-mode image acquisitions (Figure 3). For cardiac applications, images tend to be ECG and respiration-gated enabling accurate volumes of left ventricles to be determined which are not dependent on assumptions of the shape of the organs. In newer preclinical ultrasound scanners, complete 3D acquisitions are possible over a cardiac cycle (4D) enabling the dynamic movement of the heart to be viewed from any orientation. Acquisition times can be several minutes, dependent on the step-size between acquisition slices and relies upon good ECG and respiratory gating and high frame-rates. 3D imaging is also used to good effect in acquiring tumor volume data-sets, avoiding the need to make assumptions about the shape of tumor from a 2D image or the use of measurement calipers for superficial tumor volume assessment.

Doppler Techniques

Measurement of blood flow relies upon the use of the Doppler principle such that the measured change in frequency between a transmitted and received ultrasound beam is related to the velocity of the scatterers (red blood cells) from which the ultrasound beam is reflected.

Spectral Doppler

Spectral Doppler enables the Doppler frequency shift within a pre-selected region-of-interest (Doppler sample volume) to be displayed as a function of time. Most accurate measurements are made when the Doppler scatterers (red blood cells) are moving in the direction of the transmitted ultrasound beam. If the ultrasound beam cannot be aligned with the direction of blood flow, an angle correction can be made which attempts to compensate for this lack of alignment (**Figure 4**).

Color Doppler

In Color Doppler mode, the mean velocity of scatterers (red blood cells) within a pre-selected region-of-interest are color-encoded and superimposed on the gray-scale B-mode image. In clinical applications blood moving away from the transducer tends to be encoded in shades of blue and blood moving toward the transducer in shades of red. For preclinical applications, color Doppler is especially useful for the rapid location of vessels (Figure 5).

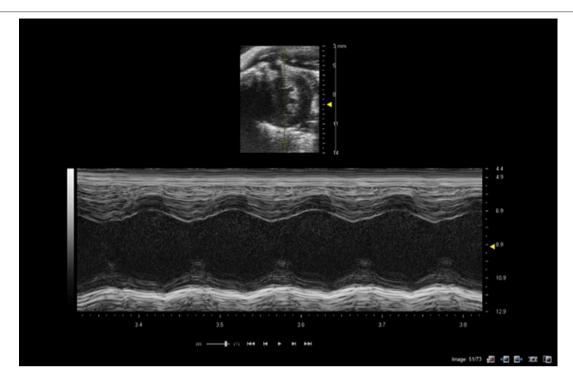


FIGURE 2 | M-mode of mouse heart showing short-axis B-mode image in top half of image with M-mode line selected (yellow line in image). Lower image shows M-mode trace through the left ventricle at level of papillary muscles. Images acquired using a 40 MHz probe focussed at 9 mm depth.

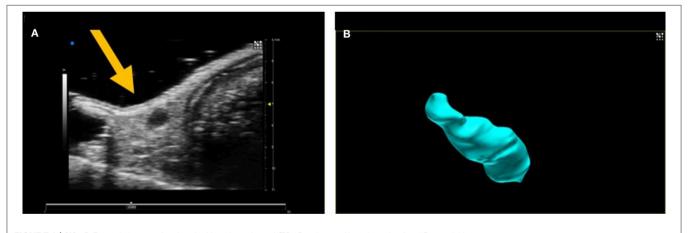


FIGURE 3 | (A) 2D B-mode image of an inguinal lymph node and (B) 3D volume of lymph node after 3D acquisition.

Power Doppler

In Power Doppler mode the power of the Doppler signal backscattered from red blood cells is displayed as a function of time within a pre-selected region of interest. The color is superimposed onto the gray-scale B-mode image. However, no directional information on blood flow is obtained but power Doppler is a more sensitive indicator of vascularity and thus useful in the detection of small vessels containing slower blood flow (**Figure 6**).

Doppler Tissue Tracking

The Doppler principle can also be applied to quantify both interand intra- regional soft tissue movement in a technique known as *tissue Doppler imaging*. In this technique, the sample volume is placed within the moving tissue of interest, and the amplitude of the high-pass filter is reduced to enable slow, high-amplitude signals corresponding to tissue to be tracked [2]. By measuring the velocities between tissues regions, velocity gradients (rate of change of velocity with distance) and strain rate information

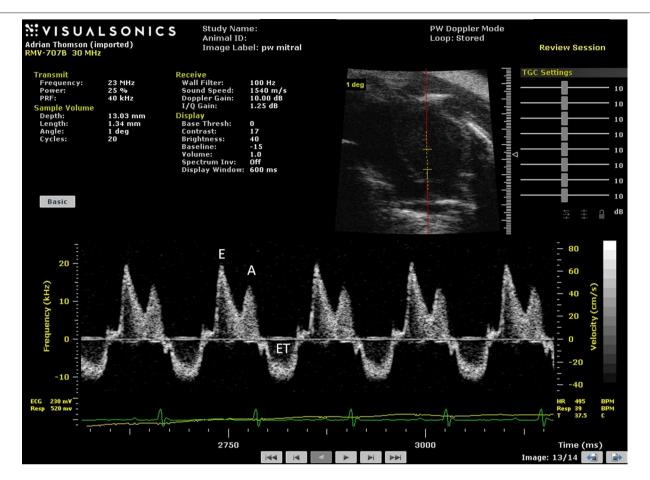


FIGURE 4 | Spectral Doppler trace with Doppler sample volume situated in center of left ventricle enables both inflow and outflow from the left ventricle to be measured with early (E) and late (atrial—A) waves and ejection time (ET) highlighted in the spectral Doppler trace. In addition isovolumic relaxation time (IVRT) and isovolumic contraction time (IVCT) may be measured where IVRT is equal to the time from the closure of the aortic valve to opening of mitral value and IVCT is the time of closure of mitral valve to opening of aortic valve.

can be calculated. However, tissue Doppler is only useful when the tissue motion is aligned with the direction of the ultrasound beam which has limitations in the assessment of cardiac radial function but has been used to good effect in studying mitral valve annulus movement.

Newer Imaging Techniques Speckle Tracking

Alternative non-Doppler techniques such as *speckle tracking* can also be used to track tissue motion and as such are not reliant on alignment between beam and direction of movement. Speckle is effectively the fine background noise on ultrasound images. It is formed by the interference between echoes from structures which are smaller than the resolution of the ultrasound system. This interference pattern (speckle) is random and unique for any volume of tissue and although it may change with movement of the tissue, image processing techniques can be used to recognize and track the movement in 2D and 3D [3]. In order to use speckle tracking techniques, high frame-rates are required (>250 frames/s) with faster heart rates requiring

higher frame-rates to ensure points of maximal and minimum strain and rate are captured. Using speckle tracking a range of parameters can be measured including displacement, velocity and strain and strain-rate.

Elastography Techniques

Ultrasound Elastography techniques are used to obtain information on the stiffness of tissue and can essentially be divided into those techniques which measure strain and those which measure shear wave velocity and from that directly measure Young's modulus (stress/strain). Strain elastography involves deformation of the tissue by application of a force (stress) and measuring the resulting degree of compression or extension of the tissue (strain) and comparing this to a reference soft tissue yielding a parameter known as the strain ratio. Since the magnitude of the stress applied is difficult to measure, strain elastography is not an intrinsic measure of tissue stiffness per se but the strain ratio can be used to infer tissue stiffness. Strain-rate is the change of tissue deformation with time. Both strain and strain-rate are routinely used in cardiac

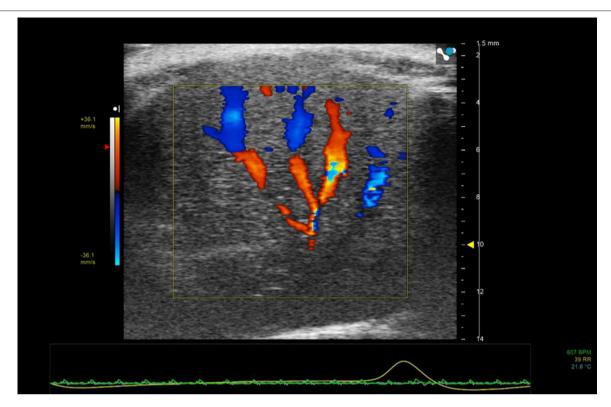


FIGURE 5 | Color Doppler region of interest superimposed on 2D B-mode image of mouse liver. Color Doppler shows the vessel network—blue indicating movement of blood away from the transducer and red toward the transducer.

applications, where strain and strain-rate values from different regions of the myocardium can be compared. Strain analysis using ultrasound is generally performed using speckle tracking techniques whereby the speckle within different pre-selected ROIs (kernals) is tracked and the relative displacement between the two kernals can be measured. The distance between the two kernals, enables strain to be calculated and the variation of strain over time is strain-rate (s^{-1}) [4] (**Figure 7**).

Alternatively, the measurement of *shear wave velocity* enables a quantitative measurement of Young's modulus of elasticity, E, provided that the tissue can be assumed to be incompressible (no change in density) and uniformly elastic (**Figure 8**). The shear modulus G is related to the Young's modulus of elasticity E, by the following equation. E = 3G. Shear wave velocity, c_s , generated as a result of a shearing force is given by, $c_s = \sqrt{(G/\rho)}$. By measuring the shear speed (usually between 1 and $10 \, \text{m.s}^{-1}$) and knowing the density, ρ , of the soft tissue (estimated at 1,000 kg.m⁻³), Young's modulus of elasticity can be calculated from the equation $E = 3\rho c_s^2$. Hence measuring the shear speed can provide quantitative information on the elastic modulus. More detailed information on elastography techniques can be found in Hoskins [5] and Bamber et al. [6].

Non-linear Imaging Techniques

Non-linear imaging techniques are utilized principally in the detection of ultrasonic contrast microbubbles (encapsulated gas bubbles). Contrast microbubbles when insonated with an

ultrasound beam will begin to oscillate, expanding during the negative phase of the cycle and contracting during the positive phase. Dependent on the frequency and amplitude of the transmitted ultrasound the microbubbles can produce a significant non-linear backscattered signal without being destroyed. Since soft tissues predominantly scatter ultrasound in a linear manner by removing or canceling the linear component of the backscattered signal the kinetics and dynamic enhancement of organs can be visualized and quantified by measuring the increase in non-linear signal as a function of time. This can then be displayed in a variety of ways such as a maximum intensity projection sequence which will enable the dynamic filling patterns to be established within a region or as a graph illustrating the backscattered intensity kinetics within a region-of-interest (Figure 9).

Ultrafast Doppler

Novel imaging techniques such as ultrafast imaging and ultrafast Doppler techniques enable exquisitely detailed images and volumes of tumor vascularity to be built up even from vessels with very slow flow which are difficult to locate with standard Doppler techniques [7].

PRECLINICAL ULTRASOUND—CARDIAC APPLICATIONS

The heart is probably the most challenging organ to image within the rodent due to its small size and rapid and



complex motion. However, rodent models of cardiac diseases and myocardial infarction (MI) give valuable insights into anatomic and physiologic changes which are often directly aligned with changes observed in human cardiac disease and thus provide opportunities to assess novel therapeutic approaches and interventions.

Adult and neonatal cardiac scanning in mice, is routinely undertaken with the mouse in the supine position, hence the standard views obtained from mouse models are not exactly comparable to images acquired from clinical subjects who are scanned while lying in the left decubitus position. The ECG, respiration and temperature of the mouse are continuously recorded and monitored to ensure minimal variation throughout the scan-time. However, due to the range of mouse strains, anesthetic choice and depth there is a wide variation in accepted normal ranges of rodent cardiac indices. A recent review recommended standardized methods of measuring and reporting cardiac physiology in the adult murine model [8] and forms a useful step toward the introduction of standardized scanning procedures similar to those introduced by the American Society of Echocardiography and the

European Association of Cardiovascular Imaging for clinical practice [9].

Similarly to clinical studies, all of the ultrasound imaging modalities: B-mode, M-mode, Doppler ultrasound and strain imaging can be used to assess cardiac function in mice.

Measurement of Cardiac Function in Adult Rodents

For adult mice scanning, transducer frequencies of 30–40 MHz are used, while for rats, ultrasound transducers operating between 10 and 25 MHz may be used—the higher frequencies for applications in smaller rats. To achieve high temporal resolution, only one focal position should be selected and placed at a depth commensurate with the region-of-interest.

There are two standard views used for initial assessment of the heart using parasternal 2D *B-mode imaging*—long-axis and short-axis views. Using these views initially provides a gross overview of the movement of left ventricular myocardial walls and mitral and aortic valve movements enabling areas of hyper-, hypo- or dyskinetic regions to be identified for further investigation. Due to the rapid heart-rate, cine-loops

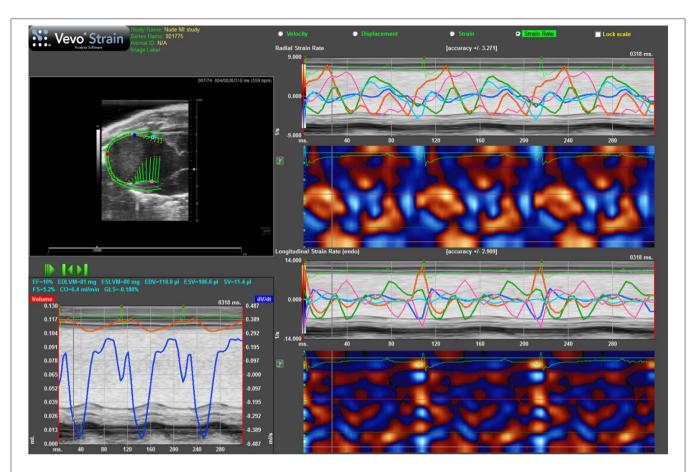


FIGURE 7 | Strain rate imaging of a nude mouse with MI as the result of ligation of left coronary artery. Top Ihs is long-axis view of heart with arrows indicating direction and magnitude of movement of endocardial border. Bottom Ihs shows change in volume of cavity over consecutive cardiac cycles alongside ECG and respiration. Top rhs shows radial strain-rate curves from five points selected on endocardial border while lower rhs shows longitudinal strain-rate curves from the same five points.

are generally acquired and can be reviewed at a much slower rate enabling key-points in the cardiac cycle such as systole and diastole to be identified. Alternatively a technique known as electrocardiogram-gated kilohertz visualization (EKV) can be used to investigate motion over one cardiac cycle with very high temporal resolution (1,000 frames/s). EKV scanning acquisition times are of the order of 30-60s with the acquisition gated on the ECG and respiration cycles. Effectively sequential Mmodes are acquired across the heart and temporally interleaved into a high temporal resolution 2D B-mode image data set of a cardiac cycle. Using this technique enables easier tracking of myocardial borders. Parameters that can be measured from Bmode or EKV images include stroke volume, ejection fraction, cardiac output, endocardial area, epicardial area, and percentage fractional myocardial area change. The formula and techniques used to measure these are beyond the scope of this review but can be found in Lang et al. [10].

M-mode is especially useful for the measurement of the maximum and minimum dimensions of the ventricles for calculation of cardiac indices such as fractional shortening and for the assessment of myocardial wall abnormalities (**Figure 2**). However, M-mode measurements of chamber size should not be

used for measurement of cardiac indices derived from volume measurements (e.g., ejection fraction) as these make assumptions re the shape of ventricles which are prone to error especially for animal models which have suffered myocardial infarctions and for which the shape of the ventricle can undergo deformation and remodeling. M-mode imaging can also provide information about valve movements with the M-mode line aligned with the tip of the mitral valve leaflets to study the thickness of the leaflets and valvular dynamics. Likewise for the aortic valve M-mode can be used to assess aortic valve cusp separation.

Four-dimensional imaging of the rodent heart is undertaken by acquiring multiple 2D EKV cineloops over a cardiac cycle. Gating on the ECG and respiration can be done either during acquisition or reconstruction of the 3D data-set. These cineloops are acquired at discrete, user-determined distances in either longor short- axis views yielding a full 4D dataset. The cineloops are then temporally interleaved and reconstructed to allow the heart to be dynamically visualized over one cardiac cycle. 4D imaging enables the volume of cardiac chambers to be established with fewer inherent assumptions re the shape and dynamics of the chambers compared to calculations using 2D images (Figure 10). As such calculation of indices requiring volume



FIGURE 8 | Shear wave elastography image of liver showing mean shear wave velocities and Young's modulus from a mouse liver (Reproduced with permission from S-Sharp Corporation).

calculations, e.g., ejection fraction are more accurate and precise than measurements undertaken using 2D acquisitions [11].

Doppler measurements are used in echocardiography to measure blood flow across the mitral and aortic valves within the heart. With the Doppler sample volume sited at mid-ventricular level, in the apical 4-chamber view, mitral valve early (E) and late [atrial (A)] inflow velocities can be seen in the mitral spectral Doppler trace—the ratio of E/A and the deceleration time of the E-wave are indicators used in the assessment of diastolic function (Figure 4). For some animals, separation of the E and A waves can be difficult to achieve due to the high heartrates displayed by adult mice. However, isovolumic relaxation time can be measured along with systolic parameters such as ejection time and isovolumic contraction time enabling the calculation of myocardial performance index, an indicator of cardiac performance (see section on embryonic imaging).

Color Doppler is used in adult rodent echocardiography for the rapid assessment of blood flow within the chambers and specifically across valves. Constriction of valves can result in jetting which can be visualized as rapid flashes of color across the valves during contraction of chambers. This enables easier localization of the spectral Doppler sample volume within the jet to measure maximal velocities for assessment of constriction of valves. Color Doppler can also be used to localize small vessels. Figure 11 shows a duplex image (color and spectral Doppler) where color Doppler has being used to localize and identify the left anterior coronary artery and spectral Doppler enabling measurement of the velocities within the artery.

Strain and Strain-Rate Imaging

Strain and strain-rate imaging are of specific value in rodent cardiac imaging providing information on regional myocardial deformation. Most commercial scanners use speckle tracking to determine strain (deformation)—by measuring the relative displacement of two kernals to determine strain and its variation over time to give strain-rate. In addition to a global strain parameter, radial, circumferential and longitudinal strain can be obtained providing information on regional segmental myocardial motion and systolic function. The timing of maximum and minimum strain and strain-rate values relative to systole and diastole can provide data on desynchronises between different myocardial regions especially relevant in infarct models (Figure 7) [12–14].

Contrast Agents

Ultrasonic contrast agents used in preclinical studies for ultrasonic enhancement are composed of lipid-encapsulated gas-filled microbubbles which are injected via the tail-vein into the rodent. The agents are purely vascular agents, mixing freely with the blood. Limited enhancement is achieved using

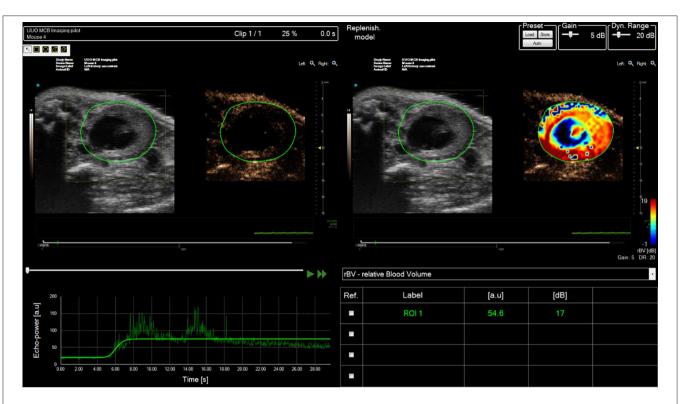


FIGURE 9 Contrast analysis of data-set acquired from right mouse kidney post ischemia-reperfusion (IRI) injury after tail-vein bolus injection of SonoVue. Mouse scanned in prone position. Multiple regions of interest (ROIs) can be drawn onto the image and the enhancement can be tracked as a function of time (bottom LHS). The relative enhancement of each ROI relative to pre-contrast image can be calculated and color-encoded (Top RHS).

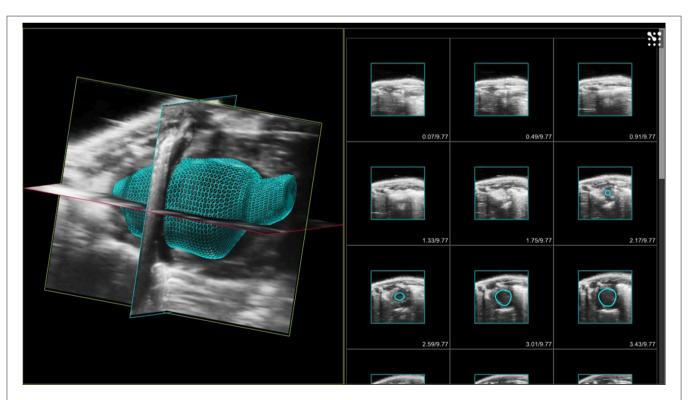


FIGURE 10 | LHS - 3D volume of murine left ventricle with aortic root. Images acquired at end-diastole. RHS 2D acquired images with endocardial borders of left ventricle highlighted in each slice.

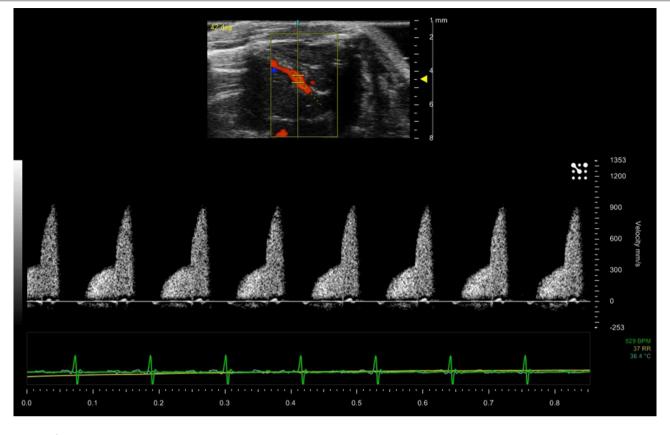


FIGURE 11 | Blood flow within the left anterior descending coronary artery of a mouse model. Maximum velocity within the artery is 900 mm/sec.

B-mode imaging, but in many instances this is sufficient to give enhancement of endocardial borders even at these high frequencies far removed from the resonant frequency of the microbubbles. Such enhancement enables better visualization and delineation of chamber volumes. The maximum recommended volume of contrast is 5 μ l/g IV for rats but for mice a bolus injection of 50 μ l is sufficient to see enhancement within the heart.

Measurement of Cardiac Function in Embryonic Mice

In embryonic mice and rats, the ultrasound backscattered signal from the circulating red blood cells is much greater than in adults. This is due to the nucleation of the red blood cells within the embryos and this enhancement can persist up to 3 to 4 days postbirth. This enhancement of the cardiac chambers, along with the complexities of determining the direction of blood flow within embryonic hearts and subsequent alignment of the Doppler beam along the direction of blood flow can make measurement of cardiac performance of embryos a challenging technique. In addition, since it is not possible to obtain an ECG from the embryos, the timing of diastole and systole is determined either by measurement of the movement of the myocardial walls or from the spectral Doppler waveform. Finally, the user needs to be mindful of the duration of anesthesia and its effect on both dam and embryos.

Since determination of the orientation of the heart can be challenging, even in older embryos, measurement of ratios calculated from the Doppler spectral trace will negate the angle dependence associated with aligning the Doppler beam with the direction of flow. Hence E/A ratios discussed above are useful indices to obtain although in embryos the A wave tends to be larger than the E wave. Likewise a parameter known as the myocardial performance (Tei) index which is a ratio of timing intervals determined from the spectral Doppler trace [summation of the isovolumic relaxation time (IVRT) and isovolumic contraction time (IVCT) divided by the ejection time (ET)] is useful and is largely unaffected by the angle of insonation. The myocardial performance is an indicator of overall cardiac performance with higher index values corresponding to an increasing dysfunctional heart. Strain rate imaging in embryonic mice is challenging and this may be due to the increased echogenicity of the blood pool, making speckle tracking more difficult.

Measurement of Cardiac Function in Neonatal Mice

Cardiac scanning of neonatal mice from day 1 post-partum (P1) is also possible. However, due to their small size and reduced hair-cover, care needs to be taken to ensure that they maintain body temperature (monitored using a neonatal rectal probe) throughout the scan. In addition, neonates can present anesthesia

challenges and use of an adaptor and nose cone to ensure sufficient depth of anesthesia is recommended. In addition, dependent on the scanning table utilized, it is often necessary to use copper-tape to extend the electrodes to ensure a good ECG signal is obtained [15]. Ultrasound probes operating up to 50 MHz can be used to image early post-partum neonates and EKV scanning can be used to acquire high temporal and spatial resolution images.

Measurement of Cardiac Function in Zebrafish

The zebrafish (*Danio rerio*) has increasingly become an important tool in medical research [16], with significant application to the investigation of an extensive range of cardiovascular human diseases [17]. Its small size and corresponding small space requirements, relatively rapid sexual maturity (\sim 3 months), generation of hundreds of embryos every week and external fertilization makes it increasingly one of the accessible animals for study.

The cardiac function of zebrafish can be imaged using preclinical ultrasound. The zebrafish heart is composed of 4 chambers—sinus venosus, atrium, ventricle and bulbus arteriosus. Light anesthesia can be induced for adult fish by injection of MS222 in the tank water. The fish can then be manipulated and placed on their dorsal side and gently restrained using plasticine that is lightly hand-molded around their bodies. Transducers up to 55 MHz can be used to image the hearts in both long and short axis views. Obtaining an ECG signal from adult zebrafish is challenging so the timing of systole and diastole is determined from cardiac chamber size and spectral Doppler traces with adult heart rates ranging from 120 to 180 beats/min. Additionally, the echogenicity of blood within adult zebrafish is similar to the surrounding tissue structures (Figure 12) making the differentiation of chamber volumes challenging.

Measurement of Cardiac Function in Embryonic Zebrafish

Assessment of cardiac function in embryonic zebrafish using ultrasound is also possible although the optical transparency of





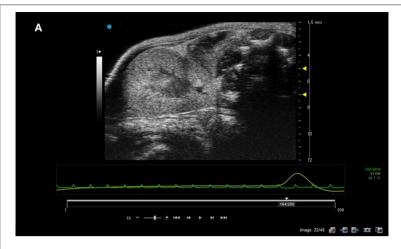
FIGURE 13 | B-mode image of a 5 day-post-fertilization zebrafish embryo suspended in agar. Embryo imaged at 55 MHz.

embryos means that cardiac function can also be studied using light microscopy techniques including video edge-detection techniques. Using Doppler ultrasound techniques, a rapid assessment of cardiac function can be undertaken with heartrates in zebrafish embryos dependent on the temperature but at 28°C are around 200 bpm [18]. Before scanning, embryos are anesthetized in a petri-dish using MS222 and then embedded in agarose. Once the agar has set, fresh aquarium water is added to the dish to limit the effects of anesthesia. Individual embryonic fish can be then identified, and the orientation of their hearts noted using a stereomicroscope. The dish is then placed on top of a heated plate and temperature maintained at 28.5°C whilst scanning is being undertaken with a thermocouple placed adjacent to the embryo to monitor temperature. The ultrasound transducer is then lowered into the water and individual embryos may then be scanned (Figure 13).

PRECLINICAL ULTRASOUND—KIDNEY APPLICATIONS

The kidneys in a mouse can either be scanned with the mouse in supine or prone position. The hair can be removed firstly with electric hair clippers and then with depilatory cream. Unless contrast agents are being used, high temporal resolution is not required for imaging the kidneys so multiple focal positions can be selected across the depth of the kidney. Frequencies used tend be between 30 and 40 MHz dependent on the size of the animal. B-mode imaging is used to locate the kidney with the cortex of the kidney tending to have increased backscatter (brighter) compared to the central medulla. Both kidneys can be scanned in the adult rodent. **Figure 14** shows an image of a mouse kidney and a duplex image using color Doppler to locate the vessel and direction of flow before placing the spectral Doppler sample volume within the vessel. Renal blood flow can be measured and the renal arterial resistive index calculated (peak systolic velocity—the end diastolic velocity) /peak systolic velocity) and its value indicative of the resistance to blood flow in the vascular bed [19].

Vascularity of the kidney can also be studied using ultrasonic contrast agents. When contrast is being used, the mouse is scanned in the prone position avoiding the potential of imaging artifacts caused by intestinal shadowing which can occur when the kidneys are scanned with the mouse in the supine position. Contrast agents are bolus-injected or infused using a syringe pump via the tail-vein. An injection of 50 μ l Micromarker (Bracco Research SpA, Geneva, Switzerland) over a 5 second period of a 1:5 dilution is a typical dosing regimen. For acquisition, baseline images are acquired in contrast-specific imaging mode immediately prior to injection of the contrast



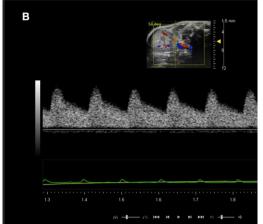


FIGURE 14 | (A) B-mode image of kidney. Note the two focal positions on the image. (B) Duplex image of mouse kidney. In the Duplex image, the sample volume is localized using the color Doppler box as an indicator to show where the vessel lies and direction of blood flow.

agent and are saved either as a separate data-set or a temporal stamp is placed on the contrast image sequence indicating when contrast is injected and images taken prior to this time-stamp are considered baseline images. An alternative approach is to inject the contrast agent, then destroy the contrast agent within the 2D plane using a short, low-frequency high pressure acoustic pulse. The low-pressure contrast-specific imaging sequence is then reinstated, with the initial frames immediately after these high pressure pulses regarded as baseline images with subsequent frames displaying contrast enhancement. After contrast injection a long sequence of 2D images are obtained, the length of sequence can be pre-set by the user. Once the sequence has been saved, either in-house software or contrast-specific software developed by the manufacturers can be used to map the intensity of the backscattered signal within the regions-of-interest (eg medulla, cortex) to study the perfusion-dynamics. Metrics of interest include area-under-the curve, time-to-peak enhancement, washin rate and these can be used as indicators of blood volume and vessel density [20]. In many instances if an ischemic-reperfusioninjury (IRI) mouse model is being studied, one kidney can act as a control and both B-mode and contrast-enhancement data can then be acquired from both kidneys.

PRECLINICAL ULTRASOUND—LIVER APPLICATIONS

The liver is a large organ within the mouse and consists of four lobes. To image the mouse liver, the mouse is again scanned in the supine position using insonating frequencies between 30 and 40 MHz (**Figure 15**). B-mode ultrasound can be used to image all 4 lobes of the liver while ultrasound enables the portal vein and hepatic artery to be identified and blood velocities measured. Identification and sizing of tumors; staging of non-alcoholic fatty liver disease [21] and determination of fibrosis in the liver can also be achieved at preclinical frequencies. For the assessment of fibrosis in the liver, shear wave imaging techniques can also

be used to measure the viscoelastic properties of mouse liver (**Figure 8**) [22]. For preclinical imaging applications, shear waves are generally generated by a lower frequency 20 MHz radiation pulse and a 40 MHz probe used to measure the shear wave propagation within the liver tissue.

