

Tissue-resident immune cells in tumor immunity and immunotherapy

Edited by

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Tissue-resident immune cells in tumor immunity and immunotherapy

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Editorial: Tissue-resident immune cells in tumor immunity and immunotherapy

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KEYWORDS

tissue-resident immune cell, macrophage, natural killer cells, dendritic cells, tertiary lymphoid structures, tumor immunity

Editorial on the Research Topic

[Tissue-resident immune cells in tumor immunity and immunotherapy](#)

Tumor microenvironment (TME) is a complex ecosystem and consists of tumor cells, multiple stromal cells and diverse immune cells (Wu et al., 2021a). From the perspective of immune cells, recent clinical practice reveals that immunotherapies have become remarkable breakthroughs in cancer treatment strategy. Clinical immunotherapies are composed of oncolytic virus, enhanced co-stimulators, vaccines, inhibitory immune checkpoint inhibitors (ICIs) and adoptive cell therapies. As a representative of ICIs, PD1/PD-L1 blockades have been approved for clinical appliance. However, they fail to generate durable responses in most patients. Our understanding of intrinsically and extrinsically immunosuppressive mechanisms for the resistance of ICIs has markedly increased (Wu et al., 2021b). Therefore, the development of strategies to reverse immunosuppressive microenvironment and surmount resistance to immunotherapy have become momentous. Tissue-resident immune cells (TRICs) are immune cells existing in non-immune organs like skin, liver, lung and gastrointestinal tract. They mainly include innate lymphoid cells, macrophages, resident memory T cells, natural killer cells, natural killer T cells, non-classical T cells, and memory B cells (Liu et al.). TRICs are deemed as a bridge that connects innate immunity to adaptive immunity. They enable to remodel the TME and can modulate tumor progression (Liu Z. et al., 2022). However, the potential mechanisms underlying TRICs to host anti-tumor immune response remain unknown. In the present Research Topic, a total of nine articles including two original articles and seven reviews are published to discuss the development, distribution, functionality and therapeutic potential of TRICs in neoplastic disease (Figure 1).

In response to foreign threats or original ontogenesis, these TRICs are capable to resident and adapt to life within diverse tissues. These site-specific immune cell compositions reflect their distinct localization within tissue niches, wherein they form an integral part of the immune sensing network, monitor for local perturbations in

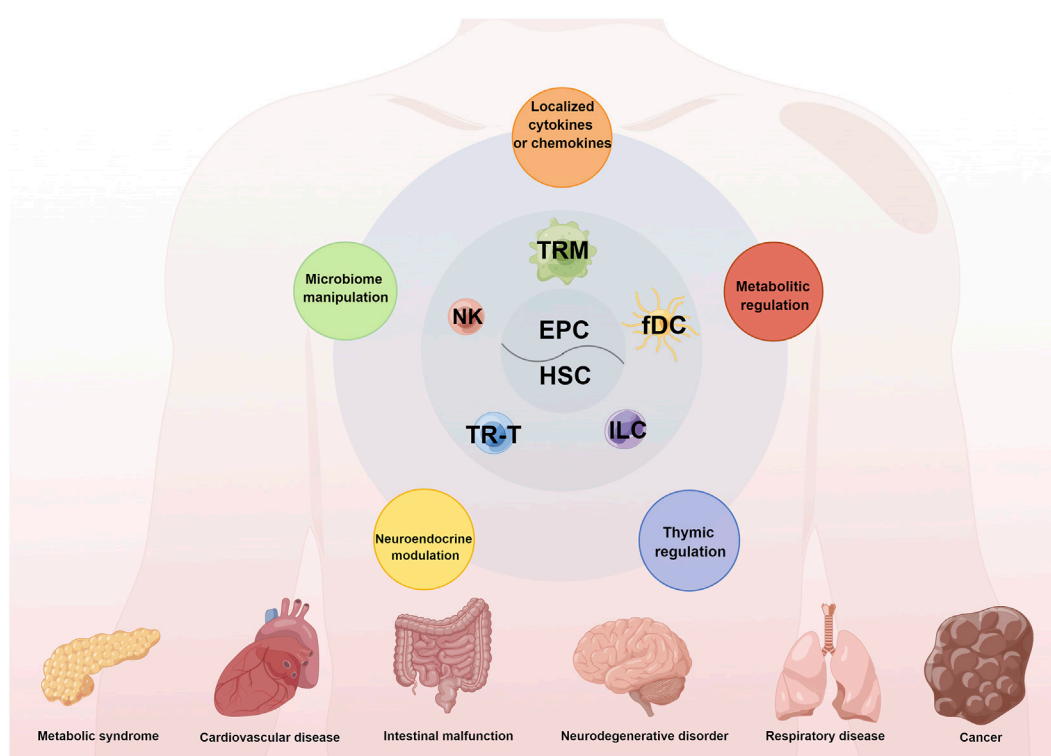


FIGURE 1

The origins, compositions, and functions of TRICs in human diseases. Tissue-resident immune cells (TRICs) mainly originate from embryonic progenitor cells (HSC) or adult haematopoietic stem cell (HSC). And TRICs mainly consist of diverse tissue-resident macrophages (TRM), NK cell, tissue-resident T (TR-T) lymphocytes, innate lymphoid cells (ILC) and follicular dendritic cells (fDC). TRICs have a vital effect on various human diseases like metabolic syndrome, cardiovascular disease and cancer through the integrated mechanisms including metabolic regulation, thymic regulation, neuroendocrine modulation, microbiome manipulation and secretion of cytokines and chemokines.

homeostasis throughout the body and provide defense against malignancies. For example, [Liu et al.](#) characterize the neuroendocrine modulation in tissue-specific immune cells, including regulations through autonomic nervous system, sensory nerves and various neuroendocrine factors. Hence, the involvement of neuroendocrine-tissue specific immunity axis in tumor biology requires to be further explored in the future and may represent a potential target for the immunotherapy of tumors.

Given the tissue-specific structure and location of TRICs, tertiary lymphoid structures (TLS) represent one of the most studied examples of TRIC aggregates. TLS are deemed as organized ectopic lymphoid organs developing in non-lymphoid tissues during chronic inflammation and cancer in response to persistent antigen stimulation ([Sautès-Fridman et al., 2016](#)). In [Rossi et al.](#), several aspects of tumor-associated TLS are described including their composition, the promoting or inhibitory mechanisms of TLS development, and their prognostic value. High level of heterogeneity has been described in TLS cellular composition, which includes innate and adaptive immune cells such as macrophages, dendritic cells, mast cells, and T and B lymphocytes which are recruited and activated by the inflammatory milieu. Upon

prolonged inflammatory stimuli including cancer, TLS can present lymphoid aggregates resembling B cell follicles with germinal centers and T cell areas supported by fibroblastic reticular cells, follicular dendritic cells and high endothelial venules ([Siliņa et al., 2018](#)). TLS are the sites where continuous tumor-antigens exposures activate local and systemic T and B cell responses, which control tumor growth, as reported for different tumor types ([Dieu-Nosjean et al., 2016](#)). A crucial role is played by the non-hematopoietic stromal component, which include fibroblasts, vascular/lymphatic endothelial cells, and epithelial cells, both in maintaining the architecture of TLS and in shaping the local cross-talk with immune cells by the production of proinflammatory cytokines and chemokines, that drive the recruitment of myeloid and lymphoid cells. Among the myeloid compartment, dendritic cells, as antigen presenting cells, are considered sufficient to TLS induction and maintenance, and are associated with better prognosis in cancer ([Sautès-Fridman et al., 2019](#)). Also, macrophages and neutrophils are present on TLS, but their role need to be better elucidated. Finally, the detrimental role of Tregs in TLS is described, with the mechanisms underlying their recruitment and expansion, and the suppressive role of follicular T regs, which are considered potential

immunotherapeutic targets for improving the efficacy of ICI therapy. Furthermore, the immunosuppressive landscape induced by Treg was carefully analyzed by [Riaz et al.](#) in non-alcoholic fatty liver disease (NAFLD)-associated hepatocellular carcinoma.

Functionally, TRICs can play a dual role since, in the remodeling of the TME, they can foster or suppress tumor response ([Liu Z. et al., 2022](#)). For example, the macrophages locating in peritoneum shape a high-energy and chronic inflammatory microenvironment that favors tumor metastasis. Likewise, the peritoneal resident macrophages impair the anti-tumor response of effector T cells and compromise therapeutic efficacy of ICIs ([Xia et al.](#)). Similarly, intestinal macrophages contribute to the regeneration of intestinal epithelial cells and the immune homeostasis in intestinal mucosa. These macrophages are capable to polarize into diverse phenotype in response to the endogenous and environmental cues. [Ma et al.](#) decipher the origin and mechanisms of maintenance of intestinal macrophages. They also describe the interplays between intestinal macrophages and internal and external stimuli, and highlight the role of intestinal macrophages in the inflammatory bowel disease occurrence and development. In addition, the review by [Busà et al.](#) analyze the contribution of innate immune cells, including NK cells, dendritic cells, macrophages, myeloid-derived suppressor cells (MDSCs), and innate lymphoid cells (ILCs), in the modulation of the tumor microenvironment and in shaping the adaptive tumor response.

Immunotherapy has allowed the field of oncology to turn a critical corner. And TRICs maybe major candidates for therapeutic manipulation. As a novel immunometabolic checkpoint, adenosine interacts with its receptors named A1, A2A, A2B, and A3 to promote cancer cell proliferation, neoangiogenesis, immunoescape and metastasis. In TME, adenosine mainly derives from the degradation of ATP, ADP, UTP, and NAD through several ectonucleotidases like CD38, CD39, and CD73. Adenosine not only enable to limit the inflammatory reaction, but also suppress anti-tumor immunosurveillance. Hence, nano-drugs targeting CD39 or CD73 deserve detailed study to increase anti-cancer immune responses ([Ferrari et al.](#)). Moreover, [Yu et al.](#) generate some novel chimeric antigen receptor (CAR) T cells *via* the construction of tumor-specific cell surface antigen on CAR-T cells. For instance, they create the CAR-T cells overexpressing glucose-regulated protein 78 (GRP78)

on cell surface (csGRP78). These engineered CAR-T cells high-efficiently eliminate tumor cells and prolong survival *in vitro* and *in vivo*. In addition, [Zhao et al.](#) demonstrate that the use of human or humanized antibody fragments for CAR construction can reduce the immunogenicity of the CAR and improve the therapeutic efficacy. However, these approaches need further clinical investigation. Therefore, developing the therapeutic strategies based on TRICs in the progressive disease is urgently required.

Collectively, this Research Topic describes the origins and biology of TRICs and the function of TRICs in tumorigenesis and malignant progression. It also confirms the importance of TRICs in cancer prevention or treatment and uncovers some unexplored knowledges in the field. In the future, the ontogeny of TRICs especially the key regulators involved in the process should be elaborated. The development of specific druggable targets of TRICs should be further explored and applied in a “personalized medicine” perspective.

Author contributions

ADP and QW contributed to the writing of Editorial.

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Humanized CD30-Targeted Chimeric Antigen Receptor T Cells Exhibit Potent Preclinical Activity Against Hodgkin's Lymphoma Cells

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CD30-directed chimeric antigen receptors (CARs) with single chain antibody fragment (scFv)-binding domains from murine HRS3 show strong cytotoxicity to Hodgkin's Lymphoma cells and have been used in clinical trials. However, murine scFv in CAR might induce specific rejective immune responses in patients, which compromises the therapeutic effects. The use of human or humanized antibody fragments for CAR construction, rather than those derived from mouse antibodies, can reduce the immunogenicity of the CAR. Importantly, this strategy might simultaneously decrease the risk of cytokine-mediated toxicities and improve CAR T cell persistence. Murine HRS3 antibody has been successfully humanized by grafting the complementarity-determining regions (CDRs) from the mouse antibody framework onto human immunoglobulin consensus sequences, followed by an *in vitro* evolutionary strategy to select functional Fab fragments with the same affinity as murine sources. In this study, humanized scFvs were utilized to construct a CD30-directed CAR (hHRS3-CAR), and its effectiveness was compared with that of HRS3-CAR. The hHRS3-CAR-T cells specifically kill CD30-positive tumor cell lines *in vitro* and eliminate lymphoma xenografts in immunodeficient mice with comparable efficiency to HRS3-CAR. The hHRS3-CAR-T could be used in clinical trials based on the previously reported advantages of humanized CARs, such as the reduction of immune rejection and better persistence of cells.

Keywords: chimeric antigen receptor, CD30, humanized HRS3 antibody, single-chain variable fragment, Hodgkin's Lymphoma, central memory phenotype

HIGHLIGHTS

- hHRS3-CAR-T cells were highly efficacious against CD30-positive tumor cells similar to HRS3-CAR-T cells
- hHRS3-CAR-T cells show higher central memory phenotype compared to HRS3-CAR-T cells

Abbreviations: AFM13, HRS3-based bispecific antibody; ALCL, anaplastic large cell lymphoma; CARs, chimeric antigen receptors; CAR-T, chimeric antigen receptor T-cells; CD19, cluster of differentiation 19; hHRS3-CAR, humanized HRS3 scFv-based CAR; CFSE, carboxyfluorescein succinimidyl ester; HL, Hodgkin's lymphoma; HRS3, murine anti-CD30 monoclonal antibody; HRS3-CAR, murine HRS3 scFv-based CAR; PI, Propidium iodide; scFv, single chain antibody fragments; Tem, central memory cells; Tem, effector memory cells; TNFRSF8, tumor necrosis factor receptor superfamily member 8.

- The CD30-directed CAR-T based on humanized HRS3 scFv might decrease immunogenicity and benefit the clinical therapy

INTRODUCTION

Chimeric antigen receptors (CARs) are artificial proteins whose basic structure is composed of an antigen recognition ectodomain and activation endodomain linked by a spacer and transmembrane domain (Eshhar et al., 1993; Sadelain et al., 2013; Boyiadzis et al., 2016). These are engineered receptors used to specifically direct patient T cells to target tumor cells (Wang et al., 2019). Adoptive cell therapy with the cluster of differentiation 19 (CD19)-directed chimeric antigen receptor T-cells (CAR-T) has induced durable clinical efficacy and has been approved for clinical first-line treatment, which provides a rationale for the development of other CARs (Kochenderfer et al., 2012; Boyiadzis et al., 2016; Turtle et al., 2016b).

Tumor necrosis factor receptor superfamily member 8 (TNFRSF8) is a 120-kDa type I transmembrane glycoprotein, more commonly referred to as CD30 (van der Weyden et al., 2017). In the normal physiological state, cell surface expression of CD30 is limited to activated T, B, and natural killer lymphocytes (Wasik et al., 2013). However, it is also strongly expressed in malignant hematopoietic cells, including Hodgkin's lymphoma (HL), anaplastic large cell lymphoma (ALCL), primary cutaneous ALCL, lymphomatoid papulosis, and certain cases of transformed mycosis fungoides (Schirrmann et al., 2014; van der Weyden et al., 2017). Thus, it was regarded as an ideal therapeutic target and a wide range of agents were developed for CD30-positive malignancies (Schwartz et al., 1989; Younes et al., 2012). Brentuximab vedotin, a CD30 antibody-drug conjugates, has achieved remarkable results against HL and ALCL (Pro et al., 2012; Younes et al., 2012). Recently, it was shown that anti-CD30 CAR-T cells can induce partial or complete remission in HL and ALCL (Wang et al., 2017; Ramos et al., 2020).

Although CD30 remains an excellent target for CAR-T therapy of HL, various obstacles should be overcome to clinically improve their efficacy, such as the persistence of CAR-T cells, trafficking to tumors, and increased tumor cytotoxicity (Ramos et al., 2017; Hong et al., 2018; Grover and Savoldo, 2019; Hombach et al., 2019). The murine anti-CD30 monoclonal antibody (HRS3), and HRS3-based bispecific antibody (AFM13) and recombinant fusion protein combined with cytokines, and CAR-T have been developed and applied to the specific immunotherapy of Hodgkin's lymphoma, including CAR-T therapy (Hombach et al., 1993; Renner et al., 2000; Jahn et al., 2012; Grover and Savoldo, 2019). Currently, most single chain antibody fragments (scFvs) are murine-derived, which, owing to immunogenicity, may weaken the efficacy of the treatment (Zou et al., 2018). One strategy to reduce the immunogenicity of CAR-T cells is to humanize scFv. Humanized CAR-T cells have also received attention because they are less antigenic and have a long survival time *in vivo* (Turtle et al., 2016a; Sommermeyer et al., 2017; Rafiq et al., 2020). Starting from the previously characterized cognate HRS3 mouse

monoclonal antibody, the bacterially produced functional Fab fragment was humanized by grafting the CDRs from the mouse antibody framework onto human immunoglobulin consensus sequences, followed by an *in vitro* evolutionary strategy to select functional Fab fragments with the same affinity as murine sources (Schlampsch et al., 2004). The humanized HRS3 antibody is fully functional in recognizing its native receptor antigen. CAR-T based on humanized HRS3-scFv has not been reported.

In this study, murine and humanized HRS3 scFv-based CARs (HRS3-CAR and hHRS3-CAR, respectively) were constructed. We used humanized scFvs to construct hHRS3-CARs, and its effectiveness was compared with that of HRS3-CAR.

MATERIALS AND METHODS

Cell Culture

L428 and L540 Hodgkin's lymphoma-derived cell lines were purchased from Shanghai Fudan-Zhangjiang Bio-Pharmaceutical Co., Ltd. (Shanghai, China). Cells were cultured in RPMI-1640 (Hyclone, United States) supplemented with 20% fetal bovine serum (FBS; Gibco). Raji cells were purchased from ATCC and cultured in RPMI-1640 medium containing 10% FBS. HEK293T cells were cultured in Dulbecco's modified Eagle's medium (Millipore, United States) supplemented with 10% FBS at 37°C and 5% CO₂. The cells were authenticated by via Short Tandem Repeat (STR) profiling and tested negative for *mycoplasma* contamination.

Construction of Plasmids Encoding anti-CD30 CARs

The CD19-specific single-chain antibody CD19-scFv was derived from anti-CD19 mAb as previously described (Yang et al., 2017). The VL and VH regions of murine and humanized HRS3 and HRS3 antibodies were obtained from the published article (Schlampsch et al., 2004). The extracellular domains containing VL and VH regions were synthesized and cloned into a lentiviral backbone containing other parts of CAR: a CD8 hinge spacer and transmembrane region, 4-1BB, and CD3ζ endo-domains under the control of the CMV promoter. The resulting plasmids were named HRS3-CAR and hHRS3-CAR, respectively.

Lentiviral Preparation and Transduction of T-Cells

Lentiviral DNA vectors were transfected with Lipo6000™ Transfection Reagent (Beyotime, China) according to the manufacturer's protocol. For lentivirus production, 20 µg of core plasmid together with helper plasmids (10 µg pCMVΔ8.9 and 4 µg pMD2. G) were transfected into 293T cells as described previously (Yang et al., 2018). Viral supernatants were collected 48 and 72 h after transfection and filtered through a 0.45 µm filter. After centrifugation at 25,000 rpm for 2.5 h at 4°C, the virus was suspended in 0.1% bovine serum

albumin (BSA) in PBS, dissolved overnight and stored in aliquots at 80°C.

Primary human T cells were isolated from healthy human blood, as previously described (Yang et al., 2019). T cells were cultured in advanced RPMI 1640 medium (Life Technologies, United States) containing 10% FBS (Life Technologies, United States) with 200 U/ml IL-2 (PeproTech, United States). T cells were activated by adding Dynabeads human T-activator CD3/CD28 kit (Life Technologies, United States) according to the manufacturer's instructions. After 48 h, at a 1:1 ratio, and on day 3, T cells were transduced with lentivirus (Multiplicity of infection, MOI = 20) in the presence of Lentibioost (Sirion Biotech), followed by a medium change after 24 h transfer to 24-well plates.

Cytotoxicity Assay

Cytotoxicity assays were conducted using a slightly modified version of a previously described assay, and cytokine concentrations were determined using enzyme-linked immunosorbent assay (ELISA) (Sun et al., 2019). For data analysis, target cells were labeled with carboxyfluorescein succinimidyl ester (CFSE) and dead target cells were identified as double-positive for CFSE and propidium iodide (PI) using a FACS Canto flow cytometer. For each sample, 10000 events of PI were collected. The percentage of specific target cell death was calculated as follows: $100 \times [\text{No. of CFSE and PI double-positive cells}] \div [(\text{No. for CFSE-positive cells}) + (\text{No. of CFSE and PI double-positive cells})]$.

Flow Cytometry

Flow cytometry was performed using the standard methods (Yang et al., 2019). The following antibodies were used: PE-anti-CD3 (Clone UCHT1, BD Biosciences or Biolegend, 981002), APC-anti-CD4 (BioLegend, 357408), FITC-anti-CD8 (BioLegend, 344704), PE-anti-CD45RO (Biolegend, 304206), APC-anti-CCR7 (BioLegend, 353214), and CD30 APC (Clone BerH8, BD Biosciences). Dead target cells were identified by double staining with CFSE and PI (BD Biosciences). All experiments were analyzed using FlowJo version 10 (Tree Star, Inc.).

Xenograft Mouse Model

The protocol was approved by the Ethics Committee of the West China Hospital of Sichuan University West China Hospital. Six-to eight-week-old female NOD-Prkdcem26ll2rgem26Nju (NCG) mice were purchased from GemPharmatech Co., Ltd (Jiangsu, China) and engrafted with 2×10^5 L428-EGFP-luci cells via tail vein injection. Five days later, CAR- or control T cells that had been expanded *in vitro* for 7 days were injected intravenously. The mice were serially imaged using 2D bioluminescence imaging as previously described to determine tumor progression (Guercio et al., 2021). All captured images were analyzed using Living Image software 4.1 (PerkinElmer, United States). The animals were examined every day for survival and sacrificed

when moribund for collection of tissue samples. At the end of the experiment (day 64), the remaining surviving mice were euthanized and animal samples were collected. Each experiment included 6 mice per group and was repeated twice (total $n = 12$ mice per group).

Cytokine Secretion Assays

Effector cells (2.5×10^5 NC, CD19-CAR, HRS3-CAR, or hHRS3-CAR-T cells) and target cells (5×10^4) were co-cultured in the absence of IL-2 at a ratio of 5:1 in 96-well plates for 24 h. Supernatants were collected and subjected to ELISA assay (BD Biosciences, United States) measurements according to the manufacturer's instructions.

Statistical Analysis

Graphs were plotted using the GraphPad Prism 8.0 statistical software. Data were analyzed using SPSS 22.0 software (IBM, United States). Statistical differences between two groups were analyzed using the unpaired Student's t-test with Welch correction. Unless otherwise stated, data are presented as mean \pm SD, and statistical significance was set at $p < 0.05$.

RESULTS

Humanized HRS3-CAR-T Cells Exert a Similar *In vitro* Anti-Lymphoma Activity Compared to HRS3-BBz T-Cells

We constructed hHRS3-CAR and HRS3-CAR for an initial validation of the humanized CAR, by cloning the scFvs of hHRS3 or HRS3, respectively, into the same CAR scaffold (Figure 1A) (Schlampsch et al., 2004). The CAR expressing anti-CD30(HRS3)-scFv was used as the positive control and that expressing anti-CD19-scFv was used as the negative control (CD19-CAR), as previously described (Sun et al., 2019). Comparing the amino acid sequences of VL and VH for HRS3-scFv and hHRS3-scFv, it was found that there were no significant changes in the amino acids in the VL; however, amino acid changes in the VH were apparent (Figure 1B).

To verify the function of hHRS3-CAR-T, we selected non-HL cells Raji and U937, and the HL cells L428 and L540. We evaluated CD30 protein expression using flow cytometry. CD30 was not detected in Raji or U937 cells, but was detected in the HL cell lines (Figure 2A, Supplementary Figure S1A). Next, we examined CAR expression and evaluated the ability of CAR-T cells to mediate the lysis of CD30⁺ HL cells (Figure 2B). CAR-T cells lysed CD30⁺ L428 and L540 cells (Figure 2C), but not Raji and U937 cells (Supplementary Figure S1B). We assessed the cytotoxicity of CD30-CAR T cells using 24-h cytotoxicity assays (Figure 2D). T cells expressing CD19-CAR served as negative controls. CAR-T cells specifically recognized and eliminated HL cells in an effector-to-target ratio-dependent manner (Figures 2E,F).

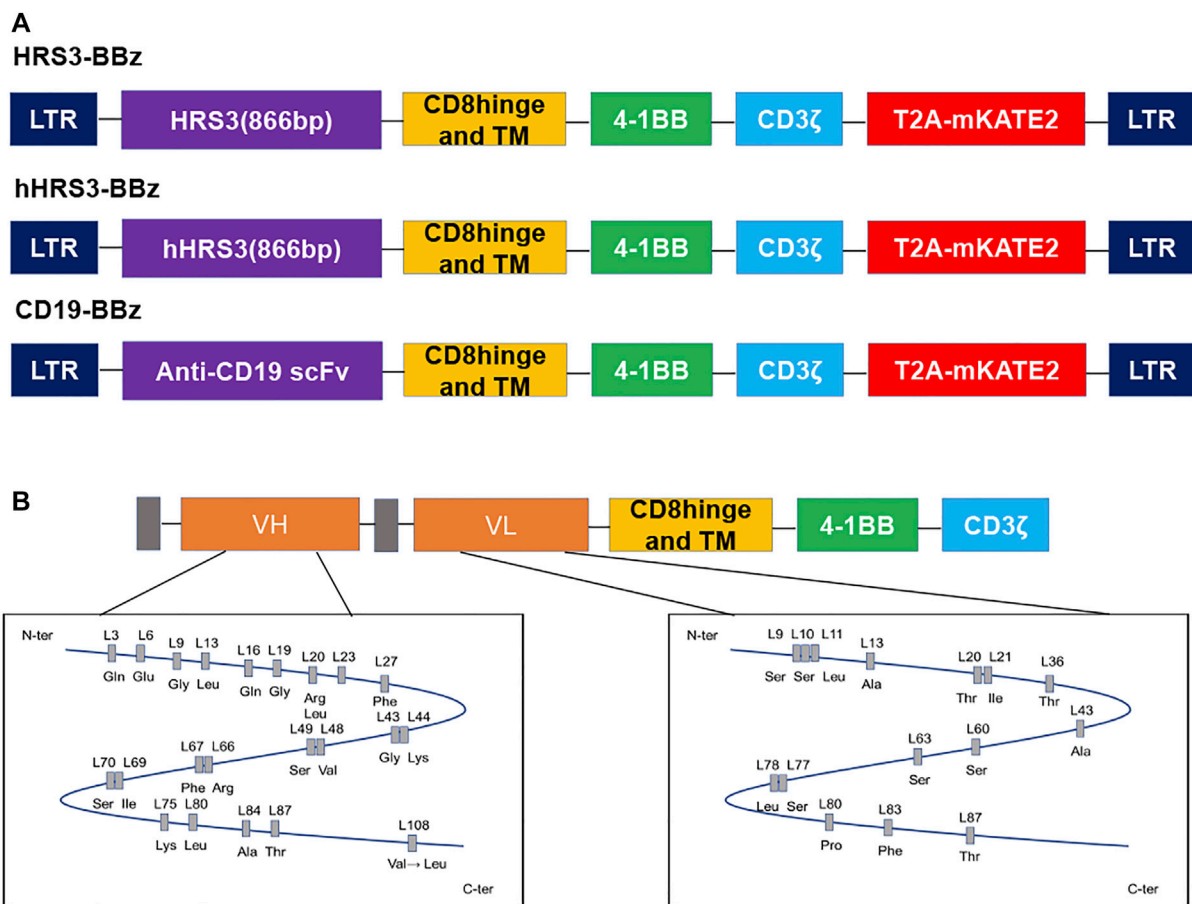


FIGURE 1 | Schematic diagram of the humanized HRS3-chimeric antigen receptor (CAR) construct and its differences from the murine receptor. **(A)** Schematic representation of CD19-CAR, HRS3-CAR, and hHRS3-CAR. All CARs had hinge, transmembrane, and CD8, and a CD3ζ T-cell activation domain. The mKATE2 is far-red fluorescent protein. In this study, the mKATE2 domain was used to trace the expression of CAR by fusing to the N-terminal of CAR via a self-cleaving T2A peptide. **(B)** Humanization of the HRS3 VL domain required 18 amino acid exchanges while retaining one amino acid from the murine framework sequence, whereas for the HRS3 VH domain, 27 amino acids were exchanged and four murine residues were retained (Schlapschky et al., 2004). The figure shows the schematic diagram of amino acids after mutation.

Humanized HRS3-CAR-T Specifically Kills CD30-Positive Cells Similar to HRS3-CAR-T

To test whether T cells expressing hHRS3-CAR were capable of specifically recognizing tumor lines expressing CD30, we co-cultured CAR-T cells with Raji cells expressing CD30 and those that did not (**Figure 2G**). CAR-T cells specifically lysed Raji-CD30 cells, but not Raji cells (**Figure 2H**). The amounts of secreted cytokines, IFN- γ and IL-2 (**Figure 2I**, **Supplementary Figure S2**), were measured. The hHRS3-CAR-T cells recognized all CD30⁺ tumor lines and secreted high levels of IFN- γ . Very low levels of IFN- γ were observed when hHRS3-CAR-T cells were co-cultured with Raji cells. In contrast, higher levels of IFN- γ were observed when CD19-CAR-T cells were co-cultured with Raji cells.

Expanded hHRS3-CAR-T Cells Express a Higher Central Memory Phenotype

To identify the effect of CAR expression on T cell phenotypes, markers of the T cell subsets were analyzed using FACS. The CD4 to CD8 ratio of CAR⁺ T cells was not significantly different between the HRS3-CAR-T and hHRS3-CAR-T cells (**Figures 3A,B**). Notably, participating effector memory (Tem) cells were significantly enriched in CD30-CAR-T cells 4 days after infection, whereas central memory (Tcm) cells were significantly enriched in CAR-T cells on the eighth day after infection (**Figures 3C,D**). The hHRS3-CAR-T cells maintained a higher proportion of CCR7⁺CD45RO⁺ Tcm cells, while HRS3-CAR-T cells had larger populations of CCR7⁻CD45RO⁺ Tem cells compared to their counterparts.

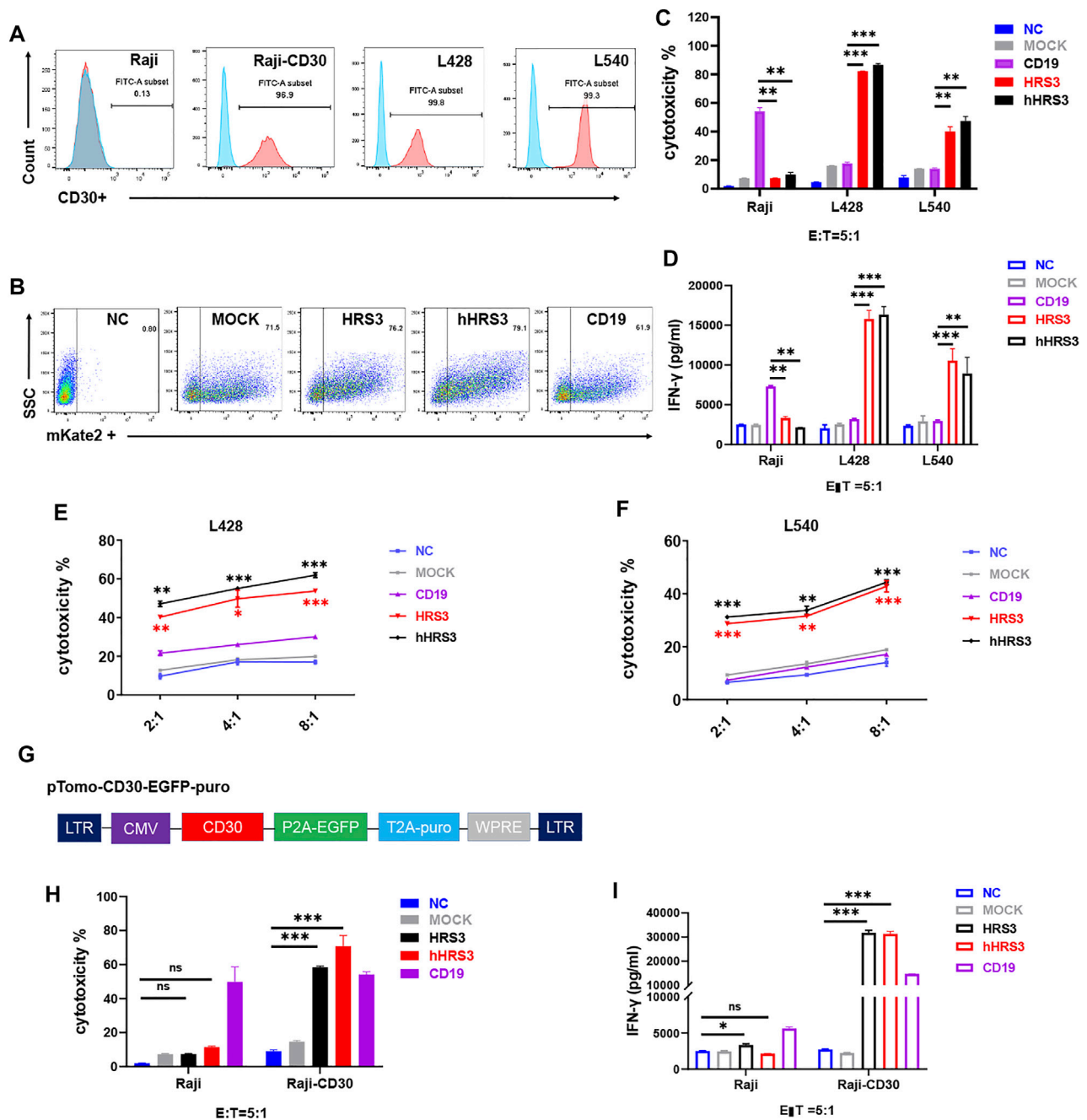
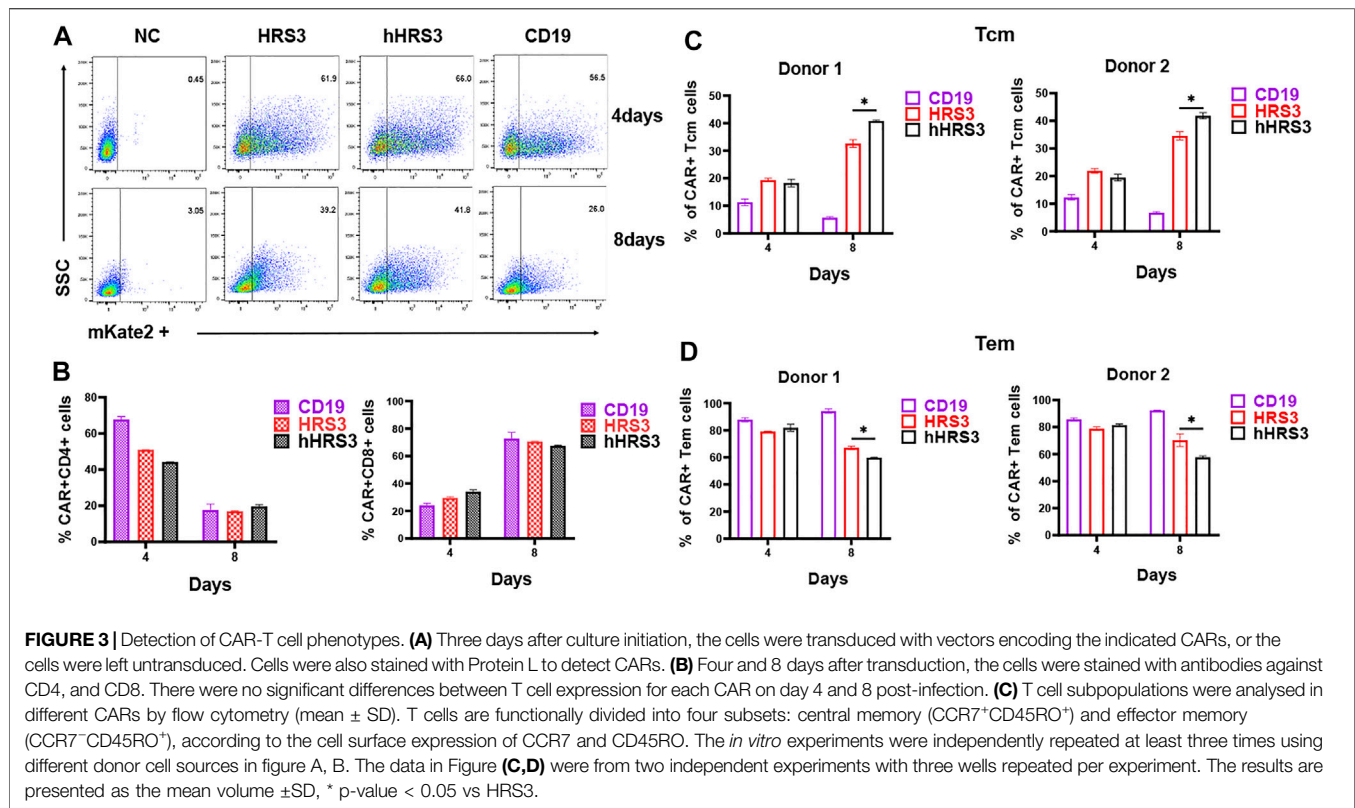


FIGURE 2 | CARs with humanized HRS3-specific scFv recognize CD30⁺ tumor cells. **(A)** B cell lymphoma and Hodgkin's lymphoma (HL) cell lines were stained with a monoclonal antibody specific for the CD30 antigen and analyzed using flow cytometry. CD30 expression was evident in a majority of the cell lines after staining with an anti-CD30 monoclonal antibody (Pink) when compared to staining with control antibody (Blue). Raji was used as negative control. **(B)** Flow-cytometry analyses in a representative donor showing CAR expression. **(C)** T cells expressing hHRS3-CAR and HRS3-CAR exhibited cytotoxicity against the non-HL and HL cell lines in a 24-h assay. Graphs show mean \pm SEM of duplicate wells. One of two representative experiments with different donor cells and similar results is shown. **(D)** IFN- γ concentrations in the supernatants of CD30-CAR-T-cells after stimulation with Raji, L428, and L540 cells for 24 h, analyzed by ELISA. **(E,F)** *In vitro* cytotoxic assay to evaluate cytolytic activity of NC T cells (Blue line), CD19-CAR-T cells (Purple line), HRS3-CAR-T cells (Red line) and hHRS3-CAR-T cells (Black line) on CD30⁺ lymphoma cell lines, namely L428 and L540 cells. The results are presented as the mean volume \pm SD, * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001 vs CD19 (CD19 as negative control). **(G)** Diagram of the full-length overexpressing human CD30 vector. **(H,I)** Detection of Raji and Raji-CD30 cell killing and cytokines (CD19 as positive control). "NC" represents uninfected T cells (negative control). "MOCK" indicates the transgenic plant that contained only the vector construct (negative control). The data were derived from different donor cells and the *in vitro* experiments were repeated independently at least three times. The results are presented as the mean volume \pm SD, * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001 vs NC.



Antitumor Responses by Humanized HRS3 Chimeric Antigen Receptor T Cells *in vivo*

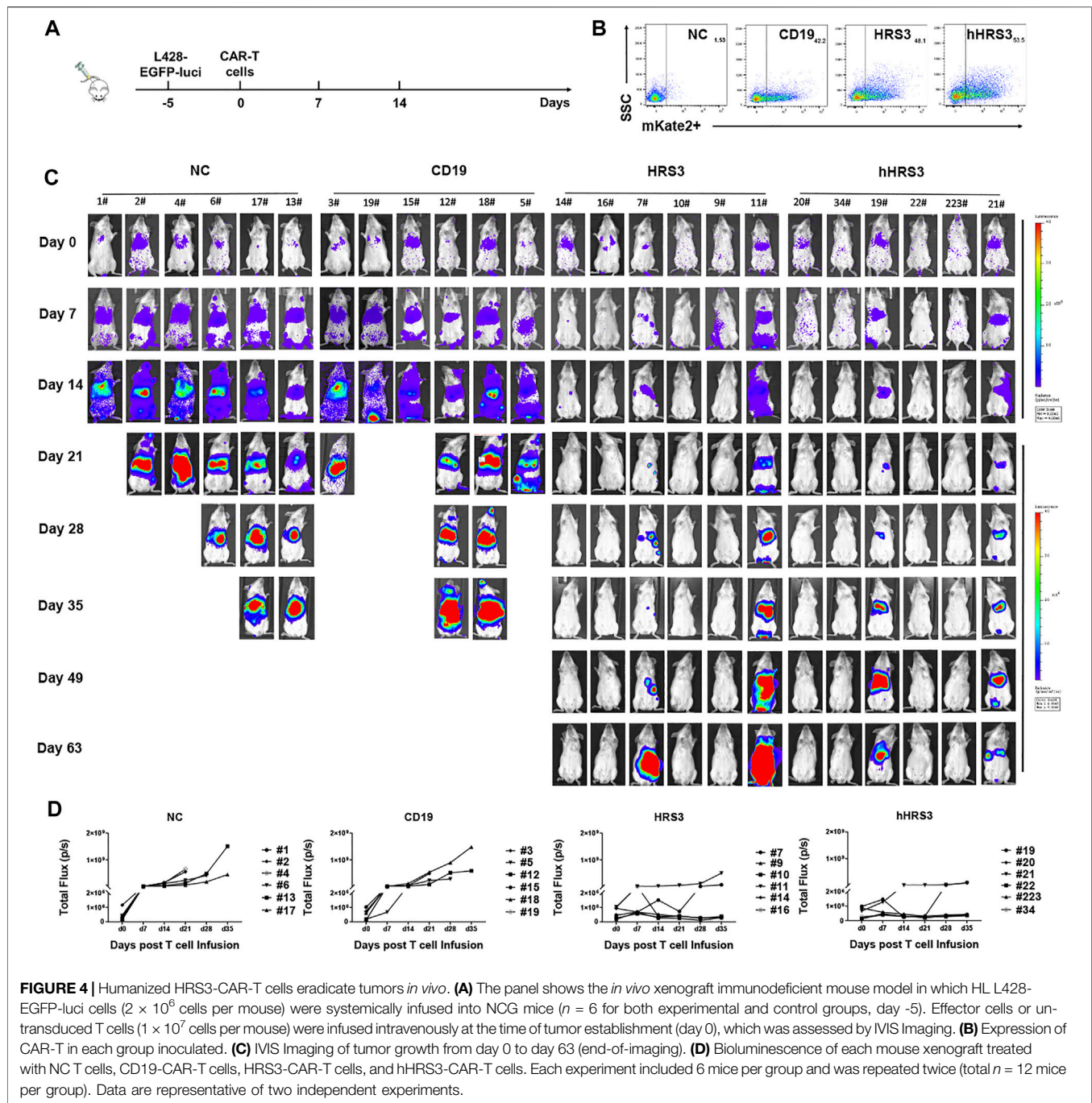
To evaluate the anti-tumor activity of hHRS3-CAR-T and HRS3-CAR-T cells in murine models, NCG mice (six per group) were injected intravenously with L428 tumor cells (2×10^6 cells per mouse). After 5 days (day 0), the tumor-bearing mice were imaged using a bioluminescence imaging system for Luc expression, and the mice were randomly divided into four groups for different treatments (**Figures 4A,B**). NC T cells, CD19-CAR-T cells, HRS3-CAR-T cells, and hHRS3-CAR-T cells (1×10^7 cells per mouse) were infused intravenously as a single dose. hHRS3-CAR-T cells showed excellent efficacy comparable to HRS3-CAR cells. In contrast, CD19-CAR-T and NC T cells exhibited progressive tumor growth (**Figure 4C**). When tumor sizes were assessed 21 days after CAR-T cell infusion, we found that T cells expressing hHRS3-CAR were more effective at reducing tumor sizes than T cells expressing HRS3-CAR (**Figure 4D**); however, survival and weight change were not statistically different when treatment with hHRS3-CAR-T and HRS3-CAR-T cells was compared. Mice in the control group died after 40 days, whereas mice in the HRS3-CAR-T and hHRS3-CAR-T groups died after 63 days. Similar relative survival curves were obtained in repeated experiments, and the survival curve data from both experiments were combined for analysis (**Figure 5A**). Owing

to significant liver ascites and death in the control group, body weight changes were only recorded for 35 days (**Supplementary Figure S3**). Previous studies have reported a class of HL tumor models that preferentially caused accumulation of tumors in the liver abdomen (Guercio et al., 2021). Macroscopic analysis of the sacrificed mice showed large tumor masses located preferentially in the liver (**Figure 5B**). Therefore, the anti-tumor activity of hHRS3-CAR-T cells was comparable to that of HRS3-CAR-T cells in this model.

Considering that hHRS3-CAR Tcm cells were significantly enriched *in vitro*, we evaluated its proportion *in vivo*. The results showed that the difference in Tcm cell ratio was not statistically significant in the blood, spleen, and bone marrow of mice treated with hHRS3-CAR-T cells versus HRS3-CAR (**Figures 5C–E**).

DISCUSSION

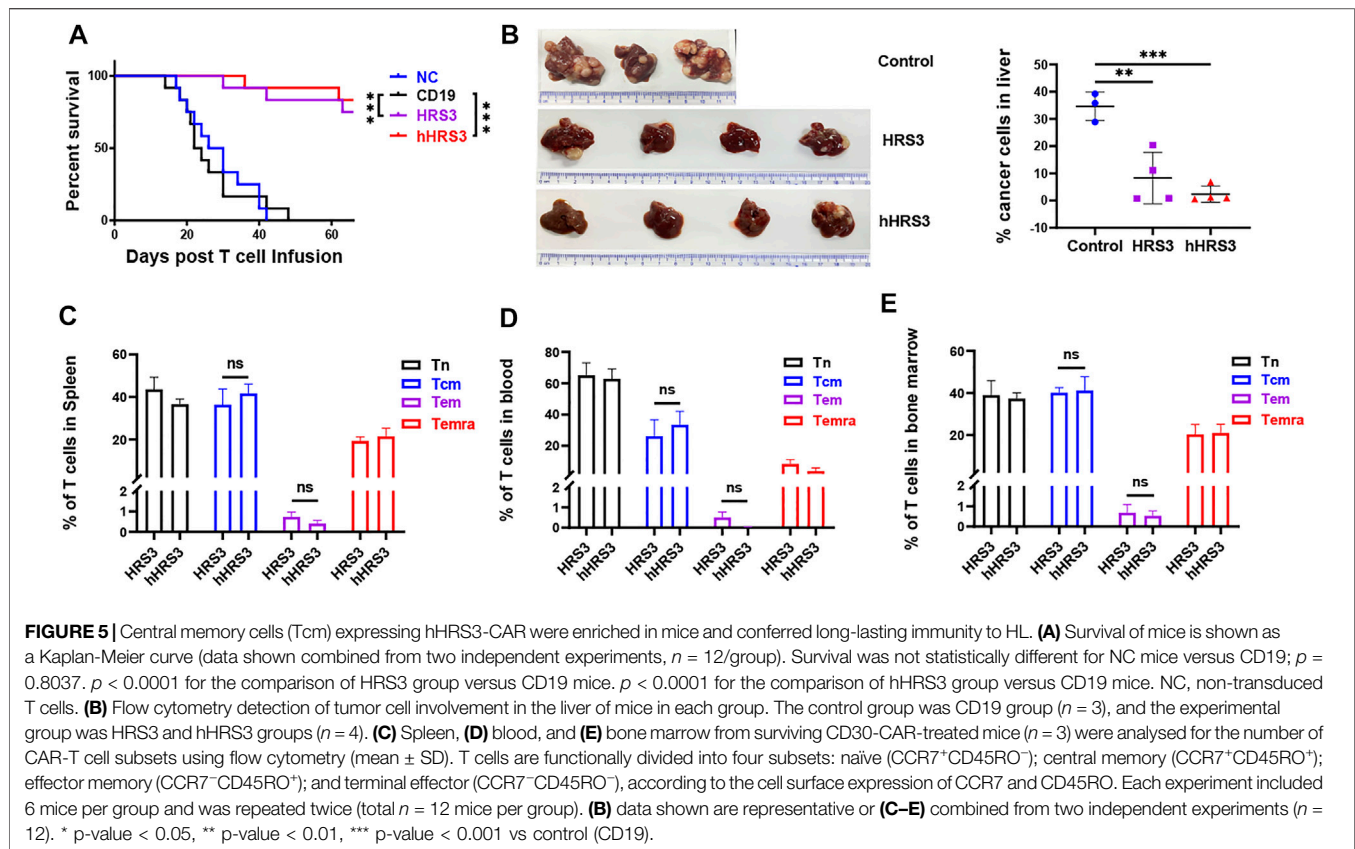
To date, several clinical trials have been conducted in adults with relapsed/refractory CD30⁺ lymphoma using different CD30-CAR-T cells (Di Stasi et al., 2009; Wang et al., 2017). Compared with the great success achieved by CD19-redirected CAR, CD30-target CAR still has room for improvement. Previous studies have demonstrated that the transfer of autologous human T-cells expressing foreign proteins, including CARs derived from murine scFvs, can elicit cellular and humoral immune responses



that may compromise CAR-T effects (Lamers et al., 2006; Wang et al., 2020; Wagner et al., 2021). The use of human or humanized antibody fragments for CAR construction, rather than those derived from mouse antibodies, such as the production of modified CD19 and Her-2 CAR-T, combination of humanized or fully human fragments, and modification of the extracellular hinge region and/or transmembrane domain, can reduce the immunogenicity of the CAR (Hombach et al., 2010;

Jonnalagadda et al., 2015). Importantly, this strategy might simultaneously decrease the risk of cytokine-mediated toxicity and improve CAR-T cell persistence (Sommermeier et al., 2017; Rafiq et al., 2020).

HRS3 is derived from a murine antibody (da Costa et al., 1992; Hombach et al., 1998); humanized HRS3 scFv was derived from HRS3 mAb, which may represent another class of anti-CD30 antibodies (Schlapschky et al., 2004). Notably, previous studies



have demonstrated that the humanized Fab fragment was fully functional with respect to CD30 binding; however, whether the CAR possessing this molecule as an extracellular recognition domain can safely and effectively eliminate target cells remains requires further investigation. In this study, we found that hHRS3-CAR-T cells were highly efficacious against antigen-specific tumor cells in both *in vitro* and *in vivo* with responses that were comparable to those of HRS3-CAR-T cells. Besides scFv, other elements of CAR may also produce rejection. In this study, the sequence of the hinge spacer and transmembrane domain in the CAR were all derived from human CD8 α to minimize immunogenicity. Furthermore, the linker of (GGGG) $_3$ that connects the heavy and light chains in the scFv has been widely used in antibodies and CARs. However, these strategies do not completely eliminate immunogenicity. Even a fully human antibody fragment might also lead to immune reactions in the human; therefore, to conclusively determine whether they are nonimmunogenic requires their application in human clinical trials.

Retrospective analysis of published CAR-T cell clinical studies revealed that an elevated proportion of Tcm or less differentiated CAR-T cells provided superior antitumor efficacy, and Tcm-derived CAR-T cells are functionally superior to those made from bulk CD8 $^+$ T cells (Chang et al., 2015; Tao et al., 2020). Tcm provides effective long-term memory responses because they have the capacity to persist long term in the circulation, have a high proliferative capacity,

and can replenish other memory T-cell subsets, including Tem (Gehad et al., 2018; Mauriello et al., 2020). Our results showed that hHRS3-CAR could produce the higher proportion of Tcm compared to parental CAR. Similar results were also observed in previous reports (Zhao et al., 2019). However, the mechanism underlying this effect remain to be elucidated up to now. We speculate that it is due to the continuous stimulation caused by antigen, such as murine scFv, accelerating the differentiation of Tcm to Tem. Although the advantages of humanized CAR-T have been proven in clinical trials, the improvement was not significant in our experiment, which may be due to the huge differences in the immune environment in immunodeficient mice and human. For example, the humanized anti-CD19 CAR did not show a difference in the ability to kill target cells *in vitro* and in mice compared to parental CAR, but it exhibited significantly lower side effects in the patients with B-cell lymphoma (Heard et al., 2021).

In conclusion, we focused on developing a CD30-specific CAR using humanized HRS3-scFv. hHRS3-CAR-T cells specifically killed CD30 $^+$ tumor cells *in vitro* with efficiency similar to that of murine HRS3-CAR-T, and these T cells significantly inhibited the established CD30 $^+$ human lymphoma tumor cells in immunodeficient mice. These findings indicate that hHRS3-CAR-T cells are a promising cellular therapeutic agent and warrants further clinical exploration.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, further inquiries can be directed to the corresponding authors.