PRECLINICAL—ULTRASOUND: GUIDED INJECTIONS

High-frequency ultrasound can also be used to guide injections into specific areas within the mouse anatomy. For injections into joints, this has recently been shown to have a higher success rate than using traditional anatomic landmarks [23]. Moreover, the less invasive approach of inducing infection within the uterus of a mouse using ultrasound-guided injections of lipopolysaccharide rather than through a mini-laparotomy clearly aligns with the principles of reduction, replacement and refinement which are central considerations for animal research [24]. Injections into fetal brains on externalized embryos, into adult kidneys and pancreas for orthotopic tumor cell injections and into the myocardium can all be undertaken.

PRECLINICAL ULTRASOUND: LYMPH NODES

Due to their size and location, identification of lymph nodes using high frequency ultrasound can be difficult within the mouse model with many lying deep within the body, encapsulated in fat pads and some, such as the mesenteric lymph node, surrounded by the intestines. However, for cancer models it is important to locate the sentinel lymph node i.e., the node to which the primary tumor drains to first. To this end, both novel contrast agents [25] and novel ultrasound imaging techniques are under development to aid the detection of the location of this node [26].



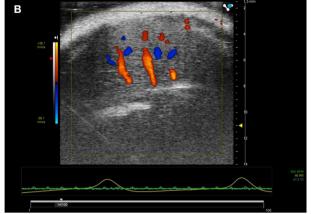


FIGURE 15 | (A) B-mode image of right lobe of normal mouse liver. Imaged using 40 MHz probe. (B) Color Doppler image of liver showing hepatic blood flow within the liver.

PRECLINICAL ULTRASOUND: CRANIAL

The use of ultrasound to study the development of the embryonic mouse brain in utero is well-established [27, 28] with development of individual embryos tracked throughout gestation. However, the effects of attenuation and resultant aberrations in the ultrasound field caused by the skull in post-natal mice and rats tend to yield poor quality images resulting in the need for either a craniotomy or thinning of the skull to remove or reduce these effects. However in recent years, the use of high frequency transcranial ultrasound to study brain vasculature and cortex activation in nonanaethetised mice enabling longitudinal studies on post-natal brain development has been demonstrated [29]. The techniques utilized ultrafast (>500 Hz) compound Doppler techniques where the backscatter from multiple plane-wave emissions acquired at a range of angles are compounded. These early studies show in exquisite detail the future potential of using ultrasound for neuroscience applications.

DISCUSSION

The real-time nature of ultrasound, its small footprint in the preclinical laboratory and the inexpensive nature of ultrasound imaging compared to MRI and PET/CT, have made it a vital element within the preclinical imaging laboratory. However, the ease of image acquisition using ultrasound by non-specialist researchers has also resulted in a lack of rigor in the reporting of the scanning planes utilized to acquire measurements. This lack of rigor has resulted in a lack of consensus on the "normal" range of physiological values. The effect of heart-rate, temperature, type and depth of anesthesia also influence cardiac measurements and are essential to report in any study [30, 31].

The vast increase in computing power has resulted in reductions in acquisition time of 3D volumes of organs and tumors and 4D acquisitions of the moving heart. Although these extra imaging dimensions will undoubtedly result in more

accurate volume measurements it is not yet clear of their potential to provide additional diagnostic information. However, for the non-specialist user of ultrasound acquiring data in 3D enables visualization of structures more easily than from a single 2D imaging plane.

Although widely used within the clinical community, techniques such as strain, strain-rate and shear wave imaging are still gaining traction within the preclinical community. Strain and strain-rate values and the timing of their maximum values within the cardiac cycle may well prove useful as early indicators of myocardial dysfunction similar to that found in clinical studies. The use of shear wave imaging to measure fibrosis in the liver has been developed on one commercial preclinical platform. Certainly, the evidence is encouraging that these techniques can provide useful diagnostic information but more studies are required to validate this for preclinical rodent models and similarly to clinical studies there must be an understanding of the limitations of the technique [4].

Contrast agent development has been ongoing for the last 30 years with initial emphasis on the development of agents to highlight the ultrasound signal from vascular structures. Since contrast-specific imaging techniques rely on generating images based on the non-linear signal scattered from the microbubbles, a transducer of sufficient frequency bandwidth and sensitivity to these signals is required. At the frequencies used in clinical applications this is easily achieved (for a 4 MHz center frequency transducer, second harmonic is at 8 MHz) and transducers used for contrast imaging are usually sensitive up to at least the second harmonic i.e., twice the fundamental transmitted frequency. However, at preclinical frequencies, this is more challenging—in order to capture signals generated at the second harmonic, a much broader bandwidth transducer is required (20 MHz center frequency with second harmonics generated at 40 MHz and sub-harmonics at 10 MHz). Consequently, it tends to be the lower frequency preclinical transducers which have been optimized for contrast-specific imaging and thus, especially in mouse and zebrafish studies, there is an

immediate reduction in spatial resolution when undertaking contrast studies. The development of capacitive micromachined ultrasound transducers (CMUTs) may provide a solution for higher resolution contrast microbubble work. CMUTS rely on a change in capacitance for generation of ultrasound rather than piezoelectricity and because they can be micromachined, lightweight 2D arrays are easily manufactured. In addition, they can be operated over a broad bandwidth and hence may be useful in the generation and detection of non-linear signals from contrast agents at higher frequencies necessary for optimal spatial resolution in preclinical animal models.

Super-resolution imaging can be used to generate very high resolution images. Using a sparse distribution of contrast microbubbles whereby single microbubbles are considered as point sources and over multiple ultrafast frame acquisitions composite images can be built up with resolution beyond the diffraction limit of the transmitted ultrasound [32]. Although the images require considerable post-processing, these images are exquisite in the detail. Improved computing power will improve the speed at which these images can be generated.

Although there is only one commercially available contrast agent manufactured for preclinical applications, lipid-encapsulated microbubbles can be made within the lab environment [33]. These microbubbles can be formulated to be used not only as contrast-enhancing agents but also as theranostic agents since targeting ligands can be relatively easily attached to the lipid shells and a drug payload incorporated within or loaded onto the microbubble shells. Although it is known that the drug payload can be released by insonation of the contrast microbubble by a high pressure acoustic pulse the translation of results obtained under highly controlled conditions in vitro have not yet been effectively translated to preclinical and clinical studies [34]. However, the development of mono-disperse microbubbles coupled with increasing access to the drive electronics within commercial preclinical scanners is likely to prompt new imaging sequences specifically tailored to these unique microbubble formulations and provide new and exciting theranostic applications.

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Finally the use of artificial intelligence (AI) is an exciting area of research undergoing evaluation in the clinical ultrasound workload pipeline. Within clinical ultrasound imaging, AI is currently being evaluated for automatic feature detection, image optimization and quantification. Within the preclinical ultrasound imaging community, AI is now incorporated in one preclinical ultrasound platform to automatically define boundaries and complete left ventricular functional measurements [35]. Although the results suggested that the quality of ultrasound images acquired was a limiting factor for AI quantification, for the non-specialist preclinical ultrasound user AI is likely to make scanners simpler to use, make image analysis easier and more rapid to implement.

CONCLUSION

In this review article, a range of applications utilizing preclinical ultrasound imaging techniques have been discussed. However, this list is not exhaustive. The range of preclinical applications for which ultrasound imaging is capable of providing meaningful diagnostic information is likely to rapidly increase over the next decade as these scanners become embedded technology within biology laboratories. The increasing use of AI and the use of contrast microbubble formulations allied with unique driving and detection mechanisms will ensure that preclinical ultrasound remains a versatile and cost-effective tool.

AUTHOR CONTRIBUTIONS

CM wrote the original manuscript. AT reviewed the manuscript and acquired almost all the images.

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Protocols for Dual Tracer PET/SPECT Preclinical Imaging

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Background: Multi-tracer PET/SPECT imaging enables different modality tracers to be present simultaneously, allowing multiple physiological processes to be imaged in the same subject, within a short time-frame. Fluorine-18 and technetium-99m, two commonly used PET and SPECT radionuclides, respectively, possess different emission profiles, offering the potential for imaging one in the presence of the other. However, the impact of the presence of each radionuclide on scanning the other could be significant and lead to confounding results. Here we use combinations of ¹⁸F and ^{99m}Tc to explore the challenges posed by dual tracer PET/SPECT imaging, and investigate potential practical ways to overcome them.

Methods: Mixed-radionuclide ¹⁸F/^{99m}Tc phantom PET and SPECT imaging experiments were carried out to determine the crossover effects of each radionuclide on the scans using Mediso nanoScan PET/CT and SPECT/CT small animal scanners.

Results: PET scan image quality and quantification were adversely affected by ^{99m}Tc activities higher than 100 MBq due to a high singles rate increasing dead-time of the detectors. Below 100 MBq ^{99m}Tc, PET scanner quantification accuracy was preserved. SPECT scan image quality and quantification were adversely affected by the presence of ¹⁸F due to Compton scattering of 511 keV photons leading to over-estimation of ^{99m}Tc activity and increased noise. However, ^{99m}Tc: ¹⁸F activity ratios of > 70:1 were found to mitigate this effect completely on the SPECT. A method for correcting for Compton scatter was also explored.

Conclusion: Suitable combinations of injection sequence and imaging sequence can be devised to meet specific experimental multi-tracer imaging needs, with only minor or insignificant effects of each radionuclide on the scan of the other.

Keywords: SPECT, PET, radionuclide, phantom, multi-modality, dual-radionuclide, dead-time, scatter

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INTRODUCTION

Individually, PET and SPECT tracers allow us to probe the underlying molecular characteristics of physiological processes, one mechanism at a time. The ability to image one tracer in the presence of another—dual radionuclide PET/SPECT imaging—enables different modality tracers to be present simultaneously, thus allowing multiple processes to be imaged in the same subject, within a much shorter period of time (removing the need to wait for tracer decay). For example, radionuclides

fluorine-18 (PET) and technetium-99m (SPECT) each possess different emission profiles and, in theory, can be imaged in the presence of the other, but the impact of each on scanning of the other (i.e. the SPECT and PET scans respectively), could be significant and lead to confounding results.

Acquiring a PET image in the presence of a SPECT radionuclide may introduce additional dead-time (the time after each photon is detected by the scanner during which the system is not able to record another event). Photons emitted from decaying ^{99m}Tc nuclei are not coincident, and their energy of 140 keV is much lower than the 511 keV PET scanner energy window, so do not contribute to the image data acquired. However, they do interact with the PET detectors, and at high enough flux, can potentially prevent true coincidence events from the positron emitter being recorded. One study in mice showed PET signal loss of 12% due to increased dead-time when ^{99m}Tc was present in an almost 10-fold higher activity compared to ¹⁸F [1]. It is worth noting that this phenomenon is not specific to mixed radionuclide effects, and dead-time is generally recognized as a performance-limiting factor at high concentrations of PET tracers [2].

Performing a SPECT scan in the presence of a PET radionuclide can also be problematic. If ¹⁸F is present during a $^{99\mathrm{m}}\mathrm{Tc}$ SPECT scan, a proportion of the photons from $^{18}\mathrm{F}$ positron annihilation will enter the SPECT 99m Tc energy window (140.5 keV, $\pm 10\%$ i.e. 20% width) due to Compton scattering the scattering of a photon by a charged particle, resulting in a decrease in energy and change in trajectory of the photon. Previous studies have shown that this down-scatter can generate significant noise and artifacts in the SPECT image [1]. A clinical study showed that the simultaneous use of 99mTc-sestamibi and [18 F]FDG (with a 99 mTc: 18 F ratio of 3.2:1) resulted in a <6 % increase in the apparent 99mTc count rate due to down-scatter from ¹⁸F [3]. This overestimation can be corrected for on clinical scanners by the use of auxiliary energy windows; such methods use the signal in parts of the spectrum outside the photopeak window to estimate an amount of signal to subtract from the imaging window to correct for scatter [4, 5]. However, these methods may be difficult to implement in a preclinical setting due to the low volume of the scatter medium (mice, rats etc.) and hardware and software constraints.

Here, we explore some of the challenges posed by dual tracer PET/SPECT preclinical imaging using radionuclides $^{18}\mathrm{F}$ and $^{99\mathrm{m}}\mathrm{Tc}$ as examples, and investigate potential practical ways to overcome these obstacles by appropriate experimental design. Mixed-radionuclide $^{18}\mathrm{F}/^{99\mathrm{m}}\mathrm{Tc}$ phantom experiments were carried out to determine the crossover effects of each radionuclide on the scans, and ultimately, to help design the optimal protocol for *in vivo* dual radionuclide preclinical imaging using $^{18}\mathrm{F}$ and $^{99\mathrm{m}}\mathrm{Tc}$.

METHODS

PET Scanner Phantoms

Plastic syringes (5 mL) were filled with either ¹⁸F only (5 MBq), ^{99m}Tc only (5 MBq), or mixtures of ¹⁸F (5 MBq) and increasing amounts of ^{99m}Tc (5, 50, 100, 150, 200, 250,

350 MBq). Activities of 5 MBq ¹⁸F and < 200 MBq ^{99m}Tc reflect routine protocols avoiding count-rate limitations of each modality separately. Volumes were made up to 3 mL by addition of water. Radioactivity in each syringe was measured using a dose calibrator (Capintec, Ramsey, NJ, USA), calibrated to the national standard. First the syringe was filled with ¹⁸F only and the activity measured. Then the required activity of 99mTc was prepared in a microcentrifuge tube, measured in the dose calibrator, and transferred to the syringe. Residual 99mTc activity in the needle and microcentrifuge tube was subtracted from the measured activity. Syringes were inverted several times for uniform distribution of radioactivity. Each syringe was placed in the pre-calibrated nanoPET/CT (Mediso, Budapest, Hungary; system sensitivity 4.67% for a 350-650 keV energy window and 4 ns coincidence window [2]). A 15 min PET scan was acquired with a 5 ns coincidence window in 1-5 coincidence mode. Subsequently, a CT scan was obtained for attenuation correction with a 55 kVp X-ray source, 600 ms exposure time in 180 projections over ~6 min. PET images were reconstructed in Nucline v.0.21 using Tera-Tomo 3D reconstruction with 4 iterations, 6 subsets, 1-3 coincidence mode, voxel sized 0.4 mm (isotropic), energy window 400-600 keV with attenuation, and scatter correction. Images were analyzed in VivoQuantTM v.3.5, patch 2 software (Invicro LLC., Boston, USA). The activity was determined within a cylindrical ROI slightly larger than the syringe. The same cylindrical ROI was used for each scan and translated or rotated to accommodate variations in the placement of each syringe. The resulting activity from the PET/CT scan was compared to the decay-corrected activity measured in the dose calibrator. Quantitative assessment of image quality was assessed by calculating the coefficient of variation for each image: a small spherical ROI was drawn over the images and the standard deviation within the ROI was divided by the mean within that ROI (Supplementary Figure 1).

SPECT Scanner Phantoms

Plastic microcentrifuge tubes (1.5 mL) were filled with either ^{99m}Tc only (1 MBq), ¹⁸F only (1 MBq), or mixtures of ^{99m}Tc (1, 10, 30, 50, 70 MBq) and ${}^{18}{\rm F}$ (1 MBq) to achieve ${}^{99{\rm m}}{\rm Tc}:{}^{18}{\rm F}$ ratios ranging from 1:1 to 70:1. Volumes were made up to 1 mL by addition of water. Radioactivity in each tube was measured using a dose calibrator (Capintec, Ramsey, NJ, USA), calibrated to the national standard. First the tube was filled with ¹⁸F only and the activity measured. Then the required activity of 99mTc was prepared in a second microcentrifuge tube, measured in the dose calibrator, and transferred to the first tube. Residual ^{99m}Tc activity in the needle and second tube was subtracted from the measured activity. Tubes were inverted several times and vortexed for uniform distribution of radioactivity. Each tube was placed in the pre-calibrated nanoSPECT/CT Silver Upgrade (Mediso Ltd., Budapest, Hungary) and imaged with acquisition time 15 min, frame time of 35 s using a 4-head scanner with 4×9 (1 mm) pinhole collimators in helical scanning mode, and CT images with a 55 kVp X-ray source, 1,000 ms exposure time in 180 projections over approximately 9 min. Images were reconstructed in a 256 × 256 matrix, voxel size 0.3 mm (isotropic) using HiSPECT (ScivisGmbH) a

reconstruction software package, and images were fused using proprietary VivoQuantTM v.3.5, patch 2 software (Invicro LLC., Boston, USA). The resulting activity from the SPECT/CT scan was compared to the decay-corrected activity measured in the dose calibrator.

Compton Scatter Data Correction

A method to correct for the effects of 511 keV scattered photons on SPECT image quantification and quality was explored. A set of phantom experiments was performed on the nanoSPECT/CT as proof-of-concept. To obtain an ¹⁸F scatter map, a microcentrifuge tube containing ¹⁸F only (2 MBq, 1 mL) was placed in a 50 mL Falcon tube of water (to mimic preclinical scatter conditions) and a 15 min SPECT scan was acquired. followed by a CT scan. Next, a tube containing a mixture of ^{99m}Tc (50 MBq) and ¹⁸F (2 MBq) was placed in a 50 mL Falcon tube on the scanner and a 15 min scan was acquired, followed by a CT scan. Finally, a tube containing ^{99m}Tc only (50 MBq) was placed on the scanner and a 15 min scan was acquired. The scatter correction was applied by subtracting the ¹⁸F-only SPECT scatter map from the mixed-radionuclide SPECT scan, according to the programming code (Python 3) in Supplementary Figure 2A. Automatic scatter correction was applied by scaling the voxel values in both the ¹⁸F-only scan and the mixed-radionuclide scan using their "COUNTS Real World Value Slope" as determined by the SPECT scanner calibration saved in the original dicom files. This allowed a matrix subtraction to be performed where each voxel value corresponded directly with real world counts, as measured by the SPECT. The images were then converted back using the Value Slope for the original mixed-radionuclide image (Supplementary Figure 2B). Both the original and scattercorrected images were analyzed in VivoQuantTM v.3.5, patch 2 software (Invicro LLC., Boston, USA). The activity in each image was determined using the same ROI, within a region slightly larger than the microcentrifuge tube. The activity quantified in both images was compared to the decay-corrected activity measured in the dose calibrator.

It is important to note that the radioactivity quantities used in these experiments reflect the doses appropriate for our scanner system specifications; tested doses may need to be adjusted for other systems.

RESULTS

Effect of 99mTc on PET Scans

The effect of the presence of SPECT radionuclide ^{99m}Tc on ¹⁸F PET scans was assessed by the use of phantoms. The PET scanner was calibrated prior to the start of the study following manufacturer procedures; ¹⁸F-only phantoms measured in the dose calibrator and PET scanner showed good agreement (within 2%).

In the presence of up to 100 MBq ^{99m}Tc, 5 MBq ¹⁸F was accurately quantified by the PET scanner: an over-estimation of < 5% activity was observed in the presence of 50 and 100 MBq ^{99m}Tc (**Figure 1**). At higher activities of ^{99m}Tc, PET scanner quantification became less accurate and consistently under-estimated the amount of ¹⁸F present. At 150 MBq of

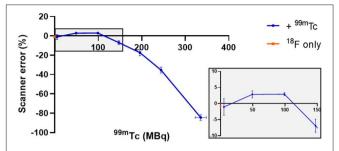


FIGURE 1 | Effect of different amounts of ^{99m}Tc on the accuracy of PET scanner quantification of 5 MBq ¹⁸F. The effect on scanner quantification was assessed by comparing the amount of ¹⁸F measured by the dose calibrator to that measured by the PET scanner; n=3, mean \pm SD. Gray box inset provides zoom of 0–150 MBq region.

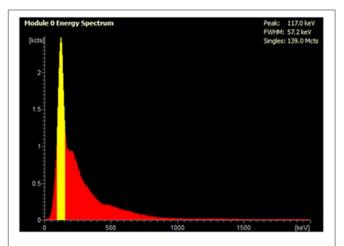


FIGURE 2 Live acquisition energy spectrum obtained during a PET scan of a mixed radionuclide phantom containing 5 MBq $^{18}\mathrm{F}$ and 250 MBq $^{99m}\mathrm{Tc}$. The yellow peak at 140 keV corresponds to the energy of $^{99m}\mathrm{Tc}$ γ photons, which reduces detection of $^{18}\mathrm{F}$ coincident photons at 511 keV.

^{99m}Tc, ¹⁸F quantification was underestimated by < 10% and became progressively worse with increasing amounts of ^{99m}Tc: at 350 MBq the scanner was underestimating activity of 18 F by >80% (Figure 1). The live acquisition energy spectrum (Figure 2, **Supplementary Figure 3**) showed that at these higher activities of ^{99m}Tc, photons at 140 keV (attributable to ^{99m}Tc decay) overwhelmed the detection of 511 keV photons originating from ¹⁸F decay suggesting that the dead-time correction could not cope with the increased singles rate. Note that the true counts decrease considerably when adding 99mTc to 18F (Supplementary Tables 1, 2). However, activity quantification showed low errors up to 100 MBq added 99mTc (Figure 1) due to the intrinsic dead-time correction of the scanner. Note also that both 99mTc only and water have similar numbers of true counts which originate from the intrinsic radiation of the LYSO:Ce crystals.

The effect of $^{99\mathrm{m}}$ Tc on PET image quality was examined (qualitatively) by observing image noise present with increasing $^{99\mathrm{m}}$ Tc activity in the field-of-view. PET image quality was

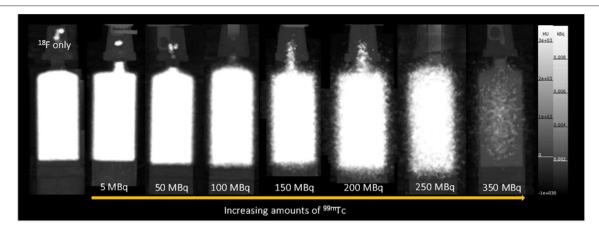


FIGURE 3 | PET-CT MIPs of mixed-radionuclide ¹⁸F + ^{99m}Tc phantoms. Each syringe contains ¹⁸F (5 MBq) mixed with increasing amounts of ^{99m}Tc (0–350 MBq). An ¹⁸F only (5 MBq) control is included for comparison.

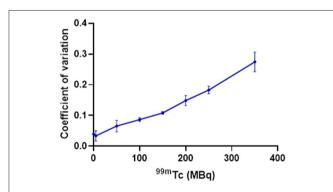


FIGURE 4 | Effect of increasing amounts of ^{99m}Tc on the PET image quality of 5 MBq ¹⁸F, quantified by calculating the coefficient of variation within an ROI for each image (SD/mean); n=3.

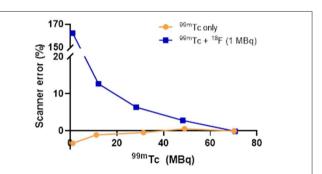


FIGURE 5 | Effect of ¹⁸F (1 MBq) on the accuracy of SPECT scanner quantification of increasing amounts of ^{99m}Tc. The effect on scanner quantification was assessed by comparing the amount of ^{99m}Tc measured by the dose calibrator to that measured by the SPECT scanner.

maintained in the presence of 5 MBq ^{99m}Tc when compared to its ¹⁸F-only control (**Figure 3**). Addition of 50 MBq ^{99m}Tc caused image quality (in terms of signal-to-noise) to deteriorate noticeably, with images becoming more diffuse and lacking in definition. Image quality became progressively worse with increasing amounts of ^{99m}Tc (**Figure 3**). These qualitative observations were supported by quantitative analysis of the images: the coefficient of variation for each image increased with increasing amounts of ^{99m}Tc present (**Figure 4**).

Effect of ¹⁸F on SPECT Scans

The effect of the presence of PET radionuclide ¹⁸F on ^{99m}Tc SPECT scans was assessed by the use of phantoms. The SPECT scanner calibration was checked prior to the start of the study: ^{99m}Tc-only phantoms measured in the dose calibrator and SPECT scanner showed good agreement (within 5%).

At equivalent activities of ^{99m}Tc and ¹⁸F (1:1), quantification

At equivalent activities of ^{99m}Tc and ¹⁸F (1:1), quantification of ^{99m}Tc was poor, with the scanner overestimating ^{99m}Tc activity by > 150% (1 MBq vs. 2.75 MBq) (**Figure 5**). A 10-fold increase in the activity of ^{99m}Tc relative to ¹⁸F dramatically

improved scanner quantification accuracy, reducing 99m Tc activity overestimation to 10% (**Figure 5**). Further increases in the quantity of 99m Tc incrementally improved scanner quantification accuracy in the presence of 1 MBq 18 F. The adverse effects of 18 F on scanner quantification accuracy were mitigated completely when 99m Tc was in 70-fold excess compared to 18 F (**Figure 5**). SPECT image quality was also affected by the presence of 18 F, with high levels of noise observed at 99m Tc: 18 F ratios of 1:1 and 10:1 (**Figure 6**). At ratios of 30:1 and above, noise levels observed qualitatively in the images were significantly reduced and images became sharper (**Figure 6**). The acquisition energy spectrum of an 18 F-only phantom on the SPECT scanner showed detection of a range of photon energies, including some in the $140 \pm 10\%$ (20% width) keV 99m Tc energy window (**Figure 7**).

Compton Scatter Data Correction

The SPECT scanner calibration was checked prior to the start of the study: ^{99m}Tc-only phantoms measured in the dose calibrator and SPECT scanner showed good agreement (within 1%): a ^{99m}Tc-only sample measured 50.8 MBq and 51.0 MBq in the

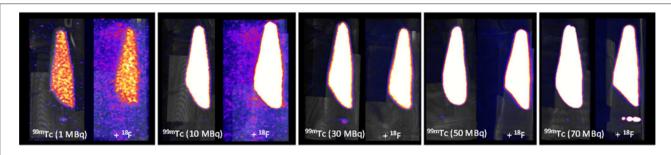


FIGURE 6 | SPECT-CT MIPs of ^{99m}Tc only and mixed-radionuclide ^{99m}Tc + ¹⁸F phantoms. Each tube contained either ^{99m}Tc only (1, 10, 30, 50, 70 MBq) or ^{99m}Tc (1, 10, 30, 50, 70 MBq) mixed with ¹⁸F (1 MBq). All images scaled to the same threshold and intensity.

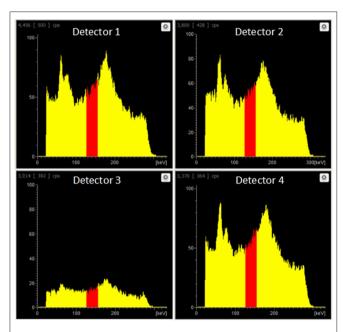


FIGURE 7 Live acquisition energy spectrum obtained during a SPECT scan of an 18 F-only phantom (1 MBq). A range of energies is evident, including energies in the 140.5 keV $\pm 10\%$ (i.e. 20% width) 99m Tc energy window (red).

dose calibrator and the SPECT scanner, respectively. The mixedradionuclide sample containing ¹⁸F (2 MBq) plus ^{99m}Tc (50.7 MBq, measured by dose calibrator) was quantified as 55.84 MBq on the SPECT scanner in the 140 \pm 10% keV window, an over-estimate of 10% resulting from the contribution of Compton-scattered 511 keV photons to the 140 keV window. Upon subtraction of the ¹⁸F-only phantom counts from the mixed ¹⁸F+^{99m}Tc counts, the resulting "scatter-corrected" data were quantified at 51.89 MBq, an over-estimation of only 2%. The coefficient of variation for the original image and scatter-corrected image was 0.098 and 0.102, respectively. The resulting image was visibly similar to the 99mTc-only control image, showing a substantial reduction in noise and comparable activity compared to the mixed-radionuclide image (Figure 8). This could be implemented in practice as data correction: initially a SPECT scan of the ¹⁸F present is acquired before injection of ^{99m}Tc, to establish the ¹⁸F down-scatter contribution; following injection of ^{99m}Tc and acquisition of the SPECT scan, the ¹⁸F down-scatter component is subtracted to provide an accurate ^{99m}Tc uptake distribution.

DISCUSSION

Our specific motivation for this work originated from the need to compare directly two PET tracers for the same biological target, both labeled with ¹⁸F, to understand subtle differences in behavior between the two tracers in vivo. Since the two tracers were labeled with the same PET radionuclide, and hence had identical physical emission profiles, they could not be compared simultaneously in the same animal. A consecutive imaging protocol (administration and PET imaging of the first tracer, followed by administration and PET imaging of the second tracer in the same animal) was possible, in theory. However, the need to allow the first tracer to decay sufficiently to prevent residual activity interfering with the second scan, combined with limits on animal exposure to anesthesia and recovery time (our specific animal license requires a minimum of 3h between mouse recovery and being re-anesthetized) means the imposed delay between tracer administration could lead to significant physiological changes (effects of anesthesia, metabolism, tumor size etc.) in the animal between the two scans. Similarly, evaluating each tracer in a different animal introduces inherent variability between mice, thus no longer maintaining a controlled environment for accurate tracer comparison.

Our solution was to adopt a paired-control approach, using a single SPECT (99mTc) tracer (for the same biological target) in conjunction with each PET tracer, where each tracer can be imaged in the presence of the other because ¹⁸F and ^{99m}Tc possess different emission profiles. Thus, the need to understand the impact of each radionuclide on the scanning of the other presented itself, and mixed-radionuclide ¹⁸F/^{99m}Tc phantom experiments were carried out to determine the crossover effects of each radionuclide on the scans. Of course, dual radionuclide PET/SPECT imaging is not only relevant to our niche example; it is of value more generally, to enable evaluation of different, but related, biological systems

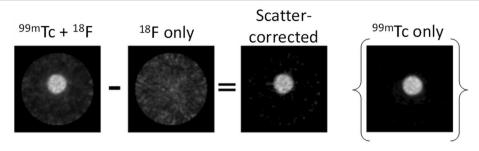


FIGURE 8 | Proof-of-concept for SPECT scatter data correction method. The ¹⁸F-only scatter map image was subtracted from the ^{99m}Tc + ¹⁸F mixed-radionuclide image to achieve the final scatter-corrected image. The ^{99m}Tc-only image is included for comparison.

at (almost) the same time using different tracers labeled with different radionuclides.

Firstly we examined the effect of 99mTc on 18F PET scans. Dead-time effects are observed on the PET scanner when there is too much of any radionuclide. A previous Noise Equivalent Counting (NEC) study performed on our PET scanner showed count-rate peaks at 430 kcps at 36 MBq and 130 kcps at 27 MBq for ¹⁸F in mouse and rat phantoms, respectively [2]. The injected activity for a mouse in our PET scanner is typically 2-10 MBq; 5 MBq ¹⁸F was used in this phantom experiment, which is well below the NEC peaks, and therefore quantification is not affected by dead-time when this quantity of ¹⁸F alone is used. However, when combined with 99mTc, we must assess the contribution of 99mTc photons emitted to scanner dead-time, and hence the effects on PET image quality and quantification. We see that when combined with lower amounts of ^{99m}Tc (<100 MBq), ¹⁸F quantification is unaffected, but 140 keV photon contribution from higher amounts of ^{99m}Tc (>150 MBq) prevents coincident 511 keV PET photons being recorded, causing the scanner to significantly underestimate ¹⁸F activity. In practice, a typical ^{99m}Tc SPECT scan requires only 10-40 MBq injection. These results enable us to assess the feasibility of a hypothetical imaging protocol as follows: (i) administration of SPECT tracer (99mTc, 40 MBq) (ii) SPECT image acquisition (1 h) (iii) administration of PET tracer (¹⁸F, 5 MBq) (iv) PET image acquisition (1 h), in the presence of ^{99m}Tc. Our phantom studies show that at these levels of activity, ¹⁸F PET quantification is not affected by the presence of ^{99m}Tc. However, even at levels of ^{99m}Tc where quantification accuracy is maintained, PET image quality does appear to be compromised. In the presence of 50 MBq ^{99m}Tc, images becomes a little more diffuse with reduced definition. While this slight decrease in image quality is unlikely to be problematic for the majority of imaging scenarios, it could make identification and visualization of very small biological structures (e.g. tumor metastases) more difficult.

Next we examined the effect of ¹⁸F on ^{99m}Tc SPECT scans. In the presence of ¹⁸F, ^{99m}Tc SPECT image quantification and quality were affected by Compton scatter, leading to an overestimation of ^{99m}Tc and increase in noise. However, when ^{99m}Tc activity was 70-fold higher than ¹⁸F this over-estimation could be mitigated completely and image quality preserved.

In practice, a good 1 h dynamic PET scan can be achieved with 3 MBq 18F alone and, taking into account decay $(t_{1/2} = 109.8 \,\mathrm{min})$, no more than 2 MBq of $^{18}\mathrm{F}$ tracer would be residual in the animal after the 1h scan. Our results enable assessment of the feasibility of an alternative hypothetical imaging protocol, as follows: (i) administration of PET tracer (18F, 3 MBq) (ii) PET image acquisition (1h) (iii) administration of SPECT tracer (99mTc, > 140 MBq, to maintain 70:1 99mTc:18F ratio) (iv) SPECT image acquisition (1 h) in the presence of ¹⁸F. Our phantom studies show that at these radionuclide activity ratios, 99mTc SPECT image quantification and quality is not affected by the presence of ¹⁸F. However, although we can control this radionuclide activity ratio at the time of SPECT tracer injection, we cannot know if this 70:1 ratio is maintained in vivo-the biodistribution of both PET and SPECT tracers would need to be similar for this to be true. This, plus the need for otherwise unnecessarily high levels of radioactivity, makes this protocol an inferior option.

From a biological perspective, it would be preferable to co-administer both tracers at the same time, but based on our findings, there is no combination of imaging sequence and tracer quantity (without waiting several hours for radionuclide decay) that would allow the two radionuclides to be injected *simultaneously* and each scanned in the presence of the other, without having a major effect on image quality and quantification. Furthermore, images of each tracer at the same time after injection could not be obtained with simultaneous injection.

We also explored simple computational methods for correcting for the effects of Compton scatter on the SPECT scanner. One approach involves using the ¹⁸F-only PET scan to identify sources of ¹⁸F, and then subtracting this from the mixed-radionuclide SPECT scan. This process becomes quite complex because we are attempting to combine data collected from two different and essentially unrelated pieces of equipment; differences between the PET and SPECT scanners must be accounted for and this requires additional calibration steps to be done for each set of measurements obtained on the scanners. An additional complication of this method is the need to maintain animal position between the two scanners

so that images can be accurately co-registered. Even with the most careful transfer between scanners (the animal bed is compatible with both scanners and could be transferred without removing the mouse), a registration step would be required using the CT scans of the mice to obtain a "best case" match for the scatter map. While it would be possible to produce a warp field for the mouse shift in position, this quickly becomes an overly-complex solution. A more practical approach might therefore be achieved using the SPECT scanner directly to obtain an ¹⁸F scatter map, prior to injection of ^{99m}Tc. This method would involve incorporating an additional SPECT scan into the scanning protocol and makes the assumption that scatter present in the ¹⁸F-only scatter map is comparable to that obtained when the SPECT tracer is also present (i.e. no change in biodistribution between SPECT scans). The scatter map must also be corrected for radionuclide decay between scans. Our proof-of-concept phantom experiment demonstrated that this scatter-correction method could be used easily and successfully to remove noise caused by Compton scattering of ¹⁸F photons. The proposed preclinical imaging protocol would then be as follows: (i) administration of PET tracer (¹⁸F) (ii) PET image acquisition (iii) SPECT image acquisition (to obtain ¹⁸F scatter map) (iv) administration of SPECT tracer (99mTc) (v) SPECT image acquisition (in the presence of ¹⁸F) (vi) scatter map image subtraction. This approach builds the scatter map acquisition into the scanning protocol, and would therefore be applicable to any PET/SPECT radionuclide combination, any radionuclide activity, and any scanner model, without requiring calibration for each experiment, making this method an attractive option for dual radionuclide PET/SPECT imaging.

The ability to obtain accurate parallel scans with PET and SPECT tracers would allow the limits of molecular imaging to be extended and would be useful for comparison of different radiotracers or to image multiple related molecular processes simultaneously to obtain a deeper understanding of interlinked processes. Examples could include temporospatial mapping of anti-cancer drug delivery (e.g. via liposomal formulation) and response in relation to the disease site [6], and in advanced cell-based therapies where the trafficking of cells to disease sites has to be quantified alongside mapping of the disease and response to therapy. Similarly, SPECT imaging of the biodistribution of therapeutic radionuclides that emit both imageable gamma photons (e.g. ¹⁷⁷Lu, ⁶⁷Cu, ¹⁸⁸Re) could be performed alongside PET imaging (e.g. with [18F]FDG or other tracer) of metabolic response to therapy. It would also enable imaging of multiple molecular characteristics of disease in an animal to obtain metabolic and gene expression profiles or characterize diseases such as cancer where heterogeneity is to be expected.

CONCLUSION

Sequential PET and SPECT data acquisition whilst both positron- and gamma-emitters are present is feasible under certain conditions without substantial influence on image quantification accuracy. Suitable combinations of injection

sequence and imaging sequence can be devised to match the biological requirements of a particular experiment, using existing commercial small animal PET and SPECT scanners, with only minor or insignificant effects of each radionuclide on the scan of the other. However, simultaneous tracer injection is not feasible under any combination of imaging sequence and tracer quantity, and does not allow images of each tracer to be obtained at the same time after injection.

DATA AVAILABILITY STATEMENT

The datasets generated for this study are available on request to the corresponding author.

AUTHOR CONTRIBUTIONS

LL and PB contributed conception of the study. LL, PB, JEB, JKB, AR, MF, HO'B, JJ, KS, JB, and CP contributed design of the study. JEB, JKB, AR, MF, JK, and CP contributed phantom data acquisition. JKB, JK, JEB, and KS contributed image analysis. HO'B and JJ contributed code development. JEB wrote the first draft of the manuscript. LL, PB, JEB, KS, and JK contributed to manuscript revision. All authors read and approved the submitted version.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fphy. 2020.00126/full#supplementary-material

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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In vivo PET/MRI Imaging of the Chorioallantoic Membrane

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The Hen's Egg Test Chorioallantoic Membrane (HET-CAM) of fertilized chick eggs represents a unique model for biomedical research. With its steadily increasing use, non-invasive *in ovo* imaging for longitudinal direct quantification of the biodistribution of compounds or monitoring of surrogate markers has been introduced. The full range of imaging methods has been applied to the HET-CAM model. From the current perspective, Magnetic Resonance Imaging (MRI) and Positron Emission Tomography (PET) appear promising techniques, providing detailed anatomical and functional information (MRI) and excellent sensitivity (PET). Especially by combining both techniques, the required sensitivity and anatomical localization of the signal source renders feasible. In the following, a review of recent applications of MRI and PET for *in ovo* imaging with a special focus on techniques for imaging *xenotransplanted* tumors on the CAM will be provided.

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INTRODUCTION

The Hen's Egg Test Chorioallantoic-Membrane (HET-CAM) of fertilized chicken eggs represents a unique model for biomedical research. During the development, the mesodermal layers of the allantois and chorion form the chorioallantoic membrane (CAM). This structure forms a rich vascular network enabling to study tissue grafts, tumor growth, metastasis formation, wound healing, drug delivery, toxicologic analysis, angiogenic and anti-angiogenic molecules [1].

The HET-CAM represents a relatively simple, quick, and low-cost model that allows screening of a large number of pharmacological samples in a short time. It has been successfully used to study cancer progression and its pharmacological treatment [2–8], angiogenesis [9], pharmacokinetics [10], properties of novel nanomaterials [9, 11], or as a model system to study microsurgical instruments and techniques [12]. Especially for xenotransplantation tumor models, the HET-CAM offers various advantages in comparison to the murine models. Since the development of the lymphoid system starts in the late stage of incubation, the HET-CAM model represents a naturally immunodeficient host, enabling xenotransplantation of many kinds of tumors without species-specific limitations [11]. The blood vessel network of the CAM thereby provides an excellent environment for primary tumor formation and a basis for angiogenic blood vessel formation [12]. Human cell line derived [13] xenografts are considered an increasingly valuable tool in oncology potentially providing biologically models of many different cancer types. Where immunodeficient rodent models

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pose barriers to widespread application due to cost and efficiency constraints, the HET-CAM model renders as efficient model especially for initial testing of tumor progression [10, 14–16], in many countries not requiring any approval for animal experiments, if sacrificed before hatching.

Due to its simplicity, the HET-CAM model appears as ideal platform for initial testing of pharmacological compounds and tissue properties, including biodistribution assessment or efficacy assessment of new compounds [1, 8, 13–19].

With the increasing use of the HET-CAM model and the need for longitudinal monitoring, non-invasive in ovo imaging of the chick embryo and especially the CAM has gained interest over recent years. Optical methods like optical coherence tomography (OCT) and Doppler techniques have successfully been applied for deriving functional and physiological properties of the embryo [20–38]. Three-dimensional microcomputed tomography (μ CT) has been applied in ovo, especially in the field of bone volume and mineral density assessment [39-46]. With the recent advances in magnetic resonance tomography (MRI) its application to in ovo imaging has rendered feasible and many applications of the technique in the live embryo as well as after sacrification have been reported for different scientific fields, including embryonal development [47-54], ophthalmology [48-57], oncology [58-63], metabolic assessment [54, 64], and initial testing of the biodistribution of new compounds [65-67]. Further, nuclear imaging methods have been translated to in ovo imaging, mainly for initial testing of new labeling strategies [19, 68–71].

Considering the capability of the HET-CAM model for monitoring the growth and progression of xenotransplanted tumors rises a huge potential for its use in the evaluation of the biodistribution of new compounds, especially in combination with specific targeting strategies. In this context the combination of the multi-contrast capabilities of MRI with the outstanding sensitivity of positron emission tomography (PET) appears promising. In the following a review of recent applications of MRI and PET for *in ovo* imaging with a special focus on techniques for imaging xenotransplanted tumors on the CAM will be provided.

THE HET-CAM MODEL

In preclinical research and drug development can-cer cell lines (CCL) are frequently used. However, in culture, CCLs often fail to retain morphology, cellular heterogeneity, and molecular profiles of the donor tissue [72, 73], and drug performance in xenografts may not perfectly reflect clinical efficacy [74]. The success of new drugs in oncology requires preclinical models that render the full heterogeneity and pathophysiology of patient tumors, and CCL or patient-derived xenografts (PDX) may mimic physiological drug effects [75, 76].

A broad range of applications for CCL and PDX have been reported using rodent models as host and their efficient use in prediction of response, development of biomarkers, and monitoring and identification of efficient treatment regimens has been proven [77]. Despite their frequent use, rodent models have practical and scientific limitations. In many applications,

rodent models have shown a very limited success rate in engraftment. Successful engraftment often takes several months. Further high, often prohibitive costs and resources are required for keeping rodents in an appropriate facility under proper hygienic conditions. They are labor-intensive, time-consuming, and require ethical approval by the regulatory authorities.

The HET-CAM model represents a well-established alternative in vivo assay. It presents a highly vascularized extra-embryonic membrane, which is connected to the embryo through a continuous circulatory system. Even though T and B cells can be detected in the chick embryo immune system by embryo development day (EDD) 11 and 12, full immune competence is not developed until EDD 18 [16]. The HET-CAM is a low-cost model with the limita-tion of developing a nonspecific inflammatory response after EDD 15 [1]. Xenotransplantation and growth of cancer cell lines on the CAM is well-established (Figure 1) and has amongst others been applied for initial assessment of the efficacy of anticancer drugs [78]. Compared to the rodent models, tumor formation on the CAM is fast, with graft vascularization and thus interface to the chick embryo vascular system normally established already after 2-5 days [79].

For xenotransplantation, fertilized chicken eggs e.g., White Leghorn (Gallus domesticus) are purchased from a hatchery and maintained at 37.8°C and a 60% relative humidity atmosphere for the whole incubation period. Upon arrival the eggs are carefully cleaned (e.g., by 70% ethanol solution) and incubation is started (EDD 0). After 4 days (EDD 4) of incubation the eggs are fenestrated and analyzed for fertilization by visual assessment of the CAM vascularization and heartbeat of the embryo. The shell access window is sealed to prevent contamination and the egg placed back into the incubator. Cancer cells are seeded on the CAM and a solid tumor, well interfaced to the extra-embryonic vascular system, forms within few days [1, 16]. The viability of the embryos needs to be monitored daily by checking the CAM vasculature for blood flow, physiological embryo movement, and the growth of the chick embryo according to Hamburger and Hamilton [80].

MAGNETIC RESONANCE IMAGING (MRI)

With its versatile image contrast, MRI raised interest in imaging of chick embryos already in the 80s. In 1986, Bone et al. [81, 82] reported first three-dimensional MR microscopy on the live chick embryo. At a 1.5T prototype system with dedicated gradient system and receive coil, they achieved a spatial resolution of 200 x 200 x 1200 μm^3 with T1 and T2 weighting, applying partial saturation (PS) and spin echo (SE) 3D-Fourier imaging techniques (3D-FT). To minimize motion-induced image artifacts, the chick embryo was immobilized by placing the egg in ice chips between 20 (EDD 11) and 90 (EDD 15) minutes. Imaging was performed at room temperature. Even though the spatial resolution and hence the fidelity of the anatomical details was still limited, Bone et al. clearly showed the potential combination of *in ovo* imaging and MRI as basis for further MRI studies. Improvements in spatial resolution were

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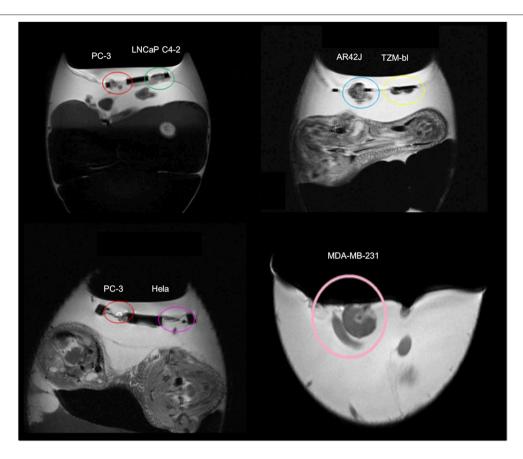


FIGURE 1 | Magnetic resonance images (MRI) of xenotransplanted tumors grown on the chorioallantoic membrane (CAM) from different cell lines (prostate cancer: PC-3, LNCaP C4-2; pancreas cancer: AR42J; adenocarcinoma: TZM-bl; cervical cancer: HELA; breast cancer: MDA-MB-231). Unpublished imaging material provided by Winter and Li.

reported by Effmann et al. [83], who used an implantable 18 mm diameter RF coil wrapped around the chick embryo, inductively coupled to an outside MR receiver [84]. With the resulting gain in signal-to-noise ratio (SNR), the PS 3D-FT could provide images with spatial resolutions of up to 50 x 50 x 600 μm^3 within 1-2 h scan times.

Assessment of metabolic developments by phosphorus ³¹P MR spectroscopy (MRS) in correlation with anatomic developments were first reported by Moseley et al. in 1989 [54], who could clearly demonstrate the decrease of the observable ³¹P volume by 80% indicating the respective tissue uptake. Further spectroscopy work was performed by Lirette et al. [85] for longitudinal quantification of the fat/water ratio (1H MRS) and the phosphormono-/phosphordiester ratio (³¹P MRS). Data were acquired with a 5 cm—diameter surface coil, in which the eggs were placed centrally. Acquisition times were below 1 h. Embryo motion was controlled by applying 1-2% halothane during scanning. Peebles et al. [86] applied ¹H MRS for monitoring of brain metabolites and diffusion MRI for assessment of changes in the apparent diffusion coefficient (ADC) in the brain during hypoxia. Immobilization of the chick embryo was achieved by dropping 5.0 mg Ketamine onto the CAM. Single voxel MRS of 6 x 6 x 6 mm³ volumes of interest were acquired in about 30 minutes acquisition time, with subsequent acquisition of the diffusion MRI by a two-point method with 230 x 230 x 2000 $\mu\,m^3$ resolution.

Falen et al. [53] and Hutchison et al. [87] applied MRI with T1 and T2—weighted imaging techniques to the assessment of the yolk structure. Both reported the applicability of MRI for the assessment of the morphology of yolk, albumen, air space, and eggshell. The inner structure of the yolk, including concentric yolk rings, could be clearly visualized by this non-destructive imaging technique. In 2000, Donoghue et al. [88] reported the application of MRI for monitoring residue transfer into egg yolk. After injection of Gd-DTPA, the transfer of the drug into the yolk was monitored by scanning the egg applying a T1-weighted (MP-RAGE) sequence. It could be shown that Gd-DTPA residues were incorporated into the yolk ring structure.

Assessment of the chick embryo vasculature by MRI was reported by Smith et al. in 1992 [89]. They performed *ex vivo* high-resolution MRI of the embryonic vasculature after perfusion fixation of the vasculature structure with gadolinium-doped gelatin. A similar approach was chosen by Hogers et al. [52] to demonstrate the benefit of ultra-highfield imaging by

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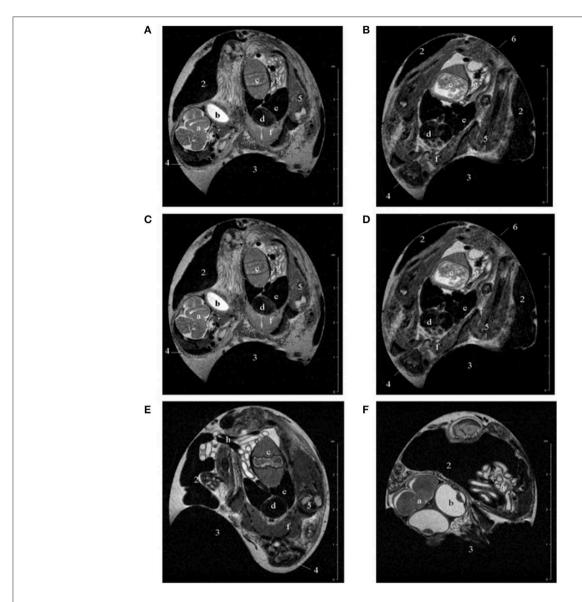


FIGURE 2 | Representative examples of T2-weighted multislice scans of chick embryos in ovo at (A) 12, (B) 15, (C) 17, (D) 18, (E) 19, and (F) 20 days of incubation. 1, albumen; 2, yolk; 3, air sac; 4, head; 5, limb; 6, rump; a, brain; b, eye; c, gizzard; d, heart; e, liver; f, pectoral muscles; g, intestine; h, umbilical vessels. The complete scans can be viewed at www.gla.ac.uk/7tmr/chickegg.htm. This research was originally published in JMRI: Noninvasive Monitoring of Chick Development In Ovo Using a 7T MRI System From Day 12 of Incubation Through to Hatching. Bain et al. [51].

comparing MRI *in vitro* microscopy between 7T and 17.6T field strength. A similar *ex vivo* technique was applied by Zhang et al. [90] and Yelbuz et al. [91, 92], who used the combination of perfusion with immersion fixation and a small molecular gadolinium agent to improve image contrast between the myocardial wall and heart lumen. Isotropic three-dimensional images with up to $25^3 \, \mu m^3$ spatial resolution were acquired with a T1-weighted spin warp technique in about 29 h scan time at 9.4T field strength. *In ovo* quantification of the cardiac function was reported by Holmes et al. [93, 94] applying a self-gating technique for cardiac synchronization of the data. Even though

adequate image quality could be obtained, the authors identified the bulk embryo motion at earlier stages as main limiting factor for reproducible image quality.

Noninvasive monitoring of chick embryo development was reported by Bain et al. [51] in 2007. For optimal image contrast a T2-weighted spin echo technique (RARE) was applied yielding 195 x 195 x 500 μ m³ spatial resolution within 25 minutes scan time at 7T (**Figure 2**). Rapid three-dimensional T1-weighted techniques provided higher spatial resolution, but organ contrast was not sufficient. For chick embryo immobilization, Bain et al. [51] used a precooling protocol, keeping the chicken eggs at

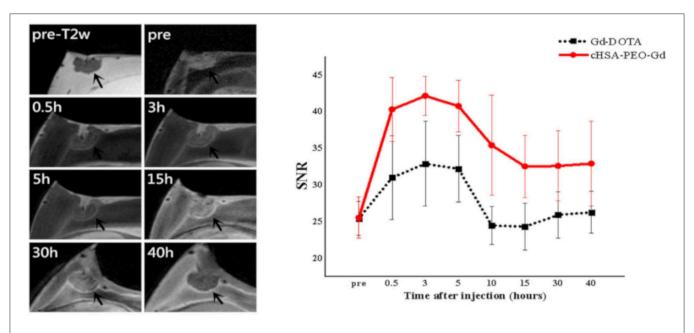


FIGURE 3 | Representative MR images of cHSA-PEO(2000)16-Gd biodistribution in solid tumor (left) and comparison of the SNR (Signal-to-Noise Ratio) of the tumor (right) over the first 40 h after systemic injection of cHSA-PEO(2000)16-Gd and Gd-DOTA. This research was originally published under the terms of the CC BY license (Creative Commons Attribution 4.0 International License) in Sci Rep: The CAM cancer xenograft as a model for initial evaluation of MR labeled compounds. Zuo et al. [65].

4°C for 60 min prior to data acquisition with subsequent data acquisition at room temperature. No slowdown or arrest of the chick embryo development was observed by the cooling or the MRI examinations. As alternative cooling protocol, Li et al. [95] suggested data acquisition at 19°C thus enabling scan times of up to 4 hours in quail embryos. More advanced imaging techniques including T1 and T2 mapping as well as magnetization transfer ratio (MTR) quantification were reported by Boss et al. [50]. Motion reduction was achieved by application of 0.5 mL Ketamine onto the CAM. Images were acquired with two-dimensional multi-slice techniques at a spatial resolution of 180 x 180 x 1000 μ m³ (T1), 260 x 260 x 1000 μ m³ (T2), and 230 x 230 x 1000 μ m³ (MTR). In 2015, Zhou et al. [49] translated developmental imaging of the brain to a 3T clinical scanner equipped with a dedicated small animal coil. T2 weighted RARE images as well as DTI data could be acquired at reasonable spatial resolution (T2w: 170 x 170 x 1000 μm³ in 8 minutes, DTI: 1.25 x 1.25 x 1 mm³ in 6 minutes), enabling noninvasive analysis of brain development including structural information. Imaging of the chick embryo brain development after Zika virus infection was reported by Goodfellow et al. [96], who could clearly demonstrate Zika virus induced microcephaly. Highresolution MRI at 7T were presented by Lindner et al. [48] for monitoring the chick embryo eye development. Immobilization of the embryo was achieved by bedding the egg on crushed ice ten minutes before scanning.

A first application of *in ovo* MRI for the assessment of the biodistribution of new compounds was reported by Dingman et al. [97] in 2003. They longitudinally investigated the distribution of a 19F-labeled L-6-heptafluorobutyryl-5-hydroxytryptophan including uptake dynamics and crossing

of the blood-brain barrier. In 2007, Oppitz et al. [98] suggested the use of chick embryo model for evaluation of the advantages and limitations of MRI to monitor the migration of superparamagnetic iron oxide (SPIO) labeled cells. A similar approach was presented by Pereira et al. [99] who showed in the chick embryo model an improved sensitivity for in vivo cell tracking after implantation by supplementing the culture medium with adequate iron sources as compared to the use of reporter genes. Faucher et al. [100] used the HET-CAM model for initial investigation of ultra-small gadolinium oxide nanoparticles for labeling of glioblastoma cells, seeded on the CAM. Taylor et al. [101] used the chick embryo model for initial evaluation of new nano- and micro-sized magnetic particles for cell tracking. All imaging was performed ex vivo. In 2017, Zuo et al. [65] reported the use of human cancer cell lines xenotransplanted onto the CAM for initial assessment of the biodistribution of MR labeled drugs. After injection of Gd-DOTA, the biodistribution of the compound in the chick embryo as well as in the xenotransplanted tumor was observed. By longitudinal imaging studies over 40 h, the accumulation and clearance of the contrast agent could be monitored. The technique was applied for demonstrating the feasibility of the HET-CAM tumor model for monitoring the fate of new MR labeled drugs by following the image contrast after intravenous administration of a gadolinium-labelled polymeric nanoparticle at high spatial resolution, applying an immobilization protocol as suggested earlier [61]. In direct comparison with conventional contrast agents, a significantly prolonged retention time of the polymeric nanoparticle in the tumor could be shown (Figure 3). For assessment of the intra-tumor distribution, 3D T1 weighted data were acquired at high spatial resolution of 100 x 100

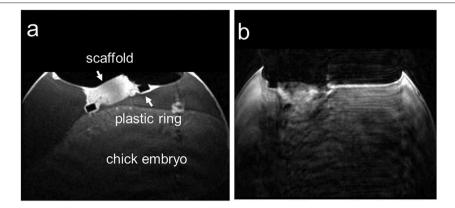


FIGURE 4 | Two in ovo T1-weighted MR images of the chick embryo on ID 14, seven days post-implantation on the CAM acquired in an axial slice through the biomaterial scaffold; (a) image without motion artifact and (b) image with motion artifacts that was excluded from further analysis. This research was originally published under the terms of the CC BY license (Creative Commons Attribution 4.0 International License) in Sci Rep: Comparison of medetomidine, thiopental and ketamine/midazolam anesthesia in chick embryos for in ovo Magnetic Resonance Imaging free of motion artifacts. Waschkies et al. [106].

x 560 μm^3 . Hafner et al. [102] used a similar approach for initial evaluation of the biodistribution of a multifunctional drug carrier.

Buschmann et al. [103] reported implantation of human osteoblasts-seeded scaffolds onto the CAM. One week after xenotransplantation, MRI (T1, T2 quantification) analysis was performed ex vivo, after intravenous injection or dripping of gadolinium onto the scaffold before sacrificing the embryo allowing for the analysis of the formation of new capillaries. The published ex vivo data clearly indicated the potential of the HET-CAM model as cheap reliable model for monitoring the angiogenesis in tissue-engineering. This work was further developed by Chesnick et al. [104] by initial testing of a new adrenolate labeled gadolinium complex for specific targeting to bone mineral. In 2015, Pfiffner et al. [105] presented in vivo MRI at 4.7T to noninvasively quantify and monitor the perfusion capacity in the HET-CAM model. After placing a biomaterial on the CAM, its perfusion capacity was quantified by relaxation rate changes after intravenous injection of the gadolinium-based contrast agent. Immobilization of the chick embryo was achieved by 5 drops of ketamine 1:100 (Ketasol-100, Graeub, Switzerland) dripped onto the CAM surface. Anatomical reference images were obtained applying a FLASH sequence at measured spatial resolution of roughly 500² μm². T1 and T2 maps were derived applying RARE sequences with multiple repetition times (TR) and echo times (TE) at spatial resolution of 200 x 200 x 1000 μ m³ before and at different time points after intravenous injection of 100 µL Gd-DOTA (0.5M) MRI contrast agent. Relaxation rate changes over the scaffold could be clearly assessed indicating different vascular density, which was confirmed by histology.