ETHICS STATEMENT

The animal study was reviewed and approved by the Animal Ethics Committee of West China Hospital of Sichuan University.

AUTHOR CONTRIBUTIONS

JG, DY, and XZ: conception and design. JG and DY: methodology, validation, data collection, analysis, writing—original draft and editing. SH and WY: methodology, validation, data collection, analysis. YZ and XZ: administrative, writing, or material support.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fcell.2021.775599/full#supplementary-material>

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Potentiating Cancer Immune Therapy via Nanomaterials and Purinergic Signaling

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INTRODUCTION

Adenosine, an autacoid nucleoside interacting with P1 receptors, activates four G protein-coupled receptors named A₁, A_{2A}, A_{2B}, and A₃, crucially regulating several human pathologies (Borea et al., 2018). It affects both neoplastic and immune cells, promoting cancer cell proliferation, neo-angiogenesis, immunoevasion, and metastasis (Arab and Hadjati, 2019). Extracellular nucleotides such as ATP, ADP, and UTP also function as cell-to-cell communication signals by binding and activating P2 receptors belonging to the P2X and P2Y subfamilies (Kennedy, 2021). These receptors are further subdivided into different subtypes (Khakh et al., 2021). The differential expressions of P1 and P2 receptors both in immune and tumor cells generate a complex picture. Cancers are able to convert extracellular ATP into immunosuppressive adenosine, through the activation of CD39 ectonucleotidase that hydrolyzes ATP to AMP, and a subsequent CD73 enzyme that transforms AMP into adenosine, with the stimulation of adenosine receptors on immune cells activating numerous immunosuppressive effects (Borea et al., 2018; Boison and Yegutkin 2019). The shift from P2 to P1 activation is important for limiting the inflammatory response, thus preventing tissue damage, but may also deleteriously inhibit immunosurveillance (Antonioni et al., 2013; Allard et al., 2019). Targeting CD39 and CD73 has, therefore, become a new way to fight cancer (Perrot et al., 2019; Moesta et al., 2020; Li et al., 2019). This review conjugates the current knowledge of purinergic signaling in cancer biology with techniques involving nanomaterials to increase anticancer immune responses.

P1 Receptors and Cancer

Two hallmarks connecting adenosine to cancer include 1) solid tumors develop hypoxia and increase adenosine from nanomolar to micromolar concentrations and 2) the A_{2A} receptor is an essential brake of immune cells (Sitkovsky M. V., 2020; Hatfield and Sitkovsky, 2020). The hypoxic activation of the master oxygen-sensitive transcriptional regulator HIF-1α upregulates ecto-5'-nucleotidase (CD73), generating adenosine accumulation associated with poor prognosis in many neoplasms (Borea et al., 2017). Adenosine activates cAMP-elevating A_{2A} receptors to inhibit CD8⁺, CD4⁺ lymphocytes, and natural killer (NK) cells but stimulates B and T regulatory lymphocytes (Treg), tumor-associated macrophages (TAMs), and myeloid-derived suppressor cells (MDSCs), thus establishing a typically immunosuppressive tumor microenvironment (TME) (Vijayan et al., 2017). This encouraged immunologists to recognize adenosine as a new “immune checkpoint regulator” that stimulated the classic anti-cytotoxic T-like antigen 4 (CTLA4) and anti-programmed death-ligand 1 (PD-L1) to increase immunoevasion (Sitkovsky M. V., 2020). Indeed, CTLA4 and PD-L1 inhibitors have been well-tolerated in cancer patients, improving overall morbidity and survival

versus standard chemotherapy. However, efficacy may be limited to relatively few patients in some tumor types, reflecting the presence of alternative immunosuppressive factors in TME. Notably, anti-PD1 therapy increased immunosuppressant A_{2A} receptors on CD8⁺ T cells; moreover, patients resistant to immunotherapy showed CD73 upregulation, suggesting that adenosine machinery counteracted the effects of immune checkpoint inhibitor drugs (Zarek et al., 2008). One improvement strategy has been implemented to inhibit (Kotulová et al., 2021) the hypoxia-HIF-1 α -A_{2A} receptor-mediated pathway in the TME through A_{2A} receptor antagonists (Hatfield and Sitkovsky, 2020; Willingham et al., 2020). Accordingly, genetic silencing of the A_{2A} receptor strongly increased inflammation and tumor rejection in mice (Ohta and Sitkovsky, 2001; Ohta et al., 2006; Sitkovsky M. V., 2020). A series of phase I/II clinical trials, evaluating the safety and efficacy of A_{2A} receptor blockers/CD73 inhibitors including oleclumab, CPI-006, BMS-986179, and NZV-930 and A_{2A} receptor antagonists such as ciferadenant, inupadenant, taminadenant, AZD4635, and preladenant alone or coadministered with immune checkpoint inhibitors such as anti-PD1 or anti-PDL1, are under evaluation (Arab and Hadjati, 2019; Arab et al., 2021; Franco et al., 2021; Thompson and Powell, 2021).

Beyond targeting the A_{2A} receptor, anticancer immunotherapy can also be potentiated by inhibiting the A2B receptor, a subtype also capable of stimulating cAMP in T cells. Phase I clinical trials of A2B blockers in patients with advanced cancer are underway (Franco et al., 2021). Arguably, this pharmacological approach might only succeed in patients bearing hypoxic tumors with a sufficient number of tumor-reactive T cells, yet this consideration remains to be resolved (Sitkovsky M. V., 2020; Fong et al., 2020).

P2 Receptors and Cancer

The TME is rich in ATP and its metabolites modulating tumor and immune cell biology and responses (Di Virgilio et al., 2018). The contribution of P2 receptors to cancer biology has been intensively investigated (Chiarella et al., 2021). The ATP-activated P2X7 receptor has emerged as a pivotal membrane molecule in tumors as it is expressed by cancer cells and by macrophages, dendritic cells, and lymphocytes infiltrating the tumor mass (De Marchi et al., 2019).

Tumor cell cytotoxicity (apoptosis or necrosis) due to prolonged P2X7 receptor activation and pore formation was a desirable anti-tumor response of this membrane molecule (Feng et al., 2006; Fu et al., 2009; Bian et al., 2013; Avanzato et al., 2016). However, subsequent identification of P2X7 receptor variants, with more precise characterization of the responses and measurement of cancer cell expression levels, indicated this subtype was upregulated in many tumor types (McLarnon, 2017; Di Virgilio et al., 2018; Zhang et al., 2019a; 2019b). More significantly, P2X7 receptor stimulation by low extracellular ATP concentrations was pro-tumorigenic, favoring cancer cell survival, proliferation, motility, and chemoresistance (Adinolfi et al., 2012; Schneider et al., 2015; Arnaud-Sampaio et al., 2020). In addition to the P2X7 receptor

subtype, the P2X4, P2X5, P2Y₆, and P2Y₁₂ receptors also have involvement in tumor biology (Roger et al., 2015). P2X4 and P2X7 receptor subtype expressions concurred with tumor cell proliferation (He et al., 2020). In contrast, P2X5 receptor mediated an anti-proliferative (Zhang et al., 2020) effect by inducing tumor cell differentiation. Cumulative reports have indicated pro-neoplastic P2Y₂ receptor-mediated responses conferring resistance to cell apoptosis, stimulation of tumor replication, and dissemination (Limami et al., 2012; Choi et al., 2013; Schumacher et al., 2013). The lack of expression of the P2X7 receptor in P2X7 KO mice induced a decrease in CD8⁺ lymphocytes while the number of Treg cells increased (De Marchi et al., 2019).

From a pharmacological and therapeutic perspective, P2 receptors have high potential to complement radiation therapy against resistant, highly malignant cancers. The stimulation of P2X7, P2Y₆, and P2Y₁₂ receptors was significant in the DNA damage response induced by γ -irradiation of adenocarcinoma A549 cells (Ide et al., 2014). B16 melanoma cells both *in vitro* and *in vivo* responded similarly to P2X7 receptor antagonists (Tanamachi et al., 2017). The use of single P2 receptor subtype inhibitors was often sufficient to block tumor cell growth and dissemination (Drill et al., 2021). The growth of human high-grade gliomas was inhibited by P2X7 subtype antagonists (Kan et al., 2020); receptor inhibitors, such as emodin, and the *Uncaria tomentosa* extract effectively counteracted the P2X7 receptor-mediated breast cancer spread (Zhu et al., 2021). P2X7 receptor antagonization could also usefully reduce pain in cancer patients with metastases. In particular, the P2X7 receptor antagonists AFC5261 and A-740003 were promising in animal models (Li et al., 2018; De Marchi et al., 2019; Falk et al., 2019). Further identification and characterization of new P2X7 receptor modulators and inhibitors were recommended (Hempel et al., 2013). Also for consideration, the expression of P2X7 and other P2 receptors by immune cells participated in immunosurveillance (Jelassi et al., 2013; Grassi and Conti, 2021). The awareness of the importance of P2-mediated signaling in cancer pathogenesis and progression (Figure 1A) has prompted therapeutic strategies targeting extracellular nucleotides. In this light, nanomaterials may improve anticancer outcomes by modulating the immune and tumor cell purinome.

Nanomaterials and Immunosurveillance

Although TME immunosurveillance may be markedly heterogeneous, most anticancer agents rely on the reactivation of homeostatic immune defense mechanisms (Joyce and Fearon, 2015; Terry et al., 2017; Ni et al., 2021). Initially, innovative nanomaterials improved upon conventional treatments yet soon drew criticism when nanoparticles elicited toxic effects from immunological alterations (Lenders et al., 2020). Nonetheless, rationally tailored nanomaterials have renewed interest in penetrant TME modulators (Zhang et al., 2021) that address tumor immune evasion (Guevara et al., 2021) by immunotherapy enhancement to promote immunogenic tumor cell death (Aikins et al., 2020) (Nogady, 2021). The multiple cell types comprising the TME provide alternative nanomaterial targets, and their

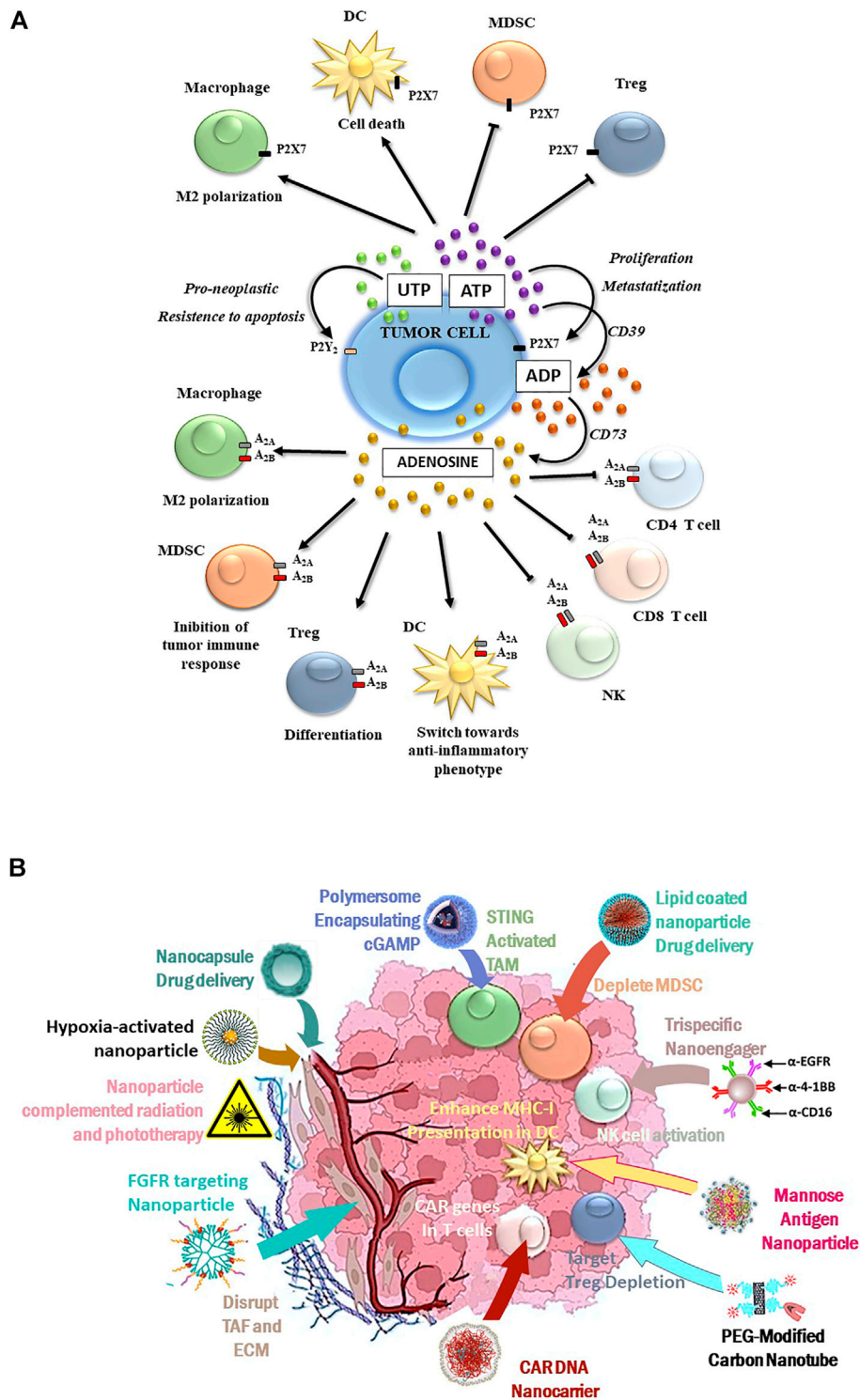


FIGURE 1 | (A) Purinergic-mediated responses occurring in the TME: P2 receptor-induced activities are summarized in the upper part of the figure, while P1 receptor-mediated responses are depicted in the lower figure part. **(B)** Schematic diagram for tailored nanoparticles targeting the TME and its immunological components to potentiate cancer immune therapy.

involvement in intervention design can be reciprocal (Song et al., 2017). For example, to counteract tumor adenosine accumulation, lipid nanoparticles mediating the knockdown of the corresponding A_{2A} receptor in memory T cells could rescue $CD8^+$ T-cell chemotaxis for infiltration into the TME of head and neck squamous cell carcinomas (Newton et al., 2021). Nanoparticle-based delivery approaches also include cell membrane-camouflaged nanocarriers (Grimaudo, 2021) such as tumor-associated macrophage membrane-coated nanoparticles (Chen et al., 2021). Cell membrane-bioinspired nanoparticles can provide superior immune regulation, nanocapsule drug delivery (Zhang et al., 2019c; Irvine and Dane, 2020), tumor targeting, and biocompatibility (Mu et al., 2021).

Yet diversity among tumorigenic cells and between individuals may still thwart nano-based delivery systems. The improved knowledge of various chronological stages of TME development remains necessary for more effective nanoplatform implementation (Yang et al., 2021) to target the more persistent subpopulation of cancer stem cells (Duan et al., 2021). The highest immunotherapeutic efficacy occurs when nanoparticles achieve precise and timely delivery, specifically targeting neoplastic cells with minimal harm to healthy cells (Muluh et al., 2021). Addressing TME traits, hypoxia-activated nanoparticles have theranostic applications (Wang et al., 2019). Since TME hypoxia blocked antitumor immunity (Singleton et al., 2021), tumor hypoxia-activated polymeric micelles were used to both activate strong cytotoxicity and stimulate a systemic antitumor immunity that effectively eradicated breast cancer in preclinical murine models (Liu et al., 2021). Hypoxia-modifier nanoparticles (Yuan et al., 2021) targeting the blood-brain barrier, enhanced immunotherapy of glioblastoma (Meng et al., 2021), a particularly aggressive form of cancer involving intracellular purine alterations (Debom et al., 2021; Giuliani et al., 2021). Cancer metastasis treatment remains a highlight of nanomedicine-based immunotherapy (Zhang et al., 2019). Excellent efficacy was observed for TME-activated nanoparticle chemodynamic immunotherapy of melanoma-derived lung metastasis (Zhai et al., 2021).

How Nanomaterials Can Be Used to Modulate TME Purinergic Signaling

Compared to the relatively heterogeneous tumor-cell population, non-tumorigenic supportive cells within the TME such as tumor-associated fibroblasts (TAFs) may present a more consistent target for nanoparticle intervention (Li et al., 2021), yet some limitations persist. Nanomaterial-based TME modulation impinging upon purinergic signaling pathways can serve to additionally recruit the immune system to provide more integrative therapy (Laplane et al., 2019; Shi and Lammers, 2019). Nanomaterials can be adapted to modulate purinergic signaling in a number of ways since nanoparticles can be size-tailored to have diameters that match pore sizes present in leaky TME vasculature, thus establishing size-related penetration and accumulation (Yu et al., 2020). Moreover, nanoparticles can assist with improved delivery of drugs such as A_{2A} antagonists that

counteracted immunosuppression (Arruga et al., 2021). It is notable that the purinergic signaling network is subjected to modulation by microRNA (miRNA) (Ferrari et al., 2016), and over 30 miRNAs directly or indirectly modulate P1 and P2 receptors and ectoenzymes, with miR-187 capable of modulating both P2X7 and CD73 (Guo et al., 2022). Notably, miRNA that bind the 3' untranslated region of the P2X7 receptor can affect the development of breast cancer by influencing the P2X7 receptor expression (Zhu et al., 2021). Nanoparticles are well-suited for precision medicine strategies to deliver purinergic signaling-specific miRNA and silencing RNA (siRNA) therapeutics (Kara et al., 2022). It has already been demonstrated that the nanoparticle delivery of siRNA-CD73 to the central nervous system blocked the CD73 expression in the glioblastoma immune microenvironment, inducing apoptosis to delay tumor growth (Azambuja et al., 2020). Smart nanomaterials can be engineered to exploit TME-specific purinergic pathway anomalies. A hydrogel of alginate conjugated with an ATP-specific aptamer hybridized with immunoadjuvant CpG oligonucleotides enabled the release of immune adjuvants in synchrony with low-dose repeated chemo/radiotherapies. This achieved a remarkable synergistic response; in addition to eliminating tumors, the evoked immune memory rejected re-challenged tumors and inhibited distant tumor metastases when combined with immune checkpoint blockade (Sun et al., 2021).

Nanoparticles Modulating TME Purinergic Pathways Potentiate Immune Therapy

Innate immune interactions include macrophage responsiveness to damage-associated molecular patterns (DAMPs) originating from the cancer cells. M2-like tumor-associated macrophages (TAMs) can efficiently engulf neighboring apoptotic cells abundant in solid tumors, an early immunosuppressive mechanism preventing a DAMP-mediated immune response. The MER proto-oncogene tyrosine kinase (MerTK) can promote an "eat me" signal on dying cells to enhance efferocytosis (Ou et al., 2021). Consequently, apoptotic cells are eliminated before releasing intracellular ATP and cyclic GMP that would otherwise activate the ATP-gated P2X7 channels of TAMs and also cytosolic nucleic acid sensor pathways, including cyclic GMP-AMP synthase (cGAS) producing cyclic guanosine monophosphate-adenosine monophosphate (cGAMP), a second messenger binding and activating the adapter protein, stimulating interferon gene (STING), expressed in TAMs and other cells of the TME. The production of stress-responsive cytokines would ultimately cause M2 macrophages to be polarized toward an immune-activated M1 phenotype (Zhao et al., 2021). Appropriately, macrophages have become key targets for nanoparticle intervention (Medrano-Bosch et al., 2021). A nanoparticle-incorporating STING activator cGAMP enhanced the antitumor immunity in PD-L1-insensitive models of triple-negative breast cancer (Cheng et al., 2018) and improved the clinical outcome of immunotherapy for melanoma (Shae et al., 2019). Cationic silica nanoparticles induced necrotic cell death and activation of the STING in the TME to enhance antitumor immunity (An

TABLE 1 | Examples of immunomodulatory nanoparticle types, tumor microenvironment (TME) interactions and co-involved purinergic pathways.

Nanomaterial	Size (nm)	TME target	Co-involved purinergic ecto-enzyme receptor subtype	Reference
CAR DNA Nanocarrier	155 ± 40	murine CD8 ⁺ T cell	P2X7	Smith et al. (2017)
FGFR targeting nanoparticle	10–200	Tumor Associated Fibroblasts (TAF)	CD73	Li et al. (2021)
Hypoxia-activated nanoparticle	254 ± 27	Hypoxia	CD39, CD73, A _{2A} , P2Y ₂ , P2X7, P2Y ₁₁	Wang et al. (2019)
Lipid coated nanoparticle drug delivery	≈30	Myeloid-Derived Suppressor Cells (MDSC)	P2X7, A _{2B}	Zhang et al. (2019)
Mannose antigen nanoparticle	210	Dendritic Cell (DC)	P2X7	Pei et al. (2021)
Nanocapsule drug delivery	100–200	Tumor Extracellular Matrix	P2X4, P2X7, P2Y ₁₂	Irvine and Dane, (2020)
PEG-modified carbon nanotube	101 ± 41	Regulatory T cells (T _{reg})	A _{2A} , A _{2B}	Sacchetti et al. (2013)
Polymersome encapsulating cGAMP	20–100	Tumor Associated Macrophage (TAM)	P2X7	Shae et al. (2019)
Trispecific nanoengager	112 ± 7	Natural Killer (NK) cell	CD39, A _{2A} , A _{2B} , A ₃ , P2X7	Au et al. (2020)

et al., 2018). Inhalable nanoparticulate agonists of STING synergized with radiotherapy to provide the long-term control of lung metastases (Liu et al., 2019). Combining nanoparticles with compatible forms of therapy such as radiation therapy (Huang et al., 2021) or photodynamic therapy (Jin et al., 2021) improved antitumor efficacy by promoting immunogenic cell death.

Nanomaterials are also capable of enhancing the trained acquired immune response (Magadán et al., 2021), and they have been rationally designed to enhance T-cell expansion, navigate physical barriers, and modulate the TME to overcome barriers to T-cell-based immunotherapies (Gong et al., 2021). Engineered immunomodulating nano-adaptor particle rafts such as trispecific natural killer cell nanoengagers (Au et al., 2020) carry more than one monoclonal antibody (mAb) to bridge effector and tumor cells. More effective responses than simply mixing the parental mAbs with T cells, NK cells, natural killer (NK) cells, or macrophages were observed (Jiang et al., 2021). Nanogels selectively released an interleukin-15 cargo upon T-cell receptor activation and expanded T cells in tumors 16-fold relative to the systemic administration of free cytokines. The higher doses of cytokines could be administered, without toxic side effects, to potentiate human chimeric antigen receptor (CAR)-T cell therapy (Tang et al., 2018). Nanoparticle versatility, exemplified in **Table 1** and

Figure 1B, has meant that numerous clinical nanomaterials and drugs potentiating immunotherapy are currently under development (Li et al., 2020; Hu and Huang, 2022).

DISCUSSION

The TME, heavily conditioned by nucleotide/nucleoside release and hydrolysis, makes purinergic signaling an extremely attractive target for strategic modulation of both cancer and immune cells, but responses to antagonists or agonists are highly context-dependent (Hreich et al., 2021). The inhibitors of specific purinome components have successfully blocked tumor progression and metastasis in animal models and preclinical studies, yet improved specific therapeutic strategies are needed. The recent implementation of nanomaterials has shown that they can be very effective agents, acting on their own, delivering mRNA or improving mAb presentation to disrupt the TME refractoriness to immune therapy.

AUTHOR CONTRIBUTIONS

DF, SG, SM, MN, AT, and JB wrote the manuscript. All authors have read and agreed to the published version of the manuscript.

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The Role of Tissue-Resident Macrophages in the Development and Treatment of Inflammatory Bowel Disease

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Inflammatory bowel disease (IBD), comprising Crohn's disease and ulcerative colitis, is a refractory disease with many immune abnormalities and pathologies in the gastrointestinal tract. Because macrophages can distinguish innocuous antigens from potential pathogens to maintain mucosa barrier functions, they are essential cells in the intestinal immune system. With numerous numbers in the intestinal tract, tissue-resident macrophages have a significant effect on the constant regeneration of intestinal epithelial cells and maintaining the immune homeostasis of the intestinal mucosa. They also have a significant influence on IBD through regulating pro-(M1) or anti-inflammatory (M2) phenotype polarization according to different environmental cues. The disequilibrium of the phenotypes and functions of macrophages, disturbed by intracellular or extracellular stimuli, influences the progression of disease. Further investigation of macrophages' role in the progression of IBD will facilitate deciphering the pathogenesis of disease and exploring novel targets to develop novel medications. In this review, we shed light on the origin and maintenance of intestinal macrophages, as well as the role of macrophages in the occurrence and development of IBD. In addition, we summarize the interaction between gut microbiota and intestinal macrophages, and the role of the macrophage-derived exosome. Furthermore, we discuss the molecular and cellular mechanisms participating in the polarization and functions of gut macrophages, the potential targeted strategies, and current clinical trials for IBD.

Keywords: inflammatory bowel disease, ulcerative colitis, Crohn's disease, tissue-resident macrophage, macrophage polarization

1 INTRODUCTION

In recent years, the morbidity of inflammatory bowel disease (IBD) has increased globally, especially in Africa and Asia, and is spreading worldwide with accelerated speed (Windsor and Kaplan, 2019). IBD is an idiopathic, refractory and chronic disease, with clinical symptoms including abdominal pain, rectal bleeding, weight loss, diarrhea, and anemia, that requires life-long medication (Roda et al., 2020; Seyed Tabib et al., 2020). Conventionally, IBD is mainly divided into Crohn's disease (CD) and ulcerative colitis (UC), along with different locations and inflammatory types, respectively (Torres et al., 2017; Ungaro et al., 2017). CD affects almost every part of the gastrointestinal tract and tissue layers, and the most frequent locations are the terminal ileum and colon (Torres et al., 2017; Roda et al., 2020). However, UC mainly involves the superficial intestinal mucosa of the colon,

including the proximal end of the rectum (Ungaro et al., 2017; Kobayashi et al., 2020). Approximately 5 million people worldwide are affected with IBD, yet the etiology of IBD is not known, and there are no cures so far (Kaplan, 2015). The continuation of this trend is likely to increase the worldwide population of patients affected by IBD to tens of millions or more in the next few decades (Ananthakrishnan, 2015). More importantly, recent discoveries revealed that patients with IBD are more susceptible to colorectal cancer (Nadeem et al., 2020). Thus, the prevention and treatment of IBD are extremely necessary and important.

The etiology of IBD arises from intricate interactions between the immune system, genetic predisposition, environmental cues, and the gut microbiome (Kobayashi et al., 2020; Roda et al., 2020). Under ideal conditions, intestinal inflammation is a self-limiting process that combats harmful pathogens and rapidly returns to homeostasis (Schett and Neurath, 2018). However, a disequilibrium between the mucosal immune system and the commensal ecosystem occurs in the exacerbation of IBD, because of the imbalance of the immunological mechanisms underlying the resolution of inflammation (Hunter, 2012; Schett and Neurath, 2018; Graham and Xavier, 2020). Intestinal macrophages are an integral part of the normal intestinal tissues that can engulf microorganisms and present antigens to activate T cells, as well as prevent excessive inflammation through specific molecular and cellular mechanisms (Smythies et al., 2005; Garrett et al., 2010; Mowat, 2018). According to the microenvironmental cues, macrophages could polarize into two different phenotypes: the classically activated (M1) or alternatively activated (M2) macrophages (Funes et al., 2018; Locati et al., 2020). When the intestinal barrier function is impaired, the efferocytosis effect leads to macrophages skewing toward M2 subtypes functionally, producing cytokines, chemokines and lipid mediators that participate in healing the intestinal mucosal barrier and maintaining homeostasis (Elliott et al., 2017; Na et al., 2019). Various cytokines and other soluble factors, including prostaglandin E2 (PGE2), bone morphogenetic protein 2 (BMP2), and WNT ligands, can be produced by gut macrophages that stimulate the expansion of epithelial cells and participate in the enteric nervous system or intestinal mucosal barrier to help maintain tissue homeostasis (Bain and Mowat, 2014). Meanwhile, intestinal macrophages maintain tolerance *via* promoting the proliferation of antigen-specific CD4⁺CD25⁺ regulatory T (T-reg) cells primarily by producing interleukin (IL)-10 in order to inhibit unrestrained inflammation as a response to innocuous commensal microbes (O'Garra et al., 2004; Hedrich and Bream, 2010).

In addition, the lack of response in patients with IBD to anti-tumor necrosis factor (TNF) therapy was found to be related to a defect in the IL-10 signaling pathway, which is crucial for biologics-induced macrophages skewing toward M2 subsets (Vos et al., 2012; Roda et al., 2016; Koelink et al., 2020). Therefore, intestinal macrophages play major roles in the establishment and maintenance of intestinal homeostasis. As a consequence, disequilibrium of intestinal macrophages could lead to a loss of tolerance to harmless microbes and food antigens, which is considered to underlie the excessive inflammation in

IBD (de Souza and Fiocchi, 2016). In view of these findings, it is important to analyze the potential contribution of macrophages to intestinal chronic inflammation, which may offer us novel insights into the pathogenesis and therapeutic strategies in IBD.

In this review, we outline the characteristics of the origin and maintenance of macrophages, as well as their interaction with other immune cells. Then, we delineate the cellular and molecular mechanisms that underlie the differentiation and function of intestinal macrophages. Furthermore, we describe the interaction between gut microbiota and intestinal macrophages, and the role of the macrophage-derived exosome. Finally, potential treatment targets, applicable drugs and current clinical trials for IBD are discussed.

2 ORIGIN AND MAINTENANCE OF INTESTINAL MACROPHAGES

The gastrointestinal tract harbors copious amounts of tissue macrophages, orchestrating innate and adaptive immune systems, helping to maintain homeostasis *via* tolerance to commensal microbes, as well as resisting potentially harmful pathogens (Yip et al., 2021). In the past, the origin of tissue macrophages was considered to be the blood monocytes, deriving from precursors in the bone marrow (van Furth et al., 1972; Bain and Mowat, 2014). With the development of novel techniques, there is mounting evidence showing that monocytes are not the exclusive origin of tissue-resident macrophages (Wu and Hirschi, 2020). Macrophages arise in two different ways: they can be differentiated from blood-derived monocytes and embryo-derived precursors, deriving from the yolk sac and/or fetal liver, established in the tissue before birth (Shaw et al., 2018; Wu and Hirschi, 2020). Intestinal tissue-resident macrophages, derived from embryonic precursors, maintain themselves *via* self-renewal *in situ* throughout adulthood but also require constant replenishment by circulating monocytes in the blood (Shaw et al., 2018). This is in contrast to macrophages in other tissues, such as microglia in the central nervous system and Langerhans cells in the liver, that maintain themselves independently and self-renew *in situ* throughout adult life (Yona et al., 2013; Ginhoux and Guillemins, 2016).

With progress in recent research, traditional understanding has been challenged, and embryo-derived macrophages were found to sustain themselves in the adult intestine (Shaw et al., 2018). In adult mice, parts of intestinal macrophages, characterized by high expression levels of CD4 and apoptotic cell-uptake receptor Tim-4 (Tim-4⁺CD4⁺ macrophages), were demonstrated to be long-lived and locally self-renewed independent of monocytes, while Tim-4⁻CD4⁺ macrophages were found to have a slow turnover from blood monocytes (Shaw et al., 2018). In contrast, Tim-4⁻CD4⁻ macrophages were short-lived and relied on continuous replenishment of blood monocytes (Shaw et al., 2018). Similar results have been found in duodenal transplant patients' mucosa, along with short-lived monocyte-derived macrophage subsets, different and dominant subsets with a slower replenishment rate were confirmed (Bujko et al., 2018). Similarly, another study in

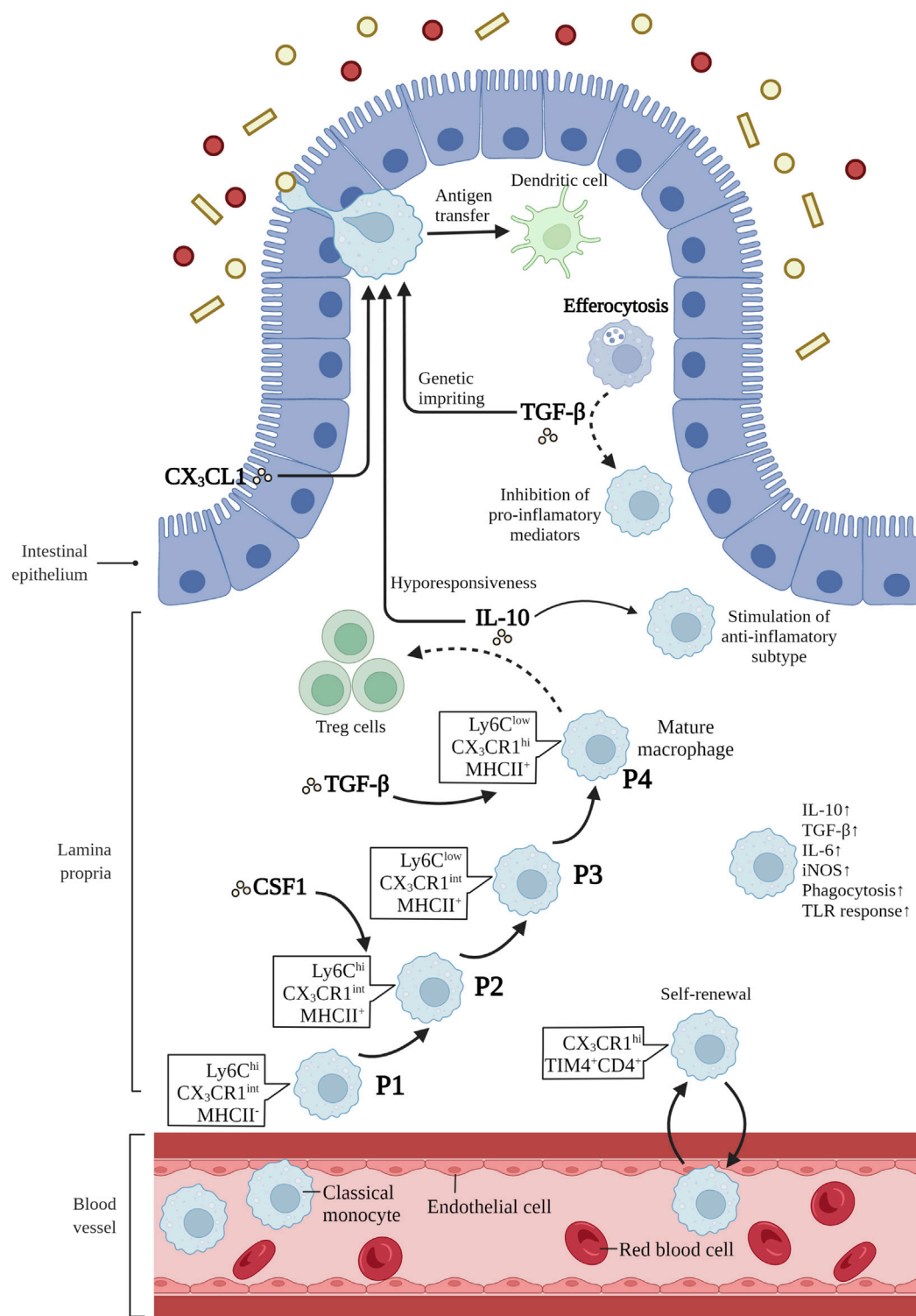


FIGURE 1 | Differentiation and function of intestinal macrophages. Intestinal macrophages are replenished by blood-derived monocytes through a series of differential intermediates in a way of “monocyte waterfall”. lymphocyte antigen 6C-high (Ly6C^{hi}) CX3C-chemokine receptor 1-intermediate (CX3CR1^{int}) major histocompatibility complex II (MHCII⁻) (P1) monocytes enter the lamina propria, acquiring the expression of MHCII (P2), and then downregulating Ly6C expression (P3). Finally, these cells upregulate the expression of CX3CR1, CD64, and F4/80, giving rise to mature macrophages (P4). T cell immunoglobulin mucin receptor 4-positive (Tim-4⁺) CD4⁺ macrophages have been demonstrated to be long-lived and locally self-renewed independent of monocytes. Macrophage colony-stimulating factor 1 (CSF1) is a critical cytokine in the survival, proliferation and differentiation of intestinal macrophages. IL-10 is crucial in inducing subtype of anti-inflammatory (Continued)

FIGURE 1 | macrophages, maintaining the hyporesponsiveness to toll-like receptors (TLRs) stimulation, and promoting antigen-specific regulatory T (Treg) cells. CX3C-chemokine ligand 1 (CX₃CL1), secreted by intestinal epithelial cells, plays a critical role in the differentiation and function of mouse intestinal macrophages. In addition, CX₃CR1⁺ macrophages form transepithelial dendrites (TEDs) with the ability to capture potential pathogens and transfer antigens to dendritic cells. The transforming growth factor- β (TGF- β) is essential for the terminal differentiation of macrophages in intestinal mucosa, and genetic imprinting of intestinal macrophages in mice. Besides, efferocytosis produce the secretion of TGF- β by macrophages, restraining the production of pro-inflammatory mediators. Mature intestinal macrophages are accompanied with the upregulation of IL-10, TGF- β , IL-6, iNOS, and the ability of phagocytosis and TLR responsiveness. Created with BioRender.com.

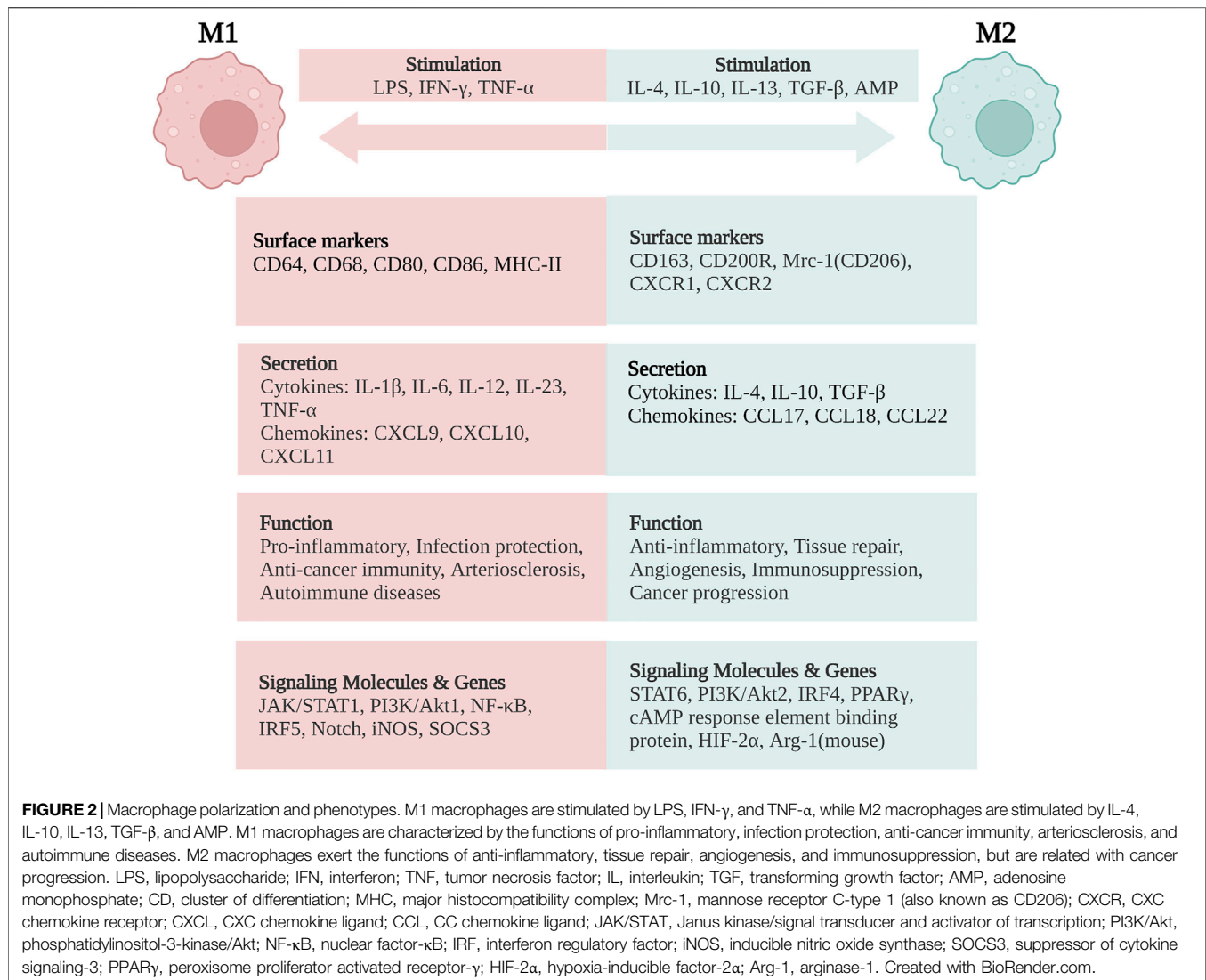
mice found that self-renewal embryo-derived macrophages and bone marrow-derived monocytes concomitantly reside in the lamina propria and muscularis externa layer of the intestine, persisting throughout adulthood (De Schepper et al., 2018). Depletion of self-maintaining macrophages could lead to a series of problems, such as injury of the submucosal vascular network, damage of enteric neurons, impaired neuro-evoked gastrointestinal section, and weakened intestinal motility (De Schepper et al., 2018). As noted above, parabiosis experiments (Guilliams et al., 2013; Hashimoto et al., 2013; Jakubzick et al., 2013; Epelman et al., 2014) and genetic fate-mapping experiments (Ginhoux et al., 2010; Hoeffel et al., 2012; Schulz et al., 2012; Yona et al., 2013) have proved that macrophages in the adult gut originating from yolk-sac precursors maintain self-renewal throughout life, thus existing independently of bone-marrow precursors for long-lasting maintenance. Given that there are different intestinal macrophage subsets with strong heterogeneity and distinct functional characteristics, future studies on macrophages in IBD should be focusing on altering the inflammatory phenotype, in parallel with keeping the protective tissue-resident subpopulations intact.

It has been proposed that macrophage precursors might compete for a limited number of niches, and the balance between embryo-derived macrophages and bone-marrow derived monocytes is delicately orchestrated by niche accessibility, availability and precursor plasticity (Guilliams and Scott, 2017; Guilliams and Svedberg, 2021). The orchestration of the niche assures that monocytes can differentiate efficiently into macrophages based on tissue-specific microenvironments only when the niche is available (Guilliams and Scott, 2017). Niche imprints play a strategic role in dictating macrophage identity and capacity for self-maintenance rather than only their origin, as was described previously (Mass and Gentek, 2021; Viola and Boeckxstaens, 2021). When the body is in a steady state, embryonic macrophages continuously renew and maintain themselves in adult tissues (Louwe et al., 2021). In the case of infection and tissue damage causing large consumption of tissue-resident macrophages, blood circulating monocytes can be used for long-term reconstruction of tissue-resident macrophages (Louwe et al., 2021). Intestinal macrophages are replenished by blood-derived monocytes through a series of differential intermediates in a step-wise continuum way, which is a process taking around 5–6 days, and has become known as the monocyte waterfall (Bain et al., 2013; Bain et al., 2014). (**Figure 1**). Lymphocyte antigen 6C-high (Ly6C^{hi}) CX3C-chemokine receptor 1- intermediate (CX3CR1^{int}) major histocompatibility complex II (MHCII⁺) (P1) monocytes seem similar to their counterparts in blood in aspects of both

phenotype and morphology (Schridde et al., 2017). As these cells enter the lamina propria, they first acquire the expression of MHCII (P2), and then downregulate Ly6C expression (P3), together with the other proteins of extravasation, and finally, upregulating the expression of CX₃CR1, CD64, and F4/80, giving rise to mature macrophages (P4) (Bain et al., 2013; Bain et al., 2014) (**Figure 1**). Notably, more and more evidences suggest that there is an analogous waterfall in the human intestinal mucosa, with classical CD14^{hi}CCR2⁺CD11c^{hi} monocytes gradually differentiating into CD14^{low}CCR2⁺CD11c^{low} macrophages (Bain et al., 2013; Bernardo et al., 2018; Bujko et al., 2018). However, there are still many questions to be answered about this process. How do macrophages differentiate into specific compartments in the distinct micro-environment of the duodenum with powerful absorptive ability or the cecum with myriad microbes? Is there a role for tissue-resident macrophages in memorizing past inflammatory injury within the intestinal tissue? Based on the aforementioned findings and potential challenges, facilitating the restoration of inflammation-imprinted resident macrophages and their niche in homeostasis may bring about a promising therapeutic avenue to prevent secondary complications in these patients.

3 FUNCTION OF INTESTINAL MACROPHAGES IN IBD

IBD is characterized by a destructive and relapsing inflammation of the gastrointestinal tract that harbors many macrophages that accumulate in the mucosa and are involved in the pathogenetic process. In IBD, the inflamed colonic mucosa can recruit a large number of macrophages, vigorously secreting IL-1, IL-6, TNF- α , IL-12, and IL-23, as well as producing reactive oxygen species (ROS), reactive nitrogen intermediates (RNIs), and proteases that could degrade the extracellular matrix. However, the characteristics of intestinal-resident macrophages in CD and UC are distinct with respect to distribution, ability to clear pathogens, and involvement in fibrosis. Macrophages mainly spread within the intestinal mucosa in UC, however, in CD, these cells also infiltrate in the muscular layer and mesenteric fat tissue (Mahida et al., 1989; Kredel et al., 2013). In the past, there was a simplified statement that CD has even been regarded as a primary immunodeficiency of macrophage (Casanova and Abel, 2009). Therefore, impaired cytokine secretion by macrophages was thought to be the reason for defective pathogenic clearance in CD (Smith et al., 2009). It is common to observe that intestinal macrophages contain *E. coli* in CD, but not in UC (Elliott et al., 2015). In contrary, bacterial pathogens were responded actively by macrophages in patients with UC (Rahman et al., 2010). As a



consequence, the formation of granulomas is generally found in CD patients but not the UC patients, because of the failure to eradicate invading pathogens effectively (Cook and Dixon, 1973). Notably, the degree of fibrosis is more pronounced in CD than in UC (Yamagata et al., 2011). Excessive wound-healing processes involve various steps with macrophages, resulting in the development of fibrosis and fibrotic strictures subsequently. In fibrotic CD, several factors produced by macrophages promote the formation of fibrosis, such as MMP-2, IL-13, TNF- α , and transforming growth factor- β (TGF- β) (Fichtner-Feigl et al., 2006; Bailey et al., 2012).

3.1 Macrophage Subsets in IBD

Mature macrophage phenotypes and functions are highly plastic and heterogeneous in response to environmental cues (Mosser and Edwards, 2008). Conventionally, a dichotomic nomenclature describes activated macrophages as having two opposite states: classically activated (M1) and alternatively activated (M2) macrophages (Gordon, 2003; Aggarwal et al., 2014). The

imbalance of M1/M2 phenotypes has been demonstrated to be involved in colitis exacerbation in the murine model of IBD (Zhu et al., 2014). Here, we summarize the stimulators of M1 and M2 macrophages, molecular marker expression, signaling pathways involved, major cytokines and chemokines secreted, as well as their functions in IBD.

In general, classically activated (M1) macrophages are characterized by secreting cytokines such as IL-12, IL-23, IL-1 β , TNF- α , ROS, and RNIs, inducing inflammation and clearing pathogens. In lamina propria of inflamed gut, pro-inflammatory M1 macrophages break down the tight junction proteins, damage the epithelial barrier, and induce epithelial cell apoptosis, leading to excessive inflammation (Cosín-Roger et al., 2013; Steinbach and Plevy, 2014; Lissner et al., 2015). In addition, the M1 subsets are also involved in the induction of T helper 1 cells (Th1) and Th17 responses. The transformation of macrophages into the M1 phenotype involves many key transcription factors, such as Janus kinase/signal transducer and transcription activator 1 (JAK/STAT1) (Hu et al., 2002; Gordon and Martinez, 2010),

TABLE 1 | Different subclasses of M2 macrophage.

Subclass	Stimuli	Cell markers	Chemokines	Cytokines and mediators	Functions
M2a	IL-4, IL-13	Mouse: Arg1, Fizz1, Chi3l3, CD206 Human: CD206, CD163 ^{low} , IL-1R, CD14 ^{low}	CCL13, CCL17, CCL18, CCL22, CCL24	IL-10, Arg1, TGF- β , IGF, Fibronectin	Anti-inflammatory, wound healing, elimination of parasites
M2b	LPS, IC, IL-1 β	Mouse: CD80, CD86, IL-10 ^{high} , IL-12 ^{low} , HLA-DR ^{low} , MHC II Human: CD14 ^{high} , CD80 ^{high} , CD200R ^{low}	CCL1	IL-1, IL-6, IL-10, TNF- α	Th2 activation, immunoregulation, promoting infection, tumor progression
M2c	IL-10, Glucocorticoids, TGF- β	Mouse: Arg1, CD206 Human: CD86 ^{low} , CD163 ^{high} , CD206, TLR1, TLR8	CCL16, CCL18, CXCL13	IL-10, TGF- β , Arg1, MerTK	Anti-inflammatory, tissue remodeling, phagocytosis, immunosuppression
M2d	A2R ligands, LPS, IL-6	Mouse: IL-10 ^{high} , IL-12 ^{low} , TNF- α ^{low} , VEGF Human: VEGF, IL-10, TGF- β	CCL5, CXCL10, CXCL16	IL-10, VEGF, TGF- β	Anti-inflammatory, angiogenesis, tumor progression

A2R, A2 adenosine receptor; Arg-1, arginase-1; CCL, chemokine (C-C motif) ligand; CD, cluster of differentiation; CXCL, chemokine (CX-C motif) ligand; Chi3l3, chitinase 3-like 3 (also known as Ym1); FIZZ1, found in inflammatory zone 1; IC, immune complex; IGF, insulin-like growth factor; LPS, lipopolysaccharide; MerTK, Mer receptor tyrosine kinase; TLR, Toll-like receptor; VEGF, vascular endothelial growth factor.

phosphoinositide 3-kinase (PI3K)/Akt1 (Lu et al., 2017; Vergadi et al., 2017), nuclear factor (NF)- κ B (Oeckinghaus et al., 2011; Zhang et al., 2018), interferon regulatory factor 5 (IRF5) (Chistiakov et al., 2018), and Notch (Xu et al., 2012; Siebel and Lendahl, 2017). On the other hand, sustained M1 phenotype expression has been shown to aggravate the inflammatory response and ultimately cause tissue damage (Figure 2).

On the contrary, alternatively activated (M2) macrophages are usually characterized by upregulated factors such as IL-4, IL-10, mannose receptor C-type 1 (Mrc-1, also known as CD206), CD163, arginase-I, IL-1 receptor antagonist, and stabilin-1, which could prevent excessive inflammation, and promote tissue healing. M2 polarization is mainly induced by transcription factors including STAT6 (Ohmori and Hamilton, 1997; Martinez et al., 2009), PI3K/Akt2 (Lu et al., 2017; Vergadi et al., 2017), IRF4 (Sato et al., 2010; Chistiakov et al., 2018), peroxisome proliferator-activated receptor (PPAR) γ (Bouhelle et al., 2007; Odegaard et al., 2007), and cyclic adenosine monophosphate (cAMP) response element binding protein (Ruffell et al., 2009; Luan et al., 2015). M2 macrophages promote resolving inflammation and remodeling tissue by producing several factors, especially IL-10. Some research has shown that the inhibition of M2 polarization or the synthesis of its cytokines may result in the exacerbation of colitis (Hunter et al., 2010; Zhu et al., 2014). M2 macrophages activate TGF- β by promoting Th2 responses to further promote fibrosis that is intimately involved in tissue remodeling (Murray and Wynn, 2011; Locati et al., 2013; Wynn and Vannella, 2016). In addition, M2 macrophages promote matrix metalloproteinases (MMPs) that control extracellular matrix (ECM) turnover to remove debris, apoptotic cells, and various ECM components, which could help to prevent tissue-damaging M1 macrophage responses (Murray and Wynn, 2011). Moreover, the expression of Arg1, Fizz1, and Ym1 has been shown to decrease inflammatory responses and promote tissue remodeling (Lawrence and Natoli, 2011; Kühl et al., 2015).

According to different stimuli and transcriptional changes, the M2 macrophages could be subdivided into several subsets (M2a, M2b, M2c, and M2d subsets) with distinct pathophysiological characteristics (The details are summarized in Table 1) (Röszer, 2015; Wang et al., 2019; Du et al., 2021). Based on these findings, the importance of macrophage polarization in the progression and prognosis of inflammation is becoming increasingly appreciated (Figure 2).

3.2 Intestinal Macrophages and Gut Microbiota in IBD

Gut commensal microbiota has continuous interaction with epithelial cells, which is essential in shaping the function of intestinal barrier structure (Hayes et al., 2018). The dysbiosis of gut microbiota has been considered as the key of IBD etiopathology (Gilbert et al., 2018). Pathogen/microbial-associated molecular patterns (PAMPs/MAMPs) are microbial signature molecules, which are recognized and attached by the innate intracellular receptors of macrophages. The macrophages present antigens to activate T cells, leading to the production of cytokines, chemokines, and antimicrobial peptides (AMPs) to maintain the integrity of intestinal barrier (Wells et al., 2011). Besides, the recruitment and differentiation of intestinal macrophage also need the crucial mediator of the microbiota, aside from the induction of local cytokines, growth factors, and chemokines (Fiocchi, 2008). A few of studies have shown in germ-free mice or in mice with depletion of microbiota with broad-spectrum antibiotics, could decrease the number of monocyte-derived or tissue-resident macrophages (Bain et al., 2014; Muller et al., 2014; Shaw et al., 2018). The metagenomic sequencing of microbial RNA has revealed that there are significant alterations in microbial composition, location and biodiversity between IBD patients and healthy individuals (Wallace et al., 2014).

For instance, the adherent invasive *E. coli* (AIEC) showed significant increased amount in IBD patients, and it is involved in

IBD pathogenesis through evading the immune system of the host, linking to intestinal epithelial cells, and promoting excessive inflammation (Lloyd-Price et al., 2019). Besides, AIEC is associated with the ability to transverse the intestinal wall into the lamina propria, even survive and replicate within macrophages by escaping autophagy (Palmela et al., 2018). *Campylobacter concisus* (*C. concisus*) is a kind of adherent and invasive proteobacterium, participating in the pathogenesis of IBD (Underwood et al., 2016). Some *C. concisus* strains acquired zonula occludens toxin (zot) gene from a virus (prophage), damaging epithelial tight junctions, inducing macrophage production of undue pro-inflammatory cytokines, such as TNF- α , and ultimately causing the chronic relapse of IBD (Zhang et al., 2014). *Akkermansia muciniphila* (*A. muciniphila*) is a Gram-negative anaerobic bacterium, that revealed protective potential with reduced abundance both in CD and UC (Png et al., 2010). *A. muciniphila* or a specific outer membrane protein Amuc_1100 could improve colitis, with the decreased number of infiltrating macrophages and CD8⁺ cytotoxic T lymphocytes in the gut (Wang et al., 2020). In a word, it is recognized as a crucial challenge to reconstitute the relationship between the host and the microbiome to an effective symbiotic state.

3.3 Macrophage-Derived Exosome

Macrophage-derived exosome has been shown to play an important role in the pathogenesis of inflammatory exacerbation and resolution by interacting with intestinal epithelial cells (IECs) and other cells. Exosome-derived miR-21a-5p from M1 macrophages could be absorbed by IECs, correlated with downregulation of E-cadherin and activation of group 2 innate lymphoid cells, aggravating dextran sulfate sodium (DSS)-induced colitis in mice (Lu et al., 2021a). In addition, the M2 macrophage-derived exosome miR-590-3p targets large tumor suppressor kinase 1 and then activates Yes-associated protein/ β -catenin transcription in IECs, hence reducing colonic inflammation, strengthening mucosal healing, and alleviating DSS-induced colitis in mice (Deng et al., 2021).

4 REGULATION MECHANISM OF MACROPHAGES IN IBD

Generally speaking, as specialized phagocytic cells of the innate immune system, macrophages exhibit multiple functions such as the maintenance of systematic homeostasis, protective defense of the host, and regulation of inflammatory response, as well as re-establishing tissue barriers upon mucosal disruption (You et al., 2016; Dionne et al., 2017). In addition, intestinal macrophages have also been found to secrete various cytokines to maintain tissue homeostasis (Grainger et al., 2017). Here, we summarize the critical regulation mechanisms of macrophages in IBD.

CSF-1. Macrophage colony-stimulating factor 1 (CSF1) is the primary cytokine, which shows a critical role in the survival, proliferation and differentiation of intestinal macrophages. It has been demonstrated that the number of intestinal macrophages

appears significant decrease in Csf1-null mice and these with the administration of anti-CSF1R antibody (MacDonald et al., 2010). Besides, following anti-CSF1R treatment, the depletion of macrophage leads to restraining Paneth cell differentiation, reducing Lrg5⁺ stem cells, and ultimately impairing the development of IECs (Sehgal et al., 2018).

IL-10/IL-10R Axis. The IL-10/IL-10-receptor (IL-10R) axis is crucial in regulating phenotype of intestinal macrophages in both mice and humans. Lack of IL-10 signaling results in macrophage hyper-responsiveness to toll-like receptors (TLRs) stimulation, causing the development of spontaneous intestinal inflammation (Zigmond et al., 2014). Disrupted IL-10/IL-10R axis can affect several regulatory pathways involved in macrophage activation, such as STAT1, STAT3, nuclear factor- κ B (NF- κ B), and TREM-1, as well as increase chromatin accessibility to pro-inflammatory genes (Hirotsu et al., 2005; Schenk et al., 2005; Simon et al., 2016). Besides, macrophage-derived IL-10 has been demonstrated that it is crucial for maintaining and promoting antigen-specific Treg cells in the intestinal mucosa in mice (Hadis et al., 2011).

CX₃CL1-CX₃CR1. The CX₃CL1-CX₃CR1 axis plays a critical role in the differentiation and function of mouse intestinal macrophages, considering that the high expression of CX₃CR1 and their special localization near by the CX₃CL1-positive intestinal epithelial cells. Lack of CX₃CR1 expression of intestinal macrophages leads to the decrease of IL-10 and defect in promoting Treg cells in the lamina propria, which may exacerbate the DSS-induced colitis in mice (Hadis et al., 2011). In patients with CD, a missense mutation in the CX₃CR1 gene was identified, which was related with an impaired antifungal ability and may lead to progression of extra-intestinal inflammatory diseases (Leonardi et al., 2018). In addition, CX₃CR1⁺ macrophages can form transepithelial dendrites (TEDs) with the ability to capture soluble antigens or potential pathogens, and even migrate into the colonic lumen to execute the mission (Rescigno et al., 2001; Vallon-Eberhard et al., 2006).

TGF- β . The TGF- β /TGF- β -receptor (TGF- β R) axis is essential for the terminal differentiation of macrophages in intestinal mucosa, and genetic imprinting of intestinal macrophages in mice, including CX₃CR1, IL-10, and α v β 5 integrin genes (Schridde et al., 2017). In line with this, the expression of the Runt-related transcription factor 3 (RUNX3), which is regulated by TGF- β , is a unique feature of intestinal macrophages (Lavin et al., 2014). In addition, macrophage turnover is regulated by the TGF- β /TGF- β R axis by controlling the expression of CCL8 (Schridde et al., 2017). Besides, efferocytosis produce the secretion of TGF- β by macrophages, restraining the production of pro-inflammatory mediators by a mechanism of autocrine/paracrine way involving TGF- β (Fadok et al., 1998).

5 TARGETING MACROPHAGES FOR IBD

There is a huge driving force for exploring innovative treatment options in IBD, because existing therapeutic strategies remain ineffective in many patients (Papamichael et al., 2015). It has been

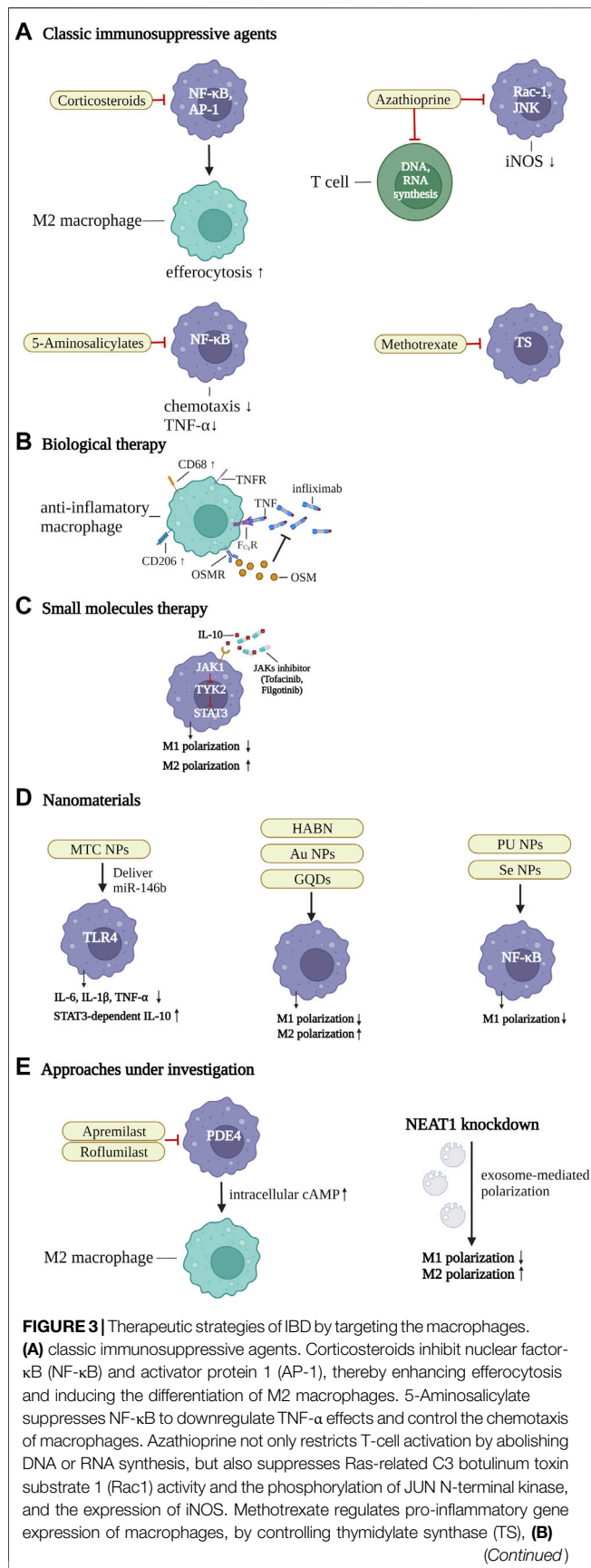


FIGURE 3 | biological therapy. Infliximab blocks TNF and TNF receptor (TNFR)-mediated inflammatory response in intestinal macrophages, by binding with Fc γ receptor (Fc γ R), and inducing CD68⁺CD206⁺ regulatory macrophages. The numbers of oncostatin M (OSM) and the receptor (OSMR- β) are associated with unresponsiveness to TNF- α blockers. **(C)** small molecules. JAK inhibitors inhibit the IL-10-JAK1-tyrosine kinase 2-STAT3 signaling pathway, which is crucial for maintaining mature macrophages in intestinal homeostasis. In addition, they can downregulate M1 and promote the differentiation of M2 macrophages. **(D)** nanomaterials. A series of macrophage targeting nanoparticles (NPs) could be synthesized to deliver specific pathway inhibitors or agonists to control inflammatory-related pathways and promote the polarization of anti-inflammatory macrophages, such as mannose-modified trimethyl chitosan (MTC) NPs, Hyaluronic acid-bilirubin nanomedicine (HABN), gold (Au) NPs, graphene quantum dots (GQDs), polyurethane (PU) NPs, and selenium (Se) NPs. **(E)** approaches under investigation. Apremilast and roflumilast are two new phosphodiesterase 4 (PDE4) blockers. The intracellular cAMP level was increased by inhibition of PDE4, thereby blocking inflammation-related factors and promoting pro-resolving macrophages. Inhibition of the Nuclear Enriched Abundant Transcript 1 (NEAT1), a new nuclear long non-coding RNA, can regulate the intestinal mucosal barrier and induce exosome-mediated differentiation of macrophages. Created with BioRender.com.

shown that modulating the polarization of M2 macrophages or suppressing inflammation-related cytokines could be an innovative therapeutic strategy to regulate intestinal inflammation and restore tissue homeostasis (Na et al., 2019; Du et al., 2021). Modulating the phenotypes of macrophages by inhibiting the pro-inflammatory M1 subset and/or inducing the anti-inflammatory M2 subset, may ameliorate IBD effectively (Ma et al., 2019). It has also been shown that macrophage functions can be affected and modulated by classic IBD agents (such as, infliximab or mesalazine) in many ways, for instance, by downregulating inflammatory signaling pathways and/or skewing to the M2 subpopulation (Bantel et al., 2000; Vos et al., 2012). In the following paragraphs, the current treatment strategies involving macrophages and potential new options to enhance the accumulation of the pro-resolving subpopulation in IBD are summed up in detail (Figure 3).

5.1 Classic Immunosuppressive Agents

Conventional treatment strategies usually rely on modulating the systemic immune responses by mitigating progression of mucosal inflammation. These conventional strategies are mainly based on immunomodulatory medications such as corticosteroids, aminosalicylates, antibiotics, and thiopurines, as well as folic acid antagonists (methotrexate) (Sales-Campos et al., 2015; Chen et al., 2021).

As the central medication for acute exacerbations of IBD patients, both UC and CD, corticosteroids remain the cornerstone of therapeutic options at present (Mowat et al., 2011). Corticosteroids comprise a series of drugs that exerts anti-inflammatory effects by binding to particular cytosolic receptors and suppressing transcription factors, for instance, NF- κ B and activator protein 1 (Oakley and Cidlowski, 2013). Moreover, the activation of immune cells and the production of adhesion molecules are suppressed by corticosteroids in inflamed sites (Sales-Campos et al., 2015; Chen et al., 2021). In addition, corticosteroids have several effects on macrophages, ranging from

enhancing efferocytosis to inducing the polarization of the M2 subpopulation (Giles et al., 2001; Ehrchen et al., 2007). Nevertheless, if corticosteroids are administrated chronically, the occurrence of side effects (e.g., osteoporosis, metabolic disease, cardiovascular syndrome), along with the non-responsive subpopulation, will appear and remain a primary obstruction to sustained remission (Ford et al., 2011; Sales-Campos et al., 2015).

5-Aminosalicylates could control the chemotaxis of macrophages or promote the proliferation of intestinal mucosa cells by downregulating TNF- α effects as well as suppressing NF- κ B signaling pathways directly, which play an integral role in pro-inflammatory macrophages in UC patients (Kaiser et al., 1999; Bantel et al., 2000). In addition, 5-aminosalicylates are often combined with corticosteroids in UC patients to reinforce the anti-inflammatory effects (Allgayer, 2003).

Azathioprine and methotrexate are the other two classic immunosuppressive drugs for IBD (Feagan et al., 2000). They not only restrict T-cell activation by abolishing DNA or RNA synthesis but suppress RAC1 activity *via* binding to 6-thioguanine triphosphates, resulting in anti-inflammatory functions in the mouse model by inhibiting the phosphorylation of JUN N-terminal kinase and the expression of iNOS. (Elion, 1989; Marinković et al., 2014). By controlling thymidylate synthase, methotrexate regulates pro-inflammatory gene expression of macrophages (Municio et al., 2016). Based on the aforementioned evidence, macrophage-modulating strategies play an important role in treating IBD patients.

5.2 Biological Therapy

TNF- α is a pro-inflammatory mediator that can be produced by macrophages and other cells including B cells, T cells, natural killer (NK) cells, dendritic cells (DCs), neutrophils, and epithelial cells (Kany et al., 2019). Macrophages are the major producers of TNF- α and interestingly are also highly responsive to TNF- α (Parameswaran and Patial, 2010). There is increasing evidence reinforcing that TNF- α plays a crucial role in the pathogenesis of IBD (Targan et al., 1997; D'Haens et al., 1999; Rutgeerts et al., 1999). The anti-TNF treatment remains a crucial strategy for IBD patients, given that it has the ability to promote the differentiation of regulatory macrophages (Vos et al., 2012).

TNF- α blockers have been used to prevent TNF- α -mediated intestinal mucosal damage and reduce or terminate the biological effects of TNF- α . Since the anti-TNF agent infliximab was approved by U.S. Food and Drug Administration in 1997, biologics have become the primary medications in the treatment of IBD patients (Stack et al., 1997; Targan et al., 1997). Thalidomide is a TNF- α inhibitor, which has been demonstrated to be effective for inducing remission in pediatric CD and adults with refractory CD (Sabate et al., 2002; Lazzerini et al., 2013). By blocking the production of interferon-regulatory factor-5 (IRF-5), thalidomide significantly inhibits the differentiation of M1 macrophage, with downregulated surfaced markers including CD86 and CCR7, as well as decreased pro-inflammatory cytokines including IL-12 and IFN- γ , that attenuates intestinal inflammation and facilitates mucosal healing (Lu et al., 2021b). Several new anti-

TNF α agents, such as adalimumab, certolizumab pegol, and golimumab, have been applied in clinical research (Danese et al., 2015; Billmeier et al., 2016; Holleran et al., 2017; Chudy-Onwugaje et al., 2019; Na et al., 2019). The ENVISION I study is a phase III double-blind randomized controlled clinical trial (RCT) investigating the clinical efficacy of adalimumab in pediatric patients with moderate-to-severe UC (Croft et al., 2021). After 8 weeks of treatment, the adalimumab group had significantly more frequent clinical remission than the placebo group (adalimumab group vs. placebo group; 60 vs. 19.8%, $p = 0.0001$) (Croft et al., 2021). Therefore, moderate-to-severe UC in children could be efficaciously and safely treated by adalimumab (Croft et al., 2021).

TNF- α inhibitors can specifically bind to receptors to form immune complexes (ICs) to neutralize TNF- α . Once bound to the antibody, TNF- α receptor activation is blocked, leading to decreased permeability of cytomembranes and paracellular tight junctions, as well as blocking the accumulation of inflammatory cells in the local intestinal mucosa (Baert et al., 1999; D'Haens et al., 1999; Rutgeerts et al., 1999; Koch and Nusrat, 2012; Vos et al., 2012; Olesen et al., 2016). In addition, by hindering lipid rafts, infliximab could rebuild equilibrium between the intestinal mucosal barrier and adherent invasive *E. coli* in CD (Yakymenko et al., 2018). In addition, anti-TNF medications could not only reduce the secretion of inflammatory cytokines and infiltration of T cells but also skew monocytes to differentiation into regulatory macrophages (CD68⁺CD206⁺), concurrently (Vos et al., 2012; Olesen et al., 2016). Compared to anti-TNF- α monotherapy, TNF- α inhibitors combined with thiopurines have been demonstrated to promote the differentiation of regulatory macrophages and enhance immunosuppressive efficacy (Vos et al., 2012). However, a majority of IBD patients are intolerant to the therapeutic regimen of anti-TNF α combined with thiopurine, which makes the strategy difficult to carry out (Jharap et al., 2010). Hence, ongoing studies should focus on finding novel alternatives for anti-TNF α combined treatment.

In addition, anti-TNF agents can induce alternative macrophage polarization *via* Fc γ receptor ligation (Lucas et al., 2005; Colombel et al., 2010; Pander et al., 2011; Vos et al., 2011; Vos et al., 2012) and increase IL-10 production of macrophages (Pander et al., 2011; Vos et al., 2011; Levin et al., 2016; Bloemendaal et al., 2017; Koelink et al., 2020). After TNF- α blocker treatment, there was obvious differentiation of the M2 subpopulation in patients with mucosal healing, whereas those without mucosal healing had no such induction (Vos et al., 2012). However, the anti-inflammatory subpopulation cannot be induced by biologics without the Fc fragment, for example, certolizumab pegol, indicating that the research on novel antibody-based strategies may be a broad avenue for IBD therapy (Boyer et al., 2016).

Moreover, the expression of oncostatin M (OSM) is elevated in IBD patients and is associated with unresponsiveness to TNF- α blockers (West et al., 2017). As a member of the IL-6 cytokine family, OSM comprises IL-11, IL-31, and leukemia inhibitory factor (Rose and Bruce, 1991). When the OSM gene was deleted or blocked, experimental colitis was significantly alleviated in

animal models with resistance to TNF- α blockers (West et al., 2017). It's worth noting that OSM aggravates the inflammatory response and damages the intestinal mucosal barrier *via* initiating the expression of cytokines, chemokines, and adhesion factors, which produce large numbers of the receptor (OSMR- β) (Pothoven and Schleimer, 2017; West et al., 2017). Thus, OSM emerges as a novel therapeutic target for IBD patients, especially for those who are non-responsive to TNF- α inhibitors, and it may also promote remodeling of the intestinal tissue.

Even if some protocols of IBD therapy use biologics in an early top-down way in high-risk CD patients, the ineffectiveness of the therapy is still an intractable problem that drives patients to increase dosage of medications or try other therapeutic regimens (Berg et al., 2019; Maronek et al., 2020; Roda et al., 2020). As mentioned above, TNF- α blockers can exert anti-inflammatory effects and remodel the intestinal mucosal barrier by inducing the polarization of M2 macrophages, but further research is needed, especially in unresponsive patients.

5.3 Small Molecules

Janus kinases (JAKs) are non-receptor tyrosine kinases that comprise JAK1, JAK2, JAK3, and tyrosine kinase 2 (TYK2) (Darnell et al., 1994). Once the JAK cytokines bond to the cell-membrane receptors, the signaling transducers with activators of transcription (STATs) are activated, leading to STAT homo-dimerization and activate downstream transcription (Boland and Vermeire, 2017). Cytokines essential for intestinal homeostasis and those that are well-described mediators of pathological responses in IBD are all dependent on JAK/STAT-mediated signaling (Villarino et al., 2017; Paramsothy et al., 2018; Salas et al., 2020). Inhibition of the JAK/STAT pathway results in a decrease in several pro-inflammatory factors, for instance, IL-6, IL-12, and IL-23 (Schwartz et al., 2017). Therefore, JAK inhibitors may represent an emerging option for treating IBD (Na et al., 2019; Salas et al., 2020).

Tofacitinib, an oral pan-JAK blocker, has recently been approved for oral treatment of moderate-to-severe active UC (Kremer et al., 2012; Machado et al., 2018; Tripathi and Feuerstein, 2019; Rogler, 2020). It inhibits JAK1 and JAK3 preferentially, parts of the tyrosine kinase family, modulates cytokine secretion, and controls immunomodulation of IBD (Shivaji et al., 2019; Sandborn et al., 2021). Three phase III trials, with 1,732 patients in total, showed that tofacitinib was more effective efficacy than placebo in inducing and maintaining remission in patients with moderately to severely active UC (Sandborn et al., 2017). However, another two phase II double-blind RCT in CD patients, tofacitinib did not show significant results compared with placebo (Sandborn et al., 2014; Panés et al., 2017). Patients on high steroid dosages, some distinct disease characteristics, and details in research design (e.g., no endoscopic confirmation in center) may explain why the lack of efficacy was observed in CD, as opposed to UC.

Filgotinib, a selective JAK1 inhibitor, has emerged as a potential reliable therapy strategy in IBD patients. A phase II double-blind RCT, the FITZROY study, included patients with

moderate-to-severe CD (Vermeire et al., 2017). After 10 weeks of treatment, patients who were given filgotinib (200 mg, once daily) showed significantly more frequent clinical remission than patients taking placebo (filgotinib group vs. placebo group; 47 vs. 23%, $p = 0.0077$) (Vermeire et al., 2017). Another phase IIb/III double-blind RCT in patients with moderate-to-severe UC, the SELECTION study, showed that filgotinib (200 mg, once daily) was well tolerated and effective in induction and maintenance of clinical remission compared with placebo (Feagan et al., 2021). A number of studies focusing on the efficacy of this JAK inhibitor in CD patients are under way. The Divergence 2 study (NCT03077412), focusing on analyzing the efficacy of filgotinib in the treatment of perianal fistula in CD, has been completed but no results have yet been reported. Another phase III double-blind RCT, The DIVERSITY1 (NCT02914561), will evaluate the effectiveness and safety of filgotinib in induction and maintenance therapy in patients with moderate-to-severe CD groups, who are biologic-naïve and biologic-experienced. In addition, the DIVERSITYLTE trial (NCT02914600), aimed at evaluating the long-term safety in CD patients, is the extension of the DIVERSITY1 study.

JAK blockers could modulate functions of T cells, but also inhibit the IL-10-JAK1-tyrosine kinase 2-STAT3 signaling pathway, which is crucial for maintaining mature macrophages in intestinal homeostasis (Pattison et al., 2012). Interestingly, recent studies have shown that tofacitinib may affect the phenotype of macrophages, which was not investigated in previous related studies (Shiratori et al., 2018; De Vries et al., 2019). Studies have found that tofacitinib can downregulate M1 and promote M2 polarization (CD206, CD163, and IL-10) in murine bone marrow-derived or blood-derived macrophages (Shiratori et al., 2018; De Vries et al., 2019). In UC patients, tofacitinib significantly inhibited the M1 pro-inflammatory pathway, resulting in reduced expression of inflammatory factors; the M2 anti-inflammatory pathway was not affected, such as IL-10 secretion and expression of CD39 and CD206, even though the M2 markers were not upregulated (Cordes et al., 2020).

Targeting multiple pro-inflammatory cytokines, especially the JAK-STAT signaling pathway, may play an important role in novel IBD strategies, especially when patients are unresponsive to current regimens. The therapeutic mechanism of macrophage involvement in JAK blockers, especially in the process of resolving intestinal inflammation, needs to be confirmed in further research. In addition, side effects of JAK blockers are still of concern, such as the threat of thromboembolic events, opportunistic infections, or unknown long-term effects. The potential value of JAK blockers in the treatment of IBD needs to be further evaluated in high-quality and long-term RCTs, based on the risk-benefit ratio criterion.

5.4 Nanomaterials

Traditional medical regimens mainly rely on immunosuppressive agents, which could result in off-target systemic adverse effects and toxic reactions. As an emerging and prospective strategy, nanotechnology could be used for targeted delivery of medications to the inflamed lesions, enhancing local

concentration as well as minimizing systematic adverse effects (Hur et al., 2012; Beloqui et al., 2016; Sohail et al., 2019). It has been shown that macrophage-targeted drug delivery systems can improve drug-delivery efficiency and decrease side effects by making full use of the phagocytic function of macrophages. This strategy has been widely explored in rheumatoid arthritis (Barrera et al., 2000), adiposis (Bu et al., 2013), and malignant tumors such as hepatocellular carcinoma and melanoma (Piaggio et al., 2016).

Intriguingly, macrophage-targeting nanoparticles have been synthesized to deliver inhibitors or agonists of inflammation-related pathways to modulate transition of macrophage phenotype (Singh et al., 2017). Nanomaterials-based therapeutics have shown great promise in the therapy of IBD, because of their useful properties in food and medicine (Cui et al., 2020). For example, miR-146b can be specifically delivered to intestinal macrophages by mannose-modified trimethyl chitosan (MTC)-conjugated nanoparticles (NPs), resulting in remarkable restoration of mucosal barrier function in the mice models (Deng et al., 2019). MTC-NPs can dramatically inhibit the activation of the M1 subset and induce the M2 phenotype by suppressing the TLR4 signaling pathway, thereby inhibiting the secretion of IL-6, IL-1 β , and TNF- α (Deng et al., 2019). Moreover, by producing STAT3-dependent IL-10, the proliferation of co-cultured colonic epithelial cells was significantly increased (Deng et al., 2019). In addition, surface-functionalized polyurethane (PU) NPs showed remarkable immunosuppression of THP-1 macrophages, suppressing the secretion of inflammation-related cytokines in phenotypic M1, controlling the NF- κ B signaling pathways, and ultimately modulating the differentiation of macrophages (Huang et al., 2018; Nakkala et al., 2021). Additionally, oral nanomedicine delivery systems for treating IBD have great promise, because of their expandability, biocompatibility, and potential targeted efficacy. Hyaluronic acid-bilirubin nanomedicine (HABN) is responsive to ROS, accumulating in inflammatory mucosa and remodeling the colonic tissue in experimental colitis. Importantly, HABN showed significant treatment efficacy *via* differentiating pro-inflammatory M1-like subtypes into the M2-like subtypes and elevating the expression of anti-inflammatory phenotypes such as CD3⁺CD4⁺Foxp3⁺ Tregs and CD11b⁺Ly6C⁺Ly6G⁺MHCII⁺ tissue-resident macrophages (Lee Y. et al., 2020; Xiao et al., 2021).

In recent years, metal-based engineered nanomaterials have shown advantageous properties in medicine. A classical case is that gold NPs (AuNPs) can induce M2 macrophage polarization, leading to inhibition of pro-inflammatory cytokines and increasing IL-10, Arg1, and PPAR γ with decreased iNOS (Taratummarat et al., 2018). In addition, lines of evidence have demonstrated that nonmetal-based nanomaterials are capable of regulating macrophage phenotype. For example, graphene quantum dots (GQDs) could effectively alleviate intestinal inflammation and prevent tissue degeneration, *via* suppressing TH1/TH17 polarization (Lee B.-C. et al., 2020). Furthermore, GQDs can not only switch the differentiation of macrophages from pro-inflammatory M1 to anti-inflammatory M2 but also induce infiltration of intestinal Tregs (Lee B.-C. et al., 2020). A similar study also investigated the effect of nonmetal-

based nanomaterials on macrophage polarization by using selenium (Se) (Zhu et al., 2017). Se is an indispensable nutrient and its decreased level may be associated with the exacerbation of IBD (Castro Aguilar-Tablada et al., 2016; Zhu et al., 2017; Ala and Kheyri, 2021). SeNPs have anti-inflammatory activity and low toxicity. Mechanistically, by inhibiting the nuclear translocation of NF- κ B, SeNPs strongly suppressed M1 subsets, leading to alleviation of DSS-induced acute colitis in mice models (Zhu et al., 2017). Nanomaterials could be a promising therapeutic strategy for IBD with great potential in the near future.

5.5 Approaches Under Investigation

Inflammatory events are like a complex cascade, modulated by various cytokines and chemokines. Enhancing the pro-resolving phenotype by pharmacological modulation of the Inflammation-related molecules is of high importance to modulate macrophages in IBD. cAMP plays a key role in the modulation of inflammation-related process. Phosphodiesterase-4 (PDE4) is a critical enzyme, regulating intracellular signaling by controlling cAMP, emerging as a novel therapeutic target. Apremilast and roflumilast are two new PDE4 blockers, introduced as new regulators of intracellular signaling pathways in treating IBD patients (Spadaccini et al., 2017; Sabino et al., 2019). The intracellular cAMP level was upregulated by inhibition of PDE4, thereby blocking inflammation-related factors and increasing secretion of anti-inflammatory proteins (Mazur et al., 2015; Spadaccini et al., 2017). Moreover, a double-blind phase II trial of apremilast in patients with active UC showed significant remission of clinical symptoms, changes in endoscopic features, and decrease in markers of inflammation than in the placebo group (Danese et al., 2020).

Nuclear Enriched Abundant Transcript 1 (NEAT1), a new nuclear long non-coding RNA, anchors on particular nuclear structures and participates in various aspects of the immune process (Liu et al., 2018). It has been demonstrated that suppression of the NEAT1 can regulate the intestinal mucosal barrier and induce exosome-mediated differentiation of macrophages, thereby inhibiting the inflammatory response in IBD (Liu et al., 2018).

Targeting PDE4 or NEAT1 might represent a novel strategy in the future, but more high-quality clinical trials are still required to be carried out.

SUMMARY AND PROSPECT

IBD is a prevalent gastrointestinal inflammatory disease, characterized by chronic and excessive inflammation, alternates states of relapse and remission, and needs for lifelong medical therapy (Hazel and O'Connor, 2020). Therefore, new strategies to prevent inflammatory relapse, tissular damage, and non-responsiveness to medications, are urgently needed.

The infiltration and activation of macrophages can phagocytize pathogens, as well as produce various cytokines under certain circumstances, and cooperate with distinct immune cells in many

aspects of the pathogenesis of IBD. Disequilibrium of macrophage polarization results in the exacerbation of IBD, and the production of particular cytokines and/or chemokines relies on the ratio of the pro-inflammatory M1 and anti-inflammatory M2 subsets. Therefore, targeted therapy of macrophages is a novel option to modulate the immune microenvironment and remodel intestinal tissue.

In recent years, remarkable advances have been achieved in the understanding of intestinal macrophage immunobiology. The advancement of single-cell sequencing technologies and fate-mapping approaches has helped to confirm new subsets and distinct transcriptional profiles of intestinal macrophages (Ginhoux et al., 2010; Yona et al., 2013; Bian et al., 2020). Emerging evidence strongly points to an accumulation in the pro-inflammatory monocyte/macrophage in the chronic relapse and remission in patients with IBD. Therefore, it is very crucial to elucidate the mechanisms of new molecules and signaling pathways that participate in the polarization and increase of pro-resolving macrophages. However, many aspects of intestinal macrophages are still under-investigated, including mechanisms underlying macrophage polarization and heterogeneity, the signaling pathways of macrophage functions, environmental cues regulating phenotypes, and interactions during the process of IBD. For instance, it will be crucial to explore the characteristics of distinct subpopulations of macrophages, particularly the tissue-resident macrophages deriving from the embryo. This will facilitate finding out differences among distinct macrophages, expanding our comprehension of the functions of macrophages. In addition, the identification of microenvironmental factors that modulate phenotypes and functions of intestinal macrophage has helped us to understand their fundamental role in homeostasis and autoimmune disease. Moreover, research on cross-talk of intestinal macrophages, gut microflora, and metabolites will be conducive to decreasing chronic inflammation. It is also crucial that future investigations probe the synergistic mechanisms of cross-talk between macrophages and other immune cells in IBD.

Nanomedicine-based approaches have emerged as novel and targeted therapeutic strategies for IBD, by improving delivery efficiency to the intestinal inflammatory sites (Hua et al., 2015; Giron et al., 2019). Even though potential application of NPs has been broadly investigated in mammalian models *in vitro* or *in vivo*, human studies are still insufficient, and some findings in humans are distinct from the ones observed in murine models to some degree (Nunes et al., 2019). In addition, since the studies of

toxicity and interaction of NPs have been mainly observed in animal models, efficacy in human intestinal cells is not fully applicable. The complexity of NP design and suitable methods for administration are two main difficulties with NPs, which impede the manufacturing process. Up to now, there has been no optimal size range of NPs determined to enable effective delivery to the cells in inflamed sites. In addition, the fate of the NPs after the body's uptake is still unknown, because the majority of the studies have focused on delivery efficiency but not safety of the nanoparticle. Safety issues should be addressed first before moving toward clinical studies. Moreover, evaluation of the effectiveness of drug delivery is also critical. Using non-invasive methods, such as positron emission tomography, to image and trace macrophages in pharmacological responses is a potential option to evaluate the safety and delivery efficacy (Weissleder et al., 2014; Kim et al., 2018; Heo et al., 2019).

Many investigations have explored inventing novel medications and repurposing classical drugs, as well as searching for alternative strategies or improving the existing ones in the effort to eradicate IBD. More efforts are needed to create new strategies for treatment options, incorporating existing therapies, and adjusting the therapeutic schedules to better fit individualized treatment. Hence, future research needs to focus on translating the results from pre-clinical studies to be further explored in clinical trials, ultimately benefiting patients with IBD.

AUTHOR CONTRIBUTIONS

SM contributed significantly to complete manuscript writing. JZ and HL contributed to the constructive discussions. SL and QW contributed to the supervision of the review. All authors read and approved the submitted version.

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Tissue-Resident Innate Immune Cell-Based Therapy: A Cornerstone of Immunotherapy Strategies for Cancer Treatment

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Cancer immunotherapy has led to impressive advances in cancer treatment. Unfortunately, in a high percentage of patients is difficult to consistently restore immune responses to eradicate established tumors. It is well accepted that adaptive immune cells, such as B lymphocytes, CD4⁺ helper T lymphocytes, and CD8⁺ cytotoxic T-lymphocytes (CTLs), are the most effective cells able to eliminate tumors. However, it has been recently reported that innate immune cells, including natural killer cells (NK), dendritic cells (DC), macrophages, myeloid-derived suppressor cells (MDSCs), and innate lymphoid cells (ILCs), represent important contributors to modulating the tumor microenvironment and shaping the adaptive tumor response. In fact, their role as a bridge to adaptive immunity, make them an attractive therapeutic target for cancer treatment. Here, we provide a comprehensive overview of the pleiotropic role of tissue-resident innate immune cells in different tumor contexts. In addition, we discuss how current and future therapeutic approaches targeting innate immune cells sustain the adaptive immune system in order to improve the efficacy of current tumor immunotherapies.

Keywords: innate immune cells, macrophages, innate lymphoid cells (ILC), NK cells, tissue-resident immune cells, cancer, MDSC (myeloid-derived suppressor cell)

1 INTRODUCTION

Cancer is considered a major public health concern worldwide and is characterized by an uncontrolled division of altered cells. The human immune system recognizes tumor cells and induces a protective response to eliminate those cells. However, sustained tumors may protect themselves by developing immune escape mechanisms through multiple soluble and cellular mediators. In the last decades, the deep knowledge of tumorigenesis and the study of the complex interaction between the host and the immune system has been the goal for significant advances in anticancer therapy. Conventional anticancer therapy, such as surgical resection, radiotherapy, and cytotoxic drugs, involves multiple targeting of tumor cells. Though, the tumor tissue microenvironment can present a dysregulated, or weakened immune response which, in turn, uncovers pro-tumor activities favouring tumor expansion and progression (Dhara et al., 2022). Recently, new potential targets have been identified based on immunomodulatory therapies, with the aim to re-establish the host anti-tumoral immune response. Since the effect of cancer

immunotherapy is largely dependent on the status of the immune system in the tumor microenvironment, the choice of therapy and the development of new therapies based on the immune status in the tumor microenvironment would be predicted to be effective (Sambi et al., 2019). Tissue-resident innate immune cells could be found in different human tissues, performing a strategic role at all stages of the immune response, from maintaining homeostasis to responding to infectious challenges to the resolution of inflammation to tissue repair and finally, to initiating antitumor response (Goff and Danforth, 2021). In humans studying immune cells and responses in tissues is challenging, due to the difficult accessibility of tissue-resident innate immune cells, the biggest pieces of knowledge concerning their responses in tissues have been obtained using murine models or studying immune cells drawn from blood (Segura et al., 2010; Gray and Farber, 2022). In recent years thanks to new knowledge obtained from these studies it has emerged that not only adaptive immune cells are the only effective cells able to eliminate tumors, but also innate cells are able to do it. Indeed, it emerged that natural killer cells (NK), dendritic cells (DC), macrophages, Myeloid-derived suppressor cells (MDSC) and innate lymphoid cells (ILCs), represent important contributors to modulating the tumor microenvironment and shaping the adaptive tumor response (Wang et al., 2019b). This review provides an overview of the different types of tissue-resident innate immune cells involved in the suppressor activity of anti-tumor immunity. The deep knowledge of the mechanisms underlying these processes could significantly improve the clinical utility of tissue-resident innate immune cells in cancer and eventually can support the identification of biomarkers for cancer prognosis and the development of novel therapeutic approaches for cancer treatment.

1.1 Tissue-Resident Dendritic Cells in Tumor Immunity

Dendritic cells (DCs) represent a heterogeneous family of immune cells, consisting of various subgroups of specialized antigen-presenting cells, mainly involved in initiating and regulating innate and adaptive immune responses (Wculek et al., 2020). Together with macrophages and B cells, they are considered the three major professional antigen-presenting cells (APCs). DCs play a critical role in promoting immunity by providing immunomodulatory signals, such as the secretion of cytokines and growth factors, but can also promote tolerance by presenting antigens to T cells (Patente et al., 2018; Wculek et al., 2020). They are a sort of sentinel able to collect a broad spectrum of environmental signals or stimuli such as bacterial and viral PAMPs and/or DAMPs, processing an extensive spectrum of specific tissue responses and influencing the immunological outcome, one of the most important, promoting T cell-mediated immunity (Levings et al., 2005; Steinman, 2006). DCs originate in bone marrow from unique precursor CD34⁺ that can differentiate into myeloid (MP) and lymphoid (LP) precursors. The first type of precursor gives rise to monocytes and DC precursors (MDP), which are further differentiated in common DC precursors (CDP), from which finally arise

preclassical DC (pre-cDC) and plasmacytoid DC (pDC). In the last step of differentiation, pre-cDC will give rise to the most represented cDC subpopulations, named cDC1 and cDC2. Regarding the second differentiation way, or else LP, the ontogenic pathway is not completely elucidated, so nowadays we only know that it can give rise to pDC (Geissmann et al., 2010). DCs can be found in practically all tissue, they are a very plastic and dynamic cell population that can change its phenotype based on the tissue microenvironment in which is located. DCs represent the link between innate and adaptive immune responses, without inflammatory stimuli they are in an immature or tolerogenic state contributing to immune tolerance. Immature DCs express low levels of costimulatory molecules such as CD40, CD80, and CD86, besides they can infiltrate the tumor micro-environment performing a preponderant role in beginning antitumor immune response (Ganguly et al., 2013). The biggest knowledge concerning DC subpopulations have been obtained from the studies on murine DCs, mostly due to the wide range of tissue accessibility; unfortunately, the same type of characterization cannot be done for human DCs (Segura et al., 2010). Indeed, almost all studies on human DCs were performed mainly on peripheral blood where, among others, DCs constitute a rare cell population. Initially, DCs have been simply divided according to the cell localization, dividing them into resident lymphoid tissue DCs and migratory non-lymphoid tissue DCs (Haniffa et al., 2013). Nowadays, the development of new technologies, especially single-cell RNAseq, allowed to bring light new characteristics of this very heterogeneous cell population providing more information usable for classification criteria, including phenotypical, functional, and developmental criteria (Heath and Carbone, 2013).

Currently, DCs are divided into at least four wide groups using either functional or phenotypical characteristics. From a phenotypical point of view, all human DCs show a high expression of major histocompatibility complex (MHC) class II molecules (MHC-II) and of CD11c, which are expressed also on other cells, and many other molecules which allow their classification into various subtypes. Conversely, they lack key markers of T cells, B cells, natural killer (NK) cells, granulocytes, and monocytes. DCs subset can be classified into Conventional DC Type 1 (cDC1), Conventional DC Type 2, Plasmacytoid DC (pDC), and Monocyte-derived DCs (moDC), and each subset plays a different role within tumors and during their therapy (Kim et al., 2021).

The cDC1 are characterized by the presence of specific markers surface including thrombin receptor THRM (CD141), the chemokine receptor XCR1, C-type lectin CLEC9A and the cell adhesion molecule CADM1 (homologous of CD8 α /CD103/XCR1 in mice) (Reynolds and Haniffa, 2015). The two mainly transcription factors involved in their generation are BATF3, a basic leucine Zipper ATF-Like Transcription Factor 3 and the IFN-regulatory factor 8 (IRF8). cDC1 are localized especially in peripheral blood and in lymphoid and non-lymphoid tissue, where they are specialized in cross-presentation, realizing the priming of CD8⁺ T cells against extracellular antigens such as bacteria and viruses (Haniffa et al., 2012). Recently, using

different tumor murine models emerged that cDC1 also play a critical role in the induction of the cancer-immune cycle, exercised through the transport of antigens from tumor towards draining lymph nodes, inducing a robust activation/proliferation of CD8⁺ T cells or transfer of antigen to resident myeloid cells (Roberts et al., 2016; Salmon et al., 2016; Gardner et al., 2020). The antitumor immune responses mediated by cDC1s are critical in the mechanism of tumor rejection and responses to immunotherapies, like the immune-checkpoint blockade and adoptive T cell therapy (Kim et al., 2021). In addition, the presence of cDC1 within human melanoma tumors correlated with improved response to anti-PD-1 therapy (Barry et al., 2018) as well as with higher CD8⁺ T cell infiltration into tumors (Binnewies et al., 2019) which is associated with a positive prognosis across multiple tumor types (Fridman et al., 2012). In addition to PD-1/PD-L1 expression, it was also observed clustered expression of TIM-3 on cDC cells within tumors, particularly CD103⁺ cDCs. de Mingo Pulido et al. (2018), have shown that the use of α TIM-3 antibody-induced an increase in cell death within tumors and an improvement in response to chemotherapy, suggesting a key role of TIM-3 as a target for therapy. Recently, Roberts et al. (2016) have shown that anti-tumour activity of migratory cDC1s subtype can be done through the expression of chemokine receptor CCR7; in fact, in mice with cDC1 defective for CCR7, it was observed a loss priming of T cell in lymph nodes area and a lack of antigen hand-off to resident myeloid cells, which led to a failure of immune control with consequential increased tumor growth. Moreover, an analysis of tumour-infiltrating cell populations, isolated by human melanoma biopsies, showed that only CD141⁺ DC expressed a detectable CCR7 on the surface, demonstrating that CCR7 is particularly prominent on CD141⁺ DC in human tumors. In addition, it has been demonstrated that cross-presentation activity by cDC1 is improved by I interferon (IFN) signaling, and cells that lack IFNAR1 (IFN- α/β receptor 1) are unable to perform tumor-specific T cell priming and tumor elimination (Diamond et al., 2011; Fuentes et al., 2011).

The cDC2 are a heterogeneous subset of cells that co-express high levels of CD11c and SIRP α (CD172a) (homologous of CD11b and CD172a in mice) and a range of other markers that are tissue-specific (Shortman and Liu, 2002; Reynolds and Haniffa, 2015; Wculek et al., 2020). The transcriptional factors involved in cDC2 maturation and differentiation are mainly three, ID2 (Inhibitor of DNA binding 2), IRF8 (Interferon Regulatory Factor 8) and IRF4 (Interferon Regulatory Factor 4), which seems to have a preponderant role in CD8(+) dendritic cell differentiation (Rees et al., 1990; Li et al., 2016; Wculek et al., 2020). Using single-cell RNA-seq analysis, Villani and collaborators described two novel cDC1 subpopulations, namely cDC2 and cDC3 that show both the expression of CD11c⁺ but diverged for the expression of other molecular markers, including CD163/CD36 and CD32B (Villani et al., 2017). cDC2 are the dominant DC subset in blood but they are also localized in lymphoid and non-lymphoid tissue, which are involved in the induction of Th1, Th2, and Th17 responses (Haniffa et al., 2013; Haniffa et al., 2012; Segura et al., 2012). Moreover, recent studies

in the literature suggest that cDC2 may be involved in presenting tumor-derived antigens to CD4⁺ T cells, which assist and support CD8⁺ T cells in their antitumor activity. Despite their role in tumorigenesis is still not well known, it emerged that they are effective stimulators of naïve T cell proliferation, required to mount an anti-tumor response (Villani et al., 2017). Besides, Binnewies and collaborators observed, in a murine model of melanoma, that the depletion of regulatory T cells into the tumoral site induced a cDC2 increase activity in eliciting intra-tumoral CD4⁺ T cell responses with subsequent tumor growth control (Villani et al., 2017). Similarly to the mouse model, it was observed an increase of CD4⁺ T in patients that show cDC2 abundance to the detriment of Treg suggests that the combination of high levels of cDC2 and low levels of Treg correlate with better tumor prognosis and with clinical responsiveness to immunotherapy (including anti-PD-1 therapy), though the increase of the levels of CD4⁺ T cell infiltration (Quezada et al., 2006; Balachandran et al., 2011; Wallin et al., 2016). It will be interesting to understand how the Treg may control cDC2 function and influence the anti-tumor CD4⁺ T cells response, both in melanoma and in other tumors (Sato et al., 2005; Binnewies et al., 2019).

Plasmacytoid DC (pDC) are characterized by the absence of CD11c and the expression of CD123 (IL-3R), CD303 (CLEC4C), and CD304 (neuropilin) markers (homologues to CD11c^{int} CD11b⁻ B220⁺ SiglecH⁺ CD317⁺ in mouse) (Dzionek et al., 2000; Collin et al., 2013). They arise in two different ways, directly from LP precursors and indirectly by CDP precursors, through the MP precursor's line. The transcriptional factors that are essential for pDC development belong to the family of E2.2 expressed in both humans and mice (Liu, 2005; Cisse et al., 2008; Cheng et al., 2015). pDCs are a subset of DC specialized in response to viral RNA and DNA infection thus, for this reason, they express very high levels of TLR7 and TLR9, the two toll-like receptors specialized in signal transduction of viral and self-nucleic acids (Lande et al., 2007; Gilliet et al., 2008). The ligation of viral antigens to their TLR7 and TLR9 induces a very strong release of type I interferon (IFN-I) together with other inflammatory cytokines, including IL6 and TNF α (Patente et al., 2018). The role of pDCs in human tumors is less known compared to the other DCs subset and the data in the literature sometimes results controversial. The state of the art of pDCs asserts that they have an inert role in anti-tumor immune responses, but it also emerged that most cancers, including breast cancer (Sisirak et al., 2012), melanoma (Gerlini et al., 2007), and ovarian carcinoma (Labidi-Galy et al., 2011) are highly infiltrated by pDCs (Le Mercier et al., 2013; Kranz et al., 2016). Le Mercier et al. (2013) reported that pDCs infiltrating human primary tumors, represent an important prognostic factor associated with poor outcomes (Treilleux et al., 2004). Other studies reported that pDCs are able to limit tumoral progression, probably through IFN- α secretion (Kranz et al., 2016). Additionally, in tumor sites, it has been identified tumor-associated pDCs (TApDC) that, compared to normal pDCs, express a partially mature phenotype and an altered IFN- α , TNF- α , and IL-6 production, able to induce an

increase in Treg expansion, are associated with tumor progression with a poor overall prognosis (Hartmann et al., 2003; Treilleux et al., 2004; Labidi-Galy et al., 2011). Conversely, it was observed, *in vivo*, that an intra-tumoral injection of a TLR7 ligand led to TAPDC activation displaying a potent curative effect, suggesting that TAPDC could become an efficient therapeutic target (Kranz et al., 2016). Thus, several therapeutic protocols have been developed in cancers to stimulate pDC production of IFN- α . Among these, Imiquimod, a TLR7 agonist, has notably been used in cancer therapy because of its antitumoral action associated with the activation of NF- κ B, which leads to the induction of proinflammatory cytokines such as IFN- α (Schon and Schon, 2008).

Monocyte-derived DCs (moDC) are a particular subset of DCs that differentiate separately from CD14^{hi} monocytes in humans (homologous to Ly6C⁺ in mice), in response to inflammation conditions (Jordan et al., 2020; Wculek et al., 2020). The knowledge acquired in the last years on human DCs was obtained using differentiated monocytes by *in vitro* culture with GM-CSF and IL4 (Sallusto and Lanzavecchia, 2018). The main surface marker of MoDCs overlaps with those expressed in macrophages, cDC2s and other immune cells, including CD1c, CD11b, CD14, CD209, CD172a CD1a, and CCR2 (Guilliams et al., 2014; Wculek et al., 2020). Recently, the evaluation of the Fc receptors Fc γ RI and Fc ϵ RI expression on moDCs allowed a better distinction between subsets, as moDCs express high levels of activating Fc receptors for IgG (Fc γ Rs). Even if the physiological relevance of MoDC is unclear, it was noted that moDCs are produced in response to inflammation-inducing IFN- γ by CD4⁺ T cells promoting Th1 immune response. Phenotypical and functional alterations in moDCs have been identified in patients with different types of cancer, including breast cancer (Ramos et al., 2012) chronic lymphocytic leukemia (Toniolo et al., 2016), chronic myeloid leukemia (Brown et al., 2014), colorectal cancer (Orsini et al., 2013) and cervical neoplasia (Lopes et al., 2017). The most observed phenotypical alteration was reduced levels of specific markers involved in antigen presentation and lymphocytes activation, including HLA-DR, CD80, CD86, and CD83. Besides, phenotypical alterations were related to loss of function in inducing proliferation of both CD4⁺ and CD8⁺ T cells (Toniolo et al., 2016). The peculiarity of the mo-DCs to present the antigens in both MHC class I and class II molecules have been extensively used in the clinic, mostly as vaccines to induce anti-tumor immune responses in cancer patients. In the last decade, the use of DCs is considered a hopeful adjuvant for inducing immunity to cancer and their manipulation could represent a great potential for cancer immunotherapy (Thurner et al., 1999). A series of clinical trials on cancer therapy aimed to promote DCs activation, and consequently T cell priming against tumor antigen through the administration of specific cytokines and or adjuvant, such as FLT3L, GM-CSF and/or agents blocking a series of soluble factors released by cancer cells or specific signaling pathways that contrast DCs maturation (Saito et al., 2008; Merad et al., 2013; Johnson et al., 2018; Kerdidani et al., 2019).