Motion artifacts introduced by bulk motion of the chick embryo is a major limiting factor for high-resolution imaging of the CAM (**Figure 4**). In 2015, Waschkies et al. [106] investigated the use of different anesthesia drugs for immobilization, whereas Zuo et al. [61] evaluated an age-adjusted precooling protocol for high-resolution imaging of the CAM. In Waschkies *et al*, medetomidine at a dosage of 0.3 mg/kg, was compared to

thiopental at 100 mg/kg and ketamine/midazolam at 50 and 1 mg/kg. The soluble anesthetics were applied by dropping a total volume of 0.3 mL onto the surface of the CAM. It was demonstrated that medetomidine performed best, enabling motion-free MRI for a period of about 30 min starting 10 min after application. Ketamine/midazolam yielded insufficient depth of anesthesia and thiopental anesthesia did not immobilize the chick embryo sufficiently long. In contrast, Zuo et al. investigated the use of an anesthesia-free immobilization approach. As extension to earlier published work [51], they suggested adaptation of the precooling time according to the age of the chick embryo, thereby achieving almost complete immobilization of the chick embryo for at least 60 min thus allowing multi-contrast high-resolution imaging of the chick embryo and xenotransplanted tumors on the CAM (Figures 5, 6). The suggested cooling protocol allowed in vivo imaging at high spatial resolution as 77 x 91 x 500 μm³ (T2 weighted anatomic, 2D), 200 x 200 x 500 μm³ (diffusion weighted, 2D), 104 x 98 x 500 μ m³ (T2 mapping, 2D), and 100 x 100 x 560 μm³ (T1 weighted, 3D). Tumor volume and growth could be monitored longitudinally from day 4 to day 9 after xenotransplantation. The tumor progression could be monitored for each individual case (Figure 7) and the volumes derived from MRI at day 9 excellently correlated with the respective volumes derived after resection of the tumors. In 2018, Herrmann et al. [58] reported the application of MRI to measure primary neuroblastoma tumor size and metastasis in a chick embryo model. Human neuroblastoma cells labeled with green fluorescent protein (GFP) and micron-sized iron particles were xenotransplanted on the CAM at EDD 7. At EDD 14, T2 RARE and T2-weighted fast low angle shot (FLASH) data were acquired (Figure 8) using the cooling protocol as suggested by Zuo et al. [61]. Additionally, Herrmann et al. performed timeof-flight (ToF) MR angiography (MRA) and reported a reduced blood flow if using the cooling protocol, making successful ToF acquisition unfeasible. Instead, ketamine anesthesia (3.6 mM ketamine in 500 μL PBS) was applied resulting in MRI data free

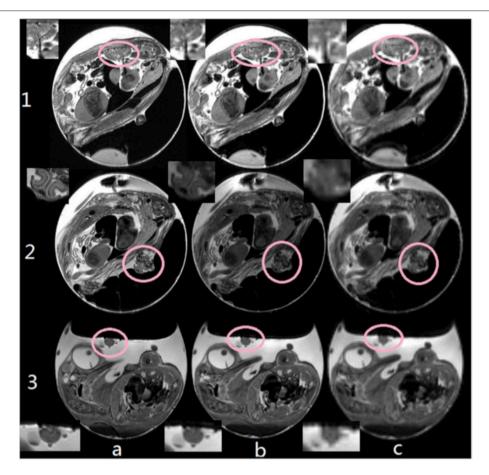


FIGURE 5 | Comparison between different image resolution: (a) 77 × 91 μm², (b) 200 × 200 μm², and (c) 500 × 500. With increasing resolution, details of e.g., the pulmonary veins (1), the beak (2, axial orientation), and tumor tissues (3) could be clearly resolved. Insets show details of the respective target structures. This research was originally published in NMR Biomed: High-resolution MRI analysis of breast cancer xenograft on the chick chorioallantoic membrane. Zuo et al. [61].

of motion artifacts for a period of 30 min. The micron-sized iron labeling of the cells allowed *in ovo* assessment of the primary tumor and detection of metastatic deposits.

POSITRON EMISSION TOMOGRAPHY (PET)

Most anatomic and functional imaging of the HET-CAM model has been performed by MRI so far. The main limitation of PET results from its rather low spatial resolution, which does not fit the high spatial resolution demands for imaging of the CAM. To gain from the outstanding sensitivity of PET, thus in almost all work published, PET (or SPECT) imaging was complimented by Computer Tomography (CT), x-ray, or MRI for providing additional anatomic details.

In 2012, Würbach et al. [71] introduced using ¹⁸F-fluoride PET for assessment of bone metabolism. For radionuclide injection, a self-built catheter made of a 30G needle and a polythene tube with 0.28 mm inner diameter was introduced into one of the CAM vessels. Imaging was performed for a

period of roughly 75 minutes yielding dynamic images (55 time frames) as well as high-quality static data. Applying an iterative ordinary Poisson maximum a posteriori reconstruction yield voxel sizes of roughly 400 x 400 x 800 μm³. The results proved the quantitative and reproducible assessment of bone metabolism in anesthetized chick embryos. Immobilization of the chick embryo during scanning was achieved by exposing the CAM to isoflurane at 1.5% concentration as suggested by Heidrich et al. [107], who investigated different anesthesia schemes for in vivo imaging of avian embryos, including isoflurane, 2,2,2-tribromoethanol (Avertin), and urethane/αchloralose (UC). UC and Avertin were directly applied as liquids onto the CAM. For isoflurane anesthesia, the egg was exposed to an isoflurane concentration of 5% in oxygen. For induction, the eggs were placed into a narcosis induction chamber. Toxic side effects and only poor correlation between narcosis depth and dose limited the application of UC and Avertin and the authors clearly favored the use of Isoflurane due to its high tolerability enabling repeated imaging of the avian embryos at a daily basis. In 2013, Gebhardt et al. [70] applied a similar approach as Würbach et al. [71] to initially

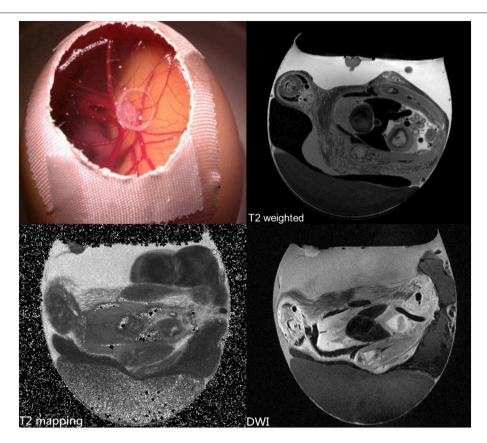


FIGURE 6 | *In vivo* high-resolution MRI with T2 and diffusion weighting (DWI), and T2 quantification of a Human breast tumor (carcinoma cell line MDA-MB-231) xenotransplanted on the CAM. Unpublished imaging material provided by Zuo obtained with precooling and MR protocols as described in [61].

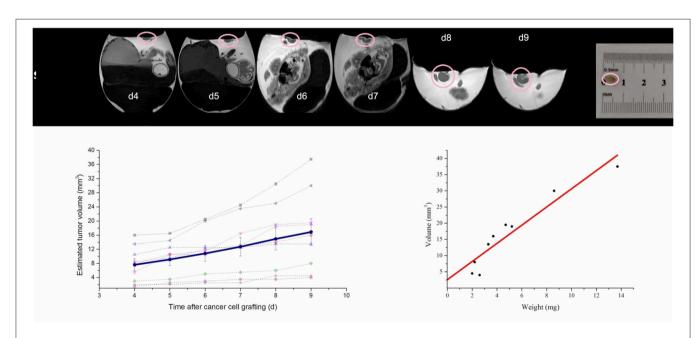


FIGURE 7 | Monitoring the progression of xenotransplanted tumor (circle) from day 4 to day 9 after cell seeding on the CAM. (Top) High-resolution T2 weighted MR images; (lower left) individual tumor volumes (n = 9) and mean volume progression (solid line); (lower right) correlation of tumor volume (n = 9) and weight after tumor resection at day 9. Modified from original research published in NMR Biomed: High-resolution MRI analysis of breast cancer xenograft on the chick chorioallantoic membrane. Zuo et al. [61].

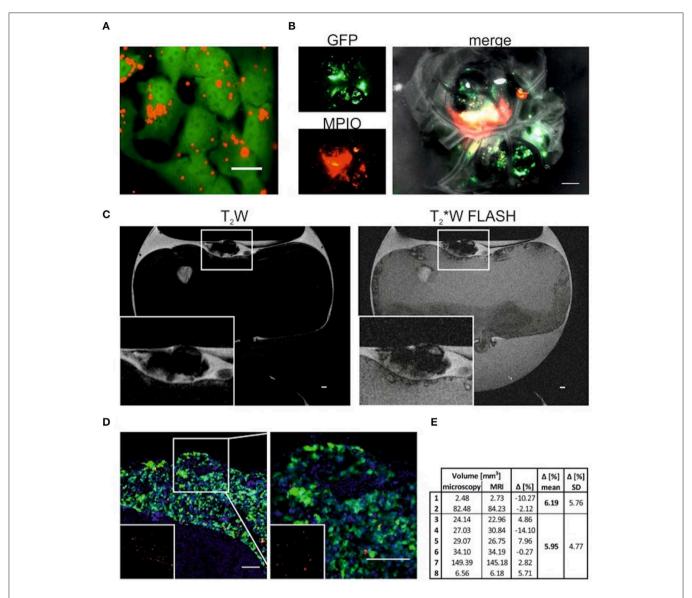


FIGURE 8 | T2W and T2*W FLASH images of tumors labeled with MPIO (A) GFP-expressing SK-N-AS cells (green) 24 h -postlabeling with 20 mM MPIO (Suncoast Yellow Encapsulated Magnetic Polymers—Bangs Beads, Red). Scale bar is 20 mm. (B) Single channel and overlay image of neuroblastoma tumor postdissection formed by GFP-expressing SK-N-AS cells (green) which were labeled with MPIO (red) 48 h prior CAM implantation. Scale bar is 1000 mm. (C) Representative sagittal T2Wand T2*W FLASH MRI images of embryonated chicken egg at E14 (A). Tumor formed by cells labeled with MPIO can be identified on top of the CAM (zoom in inset). Scale bar is 1000 mm. (D) Representative image of tumor formed on the CAM by GFP-expressing SK-N-AS cells (green) labeled with MPIO (red). Nuclei are stained with Hoechst (blue). Inset shows MPIO only (red). Right image is 2.5_ zoom. Scale bar is 100 mm. (E) Comparison of tumor volume (mm3) measured by microscopy or MRI. Tumors 1 to 2 were formed by cells without MPIO, tumors 3 to 8. This research was originally published under the terms of the CC BY license (Creative Commons Attribution 4.0 International License) in Mol Imaging: Magnetic Resonance Imaging for Characterization of a Chick Embryo Model of Cancer Cell Metastases. Herrmann et al. [58].

evaluate the dynamic behavior of new PET tracers in the chick embryo model as an *in vivo* assay. Various ¹⁸F, ⁶⁴Cu, and ⁶⁸Ga-labeled compounds were investigated and the potential of the chick embryo model as efficient *in vivo* model could be shown.

Warnock et al. [69] demonstrated the use of the CAM for screening of novel PET tracers. At EDD 11, the eggs were opened and 5 x 10^6 human U87 glioblastoma cells in 20 μ L

of culture medium xenotransplanted onto the CAM. At EDD 18 PET/CT imaging of the tumors was performed. During scanning the egg was reproducible positioned in both systems in a small animal imaging cell (Minerve equipment veterenaire) allowing temperature control and isoflurane anesthesia (2% in air). Uptake of the radiotracer was clearly demonstrated by time-activity curves and in the PET images (**Figure 9**). Contrast-agent enhanced μ CT data provided accurate anatomic correlation,

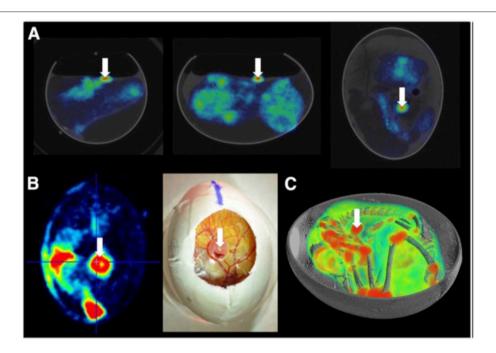


FIGURE 9 | (A) Two-dimensional coregistered PET and CT images of the chicken egg after [18F]-FDG injection and 45 min tracer uptake. (B) Visual comparison of 18F-FDG uptake in glioblastoma at level of CAM to photograph illustrating tumor localization. (C) 3D visualization of overlaid PET and CT images for [18F]-FDG uptake in embryo and U87 human glioblastoma tumor (white arrow). This research was originally published in JNM: *in vivo* PET/CT in a human glioblastoma chicken chorioallantoic membrane model: a new tool for oncology and radiotracer development. Warnock et al. © by the Society of Nuclear Medicine and Molecular Imaging, Inc. [69].

enabling distinction of the uptake in the joints and the tumor. Their outcome clearly indicated the potential of the suggested HET-CAM model for initial assessment of the pharmacokinetics of new compounds.

Haller et al. [19] investigated the tissue distribution and stability of different ¹⁸F, ¹²⁵I, ^{99m}Tc, and ¹⁷⁷Lu—labeled radiopharmaceuticals. For imaging purposes the chick embryos were euthanized by shock-freezing in liquid nitrogen at different time points after administration of the radioactivity. In comparison with the established mouse models, they concluded a similar tissue distribution and stability of radiopharmaceuticals in the chick embryo. The very similar behavior in the two in vivo models indicate the potential of using the chick embryo as an inexpensive and simple test model for preclinical screening of novel radiopharmaceuticals. To overcome the limitations of the small anatomies with respective requirement of dedicated highresolution imaging equipment, Freesmeyer et al. [108] suggested the translation of the work into ostrich eggs and demonstrated the potential use for different radiotracers even on conventional PET/CT systems. Even though overcoming the issues with small anatomy and high-spatial resolution requirements, ostrich eggs cannot be seen as a real alternative to chick embryos, since they are not readily available, hardly established in science, expensive and often do not fit into conventional small animal imaging equipment.

In a recent work of Zlatopolskiy et al. [68] the HET-CAM model was used for evaluation of radiotracers addressing

the tryptophan metabolic pathway. An efficient method for the synthesis of fluorotryptophans, labeled in different positions with ¹⁸F is presented and their biological evaluation regarding tumor targeting evaluated in the HET-CAM model. Therefor MCF7, PC-3, and NCI-H69 xenografts were cultivated on the CAM. The tissue distribution of the new agent 7-[¹⁸F]FTrp in comparison to conventional ¹⁸F⁻ was assessed after systemic injection. While in the ¹⁸F-scans tracer uptake was mainly observed in bones, joints, and beak of the chick embryos, 7-[¹⁸F]FTrp clearly delineated the tumor.

Even though CT represents an important imaging tool providing relevant anatomic information and has proven clinical success in combination with PET, its only limited soft tissue contrast is often insufficient. To that respect in 2019 Steinemann et al. [109] and Winter et al. [110] combined in ovo PET with MRI to make full advantage from the high sensitivity of PET and the excellent soft tissue contrast in MRI. Steinemann et al. used the imaging approach for monitoring the effectiveness of a new chimeric inhibitor (animacroxam, which combines histone deacetylase (HDAC) inhibitory and cytoskeleton-interfering pharmacophores) to the clinical approved HDAC in testicular germ cell tumor. Tumor plaques were grown from 10×10^6 2102EP cells mixed with 150 µl matrigel and transplanted onto the CAM. Imaging was performed three days after xenotransplantation to allow angiogenic connection of the xenograft to the CAM. Injection

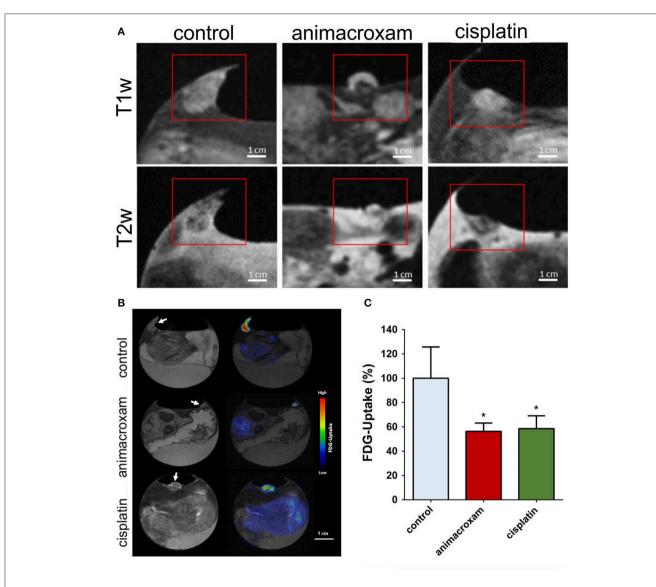


FIGURE 10 | Animacroxam induces 'cap formation' and suppresses glucose uptake in inoculated TGCT plaques. (A) T1w and T2w images of control-, animacroxam-, and cisplatin-treated tumor plaques. Animacroxam-treated tumors show a distinct viable tumor core (dark in T1w-/bright in T2w images) and a necrotic cap (bright in T1w-/dark in T2w images). (B) T1w and corresponding PET-MR images of [^18F]-FDG uptake in tumor plaques treated with NaCl, animacroxam, or cisplatin. (C) Animacroxam (5.0 μ m)- and cisplatin (2.5 μ m)-treated tumor plaques showed a reduced uptake of [^18F]-FDG. Results are shown as means \pm SEM of at least n=3 independent experiments. Scale bar = 1 cm. *P-values of \leq 0.05, unpaired t-test. This research was originally published under the terms of the Creative Commons Attribution License (CC BY) in Molecular Oncology: Antitumor and antiangiogenic activity of the novel chimeric inhibitor animacroxam in testicular germ cell cancer, Steinemann et al. [109].

of the compounds [concentrations calculated assuming 1 mL blood volume: 5 μM animacroxam, 2.5 μM cisplatin, or NaCl (0.9%)], was done intravenously via a 30G syringe. The tumor volume was derived from MRI measurements (3D T1w-GRE, 290 x 290 x 500 μm^3 , TR/TE = 50 ms/2.7 ms; 2D RARE, 290 x 290 x 700 μm^3 , TR/TE = 8885 ms/100 ms) prior and 7 days after treatment. Immobilization of the chick embryos was obtained by 1 h precooling. Tumors could be clearly delineated in the MRI data and respective volumes quantified. Respective glucose uptake of the tumors was assessed by [18 F]-FDG PET imaging (0.1 mL of 12 MBq). Fusion of the PET and MRI

data showed excellent agreement between tumor extend and FDG uptake (**Figure 10**). The observed reduction in tumor volume under treatment correlated well with the observed reduced glucose uptake. Winter et al. evaluated the HET-CAM for initial testing of the binding specificity of targeted compounds. They used the well-characterized PSMA-specific PET radiotracer [⁶⁸Ga]-PSMA-11 to demonstrate the principle of the HET-CAM model for evaluation of specific radioligand accumulation in prostate cancer xenografts (**Figure 11**). At EDD 6, tumor cells of the PSMA-positive cell line LNCaP C4-2 (1 x 10⁶ cells) and the PSMA-negative control PC-3 (7.5 x 10⁵

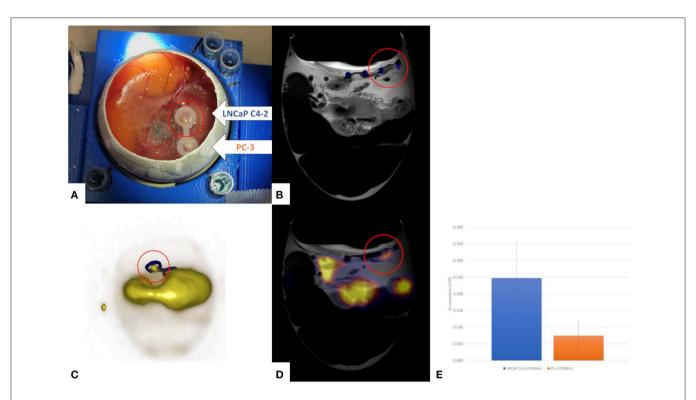


FIGURE 11 | PET/MRI for quantification of the PSMA-specific PET radiotracer [68 Ga]-PSMA-11 in the HET-CAM model with dual tumor seeding (LNCaP C4-2, PSMAQ17 positive; PC-3, PSMA negative) (A). The tumors can be nicely visualized by high-resolution MRI (B, red circle). Distribution of the [68 Ga]-PSMA-11 by PET reveals strong signal at one location of the CAM and some general accumulation in the chick embryo (C). Fusion of the PET and MRI data (D) reveals tracer accumulation in the PSMA positive tumor (red circle), which is proven by gamma counting after resection of the tumors (E). Unpublished imaging material provided by Winter G, and Li H

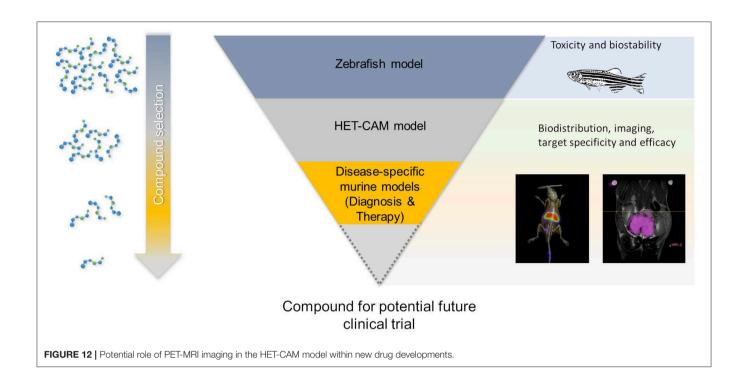
cells) mixed in Matrigel (40%, v/v) were grafted on the CAM in two silicon rings. MR and PET imaging was performed starting on EDD 12. Anatomical information was provided by high-resolution imaging using a small animal MR based on the protocol of Zuo et al. [61, 65]. For PET, 150 µl of [68Ga]-PSMA-11 solution was injected into a chorioallantoic membrane vessel followed by a dynamic 60 minutes PET scan. Registration between both imaging modalities was achieved by a self-built animal holder with PET and MRI visible fiducial markers. Tumor growth could be quantified by MR imaging. In addition to PET imaging the tumor entities were excised from the membrane after measurement and the accumulated activity was separately quantified by y-counter (COBRA II, Perkin Elmer) detection. As expected, in comparison to the PC-3 tumors, higher accumulation of [68Ga]-PSMA-11 was observed in the LNCaP C4-2 tumors, indicating the applicability of the HET-CAM model for initial testing of binding specificity of targeted compounds.

DISCUSSION

The HET-CAM model has been exerted to numerous applications. It represents a simple, quick, and low-cost model, not rising any regulatory concerns in many countries

if sacrificed before hatching. However, there is a consensus in the scientific community that it is illogical to conclude that the neural capacity to experience pain is not fully developed prior to hatching and that beyond a critical point in development avian embryos are capable of experiencing pain. The exact stage of development at which this capacity is sufficiently developed to warrant concern has not yet been determined. Society recognizes that a critical period in chick embryo development occurs 72 h prior to hatching and from an ethical point of view embryos should be sacrificed prior to EDD 18.

Since the HET-CAM model represents a naturally immunodeficient host, xenotransplantation of many kinds of tumors without species-specific limitations are possible. Even considering the fact that not all organs are fully developed, the established circulation and the highly vascularized CAM, which is connected to the embryo through a continuous circulatory system make it a natural candidate in-between cell culture and animal experiments, especially for initial testing of new compounds. Even though not finally established, it will likely play an important role in early drug development as pointed out in **Figure 12**. Compounds without detectable toxicity in cell and eventually zebra fish assays, may be initially evaluated regarding efficacy and biodistribution in the HET-CAM model, thereby reinforcing the potential of this convenient, 3R compliant, *in vivo*



model for cancer research. Only compounds showing promising properties will then further be evaluated in animal models, thus reducing the need for animal studies and related costs.

Non-invasive imaging will likely play an increasingly important role for direct visualization of the biodistribution of respectively labeled compounds and longitudinal monitoring of surrogate markers such as tumor progression and metabolism. MRI appears as an attractive imaging approach providing flexible image contrast and assessment to different tissue-specific parameters like MR relaxation times, diffusion and perfusion. Even though it offers the possibility of tailoring image contrast to the specific application, its intrinsic low sensitivity often limits its application in identification of small amounts or only traces of compounds. This limitation raises the increasing interest in using PET in the context of HET-CAM imaging. The excellent sensitivity of PET combined with the excellent anatomic detail of MRI appears as an ideal combination for anatomic, metabolic, and molecular imaging in the HET-CAM model.

Even though in PET motion compensation of the embryo may not be of paramount importance due to its only limited spatial resolution, in MRI coping with embryo motion is one of the major challenges to finally achieve the required high-spatial resolution. Over the last years efficient immobilization approaches of the chick embryo have successfully been evaluated in ovo (Table 1). Promising approaches include the precooling of the egg prior to scanning, the application of halothane and isoflurane, and the use of anesthesia agents dropped directly onto the CAM. Good to excellent immobilization could be achieved with almost all approaches. Major differences were reported regarding immobilization duration and resulting possible image

acquisition times, tolerability by the chick embryo, side effects, and easiness to use. For high-resolution anatomic imaging, precooling appears as an excellent approach, allowing long scan times of up to one hour and being easy-to-use. However, the related slowdown in metabolism [113] and blood flow [58] may limit its application in cases where physiological properties are under investigation. Here, in contrast to halothane, isoflurane was reported to not impact aortic blood flow and cardiac performance [114] and may be a good alternative with the limitation of a quite complex imaging setup. Both approaches are well tolerated by the chick embryo allowing for repeated measurements in longitudinal studies. Liquid anesthetics applied by directly dropping onto the CAM are easy to use and a variety of agents have been reported with widely varying anesthesia efficiency and often toxic side effects [58, 106, 107]. Even though, ketamine was reported to reduce cardiac contraction force in isolated chick embryo heart at EDD 4 and EDD 7 [115], Herrmann et al. reported the advantage of ketamine over precooling for time-of-flight MRI [58] and showed its possible use in applications being sensitive compromised circulation or metabolism in cases of rather short acquisition times.

This review specifically addresses MRI/PET imaging techniques for HET-CAM applications. Even though highly attractive for high-quality multi-contrast morphological and functional imaging in combination with high-sensitive imaging of radio-labeled compounds, both represent high-cost imaging techniques requiring long acquisition times with only limited applicability to high-throughput applications. A wide range of alternative somehow competing techniques have been proposed over recent years. Most prominent to mention at this point are

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TABLE 1 | Overview of reported *in vivo* in ovo imaging and spectroscopy studies.

References	Modality	Application	Imaging technique	Dimension	Spatial resolution	Immobilization	EDD	Scan time
Bone et al. [81]	MRI (1H, 1.5T)	Embryonic anatomy	T1-/T2-weighted SE	3D	200 × 200 × 1200 μm ³	Precooling (EDD 11 20 minutes, EDD15 90 minutes) on ice chips	11, 15	Not reported
Effmann et al. [83]	MRI (1H, 2T)	Embryonic anatomy	T1-weighted SE	2D	$50\times50\times600~\mu\text{m}^3$	Not reported	4,6,9	1–2 h
Moseley et al. [54]	MRS (31P, 2T), MRI (1H, 2T)	Metabolic (MRS) and anatomic (MRI) development	T1/T2-weighted SE	Single voxel (MRS), 2D (MRI)	Whole egg (MRS) 270 \times 270 \times 2000 μ m³ to 350 \times 700 \times 3000 μ m³ (MRI)	Not reported	4, 9, 12, 15, 17, 18, 19, 20, 21 (MRS), 5, 9, 15, 23 (MRI)	20 min (512 NSA, MRS), not reported (MRI)
irette et al. [85]	MRS (31P, 1H, 2T)	Metabolic development, fat-water fraction		Single voxel	Whole egg	Halothane	0, 2, 4, 6, 8, 10, 12, 14, 16, 17, 19, 20	
Peebles et al. [86]	MRS (1H, 7T), MRI (1H, 7T)	Metabolic (MRS) and diffusion (MRI) response to hypoxia and recovery	PRESS, 2pt diffusion	Single voxel (MRS), 2D (MRI)	$6\times6\times6~mm^3~(MRS),$ $230\times460\times2000$ $\mu m^3~(MRI)$	Ketamine	19	21.3 min (MRS), no reported (MRI)
Falen et al. [53]	MRI (1H, 2T)	Yolk structure	SE	2D	$250 \times 250 \times 1250$ μm^3 to $500 \times 500 \times$ $1250 \ \mu m^3$	Not reported	daily	1 h
Hutchison et al. [87]	MRI (1H, 2T)	Yolk structure	T1-/T2-weighted SE	2D	$235 \times 310 \ \mu\text{m}^2$	Not reported	1	Not reported
Donoghue et al. [88]	MRI (1H, 1.5T)	Residue transfer	IR-FLASH (MP-RAGE)	3D	$1000 \times 780 \times 1250$ μm^3	Precooling	not reported	Not reported
Holmes et al. [93]	MRI (1H, 7T)	Cardiac function	T1-weighted GE	2D	$300\times300\times1500$ μm^3	Self-gated	8, 13, 16, 20	Not reported
Bain et al. [51]	MRI (1H, 7T)	Chick embryo development	T2-weighted SE	2D	$192 \times 195 \times 500 \ \mu m^3$	Precooling	12, 15, 17, 18, 19, 20	25 min
Boss et al. [50]	MRI (1H, 7T)	MR relaxation parameter changes during embryonic development	IR-TSE (T1-mapping), HASTE (T2-mapping), MT- prepared GE	2D (T1/T2- mapping), 3D (MTR)	$\begin{array}{l} 180 \times 180 \times 1000 \\ \mu m^3 \; (T1-mapping), \\ 260 \times 260 \times 1000 \\ \mu m^3 (HASTE), 230 \times \\ 230 \times 1000 \; \mu m^3 \\ (MTR) \end{array}$	Ketamine	5, 8, 11, 16	Not reported
Zhou et al. [111]	MRI (1H, 3T)	Muscle fiber tracking during embryonic development	T1- / T2- weighted TSE, DTI	2D	$\begin{array}{l} 200\times200\times2000 \\ \mu\text{m}^3 \; (\text{T1w}), 200\times200 \\ \times \; 1200 \; \mu\text{m}^3 \; (\text{T2w}), \\ 600\times600\times1200 \\ \mu\text{m}^3 \; (\text{dti}) \end{array}$	No, single- and double-precooling	4, 5, 6,7, 8, 9, 10, 11, 12, 13, 18, 19	2 min 17 s (T1w), 12 min 23 s (t2w), 31 min 14 s (DTI)
Lindner et al. [48]	MRI (1H, 7T)	Embryonic development of the eye	T2-weighted TSE	2D	$74\times74\times700~\mu\text{m}^3$	Bedding on crushed ice for EDD > 10	1-20 daily	
Dingman et al. [112]	MRI (19F, not reported)	Biodistribution of 19F-labeled compound	Not-reported	Not-reported	Not-reported	Not-reported	15, 16, 17, 18	
Oppitz et al. [98]	MRI (1H, 3T)	Migration of iron labeled melanoma cells	T2*-weighted	3D	$300^3 - 1000^3 \ \mu m^3$	Not reported	6, 9, 18, 20	12 s / slice

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TABLE 1 | Continued

References	Modality	Application	Imaging technique	Dimension	Spatial resolution	Immobilization	EDD	Scan time
Faucher et al. [100]	MRI (1H, 1.5T)	Localization of Gd—labeled GL-261 glioblastoma cells	T1-weighted GR	3D	$350\times350\times500~\mu\text{m}^3$	Precooling	10, 11, 13	6–7 min
Zuo et al. [61]	MRI (1H, 11.7T)	CAM tumor morphology	T2-weighted TSE, T2 mapping, diffusion weighted, T1-weighted GE	2D (T2, T2-mapping, DWI) 3D (T1 weighted GE)	$77 \times 91 \times 500 \ \mu\text{m}^3$ (t2w), 200 × 200 × $500 \ \mu\text{m}^3$ (DWI), 104 × $98 \times 500 \ \mu\text{m}^3$ (T2 mapping), 100×100 × $560 \ \mu\text{m}^3$	Precooling	11–16, daily	15 min 32s (t2w), 60 min (DWI), 34 min (T2 mapping), 4 min 9 s (t1w)
Zuo et al. [65]	MRI (1H, 11.7T)	Biodistribution of Gd-labeled compounds	T1-weighted GE, T2-weighted SE	3D (T1w), 2D (T1w)	$100 \times 100 \times 560 \mu\text{m}$ (T1w), 77 × 91 × 500 μm^3 (t2w)	Precooling	16 (injection), pre- and 30 min, 3 h, 20 h, 40 h after injection	4 min 9 s (T1w), 15 min 32 s (t2w)
Pfiffner et al. [105]	MRI (1H, 4.7T)	Perfusion capacity of 3D biomaterials	T1-weighted GE, T1-/ T2-mapping	2D	$500\times500\times1000$ μm^3	Ketamine	14	25 s (GE), 9 min 40 s (mapping)
Waschkies et al. [106]	see Pfiffner et al. [105]	See Pfiffner et al. [105]	See Pfiffner et al. [105]	See Pfiffner et al. [105]	See Pfiffner et al. [105]	Metetomidone, thiopental, ketamine/midazolam	see Pfiffner et al. [105]	See Pfiffner et al. [105]
Herrmann et al. [58]	MRI(1H, 9.4T)	Tracking of magnetic particle labeled tumor cells	T2-weighted TSE, T2*-weighted GE, Time of flight (TOF)	2D	$\begin{array}{c} 88/166\times88/166\times\\ 400/500\text{ mm3 (t2w), 88}\\ \times88\times400\mu\text{m}^3\text{ (t2*,}\\ \text{tof)} \end{array}$	Precooling (T2-/T2*w), ketamine (Tof)	14	13 min 24 s-31 min 56 s (t2w), 22 min 35s (T2*), 12 min 4 s (Tof)
Würbach et al. [71]	PET (¹⁸ F)	Bone metabolism	Static, dynamic	3D	$400\times400\times800~\mu m^3$	Isoflurane	13–18	75 min
Heidrich et al. [107]	PET/μCT	Immobilization	Static	3D	Not reported	Isoflurane, 2,2,2-tribromoethanol, urethane/α-chloralose	11–18	6 min
Warnock et al. [69]	PET (¹⁸ F) / μCT	Screening of novel PET tracer	Dynamic, static	3D	$433 \times 433 \times 796 \ \mu\text{m}^3$ (PET), $100^3 \ \mu\text{m}^3$ (μ ct)	Isoflurane	18	45 min (PET), not-reported (μct)
Zlatopolskiy et al. [68]	PET (¹⁸ F)	Tracer accumulation in CAM tumor	Static	3D	1.4 ³ mm ³ (PET)	Isoflurane	7	30 min
Steinemann et al. [109]	PET (¹⁸ F) / MRI (1H, 1T)	Tumor growth and metabolism	T1-weighted GE, T2-weighted TSE, static (PET)	3D (GE, PET), 2D (TSE)	$\begin{array}{l} 290\times290\times500~\mu\text{m}^3\\ \text{(GE), } 290\times290\times700\\ \mu\text{m}^3\text{ (TSE), not}\\ \text{reported (PET)} \end{array}$	Precooling	10, 17	Not reported
Winter et al. [110]	PET (⁶⁸ Ga), MRI (1H, 11.7T)	Binding specificity of target-specific radioligands	Dynamic (PET), T2-/T1-weighted SE (MRI)	3D (PET), 2D (MRI)	$\begin{array}{l} 1.4^{3} \text{ mm}^{3} \text{ (PET), } 100 \times \\ 100 \times 560 \mu\text{m} \text{ (T1w),} \\ 77 \times 91 \times 500 \mu\text{m}^{3} \\ \text{(t2w)} \end{array}$	Precooling (MRI), none (PET)	12	

MRI, magnetic resonance imaging; MRS, magnetic resonance spectroscopy; PET, positron emission tomography; μCT, microscopy computer tomography; SE, spin echo; TSE, turbo spin echo; GE, gradient echo; IR, inversion recovery; MT, magnetization transfer; FLASH, fast low angle shot; HASTE, half-Fourier single-shot turbo spin echo.

optical methods [116, 117] including bioluminescence [118], fluorescence [119], and tomographic [120, 121] techniques. Furthermore, ultrasonographic imaging [122], x-ray based tomographic [45] and even photoacoustic techniques [123] have been introduced, the latter of which with the potential for label-free imaging. In combination with single photon emission tomography (SPECT), tomographic x-ray techniques have been applied to initial evaluation of radiopharmaceuticals in chick embryos [19].

In conclusion, the expected increasing interest in the HET-CAM model as an intermediate step between cell culture and animal model for initial testing of new compounds makes *in ovo* imaging an important tool for monitoring the fate of compounds after systemic injection or surrogate markers. The combination of MRI and PET appears promising by combining the sensitivity of PET with detailed anatomic and functional information provided by MRI.

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AUTHOR CONTRIBUTIONS

GW, AK, JL, AA, AB, HL, and ZZ performed measurements in the context of the presented work. FJ and ML provided in-depth knowledge on nano-particles. GW and VR wrote the manuscript, and are responsible for the in ovo experiments.

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Technical Aspects of *in vivo* Small Animal CMR Imaging

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Cardiovascular magnetic resonance (CMR) imaging has become an accurate and versatile imaging modality to visualize the cardiovascular system in normal or abnormal conditions. In preclinical research, small rodent animal models of human cardiovascular diseases are frequently used to investigate the basic underlying mechanism of normal and abnormal cardiac function and for monitoring the disease progression under therapy. Technical improvements have enabled the transfer of CMR to small animal research, and as such made this non-invasive technique available to provide insights into cardiac morphology, function, perfusion, and pathophysiology in small animal cardiac disease models. This article reviews the basic technical approaches to *in vivo* small animal magnetic resonance imaging and its variants for the most promising applications.

Keywords: cardiac MRI, cardiac MRS, imaging techniques, small animals, cardiovascular diseases, cardiac function

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INTRODUCTION

Cardiovascular disease is considered the leading cause of death in the developed world, with high morbidity and mortality [1, 2]. In preclinical research, small rodent animal models of human cardiovascular disease are frequently used to investigate the basic underlying mechanism of normal and abnormal cardiac functions and for monitoring the disease progression under therapy [3]. Over the past decades, the use of small animal models has provided improved understanding of cardiac diseases [4, 5].

Translational research accounts for a large proportion of animal studies performed each year. Since the implementation of the 3 Rs principles (replacement, refinement, reduction) into the European Directive 2010/63/EU, medical imaging is highly recommended in translational research, because it can visualize the progression of the disease longitudinally often in a quantitative and non-invasive way. It thus has the potential to significantly reduce the number of experimental animals. Due to the high spatial and temporal resolutions, a versatile image contrast, and access to metabolic information, magnetic resonance imaging (MRI), and spectroscopy (MRS) have been proven to be promising diagnostic tools to monitor disease progression and response to treatment in small animal models. Its versatility, accuracy and high reproducibility has made cardiovascular magnetic resonance (CMR) imaging the non-invasive reference modality in preclinical research. MRI offers exceptional accuracy in the investigation of cardiac anatomy, perfusion, wall motion, and contractility, and its excellent soft-tissue contrast enables advanced myocardial tissue characterization [6–9].

However, the small size of the mouse heart $[5-6\,\mathrm{mm}$ left ventricle (LV) diameter, $\sim 0.2\,\mathrm{g}$ of heart weight] [10], high heart (about 250–600 beats per minute [bpm]), respiratory (about 60–160 cycles per minute [cpm]) rates, and fast systemic blood circulation times (4–5 heartbeats) impose substantial challenges for functional assessment by MRI. Over the past decades, major

improvements in MRI methodology and instrumentation have been achieved, including rapidly switching high-performance gradient systems, ultra-high magnetic fields (>7 T), and non-Cartesian k-space encoding strategies such as spiral [11, 12] and radial trajectories [13, 14]. In combination with advanced mathematical concepts for image reconstruction [15–17] rapid data acquisition techniques, providing a high temporal resolution while preserving adequate spatial resolution and sufficient volume coverage, have been realized.

The main objective of this manuscript is to summarize the most important technical aspects of *in vivo* small animal CMR imaging and the required variants for specific applications. For the physiological, biological and pharmacological applications and perspective, please refer to comprehensive recent reviews [18–22]. With the included brief description of hardware demands and animal handling strategies, the reader will get familiar with the basic principle and challenges of small animal CMR imaging.

TECHNICAL CONSIDERATIONS AND METHODOLOGIES

Hardware

Small animal MRI systems usually possess high field strength ranging from 4.7 up to 21 Tesla and strong gradient systems with bore diameters typically ranging between 10 and 40 cm. Higher field strengths provide an increased signal-to-noise ratio (SNR), thus enabling a higher spatial resolution. Disadvantages arise from changes in relaxation parameters, a higher chemical shift, a higher magnetic field inhomogeneity, susceptibility to artifacts, and increased specific absorption rate (SAR) [23], which often limits the translation of the results to clinical settings. Even though the lower SNR can partly be compensated with dedicated coils at 1.5T and 3T scanner [24, 25], and high-resolution mouse embryonic cardiac images were acquired at 17.6T [26], due to the high costs of ultra-high field instruments, field strengths between 7 and 11.7T are most commonly used in small animal CMR imaging [7, 27, 28].

Further SNR improvement is achieved with dedicated radio frequency (RF) coils [29, 30]. Especially phased-array coils, additionally enabling parallel imaging [31, 32], have become standard in small animal CMR imaging. Further improvements have been reported by Wagenhaus et al. [33] and Dieringer et al. [34], who showed a 3–5-fold gain in SNR when comparing a 4-element room-temperature heart coil with a cryogenic coil.

As a further major progress, gradient systems that, depending on their inner diameters, provide amplitudes of up to 1,000 mT/m with slew rates of up to 9,000 T/m/s, have been introduced. In combination with efficient water-cooling high-duty cycles have been achieved, thus enabling rapid imaging at a high spatial resolution and a large field-of-view (FOV).

Animal Handling

Motion is one of the main challenges for *in vivo* imaging. In contrast to human studies, suitable anesthesia is generally required in small animal imaging to prevent animal motion. During scanning, the physiological status of the animal needs

to be carefully monitored (e.g., ECG, respiration sensor, rectal temperature probe) and heating blankets are required to avoid temperature loss of the animal during anesthesia. General anesthesia is achieved using injectable or inhalational agents, or a combination of the two methods, to achieve the loss of consciousness, analgesia, suppression of reflex activity, and muscle relaxation [35]. An ideal anesthetic agent for animal CMR imaging should be easy to administer, and provide adequate and reproducible immobilization, preferably without changes in cardiac function and heart rate. However, since such agents are not available, the impact of the agent on cardiovascular physiology, especially depression of cardiac function and heart rate, respiratory function and induced hypothermia [36], has to be carefully considered.

Compared with inhalant agents, injectable anesthetics have several advantages. Their administration is more convenient to perform, and complex and expensive equipment such as precision vaporizers and specific breathing systems are not required. Due to its large safety threshold and compatibility with other drugs, ketamine is one of the most widely used anesthetics in animal research [37]. However, because of muscle rigidity, it is usually combined with xylazine, resulting in cardiac and respiratory depression. Berry et al. [38] reported deep sedation by subcutaneous injection of morphine and midazolam causing significantly less depression of heart rate and ejection fraction than imaging during general anesthesia with isoflurane in mice with normal cardiac function. Pachon et al. [39] suggested that ketamine was the least effective on the LV function and the heart rate, followed by Avertin, isoflurane (see below), and ketaminexylazine combination. Other agents such as pentobarbitone, fentanyl/fluanisone, and urethane were shown to result in profound cardiovascular depression or prolonged recovery time and are not recommended in cardiac imaging. A general major drawback of injectable agents results from the limited anesthesia duration and adjustment possibilities during scanning.

Even though more complicated, in most cases inhalation anesthesia by halothanes is suggested. Here, the preferred approach is isoflurane inhalation [40]. Major advantages comprise short induction and fast recovery times, convenient adjustment during scanning, rather low hemodynamic depression, and flexible maintenance. In order to achieve high reproducible experiments, isoflurane (5% for induction, 1–1.5% for maintenance) in medical air (0.1 L/min) [7] is normally used.

Cine Imaging

For the quantification of cardiac function by CMR, rapid data acquisition techniques are required. Where for clinical applications mainly steady-state-free-procession (SSFP) sequences are applied for improving myocardium-blood contrast. In small animal CMR, fast low-angle shot (FLASH) gradient-echo [41] techniques are applied to avoid banding artifacts caused by off-resonances. Because of high heart and respiratory rates, real-time imaging of cardiac function is normally not possible and CMR imaging generally requires synchronization of the data acquisition to the cardiac and

respiratory motion. In current practice, prospective triggering and retrospective/self-gated gating are used.

Prospective Trigger

For the prospective triggering, the ECG signals are simultaneously recorded for synchronization [42, 43]. ECG signals are normally drawn from two electrodes attached to one front and rear paw. After detecting the R wave, data acquisition is performed either at a specific phase of the heart (single-phase imaging) or continuously over multiple consecutive phases of the cardiac cycle (multi-phase or cine imaging, **Figure 1A**). Simultaneously, the respiration phase is measured with a balloon pressure sensor, and respiratory gating is additionally applied to avoid respiratory motion artifacts.

However, radiofrequency pulses and gradient switching induce interferences in the ECG signal and may cause false triggers, which are more prominent at ultra-high magnetic fields. Further, the magneto-hydrodynamic effect is more prominent at higher field-strengths, often limiting the detectability of the R-peak. To avoid severe susceptibility artifacts, non-metallic materials like carbon wires have been introduced almost 30 years ago [44]. Recently, Choquet et al. [45] tested carbon wire electrodes in an 11.7T magnetic field. Even though Rpeaks were usually detectable, a clear distortion in the ECG signal still persisted. Other types of trigger devices such as optical fiber-based gating were developed, and excellent ECG signal quality has been reported [46]. Meanwhile, different filter techniques were developed to reduce ECG distortion during MRI examinations [47-49]. In principle, these filter techniques allow electrical ECG recordings for scan synchronization even at high field strengths. However, a principal limitation of prospective triggering is the required gap prior to the R-peak to ensure its proper detection. This causes loss of the end-diastolic phase or, in case only every second heartbeat is used for triggering, doubling of the scan times.

Retrospective Gating

In the clinical setting retrospective gating refers to simultaneous recording of the ECG signal with the data acquisition and subsequent reordering of the data into different cardiac phases according to the recorded ECG (**Figure 1B**). In small animal research, the term is related to self-gating techniques. Here, data synchronization is not based on physiological signals and no ECG recording is required. Instead, an additional navigator signal is acquired prior to each data acquisition (echo). After the scan, this navigator signal is analyzed and used to assign each echo to its correct position in the cardiac and respiratory cycles (**Figure 1C**).

Two of the most widely used retrospective gating sequences are self-gated FLASH (IgFLASH) and ultra-short echo time (IgUTE). The advantage of IgUTE compared to its Cartesian counterpart IgFLASH is the shorter achievable echo time (TE), which helps to reduce flow artifacts. Hoerr et al. [50] reported an IgUTE sequence with a minimal TE of 314 μs , clearly showing superior image quality especially for the delineation of small morphological structures like valves or papillary muscles. When compared with igFLASH, a substantial reduction of flow artifacts

but maintained functional parameters were reported for IgUTE by Motaal et al. [13].

Compared with prospective triggering, retrospective approaches yielded similar global cardiac function data [43, 51]. As the data are acquired continuously, a flexible number of reconstructed cardiac phases and different temporal resolution can be achieved. However, the data acquired during certain periods of motion are not used for reconstruction. Thence, data oversampling is required to compensate for excluded data [52]. More importantly, the retrospective gating allows for steady-state acquisition, which is essential for mapping myocardial relaxation times [53, 54] or for quantifying image contrast as required in molecular CMR imaging with contrast agents [53, 55].

Real-Time Imaging

The self-gating techniques enable high-quality cardiac MRI with high reproducibilities [7]. However, the acquisition times in the minute range for a single slice still limit their applications in time critical settings such as pharmacological stress or firstpass perfusion imaging. Recently, based on technical progress in hardware and software, real-time concepts have been introduced and applied in CMR imaging. Real-time imaging refers to the rapid and continuous data acquisition followed by image reconstruction and visualization. To reduce acquisition times, dedicated real-time methods, including parallel imaging [56-58], k-t acceleration methods [59–61], and compressed sensing (CS) [15, 62, 63], have been suggested and initially evaluated [64] for the rapid and continuous acquisition of image series. Realtime methods utilize undersampling techniques, thus reducing the amount of acquired data for a single frame of an image series. Iterative reconstruction algorithms ensure image fidelity, e.g., by adding spatial and temporal regularization. Recent progress in real-time MRI results in high-quality images with high SNR, adequate spatial resolution and unsurpassed temporal resolution [65-68].

Dai et al. [69] first reported real-time cine MRI in mice with a single-shot echo-planar sequence with the Karhunen-Loeve transform (KLT) filter. Radial trajectories have shown favorable properties for real-time imaging by their intrinsic low motion artifact level. Further, due to the continuous recording of all spatial frequencies with every single spoke, undersampling results in almost incoherent artifacts, often showing no noticeable effect on the reconstructed images [70]. Winkelmann et al. [71] showed that a uniform profile distribution is guaranteed with a constant golden angle (111.246°) increment. The concept of Golden Angle (GA) angular spacing enabled data acquisition with optimal kspace coverage almost independent on the number of projections (Fibonacci sequence) and ensured incoherent undersampling artifacts [72]. Wech et al. [64] investigated the application of radial generalized autocalibrating partially parallel acquisitions (GRAPPA) with large golden angle (111.25°) real-time imaging in mice. However, only mid-ventricular slices were reported, and fully left-ventricular functions were not assessed. Its extension to the tiny golden angle (tyGA) [72] enabled the translation of the GA principle to higher field strength and provided even larger flexibility in the selection of the number of projections used for reconstruction of a single frame (generalized Fibonacci

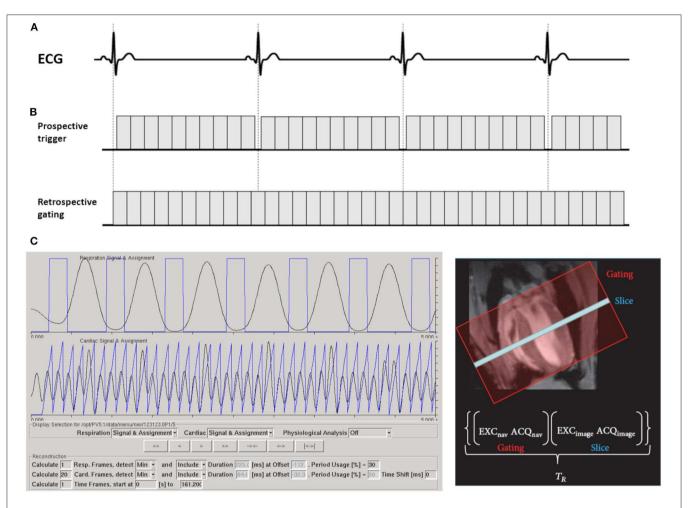


FIGURE 1 | Strategies for the synchronization of cardiac cine MRI with the cardiac cycle. (A) In the prospective triggering scheme, the acquisition is synchronized with the ECG signal. After detecting the R wave, a suitable trigger delay is set due to application, then cardiac acquisitions can be performed at a specific phase of the heartbeat or to acquire multiple consecutive cardiac phases of the cardiac cycle. (B) In the retrospective gating scheme, data are acquired continuously while simultaneously recording the ECG and respiratory signals. (C) As an alternative, an additional navigator signal is acquired prior to each echo. Primary signals are calculated from navigator scans. The navigator signals are automatically analyzed and weighted according to their contribution to respiration and cardiac signals. The weighted physiological signals are retrieved (with demerging) and/or frequency filtered (with Fourier Filter) to create respiration and cardiac signal, which are used to assign each echo to its correct position in the cardiac and respiratory cycles. Retrospective gating signal is acquired with ParaVision 5.1 (IntraGate®, Bruker Biospin, Ettlingen, Germany). The partial figure is reproduced with permission from Zuo et al. [7].

sequence). Our group investigates the feasibility of tyGA radial sparse MRI for real-time imaging of cardiac function in healthy mice [73] and a nexilin induced heart failure model [74]. Real-time cardiac tyGA radial sparse sense (tyGRASP) MRI in mice appears feasible with sufficient image quality for the quantification of global functional parameters. It enables a flexible number of projections for image reconstruction and thus offers the possibility for cardiac-phase dependent adjustment of the temporal resolution.

Accelerated Methods for CMR Imaging

MRI is an essential medical imaging tool with inherently slow data acquisition (**Figure 2A**), which imposes limitations to spatial and temporal resolution and volumetric coverage for dynamic cardiac imaging. The reduction of acquisition times can be achieved by incomplete sampling of *k*-space data.

However, related aliasing artifacts often cause degrading of the diagnostic quality. During recent years, various techniques have been developed and applied to increased undersampling, while maintaining diagnostic image quality by advanced reconstruction techniques.

Compressed Sensing

The mathematical foundation of compressed sensing (CS) was first introduced by Donoho [75] and Candès et al. [76] and translated to MRI by Lustig et al. [15]. CS aims to reconstruct signals and images from a reduced number of k-space samples not following the Nyquist criterion. As the MRI data are redundant and naturally compressible by sparse coding in some appropriate transform domain, CS has the potential to significantly reduce scan time.

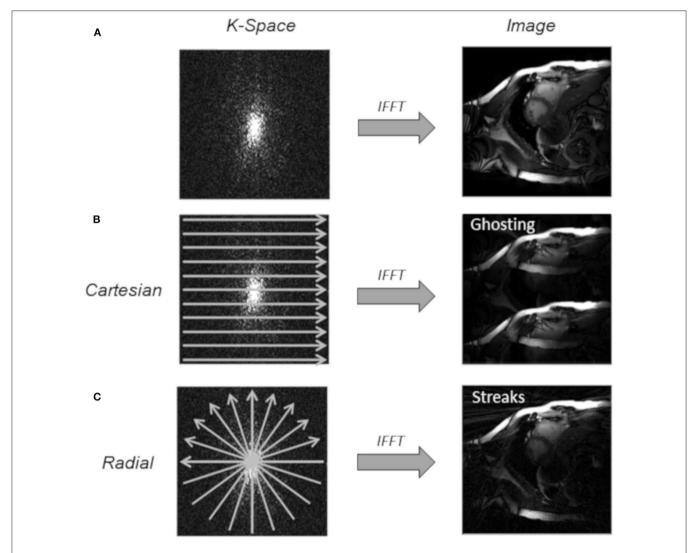


FIGURE 2 | Undersampling techniques used for cardiac imaging. (A) Fully sampled k-space. (B) Regular Cartesian undersampling (2-fold), which results in discrete aliasing artifacts in the reconstructed image with an inverse fast Fourier transform (IFFT). (C) Uniform radial undersampling (2-fold) leads to low-intensity streaking artifacts.

A successful application of CS has three basic requirements [16]. First, the desired images have a sparse representation in a known transform domain, and they can be characterized by only a small number of non-zero coefficients. Especially for dynamic CMR imaging, the quasi-periodicity of the heartbeat causes a sparse temporal Fourier transform, and data are as such highly compressible. This enables higher acceleration for dynamic imaging than static imaging [77]. Second, the aliasing artifacts should be incoherent, i.e., that they must manifest as noise-like patterns. Regular undersampling patterns lead to fold over artifacts, known as coherent aliasing (Figure 2B). In the Cartesian sampling, some *k*-space lines can be pseudo-randomly omitted, resulting in more incoherent artifacts. Alternatively, due to its highly incoherent undersampling property, many non-Cartesian trajectories, such as radial trajectories [64, 73] (Figure 2C), are widely used in CS applications. Especially radial trajectories with golden or tiny golden angle angular increments have proven to be beneficial undersampling properties since almost any arbitrary number of projections provides uniform k-space coverage [78]. Motaal et al. [13] reported UTE Cine images in the rat model, and successfully reconstructed from up to 5-fold undersampled kt-space data utilizing a CS algorithm. Wech et al. [64] and Li et al. [73] investigated CS with golden angle radial real-time imaging in the mouse model. Third, a non-linear reconstruction algorithm should be applied to enforce sparsity constrains and data consistency, to suppress incoherent aliasing artifacts [64, 72].

Several studies have shown the feasibility and accuracy of CS to accelerate CMR imaging [79–81]. Further acceleration was reported by combining CS and parallel imaging [64, 82].

Parallel Imaging

Parallel imaging is a robust method to accelerate the acquisition of MRI data using a reduced number of *k*-space data

simultaneously acquired with multiple receive coils. However, simply reducing the number of measured k-space data results in aliasing artifacts, mainly represented as well-known ghosting artifacts in Cartesian sampling and streaks in radial sampling [83]. The sensitivity encoding (SENSE) and GRAPPA are two principal methods in parallel imaging to correct for aliasing artifacts. The separate images reconstructed from the signals acquired with the different receive coil elements will have different relative intensities of the aliased component of the image. SENSE makes use of this property to separate the aliased components from the true structures in the image [84]. GRAPPA uses autocalibration signals and neighboring points in k-space to perform reconstruction of the missing portion in the kspace [85]. For the proper application of SENSE and GRAPPA, the signal at each point in the FOV has to be simultaneously recorded by several independent receive coil elements and careful alignment of the coil-array with the FOV is required. Theoretically, the maximum acceleration is only limited by the number of independent coils, but SNR limitations normally restrict the possible acceleration [83]. Wagenhaus et al. [33] investigated cardiac functional imaging of mice using a cryogenic quadrature RF coil with parallel imaging of an acceleration factor of 2. Ratering et al. [86] reported accelerated CMR of the mouse heart using self-gated parallel imaging strategies with a high acceleration factor up to 3.

k-t Acceleration

Cardiac dynamic images are sparse in an appropriate transform domain and exhibit correlations in *k*-space and time, enabling the recovery of missing data in undersampled data acquisitions. Based on this hypothesis, the k-t broad-use linear acquisition speed-up technique (k-t BLAST) and k-t sensitivity encoding (k-t SENSE) were developed to improve the performance of dynamic cardiac imaging. As a further generalization of the original method, k-t principal component analysis (k-t PCA) constrains the reconstruction using a standard data compression technique, thus enabling higher acceleration [87]. Signal correlations are learned from a small set of training data with low spatial but high temporal resolution, with subsequent reconstruction using temporal correlations [88].

Marshall et al. [89] investigated the k-t BLAST with an acceleration factor of three in healthy and myocardial infarction mice. Compared with the gradient echo cine sequence, the k-t BLAST scanning showed no significant differences. Makowski et al. [90] reported first-pass perfusion imaging with 10-fold undersampling in mice on a clinical 3 Tesla MR scanner using the k-t PCA technique.

PRECLINICAL CMR IMAGING APPLICATION

Cardiac Function

The heart can be considered as a central circulatory pump, generating the driving force to pump the blood through the vascular system. The visualization and quantification of the cardiac function are crucial, as many diseases have an impact on the performance of the heart.

Global ventricular performance parameters such as end diastolic/systolic volume (EDV/ESV), stroke volume (SV), ejection fraction (EF), and left ventricle mass (LVM) are widely used to evaluate cardiac function, which means the capability of the ventricles to eject blood into the great vessels. To derive accurate and reproducible volumetric quantification from a stack of parallel slices entirely covering the whole ventricle, the Simpson's rule is applied (**Figure 3**). The CMR assessment of the biventricular function is normally acquired with ECG-triggered or self-gated bright-blood contrast gradient-echo techniques [7, 43, 50]. Recently, the concept of real-time imaging was translated to preclinical research [64, 73, 91].

The assessment of systolic function in different mouse models has been investigated and the impact on, e.g., the EF, has been validated [92–94]. In contrast, the assessment of diastolic function in rodents is challenging. Normally the quantification is based on the filling rates at early left ventricular relaxation and late atrial contraction derived from time-volume curves of the left ventricle. Thus, a high temporal resolution acquisition (>60 frames per cardiac cycle) is highly recommended for reliable assessment. Coolen et al. [52] investigated diastolic dysfunction in diabetic mice with frame rates up to 80 frames per cardiac cycle. Later, a temporal resolution of 1 ms was reported by Roberts et al. [95] and the diastolic function was comparable to ultrasound analysis in normal mice.

Pharmacological Stress Imaging

Assessment of the left ventricular function under pharmacological stress is widely used in cardiovascular research to detect myocardial viability, ischemia or cardiac reserve and to determine the risk of subsequent cardiovascular event. However, due to the fast half-life and rapid metabolism of special drugs, a rapid quantification technique is highly required to visualize acute changes of cardiac morphology and function during pharmacological stress in the preclinical research.

Vasodilator and dobutamine are the main pharmacological agents used in stress CMR imaging [96]. By activating the adenosine receptors, the vasodilator agents can trigger coronary vasodilation and directly increase coronary flow [97]. Dobutamine is a synthetic catecholamine that primarily stimulates β_1 -adrenergic receptor and mildly stimulates α_1 , β₂-adrenergic receptor, and augments myocardial contractility [98]. Wiesmann et al. [99] firstly used dobutamine stress MRI to reveal the loss of inotropic and lusitropic response in transgenic heart failure mice with myocardial infarction and diastolic dysfunction as an early sign of cardiac dysfunction. Since then, more and more studies using the dobutamine stress MRI to investigate cardiac function in the mouse model have been reported [93, 100, 101]. Different dobutamine doses and ways of administration were reported (4 to 40 μg/min/kg intravenous infusion [i.v.] or 1.5 µg/g body weight, intraperitoneal bolus injection [i.p.]). To comply with the rapid imaging demands, real-time techniques combined with tyGA radial sparse MRI have been reported to characterize the acute changes of murine cardiac function from baseline to physiologically stress conditions in vivo without ECG and respiration synchronization [102].

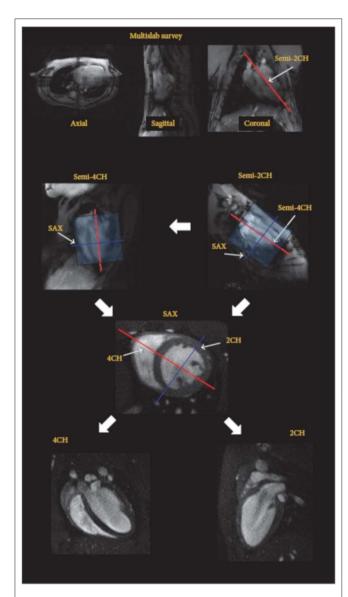


FIGURE 3 | Imaging protocol for highly reproducible imaging of cardiac function and anatomy (2/4CH: 2/4-chamber, SAX: short axes orientations). After the acquisition of a fast survey in axial, sagittal, and coronal orientation a long axis (LAX) scans are acquired in semi-2 chamber (2CH) and semi-4 chamber (4CH) orientation, which are used for accurate planning of the short axis stack (SAX). The final 2CH and 4CH orientations are planned on the SAX stack. Reproduced with permission from Zuo et al. [7].