1.2 Tissue-Resident Macrophages in Tumor Immunity

Tissue resident macrophages (TRMs) represent an important cell component of the innate immune system, with a wide distribution in every tissue throughout the body (Epelman et al., 2014b). Despite macrophage's origin being thought to be derived from circulating blood monocytes infiltrating the tissue and differentiating into macrophages, recent literature has demonstrated that macrophage ontology is not that simple (Locati et al., 2020). Several recent pieces of evidence showed that TRMs can have embryonic progenitors, such as liver resident Kupffer cells (KCs), lung alveolar, microglia, splenic, and peritoneal macrophages (Hashimoto et al., 2013; Yona et al., 2013). Interestingly, these cells are fully differentiated before birth and self-renew in a monocytes-independent manner. However, some classes of TRMs, such as adult cardiac and skeletal muscle, derive from yolk-sac, and foetal monocytes progenitors, thus they can be substituted by blood monocytes (Epelman et al., 2014a; Wang et al., 2020). TRMs have a key role in innate immunity, as they represent the first line of defence that our body put in place upon infection with pathogens or microbes. In addition, they function by presenting antigens to T cells thus stimulating T cell response in a different types of disease conditions (Greenhalgh et al., 2018). Furthermore, macrophages maintain tissue homeostasis, by specifically contributing to the clearance of cellular debris (Herzog et al., 2019), tissue repair and remodelling (Bosurgi et al., 2017). In order to exert their functions, macrophages get activated by different stimuli coming from the tissue microenvironment *in vivo* and *in vitro* by a specific cocktail of cytokines. For a better comprehension of macrophages phenotype, Mills and collaborators classified them as classically activated TRMs (M1) and alternatively activated ones (M2) (Mills et al., 2000). While M1 macrophages release proinflammatory cytokines (TNF- α , IL-1 β , IL-6, among others) and produce reactive oxygen species (ROS) to promote inflammation and defend against external pathogens, M2 ones stimulate the secretion of IL-10 and TGF- β to inhibit inflammation and to promote tissue repair and angiogenesis. However, a defined difference between these two classes of macrophages cannot be done, as their polarization can be switched according to the tissue conditions, whether it is in a steady-state or a pathological state. Thus, despite the efforts recently done to characterize M1 and M2 macrophages, a real definition of how TRMs work in physiological conditions is far from being achieved. Given their role within organs, TRMs have an important role during tumorigenesis, as they interact directly with tumor cells during progression and metastasis. Together with monocytes-derived macrophages, they represent the most abundant cells within a tumor, representing an important component of the tumor microenvironment (TME). It has been proposed that almost 50% of the tumor mass is generally represented by tumour-associated macrophages (TAMs) (Poh and Ernst, 2018). Thus, TAMs can have then different origins, although they all exert similar functions even if with different molecular mechanisms. For instance, it has been shown in transgenic mouse models of lung adenocarcinoma that while

monocyte-derived macrophages stimulate tumor dissemination, TRMs are sufficient to induce tumor growth (Loyher et al., 2018). Similar results were obtained in TRMs-depleted transgenic mouse model (Csf1^{op/op}), showing that alveolar macrophages depletion did not affect the dissemination of mammary tumor cells (Qian et al., 2009). However, this is not the case of pancreatic ductal adenocarcinoma (PDAC), where the pro-tumoral role of TRMs and monocyte-derived macrophages seems to be the exact opposite (Zhu et al., 2017c). These observations clearly suggest that the contribution of each macrophage population to tumor progression is strictly correlated with the tissue they reside. On the same lines of evidence, even the response to chemotherapy is different between TRMs and monocyte-derived macrophages, as it might change according to the type of tumor. Indeed, Loyher et al. (2018) elegantly demonstrated that monocyte-derived macrophages recovered faster from cyclophosphamide treatment when compared with TRMs in a transgenic mouse model of lung cancer. TAMs, either monocyte-derived macrophages or TRMs, are associated with tumor progression and poor prognosis, because of their role in controlling tumor survival and resistance to conventional therapies. In particular, different studies support the hypothesis that tumor-promoting macrophages have a M2-like phenotype (Mantovani et al., 2002; Boutilier and Elswa, 2021), while the M1-like one is associated with anti-tumor properties (Noy and Pollard, 2014; Ubil et al., 2018; Wanderley et al., 2018). However, as discussed above for macrophages during homeostasis, macrophage polarization is influenced by cues and stimuli by the microenvironment (Sica and Mantovani, 2012; Najafi et al., 2019; Gunasekaran et al., 2021). For instance, different studies showed that TGF- β increased in hepatocellular carcinomas the expression of TIM-3, an immune checkpoint blockade inhibitor, thus leading to 1) M1 to M2 macrophages polarization, and 2) increased tumor progression and metastatization (Yan et al., 2015). This is a very important aspect, as the induction of an M1-like polarization could be an important therapeutic strategy to generate tumor-suppressive macrophages. TAMs have a pivotal role in defining therapeutic efficiency (Zitvogel et al., 2008; Hughes et al., 2015). For instance, they inhibit T cell response *via* inhibition of cytotoxic CD8⁺ T cells, either by expressing inhibitory immune checkpoint molecules (PD-L1 and PD-L2), blocking antigen presentation or by the secretion of immunosuppressive proteins, such as IL-10, TGF- β , and prostaglandin E₂ (Blumenthal et al., 2001; Munn and Mellor, 2003; Matlack et al., 2006). In addition, they modulate T cell exclusion from the tumor by the activation of MMPs and cathepsins, and by stimulation of fibrotic mechanisms (Nielsen et al., 2016; Zhu et al., 2017c; Quaranta et al., 2018). Interestingly, it has been shown that when TAMs are depleted, cytotoxic CD8⁺ T cells increased their presence in the tumor context, thus improving the therapeutic outcome of the treatments (Denardo et al., 2009; Andreu et al., 2010). Along with inhibition of T cell response, TAMs are also responsible for chemotherapy and radiotherapy resistance and tumor relapse. Recent works demonstrated that standard care of treatment for several tumors determine a release of bioactive factors, such as VCAM1 and CCL2, that are involved in the increased macrophages infiltration in the tumor

microenvironment (Kalbasi et al., 2017; Takahashi et al., 2020). In addition, *in vivo* studies on the prostate cancer model clearly showed that macrophages depletion further improve the docetaxel chemotherapy response by reducing tumor progression (Guan et al., 2019). Furthermore, macrophages induce resistance to chemotherapy by suppressing cancer cell apoptosis *via* release of soluble factors (colon and ovarian cancer model) (Feng et al., 2011; Au Yeung et al., 2016), or by exosomal delivery of miRNA-21 (gastric cancer cells) (Zheng et al., 2017). Finally, TAMs reduce immune checkpoint blockade therapy (ICB) *via* the expression of inhibitory immune checkpoint molecules (PD-L1, PD-L2, and TIM-3), thus blocking T cell response (Thommen et al., 2015; Anfray et al., 2019). For all these reasons, TAMs have been considered an important target in tumor immunity, although preclinical studies, as well as clinical trials, did not define in the past a proper clear-cut on possible therapies aiming at TAMs eradication. Thus, different approaches are currently understudies to target macrophages for anti-cancer therapies. Among others, therapies to deplete macrophages, inhibit monocyte-derived macrophages recruitment, and stimulate TAMs repolarization towards an M1 phenotype are currently under investigation in a preclinical stage, as well as in clinical trials. Macrophages depletion *via* CSF-1R blockade as monotherapy to affect tumor growth, despite the encouraging preliminary data in preclinical studies (Strachan et al., 2013; Quail et al., 2016), did not provide substantial benefits for the treatment of established solid tumors (O'Brien et al., 2021). On the contrary, a combination of tumor resection followed by macrophage depletion did provide a valuable reduction of melanoma recurrence and metastasis (Tham et al., 2015). Thus, combined therapies, along with the identification of the right timing of the treatment itself, might be the path to contrast tumor progression. Different approaches have been described to deplete macrophages, either in normal or tumoral tissues. For instance, liposomes loaded with clodronate have been shown to reduce tumor growth in mouse models of mammary cancer. In addition, its combination with protein kinase inhibitors, such as sorafenib, was able to drastically diminish tumor angiogenesis and metastasis in a hepatocellular carcinoma model (Zhang et al., 2010). Interestingly, different groups successfully attempted to eradicate TAMs using trabectedin, a chemotherapeutic used for the treatment of ovarian cancer and sarcomas. Trabectedin acts by stimulating macrophages apoptosis *via* activation of TRAIL-R2, a death receptor specifically expressed in macrophages (Allavena et al., 2005; Germano et al., 2013; Gordon et al., 2016). Thus, trabectedin is currently under analysis in combined therapies in several clinical trials. TAMs depletion can be obtained also by inhibiting CSF1/CSF-1R signaling axis, *via* monoclonal antibodies or small molecule inhibitors. In addition, targeting macrophages' surface receptors (CD52, CD206, FR- β , among others) is another approach that has been recently taken for the same purpose. In all cases, these attempts result quite encouraging in the preclinical set, and some of them are now in clinical trials in combined chemotherapies for the treatment of lymphomas and chronic lymphocytic leukemia (NCT00069238, NCT01361711, and NCT01030900). Blocking monocyte-derived

macrophages recruitment in the tumor microenvironment is another approach that has been tried to target TAMs. This type of therapy mostly relies on monoclonal antibodies aiming at the inhibition of the interaction between monocyte chemokines and their specific receptors. The most studied signaling axis in this context has been the CCL2/CCR2, as CCR2 is highly expressed in tumors and have been shown to stimulate macrophages recruitment in the tumor microenvironment (Lim et al., 2016). Also, in this case though, while the pre-clinical studies were encouraging, the clinic ones did not provide important results for the treatment of some type of prostate cancers (Pienta et al., 2013). However, the combination with anti-PD-1 immune checkpoint blockade therapy demonstrated quite efficiency for metastasis inhibition of mouse models of bladder and lung cancer (Tu et al., 2020).

Finally, TAMs repolarization towards an M1-phenotype is another valid strategy that has been developed in recent years. Macrophage re-polarization has been obtained with different methods, including treatments with TLR agonists (van Dalen et al., 2018), CSF-1R (Pyonteck et al., 2013) and PI3K γ (Kaneda et al., 2016) inhibition. TLR agonists, including LPS and several lipoproteins, determine the activation of the NF κ B signaling pathway, thus stimulating the production of pro-inflammatory cytokines typical of the M1 phenotype. For instance, Poly:IC, a synthetic molecule mimicking viral dsRNA, binds to TLR3 and induces macrophages polarization and colon cancer arrest. However, TLR agonists result cytotoxic for use in anti-cancer therapies, thus stimulating alternative methods for their *in-situ* delivery. Interestingly, TLR7/8 agonists loaded into nanoparticles induced *in vitro* and *in vivo* polarization of M1-like macrophages in different models of solid tumors, including lung and colon adenocarcinoma (Rodell et al., 2018). CSF-1/CSF-1R axis inhibition, despite being firstly considered a valid strategy for TAM depletion, is now a well-accepted method to repolarize macrophages. An elegant work published in 2013 clearly demonstrated in a glioblastoma multiforme (GBM) tumor model that CSF-1 blockade did not eradicate TAMs, but instead “re-educate” them within the tumor microenvironment by decreasing M2 macrophage gene signature, and at the same time promoting overall survival in patients with GBM (Pyonteck et al., 2013). Furthermore, CSF-1 blockade was found to stimulate TAMs polarization and improved animal survival in mouse models of hepatocellular carcinoma and PDAC (Zhu et al., 2014; Ao et al., 2017). Finally, PI3K γ selective small molecules inhibitors nicely demonstrated their effectiveness in polarizing TAMs in mouse models of PDAC, thus promoting CD8 $^{+}$ T cell infiltration and tumor arrest.

1.3 Tissue-Resident Myeloid-Derived Suppressor Cells in Tumor Immunity

Myeloid-derived suppressor cells (MDSCs) are a heterogeneous group of immature myeloid cells, derived from the bone marrow hematopoietic precursor cells, which constitute one of the main suppressive cell populations of the innate immune system (Veglia et al., 2018). In physiological conditions, immature myeloid cells differentiate into the different innate immune cells, such as

macrophages, granulocytes, and dendritic cells, and migrate to the corresponding tissues, exerting their normal immune functions (Groth et al., 2019). In pathological conditions, such as infectious diseases, cancers or autoimmune disorders, deregulation on myeloid differentiation occurs, which, combined with a persistent stimulation of myelopoiesis, results in the expansion of MDSCs (Consonni et al., 2019; Lim et al., 2020). This deregulated generation and expansion of immunosuppressive MDSCs is promoted by a series of cytokines, such as GM-CSF, VEGF, IL-1 β , IL-6, and IL-10 (Cheng et al., 2021). Significantly increased immature myeloid cells have been observed in the bone marrow and peripheral blood of patients with cancer (Cheng et al., 2021), and the presence of enriched MDSCs have been related to poor prognosis for multiple types of cancer (Jiang et al., 2015; Tian et al., 2015; De Cicco et al., 2020). In fact, throughout the entire pathological process that leads to tumor formation, MDSCs increase up to 10-fold and migrate to the periphery, exerting their suppressor activity interfering with the normal functions of circulating T and other immune cells involved in the anti-tumor immunity (Safarzadeh et al., 2019; Nakamura and Smyth, 2020; Ma et al., 2022). Unlike mice's MDSCs, where these cells have been well characterized, human MDSCs are less clearly defined. Typically, they are described as lineage cells that co-express high levels of CD33 and CD11b surface markers but lack HLA-DR. Human CD33 $^{+}$ CD11b $^{+}$ HLA-DR $^{-}$ MDSCs can also be subdivided in three distinct populations of CD14 $^{+}$ CD15 $^{-}$ monocytic-MDSCs (M-MDSCs), CD15 $^{+}$ CD66b $^{+}$ CD14 $^{-}$ granulocytic-MDSCs (G-MDSCs) and CD14 $^{+}$ CD15 $^{-}$ early-MDSCs (E-MDSCs), which comprised more immature progenitors (Gabrilovich and Nagaraj, 2009; Mandruzzato et al., 2016; Ma et al., 2022) myeloid markers, such as PD-L1, CD40, CD49d, CD80, CD115, and CD124, which all mediate immunosuppression, has also been discovered to describe specific patterns of MDSCs (Gabrilovich and Nagaraj, 2009; Mandruzzato et al., 2016; Ma et al., 2022). Two functional proteins, such as CCAAT/enhancer-binding protein (c/EBP β) and STAT3, which promote generation, differentiation, and expansion of MDSCs, despite are not surface markers, could help to define two different MDSCs subgroups (CD11b $^{+}$ HLA-DR $^{-}$ c/EBP β $^{+}$ and CD33 $^{+}$ HLA-DR $^{-}$ STAT3 $^{+}$) and could provide new diagnostic and therapeutic tools for cancer immunotherapy (Lechner et al., 2011; Wu et al., 2011; Wang et al., 2019a). MDSCs have a key role in accelerating the progression of cancer, by producing a broad range of suppressive factors that prevent immune cells' anti-tumor reactivity (Ma et al., 2022). The main mechanisms by which MDSCs act as immunosuppressive cells are oxidative stress, amino acid consumption, cytokines secretion, cell-cell interaction and exosomes release. MDSCs mediate immunosuppressive effects under oxidative stress, producing reactive oxygen species (ROS), nitric oxide (NO), and reactive nitrogen species (RNS). Increased ROS production induces damages on adaptive immune response by interfering with TCR CD3 ζ expression, which acts on IFN- γ expression, hampering activation, viability and proliferation of T cells (Belikov et al., 2015; Ohl and Tenbrock, 2018; Cheng et al., 2021). MDSCs express nitrogen-oxygen synthase 2 (iNOS). The

upregulated expression of iNOS leads to NO production that suppresses T cell's function by inhibiting JAK3/STAT5 activation (Bingisser et al., 1998) and decreasing MHC class II expression (Harari and Liao, 2004). NO also induce T and NK cell apoptosis in tumor microenvironment through different mechanisms, such as impaired expression of the Bcl-2 family proteins, increased expression of the p53 tumor suppressor protein, damage of mitochondrial functions, DNA fragmentation, and activation of the caspase cascade (Umansky and Schirmacher, 2001). Additionally, in tumor cell aggregation sites enriched with MDSCs, NO reacts with superoxide forming the RNS, namely peroxynitrite, a strong nitrifying agent. It can nitrate tyrosine residues in T cell receptor, inducing reduced IL-2 production with a consequent impaired T cell activation and proliferation (Bentz et al., 2000; Cobbs et al., 2003; Szabo et al., 2007; Gabrilovich et al., 2012; Cheng et al., 2021) (Feng et al., 2018). Besides, peroxynitrite can modify TCR conformational flexibility affecting its interaction with MHC class I molecules, causing the decreased response of cytotoxic CD8 T cells to antigen-specific stimulation (Nagaraj et al., 2007). Additionally, peroxynitrite prevents antitumor infiltration of antigen-specific CD8 T cells by nitration of CCL2 chemokine (Molon et al., 2011). The second MDSCs' immunosuppressive mechanism consists in the exhaustion of some amino acids with a key role in T cell functioning. The high production of arginase-1 (Arg-1) by MDSCs causes L-arginine deficiency in the tumor microenvironment, which either provokes the cell cycle arrest to the G0–G1 phase of T cells (Rodriguez et al., 2007) and the downregulation of TCR expression, inducing T cell dysfunction and tumor escape *in vivo* (Rodriguez et al., 2002). Another essential amino acid for T cell activation is cysteine (Levring et al., 2015). Dendritic cells (DC) and macrophages can import extracellular cysteine and export it in the tumor microenvironment, making this amino acid available for T cell utilization. MDSCs competitively import extracellular cysteine, but, contrary to DC and macrophages, MDSCs are not able to export cysteine, due to the lacked expression of cysteine transporters, preventing T cell activation (Srivastava et al., 2010). The MDSCs overexpression of indoleamine 2, 3-dioxygenase (IDO), an enzyme that, metabolizing tryptophan, has been referred to support immunosuppressive properties of these cells. Tryptophan depletion causes T cell proliferation arrest (Srivastava et al., 2010) and antigen presentation impairment (Fallarino et al., 2006). Besides, highly IDO levels produced by MDSCs promotes the differentiation and expansion of T regulatory (Treg) cells, exacerbating the inhibition of anti-tumor T cells function (Curti et al., 2007). In response to tumor microenvironment, MDSCs acquire the ability to produce multiple immunosuppressive molecules, such as cytokines, chemokines, and growth factors (Lechner et al., 2010). The tumor microenvironment is characterized by high levels of IL-10 and MDSCs are the principal producers of this cytokine (Cheng et al., 2021) IL-10, in turn, strengthens the immunosuppressive ability of MDSCs in a vicious cycle, by upregulating the expression of different immunosuppressive molecules (Xiu et al., 2015; Lamichhane et al., 2017). IL-10 produced by MDSCs induce increased expression of

lymphocyte activation gene 3 (LAG3) and the consequent decreased IL-2, IL-12, and IFN γ secretion by T cells, which hampered their proliferation and anti-tumor activity (Vuk-Pavlovic et al., 2010; Li et al., 2015). As IL-10, increased TGF β production by MDSCs has been reported in various tumor types. TGF β is a potent immune regulator cytokine that can inhibit proliferation, activation, differentiation, and cytotoxic activity of effector T cells (Cheng et al., 2021). This cytokine blocked Th1 differentiation and activation by silencing the expression of TBET and STAT4, which are key transcription factors for the formation of this important subset of anti-tumor T cells (Gorelik et al., 2002). Moreover, acting on Smad3 signaling, TGF β could decrease IL-2 production (McKarns et al., 2004) and downregulated the expression of granzyme B and IFN γ (Zhang and Bevan, 2012). Highly production of IL-10 and TGF β by MDSCs can also lead to the differentiation and expansion of Treg cells, by inducing FoxP3 and CD25 expression on naïve CD4 T cells (Fu et al., 2004; Heo et al., 2010). Besides, MDSCs can produce high levels of some chemokines, such as CCL3, CCL4, and CCL5, which drive CCR5-expressing Treg cells through the tumor microenvironment, supporting the tumor growth (Schlecker et al., 2012). MDSCs could also impair T cell trafficking in tumor-bearing hosts. ADAM17 (a disintegrin and metalloproteinase domain 17) expressed on MDSCs directly cleaves the ectodomain of L-Selectin on T cells to inhibit their homing to tumor sites and peripheral lymph nodes (Li et al., 2021). Other than suppressing anti-tumor immunity, MDSCs can directly promote tumor progression and metastasis by inducing stemness of tumor cells, angiogenesis, and degradation of extracellular matrix (ECM). Many immunosuppressive factors, such as IL-10, TGF β , and IL-6 produced by MDSCs, are able to induce stem cell properties in various tumor cells (Schlegel et al., 2015; Zhu et al., 2017a; Yang et al., 2019). MDSCs produce high levels of VEGF (Shojaei et al., 2009), the most important cytokine involved in angiogenesis, which binding its receptor (VEGFR) on epithelial cells, promoting neo-angiogenesis by activating JAK2/STAT3 pathway. MDSCs also express high levels of VEGFR2, which, activated by VEGF secreted either by tumor cells or by themselves, lead to a vicious cycle that contributes to maintaining MDSCs angiogenic activity (Min et al., 2017). Besides, MDSCs produce matrix metalloproteinases (MMPs) that, degrading the ECM, contribute to tumor metastasis (Zhang et al., 2020). Another mechanism provided by MDSCs to suppress immune response is through cell-to-cell contact. MDSCs constitutively express on their surface molecules involved in the suppression of immune cells. Among these molecules, Fas ligand (Fas-L) is highly expressed by tumor-infiltrating MDSCs and can induce apoptosis of CD8 cytotoxic T cells by activating Fas-Fas-L axis, with a consequent local immune suppression as demonstrated in mice models (Zhu et al., 2017b; Rashid et al., 2021). Besides, MDSCs in tumor microenvironment bear high levels of ligands of negative immune checkpoint regulators, such as PD-L1 and Galectin-9, which respectively binding PD-1 and TIM3, inducing T cell anergy (Cheng et al., 2021). Moreover, it has been reported that MDSCs are able to induce decreased cytotoxicity, reduced IFN γ production and downregulated

expression of NKG2D of NK cells, due to membrane-bound TGF β in a cell-cell contact mode (Li et al., 2009). Additionally, through the cell-to-cell transfer of the metabolite methylglyoxal, MDSCs could paralyze T cells, reducing their anti-tumor activity (Baumann et al., 2020). Finally, MDSCs can also exert their immunosuppressive function by releasing exosomes. Similarly, to parental MDSCs, exosomes secreted from MDSCs contain pro-tumorigenic factors and can play a crucial role in immunosuppression, tumor growth, angiogenesis, invasion, and metastasis by distributing their contents into the tumor milieu. It has been demonstrated that MDSCs-derived exosomes contain matrix metalloproteinases (MMPs) and different cytokines, chemokines, and growth factors (CSF, VEGF, MCP, SDF1 α , TNF α , and IFN γ), which establish a pro-metastatic microenvironment that allows the metastatic progression of tumor cells (Umansky et al., 2016). Moreover, MDSCs-derived exosomes can induce exhaustion and apoptosis of CD8 T cells by either increasing ROS production or inducing the activation of Fas/Fas-ligand pathway (Rashid et al., 2021). Additionally, MDSCs-derived exosomes bearing the membrane-bound PD-L1, could induce the transformation of naïve B cells into B regulatory cells, recently identified as an immunosuppressive cell population (Rosser and Mauri, 2015), thus inhibiting antitumor immune response (Lee-Chang et al., 2019). Finally, some microRNA contained in MDSCs-derived exosomes, such as miR-126a and miR9, promotes tumor angiogenesis by reprogramming endothelial cells (Baroni et al., 2016; Deng et al., 2017). The deep knowledge of the mechanisms by which MDSCs exert their powerful immunosuppressive functions and pro-tumoral activity could help to develop new effective immunotherapeutic strategies for the treatment of tumors or could intensify the effectiveness of tumor treatments already used. For these reasons, several clinical trials targeting MDSCs and their products are ongoing. Among these, the use of monoclonal antibodies (mAb) against immune checkpoints inhibitors seems to improve cancer patients' outcomes, in combination with other anti-cancer therapies. Ipilimumab is a fully humanized mAb that acts blocking CTLA-4. Ipilimumab, alone or in combination with other anti-tumoral treatments, could potentiate the anti-tumor T cell response and could lower the frequency of MDSCs in tumor microenvironment, ameliorating the outcome of patients with different kinds of solid tumors (Hodi et al., 2010; Sade-Feldman et al., 2016; Tobin et al., 2018). Pembrolizumab, a PD-1 blocking mAb, alone or in combination with BL-8040, a CXCR4 antagonist, was approved to treat unresectable or metastatic solid tumors, due to its ability to reduce MDSCs number and increase effector T cell tumor infiltration (Redman et al., 2016; Vachhani and Chen, 2016; Syn et al., 2017; Bockorny et al., 2020). Another target of immunotherapies is the blockade of MDSCs' recruitment into the tumor microenvironment, by the antagonist of some chemokine receptors highly expressed on these cells. A CCR2 antagonist, namely 747, displayed anti-cancer properties and potentiate the efficacy of sorafenib in a model of hepatocellular carcinoma (Yao et al., 2017). Other chemokine receptors antagonists, such as reparixin (anti-CXCR1/2), LY2510924 and ulocuplumab (anti-CXCR4), in association

with chemotherapies agents, have shown significant results in the treatment of different solid tumors (Galsky et al., 2014; Schott et al., 2017; Ghobrial et al., 2020). Another important strategy for cancer treatment is the inhibition of MDSC activation, by inducing the transition of immature MDSCs in mature myeloid cells. All-trans retinoic acid (ATRA) and the active form of vitamin D have been recognized as ideal inducers of MDSCs differentiation and have been used for different types of both hematopoietic and solid tumors (Iclozan et al., 2013; Tobin et al., 2018; Fleet et al., 2020; Makitie et al., 2020). More recently, the use of CSF-1R inhibitors, such as GW-2580, Imatinib, and pexidartinib, due to their ability to inhibit the expansion of MDSCs, have revealed important results in different solid and hematopoietic cancer treatments (Giallongo et al., 2018; Edwards et al., 2019; Wesolowski et al., 2019). Finally, Arg-1 and iNOS, critical factors in MDSC-mediated immunosuppression, are the targets of inhibitor agents (INCB001158 for Arg-1 and L-NMMA for iNOS), which, in combination with immunotherapy or chemotherapy, have shown good results in some solid tumors treatment (Cheng et al., 2021; Chung et al., 2021).

1.4 Tissue-Resident Natural Killer and Natural Killer T Cells in Tumor Immunity

Natural Killer (NK) and Natural Killer T (NKT) cells are lymphocytes of the innate immune system playing pivotal roles in immune surveillance and response against virus-infected and tumor cells. NK and NKT cells share some common phenotypes and function such as the secretion of interleukin-2 (IL-2), interferon- γ (IFN- γ) and tumor necrosis factor α (TNF α) upon interaction with the ligand or antigen (Shimizu et al., 2020). However, they express distinct lineage development, tissue distribution, antigen recognition and regulatory mechanisms in health and cancer (Vivier et al., 2012).

1.4.1 Natural Killer Cells

Human NK cells are commonly divided into two subsets: immune-regulatory cytokine-responsive CD56^{bright}CD16⁻ and cytotoxic CD56^{dim}CD16⁺ with potent IFN- γ , TNF- α , and GM-CSF secretion activity upon stimulation (Cooper et al., 2001). The diatribe of whether CD56^{dim} are a mature form of CD56^{bright} (Romagnani et al., 2007) or a distinct subpopulation originating from a separate lineage is still a matter of debate (Cichocki et al., 2019).

NK cells infiltrate has been found in several types of cancers (Mamessier et al., 2011; Ali et al., 2014). Interestingly CD56^{bright} more efficiently traffic to the TME as they respond to the chemokines produced within the tumor bed. For example, IFN- γ stimulates tumor-infiltrating immune cells to release CXCL9-11, which is known to recruit CD56^{bright} NK cells (Wendel et al., 2008). By contrast, highly cytotoxic CD56^{dim} usually express receptors for chemokines produced at low levels and their traffic within the tumor site is often insufficient (Berahovich et al., 2006). NK cells vary expression of chemokine receptors following cytokine stimulation and therefore the composition of the NK cells in the TME changes accordingly (Pachynski et al., 2012). For example, CD56^{bright} NK

cells respond to IL-15 by upregulating the expression of the chemokine receptor CCR5 and induce migration to the TME. Conversely, the same cytokine inhibits infiltration of cytotoxic CD56^{dim} cells by dampening expression of CXCR4 and CX3CR1 receptors (Sechler et al., 2004). In patients with advanced melanoma, an inverse correlation between the abundance of circulating CD56^{bright} NK cells and patients' survival was found, pointing out a role of these cells in the modulation of cancer response (de Jonge et al., 2019). Likewise, the proportion of CD56^{bright} cells and production of IFN γ have been reported to be significantly lower in patients with prostate cancer than in controls (Koo et al., 2013).

Recently, by single-cell profiling a population of CD56^{bright}CD127⁺CD160⁺CD52⁺ cells, NK0 was identified from human bone marrow and represent the precursors of conventional NK2/CD56^{bright}CD160⁺CD52⁺ cells and NK1/CD56^{dim}Perforin^{high} cells (Crinier et al., 2021). In patients with acute myeloid leukemia, transcriptomic analysis of the bone marrow revealed inhibition of the NK cell effector function and, importantly, patients with a good prognosis exhibited increased levels in the population of CD160⁺ NK cells (Crinier et al., 2021). Differently to T cells, NK cells recognize their target with a mechanism known as “missing self,” where the specificity for a given antigen is dispensable. NK cell function is modulated by a dynamic balance of activating and inhibitory signals and adhesion receptors in response to “altered self” cells such as tumor cells. When the inhibitory receptors do not recognize their target *via* the interaction with “self-identifier” (HLA) molecules, NK cells kill their target (Elliott and Yokoyama, 2011). NK inhibitory receptors are killer cell Ig-like receptors (KIRs) which engage with HLA types A, B or C (Harel-Bellan et al., 1986; Marsh et al., 2003), and NKG2A which binds to the highly conserved HLA-E (Sivori et al., 1996; Islam et al., 2021). More lately, other inhibitory molecules have been added to the list such as CD161, KLRG1, SIGLEC7, SIGLEC9, PD-1, TIGIT, LAG3, and TIM3 (Cozar et al., 2021). Conversely, activation receptors include CD16, NKp30, NKp44, NKp46, NKG2D, NKG2C, and activating KIRs. NK-cell activity is also enhanced by co-receptors like DNAX accessory molecule 1 (DNAM1) (Sanchez-Correa et al., 2012), NKp80 and 2B4 (Freud et al., 2017). For many years, it has been believed that NK cells uniformly recirculate. However, alongside conventional NK (cNK) cells, NK cells resident in the peripheral tissues, termed tissue-resident NK (trNK) cells have been reported in liver, kidney, skin uterus, salivary glands, and adipose tissue (Sojka et al., 2014; Fan and Rudensky, 2016; Sun et al., 2019). These tissue-resident lymphocytes do not recirculate in the blood or lymphatic system and have a distinct phenotype, like for example, the tissue-resident EOMES⁺T-bet⁺CD49a⁺ NK cells in the human liver (Sun et al., 2019). NK cells present immune-regulatory functions as they promote the activation of other innate and adaptive immune cells both by releasing cytokines and chemokines, or through direct cell–cell contact (Vivier et al., 2011). NK cells shape adaptive immune responses through the cross-talk with other cells such as T cells, B cells, and dendritic cells (DCs) (Malmberg et al., 2017). By inducing maturation of DC, NK cells trigger T cells mediated response; by producing

IFN- γ , NK cells promote Th1 polarization (Moretta et al., 2008). Additionally, it has been proposed that NK cells can increase the function of cytotoxic CD8⁺ T cells by suppressing their state of exhaustion (Zheng et al., 2016) and, importantly, NK cell play a fundamental role in checkpoint blockade therapy by exacerbating antitumor or antiviral function of CD8⁺ T cells (Zhang et al., 2018). NK cells rapidly kill newly arising tumors or metastases, but their anti-tumor potency is less efficient against established solid formations. This is the result of the many strategies developed by tumors to escape immune surveillance, accompanied by a scarce capacity of NK cell to infiltrate the tumor site, as they tend to accumulate at the margins (Platonova et al., 2011). The tumor microenvironment (TME) is hostile to immune cells. NK cell effector function is limited by mechanisms of defense such as hypoxia, where tumor cells release abundant H2O2, thus limiting infiltration of CD56^{bright} NK cells (Izawa et al., 2011; Terrén et al., 2019). Additionally, excessive production of the metabolic enzyme Indoleamine 2, 3-dioxygenase 1 (IDO1) causes immunosuppression and NK and T-cell (Pietra et al., 2012). Likewise, Prostaglandin-E2 (PGE2) produced by cancer cells decreases NK-cell cytotoxicity (Galland et al., 2017). Additionally, tumor cells directly inhibit the expression of NK cell markers such as NKp30, NKp44, NKp46, and NKG2D by releasing soluble factors such as TGF β (Lee et al., 2004; Sconocchia et al., 2012; Close et al., 2020). NK cells show impaired cytotoxic function hampered by cancer cells and upregulation of inhibitory receptors like NKG2A (Mamessier et al., 2011). The TME is also populated by different cell types that orchestrate suppression of the anti-tumor immune response. These include stromal cells, regulatory T cells (Treg), fibroblasts and myeloid-derived suppressor cells (MDSC). Inhibition of CD8⁺ T and NK cells is exerted by cell-to-cell contact or *via* release of TGF β and IL10 or production of nitric oxide (Ghiringhelli et al., 2005). The TME negatively influences NK cell immune response. The phenotype, metabolism and function of intra-tumor NK cells dynamically change during the different stages of tumor occurrence and progression (Liu et al., 2021). In the early stages of breast cancer development, NK cells have cytotoxic functions, which are lost at a later phase, thus promoting tumor progression. NK cells have impaired functions and are exhausted in advanced cancers and are characterized by increased glucose and lipid metabolism (Liu et al., 2021). Downregulation of cytotoxicity genes was reported in biopsies of chemotherapy-resistant breast cancer samples by microarray expression assay (Garcia-Chagollan et al., 2018). In gastric cancer, the overall phenotype of NK cells did not differ between the population of circulating and infiltrating NK cells. What was reported, however, was impaired function in tumor infiltrating NK cells, with reduced IFN γ , TNF α , and proliferation (Peng et al., 2017). Likewise, in HCC tissues, a population of tumor infiltrating CD11b⁺CD27⁺ double negative NK cells was found to be characterized by poor effector functions and cytokine release (Zhang et al., 2017). In the TME, prolonged exposure to NKG2D ligands is associated with a reduction NKG2D expression, which causes NK cell function impairment and evasion of immune surveillance (Thompson et al., 2017). For example, in ovarian cancer, a reduction of the membrane-bound

MICA/B proteins has been underpinned as an immune escape strategy adopted by tumor cells. MICA/B molecules bind to the receptor NKG2D which is expressed by NK cells, but also $\gamma\delta^+$ and $CD8^+$ T cells (Xie et al., 2014). NKG2D engagement corresponds to the inhibition of NK cell cytotoxic function and tumor progression (Xie et al., 2014). The metalloproteinases ADAM 10 and 17 are expressed by tumor cells and are implicated in immune surveillance escape. These mediate the shedding of B7-H6, ligand of NKP30. Increases of the B7-H6 in its soluble form determine drop in NKP30 expression and loss of NK effector function in different cancers (Schlecker et al., 2014; Pesce et al., 2015; Semeraro et al., 2015; Mantovani et al., 2019). PD-1 is an exhaustion marker on both T cells and NK cells (Liu et al., 2017b; Pesce et al., 2017). Importantly, NK mediated tumor response can be restored by blocking the immune checkpoint PD-1/PD-L1 axes (Liu et al., 2017b). Additionally to PD1, co-expression of a second exhaustion marker like TIM-3 has been associated to impaired NK cell function in many cancers, with reduced release of Granzyme B and IFN- γ and inhibited cytotoxicity (Seo et al., 2017). An interesting immune checkpoint is represented by the inhibitory receptor NKG2A. Its ligand, HLA-E is expressed by many different tumor cells (Zhen et al., 2013; Sun et al., 2017). Blockade of NKG2A/HLA-E axes with the antibody Monalizumab, for example, has proofed to unlock both NK cell and T cells function and corroborate anti-tumor immunity (André et al., 2018). Several studies have tried to unravel the role of NK cells in tumor immunity highlighting discrepancies mainly based on the type of tumor (Rezaeifard et al., 2021). Divergent results on the rate of NK cells infiltration in solid tumors have highlighted the urge to find reliable markers to address this question. The NK Cells Receptor (NCR) NKP46 has been recently identified as a robust biomarker to quantify tumor-infiltrating NK cells (Cózar et al., 2021). Although NK cells seem to reach the tumor bed to a lesser extent than other lymphocytes such as $CD4^+$ and $CD8^+$ T cells, their presence within the tumor correlates with a higher survival rate, as reported in head and neck squamous cell carcinoma (Weil et al., 2017; Concha-Benavente et al., 2018), colorectal cancer (Sconocchia et al., 2014), prostate tumor (Izawa et al., 2011) in gastric and esophageal cancers (Lorenzo-Herrero et al., 2019) and metastatic melanoma (Cursons et al., 2019b). Patients with metastatic skin melanoma showed better survival rates if infiltrating NK cells were detected in the tumor biopsies (Cursons et al., 2019a). Moreover, increased numbers of NK cells were correlated with a better response to anti-PD-1 immunotherapy and with an accumulation of pro-active DCs with a protective anti-cancer role at the tumor site (Barry et al., 2018). By contrast, the opposite has also been reported with inverse correlation between the advance stages of cancer and NK cells infiltrating the tumor (Vgenopoulou et al., 2003) or accumulating into the lymph nodes draining the tumor (Rezaeifard et al., 2019). Recently, a subset of $CD49a^+Eomes^+$ NK cells with known proangiogenic function has been described to accumulate at the site of liver tumor. This population has impaired cytotoxic function and reduced TNF- α release, strongly suggesting a pro-oncogenic activity in HCC (Zecca et al., 2021). NK cell infiltrate has been described in metastases, solid tumors

and lymph nodes draining the tumor (Gulubova et al., 2009; Ali et al., 2014; Carrega et al., 2014). However, the extent of NK cell infiltration in the tumor greatly depends on the nature of the tumor and its localization. Some organs are more easily reached by NK cells such as the lungs, liver and kidney, while the intestinal tract appear to be less permissive (Remark et al., 2013). That said, high infiltration rate does not solely correlate with good prognostic factors. Expression of specific activating markers on NK cell surface represent a biomarker for more accurate prognosis (Schleypen et al., 2006), as described for the HLA-E receptor NKG2A and the activating marker NKG2C in endometrial cancer (Versluis et al., 2017). Tumor infiltrating NK and T cells represent a therapeutic target to tackle tumor. NK cells express the marker CD161, regulated by the gene KLRB1. CD161 expression orchestrates NK cell cytotoxic function in several cancers (Cheng et al., 2022). A good prognosis rate is observed in those cancer patients where KLRB1 is highly upregulated as infiltration of immune cells at tumor site and sensitivity to chemotherapy is KLRB1-dependent in many cancer types (Cheng et al., 2022). Nectar Therapeutics is developing an engineered IL-2 cytokine for the treatment of solid tumors. NKTR-214 is designed to sustain growth and survival of specific cancer-killing T cells and NK cells that specifically recognize a tumor target by targeting tumor infiltrating cells lymphocytes by binding to the CD122 receptor expressed by effector $CD8^+$ T cells and NK cells (Bentebibel et al., 2019). However, it has also been reported that this effect is still partial, since a portion of the patients enrolled in the study displayed a proliferation of T_{reg} cells (Sullivan, 2019).

The efficacy of this cytokine has been tested in clinical trial also in combination with checkpoint inhibitor anti-PD1 demonstrating efficacy and safety in the treatment of solid tumor like melanoma, renal cell carcinoma, and non-small cell lung cancer (Diab et al., 2020). In Soft Tissue Sarcoma (STS), compared to circulating cells, intra-tumoral NK and T cells have upregulated TIGIT, a marker of exhaustion. TIGIT+ lymphocytes are considered prognostic in STS and recently it has been proposed that TIGIT blockade may be a promising clinical strategy in STS (Judge et al., 2020). Similarly, in colon tumor biopsies, tumor-infiltrating NK cells have increased levels of TIGIT expression than circulating NK, suggesting an exhausted phenotype (Zhang et al., 2018). Finally, CD155 is the ligand of both activating receptor DNAM1 and inhibitory ligand TIGIT and is expressed in many types of cancer. DNAM1 engagement with CD155 is associated to inhibition of NK cell function (Nakai et al., 2010; Li et al., 2020). NK cells participate to response to tumors and represent potential targets for cancer immunotherapy. However, the TME negatively affects NK cell function, phenotype, survival, and rate of infiltration as a mechanism of escape. This inactivation can be however reverted by using immune checkpoints inhibitors specific, for instance, for NKG2A and TIGIT, already used in clinical trials (Galot et al., 2021). Alternatively, some studies have addressed mechanisms to increase NK cell infiltration at the tumor bed by neutralizing soluble factors that suppress NK cells function such as TGF β , already entered in clinical trials also in combination with anti-PD1 (Dodagatta-Marri et al., 2019).

1.4.2 Natural Killer T Cells

Unlike conventional T cells, NKT cells recognize lipid antigens in a CD1d-dependent or independent manner (Vivier et al., 2012). CD1d⁺ NKT cells are divided into Type I or Type II NKT cells. Type I NKT cells are also known as invariant-NKT (iNKT) cells and express the invariant Va14Ja18 TCR in mouse or Va24Ja18 in human. This TCR recognize α -Galactosylceramide (α -GalCer) lipid antigen (Terabe and Berzofsky, 2008). Human iNKT cells develop within the thymus and can be subdivided into functional subsets based on their expression of CD4 and CD8 into CD4⁺ iNKT cells, CD8⁺ iNKT cells, and DN iNKT cells (Lee et al., 2002). The DN and CD8⁺ iNKT cells have increased IFN- γ secretion and cytotoxic function upon activation while CD4⁺ iNKT cells have a pronounced helper function with release of type 2 (Th2) cytokines, such as IL-4 and IL-13 (Lee et al., 2002). In common with NK cells, human NKT cells express markers such as 2B4, NKG2D, DNAM-1, CD94, and NKG2A (Shimizu et al., 2020).

Frequency and function of intratumor or circulating iNKT cells have been assumed to correlate with overall survival in several types of cancers (Yanagisawa et al., 2002; Fujii et al., 2003; Tachibana et al., 2005; Schneiders et al., 2012), thus implying a role for iNKT cells in tumor immune surveillance. In details, reduced iNKT-cell numbers correlated with poor overall survival in head and neck squamous cell carcinoma (Molling et al., 2007) and acute myeloid leukemia (Najera Chuc et al., 2012). Conversely, increased numbers of intratumor or circulating iNKT cells have been associated with improved prognosis in colon cancer, prostate cancer, hematologic malignancies, and neuroblastoma (Metelitsa et al., 2004; Tachibana et al., 2005; Shaulov et al., 2008).

Human iNKT cytotoxicity cells against target cells may occur *via* TCR-dependent or independent signaling. During immune-surveillance, activation of iNKT cells can occur indirectly by cross-presentation of tumor lipids by APCs (Wu et al., 2003). Sialylated glycolipids on tumor cell membranes may become targets for iNKT cells and during tumor progression might be modified, representing a mechanism of immune surveillance escape. Several types of tumors, such as melanoma, small-cell lung cancer (SCLC), sarcoma, and neuroblastoma, highly express some gangliosides in comparison with corresponding normal tissue (Lo et al., 2010). These gangliosides might activate both CD4⁺CD8⁻ iNKT and CD4⁻CD8⁻ iNKT cells to produce IL-4 (Wu et al., 2003) and, acting as NKT cell ligands, might be related to prognosis in some cancers.

Activation of iNKT cells can also occur directly, *via* presentation of self-lipids by CD1d-positive tumors. CD1d expression has been found on solid tumors, such as prostate cancer (Tahir et al., 2001; Nowak et al., 2010), renal cell carcinoma (Chong et al., 2015), breast cancer (Hix et al., 2011), and tumors of the nervous system (Dhodapkar et al., 2004; Liu et al., 2013). For instance, in myeloma patients the frequency of iNKT cells in PBMCs are inversely correlated with disease progression (Dhodapkar et al., 2003; Jiang et al., 2018). This is due to the fact that primary myeloma cells express CD1d (Dhodapkar et al., 2003); however, its expression decreases in advanced stage cancer cells (Spanoudakis et al., 2009).

Furthermore, human iNKT cells have been reported to kill CD1d⁺ osteosarcoma cells, but not CD1d⁻ osteoblasts, confirming the CD1d restriction of iNKT cell-dependent cytotoxicity (Fallarini et al., 2012).

Interestingly, iNKT cells from cancer patients are not impaired; rather they are in an anergic state as they can be expanded and activated by stimulation with DCs loaded with α -GalCer, thus pointing out iNKT cells as potential target for anti-cancer therapy (Iyoda et al., 2018). In myeloid leukemia patients, for instance, purified PBMCs-derived iNKT cells are responsive to stimulation with α -GalCer/CD1d-tetramer with production of IFN- γ , TNF- α , IL-2, and IL-4 and cytotoxic against autologous leukemic cells, that are CD1d⁺ (Metelitsa et al., 2003).

iNKT cells have the capacity to alter the immune tumor microenvironment thus influencing the ability of the host to limit growth of cancer cells. iNKT cells thus represent a population to be harnessed for the development of anticancer clinical therapeutics. Indeed, the identification of strong cell agonists, such as α -GalCer and its analogues, has led to the production of synthetic lipids that have shown potential in cancer vaccination and treatment (McEwen-Smith et al., 2015). Some approaches include using nanovectors/nanoparticle-based delivery systems (Ghinnagow et al., 2017) or α -GalCer loaded exosomes (Liu et al., 2017a). Moreover, vaccination with DCs pulsed with α -Gal-Cer with the aim to expand and activate iNKT cells in human cancer patients is also being evaluated (Richter et al., 2013; Shimizu et al., 2013).

To conclude, successful therapeutic treatments should aim at increasing the rate of tumor infiltrating NK and iNKT cells and rescuing their effector function.

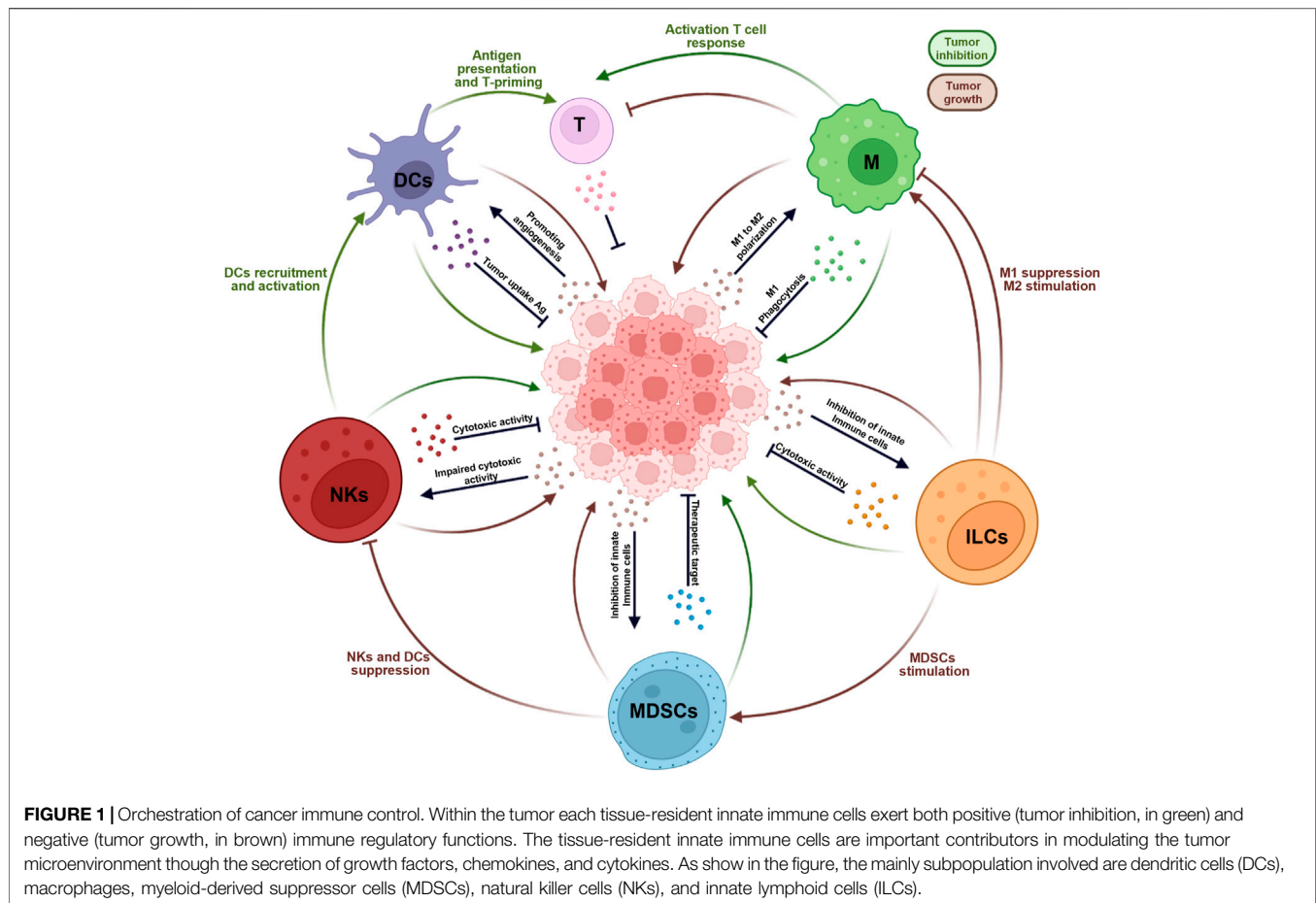
1.5 Tissue-Resident Innate Lymphoid Cells in Tumor Immunity

Although NK cells are defined as the prototypical innate lymphocyte population, over the past decade, innate lymphoid cells (ILCs) have expanded the definition of innate immune cells. ILCs are mainly located in barrier tissues including skin, intestine and lung and are involved in multiple physiological and pathophysiological processes (Mjosberg and Spits, 2016). Human ILCs are identified as Lineage⁻, CD127⁺ cells since they lack the expression of classical lymphocyte surface markers, the recombination activating gene (RAG)-rearranged antigen receptors and other surface molecules whilst express the CD127 (also known as IL-7 receptor). The lineage markers for ILCs identification in human include: CD3, CD4, CD8, CD14, CD15, CD16, CD19, CD20, CD33, CD34, CD203c, and Fc ϵ RI in order to exclude macrophages, dendritic cells, red blood cells, T, B, and NK cells (Trabanelli et al., 2018). Likewise, mouse ILCs are identified as Lin⁻, CD127⁺, CD90⁺ where the lineage mix consists of: CD3 ϵ , CD5, CD8 α , CD11c, CD11b, CD19, B220, Fc ϵ RI, TCR $\alpha\beta$, TCR $\gamma\delta$, DX5, and Ter119 (Gomez-Cadena et al., 2020). ILCs are defined as the innate counterpart of T lymphocytes subpopulations. In fact, similarly to Th1, Th2, and Th17 cells, ILCs are classified in ILC1, ILC2, and ILC3 cells mirroring the expression of transcription factors and the cytokine secretion of their adaptive counterpart (Ercolano et al.,

2020b). In particular, ILC1s express T-bet and produce IFN- γ and TNF- α , ILC2s express GATA-3 and secrete IL-4, IL-5, and IL-13 and ILC3s express ROR γ t and secreting IL-17A and/or IL-22. In the human peripheral circulation, ILC3s also comprise a population of progenitor cells (referred as ILCPs) able to differentiate into all ILC subsets and natural killer (NK) cells (Lim et al., 2017). In addition, has been recently reported that ILCPs, thanks to the expression of CD62L are able to migrate to the lymph node (Bar-Ephraim et al., 2019). As tissue-resident cells, ILCs establish close interaction with other cells in the tissues contributing to the first-line defense against different threats shaping both innate and adaptive immune response by producing their prototypic, subset specific cytokine sets. The impact of ILCs in different diseases including allergy, asthma, rheumatoid arthritis, and inflammatory bowel disease, has been widely described during the last years (Pasha et al., 2019; Wu and Shen, 2020; Ercolano et al., 2022; Trabanelli et al., 2022). Nevertheless, our group and others reported a controversial role of ILCs in cancer showing both pro and anti-tumor effects according to the tumor type and the consequent cytokines and other cells that constitute the tumor microenvironment (TME) (Ercolano et al., 2019; Ghaedi and Ohashi, 2020; Jacquelot et al., 2022). Given their ability to secrete IFN- γ and TNF- α and the expression of the natural cytotoxicity receptor (NCR) NKP46, ILC1s are often teamed to NK cells and difficult to discriminate in both human and mouse (Zhang and Huang, 2017). However, at steady state these two subsets can be distinguished according to the expression of the transcription factors Tbet and Eomes (Daussy et al., 2014; Klose et al., 2014). In addition, unlike NK cells, ILC1s show a weak cytotoxic capacity due to their poor ability to secrete granzyme B and perforin (Vivier et al., 2018). Nevertheless, recent findings based on single-cell RNA sequencing and flow cytometric analysis identified an ILC1 subset with cytotoxic ability in the liver (Di Censo et al., 2021; Friedrich et al., 2021; Chen et al., 2022). Different data demonstrated that these two populations differ in both their development and distribution. In fact, while ILC1s are predominantly tissue-resident cells, NK cells are found mostly in the bloodstream and within secondary lymphoid tissues (Gao et al., 2017). Nevertheless, has been demonstrated that, under pathological conditions, including tumor development and metastasis, NK cells can acquire an ILC1-like phenotype. In particular, in a murine model of fibrosarcoma and melanoma, has been shown that NK cells were converted in ILC1s limiting the NK cell-mediated tumor immunosurveillance (Gao et al., 2017). TGF- β resulted to be the principal mediator involved in this switching of NK phenotype suggesting that the use of antibodies targeting TGF- β and its receptors may offer a promising strategy for cancer immunotherapy inhibiting the conversion of NK cells into ILC1s. In line with these findings, Salome et al. (2019) described an uncommon population of ILC1-like cells population with cytotoxic properties which were impaired in human acute myeloid leukemia (AML) by TGF- β and AhR ligands. Together with TGF- β , different cytokines present in the TME can modulate both the pro- and anti-tumoral effect of ILC1s. For instance, an IL-15 rich environment promotes the generation of a tissue-resident

ILC1-like cells, characterized by a powerful cytotoxic activity towards cancer cells as demonstrated by using a MMTV-PyMT (PyMT) mammary tumor model (Dadi et al., 2016). Likewise, high levels of IL-15 have been observed in human colorectal cancer (CRC) biopsies, as well as high expression of T-bet and IFN- γ supporting the anti-tumoral role of ILC1s in this context (Mlecnik et al., 2014). In human melanoma, our own group reported an increase in the frequency of ILC1s in both peripheral blood mononuclear cells (PBMC) and tumor-infiltrated lymph nodes (TILN) of melanoma patients compared to healthy donors. Nevertheless, ILC1s from melanoma patients were functionally impaired as demonstrated by the reduced secretion of IFN- γ . By dissecting the different mediators present in the TME, we focused on adenosine and indoleamine. In fact, it is widely known that these two mediators are highly expressed in cancer and play a key role in the progression of melanoma and other types of cancer (Vijayan et al., 2017; Jennings et al., 2021). In particular, we observed that these two mediators are involved in ILC1 exhaustion leading to a reduction in type-1 cytokine secretion (Ercolano et al., 2020a). This effect was reverted by using an adenosine receptors inhibitor showing new evidence to sustain blocking these immunosuppressive pathways in melanoma patients by targeting the innate lymphoid cells arm.