Myocardial Strain

Myocardial strain is defined as the percentage change of myocardial length compared with the initial state in a certain direction by an internal or external force, and it is a well-validated parameter for evaluating myocardial performance. Several approaches are currently available for myocardial strain assessments.

Tagging

With the introduction of myocardial tagging in the late 1980s [103, 104], quantification of myocardial strain by CMR imaging

became possible. Later, it was introduced by de Crespigny et al. [105] into rodent research. Tagging MRI applies a series of short RF saturation pulses to spatially modulate the longitudinal magnetization prior to the conventional image acquisition, which generates regional tags with stripes or grids on the myocardium (**Figure 4**). The measurement of myocardial strain is derived from the tag deformation over the cardiac cycle.

Initially, spatial modulation of the magnetization (SPAMM) was used to generate a one- or two-dimensional grid of saturated spins [104]. However, due to longitudinal relaxation, tagging contrast is weakened in later cardiac phases. A complementary SPAMM technique (CSPAMM) was introduced by Fischer et al. [107] to improve the grid contrast by using the difference image of two acquisitions with inverted tagging grid phase.

After the tagged image acquisition, quantitative analysis of the strain is achieved by a variety of fast and accurate analysis methods, such as detecting and tracking the tag lines in the images [108], assessing temporal and spatial changes in image intensities by optical flow [109] and harmonic phase (HARP) analysis [110].

Even though tagging MRI is the most validated CMR technique to assess myocardial strain, the requirement for extra image acquisition sequences, influence of tags fading (less relevant for high field-strength and heart rates), and time-consuming post-processing limits its application.

Tissue Phase Mapping

Velocity encoded tissue phase mapping (TPM) is a valuable technique to evaluate myocardial strain, strain rate and displacement with high spatial and temporal resolutions [111-113]. TPM is based on bipolar gradients to encode myocardial velocity and enables quantitative assessments of the myocardial velocity in three directions over the whole cardiac cycle. TPM is susceptible to eddy-currents and phase distortion induced by concomitant gradient fields [114, 115], and several approaches have been developed to minimize these errors [115-117]. However, TPM-encoded acquisitions are sensitive to flow- and motion-related artifacts and require long acquisition times. Several feasible methods have been developed to accelerate image acquisition and compensate for motion artifacts. Espe et al. [112] introduced in-plane rotation of the FOV in rats to reduce directional-dependent artifacts by acquiring each slice twice. Recently, McGinley et al. [118] investigated accelerated TPM imaging by applying compressed sensing in the myocardial infarction rat model.

Displacement Encoding With Stimulated Echoes

Displacement encoding with stimulated echoes (DENSE) was introduced for high-resolution myocardial displacement mapping via stimulated echoes with a bipolar gradient by Aletras et al. [119]. It has the distinct advantage of encoding tissue displacements into the pixel phase, thus encoding motion over long periods while maintaining high spatial resolution. However, due to the stimulated echoes, DENSE has the disadvantage of a relatively low SNR. Kim et al. [120] increased SNR of 15–34% by extracting a pair of subsampled DENSE images with uncorrelated noise from the CSPAMM

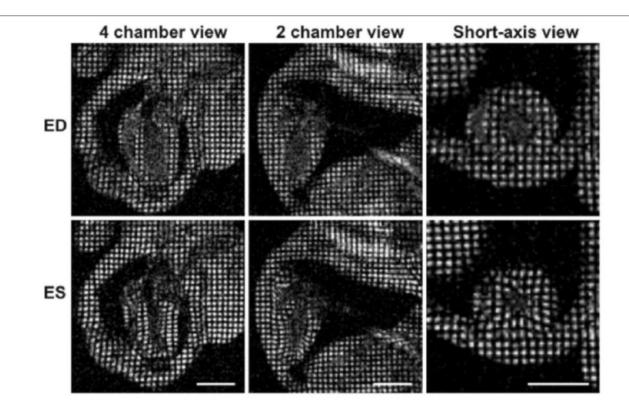


FIGURE 4 | Myocardial tagging in the mouse. Four-chamber, two-chamber, and short-axis views of a mouse heart at the end-diastole are shown in the top row, and the end-systolic frames are depicted in the lower row. The movement of the tagged myocardial tissue can be tracked to calculate myocardial strain. Reproduced with permission from Price [106].

image, and combined them during image reconstruction. After initially being implemented as single-frame imaging, DENSE was subsequently extended to cine imaging. In diet-induced obesity mice, high reproducibility was reported in the quantification of the LV function, including strain, torsion, and measures of synchrony [121]. Zhong et al. [122] investigated a 3D cine DENSE sequence with a spiral k-space trajectory in mice. Vandsburger et al. [123] combined DENSE with pharmacological stimulation to investigate the mechanics of endothelial nitric oxide synthase and neuronal nitric oxide synthase in modulating contractions and calcium influx in mice. DENSE has also been shown to be benefited from acceleration techniques, such as parallel imaging and compressed sensing [124, 125]. However, the feasibility of acceleration techniques in preclinical research needs further investigation.

Feature Tracking

Recently, CMR feature tracking (CMR-FT) was introduced for deriving global and regional myocardial strain [126]. It is mainly based on a block-matching approach. After manual defining endocardial and epicardial borders at end-diastole, in CMR-FT the borders are automatically tracked over the cardiac cycle by correlation of similar regions in the subsequent images (**Figure 5**). As CMR-FT is a promising novel method for the quantification of myocardial strain from routinely acquired cine CMR images without excessive post-processing times, it has

the potential for a fast assessment of myocardial mechanics. Its clinical potential has recently been described [128–130], and excellent inter- and intra-observer agreement and high interstudy reproducibility were reported. However, to the best of our knowledge, only one preliminary study with limited temporal resolution of 15 phases per cardiac cycle has been reported in preclinical research [131]. There, feature tracking showed high reproducibility in left ventricle global circumferential and longitudinal strain in healthy mice, whereas reproducibility of radial strain was limited.

Perfusion

Assessment of myocardial perfusion is considered to be a key parameter in the characterization of cardiac pathology, especially in ischemic heart disease or microvascular dysfunction. In normal conditions, a myocardial oxygen supply is balanced to the continuously changing myocardial oxygen demand. The imbalance of supply and consumption may result in myocardial ischemia. Currently, myocardial perfusion in rodents is typically assessed using arterial spin labeling (ASL) or first-pass perfusion imaging.

Arterial Spin Labeling

ASL is a valuable CMR technique utilizing arterial blood water protons as an endogenous diffusible tracer to non-invasively quantify regional myocardial blood flow without contrast agents

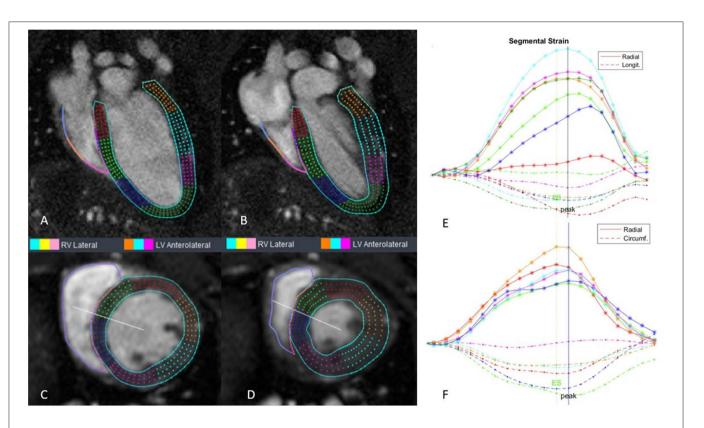


FIGURE 5 | Cine CMR images with CMR-FT myocardial strain curves in mouse. (A) 4-chamber at end-diastole; (B) 4-chamber at end-systole; (C) short axis at the end-diastole; (D) short axis at the end-systole; (E) segmental strain for 4-chamber; (F) segmental strain for short axis. Stain analysis was done using Segment v3.0 R7732 [127].

[132]. RF pulses are applied to label arterial blood which then acts as endogenous tracer. ASL requires the subtraction of two images. One image is acquired after the labeled blood flow into the target tissue and the other one is acquired without labeling. The difference between both images can be utilized to calculate the tissue's blood perfusion. The signal difference depends on labeling decays with the time-constant equal to the blood T1 relaxation time. It can be made directly proportional to myocardial blood flow in units of ml-blood per g-tissue per minute. However, the contrast differences created by magnetic labeling of blood are inherently limited, which results in relatively low SNR. To compensate for low SNR, high field strength is beneficial.

ASL was firstly demonstrated in the rodent brain by Detre et al. [133]. Later, it was applied to the perfused excised rat heart by Williams et al. [134]. However, ASL suffers from relatively long acquisition times and it is sensitive to variations in heart and respiratory rates [135].

The flow-sensitive alternating inversion recovery (FAIR) combined with the Look-Locker readout scheme is the most widely used technique in ASL (Figure 6). Belle et al. [136] employed an LLFAIR-FLASH sequence to quantify myocardial blood flow (MBF) in rats. Due to blood flow, non-excited spins enter the detection slice, which leads to an increase in the relaxation rate. The relative difference in the apparent T1 relaxation times corresponding to selective and non-selective

inversion is related to perfusion via a two-compartment tissue model. Kober et al. [137] improved MBF quantification using a respiration and ECG gated LLFAIR single-gradient echo technique in a mouse model. A nearly 10-fold increase in spatial resolution was achieved with respect to previous study in rats [138]. However, this led to a significantly increased acquisition time of about 25 min. Vandsburger et al. [139] investigated a cardio-respiratory gated ASL sequence using a fuzzy C-means algorithm to better cope with respiratory motion and heart rate variations in a myocardial infarction mice model. Abeykoon et al. [140] introduced an ASL method based on the signal intensity of flow sensitized CMR to shorten scan time to 2-4 min. In order to benefit from sensitivity advantages of continuous ASL, Troalen et al. [141] proposed cine-ASL, which is based on an ECG-gated steady-pulsed labeling approach combined with simultaneous readout over the cardia cycle. The cine-ASL led to shorter acquisition time than the LLFAIR technique while preserving spatial resolution and robustness with respect to cardiac motion.

First-Pass Perfusion

The basic principle of first-pass perfusion imaging involves intravenous injection of a bolus of a suitable contrast agent (CA), with subsequent monitoring of the passage of the CA through the heart. However, the high heart rate (400–600 bpm) and fast systemic blood circulation time limit its application in rodents.

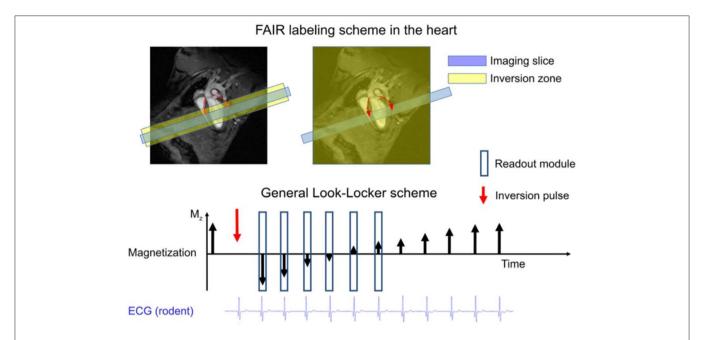


FIGURE 6 | The FAIR labeling scheme (upper part) consists of two inversion recovery measurements. In the first measurement the labeled zone is only around the imaging slice, and in the second measurement the inversion is global. FAIR is the most commonly used ASL technique in the heart. The timing of the inversion and that of the readout modules should be ECG-gated and occur in the same cardiac phase. The Look-Locker inversion-recovery readout (lower part) has been used mainly in the rodent heart, where the rapid heart rate permits dense sampling of the magnetization recovery curve. Reproduced with permission from Kober et al. [132].

Recently, the major progress in data acquisition acceleration has rendered small animal first-pass perfusion imaging feasible.

Makowski et al. [90] firstly proposed first-pass perfusion imaging in mice using a k-t SENSE technique with an acceleration factor of 10 on a clinical 3T scanner. Later, Coolen et al. [142] introduced a segmented ECG-triggered acquisition combined with parallel imaging acceleration to capture the first pass of contrast agent in healthy and myocardial infarction mice. A temporal resolution of one image per three heartbeats was reached. The same group further investigated the quantification of regional perfusion values using a dual-bolus approach in combination with a Fermi-constrained deconvolution model [143]. Later they applied this dual-bolus approach to test the feasibility of first-pass perfusion in pressure overload induced hypertrophy and heart failure mouse models after transverse aortic constriction [144]. The hypertrophic mice revealed reduced myocardial perfusion proportional to LV volume and mass, and a related decrease in LV ejection fraction. Naresh et al. [28] used k-t undersampled dual-contrast first-pass MRI with motion-compensated compressed sensing reconstruction to study myocardial blood flow in a high-fat diet mouse model. They also investigated the repeatability and variability of firstpass perfusion imaging and ASL. They concluded that firstpass MRI shows better repeatability and variability in low MBF conditions such as myocardial infarction. Due to better image quality and lower user variability, ASL is more suitable at high MBF. Recently, the tyGRASP sequence with block-wise cardiac synchronization was reported for first-pass perfusion imaging in nexilin knock-out mice [74]. During each cardiac cycle, a single block of $G_4^7 = 15$ projections with acquisition duration of t = 15

31.5ms was acquired. For suppression of the background signal and coping with arrhythmic cycles, a non-selective saturation pulse was additionally applied prior to each acquisition block with a saturation recovery time T_{SAT} of 60 ms. The trigger delay was chosen so that the acquisition was performed during end-diastole to further minimize the motion artifacts (**Figure 7**). A temporal resolution of one image per cardiac cycle was achieved. Thus, an improved temporal fidelity of the inflow and washout curves was shown.

Tissue Characterization

Because of its ability to provide superior soft tissues contrast in exquisite detail, MRI has exceeded other imaging modalities in its multi-parametric capabilities for a comprehensive myocardial tissue characterization. It can provide superior and well-validated biomarkers of important pathophysiological processes in cardiac diseases based on intrinsic relaxation properties T1, T2, and T2* with or without contrast agent. Tissue contrast is tailored by adjusting acquisition parameters such as flip angle, TE, repetition time (TR), and inversion delay (TI). Mapping techniques can further provide direct pixel-by-pixel quantitative myocardial tissue characterization to depict small variations of relaxation properties and to highlight tissue pathology.

T1 Mapping

The T1 relaxation time is the longitudinal relaxation time, describing the return of the magnetization to thermodynamic equilibrium after excitation. The native T1 value is a tissue specific constant which changes in some pathologic conditions, such as diffuse myocardial fibrosis, hemorrhage, edema,

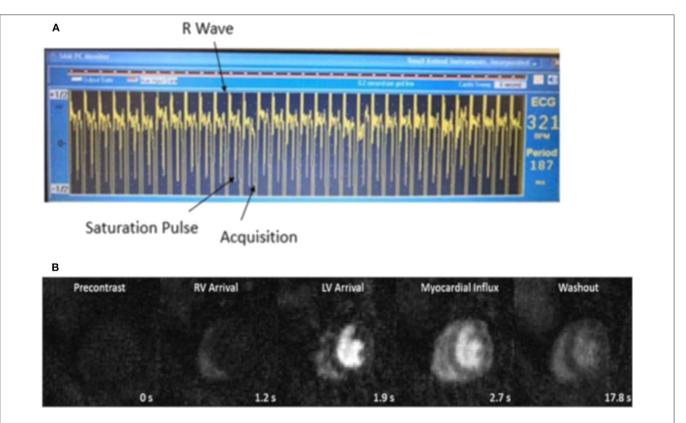


FIGURE 7 | (A) ECG signal during scan. According to the heart rate, a trigger delay was set after the detection of the R wave, then the blood and myocardial signal were approximately nulled by a non-selective saturation pulse. The acquisition was performed during end-diastole. (B) Time series of myocardial first-pass perfusion images of a nexilin wild-type mouse. From left to right: precontrast, RV arrival, LV arrival, myocardial influx, and washout.

inflammation, and acute infarction [145]. Thus, the quantitation of T1 value can be used to distinguish different soft tissues and pathologies. The general principle for T1 mapping is to acquire multiple images at different inversion times in order to assess the T1 recovery curve.

Several T1 mapping methods have been proposed in preclinical research. One of the most widely used methods for measuring myocardial T1 is a single slice inversion recovery Look-Locker technique [146-148]. With this technique, image datasets are acquired repeatedly after an inversion pulse to create multiple images along the recovery curve. However, this method has several drawbacks. The long TR results in relatively long total acquisition times. Poor ECG signals and variations in the heart rate cause inversion times to differ for subsequent acquisition thus causing k-space inconsistencies. In-plane and throughplane motion between excitations reduce accuracy [54]. An ECG-triggered saturation-recovery Look-Locker (SRLL) method has been proposed by Li et al. [149] to acquire a singleslice T1 map in about 3 min. By combining the SRLL method with a modified model-based compressed sensing method, a 50% reduction in imaging time was achieved for the in vivo T1 mapping of the mouse heart [150]. Later, Jiang et al. [151] further extended the method to multi-slice T1 mapping (MRLL) allowing for more coverage without increasing scan time. However, the SRLL sequence yields relatively low SNR and a lower accuracy compared with the inversion recovery. The single shot 2D modified Look-Locker (MOLLI) technique has shown high reproducibility and high SNR in humans [152]. However, it is challenging in mice due to the high heart rates and requirements on spatial resolution. Recently, Nezafat et al. [153] proposed a multi-shot 2D modified Look-Locker sequence for high-resolution T1 mapping in mice at a 3T MRI clinical scanner. A further method for myocardial T1 mapping in mice has been proposed by Coolen et al. [54] using a 3D intra-gate FLASH sequence in combination with a variable flip angle DESPOT1 (driven equilibrium single-pulse observation of T1) analysis. With this protocol, 3D T1 maps of the heart ventricles could be obtained in 20 min with a sufficient spatial resolution (Figure 8). Castets et al. [154] accelerated 3D T1 mapping measurements using spiral encoding with a higher spatial resolution (208 \times 208 \times 315 μ m³) in a 10–12 min acquisition time.

A promising application for T1 mapping is the quantification of myocardial extracellular volume (ECV) fraction. ECV contains the interstitial and intravascular spaces. Many disease processes affecting the myocardium can be understood through ECV changes, such as diffuse or interstitial myocardial fibrosis. ECV can be measured by combining native and post-contrast T1 mapping of blood and myocardium. Neilan et al. [155] applied and validated a Look-Locker FLASH sequence to quantify ECV in juvenile and aged mice.

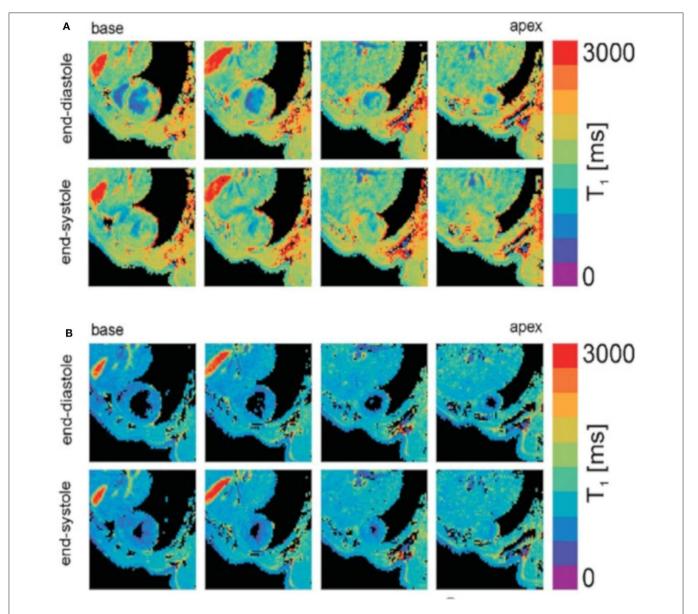


FIGURE 8 | T1 mapping of the mouse heart resulting from DESPOT1 analysis of both black-blood (A) and bright-blood (B) data. T1 maps are shown for four different slices covering the base to apex and for both the end-diastolic and end-systolic cardiac phases. Reproduced with permission from Coolen et al. [54].

T2 and T2* Mapping

The T2 relaxation time, also referred to as spin-spin or transverse relaxation time, is describing the tissue-specific decay of the transversal magnetization after excitation. Myocardial edema is the main pathology responsible for changes in the T2 value, and it was first demonstrated in a canine model of acute myocardial infarction (AMI) by Higgins et al. [156].

Two variants of T2 mapping techniques are usually used in CMR imaging: dark blood turbo spin-echo (TSE), and bright blood T2 preparation. Schneider et al. [147] mapped T2 in mice by acquiring the spin echo data with echo times ranging from 3.7 to 24 ms. Later, Bun et al. [157] performed T2 measurements with a similar sequence to quantify myocardial fibrosis in

diabetic mice at 11.75 T. However, the TSE-based T2 mapping suffered from ghosting artifacts caused by blood flow and signal loss due to through-plane motion [158]. The T2 preparation-based method is less prone to TSE-associated artifacts [159]. It mainly contains a T2 preparation module and a rapid imaging sequence such as FLASH. The T2-preparation module contains non-selective 90 and 180° pulses to create spin-spin relaxation followed by a -90° restore pulse. After the restore pulse, the longitudinal magnetization depends on the tissue T2 value. Beyers et al. [55] proposed a T2 preparation module containing a Carr-Purcell-Meiboom-Grill and Malcolm Levitt (CPMG-MLEV) weighted series of composite 180° pulses, followed by a multi-slice gradient echo readout. In this way, the resulting T2

values are less sensitive to effects of B0 and B1 inhomogeneities. Coolen et al. [160] extended this preparation module with fast steady-state-free-precession (SSFP, FISP) readout. However, the total acquisition time for one T2 measurement with three slices was about 30 min, which limited its application in fast dynamic contrast agent enhanced MRI studies. Chen et al. [161] performed rapid T2 mapping of the mouse heart using the CPMG sequence and compressed sensing reconstruction, which allowed T2 quantification at a temporal resolution of 1 min per slice (Figure 9).

T2* relaxation refers to decay of transverse magnetization caused by a combination of spin-spin relaxation and magnetic field inhomogeneity. Gradient-echo MRI with T2*-based contrast can be used to depict different lesions in diseased mouse heart. T2* cardiac MRI has been utilized to evaluate myocardial iron overload and collagen deposits. T2* is reduced in ironand collagen-laden tissues due to increased magnetic field inhomogeneity. Jackson et al. [162] measured T2* relaxation using two multi-echo gradient echo sequences with 15 echo times in the range of 0.9-14.9 ms at 1 ms intervals in a mouse model of β-thalassemia. Over 10-fold decreased myocardial $T2^*$ (0.7 \pm 0.2 ms) was observed in the iron-loaded thalassemia group, which was consistent with histological results. van Nierop et al. [163] reported reduced T2* value in myocardial infarction (MI) and transverse aortic constriction (TAC) mice using an ECG-triggered T2*-weighted 3D center-out radial sequence with TE ranging from 21 µs to 4 ms. T2*-shortening contrast agents, such as iron oxide nanoparticles (IONPs), have been used to exploit T2* contrast in mouse cardiovascular system [164, 165]. Sosnovik et al. [164] reported an iron oxide-based particle targeted at apoptotic cells in an ischemia/reperfusion injury mice model. Significantly decreased signal intensity was observed in T2*-weighted FLASH images. Zhou et al. [166] used the Sweep Imaging with Fourier Transformation (SWIFT) technique to visualize iron oxide particle labeled stem cells in the rat heart. Due to its zero echo-time properties, SWIFT images showed reduced blooming artifacts compared to gradient-echo images, and enhancement of off-resonance signals relative to the background. However, a major remaining challenge for IONPs application is to distinguish regions of signal void due to IONPs from those due to low signal tissues or susceptibility artifacts. Even though several bright-iron methods such as off-resonance techniques [167], gradient-compensation techniques [168], and post-processing methods to identify IONP-introduced magnetic field inhomogeneities [169] have been introduced, IONP-induced off-resonances can hardly be distinguished from other sources. This yields a rather low specificity of the IONP approach. Similar to SWIFT, ultrashort echo time (UTE) techniques have been used for providing endogenous T2* contrast [163, 170].

Contrast Enhanced MRI

Contrast enhanced MRI (CE-MRI) is a widely used imaging technique to investigate microvascular structure and function by injecting a contrast agent. MR contrast agents work by modifying the tissue relaxation properties and thus directly affect the image contrast. This effect is known as relaxivity and enables better

visualization of tissues in which the agent accumulates. The contrast agents can be classified as T1-weighted (i.e., gadolinium chelates, manganese chelates) or T2*-weighted (i.e., iron oxide particles). Here, we mainly discuss T1-weighted CE-MRI.

Late Gadolinium Enhancement MRI

Late gadolinium enhancement (LGE) CMR is a non-invasive reference standard for investigating myocardial viability. In AMI, cellular necrosis, lysis, and edema are the main pathological changes. In chronic infarcted tissues, fibrous scar tissues with increased extracellular space form. Compared with healthy tissues, the Gd-agent was slowly washed in and washed out in pathological tissues with expanded extracellular space. Analysis of the CA dynamics allows to distinguish between healthy and high-risk tissues and myocardial scars [171].

Kim et al. [172] initially applied LGE to study myocardial viability in a rabbit model. A clear difference in contrast kinetics between normal tissue, infarct rim, and infarct core regions could be observed. Yang et al. [173] validated the LGE technique for accurate assessment of infarct size in MI mice. After intravenously injecting a 0.3–0.6 mmol/kg bolus of Gd-DTPA, CA-enhanced images of the entire heart were acquired in 15 to 30 min. Great agreements were achieved for infarct size between LGE images and 2,3,5-triphenyl tetrazolium chloride (TTC) staining. The results were in excellent concordance with many other studies [174–176], which clearly demonstrated LGE cardiac imaging to be a reference standard to follow up myocardial viability *in vivo*.

Two main methods for LGE imaging are the inversion recovery (IR) fast gradient echo sequence and the T1-weighted cine FLASH sequence. Due to the ability to null the signal of remote myocardium, IR shows better contrast between the infarcted and non-infarcted myocardium and is widely used in humans. In preclinical research, Price et al. [177] applied LGE in small animals using a multi-slice IR gradient-echo sequence in combination with a Look-Locker sequence for assessing the optimal inversion point to null the signal from healthy myocardium (300-450 ms for rats, around 330 ms for mice, Figure 10). Thomas et al. [174] and Protti et al. [178] compared IR LGE and T1-weighted cine FLASH LGE imaging at 4.7 and 7 T. Both protocols produced reliable results for the assessment of infarction size. Cine FLASH was found to be a more robust, faster and less user dependent method for visualizing infarct size and recommended as the more promising technique in small rodents.

Manganese-Enhanced MRI (MEMRI)

Unlike gadolinium, which only allows extracellular space imaging for assessment of myocardial viability, manganese provides T1-weighted intracellular contrast through calcium handling. During myocardial contraction, Ca²⁺ enters cardiomyocytes primarily by conduction through voltage-gated L-type calcium channel that causes increase in cytosolic Ca²⁺ concentration, which then binds to troponin C and activates myocardial contraction (excitation-contraction coupling) [179]. After systolic contraction, Ca²⁺ is actively transported into the sarcoendoplasmic reticulum (SR) by Ca-ATPase and excreted from the cell through the sarcolemmal Na⁺-Ca²⁺ exchanger

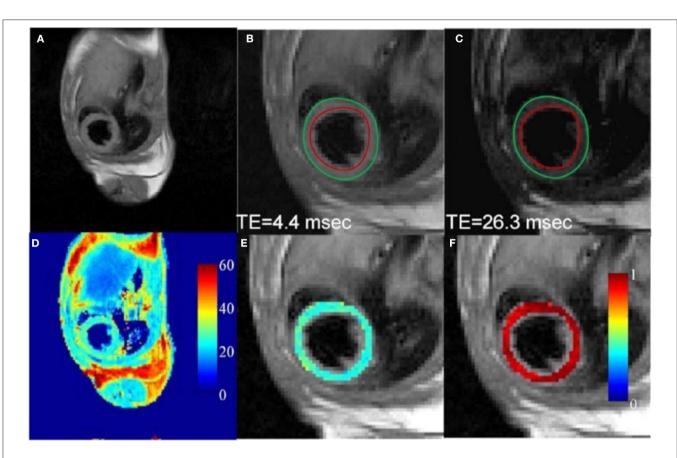


FIGURE 9 | *In vivo* T2 mapping of a mouse heart using a fully-sampled dataset. **(A)** Full FOV image of the first echo (TE: 4.4 msec). **(B,C)** Enlarged images of the heart from the first and sixth echo, respectively. Red and green circles represent endocardial and epicardial contours drawn from the first echo image, respectively. **(D)** The corresponding T2 map for the whole image. **(E)** Enlarged T2 map for the mouse heart. **(F)** Map of squared correlation coefficient for the exponential T2 fitting. Reproduced with permission from Chen et al. [161].

[179]. Alterations in calcium handling may impair the Ca²⁺ cycling between the extracellular space, cytosol, and SR, resulting in systolic or diastolic dysfunction. Manganese is a T1 shortening compound taken up through voltage-gated calcium channels into cells with active calcium handling. It has the ability to measure Ca²⁺ channel activity and myocardial viability, and has been validated in various clinical [180-182] and preclinical [183-185] studies. However, its application in clinical routine was limited by its potential toxicity causing myocardial depression. Manganese formulations using chelation or linkage to a calcium compound [186] were developed. Spath et al. [184] investigated manganese-based contrast media in healthy and infarcted rat models (Figure 11). The investigated manganese agents resulted in calcium channel-dependent myocardial T1 shortening. A good agreement between infarct size on MEMRI T1 mapping and Masson's trichrome (MTC) staining (bias 1.4, 95% CI −14.8 to 17.1, p > 0.05) was reported. In contrast, standard gadolinium delayed enhancement MRI (DEMRI) with the inversion recovery technique overestimated the infarct size (bias 11.4, 95% CI -9.1to 31.8, p = 0.0002), as did DEMRI T1 mapping (bias 8.2, 95% CI -10.7 to 27.2, p = 0.008). Recently, Toma et al. [183] proposed a dual contrast MEMRI and DEMRI technique to evaluate the physiologically unstable peri-infarct region and to track the

therapeutic effects of telmisartan on the injured myocardium longitudinally with attenuation of the peri-infarct region.