ILC2s are assigned as a primarily pro-tumorigenic subset given their ability to produce type-2 cytokines, such as IL-13 and IL-5, and other immunosuppressive mediators. Different studies reported a higher frequency of tumor-infiltrating ILC2 in gastric, breast and prostate cancer. Particularly, in a first work published by Jovanovic et al. (2014), has been reported an increase of ILC2-derived IL-13 *in vivo* by using the 4T1 syngeneic murine model. Next, Salimi et al. (2018), observed an increase of ILC2s and investigated on the expression of different activatory and inhibitory receptors in tumor-infiltrating ILCs in both human breast and gastric cancer. Similarly, Trabanelli et al. (2017), found an enrichment of ILC2s in prostate cancer patients which was correlated with tumor stage and myeloid derived suppressor cells (MDSCs) frequency. Increased numbers of ILC2 have been showed also in the tumors of gastric cancer patients infected with *Helicobacter pylori* (Li et al., 2017). Furthermore, very recently, has been reported a link between ILC2 and tuft cells (a rare population of epithelial cells present at the gastrointestinal and respiratory tract). In particular, the tuft cells/ILC2 axis seems to be involved in the development of gastric cancer as demonstrated by using a murine model of intestinal metaplasia. This result was also confirmed in tumor microarrays of intestinal-type gastric cancer patients showing a unique correlation for tuft cells, ILC2s and survival in intestinal-type gastric cancer. IL-25 and IL-13 play a key role in dictating the crosstalk between tuft cells and ILC2s, in fact, the treatment with either α -IL13 or α -IL25 neutralizing antibodies significantly restrained tumor growth which coincided with a reduced frequency of both tuft cells and ILC2s in mice (O'Keefe et al., 2022). The pro- and anti-tumoral role of ILC2s is frequently associated with the overexpression of various cytokines involved in their activation including IL-33, IL-25, and TSLP commonly defined as "alarmins" (Roan et al., 2019). Our group recently



demonstrated that IL-33 is highly expressed in tissues as well as in the serum of CRC patients. The high presence of IL-33 didn't affect the frequency of ILC2s but increased their activity in terms of IL-13 and IL-5 production which in turn sustains CRC progression through the modulation of the epithelial-to-mesenchymal transition (EMT) phenomenon (Ercolano et al., 2021). Conversely, it has been recently reported that in pancreatic adenocarcinoma, IL-33 induces ILC2 expansion that was accompanied by enhanced intratumoral CD8⁺ T cells pushing tissue-specific tumor immunity (Moral et al., 2020). Interestingly, they also reported that tumor-infiltrated ILC2s express the inhibitory checkpoint receptor PD-1 hypothesizing that PD-1 blockade could further boost ILC2 activation to enhance anti-tumor efficacy. In line with these findings, (Jacquelot et al., 2021a) demonstrated that PD-1 blockade increased ILC2 and eosinophil recruitment and enhanced anti-tumor responses in melanoma context (Jacquelot et al., 2021b). These findings suggest the need to further dissect investigation on the broad array of checkpoint inhibitors as target for ILC2 in cancer immunotherapy.

The role of ILC3s in cancer is emerging as complex and highly dependent on the tumor type as also described for their adaptive counterpart (Bruchard and Ghiringhelli, 2019). In fact, similarly to Th17 cells, ILC3s exert both pro- and anti-tumor functions showing different phenotypes according to the tissue microenvironment. Although ILC3s are generally

dependent on the transcription factor ROR γ t, there are more complex subsets that further subdivide ILC3s in NCR⁺ ILC3s and NCR⁻ ILC3s depending on the expression of the natural cytotoxicity receptors (NCRs) Nkp46 and Nkp44 in both human and mice (Melo-Gonzalez and Hepworth, 2017). In addition, lymphoid-tissue inducer (LTi) cells are a further subclass of ILC3 closely related to NCR⁻ ILC3s, involved in lymph nodes development (Spits et al., 2013). ILC3s have been associated with the pathogenesis and progression of different types of cancer. For instance, a profound reduction of ILC3 NCR⁺ cells was observed also in acute myeloid leukemia (AML) patients which was completely recovered after two cycles of treatment with standard chemotherapy (represented by daunorubicin/cytarabine) (Trabanelli et al., 2015). Conversely, Liu et al. (2019) demonstrated that NCR⁻ ILC3s were the tissue-resident cells mainly present in the liver of hepatocellular carcinoma-bearing mice. In particular, NCR⁻ ILC3s supported the early phase of tumor development by promoting the establishment of an IL-17-rich tumor microenvironment in response to IL-23 sustaining the differentiation of other IL-17-producing cells. These findings suggest that NCR⁻ ILC3s, as well as IL-23, could be an interesting target to exploit for the prevention of hepatocellular carcinoma progression. Given the essential role of LTi cells in generating secondary lymphoid tissues

during embryogenesis, it is possible to hypothesize an involvement of these cells in cancer context. In fact, has been demonstrated that an IL-12 enriched environment promotes the recruitment and proliferation of NKp46⁺ LTI cells, able to inhibit tumor growth and thwart the development of lung metastases in a murine model of cutaneous melanoma (Eisenring et al., 2010). Importantly, (Jacquelot et al., 2021b) recently reviewed that LTI cells are implicated in the development of tertiary lymphoid structures that are formed in inflamed tissues (including tumor) and are composed by different immune cells driving the immune response against tumor development and progression and improving the clinical outcome (Jacquelot et al., 2021a). Moreover, in subcutaneous melanoma, it has been showed that LTI cells exert a tumoricidal effect by increasing the expression levels of adhesion molecules in the tumor which in turn promote the recruitment of adaptive immune cells and the subsequent tumor control (Eisenring et al., 2010). The ability of ILCs to foster the recruitment of other immune cells has been recently described in bladder cancer settings. In particular, Vanoni et al. (2021) demonstrated that ILCPs (the ILC3 progenitor subset present in the peripheral blood) interact with endothelial cells inducing, on one hand, the expression of adhesion molecules on the surface of endothelial cells and acquiring and, on the other, an ILC3-like phenotype sharing some phenotypical markers with LTI cells. However, in human high-grade bladder carcinoma samples, ILCPs are barely detected and their ability to upregulate adhesion molecule expression on endothelial cells was impaired (Vanoni et al., 2021). These findings could describe one of the mechanisms through which tumour cells block the infiltration of immune cells into the tumour site highlighting a new attractive target to regulate the immune infiltration and establish an antitumor immune response.

2 CONCLUDING REMARKS

Immune system evasion is a distinctive hallmark of cancer (Hanahan, 2022). In the last decades, cancer immunotherapy

has experienced important clinical progresses in the treatment of different types of cancer. For instance, immune checkpoint inhibitors such as ipilimumab, nivolumab, and pembrolizumab, whose primary purpose is to unleash effector T cells response, have recast the treatment of aggressive forms of tumor including melanoma, non-small cell lung carcinoma and colorectal cancer (Bagchi et al., 2021). However, cancer relapse and recurrence occur for most patients increasing the need to find new therapeutic targets to improve cancer immunotherapy. The tumor milieu is a complex assortment of immune cells, blood vessels, connective tissue cells and extracellular matrix molecules, which all exert a remarkable influence on the cancerous cells they surround. The better understanding of this microenvironment, with particular attention focused on the function of immune cells within this region is today of particular interest. In this context, tissue-resident innate immune cells exert both positive and negative immune regulatory functions (Figure 1), representing important contributors in modulating the tumor microenvironment and shaping the adaptive tumor response (Wang et al., 2019b). Thus, investigate on the innate-adaptive lymphocyte crosstalk in cancer, could represent an interesting approach in order to increase the efficacy of the current immunotherapies.

AUTHOR CONTRIBUTIONS

RB, MB, EB, GZ, DM, and PC did the bibliographic research and wrote the manuscript. GE and AI critically revised the article for intellectual content. All authors contributed to the article and approved the submitted version.

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Stromal and Immune Cell Dynamics in Tumor Associated Tertiary Lymphoid Structures and Anti-Tumor Immune Responses

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Tertiary lymphoid structures (TLS) are ectopic lymphoid organs that have been observed in chronic inflammatory conditions including cancer, where they are thought to exert a positive effect on prognosis. Both immune and non-immune cells participate in the genesis of TLS by establishing complex cross-talks requiring both soluble factors and cell-to-cell contact. Several immune cell types, including T follicular helper cells (Tfh), regulatory T cells (Tregs), and myeloid cells, may accumulate in TLS, possibly promoting or inhibiting their development. In this manuscript, we propose to review the available evidence regarding specific aspects of the TLS formation in solid cancers, including 1) the role of stromal cell composition and architecture in the recruitment of specific immune subpopulations and the formation of immune cell aggregates; 2) the contribution of the myeloid compartment (macrophages and neutrophils) to the development of antibody responses and the TLS formation; 3) the immunological and metabolic mechanisms dictating recruitment, expansion and plasticity of Tregs into T follicular regulatory cells, which are potentially sensitive to immunotherapeutic strategies directed to costimulatory receptors or checkpoint molecules.

Keywords: TLS, Treg, Tfh, neutrophils, tumor stroma

Abbreviations: APC, antigen presenting cells; APRIL, proliferation-inducing ligand; BAFF, B-cell activating factor; CTLA-4, Cytotoxic T-Lymphocyte Antigen-4; DC, dendritic cells; FRC, fibroblastic reticular cell; GC, germinal center; GTR, Glucocorticoid-induced tumour necrosis factor receptor-related protein; IFN γ , interferon γ ; LN, lymph node; NSCLC, non-small cell lung cancer; PD-1, Programmed Death-1; PD-L1, Programmed-Death Ligand 1; SLO, Secondary lymphoid organs; TEM, T effector memory; Tfh, T follicular helper; Th1, T helper 1; TLS, tertiary lymphoid structures; TNF α , tumor necrosis factor α ; TRM, Tissue resident memory; TME, tumor microenvironment.

INTRODUCTION

Human solid cancers have been traditionally classified into subtypes based on disease stage and histology for prognostic purposes and selection of clinical treatments. In the past decades the development of new therapeutic strategies and the accumulating knowledge on tumor biology has called for a more comprehensive classification system that takes into account the complexity of the disease in terms of qualitative heterogeneity and response to therapies. Indeed, it is now well recognized that tumors are heterogeneous entities where the stromal components (fibroblasts, blood vessels and infiltrating leukocytes) are major determinants of disease progression and can be therapeutic targets along with transformed cells. In this view, a detailed characterization of the tumor microenvironment as a whole represents a pivotal tool to fully exploit the potential of new therapies and ultimately improve patients' survival and quality of life.

Infiltrating leukocytes often outnumber transformed cells in tumor masses and can grow in organized structures resembling secondary lymphoid organs (SLO), known as tumor associated tertiary lymphoid structures (TLS). The number and qualitative composition of TLS can vary significantly among tumor types but

there is now consensus about the overall positive effects they exert on prognosis and response to immunotherapy. It is therefore important to include the immune profile when characterizing tumors in order to make appropriate decisions in terms of therapy and disease clinical management. In this review the general features of tumor-associated TLS and of their formation will be described. The role of the TLS-associated cell types, mainly T and B lymphocytes subsets and myeloid cells, will also be discussed and related to the induction of tumor specific immunity and to the prognostic significance of these structures.

TERTIARY LYMPHOID STRUCTURES: GENERAL FEATURES AND PROGNOSTIC SIGNIFICANCE IN CANCER

TLS are ectopic lymphoid organs that originate within nonlymphoid tissues during chronic inflammatory conditions, such as persistent pathogen infection, autoimmune disorders, allograft rejection and cancer (Ansel and Cyster, 2001; Aloisi and Pujol-Borrell, 2006). TLS, also named tertiary lymphoid organs (TLO), develop in peripheral tissues in close proximity to

TABLE 1 | TLS features in human cancers and effects on prognosis and/or therapy.

Tumor	TLS features	Effect on prognosis and/or therapy	References
NSCLC	Mature DC (DC-LAMP ⁺) Th1 CD3 ⁺ CD4 ⁺ CD3 ⁺ CD8 ⁺ T cells B cells Ki67 ⁺ , plasmacells Neutrophils (APC-like)	↑ OS Mature DC not detected in metastasis	(Dieu-Nosjean et al., 2008; Germain et al., 2014; Goc et al., 2014; Singhal et al., 2016)
Breast cancer	nd ↑ Treg ↑ B cells, ↓ Treg	Association with higher tumor grade ↑ risk of recurrence and death ↑ OS	(Figenschau et al., 2015; Sofopoulos et al., 2019; Zhang et al., 2021) (Gobert et al., 2009; Miao et al., 2021; Song et al., 2019) (Germain et al., 2021)
Ovarian cancer (HGSC)	Plasmacells CD8 ⁺ T cells Neutrophils	nd nd	(Kroeger et al., 2016) (Montfort et al., 2017)
Prostate cancer	↑ Th1, CD8 ⁺ ↓ Treg	Association with spontaneous remission	(Garcia-Hernandez et al., 2017)
Colon cancer	Tfh FDC and GC B cells ↑ Th2 and macrophages ↑ Tfr (Bcl6 ⁺)	nd ↓ risk of recurrence with mature TLS ↑ risk of recurrence	(Schweiger et al., 2016) (Posch et al., 2018) (Yamaguchi et al., 2020)
Pancreatic cancer	Intratumoral localization with Th1-Th17 signature	↑ OS and DFS	(Hiraoka et al., 2015)
Gastric cancer	↑ eTreg PD-1hi	Disease progression upon nivolumab tx	(Kamada et al., 2019)
HCC	↑ T CD8 ⁺ , B cells ↓ Treg	↓ risk of early tumor recurrence	(Li et al., 2020)

NSCLC, non-small cell lung cancer; OS, overall survival; DFS, disease free survival; HCC, hepatocellular carcinoma; nd, not determined; HGSC, high grade serous cancer; APC, antigen presenting cell; eTreg, effector Treg.

pathological loci, under stress conditions and as the result of persistent antigen stimulation (Sautes-Fridman et al., 2016). TLS structure resembles that of conventional secondary lymphoid organs (for example, lymph nodes) including B cell zones, T cell zones, marginal zones with activated macrophages and dendritic cells, reticular fibroblast cell networks and vasculature permissive to immune cell extravasation (Aoyama et al., 2021). However, while lymph nodes are encapsulated, TLS represent a congregation of immune and stromal cells confined within an organ or tissue (Aoyama et al., 2021). TLS form *de novo* in the microenvironment of solid tissues in response to prolonged inflammatory stimuli including cancer and may dissipate upon the resolution of inflammation (Moyron-Quiroz et al., 2004). TLS can additionally foster tumor antigen presentation, T cell activation and clonal expansion (Joshi et al., 2015; Zhu et al., 2015), activation of antigen-presenting cells (APC) (Hughes et al., 2016), germinal center (GC) formation (Silina et al., 2018), and B cell class switching (Schroder et al., 1996). Various types of innate and adaptive immune cells comprising macrophages, DCs, mast cells, as well as T and B cells, are recruited and activated by inflammatory mediators, especially cytokines, chemokines and adhesion molecules to the site of persistent inflammation and participate to the formation of TLS (Weinstein and Storkus, 2015; Helmink et al., 2020). As compared to secondary lymphoid structures, TLS exhibit a fair amount of heterogeneity in terms of cellular composition and topographical localization within tissue types.

TLS are lymphoid aggregates characterized by two distinct B and T compartments. Fibroblastic reticular cell networks, PNA⁺ High Endothelial Venules (HEVs) and follicular dendritic cells are found within T cell zones. On the other hand, B compartment consists of B cell follicles primarily composed of naïve B cells with evidence for class switching and reactive GC in B cell zones, and expression of the enzyme activation-induced cytidine deaminase (AID), required for the initiation of somatic hypermutation and immunoglobulin gene class switching (Muramatsu et al., 2000; Neyt et al., 2012; Dieu-Nosjean et al., 2014; Jones et al., 2016). At an early stage, TLS show a different composition and primarily consist of T and B cells without formation of follicles with evidence of GC.

Tumor-associated TLS from different tumor types vary in cellular composition and organization. In fact, they variably contain B lymphocytes with immature, naïve, activated, memory and plasma cell phenotypes (Sautes-Fridman et al., 2019). In non-small cell lung cancer (NSCLC), tumor-associated TLS include large numbers of mature dendritic cells DC-LAMP⁺, which are not detected in lung metastatic neoplasms. The density of mature DC within primary lung tumor TLS has been found to be related to the amount of intratumoral Th1 and CD8⁺ T cell infiltration, and positively influences the effectiveness of antitumoral cytotoxic immune response. Thus, these findings seem to indicate mature DC as possible biomarkers of clinical outcome and as predictors of long-term survival (Dieu-Nosjean et al., 2008; Dieu-Nosjean et al., 2014; Goc et al., 2014). TLS in breast cancer commonly contain T helper follicular (Tfh) cells (Gobert et al., 2009), whereas those associated with prostate and lung metastatic colon cancer contain

large numbers of regulatory T cells (Tregs) (Kang et al., 2021). A high density of Tfh is commonly reported in TLS in breast cancer (Rubin and Kan, 1985), although it is also documented in those associated with prostatic adenocarcinoma (Garcia-Hernandez et al., 2017) and colorectal adenocarcinoma with pulmonary metastasis (Schweiger et al., 2016). Tfh and Treg cells have been shown to act in a complex balance in TLS formation and influence the composition of the neoplastic chronic inflammatory microenvironment. Gu-Trantien et al. demonstrated that, in breast cancer models, Treg accumulation occurs in response to antigen-induced IL-2 production and contributes to the suppression of Th1-mediated adaptive immune response. Later, the IL-2-depleted microenvironment induces the differentiation of some activated CD4⁺ T cells into CXCL13-producing Tfh, capable of sustaining TLS formation and tumor-infiltrating B cell recruitment (Gu-Trantien et al., 2013).

Well-organized TLS have been described in several solid tumors with different topographic locations either in close contact with malignant cells and in peritumoral areas, and are generally considered a favorable prognostic factor (Sautes-Fridman et al., 2016; Sautes-Fridman et al., 2019). Several studies documented the presence of intratumoral TLS with a non-classical organization (without the evidence of discrete T- and B-cell compartments) in hepatocarcinoma (Finkin et al., 2015) and renal cell carcinoma presenting pulmonary metastasis (Remark et al., 2013). Other studies highlighted peritumoral TLS in proximity to the tumor-invasive margin (Munoz-Erazo et al., 2020).

TLS are privileged sites where the activation and the maintenance of local and systemic T and B cell response against tumor antigens occur (Heinhuis et al., 2019) and decelerate neoplastic progression (Dieu-Nosjean et al., 2016). Several studies reported their presence in NSCLC (Germain et al., 2014), colorectal cancer (McMullen et al., 2010; Di Caro et al., 2014), breast (Martinet et al., 2011), pancreatic (Hiraoka et al., 2015; Castino et al., 2016) and gastric carcinomas (Hennequin et al., 2016), oral cancer (Wirsing et al., 2018) as well as ovarian cancer (Milne et al., 2009) and melanoma (Ladanyi et al., 2007; Engelhard et al., 2018; Sautes-Fridman et al., 2019).

Numerous preclinical and clinical studies attribute varied roles to TLS in accordance with their structure or with the neoplastic characteristics related to either the site of origin or the location of the neoplasm. Indeed TLS promote a vigorous immune response intratumorally, constituting a barrier to disease progression, and also modulate immunity in the tumor microenvironment (Engelhard et al., 2018). The presence of TLS correlates to the activation of the immune response and for this reason they are considered a biomarker for stratifying untreated cancer patients' survival risk and an intriguing and promising target for predicting the efficacy of new immunotherapies (Colbeck et al., 2017a; Helmink et al., 2020). Although the prognostic impact of tumor-associated TLS has been extensively investigated, the immune response that occurs in TLS and the significance of their prognostic role remain incomplete. Several studies have indicated a significant correlation between TLS density and higher rates of disease-free survival and overall

patient survival (Sautes-Fridman et al., 2019), although there are exceptions (Figenschau et al., 2015; Finkin et al., 2015). However, it is observed that patient survival depends strictly on TLS' classical or non-classical organization and also peri- and intratumoral localization. Tumor-associated TLS and/or stromal cells (as high endothelial venules, HEVs) can be extratumoral, positioned at or outside the tumor invasive margin, or intratumoral, located within the true tumor mass or tumor nests. The importance of TLS/HEVs in enabling infiltration of T cells into the tumor has been demonstrated. Indeed, unlike intratumoral structures, extratumoral HEVs were not associated with increased tumor-infiltrating lymphocyte (TIL) frequencies (Martinet et al., 2011; Martinet et al., 2012; Bento et al., 2015). Similarly, while extratumoral TLS density was not a prognostic marker in pancreatic cancer patients, intratumoral TLS were an independent favorable prognosticator (Hiraoka et al., 2015). However, the relationship between tumor-associated TLS and patient outcome appears to depend on many parameters, including cancer type, disease stage, and quality of the immune infiltrate (Table 1). As discussed in detail thereafter, high frequencies of regulatory T cells in TLS can suppress antitumor immune responses (Joshi et al., 2015).

For this reason, we believe that greater knowledge about TLS development, composition, and function may offer new therapeutic opportunities to modulate antitumor immunity. In recent years the tumor microenvironment has been considered as an active niche in a state of dynamic evolution (Rosenthal et al., 2019). In fact the complex cross-talk between the neoplastic sub-clones and immune cells represent a crucial event for neoplastic progression (Locy et al., 2018). Although tumor-associated TLS are usually associated with higher densities of CD8⁺ intratumoral lymphocytes, multivariate studies performed on NSCLC and colorectal cancer series have demonstrated that their prognostic value is independent of TIL density (Di Caro et al., 2014; Goc et al., 2014). Furthermore, intratumoral TLS are more significantly associated with longer patient survival than peritumoral ones in pancreatic adenocarcinoma (Hiraoka et al., 2015) and also in early stage hepatocarcinoma (Li et al., 2020). Wirsing et al. reported that oral squamous cell carcinoma patients with high TLS density tended to survive longer, although this was not statistically significant (Wirsing et al., 2014).

Bertucci et al. detected a higher expression of TLS signatures with higher sensitivity to immune checkpoint inhibitors in inflammatory breast cancer (Bertucci et al., 2021). In breast cancers, TLS were not significantly correlated with clinical variables (patient age, tumor size) but were considerably influenced by other pathological parameters (e.g., tumor differentiation grade, lymphovascular invasion status and pTNM stage), confirming their key role in the neoplastic progression (Zhang et al., 2021). Patients with HER-2⁺ breast carcinoma featuring TLS, that were treated with chemotherapy and/or HER-2 targeted therapy, showed a good treatment response to be attributed also to active antitumor immunity of TLS (Luen et al., 2017).

Some studies highlighted a correlation between TLS and a higher frequency of lymph nodal metastasis in high grade breast

carcinoma, suggesting their unfavorable prognostic value and, at the same time, the necessity of associating TLS with other prognostic parameters (Figenschau et al., 2015; Sofopoulos et al., 2019).

The prognostic value of TLS has been particularly well-explored in colorectal cancer (Schweiger et al., 2016; Posch et al., 2018; Trajkovski et al., 2018). Yamaguchi et al. performed experiments aimed to investigate the cellular composition of TLS and to assess which cytotype correlates with disease recurrence. Five types of TLS (GC-rich, B-cell rich, follicular DC rich, Th (CD4) rich, and CTL (B/Th rich) were identified in term of cellular composition, and the density of CD4⁺ T cells and macrophages was associated with a higher rate of relapse in patients (Yamaguchi et al., 2020). On the contrary, Posch et al. delineated only three types of TLS, based on the composition of the aggregates and the functional state of a single cytotype within TLS, distinguishing the early TLS (dense aggregates with undifferentiated FDC); Primary follicle-like TLS (cluster of B cells with FDC networks but without GC); and follicle-like secondary TLS (with GC), and showing that a high percentage of mature TLS correlated with a better prognosis (Posch et al., 2018). In triple negative breast cancer, Seow et al., through a multiplex imaging analysis, identified a high density of plasma cells within TLS, suggesting a functional role for B cells in outcome (Seow et al., 2020).

Schlosser et al. demonstrated that, in esophagogastric adenocarcinoma patients, B cells within TLS produced tumor-specific antibodies, confirming their functional role in decelerating tumor growth (Schlosser et al., 2019).

CELL MEDIATED AND ANTIBODY RESPONSES IN CANCER: CONNECTION WITH TERTIARY LYMPHOID STRUCTURES

The role of adaptive immune responses in controlling tumor onset and evolution is now well established and supported by substantial preclinical and clinical evidence. Cells from nascent tumors can indeed be recognized by cytotoxic T cells since they display on their membrane peptide epitopes associated with major histocompatibility complex-class I (MHC-I) molecules that can drive tumor rejection. The intrinsic genetic instability of transformed cells is a major source of tumor antigens and, as such, the trigger of tumor specific adaptive immune responses. Nevertheless, such responses can promote the selection of poorly immunogenic tumor cell variants that escape immune control and can ultimately lead to cancer development (Mittal et al., 2014; Schumacher and Schreiber, 2015).

Animal models have highlighted the protective role of T cells and IFN- γ in tumor development. Mice lacking the adaptive arm of the immune system or unresponsive to IFN- γ (IFNGR1 and STAT1 ko) show increased susceptibility to both carcinogen-induced and spontaneous tumorigenesis (Kaplan et al., 1998; Smyth et al., 2000; Shankaran et al., 2001). In human cancers the infiltration of both CD8⁺ and CD4⁺ T lymphocytes is a common characteristic of tumors that have a favorable prognosis (Fridman et al., 2017; Paijens et al., 2021). CD8⁺ T cells exert their

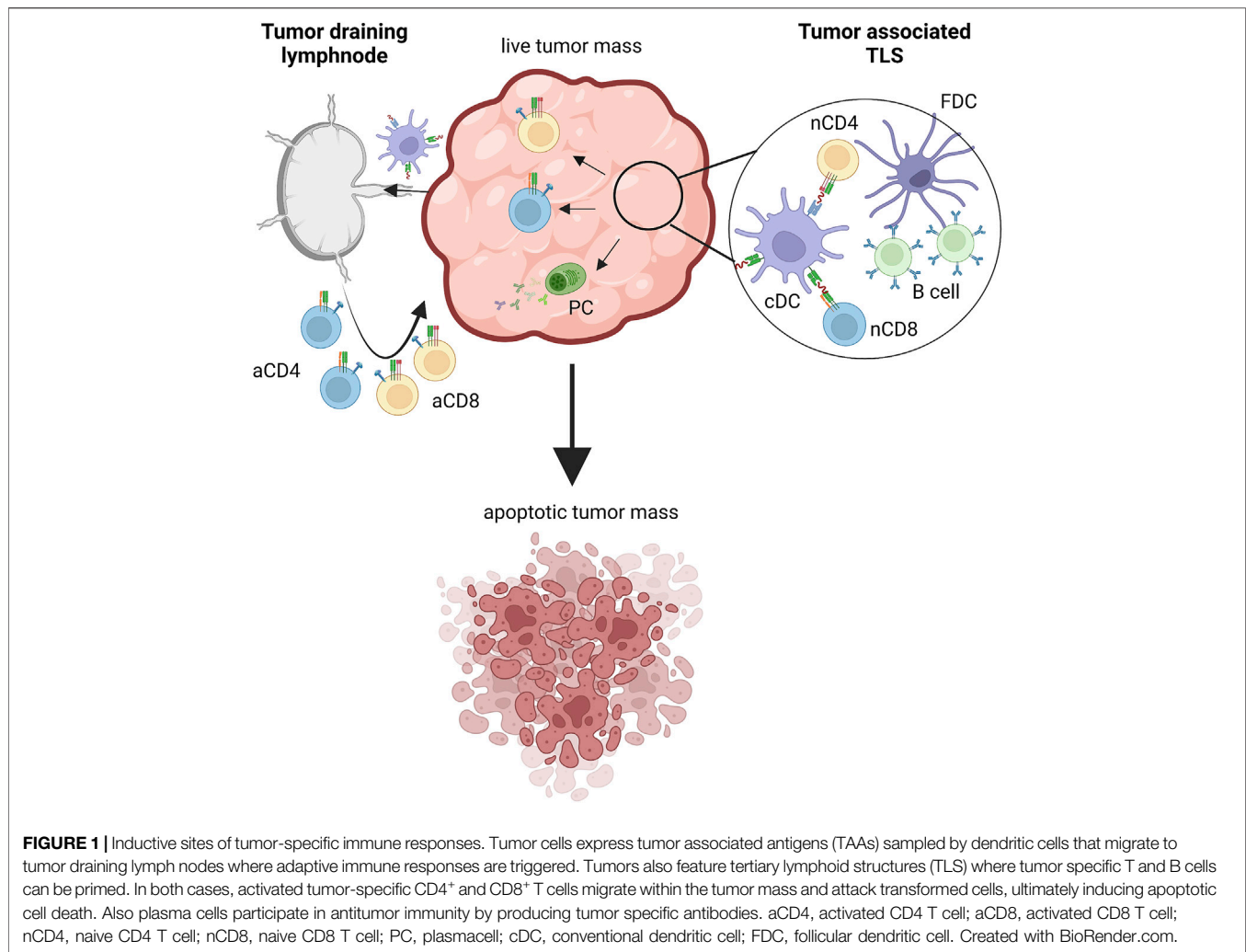
antitumor function both directly, by killing tumor cells expressing tumor-associated antigens on MHC-I molecules, and indirectly, by releasing proinflammatory cytokines (such as IFN- γ and TNF- α) that activate other leukocytes and sustain their antitumor activities. The infiltration of CD8⁺ T cells with an effector memory phenotype (TEM) positively correlates with overall and disease free survival in both colorectal and breast cancer patients (Pages et al., 2005; Galon et al., 2006; Bindea et al., 2013; Ahmadvand et al., 2019). More recently, a protective role of tissue resident memory (TRM) CD8⁺ T cells, that do not recirculate in blood, has emerged in several solid cancers. In both human and murine tumors, infiltration of CD103⁺ CD8⁺ T cells (a marker for TRM) is associated with improved survival (Paijens et al., 2021). Interestingly, non-tumor-specific TRM have been identified in tumor masses that can contribute to the antitumor immune response via a bystander effect (Simoni et al., 2018; Rosato et al., 2019). In mouse models of melanoma and colon carcinoma, boosting of virus-specific TRM via peptide vaccination resulted in recruitment and activation of both natural killer and dendritic cells and in upregulation of programmed death-ligand 1 (PD-L1), thus sensitizing tumors to immune checkpoint inhibitors-based immunotherapy (Rosato et al., 2019).

CD4⁺ T cells represent a heterogeneous subset of lymphocytes with high phenotypical and functional plasticity and can be considered as the playmakers of the immune system. Several T helper cell subsets have been characterized, each one featuring a specific molecular signature, that are required for both priming of CD8⁺ and B lymphocytes and for optimal antigen presentation by dendritic cells through the CD40L-CD40 axis. In line with their heterogeneity, CD4⁺ T cells can play important yet opposing roles in antitumor immunity. T helper 1 (Th1) polarized CD4⁺ T cells sustain inflammation and cytotoxic cell function and survival through production of IFN- γ and other cytokines (IL-15, IL-12) and are usually associated with a good prognosis in several cancer types (Bindea et al., 2013; Chraa et al., 2019). Likewise, detection of Tfh has been associated with improved prognosis in breast and colorectal cancers (Paijens et al., 2021). Tfh presence is indeed suggestive of TLS, and thus of antitumoral cytotoxic and antibody responses. On the other hand, Foxp3-expressing Tregs are the CD4⁺ T cell subset devoted to maintaining immune homeostasis by suppressing the effector functions of both innate and adaptive immunity. Tregs are expanded in tumors where they promote disease progression by inhibiting antitumor immunity through several mechanisms, including release of immune-suppressive cytokines (IL-10, TGF- β) and deprivation of nutrients, growth factors (IL-2) and costimulatory signals. Treg infiltration is predictive of poor prognosis and their targeted depletion is regarded as an appealing strategy for immunotherapy, even though clinical attempts have not achieved substantial efficacy so far. On the one side, the Treg-depleting activity of anti-CTLA4 antibodies described in mouse models (Selby et al., 2013; Simpson et al., 2013) has not been replicated in human cancers (Sharma et al., 2019) and subsequent attempts of targeting tumor infiltrating Tregs by an anti-CCR4 antibody were limited by concomitant depletion of effector CD4⁺ and CD8⁺ T cells (Kurose et al., 2015). Recently, Campbell and coworkers

proposed a CCR8-dependent depletion of tumor infiltrating Tregs based on the highly restricted expression of this receptor on tumor infiltrating Tregs as compared to both their circulating counterpart and to intratumoral effector T cells in different human tumors. Treatment of tumor bearing mice with the anti-CCR8 antibody was highly specific to tumor infiltrating Tregs, sparing both intratumoral effector T cells and Tregs in non-tumor tissues and ultimately enabling effective and long-lasting antitumor immunity (Campbell et al., 2021).

A strong endorsement to the significance of functional T cell responses in cancer control came from the licensing of immune checkpoint inhibitors (ICIs) for immunotherapy. ICIs are monoclonal antibodies targeting molecules involved in downregulation of effector T cell functions, typically CTLA-4, PD-1 and its ligand PD-L1 (Pardoll, 2012; Topalian et al., 2015). CTLA-4 and PD-1 expression is upregulated upon T cell activation and the latter has been associated with T cell functional exhaustion in both chronic viral infections and cancer (Barber et al., 2006; Keir et al., 2008). Hence, preventing PD-1 interactions with its ligands PD-L1 and PD-L2 in the tumor microenvironment is expected to restore the cytotoxic functions of exhausted tumor-specific T cells and has achieved significant success in the management of advanced stage solid tumors.

Despite having been disregarded by the majority of studies on prognosis and response to immunotherapy so far, accumulating evidence indicates that B lymphocytes can exert both anti- and pro-tumoral activities. Similarly to T cells, B cells are indeed highly versatile leukocytes endowed with both effector and modulatory functions. Besides being the source of antibodies, B cells can effectively prime CD4⁺ T cells as professional APC (Bruno et al., 2017; Hong et al., 2018; Hua and Hou, 2020) and participate in tolerance maintenance as IL-10 producing B regulatory cells (Bregs) (Rosser and Mauri, 2015). Infiltration of B cells is often associated with a good prognosis in different tumor types and can be predictive of response to immunotherapy. Both in melanoma and soft tissue sarcoma patients, B cell abundance and the concomitant detection of TLS was associated with improved survival and to a better response rate to ICI therapy with the anti-PD-1 pembrolizumab (Helmink et al., 2020; Petitprez et al., 2020). Of note, in the sarcoma study, B cells appeared to be the strongest prognostic factor, irrespective of high or low CD8⁺ T cells and other cytotoxic cell content (Petitprez et al., 2020). Evidence of antibody response induction has been identified in different tumor types, including melanoma and breast cancer (Garaud et al., 2019; N et al., 2021). Insights on the significance of antibody responses in cancer came from studies on breast cancer after the approval of the therapeutic antibody trastuzumab. Trastuzumab targets the HER2 receptor, overexpressed by a subtype of breast tumors, and has been shown over the years to induce both antibody-dependent cell cytotoxicity (ADCC) and antibody-dependent cell phagocytosis (ADCP) by engaging the Fc γ receptors on natural killer cells, monocytes and macrophages (Park et al., 2010; Tsao et al., 2019; Ehlers et al., 2021; Upton et al., 2021). The detection of high levels of HER2-specific autoantibodies in a cohort of breast



cancer patients positively correlated with the infiltration of B cells (CD20⁺) and of CXCL13⁺ cells, suggestive of TLS presence (Sato et al., 2021).

The induction and persistence of functional tumor specific adaptive immune responses can be a major barrier to disease progression. It is clear from the above discussion that both T and B lymphocytes are activated in the presence of cancer cells and both arms of the adaptive immune system play a role in disease progression and response to therapy. Several retrospective studies in humans have associated the presence of TLS with good prognosis and improved responses to ICI-based immunotherapy in distinct cancer types (Fridman et al., 2017; Sautes-Fridman et al., 2019). The beneficial effect of TLS seems mostly related to their qualitative cellular composition, with Th1-polarized CD4⁺, effector memory CD8⁺ T cells and mature dendritic cells associated to the best outcomes in colorectal and lung cancers (Dieu-Nosjean et al., 2008; Di Caro et al., 2014; Goc et al., 2014). Whether TLS are primarily involved in induction of tumor-specific immune responses and to what extent that relates to their prognostic value has not been completely elucidated yet. The concomitant

detection of dendritic cells and T and B lymphocytes in proximal vicinity may be indicative of actual antigen-specific priming occurring in TLS. In lung cancer patients, high densities of mature dendritic cells (Lamp⁺) positively correlated with infiltration of activated CD8⁺ T cells (CD69⁺ CD38⁺) and with an effector memory phenotype that localized in the tumor nest, close to target tumor cells. Notably, the concomitant detection of dendritic cells and CD8⁺ T cells identified the group with a lower risk of death as compared to CD8⁺ T cell infiltration alone (Goc et al., 2014). Additional studies from the same group also reported infiltration of mature DC and B cells staining positive for the proliferation marker Ki67 and the activation induced deaminase (AID), indicating ongoing germinal center reactions. Indeed, CD138⁺ plasma cells were also detectable that specifically recognized tumor antigens in half of patients (Germain et al., 2014). As for CD8⁺ T cells, the best clinical outcome in terms of survival was observed in patients showing concomitant infiltration of B cells and dendritic cells both in early and late stage tumors (Germain et al., 2014). In high grade ovarian cancer patients, TLS with high density of plasma cells actively synthesizing IgG were described. Again,

plasma cell infiltration correlated with cytotoxic T cells infiltration and dictated their prognostic benefit (Kroegeer et al., 2016).

These studies suggest that specific and complete immune responses can be induced at the tumor site and that TLS facilitate interactions between innate and adaptive immune cells (Figure 1). These observations are supported by some studies that implied the occurrence of active immune responses in ectopic lymphoid structures found in autoimmune conditions and infections. For instance, splenectomized mice lacking SLO and Peyer's Patches (Lymphotoxin α $-/-$) can mount functional antigen-specific CD8⁺ T cell and antibody responses upon influenza virus infection that occur at the inducible bronchus associated lymphoid tissue (iBALT) and sustain viral clearance (Moyron-Quiroz et al., 2004). Furthermore, iBALT-primed T and B cells develop a memory phenotype and provide protection against viral challenge (Moyron-Quiroz et al., 2006). Antigen-specific priming in the absence of canonical SLO has also been reported in tumor models. Schrama and colleagues grew in splenectomized LT α ^{-/-} mice B16 derived tumors that can be specifically targeted with LT α , a well-known lymphoid tissue inducer. The authors documented delayed growth of subcutaneous tumors and complete protection from pulmonary metastasis. Importantly, CD8⁺ T cells specific for the tumor associated antigen TRP-2 were detectable by *in situ* tetramer staining only within tumors where TLS had been induced (Schrama et al., 2008). Similarly, antitumoral activity was shown for adoptively transferred naive T cells even when lymphocyte egress from LN was blocked by FTY720 (Thompson et al., 2010; Peske et al., 2015). These results suggest that antitumor immune responses likely induced in TLS can restrain tumor growth and control disease evolution by protecting from metastatic spread. More recently, the generation of TLS has been associated with the composition of the gut microbiome, whose involvement in tumor development and immunity has raised much interest. Overacre-Delgoffe and coworkers assessed the occurrence of TLS in a carcinogen induced colorectal cancer model in the presence of the bacterial species *Helicobacter hepaticum* (Hhep). Hhep colonized mice developed smaller tumor numbers as compared to controls, survived longer and developed intratumoral TLS dominated by Tfh responses that appear to be the correlate of protection. Indeed, both TLS formation and the effect on disease progression were abrogated in mice specifically devoid of Tfh and rescued upon Hhep-specific CD4⁺ T cell adoptive transfer (Overacre-Delgoffe et al., 2021).

STROMAL CELL COMPOSITION AND ARCHITECTURE IN TERTIARY LYMPHOID STRUCTURES FORMATION

Within the tumor microenvironment the local cross-talk between immune cells and stromal elements leads to the production of a series of pro-inflammatory cytokines and TNF receptor family components that determines the formation of TLS (Le Hir et al., 1996; Matsumoto et al., 1996; Endres et al., 1999; Forster et al.,

1999; Lorenz et al., 2003; Cupedo and Mebius, 2005). Different non-hematopoietic stromal cells, namely fibroblasts, blood and lymphatic endothelial cells, pericytes, and epithelial cells, participate variably to TLS development (Buckley et al., 2015). Several studies have demonstrated a key role of the stromal elements, in particular fibroblasts, in chronic inflammation by the activation of pro-survival and retention signals. In fact, fibroblasts showed to promote the local recruitment of immune cells at the inflammatory site and support the maintenance of the inflammatory state by producing various factors, such as B-cell survival factors (BAFF) and inflammatory chemokines (e.g., IL-8, CCL5, CXCL1). However, fibroblasts can also participate in the formation of TLS through their capability to produce other chemokines, such as CXCL12, CCL21 and CXCL13 (Filer et al., 2008; Flavell et al., 2008; Barone et al., 2012). Soluble molecules produced by stromal cells have been harnessed to drive TLS formation for therapeutic purposes (Johansson-Percival and Ganss, 2021). For instance, in a neuroendocrine tumor mouse model, targeting endothelial cells and activated tumor infiltrating macrophages (CD68⁺) with the LN-inducing cytokine LIGHT (TNFSF14) induces production of CCL21, TNF α , and IL1 β that, overall, drive T/B cell recruitment and formation of mature TLS (Johansson-Percival et al., 2015; Johansson-Percival et al., 2017). In a distinct approach, genetically engineered DC overexpressing Tbet, and thus producing high levels of IFN γ , TNF α and IL36 γ , have been shown to induce TLS in murine colon cancer even in the absence of peripheral LN (Weinstein et al., 2017).

In 2004 Cupedo et al. highlighted the crucial role of stromal cells in the development of TLS by performing intradermal injections of cell suspensions obtained from neonatal lymph nodes, which seemed to promote the formation of ectopic lymphocyte aggregates resembling lymph node-like follicular structures. Interestingly, the major cellular actors strictly involved in this process were the mesenchymal elements showing the capability to engage and retain host-derived T and B lymphocytes organized into two distinct compartments (Cupedo et al., 2004). Subsequently, Suematsu et al. used a mouse model and performed the implantation of stromal cell scaffolds under the kidney capsule, demonstrating the generation of lymphoid structures. These structures, described as artificial lymph nodes, recapitulated the morphological characteristics of lymph node parenchyma and proved to be able to support immune responses (Suematsu and Watanabe, 2004). Furthermore, other studies supported the pivotal contribution of stromal cells in the development of ectopic lymphoid structures during chronic inflammation. In a model of atherosclerosis, the investigators described the formation of adventitial aortic tertiary lymphoid organs, due to the activation of mouse aorta smooth muscle cells expressing both VCAM-1 and chemokines CXCL13 and CCL21 (Grabner et al., 2009).

Overall, as a consequence of persistent antigen presentation due to chronic inflammatory stimuli, stromal cells acquire lymph node-like properties that allow them to recruit, activate and prime adaptive immune cells (Figure 2A). A variety of inflammatory

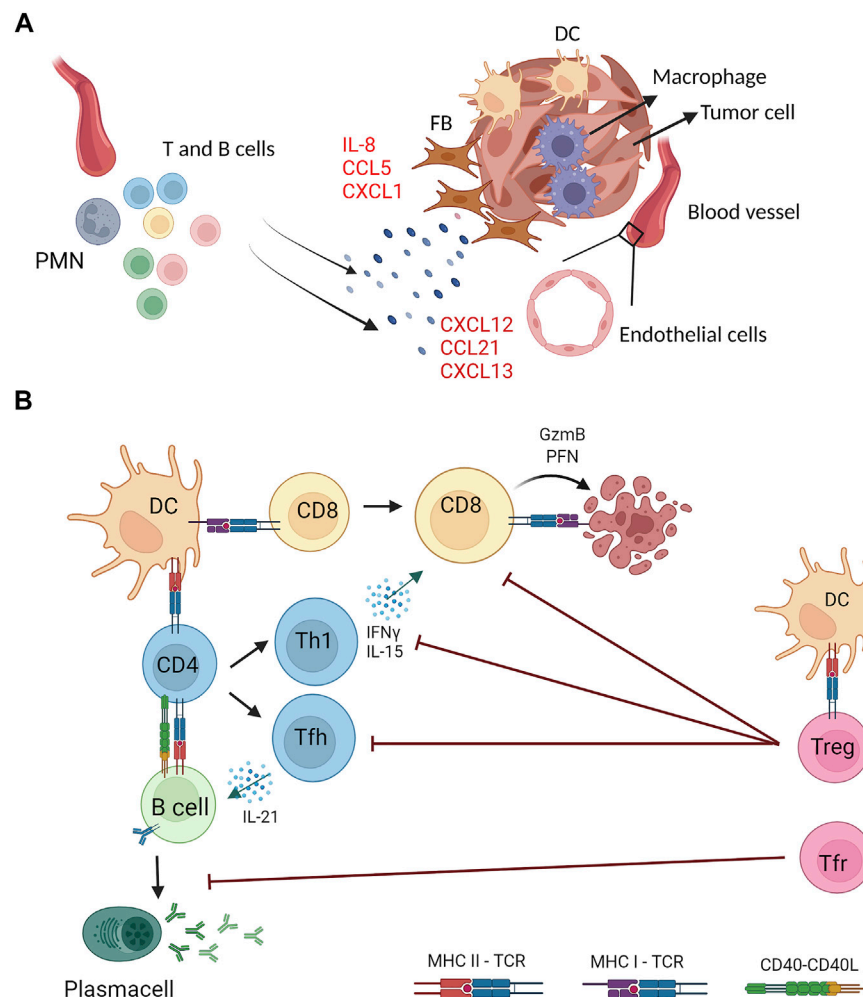


FIGURE 2 | Stromal and immune cells crosstalk in the generation and functions of tumor associated TLS. **(A)** Stromal components of tumor masses (fibroblasts, endothelial and myeloid cells) are the source of proinflammatory cytokines (e.g., IL-8) and chemokines (e.g., CXCL13) that drive recruitment and activation of lymphocytes and other myeloid cells (e.g., neutrophils) at the tumor site that generate organized lymphoid structures **(B)** Tumor associated TLS feature multiple interactions between lymphoid and myeloid cells for induction of tumor specific immune responses. Dendritic cells (DC) and B cells can present TAA on MHC class I and class II molecules to CD8⁺ and CD4⁺ T cells expressing the cognate T cell receptor (TCR) and, concomitantly, provide costimulatory signals by CD40⁺CD40L axis. Upon antigen recognition, CD8⁺ T cells differentiate into cytotoxic cells that kill tumor targets by perforin (PFN) and Granzyme B (GzmB). CD4⁺ T cells can differentiate into several T helper subsets, including T helper 1 (Th1) and T follicular helper (Tfh) that sustain, respectively, cytotoxic and B cell responses through the production of specific cytokines (IFN γ , IL-15, IL-21). Activated B cells differentiate into antibody secreting plasma cells. TAA-specific CD4⁺ T cells include regulatory T cells that, once activated, counteract effector CD4⁺ and CD8⁺ T cells. A specialized subset of Treg with a follicular phenotype (Tfr) inhibit B cell responses. Created with BioRender.com.

stimuli, either infectious, autoimmune or tumor-related, have proved to be responsible for the formation of such antigen-specific lymphoid aggregates. Thus, in the setting of a solid neoplasm, TLS formation accounts for the promotion of a tumor-specific immune response that elicits a targeted intratumoral adaptive immunity. Knowledge of these processes helps define TLS as promising prognostic biomarkers to stratify the patient's overall survival rate and may soon contribute to the development of novel immunotherapeutic agents for the treatment of different solid neoplasms (Colbeck et al., 2017a).