Diffusion Tensor Imaging

The myocardial fiber anatomy underlies the mechanical and electrical properties of the heart [187]. Within the normal LV, the myofibers follow left-handed helices in the epicardium, and transit smoothly through a circumferential orientation at the mesocardium to right-handed helices in the endocardium. A feasible and accurate technique to characterize and identify fiber structure changes can contribute to elucidating the complex cardiac structure-function relationships. MR diffusion tensor imaging (DTI) has been validated as a valuable tool to obtain non-invasive measures of myocardial microstructure in both clinical and preclinical studies [187–189]. Several quantitative parameters derived from DTI, such as mean diffusivity (MD) and fractional anisotropy (FA), helix angle (HA) and second eigenvector angulation (E2A), can be used to describe myocardial microstructural organization.

After first developed in 1990s [190], DTI has been widely used in brain imaging to study the spatial organization of white matter fiber tracts [191, 192]. The preclinical application of cardiac DTI is more challenging, due to cardiac and respiratory motion,

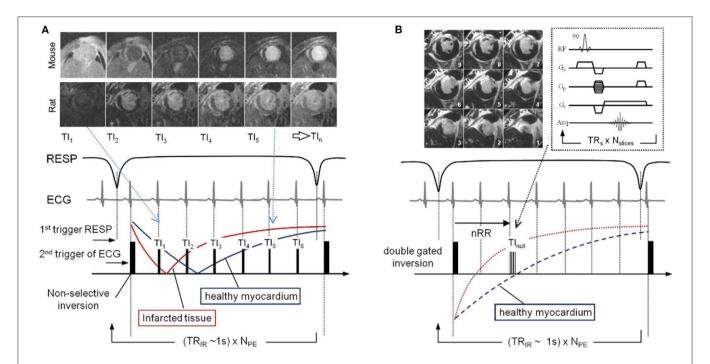


FIGURE 10 | Pulse sequence diagrams for LGE imaging. **(A)** Look-Locker pulse sequence and gating strategy used to acquire multiple inversion time (TI). Images from TI1–TI6 time points are shown for both mouse and rat, where the indices are related to the number of R-wave triggers given the double gated inversion pulse. **(B)** The LGE IR sequence diagram follows the same gating and acquisition scheme but acquires a 90° flip angle multislice GRE stack at the nearest TI value to null healthy myocardium. TR_s is the time between slice acquisition pulses, TR_{IR} is the time between inversion pulses, N_{PE} is the number of phase-encoding steps, and N_{slices} is the number of slices. Reproduced with permission from Price et al. [177].

the diffusion signal attenuation, and a short T2 relaxation time causing low SNR condition. Further, high-resolution DTI of the mouse heart is more complicated due to a low degree of diffusion anisotropy in the tissue [188]. With the developments of pulse sequence design and gradient systems, cardiac DTI has become feasible for *in vitro* and *in vivo* applications.

In the beginning, cardiac DTI was mainly performed on isolated hearts. Scollan et al. [193] introduced two-dimensional stimulated echo acquisition mode (STEAM) in perfused rabbit hearts using standard and fast spin-echo pulse sequence with half-sine diffusion gradients in six non-collinear directions. The inclination angle derived from both protocols showed high agreement with histological results. Jiang et al. [188] firstly extended a similar protocol to acquire 3D diffusion-weighted images of 12 directions in a fixed mouse heart. High spatial resolution (isotropic 100 µm) images were acquired in 9.1 h and allowed the quantification of the myocardial structure at more than 170,000 locations throughout the mouse heart, which is about 10 times better than histological studies. The FA value of 0.27 \pm 0.06 and the mean diffusion tensor eigenvalues of 0.75 ± 0.13 , 0.60 ± 0.13 , and $0.51 \pm 0.13 \times 10^{-3} \text{ mm}^2/\text{s}$ are in good agreement with other studies [193, 194]. Huang et al. [195] firstly investigated in vivo DTI-tractography of the mouse heart to follow myocardial microstructural changes in ischemia/reperfusion mouse models. It showed increased MD and FA in acute ischemia (24h after injury), but decreased values during myocardial healing (2-3 weeks after reperfusion)

(Figure 12). Later, the same group applied 3D DTI-tractography *in vivo* to study ischemic myocardium and assessed the cell therapy effect [196]. With the velocity-compensated Stejskal-Tanner diffusion sequence, they were able to obtain high-resolution 3D reconstructions of the myofibrillar tracts in the mouse heart. The derived parameters clearly showed that DTI could non-invasively reveal the microstructural features of the myocardium.

Magnetic Resonance Spectroscopy and Multi-Nuclei Imaging

CMR spectroscopy (CMRS) is a non-invasive technique to investigate the myocardial metabolism. It can use the signal from different endogenous nuclei, including ³¹phosphorus (³¹P), ¹Hydrogen (¹H), ²³Sodium (²³Na), and ¹³Carbon (¹³C), to quantify myocardial metabolism *in vivo* [197]. As the resonance frequency of nuclei is dependent on its molecular environment, different metabolites exhibit slightly different frequencies (chemical shift), thus leading to MR frequency spectra according to the chemical composition of the investigated voxel. An analysis of the frequency response (the MR spectrum) allows quantification of different metabolites [198].

³¹P-MRS is most widely used to quantify high-energy phosphates in the heart, including adenosine triphosphate (ATP) and phosphocreatine (PCr). The mutual transformation of ATP and PCr are necessary to meet the energy consumption required to maintain normal cardiac function. The impairments in energy

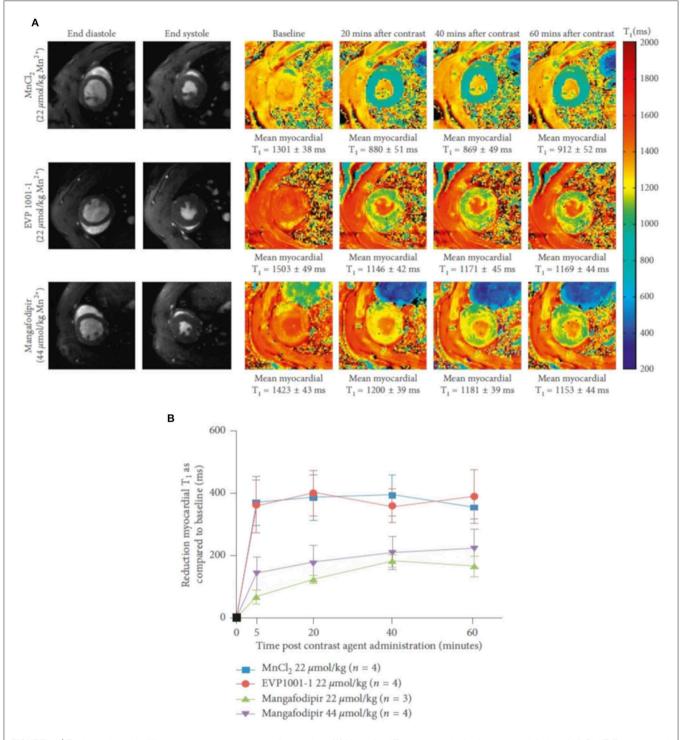


FIGURE 11 | T1 shortening with different manganese contrast media over time. (A) Normalized T1 maps acquired subsequent to infusion of MnCl₂, EVP1001-1, and mangafodipir at 20 min intervals up to 60 min. A clear decreased myocardial T1 value could be observed in all groups. (B) Reduction in mean left ventricular T1 values over 60 min with MnCl₂, EVP1001-1 and different concentrations of mangafodipir. Two-way ANOVA confirmed a dependence of mean myocardial T1 shortening between each of the contrast agents (P < 0.0001). Reproduced with permission from Spath et al. [184].

metabolism reveal pathological processes in cardiac disease. Various preclinical studies showed reduced concentrations of ATP, PCr, and PCr/ATP ratios in cardiomyopathy or heart

failure [199-201]. CMRS needs to localize signal to a certain voxel and to exclude signal from nearby structures (e.g., liver, chest skeletal muscle). Localization methods for cardiac MRS

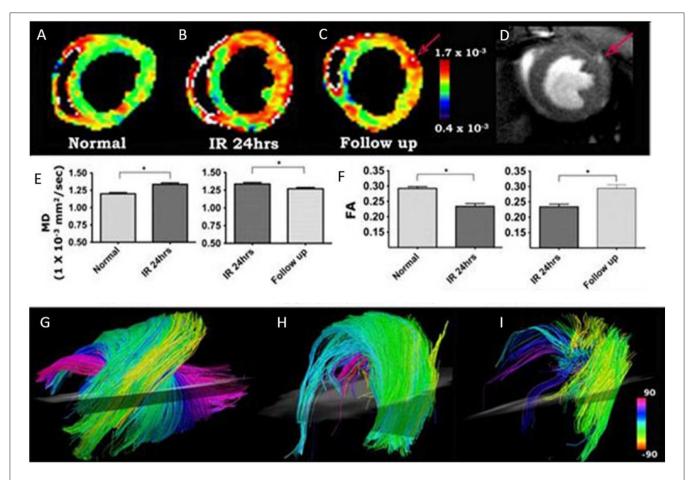


FIGURE 12 | **(A–I)** *In vivo* DTI-tractography of mouse heart at baseline, 24 h after injury and 2–3 weeks after ischemia-reperfusion. The mean diffusivity (MD) maps clearly showed that MD in the injured anterolateral wall increased acutely (24 h after injury) and subsequently returned toward baseline as the myocardium healed **(A–C,E)**. Fractional anisotropy (FA) decreased acutely and returned to baseline 2–3 weeks after injury **(F)**. **(C,D)** The left coronary artery, when present in the image, can be used for internal standardization and control. MD in the vessel and its branches (red arrow, **C,D**) will be significantly higher than MD in normal or healing myocardium. Myofibers passing through a region of interest placed in the anterolateral wall are shown in **(G–I)**. **(G)** Normal mouse heart. The characteristic arrangement of myofibers into an array of crossing helices is clearly visible. **(H)** Mouse exposed to ischemia-reperfusion with severe hypokinesis in the anterolateral wall. However, MD has remained <1.3 × 10^{\times} mm²/s and fiber architecture remains reasonably organized. **(I)** Mouse exposed to ischemia-reperfusion, also presenting with severe hypokinesis of the anterolateral wall. MD in this mouse, however, is <1.3 × 10^{-3} mm²/s and fiber architecture is severely perturbed. Reproduced with permission from Huang et al. [195].

mainly contain two approaches, single-voxel and chemical shift imaging (CSI). Both contain advantages and limitations. Single-voxel localization is usually performed with image selected *in vivo* spectroscopy (ISIS), which consists of three slice-selective 180° pulses for localization and a single nonselective 90° pulse for signal detection [202]. Bakermans et al. [203] assessed myocardial energy status *in vivo* using single-voxel ISIS-localized 31 P-MRS. Accurate localization and decreased PCr/ γ -ATP ratios were observed in TAC mice (**Figure 13**). The 31 P-CSI can be performed in 1D (column of voxel), 2D (plane of voxel), or 3D (block of voxels) mode [200, 204, 205]. CSI employs phase-encoding gradients in different directions and resolves spectra from different locations across the myocardium.

The ¹H represents the MR-active nuclei with the highest natural abundance and sensitivity in living tissues, and ensures cardiac ¹H-MRS to be a useful target for quantifying myocardial

metabolites, such as triglycerides, lactate, carnitine, myoglobin, and creatine (Cr) levels [206]. Since creatine plays a key role in the creatine kinase system, its measurement can provide additional information about myocardial energy transportation and storage. The high lipid concentration is associated with atherosclerosis and type 2 diabetes mellitus, which results in impaired cardiac function. Due to the technical restriction, it took decades for translating to in vivo imaging after first implemented ¹H-CMRS in a perfused rat heart in Ugurbil et al. [207]. Schneider et al. [208] reported cardiac ¹H-MRS in a guanidinoacetate N-methyltransferase (GAMT) deficient mouse model in vivo using a single-voxel point resolved spectroscopy sequence (PRESS). Various cardiac metabolites were detected in voxels of 2 µl and a clear decreased myocardial creatine level was observed. PRESS is the dominant method for ¹H-MRS, containing three slice-selective RF pulses (90-180-180°) applied

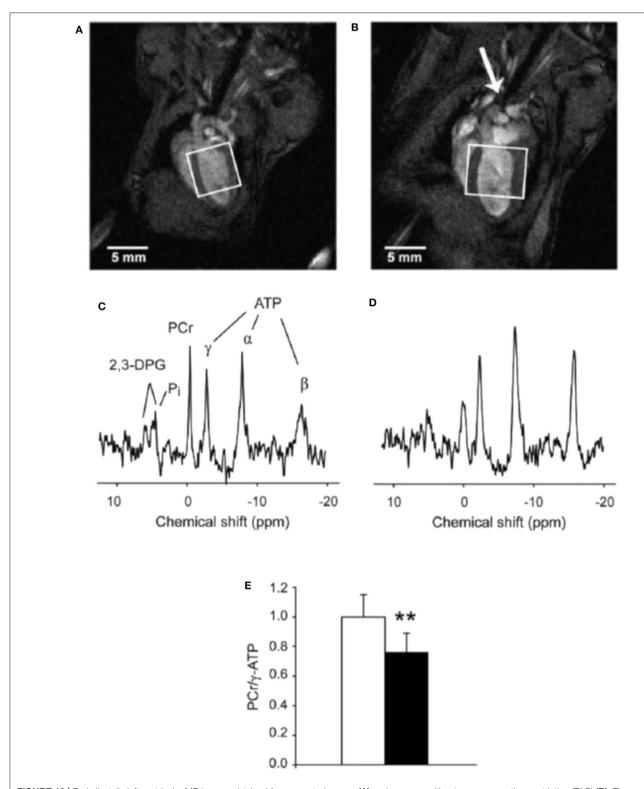


FIGURE 13 | End-diastolic left ventricular MR images obtained from a control mouse **(A)** and a mouse with a transverse aortic constriction (TAC) **(B)**. The constriction is indicated by the arrow. Dilated hypertrophic cardiomyopathy is evidenced by increased LV wall thickness and LV cavity volume in the TAC mouse. Rectangles indicate the voxels selected for localized 31P-MRS with 3D ISIS. **(C,D)** display ³¹P MR spectra acquired *in vivo* with 3D ISIS in a healthy mouse heart and a TAC heart, respectively. Myocardial PCr/ γ -ATP was lower in TAC mice (n = 8) compared to healthy controls (n = 9) **(E)**. Data are expressed as mean \pm SD. **P < 0.01. α -, β -, γ -ATP, α -, β -, and γ -phosphate groups in ATP; 2,3-DPG, 2,3-diphosphoglycerate; PCr, phosphocreatine; Pi, inorganic phosphate. Reproduced with permission from Bakermans et al. [203].

concurrently with three mutually orthogonal field gradients [209]. Another technique for ¹H-MRS is STEAM. It is similar to PRESS, but uses three 90° RF pulses. However, ¹H-MRS remains technically challenging due to the superabundance of ¹H in the water molecule, and it will result in baseline distortion and affect the quantification.

²³Na is an important component in the myocardial signal transduction pathway. The ²³Na signal is increased in myocardial ischemia. Thus, ²³Na-MRS can measure intracellular and extracellular Na⁺ changes to investigate myocardial viability without external contrast agents [210, 211]. Combination with acceleration methods such as CS has been shown [212].

As many metabolites contain carbon, ¹³C-MRS is particularly suited to study myocardial metabolism. However, traditional ¹³C-MRS is limited by low inherent sensitivity. In the last 10 years, in vivo cardiac 13C-MRS has become feasible with the development of dynamic nuclear hyperpolarization (DNP) technique. DNP is based on transferring electron to nuclear spins thus achieving substantially higher polarization through DNP. It requires the presence of unpaired electrons homogeneously distributed within the sample, which can be achieved by mixing the sample with radicals. To achieve almost 100% polarization of the electrons, DNP works at low temperature and high magnetic fields. Electron-nuclear spin transitions are induced through microwave irradiation. In the solid state, the nuclear polarizations of ¹³C can be increased to over 40% [213]. Subsequently, the solid sample is dissolved rapidly to yield a solution of molecules with hyperpolarized nuclear spins [214]. The sensitivity of ¹³C-MRS can be increased over 10,000-fold and the metabolism of infused hyperpolarized compounds be visualized in vivo [210], 1-13Cpyruvate has been the most widely used DNP hyperpolarized molecules. Pyruvate is the primary metabolites of carbohydrates. After being transported into mitochondria, it is irreversibly converted to acetyl-CoA by the pyruvate dehydrogenase enzyme complex (PDH), then participated into the tricarboxylic acid (TCA) cycle [215]. By labeling pyruvate in a unique carbon position and investigating its metabolism by MRS, insights into myocardial metabolism can be derived. Dodd et al. [216] investigated in vivo metabolism of [1-13C]pyruvate in the mouse heart and revealed metabolic differences between different mouse strains. Atherton et al. [217] used [2-13C]pyruvate to evaluate Krebs cycle metabolism in hyperthyroidism rats and increased anaplerosis was observed in the hyperthyroid heart. With infused hyperpolarized pyruvate, myocardial metabolic processes have been quantified in different rodent models, including diabetes [218], ischemia [219], cardiac inflammation [220], etc.

CONCLUSIONS

MRI is a tremendously versatile and flexible imaging modality and provides high-resolution images in any arbitrary plane without the risk of ionizing radiation. Especially its accuracy and high reproducibility have made CMR the non-invasive reference modality for deriving myocardial structure, global and regional function, perfusion, tissue characterization and myocardial metabolism in small animal research.

Even though well-established, cardiac imaging in small animals is still challenging especially due to high cardiac and respiratory rates and the small anatomical structures, often demanding dedicated hardware components for providing sufficient image quality in acceptable imaging times. Especially dedicated multielement receiver coils either placed under the chest of the animal or wrapped around its thorax ensure sufficient SNR and reduction of the acquisition time by parallel imaging approaches.

According to the nature of MRI, reliable and highly reproducible information on the cardiac condition of the animal can be obtained. However, the impact of the required general anesthesia and rather long acquisition times on the investigated parameters have to be carefully considered during data interpretation. Inhalation anesthesia is highly recommended, since it provides greater safety, lesser cardiovascular depression, and rapid recovery, and convenient adjustments and maintenance during scanning. The body temperature control of the animal seems mandatory to avoid the deterioration of the derived functional parameters by cardiovascular depression due to cooling out of the animal.

With the availability of reliably working self-gating techniques, assessment of global cardiac function has been proven to be an excellent tool for reliable quantification of systolic dysfunction. However, due to the high heart rates, the assessment of diastolic dysfunction is still challenging and demands long acquisition times to provide sufficient temporal resolution. As in human imaging, regional cardiac function has been addressed by several approaches, and the use of conventional cine images in combination with feature tracking show the potential to enable efficient regional wall motion analysis.

One of the strengths of CMR is its capability for tissue characterization. Identification of scarred tissue by means of delayed contrast enhancement imaging is straight forward using (black-blood) self-gating techniques. Although mapping of relaxation parameters by different means has been reported, it is technically more challenging and well-trained operators are required especially for ensuring accurate and reproducible numbers. More advanced techniques such as (first-pass) perfusion, diffusion-weighted imaging or DTI for deriving myocardial fiber orientation must still be seen as experimental.

Further important information on tissue composition and metabolism can be retrieved from MR spectroscopy and multinuclei imaging. Due to its high natural abundance and sensitivity, ¹H spectroscopy has been efficiently applied to quantifying triglycerides, lactate, carnitine, myoglobin, and creatine (Cr) levels. However, to make full use of the technique, different nuclei like phosphorus (³¹P), Sodium (²³Na), and Carbon (¹³C) need to be investigated to quantify myocardial metabolism *in vivo*. ³¹P-MRS can be used to quantify high-energy phosphates in the heart, ²³Na is an important component in the myocardial signal transduction pathway, and ¹³C-MRS is particularly suited to study myocardial metabolism. In general, the multinuclei techniques can be extended to imaging thus

providing the chemical composition of each voxel. Due to the low sensitivity and the need to spectrally separate the signal from the different metabolites, multinuclei MRS and MRI are mainly performed at ultra-high field strengths. Even though available in research for decades, due to the long scan times and the expertise required to performing multi-nuclei MRS and MRI in the heart, this technique must still be seen as experimental with unfortunately only little utilization. With the recent introduction of hyperpolarized ¹³C imaging, limitations from the intrinsic low sensitivity may be solved and rapid access to ¹³C-labeled metabolites may be enabled at the expense of high related costs.

CMR imaging and spectroscopy is still one of the most promising noninvasive tools for the staging and longitudinal monitoring of cardiovascular diseases in small animals. Due to its versatility, it can be applied to a wide range of translational applications and provide quantitative data from global functional assessment to metabolic characterization of the underlying myocardial substrate. Due to its complexity, the application is currently often limited to global functional assessment and scar imaging. More challenging techniques such as assessing metabolism or the structural organization of the myocardial fibers are still limited by long scan times and may need further technical developments before finally becoming routine in small animal applications.

AUTHOR CONTRIBUTIONS

HL and VR drafted the manuscript. All authors read and approved the final manuscript.

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Functional Neuroimaging in Rodents Using Cerebral Blood Flow SPECT

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The brain-wide activation patterns that underlie, generate, and change the behavioral outputs in rodents, the main animal models in biomedical research, are difficult to assess in vivo. The standard tool for whole-brain imaging of spatiotemporal activation patterns in rodents is BOLD fMRI, but the technique requires the animals to be immobilized inside the scanners. One of the few methods that can provide in vivo images of brain-wide patterns of neural activity from unrestrained animals outside scanner environments is single-photon emission computed tomography (SPECT) imaging of cerebral blood flow (CBF). During ongoing behavior, animals are intravenously injected with ^{99m}Tc-HMPAO (99m-technetium hexamethylene propyleneamine oxime), a lipophilic tracer that, after accumulation in the brain in a flow-dependent manner, is rapidly converted to a hydrophilic compound that remains trapped in the brain and shows no redistribution. The ^{99m}Tc brain distribution, reflecting the average blood flow during the time of injection, can be read out in the anesthetized animal after injection. Similar in rationale to ¹⁸F-2-fluoro-2-deoxy-glucose (¹⁸F-FDG) positron emission tomography (PET), 99mTc-HMPAO SPECT provides static images of spatial patterns of neural activity from awake behaving rodents, but the spatial resolution can be higher and the stimulation times substantially shorter. In this review, we present an overview about the underlying rationales and principles of functional CBF SPECT imaging in rodents, give a short summary of the experimental procedures, and discuss the advantages, drawbacks, and perspectives of the technique within the framework of methods for imaging brain-wide activation patterns in awake behaving rodents.

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INTRODUCTION

Rodents, in particular rats and mice, serve as the main model organisms for studying the structure and function of the mammalian brain in basic and applied neurosciences. With brain sizes in the cubic centimeter range—about 0.5 cm³ in mice and 2 cm³ in rats—these rodents pose particular challenges for neuroimaging techniques, especially techniques for *in vivo* imaging of the entire organ.

Rodent brains are several orders of magnitude larger than the brains of small vertebrates such as the zebrafish or common invertebrate model organisms such as the fruit fly *Drosophila* and the roundworm *Caenorhabditis elegans*. In addition, myelinated fiber bundles traverse the adult rodent brains, strongly increasing the scattering of electromagnetic waves in the visible range. In contrast to the transparent brains of zebrafish larvae or *C. elegans*, which can be optically imaged as a whole

at cellular resolution *in vivo* [1, 2], optical *in vivo* imaging of entire rodent brains at this resolution is not possible.

With respect to penetration depths and fields of view, rodent brains can easily be imaged with X-ray CT, MRI, PET, or SPECT, medical imaging techniques developed for human imaging. However, with brain volumes about a thousand times smaller than the human brain, substantial increases in spatial resolution are required if rodent brains should be imaged with at least the same relative resolution—relative to the brain size—as in humans

Techniques for imaging the entire brain are of particular relevance in neuroscience. Brains are characterized by high degrees of global and local anatomical and functional interconnectivities between single neurons and neuronal ensembles. This network topology implies that, as a general rule, changes in behavioral output are mediated by activation changes in distributed neuron populations. In fact, even apparently simple behaviors, e.g., fear behavior [3], have been shown to be governed by complex brain-wide network activations. Explaining the changes in behavior that genetic alterations or manipulations, protein modifications, pharmacological treatments, and artificial or natural stimulations of cell ensembles might cause requires identification of the network activation patterns.

An ideal method for functional neuroimaging would be able to image *in vivo* brain-wide patterns of neural activity with high spatial (single-cell) and temporal (millisecond) resolution in behaving unrestrained animals. High-throughput imaging, repeated imaging over long time spans, and little to no interferences with experimental set-ups would be additional benefits.

Optical methods in invertebrates and the zebrafish larva as a small vertebrate come close to these demands [1, 2]. For the mouse brain, however, no such methods are available, and it remains dubious whether techniques for single-cell-resolution *in vivo* imaging of the activation patterns of the \sim 70 million neurons in the mouse brain [4] can be developed at all. All currently available methods operate at substantially lower resolutions and suffer from more or less severe drawbacks.

The prevailing approach to assessing the brain-wide network behavior in the rodent brain is functional magnetic resonance imaging based on blood-oxygenation-level-dependent contrast (BOLD fMRI). Spatial and temporal resolutions rank among the highest in rodent whole-brain imaging, but animals have to be restrained inside scanners. In vivo images of brain-wide activation patterns in unrestrained, behaving rodents can be obtained using tracer techniques. Rodents are injected before or during the behavior of interest with tracers that accumulate in the brain in an activity-dependent manner. Tracers that show no relevant redistribution can be imaged in anesthetized animals after the experiment. Three tracers with three different imaging modalities are commonly used, the glucose analog ¹⁸F-2-fluoro-2-deoxy-glucose (18F-FDG) for positron emission tomography (PET) imaging, the calcium analog manganese for manganeseenhanced MRI (MEMRI), and the blood flow tracer 99mTc-HMPAO for SPECT imaging. As one of the main drawbacks, these methods can provide only a static view of the average activity during the uptake period. What makes these approaches attractive is that there are few constraints on the behavioral set-ups to be used and the simplicity of the methods with respect to the treatments of the animals.

We here review one of the approaches, functional neuroimaging using CBF SPECT. We first describe the historical development and the rationales of using tracers for imaging cerebral blood flow and give an overview of the principles of SPECT imaging in small animals. We then explain the experimental procedure and discuss the approach in the framework of the diverse techniques for brain-wide functional neuroimaging in rodents.

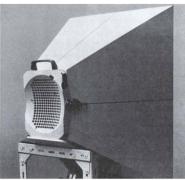
IMAGING REGIONAL CEREBRAL BLOOD FLOW USING TRACER TECHNIQUES

Functional neuroimaging has its roots in studies of cerebral blood flow in mammals. In 1948, Kety and Schmidt published a method for quantifying the global cerebral blood flow in humans based on measurements of arteriovenous differences in concentrations of nitrous oxide, a non-metabolized gas [5]. The method solved a problem inherent to earlier attempts of calculating global cerebral blood flow from arteriovenous differences in oxygen concentration. By using an inert gas, the flow could be determined independently from the oxygen metabolism [6]. The inert gas approach, which can be seen as a tracer technique for calculating global cerebral blood flow, led to the development of tracer techniques for imaging regional cerebral blood flow (rCBF). The first method for studying rCBF was published in 1955 [7]. It was based on intravenously injecting cats with 131 I-trifluoroiodomethane, an inert gas radioactively labeled with 131 iodine, and studying the spatial patterns of the flow-dependent wash-in of the gas post-mortem by means of an autoradiographic method. After tracer injection, brains were quickly removed and frozen in order to avoid back-diffusion of the tracer from the brain to plasma. Brain sectioning and autoradiography were performed at -40° C in order to minimize the loss of the volatile compound [6]. By demonstrating the increased blood flow in the visual cortex upon visual stimulation, the method was also the first to provide images of stimulusinduced brain activations [8, 9].

Interestingly, it was not generally recognized at that time that these studies formed the basis for what would later be termed "functional neuroimaging." When the data were presented in 1955 on a meeting of the American Neurological Association, Landau (as quoted from [10]) commented: "Of course we recognize that this is a very secondhand way of determining physiological activity; it is rather like trying to measure what a factory does by measuring the intake of water and the output of sewage. This is only a problem of plumbing and only secondary inferences can be made about function. We would not suggest that this is a substitute for electrical recording in terms of easy evaluation of what is going on."

In fact, in terms of spatial and temporal resolution, measurements of blood flow are orders of magnitude apart from electrophysiological recordings. Nevertheless, the following decades clearly showed the usefulness of this approach for





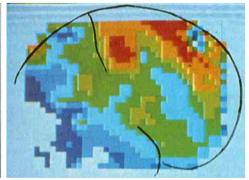


FIGURE 1 | Functional neuroimaging in humans started with 2D scintigraphic imaging of cerebral blood flow. An experimental set-up is shown in the left panel. The arrow points to a gamma camera equipped with a cone beam collimator similar to the collimator shown in the middle panel. The cone-beam collimator is placed close to the subject's head. The gamma camera is a 254 detector camera developed by Per Rommer and Edda Sveinsdottir under the leadership of Niels A. Lassen at Meditronic and commercialized by Medimatic under the name "Dynamatic 254" (Images reprinted with permission from Per Rommer). An example of the images obtained with this set-up is shown in the right panel. Brain contours and the central sulcus are outlined in black. The image shows CBF during hand gripping with the contralateral hand. Reprinted with permission from the American Medical Association. Copyright © (1976) American Medical Association. All rights reserved [12].

detecting spatial patterns of neural activity in experimental animals and in humans. The first images of functional brain activity in humans were 2D scintigraphic gamma camera images from subjects intra-arterially injected with the gamma emitter ¹³³Xe as a tracer, again an inert gas ([11]; **Figure 1**). Groundbreaking work on functional imaging in humans followed using PET with ¹⁵O-H₂O as a blood flow tracer [13–15]. The short half-life of ¹⁵O of 2.04 min made it possible to repeatedly image the same subject inside the PET scanner, and the logic of subtracting data sets from different conditions for studying cognitive processes was introduced [10].

The details of the neurovascular coupling are still under debate. Much progress has been made in elucidating signal cascades coupling energy demands in neural tissue to changes in diameter in capillaries or different segments of the arterial system [16], but the interpretation of increased or decreased flow in volumes of mixed populations of excitatory and inhibitory neurons, presynaptic and post-synaptic neuronal elements, and astrocytes has remained unclear. Under simple conditions, an excitatory input may lead to enhanced post-synaptic processing in a volume element, resulting in an increased flow. Conversely, reduced excitatory input under certain stimulus conditions may result in reduced metabolism and flow appearing as a deactivation. The complexity increases, however, when inhibitory interneurons are involved. Subpopulations of inhibitory interneurons, for instance, may have high firing rates and energy demands, but the net effect on energy demands in a volume element will depend on, among others, the densities of excitatory and inhibitory neurons as well as the local effects of the inhibition, factors that vary in different brain regions.