Even during development, TLS stroma presents a large degree of plasticity (Barone et al., 2016). Early anlagen mesenchyme can differentiate upon specific stimuli into diverse and highly

specialized stroma, which then creates functional micro domains within the TLS (Asam et al., 2021). TLS non-vascular stroma is largely represented by fibroblastic reticular cells (FRC), a fine network of canaliculi forming fibroblasts that display unique functional properties, including the ability to support the dramatic anatomical remodelling required to adapt TLS to the lymphocyte influx occurring in response to antigen stimulation (Perez-Shibayama et al., 2019). The mechanism underpinning the physical plasticity of the TLS fibroblasts has been identified in the SLO in the interaction between podoplanin, a glycoprotein broadly expressed on FRC, and its receptor CLEC2 expressed by DC, first incomers in the TLS upon antigen exposure, during inflammation or upon immunization (Acton et al., 2014). The

adaptability of the stroma during the immune response has been deemed critical to enable expansion of the B follicle required to accommodate the GC reaction upon immunization. Plasticity of the fibroblasts in TLS can therefore be defined as the most critical property required to shape an efficient immune response (Barone et al., 2016; Asam et al., 2021).

MYELOID CELLS IN TERTIARY LYMPHOID STRUCTURE FORMATION

TLS are organized formation of immune cells, which arise in tissue during chronic inflammation (e.g., autoimmunity, allograft rejection, chronic inflammation, and cancer) (Manzo et al., 2010; Thaunat et al., 2010; Neyt et al., 2012; Colbeck et al., 2017a). Similarly to lymph node and SLO, TLS displayed an inner area of CD20⁺ B cells surrounded by CD3⁺ T cells (Sautes-Fridman et al., 2019). Even though TLS are populated by a variety of T cells (CD4⁺ follicular helper T cells, CD8⁺ cytotoxic T cells, CD4⁺ T helper 1 and regulatory T cells) (Gu-Trantien et al., 2013; Goc et al., 2014; Hennequin et al., 2016; Kroeger et al., 2016) and B cells, TLS are also populated by distinct types of myeloid cells. In particular, follicular dendritic cells (FDC), characterized by the expression of CD21, localize in the inner B zone (Bergomas et al., 2011) and dendritic cell-lysosomal associated membrane protein (DC-LAMP⁺, also known as CD83⁺ DC) preferentially distribute in T cell zone and activate T cell (McMullen et al., 2010). DC may also accomplish other functions in TLS organization. Indeed, it has been suggested that antigen-presenting DC, through the activation of T cells, are sufficient to TLS induction (Ludewig et al., 1998; Neyt et al., 2012). In line with this, the depletion of DC determined the loss of existing TLS, indicating the importance of DC for structural organization and maintenance of TLS, probably through the production of chemokines (e.g., CXCL13) or by the continuous activation of T cells (GeurtsvanKessel et al., 2009; Halle et al., 2009; Muniz et al., 2011). The presence of DC in TLS, as well as of other immune cell types, has been associated with better prognosis in cancer (Goc et al., 2014; Sautes-Fridman et al., 2019).

Cancer-associated TLS can also contain scattered CD68⁺ macrophages (Dieu-Nosjean et al., 2008; Schumacher and Thommen, 2022), and the function of these macrophages has not been fully characterized. One hypothesis is that they function as scavenger cells, as it is in SLO, where T cell zone macrophages (TZM) acted as the only professional scavenger cells clearing up apoptotic cells (Baratin et al., 2017). During atherosclerosis, M1-polarized macrophages act as potential lymphoid tissue inducer cells (LTi) (Guedj et al., 2014). In this context, macrophages were identified as the inducer cells that enhanced the expression of chemokines by vascular smooth cells. Interestingly, this function in M1-polarized macrophages was independent of lymphotoxin- α 1b2 (LT β R) signaling (Guedj et al., 2014). The ability of macrophages to induce TLS has been shown in another pathological context. Indeed, using a model of *Salmonella* colitis, Kosco and colleagues demonstrated that only intestinal mucosa resident CXCR1^{hi} macrophages act as the APC responsible for the recruitment of CD4⁺ T cells and B cells at

the site of *Salmonella* invasion, leading to the formation of TLS and to the local pathogen specific IgA response (Kosco et al., 2020).

Neutrophils can infiltrate TLS and have been reported to infiltrate the TLS found in the omental metastasis of patients with high-grade serous ovarian cancer (HGSOC) (Montfort et al., 2017), and the TLS of patients with prostate cancer (Garcia-Hernandez et al., 2017). The function of neutrophils in this context has not been characterized. Neutrophils present in secondary lymphoid organs can influence antigen presentation and B-cell antibody response (Lok and Clatworthy, 2021). Indeed, neutrophils in the spleen provide helper signals to B cells through the production of BAFF, APRIL, and IL-21 (Puga et al., 2011). In lymph nodes, neutrophils expressing high level of major histocompatibility complex II (MHCII) are mostly located in proximity of T cells and natural killer cells, suggesting a role in CD4⁺ T cell activation (Lok et al., 2019). In early-stage NSCLC patients, neutrophils that can acquire APC-like features and activate CD4⁺ T cells and CD8⁺ T cells have been identified (Singhal et al., 2016). However, the precise role of neutrophils in TLS has not been elucidated and in our opinion deserves further investigation.

REGULATORY T CELLS IN TERTIARY LYMPHOID STRUCTURES: METABOLIC ASPECTS UNDERLYING THEIR FITNESS IN THE TUMOR MICROENVIRONMENT

In accordance with their well-defined and above discussed role in tumors, a detrimental role in antitumor immunity has been documented in studies focusing on TLS-associated Tregs. In mouse models of fibrosarcoma and lung adenocarcinoma, Treg depletion triggers TLS and increases T cell activation with ensuing tumor control (Hindley et al., 2012; Colbeck et al., 2017b). In human breast and prostate cancers, the presence of Foxp3⁺ cells in TLS is associated with adverse clinical outcomes (Gobert et al., 2009; Garcia-Hernandez et al., 2017; Germain et al., 2021). Interestingly, in a study on breast cancer the predictive value in terms of death and relapse was specifically associated to Tregs detected within lymphoid structures rather than to those infiltrating the tumor bed. Lymphoid tissue-associated Tregs show an activated phenotype, are in a proliferative state (Ki67⁺) and in close proximity to activated DCs and T cells. This suggests that tumor antigen specific Tregs are primed in TLS, where they can directly suppress antitumor effector T cells (Gobert et al., 2009). In support of this, Joshi and colleagues have specifically demonstrated that in a mouse model of lung cancer Tregs are preferentially detected in TLS (rather than scattered in the tumor stroma) where they maintain immune quiescence. Treg depletion by diphtheria toxin administration in a transgenic model reactivates proliferation of both CD4⁺ and CD8⁺ T cells within TLS and results in enhanced tumor destruction (Joshi et al., 2015).

While Tregs are detected in tumor associated TLS in human cancers and murine models, their contribution in the formation of these structures is still not known. Considering the favorable prognostic value played by TLS in cancer, dissecting the processes and cell types involved in their formation may have a significant therapeutic impact. Tumor infiltrating Tregs show an activated phenotype characterized by the expression of PD-1 and OX40 (Piconese et al., 2014; Kamada et al., 2019; Polesso et al., 2019), that holds potential for modulating their abundance in the tumor microenvironment with therapeutic implications. In gastric cancer patients, effector Tregs (eTreg, Foxp3^{high} CD45RA⁺) express high levels of PD-1 that impairs anti-PD-1 based therapy, inducing rapid disease progression. Kamada and colleagues observed hyperprogressive disease in 10% of patients after nivolumab treatment that was associated with the accumulation of proliferating intratumoral eTreg with enhanced suppressive potential (Kamada et al., 2019). In this view, combinatorial therapies exploiting the phenotypic heterogeneity of tumor infiltrating Tregs may be a backup strategy. In mouse models of melanoma and colon cancer, anti-PD-1 treatment induced the expansion of tumor Tregs with a follicular phenotype (Follicular regulatory T cells or Tfr, Foxp3⁺ Bcl6⁺), and Tfr depletion by pretreatment with anti-CTLA4 improved tumor control. Notably, a cohort of melanoma patients undergoing sequential anti-CTLA4 and anti-PD-1 had a survival advantage over both the corresponding monotherapies or the anti-PD-1 followed by anti-CTLA4 (Eschweiler et al., 2021).

Follicular regulatory T cells are Foxp3⁺ cells that, upon antigen recognition, co-opt the differentiation pathway of T_H and thus express the committing transcription factor Bcl6 and the chemokine receptor CXCR5, that allows relocation to germinal centers, where they modulate antibody responses (Lu and Craft, 2021). While the role of Tfr in immunization and infection models has been characterized, their significance in tumors is mostly still unknown. Nevertheless, evidence has been accumulating pointing to a central role of Tfr in modulating antitumor immunity and immunotherapy performance (Figure 2B). Increased Tfr frequencies are detected in peripheral blood of breast cancer patients (Song et al., 2019; Miao et al., 2021) and are shown to be a source of IL-10 that suppress antibodies production and promote Breg generation (Song et al., 2019). Whether a fraction of tumor infiltrating Tregs differentiate to Tfr in tumor associated TLS is not known, but a recent work supports this hypothesis. Eschweiler et al. reported that Tfr and activated Treg (4-1BB⁺) isolated from human head and neck cancer share a transcriptomic signature characterized by upregulation of genes related to activation, costimulation and suppressive functions (*TNFRSF4*, *TNFRSF18*, *TNFRSF1B*, *ENTPD1*). Importantly, a fraction of activated Tregs shared TCR with Tfr, indicating a developmental relationship between the two subsets. A similar pattern was identified in murine melanoma derived Treg/Tfr, suggesting that Tfr may actually derive from tumor infiltrating Tregs that in TLS are activated by tumor-specific antigens (Eschweiler et al., 2021). Tfr represent an attractive therapeutic target given their interactions with immune ICIs and their increased suppressive functions over Bcl6⁺ Tregs (Sage et al., 2014a; Sage et al., 2014b; Eschweiler et al., 2021).

Since the anti-tumor immune response occurs locally within the tumor mass and is not restricted to the activation of effector T cells in draining secondary lymphoid organs, the cellular composition and the metabolic events occurring at the TME contribute to TLS formation, thus impacting on tumor suppression and therapeutic response. The B-cell mediated antigen presentation to CD4⁺ T cells occurring in the TLS is finely regulated by different external stimuli and by the TME conditions. In this context, the TLS-B cell interaction is crucial to modulate the early phases of T cell activation, their co-stimulatory properties and/or cell exhaustion, driving their lineage decision. More in detail, it has been described that TLS-B density positively correlates with a specific CD4⁺ T cell signature characterized by the hyper-expression of pro-inflammatory genes including POU2AF1, which encodes for the transcriptional coactivator OCA-B (also called OBF-1) that directly stimulates the IFN- γ and IL-2 promoter activities and is required for the *in vivo* generation of CD4⁺ memory T cells (Brunner et al., 2007; Shakya et al., 2015). Recently, Germain and colleagues observed that high TLS-B density in NSCLC subjects negatively correlates with the exhausted CD4⁺ T cell compartment, expressing several Treg-cell associated genes and molecules, including CD5, CD25, GITR, and Tim-3. Conversely, they found a higher percentage of CD4⁺Foxp3⁺ Tregs in NSCLC subjects with low TLS-B density compared with those expressing high TLS-B density. This shows that high TLS-B cell density correlates positively with naïve, central memory and effector CD4⁺ T cell number but negatively with exhausted T cells and Treg cells (Germain et al., 2021).

The metabolism of the TME represents a key point in the polarization of the tumor-specific immune response. There exists evidence that low-glucose and high-lactate environment within the TME constraints T cell effector function, while promoting Treg generation and immunosuppression (Wang et al., 2018). Treg cells in tumors rely on a combination of glycolysis and fatty acid synthesis and oxidation, which allows their survival and proliferation in the hostile tumor environment (Pacella et al., 2018). A recent study has further elucidated that high-glucose conditions impair the function and stability of Tregs. Interestingly, Tregs have evolved to benefit from the symbiosis with tumors by utilizing the glycolytic by-product lactic acid (LA); indeed, they incorporate lactate-derived carbon into phosphoenolpyruvate (PEP) to provide upstream glycolytic intermediates essential for proliferation. This offers the opportunity to decrease their need for glucose, thus preserving Foxp3 induction and suppressive function (Watson et al., 2021). In addition, very recently the link between LA and PD-1 expression in TILs has been clarified; more in detail, LA upregulated PD-1 expression by eTregs through MCT1, which is controlled by Foxp3 under a low-glucose and high-LA TME. Conversely, the effect of high LA concentration on PD-1 expression by CD8⁺ T cells shows an inverse trend. This means that the efficacy of PD-1 blockade against tumors is improved by targeting the LA metabolism of Tregs (Kumagai et al., 2022). Zappasodi and colleagues recently showed that CTLA-4 blockade promotes immune cell infiltration and metabolic fitness especially in glycolysis-low tumors.

Accordingly, inhibition of tumor glycolysis ameliorates the ability of CTLA-4 blockade to induce loss of Treg stability associated with the development of anti-tumor immunity (Zappasodi et al., 2021). Moreover, increased lipid metabolism in intratumoral Tregs, which is known to boost their suppressive function, is a shared event in human and mouse cancer, occurring through the CD36 up-regulation. CD36 supports mitochondrial fitness and biogenesis *via* a peroxisome proliferator-activated receptor- β (PPAR- β)-dependent mechanism by modulating NAD⁺ levels that allow Tregs to adapt to a lactic acid-enriched TME (Wang et al., 2020). Recently, it has been reported that inhibition of fatty acid binding proteins (FABP)5, one of the lipid chaperones required to facilitate uptake and intracellular lipid trafficking, causes mitochondrial damage, mtDNA release and consequent activation of the cGAS-STING-dependent type I IFN signaling; this promotes greater suppressive capacity, a phenotype also evident in tumor Tregs (Field et al., 2020).

Recent studies have revealed the importance of Blimp1 in the regulation of effector Treg (eTreg) and Tfr cell stability and suppressive function. Tfr cells express Foxp3 and belong to eTregs, and share many features with Tfh cells, as high expression levels of PD-1 and CXCR5, which allow them to traffic to B-cell follicles in response to CXCL13 (Garg et al., 2019; Shen et al., 2019). To date, few reports reported that Tfr cells are increased in cancer patients (Cha et al., 2018; Li et al., 2019), but their mechanism of action in the tumor is still unclear. However, the formation of TLS and the increased proportion of Tfh and B cells within the tumors, as observed in mice with Blimp1-specific deletion in Treg cells, are associated with favorable outcomes and with an increased response to immunotherapy in several tumors (Dixon et al., 2021).

DISCUSSION

The development of specific immune responses is a common characteristic of tumor hosts, triggered by the inflammation resulting from recognition of antigenically aberrant transformed cells. As to whether tumor specific immune responses can be triggered locally has been long a matter of debate and the discovery of tumor associated TLS and of their composition represents a central point of discussion. Animal models of secondary lymphoid organs deficiency, such as the splenectomized LT α $-/-$ mice, have shown that the presence of tumor associated TLS is sufficient to induce effective antitumor immune responses (Schrama et al., 2008). Some characteristics of tumor associated TLS, such as the presence of mature dendritic cells, T cells and actively proliferating B cells (Ki67+) in close proximity, can be indicative of ongoing antigen specific activation. Despite very few studies have specifically associated TLS presence with tumor specific immunity (Germain et al., 2014; Kroeger et al., 2016; Overacre-Delgoffe et al., 2021), the strong prognostic value of these intratumoral lymphoid structures might indeed be related to their promoting effect on antitumor responses. Also, the predictive value of response to ICI-based immunotherapy further sustains a link between TLS and tumor specific immunity. Antibodies directed against PD-1, that

achieved the best clinical performance amongst ICIs, are thought to alleviate the suppressive signals impinging on tumor specific effector T cells in the tumor microenvironment and thus reactivate their cytotoxic functions. Also regulatory T cells can express high levels of PD-1 and other immune checkpoint molecules in the tumor microenvironment, and this may undermine the efficacy of ICIs as observed in gastric cancer (Kamada et al., 2019). It is therefore important to include TLS detection and characterization in tumor specimen analysis to improve the clinical management of the disease.

Regulatory T cells are found in tumors both scattered within the mass and associated with TLS. Studies on TLS-associated Tregs overall fit with their detrimental role in cancer and provide insight on their tumor promoting activities. Treg with a follicular phenotype (Foxp3⁺ Bcl6⁺ CXCR5⁺) have been the focus of recent studies, that highlighted a more powerful suppressive potential as compared to non-follicular Tregs (Sage et al., 2014a; Sage et al., 2014b; Eschweiler et al., 2021). In this view, follicular Tregs hold therapeutic potential to improve current therapies. There is indeed evidence that anti-CTLA-4 blocking antibodies can deplete Tfr, because of their increased expression of CTLA-4, and this improves the efficacy of subsequent administration of anti-PD-1 (Eschweiler et al., 2021). It has also been shown that tumor infiltrating Tfr share TCRs with activated Tregs and thus they derive from TAA-specific Tregs that migrate into tumors and get activated in TLS.

Tumor associated tertiary lymphoid structures represent an incredibly informative tool in tumor management and their characterization should be included in routine tumor pre- and postoperative analysis in order to provide the most accurate grade of disease management.

AUTHOR CONTRIBUTIONS

AR, BB, AL, VD, and SC wrote the main body. AR wrote the introduction and the discussion and prepared the figures and the table. AR, VD, SP, CT, and SJ organized the review structure and revised the manuscript.

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Fine-tuning of regulatory T cells is indispensable for the metabolic steatosis-related hepatocellular carcinoma: A review

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The majority of chronic hepatic diseases are caused by nutritional imbalance. These nutritional inequities include excessive intake of alcohol and fat, which causes alcoholic liver disease (ALD) and non-alcoholic fatty liver disease (NAFLD), respectively. The pathogenesis of hepatic diseases is mainly dependent on oxidative stress, autophagy, DNA damage, and gut microbiota and their metabolites. These factors influence the normal physiology of the liver and impact the hepatic microenvironment. The hepatic microenvironment contains several immune cells and inflammatory cytokines which interact with each other and contribute to the progression of chronic hepatic diseases. Among these immune cells, Foxp3⁺ CD4⁺ regulatory T cells (Tregs) are the crucial subset of CD4⁺ T cells that create an immunosuppressive environment. This review emphasizes the function of Tregs in the pathogenesis of ALD and NAFLD and their role in the progression of NAFLD-associated hepatocellular carcinoma (HCC). Briefly, Tregs establish an immunosuppressive landscape in the liver by interacting with the innate immune cells and gut microbiota and their metabolites. Meanwhile, with the advancement of steatosis, these Tregs inhibit the proliferation, activation and functions of other cytotoxic T cells and support the progression of simple steatosis to HCC. Briefly, it can be suggested that targeting Tregs can act as a favourable prognostic indicator by modulating steatosis and insulin resistance during the pathogenesis of hepatic steatosis and NAFLD-associated HCC.

KEYWORDS

regulatory (Treg) cell, forkhead box P3 (FOXP3), hepatocellular carcinoma, metabolic liver diseases, nonalcoholic fatty liver disease -NAFLD, alcoholic liver disease -ALD, NAFLD-associated HCC

Introduction

Human beings acquire a sophisticated immune system that actively exists with complex biological mechanisms to defend the host by attacking and destroying the foreign substances (antigen) and transformed or infected cells. Simultaneously, numerous immune regulatory processes are projected to dodge the auto-immune mechanisms resulting against the body's own tissues. The immune system retains a distinct CD4⁺ cells population, regulatory T cells (Tregs), known to serve essential modulatory roles in immune homeostasis by maintaining peripheral tolerance and controlling the pathological and physiological immune response (Vignali et al., 2008; Lu et al., 2017). These Treg cells assist in limiting the inflammatory responses and abolish autoreactive T cells (Peterson, 2012; Scheinecker et al., 2020).

In 1970, it was first proposed that the presence of thymic-derived suppressor T cells, other than helper T (Th) cells, plays a role in self-tolerance by restricting the effector immune reactions (Gershon and Kondo, 1970). These suppressor T cells were later found responsible for the over-production of immunosuppressive cytokines, such as transforming growth factor β (TGF- β) and interleukin 10 (IL-10), which take part in the immune suppression (O'Garra and Murphy, 1994; Cottrez et al., 2000). Afterward, Sakaguchi et al. (1995), identified the IL-2 receptor α -chain (CD25 molecule) on the surface of these suppressive T cells and named Treg cells. It has been estimated that 5% to 50% of CD4⁺ T cells in the human peripheral blood are comprised of naturally arising CD25⁺ Treg cells that suppress immune activity (Sakaguchi et al., 1995; Gregg et al., 2005). Moreover, CD25⁺CD4⁺ Tregs were determined to express forkhead box P3 (FOXP3), a transcriptional factor which regulated the development and proper functioning of Treg cells (Hori et al., 2003). Therefore, these suppressor T cells can be characterized as CD4⁺CD25⁺FOXP3⁺ Treg cells in murine and humans (Ziegler, 2006).

Multiple mechanisms have been defined for the proper functioning of Treg cells. These include the secretion of cytokines and soluble factors, cell-to-cell contact, and changes in the extracellular milieu to target a diverse population of immune cell populations, such as antigen-presenting cells (APCs), CD8⁺ T killers and cell counterparts of conventional CD4⁺ T cells (Vignali et al., 2008). Emerging evidence suggests the presence of these Treg cells population residing or infiltrating in numerous peripheral organs where they mediate tissue-specific functions. For instance, peroxisome proliferator-activated receptor- γ (PPAR- γ) expressing visceral adipose tissue-specific Treg population execute highly distinct functions, including the regulation of numerous genes known to have crucial functions in lipid and glucose metabolism (Cipolletta et al., 2012). Similarly, in muscle and lung, the presence of amphiregulin, a ligand of epidermal growth factor receptor, expressing Treg cells population can directly expedite

the tissue repairing process (Burzyn et al., 2013; Arpaia et al., 2015). Foxp3⁺ Tregs play various roles in liver homeostasis and pathogenesis by interacting with other hepatic immune cells and hepatocytes. Hepatocytes have exhibited encytosis ability to engulf CD4⁺ T cells, predominantly Tregs, during hepatic inflammation to regulate T cell population (Davies et al., 2019).

Although the non-lymphoid tissue-specific Tregs molecular signature and functions have been interrogated in numerous investigations, our knowledge of the functions and fundamental biology of these liver-specific Treg cells and how they vary from other non-lymphoid Treg cells and immune cells is yet overlooked. Here, we reviewed the currently available studies about Treg cells that infiltrate the liver, emphasizing the mechanisms in the progression of chronic liver diseases from simple steatosis to hepatocellular carcinoma (HCC).

Treg cells in hepatic microenvironment

One of the largest internal tissues, the liver, connects with the gastrointestinal tract through the portal vein, which delivers multiple pathogenic and non-pathogenic antigens derived from the gastrointestinal tract (Jenne and Kubes, 2013; Kubes and Jenne, 2018). Therefore, besides enduring non-pathogenic organisms, it plays frontline immunological functions by establishing and escalating specific immune responses (Jenne and Kubes, 2013). As a vast organ, liver retains a predominant population of cells, including T lymphocytes, which are immunologically active and maintain essential immunological functions (Parker and Picut, 2012). The phenotypic characteristics and function of Treg cells differ between intrahepatic and circulatory compartments. This difference is due to the residence of Tregs in the hepatic microenvironment, which are deprived of sufficient oxygen while supplemented with inflammatory cytokines, hormones and metabolic products (Jeffery et al., 2016).

As the gut and liver are connected *via* the portal vein, several environmental factors, including dietary nutrients and metabolites, impact the functionality of Treg cells (Zeng and Chi, 2015). It is evident that gut microbiota and their metabolites strongly affect immune responses (Wu and Wu, 2012). Several microbial metabolites and bile acids have been linked with the expansion and stability of Tregs (Hang et al., 2019; Campbell et al., 2020; Song et al., 2020; Wiechers et al., 2021). Increasing evidence suggests that intake of short-chain fatty acids (SCFAs), metabolites produced by numerous symbionts, improves the proportion of Treg cells in mice treated with antibiotics (Arpaia et al., 2013). Similarly, oral gavage of microbes or SCFAs also activates Treg cells in response to several diseases (Ben Ya'acov et al., 2015; Smith et al., 2013). These gut microbiota and their metabolites also influence the normal physiology and immune response in the

liver (Visekruna and Luu, 2021). It can be suggested that microbiota and their metabolites can also play a vital role in stabilizing the Treg cells.

Bile acids, cholesterol metabolites, are immensely produced in the liver through a multiple-step complex process that involves peroxisomal, mitochondrial, and cytosolic enzymes (Russell, 2003). These bile acids are best known to regulate metabolic processes, cellular processes, and the immune system (Chiang and Ferrell, 2019; Fiorucci et al., 2021). Bile acids exert their function by activating numerous receptors, including RAR-related orphan receptor γ (ROR γ t), liver X receptors α/β (LXR α/β), farnesoid X receptor (FXR), vitamin D receptor (VDR), constitutive androstane receptor (CAR), pregnane X receptor (PXR), and membrane-bound G protein-coupled receptors Takeda G protein-coupled receptor 5 (TGR5) (Keitel et al., 2019; Shin and Wang, 2019; Cai et al., 2021). Among these receptors, FXR and TGR5 have been acknowledged as legitimate targets for treating metabolic-associated NAFLD (Arab et al., 2017). Activation of these receptors also influences and shapes the innate immune response, thus playing critical roles in the progression and development of NAFLD-related HCC (Schubert et al., 2017). Increasing evidence indicates that bile acids and their receptors also influence the adaptive immune system (Campbell et al., 2020; Song et al., 2020); however, the role of these receptors in adaptive immune response, especially in liver resident Tregs, is not studied well. A recent study identified isoallo-LCA and 3-oxo-LCA as metabolites of lithocholic acid (LCA). Among these, 3-oxo-LCA directly binds to the ROR γ t and suppresses the differentiation of Th17 cells. Meanwhile, isoallo-LCA stimulates mitochondrial ROS production and promotes Treg differentiation by increasing FOXP3 expression (Hang et al., 2019). Interestingly, obeticholic acid (OCA), FXR agonist, was approved by FDA for the treatment of primary sclerosing (Ali and Lindor, 2016). On the other hand, OCA ameliorates fibrosis and NASH; thus, it exerts beneficial effects by reducing hepatic cirrhosis (Shah and Kowdley, 2020). However, the effect of OCA and other bile acid molecules on the population and function of FOXP3⁺CD4⁺ cells is not studied.

It has been documented that fat-soluble vitamins are highly prevalent in the liver (Stacchiotti et al., 2021). A metabolite of vitamin A, all-trans retinoic acid (RA), plays a role in the growth, differentiation and proper functioning of immune cells, including Treg cells (Liu et al., 2015). In the liver, RA is produced by stellate cells, which increases the Foxp3 in CD4⁺ T cells and takes part in the development (Dunham et al., 2013), functioning and stability of the Treg cells during the inflammatory microenvironment (Zhou et al., 2010; Lu et al., 2014). TGF- β is considered one of the essential immunosuppressive cytokines that activate the population of CD4⁺ CD25⁺ FoxP3⁺ Treg cells (Kanamori et al., 2016). RA can directly influence and promote the TGF- β -dependent differentiation of naive T cells into the FoxP3⁺ Treg cells (Mucida et al., 2009; Martínez-Blanco et al., 2021).

Besides the TGF- β in an inflammatory hepatic microenvironment, several other pro-inflammatory cytokines, including IL-1, IL-12, IL-6, IL-8, and TNF α , are also present. However, it was reported that IL-2 is deficient, which is necessary for the overall survival of Treg cells (Chen et al., 2016a). Activation of APCs is known to secrete these pro-inflammatory cytokines (Blanco et al., 2008). These intrahepatic resident Treg cells also rely on the APCs for their differentiation, proper functioning, and survival. Tregs interact with APCs by binding with CD80/86 through CD28/CTLA-4, engaging with MHC Class II through TCR in the presence of antigen, and responding to APC secretory cytokines through cytokine receptors (Goddard et al., 2004; Lai et al., 2007). However, TGF- β , in combination with higher IL-6, generates IL-17 producing Th17 cells from naive T cells, which further suppresses the induction of Treg cells (Bettelli et al., 2006). In addition, hepatocytes also play an important role in the differentiation of Foxp3⁺ Tregs upon TCR stimulation from the CD4⁺ T cells via Notch-signaling (Burghardt et al., 2014). Resident Treg cells, even present in slightly lower regulatory potential, acquire an intact functional ability and affirm short-term lineage during culturing conditions that imitate and maintain the intrahepatic microenvironment (Chen et al., 2016a).

Immune metabolic pathways have been well studied for the activation, differentiation, survival, and proliferation of the immune cells, including metabolically active Treg cells (O'Neill et al., 2016; Wang et al., 2019). The expression of Foxp3, a pivotal transcription factor of Treg, is known to involve in metabolic pathways, such as glycolysis and fatty-acid oxidation (Fontenot et al., 2003; Gerriets et al., 2016; Angelin et al., 2017). During inflammatory circumstances, the ratios of metabolic supply-and-demand dramatically alter. Inflammatory lesions induce the level of hypoxia-inducible factor-1 α (HIF-1 α) in the tissues deficient in enough oxygen. HIF-1 α plays a vital role in enhancing the population and suppressive roles of thymic Treg (Ben-Shoshan et al., 2008; Clambey et al., 2012) by directly binding the promoter region of FOXP3 (Clambey et al., 2012). However, during an oxygen-deficient environment, the ablation of mTOR signaling is found to be involved in the elimination of the HIF-1 α functions (Land and Tee, 2007). Activating transcription factor 3 (ATF3), a member of ATF/CREB transcriptional family, is induced at early inflammatory responses by cytokines, i.e., IFN- α , IFN- β , IFN- γ and IL-4 (Farber, 1992; Drysdale et al., 1996). The absence of ATF3 escalated the mTOR-dependent induction of the HIF-1 α , which minimized the Foxp3⁺ Treg cells (Zhu et al., 2018). Therefore, the hypoxic anti-inflammatory process induces HIF-1 α that improves the population and functions of Treg cells by strengthening their effectiveness and reducing the proliferation of effector cells (Ben-Shoshan et al., 2008).

Conclusively, it is evident that hepatic immune responses and Treg population and functionality are greatly dependent on the

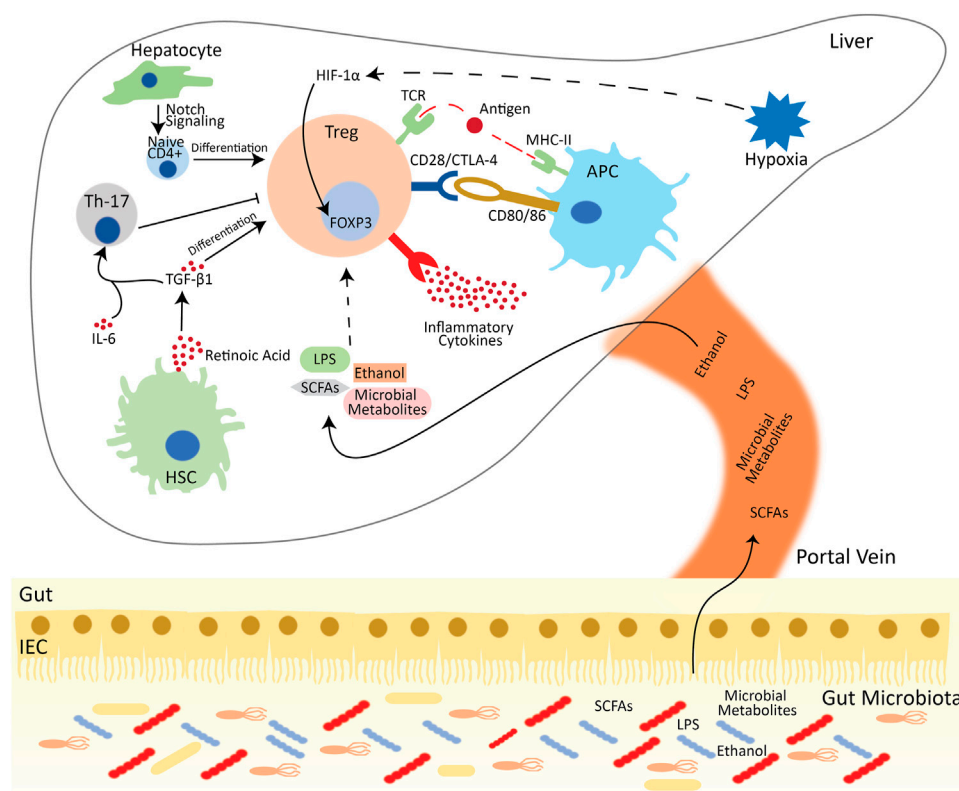


FIGURE 1

Treg mediated immune suppression in the hepatic microenvironment. Tregs are activated by interacting with the MHC-II on the surface of APCs in the presence of antigen. Tregs also suppress conventional T cells by interacting with pro-inflammatory cytokines and pairing with CD80/86 via CTLA-4/CD28 and deprive the co-stimulatory signal to responder T cells. Besides the APC, Tregs also interact with other hepatic cells. Hepatocytes differentiate the naïve CD4⁺ cells into FOXP3⁺ Tregs *via* notch signaling. HSCs release retinoic acid, which activates the TGF- β signaling and aids Tregs differentiation. Meanwhile, in the presence of IL-6, TGF- β activates Th-17 cells, which reduces the activation and development of Tregs. Additionally, in oxygen-deprived environment, HIF-1 α directly interacts with the FOXP3 and enhance the population of Tregs. Besides the intrahepatic regulation of Treg development and functions, gut microbiota and their metabolites also influence the Treg functions. Abbreviations: APC, Antigen presenting cell; Treg, regulatory T cell; Th-17, T helper 17 cell; HSC, hepatic stellate cell; IL, interleukin; CTLA4, cytotoxic T lymphocyte-associated antigen 4; DC, dendritic cell; CD, cluster of differentiation; TGF- β 1, transforming growth factor-beta 1; MHC, major histocompatibility complex; IEC, intestinal epithelial cells; LPS, lipopolysaccharide; SCFA, Short-chain fatty acids.

hepatic microenvironment (Figure 1). This hepatic microenvironment has an excessive hypoxic atmosphere due to higher blood supply, especially around zone 3 (Jeffery et al., 2016). Meanwhile, other environmental signalling, including environmental factors, microbial metabolites and metabolic pathways, also influence the transcriptional programming of Foxp3 and the functional plasticity of Treg cells.

Functions of Tregs in metabolic-associated chronic hepatic diseases

As mentioned earlier, the human liver acquires a large amount of blood supply, ~70%–80%, from the portal vein, which is intensified with numerous metabolites and nutrients (Balmer et al., 2014). Therefore, the liver-resident immune

cells, e.g., APCs, Tregs and T effector cells (Teffs), are continuously exposed to numerous signals which significantly impact their activation and alter their functions. Besides the effects of metabolites and nutrients on Tregs, innate immune cells and pro-inflammatory cytokines also impact the Tregs (Figure 2). Reported data on the immunosuppressive functions of Tregs suggest that intrahepatic suppression/overexpression or inadequate regulation of Tregs contribute to the onset of various diseases, including chronic hepatitis B&C virus (Cabrera et al., 2004), HCC (Unitt et al., 2005), autoimmune hepatitis (Longhi et al., 2004), alcoholic liver disease (ALD) (Matos et al., 2013), non-alcoholic liver disease (NAFLD) (Rau et al., 2016), primary biliary cirrhosis (Lan et al., 2006), acute rejection after liver transplant (Demirkiran et al., 2006). Here, we will be focusing on the function of

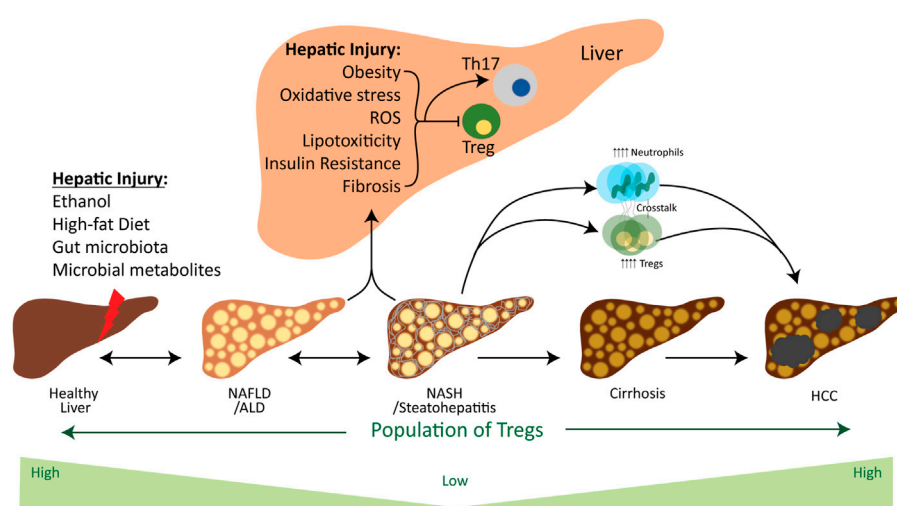


FIGURE 2

Influence of factors involved in the chronic liver disease spectrum on the Treg cells. Hepatic injury is caused by various environmental stressors, including ethanol, a high-fat diet and gut microbiota and their metabolites. These stressors initiate the simple steatosis and lead to steatohepatitis and cirrhosis in the liver, which finally progresses towards the tumor development. In the beginning, environmental stressors induce hepatic oxidative stress, ROS, lipotoxicity, insulin resistance, fibrosis and obesity, which are the pathogenic factors for ALD, NAFLD, NASH and HCC. These factors considerably contribute in downregulating the activation of Tregs and their population for the development of steatosis and fibrosis. However, the progression of NASH towards the tumor development increases the population of Tregs to establish a pro-tumor microenvironment. Meanwhile, adaptive and innate immune systems communicate with each other through Tregs and neutrophils, which aid in the progression of NAFLD-associated HCC. Abbreviations: Treg, regulatory T cell; Th-17, T helper 17 cell; NAFLD, Non-alcoholic fatty liver disease; ALD, alcoholic liver disease; NASH, non-alcoholic steatohepatitis; HCC, hepatocellular carcinoma.

Tregs in metabolic-associated chronic hepatic diseases, including ALD, NAFLD, NASH, and NAFLD-associated HCC.

Role of Treg in alcoholic liver disease

Alcohol abuse, an emerging and alarming health concern with high mortality worldwide, encompasses a broad range of injuries. These include alcoholic liver disease (ALD) with mild steatosis to steatohepatitis, fibrosis, and cirrhosis, leading to hepatocellular cancer (O'Shea et al., 2010; Breitkopf et al., 2009). It has been estimated that excessive alcohol intake is responsible for up to 4% of the yearly deaths (Singal and Anand, 2013). Ample evidence suggests that innate and adaptive immune responses are entailed in the development, pathogenesis and progression of ALD (Mille r et al., 2011; Albano, 2012; Gao et al., 2019). Alcoholic hepatic injury recruits peripheral immune-related cells, including infiltrating monocytes, neutrophils and T lymphocytes (Chedid et al., 1993; Nagy, 2015). Excessive exposure to alcohol or chronic ALD leads to the dysregulation of the balance between these immune cells and disruption of the immune activity. It contributes to the development of the unresolved inflammation features of ALD.

The role of inflammatory response activation and aberrant immune responses in worsening the ALD and its outcome has

been extensively studied. It is generally believed that mild or excessive ethanol abuse may modify the immune responses and functions (Szabo et al., 2011; Azizov et al., 2020; Luck et al., 2021). Ethanol impairs the functions of APCs and monocytes, decreases the proliferation of T cells and interferes with the expression of adhesion molecules (Szabo and Mandrekar, 2009). During the progression of ALD, there is an increase in the production of pro-inflammatory chemokines/cytokines by the liver resident macrophages, i.e., kupffer cells (KC) (Slevin et al., 2020). Meanwhile, damaged hepatocytes may produce several antigens to initiate the intrahepatic immune responses, resulting in massive intrahepatic inflammatory cell recruitment, including Treg cells (Viitala et al., 2000).

With the advancement in experimental techniques, multiple T cell subtypes have been identified. It has been recognized that alcohol exposure impacts the T cells phenotypes and Treg cells population (Matos et al., 2013). Earlier studies elucidating the molecular mechanism underlying the progression and development of ALD illustrated the presence of CD4⁺ and CD8⁺ cells in the liver biopsies from ALD patients (Chedid et al., 1993). The population of peripheral blood CD4⁺/CD25⁺ Treg cells is not altered (non-significant increase) in chronic alcoholic patients. Still, it significantly decreases with the increased inflammatory cytokines in patients with alcoholic hepatitis (AH) (Almeida et al., 2013). A similar relative and

absolute Treg population in AH, regardless of chronic hepatopathy symptoms, concluded that decreased CD4⁺/CD25⁺ Treg cells in AH depend on the acute hepatic inflammation (Almeida et al., 2013).

Similarly, Treg cells are most likely to participate in the pathogenesis of viral hepatitis in individuals with alcohol abuse. It was evident by the enhanced CD4⁺ FOXP3⁺ and CD25⁺ FOXP3⁺ Treg cell subtypes which were prompted in mice immunized with DCs, isolated from ethanol-fed mice, and loaded with HCV core (Ortiz and Wands, 2014). In contrast to decreased circulatory CD4⁺/CD25⁺ Treg cells in alcoholic patients (Almeida et al., 2013), another study reported an increased population of circulatory CD4⁺/CD25⁺ Treg cells in alcoholic patients (Ribeiro et al., 2017), suggested the role of Treg cells in reducing the detrimental effects of excessive alcohol intake on the liver. Meanwhile, it has been investigated that inflammatory immune response in ALD has resulted from the increased Th17 population (Kasztelan-Szczerbińska et al., 2015), and Treg cells reduce the development and differentiation of Th17 cells by modulating the levels of anti-inflammatory IL-10 and TGF- β cytokines (Chaudhry et al., 2011; O'Garra and Vieira, 2004; Lee, 2018). Likewise, the increased distribution of Treg cells close to the portal tract in the inflamed human liver demonstrates the close association with the suppression of immune response (Oo et al., 2010). Therefore, it can be suggested that an increased Treg cells population in patients with extreme ethanol might reduce the alcoholic hepatic inflammatory responses.

As previously described, the liver is directly connected to the gut and is continuously susceptible to harmless antigens and byproducts of gut bacteria. Currently available studies have discovered that alterations in the intestinal microbiome serve an important regulatory role in initiating ALD in humans and murine (Yan et al., 2011; Mutlu et al., 2012). Likewise, excessive alcohol intake may damage microbiome balance, distort the intestinal barrier, and lead to a dysfunctional liver and other vital organs (Bishehsari et al., 2017). Alcohol-induced intestinal barrier disruption helps the endotoxins, including lipopolysaccharide (LPS), and cytokines, including IL-6 and TNF α , to translocate into the liver and interact with hepatocytes and immune cells (Bala et al., 2014; Bishehsari et al., 2017; Zheng and Wang, 2021), which play pivotal roles in ALD and hepatic inflammation. Evidence of the ethanol-dependent modifications in the expression of CD4⁺ T Cell subsets in LPS-stimulated peripheral blood mononuclear cells suggests that ethanol impedes the Foxp3 kinetics and the production of IL-1 and TNF- α after the LPS challenge, thereby affecting the Treg/Th17 cells balance (von Haefen et al., 2011).

Ethanol intake damages the liver by reducing the population of Treg cells while increasing the Th17 cells population along with the production of IL-17 and increasing the intestinal permeability by reducing the expression of tight junction proteins (Wang et al., 2011; Chen et al., 2016b). Probiotic

supplementation is well known to improve the functions of the intestinal barrier by improving the expression of tight junction proteins and exerting protective effects in response to damaging factors, including alcohol abuse (Rao and Samak, 2013). *Lactobacillus rhamnosus* GG (LGG) is a probiotic that strives to treat and prevent various diseases by stimulating immune responses (Segers and Lebeer, 2014). A recent study showed that LGG supernatant supplementation ameliorates ALD by improving the population of Treg cells and decreasing the Th17 population (Chen et al., 2016b).

Alcohol consumption, either acute or chronic, lowers the antigen presentation by DCs, and reduces the T-cell proliferation and activation by affecting the levels of costimulatory molecules (Eken et al., 2011). Hepatic resident APCs activate the Treg cells from naive CD4⁺ precursors (Bamboat et al., 2009). In ALD-cirrhosis patients, diminished levels of circulatory IL-1 β , IL-6, IL-12, and TNF- α inflammatory cytokines, along with fewer number of circulatory DCs have been observed (Laso et al., 2007). Excessive alcohol consumption impairs the production of cytokines IL-6, IL-12, IL-17A and IFN- γ from APCs which are basically involved in initiating the adaptive immune response (Heinz and Waltenbaugh, 2007). Generally, ethanol diminishes the expression of stimulatory molecules on the surface of DCs, impairs their ability to prime T cells, affects the activation of naive T cells, and restricts the development of allogeneic T cells. Upon CpG stimulation, hepatic DCs collected from ethanol-fed mice exhibited reduced functional maturation (Lau et al., 2006). It implies that the alcohol-induced dysfunctional DCs might serve as a protective mechanism for immunosuppression by excessive alcohol drinking (Szabo, 1999; Lau et al., 2006) and may impair the Treg population.

Meanwhile, cell-cell interaction between DCs and Treg cells depends on the MHC-II for activation of Treg cells. Individuals with chronic alcohol intake may show lower MHC II-dependent T cell response (Chang and Norman, 1999). It can be advocated that besides the exclusive effects of alcohol on the cells responsible for innate immune response, early consequences on the adaptive immune system by alcohol contribute to the AH and ALD. Similarly, dysfunctional Treg cells are well known to contribute to the development and progression of these alcoholic diseases. However, the influence of alcohol on the roles of liver resident Treg cells is not studied well. Therefore, further investigations are necessary to improve our understanding of mechanisms underlying ALD and provide aid in finding novel therapeutic targets to treat AH and ALD.

Role of Treg in non-alcoholic fatty liver disease

Non-alcoholic fatty liver disease (NAFLD), affecting one-third of the population, is known for the presence of hepatic steatosis, which accelerates a series of hepatic diseases ranging

from non-alcoholic fatty liver (NAFL) to non-alcoholic steatohepatitis (NASH) and progress to cirrhosis and hepatocellular carcinoma (HCC) (Younossi et al., 2016; Younossi et al., 2018). Hypothetically, the progression of NAFLD has been illustrated in a “multi-hit” manner, which initiates the accumulation of lipids in hepatocytes. Afterward, an increase in free fatty acids secretion from adipocytes, oxidative stress, decreased adiponectin, and increased pro-inflammatory cytokines (resistin, leptin, TNF α , and IL-6) collectively prompt the development of hepatic steatosis and inflammation (Starley et al., 2010). Meanwhile, several other factors, including TGF- β 1-dependent collagen deposition, macrophage activation, hepatic reactive oxygen species (ROS), metabolically active natural killer T cells (NK-T) and CD8 $^{+}$ T cells, and imbalance between Th17 and Treg, take part in the disease progression beyond NAFL (Wolf et al., 2014; Paquissi, 2016).

Increasing evidence suggested the close association of NASH with activated innate immune response in mice (Tosello-Tramont et al., 2012) and humans (Malehmir et al., 2019). However, the role of adaptive immunity and Treg cells in NASH hasn't been studied well. A recent clinical study showed the low population of resting Tregs in the peripheral blood of NASH patients and an increase in intrahepatic Th17 cells (Rau et al., 2016), suggesting that higher Th17/rTreg is engaged in NAFL to NASH progression. Another study indicated that NAFLD-related severe hepatic inflammation in children was linked with higher intralobular Foxp3 $^{+}$ lymphocytes, while adults exhibited decreased Foxp3 $^{+}$ and higher IL-17A $^{+}$ lymphocytes in portal/periportal (P/P) tracts (Cairolì et al., 2021). Similarly, the high-fat diet (HFD)-induced NAFLD model showed an elevated population of intrahepatic Th17 cells. This increased Th17 and IL-17 are linked with the development of steatosis and the expression of pro-inflammatory cytokines (Tang et al., 2011). Subsequently, increased Th17 in liver during the chronic liver injuries exhibits a decreased proportion of Treg cells with the increased IL-6, IL-17 and IL-23 (He et al., 2017; Khanam et al., 2019).

Insulin resistance (IR), lipotoxicity and adipose inflammation are the hallmarks of NAFLD. Generally, lipotoxicity accelerates the pathogenesis of NAFLD by aggravating hepatic inflammation, adipose tissue inflammation and IR (Manco, 2017). It has been implicated that CD4 $^{+}$ T cells, especially Tregs, play critical roles in the regulation of IR, adipose inflammation and obesity. For instance, Tregs repress the immune response, whereas Th1 and Th17 cells enhance adipose inflammation (Bluestone et al., 2009; Newton et al., 2016). Upon activation, resting naive CD4 $^{+}$ T lymphocytes are differentiated into Tregs and T_H17 cells and employ immunological responses. Obesity and IR affect the Treg cells by suppressing their differentiation or impairing their functions (Feurerer et al., 2009; Cipolletta et al., 2012; Wagner et al., 2013). It was found that maintenance of Tregs in VATs of HFD-induced obese animal model significantly reduces adipocyte size and

decreases the body weight gain and visceral adipose tissue weight; thus, impairing Tregs worsens HFD-induced obesity and IR in mice (Tian et al., 2011; Cipolletta et al., 2012).

Several cellular metabolic activities, including inflammation, stress responses, and cell survival, are responsible for the oxidative stress and production of ROS within the cells (Pizzino et al., 2017). ROS production promotes hepatic inflammation, fibrogenesis and lipotoxicity in NAFLD (Delli Bovi et al., 2021). Lack of fatty acid β -oxidation along with intensive lipogenesis cause the excessive accumulation of triglycerides within the hepatocytes. During the process of NASH, increased ROS combines triglycerides and leads to IR and hepatic steatosis (Mansouri et al., 2018). Oxidative stress in the liver exerts detrimental effects on the hepatic Tregs. It was observed that oxidative stress induces Treg apoptosis and leads to their deletion within the steatotic liver (Ma et al., 2007), and consequently increases hepatic inflammation and activates TNF- α signaling pathway. This results in further hepatic injury, including the progression of simple steatosis to steatohepatitis, especially when liver is exposed to endotoxins, e.g., LPS, which can be delivered to liver or endogenously produced by gut microbiota (Ma et al., 2007; An et al., 2021). Moreover, adoptive transfer of Tregs have decreased HFD-induced intrahepatic TNF- α signaling and diminished the LPS-induced hepatotoxicity (Ma et al., 2007).

As mentioned earlier, activation of Tregs and their ability to perform suppressive functions are somehow dependent on the MHC-II. Liver sinusoidal endothelial cells (LSECs) and KCs are the key MHC-II expressing hepatic APC populations, which display antigen to Tregs and other CD4 $^{+}$ T cells (Wiegard et al., 2005). These Treg cells stimulated by KC and LSEC suppress the other CD4 $^{+}$ T cells proliferation (Wiegard et al., 2005). Similarly, hepatocytes can express MHC-II during hepatic inflammation, which helps them contribute to inflammatory immune responses by overcoming Treg suppressive functions during microbial antigenic signals (Herkele et al., 2003; Wiegard et al., 2005). The inflammatory hepatic microenvironment, i.e., TNF- α , IFN- γ and oxidative stress induced by KCs and DCs impair the survival and induce the apoptosis of Foxp3 $^{+}$ Treg cells during the apoptosis of hepatocytes and NASH (Ma et al., 2007; Roh et al., 2018). However, another study reported that the population of hepatic Tregs enhanced during the NASH, and depletion of Tregs can significantly inhibit the development of HCC from choline-deficient, high-fat diet feeding and diethylnitrosamine injection-induced NASH model (Wang et al., 2021). These opposing findings describing the functions of Tregs in NASH could have resulted from the different NASH models, or there is a probability that Tregs exert contrasting functions during the early and late NASH.

KLF10 is a well-known responsive transcription factor of TGF- β 1, which regulates the functions and differentiation of T_H17 and Tregs (Cao et al., 2009). A recent study concluded that the expression of KLF10 is significantly reduced in T_H17 and

Tregs isolated from peripheral blood and spleen of HFD-induced and obese mice (Wara et al., 2020). It is known that diet-induced obesity and liver diseases increase the immune cell accumulation in the liver and aggravate hepatic inflammation and lipid metabolic dysfunction (Dallio et al., 2021). CD4⁺ T cell-specific KLF10 deficiency leads to inflammation in adipose tissue, IR, obesity and the onset of NAFLD with impaired Treg accumulation (Wara et al., 2020). However, adoptive transfer of Tregs in CD4⁺ T cell-specific KLF10 deficient mice impede obesity, IR, adipose tissue inflammation and fatty liver phenotype (Wara et al., 2020). Overall, Foxp3⁺ Tregs exert protective roles during the progression of NAFLD from simple steatosis to steatohepatitis. Therefore, it can be concluded that despite the activation and marginal clonal expansion of hepatic T cells in NASH, the increased population of Treg counterbalance these effects. Meanwhile, the adoptive transfer of Treg in NASH aggravates the disease severity (Dywicki et al., 2022). Overall, the current understandings of the protective function of Tregs are still limited and need additional investigations to provide aid in treating NAFLD and NASH through Treg targeted therapy.

Role of Treg in NAFLD-associated HCC

HCC is deemed a major histological type of primary liver cancer which accounts for approximately 75% of all hepatic cancers (McGlynn et al., 2015). Leading evidence suggests that a high incidence of NAFLD and the ultimate progression of liver diseases are the leading causes of HCC. NASH leads to the hepatocytes' death and compensatory proliferation, and converts the mild fibrosis to advanced fibrosis with elevated levels of TNF α , TGF- β 1 and IL-18, which increase the risks of HCC (Anstee et al., 2019). The tumor microenvironment comprises cancer cells, immune cells and their mediators, and pro-inflammatory cytokines and chemokines (Gallimore and Simon, 2008). In the liver, the pathogenesis of NASH-associated HCC exclusively depends on the intrahepatic inflammatory and immune responses, autophagy, oxidative stress and DNA damage (Wolf et al., 2014; Anstee et al., 2019). Immune evasion of cancer cells is regulated by various immune suppressor mechanisms, which involve different subsets of immune cells and contribute to the initiation and progression of HCC (Greten et al., 2015). Meanwhile, lymphocytic infiltrate at the tumor site decreases the risk of a recurrent tumor and increases the overall survival rate (Greten et al., 2013). However, the role of T cells, especially Tregs, in NASH-associated HCC is not understood well. Striking evidence advocated that the Tregs population increases in peripheral blood and tumor tissues collected from HCC individuals (Guo et al., 2014). Therefore, researchers believe that increase in Tregs may exert adverse

effects on the HCC disease prognosis (Wilke et al., 2010), and an augmented ratio of effector CD4⁺/Treg cells represent a better prognosis for HCC (Kalathil et al., 2019).

Several studies have determined the critical role of CD4⁺ T cells in the initiation and progression of HCC. CD4⁺ T cells generally impede the HCC initiation and progression, thereby contributing to the tumor regression (Rakhra et al., 2010). Tregs adversely affect the local immune microenvironment (Nishida and Kudo, 2017). FOXP3⁺ Tregs exert immunosuppressive functions in the tumor settings by restricting the development and activation of anti-tumor effector cells and facilitating the tumor immune escape (Khazaie and von Boehmer, 2006). Thus, elevated population of CD4⁺ CD25⁺ FoxP3⁺ Tregs promotes the disease initiation and progression by impairing the functions of effector CD8⁺ cells (Fu et al., 2007; Gao et al., 2007; Shi et al., 2018). Earlier studies have indicated that Tregs could regulate the differentiation and development of T cells by secreting anti-inflammatory IL-10 and TGF- β 1 or repressing the IFN- γ and the T cells proliferation, thereby inhibiting their immune function (Bergmann et al., 2011). Meanwhile, HCC tumors themselves secrete TGF- β 1, which serves as the foremost vital source of TGF- β 1 in HCC patients (Wang et al., 2016). This TGF- β 1 could be a major factor in activating the regulatory phenotype of Tregs and maintaining their biological functions (Marie et al., 2005).

The functional heterogeneity of CD4⁺ T cells embraces Teff and Treg cell functions depending on their differentiation (Sallusto and Lanzavecchia, 2009). HCC pathogenesis greatly depends on the selective loss of hepatic resident CD4⁺ T cells, which accelerates the progression of HCC from NAFLD liver (Ma et al., 2016). It is obvious that IFN- γ secreting cytotoxic CD4⁺ Th1 cells monitor and clear the premalignant senescent hepatocytes (Kang et al., 2011). However, FOXP3⁺ Tregs inhibit the proliferation and function of Th1 and other Teffs. Therefore, despite the decreased population of total CD4⁺ in NASH liver, an enhanced population of Tregs has been observed, which aggravates the inflammation in NASH by establishing the pro-tumorigenic settings and leading to the initiation of the NASH-HCC malignant process (Wang et al., 2021).

Yes-associated protein-1 (YAP1) is a transcriptional coactivator and downstream effector of the Hippo signaling pathway (Manmadhan and Ehmer, 2019). Several studies have reported the positive correlation of YAP1 with the severity of hepatocyte injury and the progression of NAFLD and NASH (Chen et al., 2018; Salloum et al., 2021). Moreover, inhibiting the YAP1, reported as an independent prognostic marker and associated with the disease-free survival HCC patients (Xu et al., 2009), restores hepatocyte differentiation, and reduces the tumor development and the advancement of HCC (Fitamant et al., 2015). Besides the direct evidence of YAP in the development of NAFLD-HCC, it was investigated that YAP is

necessary for the differentiation and immunosuppressive functions of Treg cells (Fan et al., 2017; Ni et al., 2018).

Mounting evidence indicated the potential role of gut microbiota in modulating T-cell immunity directly or *via* their metabolites, including SCFAs (Asarat et al., 2016). Microbial dysbiosis leads to the generation of excessive amounts of SCFA, especially butyrate, which aid in setting the tumor microenvironment (Singh et al., 2018). An ex-vivo investigation showed a positive correlation between Treg and butyrate. It indicated that gut microbiota in the NAFLD-HCC model expands the population of total and effector IL-10⁺ Tregs while decreasing the expansion of CD8⁺ cells (Behary et al., 2021). Similarly, it has been verified that IL-2 plays important role in the activation and expansion of CD8⁺ T cells (Chinen et al., 2016). The presence of peripheral Tregs consumes the IL-2, thereby attenuating the functions of CD8⁺ T cells (Chinen et al., 2016). Previous ex-vivo investigation implied that this T cell expression profile is triggered by the gut-microbiota isolated from NAFLD-HCC patients, but not cirrhosis, and demonstrated the microbiota and metabolites-specific regulatory effects on T cells in NAFLD-HCC (Behary et al., 2021). Together, all these investigations highlight the role of Treg in the onset of NAFLD-HCC. However, detailed mechanistic studies are still required to thoroughly understand the functions of Tregs in the pre-tumor process from NAFLD to HCC.

Conclusion

Chronic hepatic diseases, such as ALD and NAFLD, are emerging as the foremost cause of liver cancer and morbidity worldwide. It has been estimated that the prevalence of NAFLD-associated HCC will drastically increase (up to 45%–130%) in a decade (Grgurevic et al., 2021). The progression of hepatic diseases largely depends on several factors, such as ROS, oxidative stress, lipotoxicity, IR and gut microbiota. In the hepatic microenvironment, numerous hepatic parenchymal, non-parenchymal, innate immune cells, adaptive immune cells, and inflammatory cytokines and chemokines interact with each other to maintain immune homeostasis. However, factors contributing to metabolic steatosis disrupt this homeostasis which greatly affects the population of T cells in the hepatic microenvironment and leads to the CD4⁺ T cell infiltration in the liver. Numerous CD4⁺ T cell subsets participate in regulating the ALD, NAFLD, and NAFLD-related HCC disease progression. Among these T cells, FOXP3⁺ Tregs play pivotal roles in the progression of steatohepatitis and in creating pre-tumor microenvironment settings. It was suggested that during the hepatic injury, factors contributing to the disease progression reduce the activation and development of FOXP3⁺ Tregs. However, an

increase in Tregs is involved in tempering the features of ALD and NAFLD by reducing the steatohepatitis and fibrosis, and exerting the immunosuppressive effects by hindering the inflammatory cellular immunity (Albano, 2012; Ikeno et al., 2020). Meanwhile, an increased population of Tregs promotes tumor development by setting a premalignant stage for the progression of HCC in the NASH-associated liver (Wang et al., 2021). It is noteworthy that various parenchymal and non-parenchymal cells in the liver interact to induce an immune response. Increasing evidence demonstrates that various factors influence the activity and function of Tregs. However, studies reporting the impacts of Tregs on the hepatic parenchymal and non-parenchymal cells are not illustrated.

Tregs-targeted therapy is regarded as a prospective HCC therapeutic strategy. So far, numerous innovative therapeutic strategies have been reported to target Tregs in clinical trials. These strategies, including using small molecules or antibodies, disrupt the function or differentiation of Tregs (Tsung and Norton, 2015). Despite advancements in biological and cancer research, little attention has been paid to developing strategies targeting the Tregs, especially in NAFLD-associated HCC. Various effective therapies, including monoclonal antibodies (anti-PD-1, anti-PD-L1, and anti-CTLA-4), have shown favorable prognosis and improved overall survival rates in patients with solid tumours (Saleh and Elkord, 2020a). However, studies demonstrating the effect of these monoclonal antibody usages in treating NAFLD-associated HCC are limited and need attention. More importantly, considering the side effects and low efficacy of these monoclonal antibodies, it is important to identify new anti-tumor drugs and validate the efficacy of newly identified drugs alone or in combination with other immune checkpoint inhibitors. Treg-targeted therapy represses tumor growth by enhancing the infiltration of CD8⁺ cells at the site of the tumor, improving the functions of APCs and minimizing the infiltration of myeloid suppressive cells in TME (Saleh and Elkord, 2019; Saleh and Elkord, 2020b). Thus, realizing the significant effects of the adoptive transfer of Tregs in the NAFLD and NAFLD-related HCC (Van Herck et al., 2020), it is important to evaluate the efficacy of natural or engineered Tregs along with other immune checkpoint inhibitors in NAFLD, premalignant NAFLD and NAFLD-related HCC. Meanwhile, it is worthwhile to understand the effects and function of Tregs in HCC tumors induced by different causative agents and varying disease stages and histological grades.

In conclusion, the cell-cell interactions, production of inflammatory cytokines and chemokines, and antigens in the tumor microenvironment diversify the functional studies of Tregs in HCC tumors. A comprehensive and clear mechanistic understanding of the biology of hepatic Treg cells in the steatosis and premalignant process may lead to inventing novel therapeutic approaches that target Tregs to restrict and

treat chronic hepatic diseases, metabolic steatosis and NAFLD-associated HCC.

Author contributions

FR and PW prepared the draft. FP outlined the topic and edited it.

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Chimeric Antigen Receptor T Cells Targeting Cell Surface GRP78 to Eradicate Acute Myeloid Leukemia

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Acute myeloid leukemia (AML) is a serious, life-threatening hematological malignancy. The treatment outcome of relapsed or refractory AML patients remains dismal, and new treatment options are needed. Chimeric antigen receptor (CAR) T cells have been successful in improving the prognosis for B-lineage acute lymphoblastic leukemia and lymphoma by targeting CD19. However, CAR T-cell therapy for AML is still elusive, owing to the lack of a tumor-specific cell surface antigen and spare hematopoietic stem cells (HSCs). This study generated a novel CAR construction that targets the cell surface protein glucose-regulated protein 78 (GRP78) (csGRP78). We confirmed that GRP78-CAR T cells demonstrate an anti-tumor effect against human AML cells *in vitro*. In xenograft models, GRP78-CAR T cells effectively eliminate AML cells and protect mice against systemic leukemia, in the meanwhile, prolonging survival. In addition, GRP78-CAR T cells also specifically eradicate the primary AML patient-derived blast. In particular, GRP78-CAR T cells spare normal HSCs, highlighting that GRP78-CAR is a promising approach for the therapy of AML.

Keywords: GRP78, CAR T cell, acute myeloid leukemia (AML), hematopoietic stem cells (HSCs), cell surface

INTRODUCTION

In recent years, chimeric antigen receptor (CAR) T-cell treatment has achieved great success in clinical trials, especially those in which CAR T cells targeting CD19 have shown excellent response against B-cell lineage hematological malignancies (Scheuermann and Racila, 1995; Porter et al., 2011; Maude et al., 2014; Sommermeyer et al., 2017; Park et al., 2018). However, other subtypes of hematological malignancies, including acute myeloid leukemia (AML) with deficiency of a specific target on the cell surface lack effective therapy.

AML, the most common acute leukemia in adults, is characterized by a clonal expansion of myeloid blasts in the bone marrow, blood, and other tissues. The prognosis of AML patients is still poor, and the 5-year survival rate remains below 50% owing to resistance to the treatments and relapse of the disease. Unlike the B-cell malignancies with antigens that are exclusively expressed in B-cell lineages and B-cell aplasia, which is clinically tolerable, CAR-targeted antigens for myeloid cells are shared with normal hematopoietic stem cells (HSCs); thus, no ideal surface marker can distinguish between normal and tumor cells (Mardiana and Gill, 2020). Several CARs targeting CD33 (Wang et al., 2015) or CD123 (Ruella et al., 2016) show potency in the pre-clinical model; however, these CAR T cells are targeting both normal HSCs

and leukemic cells, which lead to myeloablation and bone marrow failure and induce significant cytokine release syndrome (Ehninger et al., 2014; Wang et al., 2015). To prevent the severe side effect induced by the CAR T-cell treatment, several approaches were utilized including limiting the persistence of CAR T cells through engineering a “safety switch” (Di Stasi et al., 2011); novel developed CAR T cells targeting CLL-1 or CD70 are efficient against AML without being toxic to normal HSCs (Tashiro et al., 2017; Wang et al., 2018; Sauer et al., 2021). In the past decades, numerous tumor antigens such as CD33, CD123, CLL1, and CD38 have been explored as target antigens for AML treatment (Jin et al., 2009; Walter et al., 2012; Wang et al., 2018; Cui et al., 2021), and the clinical trials for these CAR T-cell therapies reported improved outcomes. A phase I clinical trial showed that CLL1 CAR T-cell therapy has high efficacy and limited toxicity in relapsed and refractory AML patients (Zhang et al., 2021). Another clinical trial reported that four out of six (66.7%) relapsed patients achieved complete remission (CR) or CR with incomplete count recovery (CRi) after CD38-CAR T-cell infusion, and the clinically adverse effects of patients are manageable (Cui et al., 2021). Since the number of cases in these studies is limited, the safety and efficacy of CAR T-cell therapy for patients with relapsed/refractory AML requires further investigations.

Glucose-regulated protein 78 (GRP78; also known as Bip) as an endoplasmic reticulum (ER) chaperone protein is essential for protein quality control (Quinones et al., 2008). The accumulation of evidence shows that GRP78 contains anti-apoptotic function through activation of UPR and blocking caspase activation to enhance cell survival and contribute to tumor progression (Fu et al., 2007; Casas, 2017). In particular, GRP78 is expressed and located mainly within the ER lumen. However, a small fraction of GRP78 could re-locate to the cell surface on a certain type of cells, particularly tumor cells (Shin et al., 2003; Arap et al., 2004; Gonzalez-Gronow et al., 2009; Zhang et al., 2010). GRP78 on the cell surface of tumor cells promotes cell proliferation, metastasis, and resistance to drug therapy (Lee, 2007; Li and Li, 2012).

A proof-of-concept study reported that the cell surface GRP78 could be specifically targeted by peptidic ligands to induce tumor cell death in prostate and breast cancer models (Arap et al., 2004; Kim et al., 2006). The GRP78 monoclonal antibody MAb159 specifically shows inhibition of tumor cell proliferation and metastasis and leads to tumor regression (Liu et al., 2013). The inhibition of cell surface GRP78 by polyclonal N-20 antibody can suppress glioma cancer cell survival and proliferation (Kang et al., 2016). GRP78 was proven to be highly expressed on the cell surface of AML patients' peripheral blood cells, and it is also over-expressed in chronic lymphocytic leukemia patients' cells than in normal B cells, but not in T cells (Huergo-Zapico et al., 2012; Staquicini et al., 2018). Therefore, the overexpression of GRP78 on the plasma membrane of leukemia cells potentially provides a novel target for the therapy of hematological malignancies.

Here, we developed CAR T cells targeting cell surface GRP78 to specifically eradicate AMLs cells *in vitro* and *in vivo*.

METHODS

Cell Lines and Primary Samples

KG1a, HL-60, and U937 cell lines were from ATCC and were purchased from the China National Collection of Authenticated Cell Cultures and Conservation Genetics CAS Kunming Cell Bank. HL-60 and U937 cells were cultured in RPMI (Gibco) supplemented with 10% FBS, 100 U/ml penicillin, and 100 mg/ml streptomycin sulfate at 37°C with 5% CO₂. KG1a cells were cultured in RPMI (Gibco) supplemented with 20% FBS, 100 U/ml penicillin, and 100 mg/ml streptomycin sulfate at 37°C with 5% CO₂. Primary human AML blood samples were obtained from the West China Hospital of Sichuan University with the approval of patients. Blood and bone marrow from healthy donors were provided by the West China Hospital of Sichuan University with the approval of donors (#2022151).

Chimeric Antigen Receptor T-Cell Production

Primary T cells were isolated from peripheral blood of healthy donors using the RosetteSep Human T Cell Enrichment Cocktail (Stemcell Technologies) according to the manufacturer's protocol. The isolated T cells were confirmed by flow cytometry using phycoerythrin-conjugated anti-human CD3 (BioLegend, 300408). T cells were cultured in Advanced RPMI1640 (Gibco) supplemented with 10% FBS, 100 U/ml penicillin, 100 mg/ml streptomycin sulfate, and 200 U/ml IL2 (PeproTech). T cells were counted and stimulated by CD3/CD28 beads (Life Technologies) for 72 h and infected with lentiviral particles at an MOI of 100.

Cytotoxic T Lymphocyte Assay

The specific cytotoxicity of the CAR T cells was measured against the CFSE-labeled target cancer cells at indicated effector/target (E/T) ratios in triplicate wells. After 24 h of culture in Advanced RPMI 1640 (Gibco) supplemented with 10% FBS, 100 U/ml penicillin, and 100 mg/ml streptomycin sulfate, total cells were harvested, and dead cells were labeled with PI following flow cytometry analysis.

Cytokine Production Assay

Effector cells and target cells were cultured at varied E/T ratios in Advanced RPMI 1640 (Gibco) media for 24 or 48 h. Human interferon gamma (INF-γ; #KHC4021, Invitrogen), tumor necrosis factor (TNF; #550610, BD Biosciences), and granzyme B (#ab235635, Abcam) in the supernatant of culture were analyzed using a commercial assay according to the manufacturer's instructions.

Immunofluorescence

A total of 0.5×10^6 cells were collected and washed once with ice-cold PBS (pH 7.4) and incubated with anti-GRP78 (#PA1-014A, Thermo Fisher Scientific; 1:200 in 2% FBS PBS) for 60 min at 4°C. Cells were centrifuged and washed once with PBS followed by fixation in ice-cold methanol (100%) for 10 min at 4°C and washed once again with PBS. Cells were incubated in blocking buffer (2.5% BSA/10% goat serum/

0.1% Tween-20) for 30 min at RT. Incubation with goat anti-rabbit IgG (H+L) secondary antibody conjugated with Cyanine3 (#A10520, ThermoFisher Scientific, 1:200) in blocking buffer for 1 h at RT. After washing once with PBS, cell nuclei were stained with DAPI in PBS for 10 min in the dark. The cells were centrifuged and washed once with PBS, resuspended in 30 μ l PBS and dropped on the coverslip, mounted with Aqua-Polymount on the slide (#1860620, Polysciences Inc.).

Xenograft Animal Model

Six-week-old female NOD-Prkdcem26ll2rgem26Nju (NCG) mice were purchased from GemPharmatech Co., Ltd. (Jiangsu, China) and housed in a pathogen-free animal facility. Then, 1.0×10^6 KG1a-Luci or U937-EGFP-Luci cells were intravenously injected into NCG mice *via* the tail vein 1 week after arriving at the local animal facility. Moreover, 5.0×10^6 Non-CAR, MOCK-CAR, and GRP78-CAR T cells were intravenously injected via the tail vein on day 6 for U937-EGFP-Luci-injected mice and day 7 for KG1a-Luci-injected mice after leukemia cells were transplanted, followed by serial bioluminescence imaging to quantify the progression of the tumor. The bioluminescence images were captured using an IVIS imaging system and quantified by Living Image software 4.1 (PerkinElmer). Mice were injected intraperitoneally with Avertin (375 mg/kg) and D-luciferin (150 mg/kg) and imaged under anesthesia. Mice were sacrificed when they were in the moribund state or when they showed signs of hind limb paralysis or at end of the experiment time point (50 days post leukemia cell injection for U937-EGFP-Luci or 100 days for KG1a-Luci).

Flow Cytometry

Primary AML cells were isolated through density gradient centrifuge, and then the remaining red blood cells were lysed. For the cell lysis analysis of CD34⁺ progenitor/stem cell subsets, CD34-FITC mAbs (Clone 4H11, Invitrogen) were stained, and the positive subset was analyzed using the percentage of lysis after staining with PI. The transduction rate of CAR into T cells was detected using mKate signal. Flow cytometry was performed on a BD Fortessa flow cytometer, and results were analyzed using the software FlowJo v10.

RESULTS

Glucose-Regulated Protein 78–Chimeric Antigen Receptor T Cells Demonstrated Robust Cytotoxicity Against Leukemia Cells *In Vitro*

To access the expression of GRP78 on the cell surface, we performed live-cell staining with GRP78, observing enhanced GRP78 expression on the plasma membrane of multiple AML cell lines (**Figure 1A**; **Supplementary Figure S1**). Thus, the enriched GRP78 on the cell surface provides the opportunity to be targeted.

We constructed a Pep42 peptide into a second-generation CAR construct to generate GRP78-CAR that contains 4-1BB and CD3 ζ costimulatory signaling domains (**Supplementary Figure S2A**). Healthy T cells were expanded and transduced by a GRP78-CAR lentivirus, and Non-CAR, MOCK-CAR, and CD19-CAR were used as controls. The CAR lentivirus transduction is efficient in that more than 50% of T cells expressed CAR (**Supplementary Figure S2B**). The cytotoxicity of CAR T cells was assessed by co-culturing with leukemia cells *in vitro* for 24 h. It was observed that GRP78-CAR T cells robustly elicited specific cytotoxicity against all three AML cell lines (**Figure 1B**; GRP78-CAR vs. Non-CAR, MOCK-CAR, and CD19-CAR). Next, we evaluated the dose-dependent cytotoxicity of the CAR T cells by progressively increasing the E/T ratio from 0.5:1 to 5:1. GRP78-CAR T cells exhibited robust lysis against AML cells, even at the 0.5:1 ratio for KG1a and U937 cells (**Figure 1C**). Considerable amounts of released cytokines including IFN- γ , TNF- α , and granzyme B were detected in the supernatant of the medium after GRP78-CAR T cells were co-cultured with AML cells (**Figure 1D**). Together, the result of the *in vitro* cytotoxicity assay provides compelling evidence that GRP78-CAR T cells can effectively kill AML cells *in vitro*.

Glucose-Regulated Protein 78–Chimeric Antigen Receptor T Cells Eliminate Human Acute Myeloid Leukemia *In Vivo* in Xenograft Mouse Models

The anti-leukemia cytotoxicity *in vivo* was validated through the human AML xenograft mouse model, in which 1×10^6 U937-EGFP-Luci leukemia cells were intravenously injected into NSG mice, followed by 5.0×10^6 Non-CAR T cells, MOCK-CAR T cells, and GRP78-CAR T cells injection at day 6 (**Figure 2A**). The burden of tumor cells was monitored over a series of days by luminescence imaging.

The mice injected with Non-CAR T cells and MOCK-CAR T cells showed first signs of disease, such as reduced mobility, hypothermia, and scruffy fur, within 17 days post injection, strikingly compared to 34 days for the mice injected with GRP78-CAR T cells (**Figure 2B**). Control mice that received Non-CAR T or MOCK-CAR T-cell injection displayed rapid progression of leukemia that 50% of animals succumbed 19 days post leukemia cell injection. In sharp contrast, among GRP78-CAR T-cell-treated mice, 50% survived more than 45 days after leukemia cell injection (**Figure 2D**). Moreover, three out of seven mice survived healthy for 50 days after tumor cell challenges, and tumor burden imaging confirmed that the vast majority of the leukemia cells were eliminated *in vivo* (**Figures 2C,D**).

We also tested the therapeutic efficacy of GRP78-CAR T cells by intravenous injection of AML KG1a-Luci cells into NSG mice, and the groups of mice treated with Non-CAR T cells, MOCK-CAR T cells, or GRP78-CAR T cells were monitored by bioluminescence at indicated days post injection (**Supplementary Figure S3A**). The AML burden in mice was

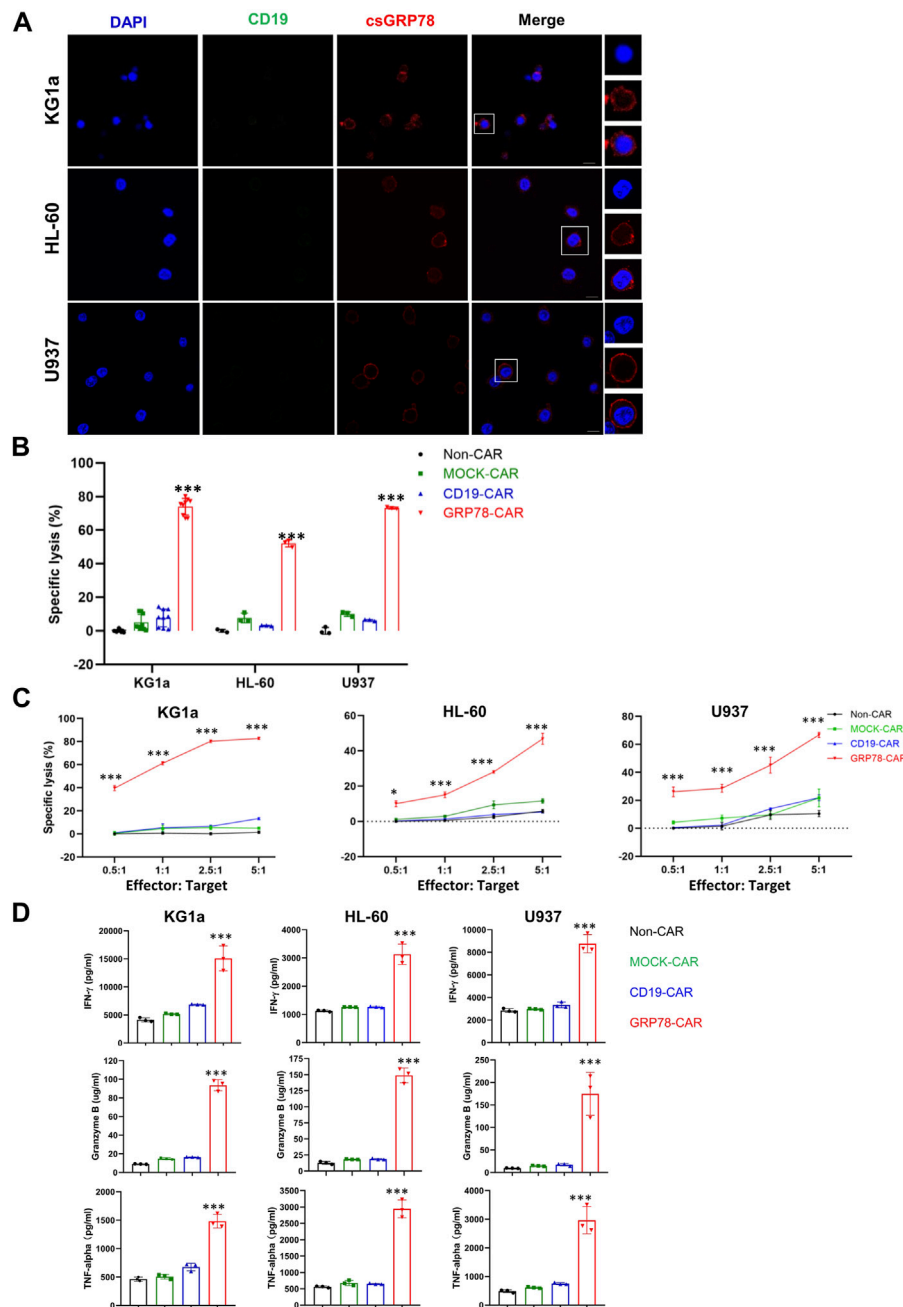


FIGURE 1 | Glucose-regulated protein 78 (GRP78)-chimeric antigen receptor (CAR) T cells demonstrate anti-leukemic effect against acute myeloid leukemia cells.

(A) Confocal image of representative immunofluorescence staining of cell surface GRP78 (red) and CD19 (green) on indicated leukemia cell lines. The denoted cells are zoomed on the right. The bars indicated 10 μ m length. **(B)** cytotoxic assay measuring the specific lysis of target cells. CFSE-labeled AML cell lines KG1a, HL-60, and U937 cells were co-incubated with Non-CAR T, MOCK-CAR T, CD19-CAR T, and GRP78-CAR T cells at an effector/target (E/T) ratio of 5:1 for 24 h. Experiments were repeated with at least triplicate samples. Data represent means \pm SDs. Two-sided Student's t-test was performed between GRP78-CAR and Non-CAR, MOCK-CAR, and CD19-CAR, *** p < 0.01. **(C)** leukemia cells were incubated with Non-CAR T, MOCK-CAR T, CD19-CAR T, and GRP78-CAR T cells at various (E/T) ratios as indicated. Percentages of lysis cells are shown as means \pm SDs. All experiments were repeated with at least triplicate samples. GRP78-CAR vs. Non-CAR, MOCK-CAR, and CD19-CAR T cells with the two-sided Student's t-test, *** p < 0.01. **(D)** ELISA measurements of cytokines interferon gamma (IFN- γ), tumor necrosis factor- α (TNF- α), and granzyme B in the cell supernatant were determined following 24-h incubation of target cells with specified CAR-T cells. Two-side Student's t-test was performed between GRP78-CAR T cell treatment and Non-CAR, MOCK-CAR, and CD19-CAR T cells. All experiments were repeated with at least triplicate samples. Data represent means \pm SDs. *** p < 0.01.

quantified and surrogated as bioluminescence, and the group of mice with GRP78-CAR T-cell injection exhibited strikingly lower bioluminescence signal than mice treated with Non-CAR T cells and MOCK-CAR T cells, indicating that the vast majority of KG1a leukemia cells were eradicated by GRP78-CAR T cells *in vivo* (Supplementary Figures S3B,C). After analysis of lymphoid organs of sacrificed mice, the residual leukemia cells in lymphoid organs are rarely detectable in mice injected with GRP78-CAR T cells (Supplementary Figures S3D,E).

Altogether, the *in vivo* AML xenograft mouse experiment is consistent with the *in vitro* cytotoxicity assay that GRP78-CAR T cells can eliminate leukemia cells both *in vitro* and *in vivo*.

Glucose-Regulated Protein 78–Chimeric Antigen Receptor T Cells Eradicated Primary Acute Myeloid Leukemia Blast

Next, we determined whether GRP78-CAR T cells could elicit cytotoxicity against primary AML blasts. A panel of normal

and primary AML blood samples obtained from healthy donors and AML patients were co-cultured with CAR T cells at an E/T ratio of 10:1 for 48 h. Cytotoxicity induced by CAR T cells against normal or patients' samples *in vitro* was determined by cytotoxic T lymphocyte assay. In total, 24 patients' blood samples were collected, and the fraction of blasts in peripheral blood cells varied from 18% to 99% including variable FAB subtypes (Supplementary Table S1). GRP78-CAR T cells induced significantly higher cytotoxicity against AML blast samples (6 out of 24, 25%), but no cytotoxicity to normal samples (Figure 3A). In contrast to control CAR T cells, GRP78-CAR T-cell treatments released significantly higher levels of cytokine IFN- γ to the supernatant, which indicates that GRP78-CAR T cells specifically elicit immune cytotoxicity to patients' AML blasts (Figure 3B). Furthermore, immunofluorescence staining was performed on GRP78-CAR T-cell response samples and confirmed that GRP78 is enriched on the plasma membrane of patients' tumor samples (Supplementary Figure S4).

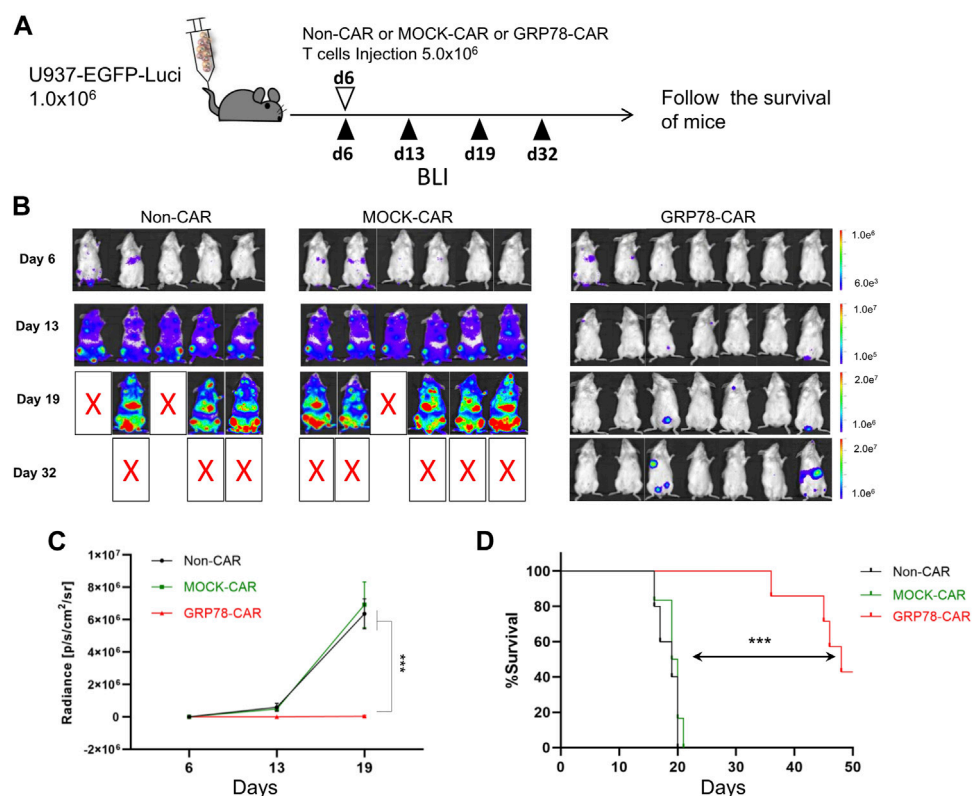
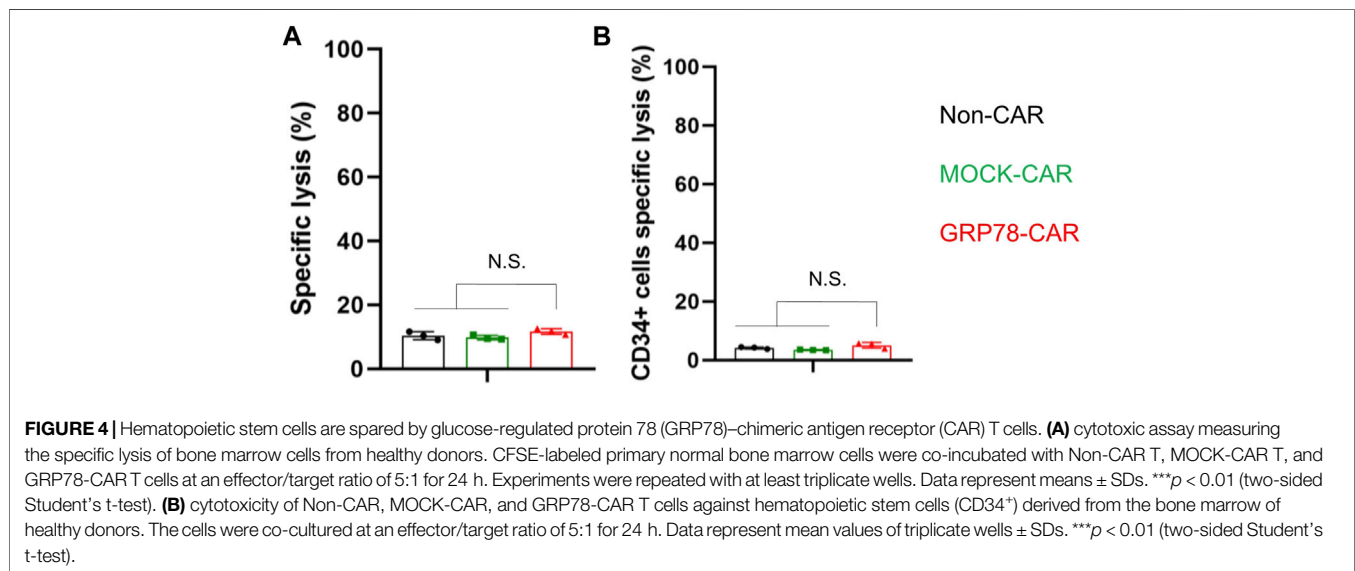
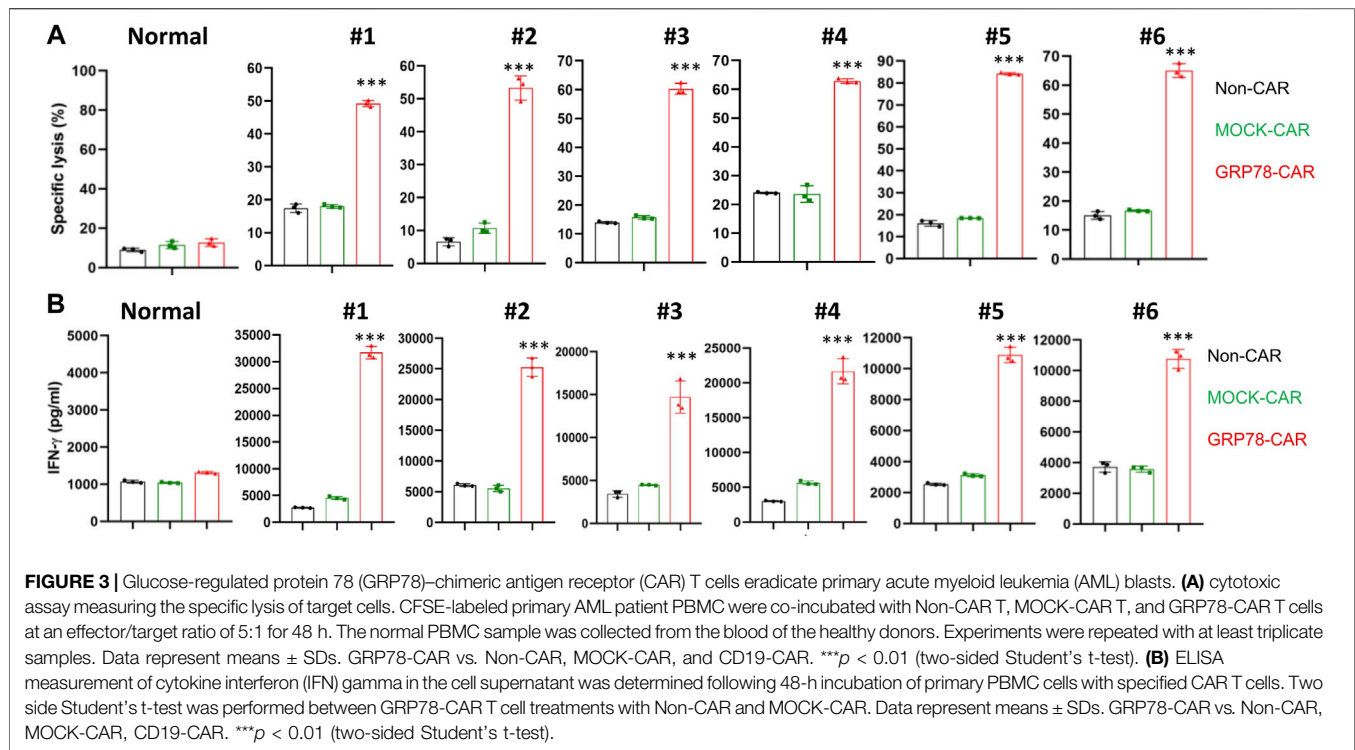


FIGURE 2 | Glucose-regulated protein 78 (GRP78)–chimeric antigen receptor (CAR) T cells eliminate human acute myeloid leukemia (AML) *in vivo* in xenograft mouse models. **(A)** Schematic of the U937 leukemia cell xenograft model. NSG mice were injected via the tail vein with 1×10^6 U937-EGFP luciferase (U937-EGFP-Luc) on day 0. Bioluminescent imaging (BLI) was performed on day 6 to quantify engraftment and for randomization of treatment groups. GRP78-CAR T cells (5×10^6), MOCK-CAR T cells (5×10^6), or Non-CAR T cells (5×10^6) were injected via the tail vein on day 6, followed with serial BLI. BLI radiance was measured as a surrogate quantification of tumor burden. **(B)** tumor burden was visualized by BLI on days 6, 13, and 19 following U937-EGFP-Luc cell transplantation. **(C)** bioluminescent signal for each treatment group over time. Data represent mean values of each group \pm SEMs. The number of mice in each group is listed in **(B)**. Two-way ANOVA test was performed between GRP78-CAR T-cell treatment and Non-CAR and MOCK-CAR T cells. *** $p < 0.01$. **(D)** Kaplan–Meier analysis of survival. Log-rank (Mantel–Cox) tests were used to perform statistical analyses of survival between groups.



Hematopoietic Stem Cells Are Spared by Glucose-Regulated Protein 78–Chimeric Antigen Receptor T Cells

The limitation of CAR T-cell treatment for AML is because of the lack of a tumor-specific antigen enriched in leukemia cells but not in normal cells and HSCs. Therefore, we isolated cells from the bone marrow of healthy donors after lysis of red blood cells to co-incubate with CAR T cells. GRP78-CAR

T cells exhibit a comparable level of cytotoxicity with Non-CAR and MOCK-CAR T cells (Figure 4A). Next, the cytotoxicity of engineered CAR T was tested on the HSCs (CD34⁺) derived from the bone marrow of healthy donors. After 24 h of co-culture of CAR-T cells with the cell mixture, no increment of cell lysis was observed on the CD34⁺ cell subpopulation (Figure 4B). Another sample from healthy donors showed a consistent result (Supplementary Figure

S5). Overall, stem cells derived from the hematopoietic system are not targeted by GRP78-CAR T cells, suggesting that the engineered GRP78-CAR T cell is a safe therapy for AML without the potential toxicity.

Regarding CAR lentivirus transfection that may lead to CAR T cells fratricide via self-targeting, we tested the GRP78-CAR T cells' induced cytotoxicity to primary T cells. It was confirmed that no significant cytotoxicity was induced by GRP78-CAR T cells in comparison to control CAR T cells and accompanied by a similar level of cytokine production (**Supplementary Figures S6A,B**). GRP78-CAR lentivirus transfection also exhibits no impairment to the T-cell proliferation (**Supplementary Figure S6C**), which facilitates the expansion and preparation of GRP78-CAR T cells *in vitro*. Furthermore, GRP78 was barely detected on the cell surface of normal T cells by immunostaining, which is consistent with the above observation (**Supplementary Figure S6D**).

DISCUSSION

AML is the most common acute leukemia in adults. Although for AML patients, CR is achieved in 60–80% of younger adults and 40–60% of older adults after standard chemotherapy, in the majority of cases, AML will relapse within 3 years (Döhner et al., 2010; Döhner et al., 2015; Döhner et al., 2017). CAR T-cell therapy is an emerged technology that is developed and proven to be an effective treatment for hematological malignancies, such as CAR T cells targeting CD19 for B-cell malignancies. However, the lack of effective CAR-T for the therapy of AML is because of the short of specificity. Previous studies reported that CAR-T cells targeted CD33/CD123, which antigens targeted both leukemia cells and hematological stem cells, indicating CD33/CD123 CAR-T treatment might result in the bone marrow failure (Pizzitola et al., 2014).

Current CAR T cells targeting CLL-1 and CD70 demonstrated cytotoxicity to tumor cells and spared CD34⁺ stem cells, indicating the potency of clinical implications for these two CAR T-cell treatments. However, it is well known that AML is featured with genetic heterogeneity and variable fusion genes as tumorigenesis drivers. Only a fraction of AML cells expresses CLL-1 or CD70 on the plasma membrane as the target for CAR T cells. Furthermore, relapse after CAR T-cell therapy remains a challenge owing to the mutation or down-regulation of the antigen on the tumor cell surface, which leads to the tumor escaping from CAR targeting and consequently results in resistance to therapy (Ruella and Maus, 2016; Shah and Fry, 2019). To overcome tumor antigen escape, the CAR is designed to simultaneously target multiple cell surface antigens, such as CD22 and CD20 (Zah et al., 2016; Fry et al., 2018). Therefore, it underscores the necessity of developing novel CAR T cells that target diverse antigens to combine or complement the current CAR T-cell therapy for AML and provide more options for patients.

GRP78, a chaperone protein that belongs to the heat-shock protein family, plays a crucial role in maintaining cellular homeostasis. It is an evolutionarily conserved protein that

presents in multiple subcellular positions and exerts distinct functions: retains in the ER to produce unfolded protein response, binds to mitochondria to interact with apoptotic executors, and resides in the plasma membrane to transduce proliferative signal as a receptor (Zhang and Zhang, 2010). The plasma membrane GRP78 has been uncovered in various human cancers, including leukemia (Staquicini et al., 2018), melanoma (de Ridder et al., 2011), prostate cancer (Arap et al., 2004), and colorectal cancer (Shin et al., 2003; Li et al., 2013). In the tumor cells, the cell surface GRP78 has a crucial role in protection from apoptosis, promotion of proliferation, evasion from immune surveillance, and resistance to various therapies (Gonzalez-Gronow et al., 2009; Zhang and Zhang, 2010). However, the mechanisms by which GRP78 is translocated to the cell surface remain elusive. Noting that the tumor cells exhibit a high level of GRP78 on the plasma membrane, targeting GRP78 to induce cytotoxicity of tumor cells becomes an attractive method. Several studies designed GRP78-binding peptides conjugated with cytotoxic drugs to precisely target cancer cells, which demonstrated promising results *in vitro* and *in vivo* (Arap et al., 2004; Kim et al., 2006; Yoneda et al., 2008). Jiang et al. (2019) constructed GRP78-targeted nanocage to specifically target and kill hepatocellular carcinoma and suppress lung metastasis. Here, we cloned Pep42, a cyclic oligopeptide that specifically targets cell surface GRP78, into a second-generation CAR construct to generate GRP78-CAR and demonstrated that GRP78-CAR T cells can effectively induce cytotoxicity of AML cells *in vitro* and eradicate explanted leukemia cells *in vivo*. Furthermore, in a cohort of 24 AML patients, we found that GRP78-CAR T cells effectively eradicated AML blasts in a fraction of AML specimens (25%) with different FAB subtypes, supporting its promising application for AML treatment.

In normal cells, previous studies reported that the functions of GRP78 are binding to polypeptides in the ER and activating unfolded protein response when polypeptides are overproduced. Thus, GRP78 resides in the lumen of the ER to maintain intracellular homeostasis. Besides, several studies have uncovered that GRP78 can also express on the plasma membrane of various cancer cells and endothelial cells (Davidson et al., 2005; Lee, 2007; Gonzalez-Gronow et al., 2009). Therefore, GRP78 serves as a suitable target for CAR T-cell therapy. In principle, CAR T cells targeting the cell surface of GRP78 have the advantage of sparing normal cells and specifically inducing cytotoxicity of tumor cells. In particular, for the therapy of AML, which requires greater cancer cell specificity, in pioneer studies, CAR T cells targeting antigens CD33, CD44, and CD123 have been developed (Jin et al., 2006; Jin et al., 2009; Walter et al., 2012). However, these treatments exhibit side effects when normal HSCs are targeted accompanied by bone marrow toxicity, which leads to myeloablation. Our result supports that GRP78-CAR T cells are not targeting the normal cells and avoid cytotoxicity to HSCs, which ensures the safety of GRP78-CAR T-cell therapy.

Aligned with our study, a recent study by Hebbar et al. (2022) also reported that GRP78 is a promising target for CAR

T cells in the therapy of AML. Both studies highlighted that GRP78-CAR T cells are able to eradicate the malignant cells *in vitro* and *in vivo* and the same peptide (Pep42) was chosen to construct CAR. Both studies confirmed that GRP78-CAR T cells are safe and would not impair the HSCs. In our study, we confirmed that 6 out of 24 fresh AML primary blasts can be eradicated by GRP78-CAR T cells, while they measured the expression of GRP78 in 14 primary AML samples without testing the cytotoxicity of GRP78-CAR T cells. Thus, we might provide more direct evidence of GRP78-CAR T cells' induced cytotoxicity to primary AML samples. In their study, flow cytometry was performed and demonstrated that GRP78 is expressed on the cell surface of more than half of primary AML samples using an antibody for ER retention sequence (KDEL) and a biotin-conjugated peptide, but the antibody used in the study is no longer supplied by the company. In our study, we performed immunostaining to assess the expression and visualize the localization of GRP78 for living AML cells and primary samples. We observed that GRP78 is expressed on the plasma membrane of three AML cell lines and 25% of primary AML samples, which is consistent with the cytotoxicity induced by GRP78-CAR T cells. The lower percentage of GRP78 we detected might be because of the difference in antibodies, more stringent criteria used in immunofluorescence staining, and the sizes of samples. Furthermore, the GRP78-CAR T cells generated in our study might be more effective than those generated by Hebbar et al. (2022). Their study proved the anti-AML activity of GRP78-CAR T cells *in vivo* by injection of 5×10^3 MOLM13 AML cells following 3×10^6 CAR T cells on day 7, whereas our study demonstrated that 5×10^6 GRP78-CAR T cells can eradicate explanted 1×10^6 of U937 or KG1a AML cells in the xenograft mouse models. Together, both studies uncover the anti-AML activity of GRP78-CAR, thus highlighting GRP78-CAR T-cell therapy as a promising approach in the clinic.

In this study, we constructed the GRP78-CAR and demonstrated that GRP78-CAR T cells manifested high cytolytic effects against AML cells *in vitro* and significantly eradicated the tumor in xenograft mouse models. Moreover, GRP78-CAR T cells could notably eliminate primary AML blasts, which indicates a substantial fraction of AML patients could benefit from GRP78-CAR T-cell therapy in the future. GRP78-CAR T cells showed no cytotoxicity on normal bone marrow cells and HSCs. Together, GRP78-CAR T cells can effectively eradicate AML and have the potency to be applied in clinical therapy.

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DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/**Supplementary Material**, and further inquiries can be directed to the corresponding authors.

ETHICS STATEMENT

The studies involving human participants were reviewed and approved by the Ethics Committees of West China Hospital of Sichuan University (#2022151). The patients/participants provided their written informed consent to participate in this study. The animal study was reviewed and approved by the Animal Ethics Committee of West China Hospital of Sichuan University.

AUTHOR CONTRIBUTIONS

WY, TL, and XZ conceived and designed the experiments. WY, HZ, and JT performed the experiments. YC provided the CAR plasmids. HZ collected the normal and patients' samples. XC provided the clinical data. All authors read and approved the final manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fcell.2022.928140/full#supplementary-material>

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Peritoneal resident macrophages in tumor metastasis and immunotherapy

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Macrophages residing in various tissues play crucial roles in innate immunity, tissue repair, and immune homeostasis. The development and differentiation of macrophages in non-lymphoid tissues are highly regulated by the tissue microenvironment. Peritoneum provides a unique metastatic niche for certain types of tumor cells. As the dominant immune cell type in peritoneal cavity, macrophages control the immune response to tumor and influence the efficacy of anti-tumor therapy. Considering the heterogeneity of macrophages in origin, metabolism, and function, it is always challenging to define the precise roles of macrophages in tumor microenvironment. We review here recent progresses in peritoneal resident macrophage research in the context of physiological and metastatic tumor conditions, which may benefit the development of new anti-tumor therapies through targeting macrophages.