Stimulus-induced changes in cerebral blood flow as measured with $^{15}\text{O-H}_2\text{O}$ PET in humans increase up to 30% upon intense stimulation [17]. These changes are relatively large compared to changes in cerebral blood volume (CBV) or in the BOLD response. This may compensate to some degree

for the fact that, in contrast to BOLD fMRI or functional ultrasound (fUS) measurements of CBV, usually only one image is taken per individual and condition in CBF studies. Comparisons of the sensitivities of the different methods are difficult, however, as they strongly depend on image noise, which can vary substantially with different imaging protocols and in radionuclide imaging is strongly affected by injected dose and acquisition times.

A number of chemically quite diverse molecules can be used as tracers for imaging cerebral blood flow: inert gases, ¹⁵O-labeled water, or labeled lipophilic compounds such as ¹⁴C-iodoantipyrine [18]. A key feature of all these compounds is that they can readily pass the blood-brain barrier. With all these compounds, the passage through the BBB is bi-directional. In order to measure the blood-flow-dependent wash-in of these compounds into the brain, measurements have to be done quickly after injection—usually within the first minute—as long as there is unidirectional flow of the tracers from plasma to brain. Even if the half-life of ¹⁵O were much longer, ¹⁵O-H₂O PET CBF measurements would still have to be done in subjects inside the PET scanner. For autoradiographic measurements in experimental animals, the brains have to be quickly removed after injection [18].

Routine SPECT imaging of CBF differs from these approaches because tracers can be used that are trapped in the brain after passage through the BBB. This makes it possible to image the tracer distributions, or the distributions of the radioactive labels, resp., after trapping. In theory, measurements of CBF using trapped tracers are less straightforward than measurements with inert, non-metabolized compounds, because additional factors come into play, in particular the rates of the trapping reactions and potential redistributions of tracers or trapped labels. In practice, however, the two most commonly used tracers for SPECT imaging of brain perfusion, ^{99m}Tc-HMPAO [19] and ^{99m}Tc-ethyl cysteinate dimer (^{99m}Tc-ECD), have been shown to rather accurately reflect CBF [18].

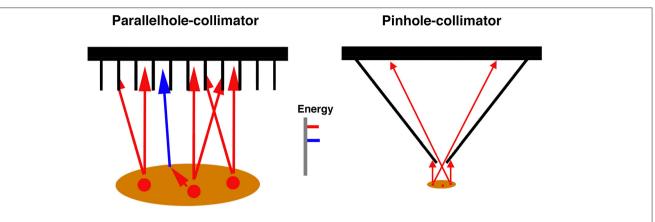


FIGURE 2 | Two collimator types used in SPECT imaging. Parallel-hole collimators, frequently used in SPECT imaging in humans, absorb photons that would reach the detector—within limits—at oblique angles after emission from the sources. The sources are depicted in red. Scattered photons (blue, shown only for the parallel-hole collimator) can be distinguished from non-scattered photons due to their lower energy. When pinhole collimators are used, magnified 2D projection images form on the detector if the imaged objects are close to the pinhole.

Both tracers are trapped by rapid conversion to hydrophilic compounds after passage through the BBB. The available data indicate that 99mTc-HMPAO is metabolized to hydrophilic compounds in reactions that, at least in part, depend on glutathione and may take place preferentially in astrocytes [20, 21]. 99mTc-ECD is metabolized to a monoacid form that is retained in brains of primates. ^{99m}Tc is not retained in rat and mouse brains after intravenous ^{99m}Tc-ECD injections [22, 23]. Studies in mice have shown that the ^{99m}Tc monoacid is quickly extruded by the organic anion transporter OAT3 [24], which is highly expressed in endothelial cells. In addition to the ^{99m}Tc-labeled tracers, there is also a ¹²³I-iodine-labeled tracer available for SPECT imaging, ¹²³I-iodoamphetamine (¹²³I-IMP). In humans, the tracer redistributes already within the first hour after administration [25, 26], a fact that has limited its use. To our knowledge, its redistribution has not been studied with smallanimal SPECT in rodents, but the tracer has been used for an ex vivo SPECT imaging study [27]. Currently, 99mTc-HMPAO can be regarded as the tracer of choice for functional neuroimaging using CBF SPECT in rodents.

PRINCIPLES OF SPECT IMAGING IN SMALL ANIMALS

As mentioned above, the first *in vivo* images of brain activity were 2D scintigraphic images of cerebral blood flow in humans with pixel sizes on the order of 1 cm². These images were taken with a gamma camera, a device developed in the 1950s by Anger [28, 29].

The traditional Anger camera records the spatial positions and intensities of scintillation events that occur in relatively large crystals—usually flat thallium-activated sodium iodide crystals a few hundred square centimeters in size—upon absorption of gamma photons. In order to relate the spatial position of a scintillation event in the crystal to a restricted volume of possible emission sites in the subject, the cameras are equipped with

so-called collimators, a term derived from a false reading of Latin *collineare*, meaning "to direct in a straight line" (Merriam-Webster online dictionary: https://www.merriam-webster.com/dictionary/collimate).

No different from light emitted from a light source, gamma rays are emitted isotropically from gamma ray sources. Collimators, placed between the sources and the scintillation crystal, limit the possible angles at which gamma rays from different positions in the field of view can reach the crystal (for a review on collimators, see [30]). A parallel-hole collimator, for instance, is a sieve-like structure made of heavy metals that absorbs most of the gamma photons reaching the detector at oblique angles (Figure 2). The 2D projection image of the source distribution is formed from parallel bundles of gamma rays that can pass through the collimator. Absorptive collimation with different collimator geometries is the prevailing method for forming 2D projection images in SPECT. In general, small fractions of <1% of the gamma photons that could theoretically reach the detector pass through the collimator and can be used for image formation [30].

The first systems for 3D imaging of gamma emitters were developed in the 1960s [31, 32]. Scanners with rotating gamma cameras, similar to currently prevailing clinical scanners, were introduced in the 1970s [31]. The development of SPECT imaging was driven not only by advancements in the imaging technology but also by the discovery of the radionuclide ^{99m}Technetium [33]. With a physical half-life of 6 h, an energy of the emitted gamma photons of 140 keV, which is low enough for efficient detection with NaI-scintillator crystals but high enough for efficient emissions out of the human body, and easy onsite availability from ^{99m}Tc generators, this radionuclide proved to be ideal for SPECT imaging. ^{99m}Tc became the most used radionuclide for diagnostic imaging worldwide [33].

With spatial resolutions in the range of a cubic centimeter in clinical routine, SPECT has been notoriously regarded a low-resolution imaging modality that is inferior to PET in any respect. However, the spatial resolution of SPECT

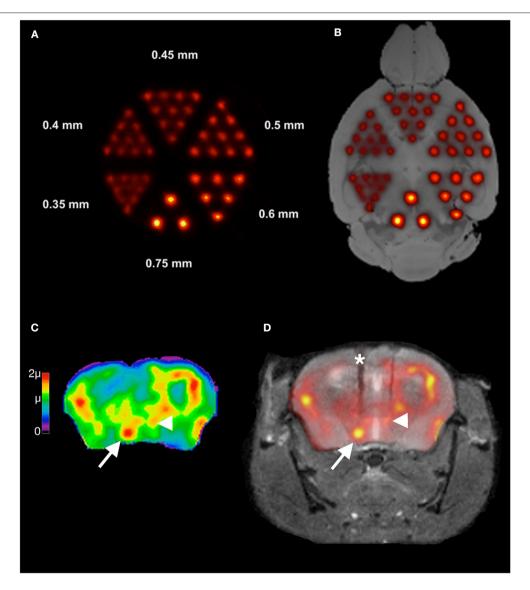


FIGURE 3 | Illustration of spatial resolutions with multi-pinhole SPECT imaging in mouse brain. Shown in (A) is an image of a SPECT measurement of a micro-Jaszczak hot-rod resolution phantom filled with ^{99m}Tc. The phantom was scanned with custom-made 0.3 mm multi-pinhole apertures at the Leibniz Institute for Neurobiology. Rods down to the size of 0.4 mm can be resolved. In (B), an overlay of the image in (A) onto an anatomical reference MR image [38] of a mouse brain is shown to illustrate these spatial resolutions in relation to the mouse brain anatomy. Resolutions in the range of 0.75 mm that can easily be achieved in SPECT imaging are already quite useful for imaging brain regional tracer distributions. In (C) a high-resolution ^{99m}Tc-HMPAO SPECT image is shown from the CBF of a mouse during intracranial self-stimulation of the medial forebrain bundle (mfb). This image was overlaid on the MR of the same animal in (D). The MR is a post-mortem MR after removal of the self-stimulation setup. The electrode track is marked by an asterisk in (D). Images were taken with the same setup as for the measurement in (A). The color scale in (C) is in units of the global mean intensity μ. Note in (C) the clear delineation of the mfb (arrow) and the small hypothalamic region with a relatively high uptake (arrowhead).

critically depends on the collimators used and can exceed that of PET.

Magnified projection images of gamma ray sources can be obtained when pinhole collimators (**Figure 2**) are used, with the magnification depending on pinhole-detector and pinhole-object distances and the resolution depending on pinhole diameters and detector resolutions. High system resolutions can be achieved this way even with detector resolutions in the range of a few millimeters. In principle, microscopic resolutions could be

achieved [34], the main limiting factor being the decreasing sensitivity with decreasing pinhole diameter. The system's sensitivity increases with increasing number of pinholes for a given field of view, the maximum number of pinholes depending on the geometries of pinhole and detector arrangements. Current commercially available small-animal SPECT scanners make use of this multi-pinhole technology ([35]; for reviews on small-animal SPECT, see also [36, 37]; **Figure 3**). Spatial resolutions down to ca. 250 µm have been reported for *in vivo* imaging [39].

These spatial resolutions cannot be achieved in PET imaging of conventional positron emitters in brain tissue. In clinical routine and in most preclinical scanners, PET imaging is based on coincidence detection of two 511 keV-photons emitted in nearly opposite directions from positron-electron annihilation sites (but see Walker et al. [40] for a preclinical PET scanner with pinhole collimation). Positrons have to lose most of their kinetic energy before an annihilation event is possible. Annihilation events occur at certain distances from the positron emitting radionuclide or tracer molecules labeled with the radionuclide, a factor limiting the spatial resolution of PET, irrespective of the way the emitted photons are detected. The mean distances between the sites of positron emissions and the sites of annihilations, the so-called positron ranges, depend on the kinetic energies at which positrons are emitted and the probabilities with which the emitted positrons can interact with their environment. On average, positron ranges decrease with increasing tissue density. Positrons emitted from ¹⁸F have a favorably low maximum energy of 0.634 MeV [41], and it seems possible to detect this radionuclide in mouse brain at a spatial resolution close to 600 µm [42]. For comparison, ¹⁵O emits positrons at a maximum energy of 1.732 MeV, resulting in a mean positron range of three millimeters in water [41]. While detection of photons from annihilations rather than detection of photons emitted from radionuclide atoms limits the spatial resolution of PET, there is at the same time a substantial gain in sensitivity when coincidence detection is used, as no collimators are necessary for imaging radionuclide distributions.

In preclinical practice, the spatial resolution advantage of SPECT vs. the sensitivity advantage of PET may in many cases be of minor relevance: Newest-generation small-animal PET scanners approach the fundamental limit in spatial resolution for ¹⁸F, which is similar to the resolutions in many routine measurements with small-animal SPECT. On the other hand, SPECT imaging at a resolution of about 700 µm is possible with doses that are well within nano- to picomolar ranges. 100 MBq ^{99m}Tc corresponds to ca. 5 pmol (see [43] for details of calculations). With about 1.5 MBq of this amount reaching the mouse brain in a typical CBF imaging experiment [22, 44], this would correspond to ca. 0.075 pmol/0.5 cm³ brain tissue corresponding to a concentration of 150 pmol/L (assuming 1 $cm^3 = 1 \text{ mL}$). For estimating pharmacological or toxicological effects, it has to be taken into account that HMPAO labeled with ⁹⁹Tc, the decay product of ^{99m}Tc, also enters the brain. However, even with amounts of 99 Tc-HMPAO exceeding those of ^{99m}Tc-HMPAO by an order of magnitude, the total concentration of labeled HMPAO would still be outside of the range of pharmacological effects.

In general, the ratio of radioactively labeled tracers vs. tracers labeled with decay products is higher with ^{99m}Tc-labeled compounds than with PET tracers because of the longer half-life of ^{99m}Tc and delivery of the radionuclide from ^{99m}Tc generators at high specific activities, i.e., high amounts of radioactive atoms per total number or mass of the atoms. With activities of ^{99m}Tc of 1 GBq delivered in a few hundred microliters of physiological saline solution, volume loads usually

are also within limits of good practice for i.v. injections in rodents.

Radionuclide contents can be quantified quite accurately in SPECT and PET imaging if the data sets are corrected for the various factors that affect how many of the emitted photons can finally be counted and selected for 3D image reconstructions, e.g., collimator effects in SPECT, random coincidences in PET, and effects of absorption and scattering in the imaged subjects [45]. Underestimations of the true activities due to gamma ray attenuation in the subjects can be more severe in PET than in SPECT imaging despite the higher photon energies in PET, because a true coincidence event is missing if only one of the two annihilation photons does not reach the detector in a line of response [45]. Without attenuation correction, radionuclide contents would be underestimated in small-animal PET imaging by about 40% in rats [46] and 20% in mice [47]. In small-animal SPECT imaging, the combined effects of scattering and absorption can result in underestimations of true activities by about 12% in mice [48, 49] and 23% in rats [50] when using the radionuclide ^{99m}Tc. Attenuation correction is computationally simpler in PET imaging [45, 51], but algorithms have been developed that reduce the errors in small-animal SPECT imaging to <5% [50]. It can be expected that the accuracy will increase further when corrections will be based on calculations of attenuation coefficients from X-ray CT scans or more indirectly from MR images of the same individual, as increasingly done in humans [51]. Finally, when using SPECT for functional neuroimaging in rodents, the focus is on comparing differences in radionuclide distributions in brains from animals of different experimental groups. Due to little variations in brain and skull anatomy, absorption and scattering will also differ little within and between the groups. This tends to reduce attenuation effects in voxel-wise statistical comparisons.

The radionuclide doses given per body weight are generally higher in small-animal imaging as compared with human imaging [52], resulting in higher radiation exposures. Data for ^{99m}Tc-HMPAO in rats [19] and calculations for other ^{99m}Tc-compounds in mice and rats [52] indicate that whole-body radiation doses in CBF SPECT at commonly used ^{99m}Tc doses, e.g., 100 MBq in mice, can be estimated to be in the lower to mid centigray range, which is well within usual dose ranges in small-animal PET and SPECT imaging [52].

The choice between PET and SPECT in preclinical imaging may frequently depend on scanner availabilities and suitable tracers for the questions to be studied. The logistics of small-animal SPECT are simpler due to the relatively long half-lives of the radionuclides used. An interesting opportunity in SPECT imaging is dual-isotope SPECT [36, 37]. Two or more tracers can be detected simultaneously if they emit gamma or X-ray photons at energies sufficiently different for being resolved with the detectors used. In principle, images of CBF under two different conditions in the same animal could be obtained by sequentially injecting the two tracers ^{99m}Tc-HMPAO and ¹²³I-IMP in one session. Because of potential redistributions of ¹²³I-IMP, the feasibility of this approach for *in vivo* imaging is currently unclear, but it could be of interest for high-resolution *ex vivo* imaging.

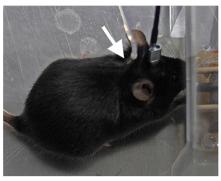




FIGURE 4 I Images of mice implanted with chronic external jugular vein catheters. The image on the left shows a mouse during optogenetic stimulation, the image on the right a volume-rendered CT from a mouse that was injected with an X-ray-dense contrast agent during CT acquisition. The arrows point to the dorsal exit of the catheter. The subcutaneous part of the tunneled catheter can be seen in the CT. The tip of the catheter (asterisk) is at or close to the right atrium.

FUNCTIONAL NEUROIMAGING IN RODENTS USING 99mTc-HMPAO SPECT—THE EXPERIMENTAL PROCEDURE

SPECT imaging of cerebral blood flow in rodents dates back to experiments in the 1990s in rats [53, 54]. High-resolution images of cerebral blood flow in mice were demonstrated much later with a multi-pinhole system in 2009 [55].

These experiments were done to demonstrate the spatial resolution of imaging systems using pinhole collimators. ^{99m}Tc-HMPAO was intravenously injected via the tail vein—the common approach of i.v. injections in rodents. The highly lipophilic compound is rapidly cleared from the plasma. Andersen et al. [56] found a high first-pass extraction of about 80% in rats. The images obtained after a tail vein bolus injection thus mostly represent the mean CBF during the short time span during and shortly after tail vein injection.

In order to make use of the approach for mapping stimulus-dependent changes in blood flow, the tracer has to be injected during the stimulation period. To the best of our knowledge, the first study using a dedicated small-animal SPECT scanner for imaging brain activation patterns was performed by Wyckhuys et al. [57] in restrained rats.

For the method to be used for repeated imaging of unrestrained behaving animals, we developed an approach for continuously injecting the tracer during ongoing behavior via catheters in the right external jugular vein. External jugular vein catheterization is a well-established approach for chronic intravenous injections or blood sampling in rodents (for instance [58–67]). From our experience, the complexity of the approach is frequently overestimated. In experienced hands, the surgery takes about 30 min. The catheters are subcutaneously tunneled and exit shortly behind the scapulae (**Figure 4**). For i.v. injections, the catheters are connected to perfusion pumps via polyethylene tubes with little interference with ongoing behavior. We used

this approach in a number of studies including different learning paradigms [68, 69].

We have developed a protocol for simple, inexpensive onsite synthesis of ^{99m}Tc-HMPAO close to the behavioral setup [44]. ^{99m}Tc is a so-called generator radionuclide [33]. It is a decay product of ⁹⁹Mo-molybdenum, a radionuclide with a half-life of 66 hours. ⁹⁹Mo can conveniently be transported over long distances to hospitals for on-site delivery of ^{99m}Tc. ^{99m}Tc generators contain the divalent molybdate anion ⁹⁹MoO4²⁻, from which the monovalent pertechnetate anion ^{99m}TcO4⁻ forms when ⁹⁹Mo decays. The change in valency facilitates separating ^{99m}TcO4⁻ from ⁹⁹MoO4²⁻ by elution with NaCl solutions. ^{99m}Tc generators are present in practically every department of nuclear medicine. The logistics of supplying a small-animal SPECT lab with ^{99m}Tc are very simple.

For synthesis of ^{99m}Tc-HMPAO, the solution of ^{99m}TcO4⁻ in saline is added to the organic compound exametazime (HMPAO) in the presence of the reducing agent Sn(II)Cl₂. HMPAO and Sn(II)Cl₂ are commercially available as kit preparations delivered as a lyophilized mixture under nitrogen in amounts for use in humans. For use in rodents, we store aliquots of such a kit preparation frozen in saline solutions. Upon use, we add freshly prepared Sn(II)Cl₂ solution in order to compensate for potential losses due to oxidation during storage [44]. ^{99m}Tc-HMPAO synthesis from kits or stored aliquots takes a few minutes.

We inject the tracer during ongoing behavior over a period, in most experiments, of about five to 10 min. After injection, animals are anesthetized and scanned (for a scheme of the workflow, see **Figure 5**). We use co-registered CT scans as anatomical references. In most studies, we repeatedly image the same animals under different behavioral conditions. We use intervals between the measurements of 2 days. For data analysis, we align the SPECT/CTs to reference MRs and calculate parametric voxel-wise statistical maps from global mean normalized data of brain ^{99m}Tc content.

In humans, arterial input functions can be determined and cerebral blood flow or glucose metabolism can be fully quantified

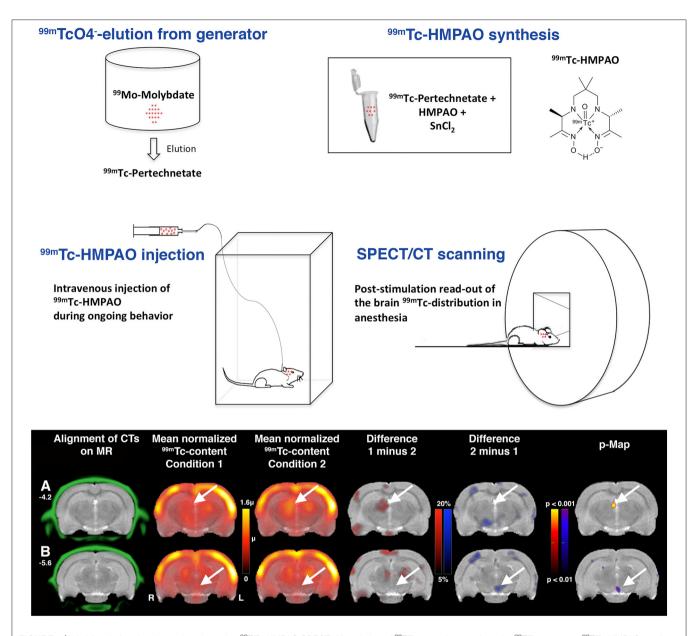


FIGURE 5 | Workflow in functional neuroimaging using ^{99m}Tc-HMPAO SPECT. After elution of ^{99m}Tc-pertechnetate from the ^{99m}Tc generator, ^{99m}Tc-HMPAO can be synthesized on-site in the small-animal SPECT lab. Rodents are intravenously injected with the tracer during ongoing behavior. For SPECT scanning of the distribution of the trapped tracer, the animals are anesthetized. Data analysis starts with aligning of the SPECT data sets to reference MRs or atlases by using the landmarks of the co-registered CT. Here, previously unpublished images from data of a subgroup of rats from the study of innate fear behavior in Vincenz et al. [70] are shown to illustrate the data analysis. Sections at two different Bregma levels are shown (A Bregma –4.2; B Bregma –5.6). The color scale on the left is in units of the global mean intensity. Arrows point to the habenula and interpeduncular nucleus where significant increases or decreases, resp., in flow were found.

with PET imaging. In rodents, and in particular in mice, arterial blood sampling is difficult and impractical in behaving animals. Therefore, intensity normalization is the standard approach to comparing individual and group data in functional small-animal radionuclide imaging [71, 72]. Especially when used for imaging normal behaving animals, where global metabolic rates and blood flow can be assumed to vary only within narrow limits, the effects of the normalization can be expected to be minor.

CBF SPECT IN THE CONTEXT OF TECHNIQUES FOR IMAGING BRAIN-WIDE ACTIVATION PATTERNS IN AWAKE BEHAVING RODENTS

We have reviewed above the rationales underlying functional neuroimaging using CBF SPECT in rodents and outlined the experimental procedure that we developed in our lab. We have used this approach in a number of different studies including artificial stimulations—electrical as well as optogenetic [44, 73, 74]—pharmacological manipulations [75], studies of baseline metabolism under physiological or pathological conditions [76], or changes in activation patterns due to sensory stimuli in conjunction with [68] or without [70, 77] learning paradigms. Our findings matched well with data from other groups using other methods as far as such data were available. The involvement of the habenulo-interpeduncular system in innate fear behavior [70], for instance, or of the supramammillary nucleus in food reward [75] as described in our SPECT studies has also been found with optogenetic or electrophysiological methods, resp. [78–80].

The scope of most of our studies was on screening for brainwide activation patterns in behaving rodents. Many of these studies would have been very difficult or impossible to perform with BOLD fMRI, especially those that require active locomotor behaviors as the intracranial self-stimulation studies or studies with complex learning paradigms [68].

Some of the studies might have been performed with ¹⁸F-FDG PET. In fact, the scopes of applications of ¹⁸F-FDG PET (see, for instance, [71, 72, 81–83]) and ^{99m}Tc-HMPAO SPECT are very similar. As mentioned above, both methods provide static images of spatial patterns of neural activity averaged or integrated resp. over certain periods of time. However, due to differences in tracer kinetics, the integration times differ considerably between the two methods.

As studied in detail by Sokoloff et al. when they introduced the autoradiographic technique for mapping cerebral glucose metabolism using 2-deoxyglucose (2-DG) labeled with 14C, it takes about 30-45 min until, after a single bolus injection, sufficient amounts of the tracer are trapped in the brain [84]. 2-DG can enter and leave the brain via facilitated diffusion through glucose transporters in the BBB. The brain regional 2-DG distribution shortly after injection reflects spatial patterns of 2-DG influx in relation to blood flow. In a relatively slow process, 2-DG is phosphorylated to 2-DG-6-phosphate, which is trapped intracellularly and does not redistribute. Images taken earlier than about 30 min reflect to varying degrees the influx, efflux, and phosphorylation of 2-DG. In order to image with ¹⁸F-FDG PET a tracer distribution that solely or at least largely reflects tracer uptake and phosphorylation in the unrestrained awake state outside the scanner and that remains stable during subsequent image acquisition under anesthesia inside the scanner, animals cannot be imaged much earlier than about 30 min after ¹⁸F-FDG injection.

On the other hand, the long uptake and phosphorylation times of ¹⁸F-FDG make it possible to inject a single tracer dose i.v. or i.p. before the behavioral experiment starts. Repeated imaging of the same individual over long time periods such as weeks or months is easier with ¹⁸F-FDG because there is no need for implanting intravenous catheters.

In contrast to ¹⁸F-FDG, ^{99m}Tc-HMPAO is rapidly cleared from the plasma and rapidly trapped in the brain. We mentioned above the high first-pass extraction of about 80% [56]. In humans, count rates in the brain reach maximum values 30–40 s after injection, then decrease slightly to 91% and remain constant

2 min after injection [85]. The 40-s period until the net uptake of ^{99m}Tc-HMPAO ceases can be seen as the maximum temporal resolution that might theoretically be achieved when using CBF SPECT for assessing the spatial patterns of neural activity in unrestrained animals outside scanner environments, the limiting factor in practice being the volume load if the dose necessary for imaging at high resolution and high signal-to-noise ratio should be injected in one single bolus. In our routine protocols, we use time spans of several minutes over which ^{99m}Tc-HMPAO is injected. The time spans might be adjusted to the behavioral paradigms under study.

Among the different tracer techniques for *in vivo* imaging of brain-wide activation patterns in rodents, the highest spatial resolution can be achieved with MEMRI [86], but without opening the BBB, manganese reaches detectable levels only slowly. The long stimulation times on the order of several hours limit the scope of applications.

The static images that are usually acquired with all of these tracer techniques provide insight into temporal dynamics only insofar as the temporal dynamics might affect the average spatial patterns of network activities. In theory, nuclear imaging techniques are well-suited for imaging temporal dynamics. Motion-correction algorithms have been used to obtain images of awake behaving animals inside scanners [87-89], and miniaturized, wearable PET scanners for brain imaging in behaving rats have been developed [90]. The methods can be of high value for imaging tracers that are not trapped and the distribution of which might change under anesthesia as compared with that in the awake state, e.g., neurotransmitter receptor ligands. Imaging at both high spatial resolutions and short acquisition times in the range of seconds or lower would require high sensitivities and/or high radionuclide doses and might be challenging. It remains to be seen whether approaches for 4D functional neuroimaging in awake behaving rodents, based on imaging, e.g., CBF, CBV, or displacement of receptor ligands, might emerge from nuclear imaging techniques and what spatial and temporal resolutions these could provide.

Four-dimensional whole-brain imaging of spatiotemporal patterns of neural activity in behaving rodents is possible with ultrasound imaging of changes in CBV [91]. As a major drawback compared to fMRI, PET, and SPECT, animals have to undergo skull surgery in order to enable ultrasound imaging. Measurements have been performed through the thinned skull in rats [92], ultrasound-clear skull prostheses [93], or large cranial windows in head-fixed mice [94]. In the latter study [94], high spatial resolutions of about $100\,\mu\mathrm{m}$ in-plane and $300\,\mu\mathrm{m}$ off-plane have been obtained, but relatively long imaging times were used ranging from 14 min to several hours.

In the context of the array of *in vivo* whole-brain functional neuroimaging techniques, we see the attractiveness of functional CBF SPECT imaging in the combination of minimal invasiveness with relatively high spatial resolution and simple logistics.

The temporal resolution might be improved with stimulustriggered short bolus injections of ^{99m}Tc-HMPAO, but it certainly cannot compete with that of BOLD fMRI. When effects of anesthesia or restraints can be tolerated or expected to be minor, BOLD fMRI is certainly the method of choice. From the underlying physics, the spatial resolution of 99m Tc-HMPAO SPECT could be further increased, the limiting factor in practice being the limited sensitivity that, to our experience, can make imaging well-beyond the range of about $500\,\mu m$ difficult for routine use, as it requires injections of large doses or volumes resp. and/or long scan times. It remains to be seen whether technical improvements could increase the sensitivity in small-animal SPECT imaging.

Despite the variety of new methods for in vivo imaging of neural activity, there are still only three approaches to noninvasively—in particular without the need for head surgery obtain images of brain-wide patterns of neural activity in awake unrestrained rodents, ¹⁸F-FDG PET, MEMRI, and ^{99m}Tc-HMPAO SPECT. Currently, the vast majority of studies aiming at elucidating brain-wide patterns of neural activity in rodents are done by post-mortem readout of the patterns of immediate early genes (IEGs) expressed in an activity-dependent manner in vivo [95]. IEG expression patterns can be mapped with cellular resolution, but data acquisition and analysis are time consuming. Similar to tracer techniques, IEG mapping studies provide little information on temporal dynamics on timescales of neuronal signal-processing rates, but the decades of its use demonstrate at the same time the value of this spatial information for elucidating network activation patterns.

Within this array of methods for imaging brain-wide spatial patterns of neural activity in unrestrained rodents, ^{99m}Tc-HMPAO SPECT is, in our opinion, a highly attractive technique. When aiming at regional spatial resolutions, it

provides 3D data sets of functional brain activations at substantially higher throughput than IEG-mapping approaches, and stimulation times in the minute range make the method less sensitive to the effects of behavioral habituation than ¹⁸F-FDG PET and MEMRI.

ETHICS STATEMENT

All experiments were conducted according to the guidelines of the European Community (Directive 2010/63/EU) and approved by a local ethics committee of the Federal state of Saxony-Anhalt.

AUTHOR CONTRIBUTIONS

JG and AO conceived the review and wrote the manuscript.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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