KEYWORDS

resident macrophage, peritoneal metastasis, tumor immunity, immunotherapy, ontogeny, immune evasion, tumor microenvironment, tumor associated macrophage

1 Introduction

Macrophages are critical for immunity, tissue repair, and organ regeneration. Tissue resident macrophages are observed in multiple tissues and defined as a population genetically and developmentally distinct from inflammatory macrophages (Cox et al., 2021). Unlike blood monocytes or differentiated inflammatory macrophages, tissue resident macrophages maintain their population in-site *via* self-renewal without the contribution of blood monocytes and hardly move to other tissues (Yona et al., 2013; Dick et al., 2019). Genetic fate-mapping strategies in mouse developmental model indicates most of the tissue resident macrophages originate from colony-stimulating factor 1 receptor (*Csf1r*)-expressing erythromyeloid progenitors (EMPs) which arise at approximately embryonic day 8 (E8) from the yolk sac hemogenic endothelium (Gomez Perdiguero et al., 2015). At about E10, hematopoietic stem cells (HSCs) migrate into the fetal liver, which serves as the major organ of HSC differentiation until birth (Gekas et al., 2005). Meanwhile, HSCs progenitors replenish part of tissue resident macrophages under physiological and pathological contexts (Hashimoto et al., 2013; Bain et al., 2014). Although tissue resident macrophages in different tissues share

certain core activities, they display functional diversity to support the homeostasis of each tissue. Dysfunction of tissue resident macrophages causes severe and often fatal developmental disorders as reported in recent experimental works in mice (De Schepper et al., 2019; Oosterhof et al., 2019). Understanding their diversity and contribution to pathophysiological processes may provide new therapeutic targets for human diseases, especially tumor.

Tumorigenesis is mediated by mutated genes which not only support uncontrolled tumor cell growth but also protect them from immune surveillance. Tumor associated macrophages (TAMs) represent the dominant myeloid cell population in most types of solid tumors of both humans and mice. TAMs contribute to the immunosuppressive tumor microenvironment (TME) which protects tumor cells from anti-tumor immune response (Pittet et al., 2022). However, the connection between tissue resident macrophages and TAMs in different solid tumors is still not well understood. Monocytes have been considered as the precursors of TAMs for many years since CCL2/CCR2 signaling which recruits monocytes from bone marrow to tumor facilitates breast cancer metastasis (Qian et al., 2011). Furthermore, detailed research points out monocyte-derived macrophages, but not mammary tissue macrophages, promote the breast cancer development (Franklin et al., 2014). Recently, new research revealed the pro-tumoral role of tissue resident macrophages, similar to monocytic macrophages, in tumorigenesis and tumor growth among certain types of tumors. For example, the pancreatic tissue resident macrophages originate from embryonic hematopoiesis and promote pancreatic ductal adenocarcinoma (PDAC) progression (Zhu et al., 2017). Consistently, the lung resident interstitial macrophages contribute to the pool of TAMs together with CCR2-dependent recruited macrophages (Loyher et al., 2018). Moreover, we and other groups demonstrate that the peritoneal resident macrophages promote ovarian cancer development and metastasis into peritoneal cavity (Casanova-Acebes et al., 2020; Etzerodt et al., 2020; Xia et al., 2020). Therefore, the involvement of tissue resident macrophages may decide the fate of tumor progression.

Peritoneal cavity is a fluid-filled space located between the wall of the abdomen and the organs found in the abdomen. Peritoneal resident macrophages are well-studied as mouse primary macrophages in peritoneal cavity and share very similar characters with macrophages obtained from both pleural cavity and pericardial cavity. Peritoneal resident macrophages maintain serosal homeostasis and provide immune surveillance in the etiology of pathologies including peritonitis, endometriosis, and metastatic cancers. Here, we summarize the new concepts related to the development and differentiation of cavity-resident macrophages, especially peritoneal resident macrophages, and their roles in tumor metastasis and immunotherapy.

2 The basic biology of peritoneal resident macrophages in steady-state mouse

2.1 The phenotypes of peritoneal resident macrophages

Peritoneal macrophages have been used as the source of primary mouse resting macrophages for almost 60 years since Cohn and collaborators started to collect and analyze them in the 1960s (Steinman and Moberg, 1994). At that time, these cells were considered as an individual macrophage population since they are characterized by the classical mouse macrophage markers CD11b and F4/80. Further, peritoneal resident macrophages have been divided into large peritoneal macrophages (LPMs) and small peritoneal macrophages (SPMs) based on their size (Ghosn et al., 2010). In the meantime, the two subsets display phenotypic differences that LPMs have been found to be F4/80^{High}MHC-II^{Low} while SPMs to be F4/80^{Low}MHC-II^{High}. The LPMs are the long-lived macrophages since they express more mature markers as CD40, CD80, and CD86 (Ghosn et al., 2010). Some unique markers are specifically expressed on each subsets, for example T-cell immunoglobulin and mucin domain containing 4 (TIM4) and Intercellular adhesion molecule 2 (ICAM2) expressed on LPMs while CCR2 and CD226 expressed on SPMs (Kim et al., 2016) (Table 1). In steady-state mouse, LPMs are the dominant population (more than 90%) with very identical profiles while SPMs are a very small (less than 10%) and heterogeneous population consisted with several monocytic subsets (Bain et al., 2016; Kim et al., 2016).

2.2 The determinants of peritoneal resident macrophage differentiation

Several critical factors determine the formation of macrophage niches which control the size of the macrophage population and imprint their tissue-specific identity in peritoneal cavity, including the ontogeny, intrinsic factors, and local environment (Figure 1).

2.2.1 Ontogeny

It is important to understand how the tissue macrophages establish their compartment during mammalian development and aging. The population of tissue resident macrophages in different location and at different time points can arise from three distinct waves of precursors: early yolk sac macrophages, fetal liver monocytes, or bone marrow derived monocytes (Bleriot et al., 2020). In the steady state condition, most tissue resident macrophages in mice and humans originate from the embryonic stage and are maintained by self-renew but not differentiated from adult hematopoiesis (Ginhoux and

TABLE 1 The phenotypic difference between LPMs and SPMs in steady-state mice.

Surface markers	Peritoneal resident macrophages (LPMs)	Monocyte derive macrophages (SPMs)	References
CCR2	–	+	(Kim et al., 2016; Xia et al., 2020)
CD9	High	Low	Rosas et al. (2014)
CD11b	High	Low	(Ghosn et al., 2010; Gautier et al., 2012)
CD11c	+	+/-	(Ghosn et al., 2010; Bain et al., 2016)
CD24	+	–	Rosas et al. (2014)
CD40	High	Low	Ghosn et al. (2010)
CD49f	+	–	Okabe and Medzhitov, (2014)
CD64	+	–	Gautier et al. (2012)
CD73	+	–	(Okabe and Medzhitov, 2014; Rosas et al., 2014)
CD80	High	Low	Ghosn et al. (2010)
CD86	High	Low	Ghosn et al. (2010)
CD93	+	–	(Okabe and Medzhitov, 2014; Rosas et al., 2014)
CD102 (ICAM2)	+	–	(Okabe and Medzhitov, 2014; Kim et al., 2016; Bain et al., 2020)
CD206	–	+	Accarias et al. (2016)
CD209b	High	Low	Rosas et al. (2014)
CD226	–	+	Kim et al. (2016)
CRlg	+	–	(Rosas et al., 2014; Xia et al., 2020)
F4/80	High	Low	(Ghosn et al., 2010; Gautier et al., 2012; Okabe and Medzhitov, 2014; Bain et al., 2016)
MerTK	+	–	Gautier et al. (2012)
MHC-II	Low	High	(Ghosn et al., 2010; Okabe and Medzhitov, 2014; Bain et al., 2016; Kim et al., 2016)
TIM4	+	–	(Rosas et al., 2014; Bain et al., 2016; Xia et al., 2020)
TLR4	High	Low	Ghosn et al. (2010)

Level of expression: + positive; – negative.

Guilliams, 2016). Indeed, the fate-mapping studies demonstrate the precursors of LPMs migrate and reside in the peritoneal cavity during embryonic stage and are shaped by the tissue microenvironment (Yona et al., 2013; Bain et al., 2016). In the young mice, embryonic derived LPMs depend on self-proliferation to sustain their numbers. However, bone marrow derived macrophages can differentiate and acquire key characteristics of the embryonic population in peritoneal cavity and finally replenish the embryonic derived LPMs with aging (Bain et al., 2016).

2.2.2 Intrinsic factors

In addition to ontogeny, intrinsic factors also have an important effect on the peritoneal macrophage differentiation, such as genetic background, sex difference, and phagocytosis. Systematic genetic and epigenetic analyses of tissue resident macrophages from five diverse strains of mice discovered the macrophage identity was linked to more than 100 transcription factors that in turn bind to hundreds of connected cis-regulatory domains (Link et al., 2018). Therefore, mutation of these regulatory elements might disturb the specific macrophage

identity. For example, deletion of a specific enhancer of *Csf1r* gene, the *fms*-intronic regulatory element (FIRE), selectively affects peritoneal resident macrophage populations (Rojo et al., 2019). In addition, CCAAT/enhancer binding protein (C/EBP)- β , functioning as macrophage restricted lineage determining transcription factor, plays an intrinsic role in the generation of LPMs (Cain et al., 2013). Sex differences modulate the immune response (Wilkinson et al., 2022). Sex has been proposed to affect brain microglia differentiation (Thion et al., 2018). Similarly, peritoneal resident macrophages exhibit sexually dimorphic traits that their replenishment from the bone marrow is higher in males compared to that in females, which is driven by changes in the local microenvironment that arise upon sexual maturation (Bain et al., 2020). Phagocytosis, the phagocytes restricted activity to uptake the particles discovered by Ilya Metchnikoff in starfish larvae in 1880s (Epelman et al., 2014), transiently decides the resident macrophage identity by polarizing the cell toward an anti-inflammatory phenotype (A-Gonzalez et al., 2017). But the abilities of phagocytosis between LPMs and SPMs are not the same. At the early stage of infection, LPMs are the major bacterial

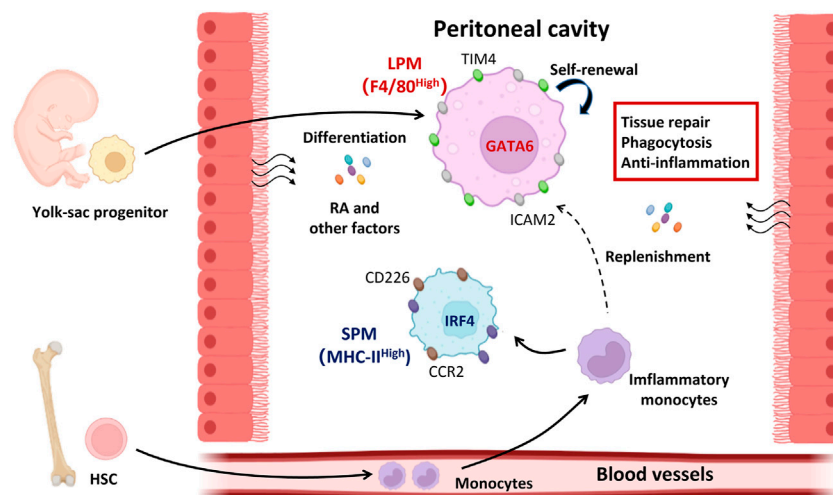


FIGURE 1

The determinants of peritoneal resident macrophage differentiation. Under steady state, both LPMs and SPMs represent the peritoneal resident macrophages. LPMs are dominant in the peritoneal cavity and function in tissue repair, phagocytosis, and anti-inflammation. LPMs are differentiated from the yolk-sac progenitors and maintain their numbers by self-renewal. Local environment supports the LPMs differentiation by secreting the retinoic acid and other factors. Different from LPMs, SPMs are differentiated from HSC derived monocytes and expand themselves in peritoneal cavity once inflammation occurs. The differentiation of LPMs is mediated by transcriptional factor GATA6 while that of SPMs is IRF4. GATA6, GATA binding protein six; HSC, hematopoietic stem cells; IRF4, interferon regulatory factor 4; LPMs, large peritoneal macrophages; RA, retinoic acid; SPMs, small peritoneal macrophages.

phagocytic cells beyond SPMs (Ghoshn et al., 2010). Consistently, it is convinced in the context of apoptotic cells clearance by peritoneal and pleural resident macrophages which is shown the transcription factors KLF2 and KLF4 initiate the apoptotic cell clearance program in tissue residential macrophages (Roberts et al., 2017). This type of program in peritoneal resident macrophages is context dependent and reversible.

2.2.3 Local microenvironment

The local microenvironment, so-called “niche of residence” (Guilliams and Scott, 2017), provides signals necessary for the maturation of functional resident macrophages from any precursor in a time-dependent manner. The transcriptional factor GATA binding protein 6 (GATA6) is responsible for the development and identity of peritoneal resident macrophage, specifically expressed in LPMs but not SPMs (Gautier et al., 2012; Gautier et al., 2014; Okabe and Medzhitov, 2014; Rosas et al., 2014). Retinoic acid, a metabolite of vitamin A, induces tissue-specific localization and functional polarization of LPMs through the induction of GATA6 expression (Gautier et al., 2014; Okabe and Medzhitov, 2014). The omentum which is formed by a double layer of mesothelial cells in peritoneal cavity provides continuous retinoic acid and other factors to support the LPMs profiles (Okabe and Medzhitov, 2014). Furthermore, transcription factor Wilms’ tumor 1 (WT1) positive mesothelial and fibroblastic stromal cells induce retinoic acid-dependent and -independent

hallmark genes of GATA6⁺ macrophages by expressing two rate-limiting enzymes, aldehyde dehydrogenases (ALDH)-1 and -2, in retinol metabolism (Buechler et al., 2019). Hence, serous cavity restricts the peritoneal resident macrophage identity.

2.3 The homeostasis of peritoneal resident macrophages

In newborn mouse, LPMs expand *via* local proliferation which is considerably reduced and most likely provides homeostatic control of cell numbers in the adult (Davies et al., 2011). The proliferative capacity of LPMs is determined by signals from the local microenvironment rather than their genetic heterogeneity and origin (Bain et al., 2016; Bain et al., 2020). CSF1-Fc or IL-4c is known to drive proliferation of peritoneal macrophages in steady state or TH-2 inflammation (Jenkins et al., 2011; Jenkins et al., 2013). During the resolution of inflammation, LPMs survive and then undergo a transient and intense proliferative burst *in situ* to repopulate the tissue which is M-CSF dependent and highly decided by the expression of GATA6. Selective GATA6 deficiency resulted in dysregulated peritoneal macrophage proliferative renewal during homeostasis and in response to inflammation, which was associated with delays in the resolution of inflammation (Rosas et al., 2014). In addition, GATA6-deficient macrophages are vulnerable to death and lead to a reduction of peritoneal resident macrophages by

lacking functional aspartoacylase (Gautier et al., 2014). Accordingly, mammalian target of rapamycin complex 2 (mTORC2) has been found negatively regulate the GATA6 expression by controlling forkhead box O1 (FOXO1) activation. Hence, mTORC2 deficiency enhances the generation of tissue-resident peritoneal cells through increased proliferation and cell survival (Oh et al., 2017).

Notably, the proliferation activity of peritoneal macrophage displays a sexual dimorphism that LPMs proliferate faster at the resolution stage of inflammation in male mice than that in female mice. Consistently, the signature of male peritoneal macrophages was dominated by cell cycle-associated genes compared to genes associated with lipid uptake and transport as well as immune response in female (Bain et al., 2020). Interestingly, peritoneal macrophages express estrogen receptors which mediated enhanced proliferation in response to exogenous estrogen. Furthermore, ovariectomy leads to a reduction in the number of macrophages which imply the sex maturation influences the biology of the peritoneal resident macrophages (Pepe et al., 2017).

2.4 The metabolic profiles of peritoneal resident macrophages

The metabolism of macrophage is highly linked with their activation, polarization, and function (Leone and Powell, 2020). Macrophages in tissue establish metabolic adaptation to support homeostatic tissue function and facilitate wound healing. The peritoneal resident macrophages express the GATA6 associated gene *Aspa*, which encodes the hydrolase enzyme aspartoacylase to catalyze the deacylation of N-acetylaspartate into aspartate and acetate (Gautier et al., 2014). The peritoneal cavity is enriched for N-acetylaspartate relative to its abundance in serum. Considering the acetate is the precursor of acetyl-CoA which has been used as fuel for the tricarboxylic acid (TCA) cycle, peritoneal resident macrophages displays higher level of mitochondrial oxygen-consumption rates compared with that in bone marrow derived macrophages *in vitro* (Davies et al., 2017). In addition, the concentration of glutamate is higher in the peritoneal cavity than in serum which is able to supplement glutamine to maintain respiratory burst during phagocytosis *via* enhancing mitochondrial complex-II metabolism in peritoneal resident macrophages (Davies et al., 2017). Consistently, peritoneal resident macrophages increase TCA cycle-associated genes and mitochondrial mass compared with monocyte derive macrophages. Inhibition of mTORC2 increases TCA cycle-associated genes expression and mitochondrial mass which may be due to the elevated GATA6 expression (Oh et al., 2017). Hence, the diversity of metabolites in peritoneal cavity may determine the metabolic profiles through modulating GATA6 expression in peritoneal resident macrophage.

3 The role of peritoneal resident macrophages in tumor metastasis into the cavity

TAMs are a key component of the TME which promote angiogenesis, tumor metastasis, and immune evasion (Mantovani et al., 2017). The serous cavity is a common metastatic site for a variety of malignant cancers, including colorectal cancer (Ceelen et al., 2020), gastric cancer (Song et al., 2019), ovarian cancer (Etzerodt et al., 2020; Xia et al., 2020), and lung cancer (Chow et al., 2021). When tumors metastasize into the peritoneal cavity, resident macrophages not only support tumor cell colonization and proliferation but also suppress the anti-tumor immune response (Figure 2).

3.1 The metastasis of tumors into peritoneal cavity relies on macrophages in omentum

The omentum is an adipose tissue layer containing certain milky spots (clusters of leukocytes) which are mainly composed of macrophages and B1 cells, resembling the cellular composition found in the peritoneal cavity. However, the phenotype of omental macrophages is different from peritoneal residential macrophages (Louwe et al., 2022). CD169 and LYVE1 are used to identify three omental macrophage subsets, in which the CD169^{High}LYVE1⁺ subset can be further divided into four subpopulations based on the expression of CD163 and TIM4. Interestingly, many of the CD163⁺TIM4⁺ cells are embryonic origin and support the growth of metastatic ovarian cancer (Etzerodt et al., 2020). In peritoneal metastasis, the colonization of omentum is always associated with poor prognosis which provides a critical basement for tumor metastasis into the peritoneal cavity (Coccolini et al., 2013). Consistent with this observation, omentectomy inhibits tumor growth in the peritoneal cavity through a surgical procedure to remove the omentum (Etzerodt et al., 2020). Mechanically, ovarian cancer frequently colonizes the omentum which is observed passively through the milky spots (Rangel-Moreno et al., 2009), or fascinated by neutrophil extracellular traps (Lee et al., 2019), or recruited by the chemokines like IL-8 and CXCL12 (Nieman et al., 2011; Kasagi et al., 2016). Macrophages play an important role to assist the tumor cell colonization into omentum. It is reported that omental macrophages promote the migration and colonization of ovarian cancer cells to the omentum through the secretion of chemokine ligands that interact with chemokine receptor 1 (CCR1), and inhibition of CCR1 reduces ovarian cancer colonization (Krishnan et al., 2020). In addition, macrophages are supposed to form the immune suppressive microenvironment in the milky spots which are selectively invaded by tumor cells (Oosterling et al., 2006; Clark et al., 2013).

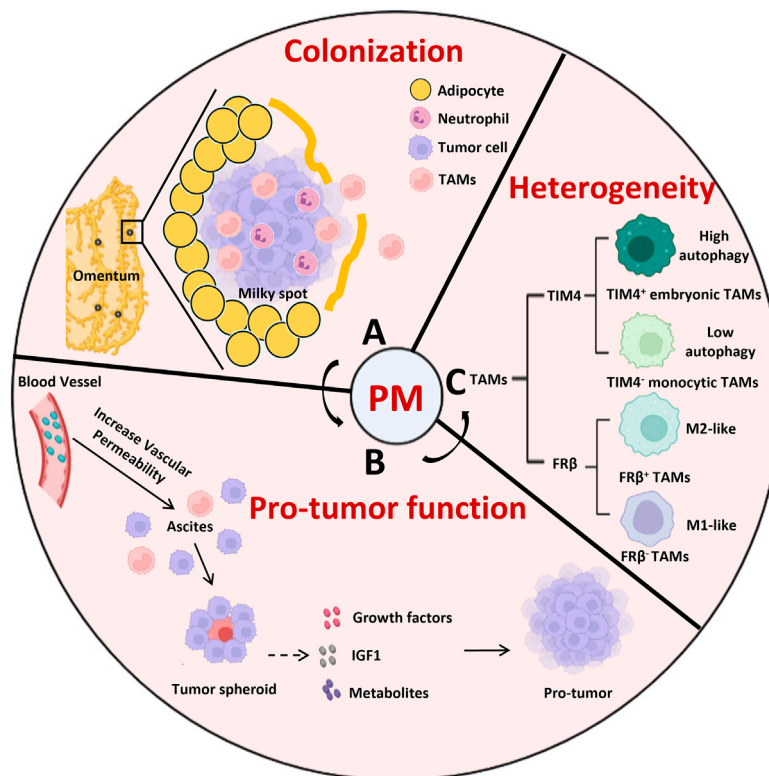


FIGURE 2

The role of peritoneal resident macrophages in the tumor metastasis into the cavity. (A) The colonization of omentum is a critical step for tumor metastasis, which is occurred passively through the milky spots. (B) TAMs promote the tumor peritoneal metastasis through gathering tumor cells to form the spheroid and secreting growth factors, IGF1, metabolites to support the tumor growth. (C) The heterogeneity of TAMs distinguished by TIM4 or FR β in peritoneal metastasis. Compared to TIM4⁺ monocytic TAMs, TIM4⁺ embryonic TAMs express more OXPHOS genes and adapt to autophagy to support their survival. FR β ⁺ TAMs display a round shape that was more monocytic in appearance and consistent with M1 phenotype while FR β ⁺ TAMs exhibited an elongated cell shape with a M2-polarized pro-tumor profiles. IGF1, insulin-like growth factor 1; PM, peritoneal metastasis; TAMs, tumor associated macrophages.

3.2 The promotion of tumor metastasis by peritoneal resident macrophages

3.2.1 Support tumor growth and ascites formation

TAMs directly promote the development of metastases in ovarian cancer through the production of cytokines IL-6 (Isobe et al., 2015), vascular endothelial growth factor (VEGF) (Song et al., 2019), and transforming growth factor β (TGF β) (Rodríguez et al., 2001), among others. In addition, insulin-like growth factor 1 (IGF1) expressed by TAMs increased the proliferation and migration of ID8 mouse ovarian cancer cells; while blockade of the IGF1 pathway in ID8 cells with an IGF1 neutralizing antibody effectively inhibited the ID8 caused tumor growth (Liu et al., 2018). Moreover, TAMs derived metabolites also contribute to the tumor growth. In peritoneal metastasis, GATA6⁺ residential macrophages elicit a fatty acid oxidation mediated an increase in oxidative phosphorylation (OXPHOS). Itaconic acid, a peritoneal

resident macrophage specific metabolite which is produced by immune responsive gene 1 (IRG1) mediated catabolism of mitochondrial cis-aconitate, can promote tumor progression into the peritoneum. Knockdown of IRG1 significantly reduced peritoneal tumors with reductions in OXPHOS and ROS in TAMs and ROS-mediated MAPK activation in tumor cells (Weiss et al., 2018).

Patients with advanced peritoneal tumors often develop malignant ascites with fluid accumulation in the peritoneal cavity. The formation of peritoneal ascites is associated with increased vascular permeability and obstructed lymphatic drainage. The overexpression of VEGF causes the increased vascular permeability (Herr et al., 2012) accompanied with IL-6 and IL-10, as well as CXCL12 in ascites (Zeng et al., 2019). As the major source of VEGF, macrophages resided in peritoneal cavity promote the ascites formation in ovarian cancer and gastric cancer peritoneal metastasis (Song et al., 2019). The CSF1 antibody blockade and clodronate liposomes depletion inhibit peritoneal resident macrophage accumulation and

prevent ascites formation in ovarian cancer (Robinson-Smith et al., 2007; Moughon et al., 2015). Ascites-derived spheroids in ovarian cancer facilitate tumor growth and progression. At early stages of transcoelomic metastasis of mouse epithelial ovarian cancer, M2 macrophage-like TAMs formed spheroids and secreted EGF, which upregulated $\alpha\text{M}\beta 2$ integrin on TAMs and ICAM-1 on tumor cells to enhance association between tumor cells and TAMs, then to support tumor cell proliferation and migration (Yin et al., 2016).

3.2.2 Facilitate immune evasion

In TME, TAMs have been summarized to be the dominant suppressive cells associated with immune evasion (Mantovani et al., 2017; Pathria et al., 2019). It is known that macrophages can directly target and eliminate the tumor cells. However, tumor expressed CD24 in ovarian cancer prevents macrophage-mediated phagocytic tumor clearance and promotes immune evasion by interacting with the inhibitory receptor sialic-acid-binding Ig-like lectin 10 (Siglec-10) expressed on TAMs (Barkal et al., 2019). Meanwhile, the presence of tumor infiltrating CD8^+ T lymphocytes is highly associated with longer survival in ovarian cancer (Zhang et al., 2003; Peng et al., 2015). However, it is observed that the level of cavity resident macrophages is associated with reduced numbers of CD8^+ T cells in pleural effusions and peritoneal ascites from patients with cancers. Mechanistically, TIM4 on the surface of cavity-resident macrophages interacts with its receptor phosphatidylserine (PS) upregulated on the surface of activated cytotoxic CD8^+ T cells, which leads to CD8^+ T cells sequestered away from tumor targets and proliferation suppression by TIM4^+ macrophages (Chow et al., 2021). In addition, canonical autophagy in peritoneal resident macrophages shows a suppressive effect on their $\text{IFN}\gamma$ pathway activation (Wang et al., 2020). In mouse ID8 ovarian cancer metastasis, the depletion of autophagy related gene FIP200 in peritoneal TAMs induced T cell mediated anti-tumor response which may be due to the spontaneous $\text{IFN}\gamma$ mediated immune activation in autophagy deficient TAMs (Xia et al., 2020). Hence, increased autophagy in peritoneal TAMs promotes ovarian cancer immune evasion.

3.3 The polarization of peritoneal tumor-associated macrophages remodeled by tumor cells

The plasticity of TAMs makes them polarized into two functional types, M1 (pro-inflammatory with anti-tumor activity) and M2 (anti-inflammatory with pro-tumor activity) macrophages, determined by their local TME (Murray et al., 2014; Muller et al., 2017). It is reported ovarian cancer cells polarize macrophages toward an M2 phenotype *in vivo* which gradually gain expression of M2-like marker genes, such as

CD206, Arg1, and CD163, at 4–8 weeks after tumor injection (Yin et al., 2016). The homeobox A9 (HOXA9) expression in ovarian cancer cells stimulated chemotaxis of peritoneal macrophages and induced macrophages to acquire M2-like features (Ko et al., 2014). In a mouse ovarian metastatic model, tumor cells promote membrane-cholesterol efflux and depletion of lipid rafts from macrophages which promotes IL-4-mediated reprogramming but inhibits $\text{IFN}\gamma$ -induced gene expression to accelerate tumor progression (Goossens et al., 2019). In addition, tumor-derived ubiquitin protein ligase E3 component N-recognin 5 (UBR5), an E3 ligase overexpressed in human ovarian cancer associated with poor prognosis, promotes TAMs recruitment and polarization *via* key chemokines and cytokines (Song et al., 2020). Meanwhile, M2-like TAM polarization could be repressed by sorbin and SH3 domain containing 2 (SORBS2) through stabilizing WAP four-disulfide core domain 1 (WFDC1) and IL-17D in ovarian cancer (Zhao et al., 2018). Furthermore, $\text{IFN}\gamma$ secreted by tumor-infiltrating lymphocyte (TIL) is critical for M1 TAMs polarization. However, epigenetic silencing of CCL5 expression through DNA methylation in ovarian cancer cells leads to the TIL desertification and reduced $\text{IFN}\gamma$ polarized M1 TAMs (Dangaj et al., 2019). Hence, the conversion of M2 TAMs to M1 TAMs provides an approach to improve the anti-tumor response by targeting TAMs.

3.4 The accumulation and discrepancy of peritoneal resident macrophage subsets in peritoneal metastasis

The accumulation of TAMs in peritoneal cavity reflects the development of peritoneal metastasis. Tumor derived factors, such as M-CSF and IL-4, promote the peritoneal residential macrophages self-proliferation or differentiation from monocytes. Due to the different ontogeny of peritoneal resident macrophages, the accumulation of peritoneal TAMs may originate from different precursors. In our work, the expression of TIM4 can be used to distinguish TIM4^+ embryonic TAMs from TIM4^- monocytic TAMs which share very similar gene signatures with LPMs and SPMs in tumor free mice (Xia et al., 2020). Both TAM subsets expand in ID8 metastatic models. Further, we observe TIM4^+ embryonic TAMs only depend on the self-proliferation while most of TIM4^- monocytic TAMs differentiate from infiltrated monocytes which were recruited by the tumor caused inflammation in peritoneal cavity. Compared to TIM4^- monocytic TAMs, TIM4^+ embryonic TAMs express more OXPHOS genes and adapt to autophagy to support their survival in ovarian cancer metastasis. As the dominant TAMs in early tumor stage, TIM4^+ embryonic macrophages promote the tumor metastasis (Xia et al., 2020). Similarly, surface expression of folate receptor (FR) β also can be used to identify two different peritoneal TAM subsets. $\text{FR}\beta^-$ TAMs display a round shape that is more monocytic in appearance and consistent with

M1 phenotype. However, FR β^+ TAMs exhibit an elongated cell shape with a M2-polarized protumor profile (Rodríguez-García et al., 2021). In addition, the monocytic TAMs increase their percentage in total TAMs following the tumor growth and show some effects on tumor metastasis. At the advanced tumor stage, monocytic TAMs accumulate a lot from blood and elicit pro-tumor effect. For example, F4/80^{Low} SPMs can directly enhance ovarian cancer cell growth with expression of protumor and proangiogenic molecular mediators upregulated by IL-17 (Rei et al., 2014). Transcription factor ZEB1 expressed in F4/80^{Low} TAMs enhances tumor progression with the induction of a CCR2-MMP9-CCL2 positive loop between TAMs and cancer cells (Cortes et al., 2017).

Noticeably, the macrophages also reside within mesothelial membranes lining the peritoneal cavity which can be divided into LYVE1^{High}MHC-II^{Low} and LYVE1^{Low/-}MHC-II^{High} subsets. LYVE1^{High} macrophages predominantly originate from embryonic-derived progenitors and promote epithelial ovarian tumor growth. The LYVE1^{High} mesothelial macrophages express similar profiles with ovarian tumor-associated macrophages previously described in the omentum. These data reveal that the peritoneal compartment contains other two resident macrophage populations and that LYVE1^{High} mesothelial macrophages drive tumor growth (Zhang et al., 2021).

4 Targeting peritoneal resident macrophages to enhance anti-tumor immunotherapy

Harnessing the immune system provides an important approach to combating cancer. Several strategies have been developed to manipulate the immune response, including immune checkpoint blockade (ICB), chimeric antigen receptor T cells (CAR T cells), dendritic cell vaccines, and cytokine therapies. Peritoneal resident macrophages assist tumors to suppress the immune response which should be a good target to improve the effect of immunotherapy (Duan and Luo, 2021). Several strategies have been developed to target the TAMs in peritoneal cavity:

4.1 Myeloid checkpoint blockade

Blocking the PD-1/PD-L1 or CTLA-4 pathways with antibodies relieves the cytotoxic function of T cells to control the tumor growth (Zou et al., 2016). However, patients with peritoneal metastasis are hardly responsive to the PD-1/PD-L1 blockade indicating that there are other checkpoints involved to hinder the effect of ICB in peritoneal metastasis. Along with the immune checkpoints on T cells, several checkpoints that are mainly associated with macrophages have been discovered. TIM4⁺ cavity TAMs sequester and impair

proliferation of CD8⁺ T cells under the ICB treatment through the interaction between TIM4 and PS. Hence, TIM4 blockade abrogates this sequestration and proliferation suppression and enhances anti-tumor efficacy in models of anti-PD-1 therapy and adoptive T cell therapy in mice (Chow et al., 2021). CD47 on the tumor surface acts as a “don’t eat me” signal and prevents macrophage-mediated phagocytosis through its direct interaction with signal regulatory protein- α (SIRP α). Blockade of CD47 signaling by using targeted monoclonal antibodies restores the phagocytic capacity of TAMs which enables macrophage phagocytosis of ovarian cancer cells (Willingham et al., 2012; Liu R. et al., 2017). Furthermore, a phase I trial of an anti-CD47 antibody Hu5F9-G4 demonstrated two patients with ovarian/fallopian tube cancers had partial remissions for 5.2 and 9.2 months (Sikic et al., 2019). In addition, the CD24/Siglec-10 signal also provides a target for restoring the phagocytosis of peritoneal resident TAMs in ovarian cancer (Barkal et al., 2019).

4.2 Tumor-associated macrophages depletion

Emerging evidence shows the loss of TAMs destroys the suppressive TME and promotes anti-tumor immune response. Targeting the differentiation and proliferation of TAMs always influences their population. Administration of GW2580, an inhibitor of CSF1 receptor, reduced infiltration of M2-like macrophages and dramatically decreased ascites volume in the late stages of ovarian cancer metastasis (Moughon et al., 2015). Depletion of GATA6 induces peritoneal residential macrophage apoptosis which dramatically decreases their numbers (Gautier et al., 2014; Rosas et al., 2014). Blocking the induction of GATA6 or inhibiting its transcriptional activity should strongly impair the identity of peritoneal resident macrophages and reduce their numbers. For example, retinoid X receptors (RXRs) control mouse serous-macrophage identity by regulating chromatin accessibility and the transcriptional regulation of canonical macrophage genes, partially through GATA6. RXRs deficiency impairs neonatal expansion of the LPM pool and reduces the survival of adult LPMs through excess lipid accumulation. Depletion of RXR diminishes LPMs accumulation in ovarian cancer and strongly reduces tumor progression in mice which indicates targeting RXR signaling may improve ovarian cancer outcomes *via* interfering the maintenance of the serous macrophage pool (Casanova-Acebes et al., 2020). In addition, the peritoneal resident TAMs highly relied on the autophagy for survival compared to the migrated TAMs. Autophagy can be used as a target to selectively reduce the TIM4⁺ residential TAMs and tumor growth (Xia et al., 2020).

Some artificial materials are developed to destroy the peritoneal TAMs. Clodronate liposome elicits toxic effects on

macrophages *via* phagocytosis. The administration of clodronate liposome reduces the number of peritoneal TAMs and metastasis in ovarian cancer (Etzerodt et al., 2020; Xia et al., 2020). CAR T cells are a type of immunotherapy that involves T cells genetically modified to express receptors that recognize cancer-specific antigens (Kershaw et al., 2013). Interestingly, Rodriguez-Garcia et al. (2021) developed mouse and human FR β -specific CAR T cells which recognize and deplete the FR β ⁺ TAMs in ovarian cancer metastasis. Furthermore, pre-treatment of the TME with anti-TAM CAR T cells improves the efficacy of tumor-specific CAR T cells against ovarian cancer metastasis. Similarly, G5-methotrexate (G5-MTX) nanoparticles restrict tumor growth by targeting and depleting the FR β ⁺ TAMs in ascites models of ovarian cancer (Penn et al., 2018).

4.3 Metabolic remodeling

It is well known that aggressively proliferated tumor cells consume amount of nutrients and fulfill the TME with their metabolic products which crosstalk with TAMs and form immune suppressive TME (Chang et al., 2015). This immunosuppressive remodeling seems not because of direct nutrient competition since cell-intrinsic programs drive the preferential acquisition of glucose and glutamine by immune and cancer cells (Reinfeld et al., 2021). Cancer cells show the highest uptake of glutamine which is not only their fuel but also drives M2-like macrophage polarization *via* epigenetic modifications (Liu P. S. et al., 2017). In addition, certain tumor derived metabolites function to promote the polarization of M2 TAMs phenotype, including lactic acid (Colegio et al., 2014), succinate (Wu et al., 2020), and so on. Hence, alteration of the tumor or macrophage metabolism provides an approach to convert the anti-inflammatory TAMs into pro-inflammatory TAMs. For example, genetic depletion of glutamine synthetase skews macrophages toward an M1-like phenotype and inhibits tumor metastasis (Palmieri et al., 2017).

In the context of peritoneal grafted cancer models, it is observed that the fatty acid oxidation (FAO), a way to break down a fatty acid into acetyl-CoA, increase in peritoneal resident macrophages (Weiss et al., 2018). Lipid metabolism is critical for the identity and homeostasis of LPMs and RXR-deficient peritoneal TIM4⁺ LPMs leads to lipid accumulation and apoptosis (Casanova-Acebes et al., 2020). Considering the LPMs represent the dominant peritoneal TAMs, interrupting their lipid metabolism may have the effect to control the ovarian cancer metastasis by inducing their apoptosis. Moreover, hyaluronic acid secreted by ovarian cancer cells promotes plasma membrane cholesterol efflux in TAMs *via* binding to CD44, which enhances IL-4 receptor signaling *in vitro* and *in vivo* associated with reduced intracellular cholesterol, finally promoting the expression of the typical M2 marker Arg1 while inhibiting proinflammatory IL-12 expression

(Goossens et al., 2019). Deletion of cholesterol efflux genes ATP-binding cassette transporter A1 (ABCA1) and ATP-binding cassette transporter G1 (ABCG1) in peritoneal TAMs has been found to significantly impair tumor progression (Goossens et al., 2019). In addition, mTORC2 is important for the metabolic reprogramming of tissue-resident macrophages (Oh et al., 2017) and TAMs (Huang et al., 2016), so mTORC2 can be a potential target to remodel TAMs from an anti-inflammatory to an anti-tumor phenotype. Hence, metabolic rewiring of peritoneal TAMs should be an alternative strategy to enhance the anti-tumor immunity.

5 The human counterpart of peritoneal resident macrophages in cavity metastasis

Human studies on peritoneal macrophage populations divide them into three distinct subsets based on the expression of CD14/CD16 (CD14⁺⁺CD16⁻, CD14⁺⁺CD16⁺, and CD14^{High}CD16^{High}). The CD14^{High}CD16^{High} subset represents the mature phenotype of steady-state human resident peritoneal macrophages based on the expression of GATA6, and other resident macrophage markers, such as CD206 and Slan (Ruiz-Alcaraz et al., 2016; Ruiz-Alcaraz et al., 2018). Consistent with mouse models, emerging evidence demonstrate that human peritoneal resident macrophages promote human cancer metastasis into cavity. For example, gastric cancer (GC) patients with peritoneal metastasis had increased levels of alternatively activated macrophages in the peritoneum compared to those without dissemination. Macrophages in the peritoneal cavity produce EGF and VEGF to enhance the angiogenesis in GC patients bearing peritoneal metastasis. Hence, patients bearing more macrophages in the peritoneum had a poorer prognosis (Song et al., 2019). The ascites provides a convenient way to isolate high amount of pure human macrophages which can be analyzed through their transcriptome and proteome. It is reported TAMs from human ovarian carcinoma ascites shared similar character with peritoneal resident macrophages, but not monocyte-derived macrophages. The elevated signature genes in human TAMs are highly related to extracellular matrix (ECM) remodeling which indicates the role for TAMs in cancer cell invasion and ovarian cancer progression (Finkernagel et al., 2016). Meanwhile, two subgroups of ascites macrophages have been identified in ovarian cancer patients. Subgroup A has a high expression of pro-tumor markers (CD163, PCOLCE2, IL-6) related to immune suppression and ECM remodeling while subgroup B has a low expression of pro-tumorigenic and immunosuppressive markers with an upregulation of genes linked to interferon signaling (Adhikary et al., 2017). Furthermore, the expression of complement receptor of the immunoglobulin superfamily (CRIg) and CCR2 have been used to define two phenotypically and functionally distinct human peritoneal

macrophage subpopulations (Irvine et al., 2016). CRIG^{High} cells are transcriptionally, metabolically, and functionally similar with the mouse F4/80^{High} resident peritoneal macrophages in cirrhosis (Irvine et al., 2016) and ovarian cancer patients (Xia et al., 2020).

6 Conclusion

As the dominant myeloid cells infiltrating TME, TAMs promote immune evasion through multiple routes, including triggering of inhibitory immune checkpoints in T cells. Understanding the ontogeny and modulation of those immunosuppressive cells is critical for overcoming their disadvantages. Different from monocytic macrophages, peritoneal resident macrophages originate from embryonic precursors which locate in peritoneal cavity during development and can self-maintain locally throughout life with tissue-specific levels of replacement by circulating precursors (Bain et al., 2016). After tumor cells infiltrate into the peritoneal cavity, peritoneal resident macrophages become the primary macrophages surrounding the tumor cells and promote the tumor growth at the early stage. Meanwhile, inflammatory macrophages differentiated from blood monocytes gradually increase in numbers as the tumor progresses, contributing to peritoneal metastasis at the late stage. Determining whether peritoneal resident TAMs are predictive biomarkers for early peritoneal metastasis is important for personalized patient care in clinical applications.

Targeting the peritoneal resident TAMs elicits anti-tumor immune response and controls tumor metastasis. The tumor spheroids, angiogenesis, and immune suppression microenvironments supported by peritoneal TAMs promote tumor survival and growth. Understanding the differentiation, polarization, and metabolism of peritoneal TAMs is beneficial for exploring different approaches to reduce or remodel TAMs. The development of new technologies, such as CAR-macrophage and CAR-T targeting to macrophages, extend the potential immunotherapy by modulating peritoneal macrophages. Given the peritoneal resident macrophages can be recruited to injured organs in peritoneal cavity, it is still unknown if the peritoneal resident macrophages have effects on the orthotopic tumor growth and initiate the tumor transformation and metastasis. In the future, more challenges need to be addressed to manipulate TAMs in peritoneal metastasis, including 1) to

understand the metabolic consumption of peritoneal TAMs and the pro-tumor effects of TAMs related metabolites; 2) to discover peritoneal specific transcriptional factors and surface markers to distinguish pro- and anti-tumoral peritoneal TAM subsets; 3) to prevent the clearance of the tumor neo-antigens by peritoneal TAMs; 4) to reduce the interference of peritoneal TAMs in antigen presentation; 5) to explore peritoneal macrophage related epigenetic regulations of their profiles; 6) to avoid peritoneal TAMs mediated immunotherapy resistance. In summary, peritoneal resident macrophages promote tumor metastasis into peritoneal cavity and can be targeted to enhance T-cell immunity, to modify polarization of TAMs, and to enhance phagocytosis of cancer cells with or without other therapies.

Author contributions

YZ and HX wrote the text. YC and DO revised the content. All authors discussed on the contents of the manuscript.

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Conflict of interest

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Neuroendocrine regulations in tissue-specific immunity: From mechanism to applications in tumor

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Immune responses in nonlymphoid tissues play a vital role in the maintenance of homeostasis. Lots of evidence supports that tissue-specific immune cells provide defense against tumor through the localization in different tissue throughout the body, and can be regulated by diverse factors. Accordingly, the distribution of nervous tissue is also tissue-specific which is essential in the growth of corresponding organs, and the occurrence and development of tumor. Although there have been many mature perspectives on the neuroendocrine regulation in tumor microenvironment, the neuroendocrine regulation of tissue-specific immune cells has not yet been summarized. In this review, we focus on how tissue immune responses are influenced by autonomic nervous system, sensory nerves, and various neuroendocrine factors and reversely how tissue-specific immune cells communicate with neuroendocrine system through releasing different factors. Furthermore, we pay attention to the potential mechanisms of neuroendocrine-tissue specific immunity axis involved in tumors. This may provide new insights for the immunotherapy of tumors in the future.

KEYWORDS

neuroendocrine regulation, neurotransmitter, neuropeptide, tissue-specific immunity, cancer

1 Introduction

Tumors develop in complicated tissue environments, which they rely on for growth, invasion and metastasis (Quail and Joyce, 2013). The tumor microenvironment (TME) is a heterogeneous ecosystem composed of all the structures at the site and those that are recruited to the area—immune cells, mesenchymal stem cells, vascular vessels, nerves and matrix components (Hanahan and Coussens, 2012). Tumors are derived from the complex interactions that occur between them (Gysler and Drapkin, 2021). With the constant exploration of new ways to treat tumors, therapies targeting the TME have

emerged as a promising approach for cancer treatment for the past few years (Bejarano et al., 2021). Research has progressed, but there are remaining unknowns. The composition of the TME is being elucidated, with the neurological, immunological and microbiological components being identified. However, other characteristics and the dynamic evolution of the TME require further in-depth exploration.

Tissue-specific immunity occurs when immune cells establish permanent tissue residency in different organs, thus creating a defensive system (Klose and Artis, 2020). Numerous immune cells reside in nonlymphoid tissues. These tissue-resident populations do not recirculate and adopt a unique phenotype that is distinct from immune cells in the blood or lymphatic system (Mackay and Kallies, 2017). The origin of tissue-resident immune cells is complex and includes tissue innate immune cells and immune cells that have migrated from the peripheral blood. Innate immune cells, including macrophages, dendritic cells (DCs) and innate lymphoid cells (ILCs), exhibit tissue-specific subset compositions in the lung, skin, intestines and comprise the early responders to pathogen encounters. Adaptive immune cells, such as T cells and B cells, also have tissue-resident subsets that help to build immune memory. For example, tissue-resident memory T cells persist as tissue-resident populations in mucosal and exocrine sites, while memory B cells predominate in the intestines. In general, the human immune system is localized in a tissue-specific manner in diverse sites (Weisberg et al., 2021). Functionally, tissue-specific immunity is observed to play a part in tumor development through various regulatory mechanisms (Lei et al., 2020; Liu et al., 2022a).

Recently, the contribution of nerves to the pathogenesis of malignancies has emerged (Zahalka and Frenette, 2020). Several landmark studies have demonstrated that the nervous system plays an active role in tumorigenesis (Reavis et al., 2020). Meanwhile, some studies have suggested that tumor innervation is associated with accelerated tumor progression in multiple cancers (Albo et al., 2011; Magnon et al., 2013; Huang et al., 2014; Kappos et al., 2018; Renz et al., 2018). The nervous system is composed of the central nervous system (CNS) and the peripheral nervous system (PNS). The CNS is the main part of the nervous system and is composed of the spinal cord and brain, which play a part in tumor development. Studies have reported that chronic stress causes disorders in the CNS and promotes tumor initiation and progression (Saul et al., 2005; Goldfarb et al., 2011; Levi et al., 2011; Partecke et al., 2016). β -adrenergic activation by the cAMP–PKA signaling pathway, e.g., β -adrenergic receptors (ARs) stimulated by norepinephrine (NE), is a major mechanism by which stress can enhance tumor development and increase vascularization (Thaker et al., 2006). Furthermore, immune regulation also plays a vital role in stress-induced tumor development (Dhabhar, 2009). Studies have shown that chronic stress causes a large-scale alteration of immune cells in tissues and induces

suppression or dysregulation of immune function (Dhabhar et al., 2012; Dhabhar, 2014). The PNS emanates from the CNS and is divided into the autonomic systems and somatosensory, which are responsible for communicating with all parts of the body. Autonomic nerve density was reported to be associated with tumor prognosis and progression (Silverman et al., 2021). In terms of mechanism, infiltrating sympathetic nerves facilitated tumor progression and invasion through β -adrenergic activation (Pon et al., 2016). Adrenergic nerves also facilitate tumor growth by releasing NE to stimulate angiogenesis via VEGF signaling (Zahalka et al., 2017). In light of neural receptors are expressed by many immune cell types, it follows that immune cells may also participate in oncogenesis through adrenergic signaling (Silverman et al., 2021). Neuroendocrine factors contain neurotransmitters, neuropeptides and many other factors secreted by the nervous system mediate stimulatory or inhibitory functions by binding to their respective receptors. In recent decades, many discoveries have elucidated their regulatory roles in tissues and organs (Jiang et al., 2020a). For instance, studies in nerve growth factor (NGF) has reported that this factor acts not only on the PNS and CNS but also on nonneuronal and cancer cells (Aloe et al., 2016). NGF and its receptor TrkA have been implicated in the development of many aggressive cancers. However, NGF pathway has been proved to be critical to inflammation control and the immune response in tumor (Campos et al., 2007; Retamales-Ortega et al., 2017; Wehkamp et al., 2018; Triaca et al., 2019; Jiang et al., 2020b). Nerves regulate multiple components of the TME. Importantly, with the development of high-throughput sequencing techniques including single-cell RNA sequencing and spatial transcriptomics (Liu et al., 2022b), researchers found that immune and neuronal cells are often colocalized to form neuroimmune cell units (Huh and Veiga-Fernandes, 2020). And, both immune cells and neurons express receptors to sense neurotransmitters and cytokines, allowing direct interactions between the two systems (Seillet and Jacquilot, 2019).

Relatively few studies have investigated the functional role of neuroendocrine in carcinogenesis and regulation of the TME. Here, we summarize the mechanisms of neuroendocrine regulation of tissue-specific immunity based on the neuroendocrine signal transmission medium and how tissue-specific immune cells communicate with nerves by releasing different factors. We then focus on the role of neuroendocrine regulation in tumor immunity and how it informs prognosis and treatment.

2 Neuroendocrine regulation in tissue-specific immunity

The nervous system is composed of various components such as the CNS, sympathetic nerves, parasympathetic nerves, and sensory nerve nociceptors, and it mediates immune cells

primarily by secreting neuroendocrine factors such as neurotransmitters and neuropeptides. These molecules can regulate tissue-specific immunity by binding to their corresponding receptors expressed on immune cells in various tissues. Here, we summarize the neuroendocrine regulation of tissue-specific immunity, categorized by signaling mediator.

2.1 Adrenergic regulation

The adrenergic system is composed of NE and epinephrine, which are the primary neurotransmitters secreted by postganglionic sympathetic neurons. They regulate cellular function through ARs, including the α 1-, α 2-, β 1-, β 2-, and β 3-ARs (Tanner et al., 2021). The immune effects of adrenergic signaling are primarily transmitted by β 2-ARs, which are expressed on nearly all major immune cell types (Marino and Cosentino, 2013). NE has been shown to mediate the cell trafficking and effector activities of immune cells *via* β 2-AR.

NE affects the function of the CNS. Microglia are the most common resident innate immune cells in the CNS and monitor brain homeostasis by producing ligands that support neuronal survival, pruning non-functional synapses and removing dying neurons (Nayak et al., 2014; Werneburg et al., 2017). Studies have shown that NE upregulates the expression of the amyloid beta peptide (A β) receptor mFPR2 through activation of β 2-AR in microglia, which helps to maintain the adequate uptake and clearance of A β (42). Moreover, increased secretion of NE suppresses the microglial response and reduces the upregulation of both anti- and pro-inflammatory cytokines through β 2-adrenergic signaling (Lechtenberg et al., 2019). In general, NE can modulate microglial motility, which can affect the function of microglia in some pathogenic situations (Gyoneva and Traynelis, 2013; Umpierre and Wu, 2020).

Tissue-resident macrophages, ILCs, tissue-resident T cells and NK cells are common tissue-resident immune cells in the periphery. They act in a tissue-specific manner in adipose tissue, liver, lung and gut, where NE has been shown to modulate these cells *via* β 2-adrenergic signaling. In adipose tissue, adipose tissue macrophages (ATMs) and ILC2s are common resident immune cells that act as dominant initiators of type 2 inflammation and tissue repair (Cording et al., 2016). Some studies have shown that sympathetic nerves maintain an anti-inflammatory state in mice by inhibiting TNF- α level in macrophages (Tang et al., 2015). Additionally, NE can promote extracellular fatty acid uptake and storage as triglycerides and reduce free fatty acid release from triglyceride-laden macrophages (Petkevicius et al., 2021a). However, another study found that the sympathetic nervous system exerts an indirect effect on ATMs through the modulation of adipocyte function instead of modulating the phenotype of ATMs directly (Petkevicius et al., 2021b). Similar findings were also found for ILC2s, in which PDGFRA + adipose stem cell

(ASC) could serve as a messenger between the immune cells and nervous system. The sympathetic nerve can act on ASCs *via* β 2-AR to control the level of glial-derived neurotrophic factor and indirectly regulate the activity of adipose tissue ILC2s *via* the neurotrophic factor receptor RET (50). Likewise, β -adrenergic signaling was also reported to regulate the production of IL-33 by a DPP4+PDGFRB + ASC subpopulation and enhance ILC2 accumulation indirectly (Shan et al., 2021).

In the intestine, tissue-specific immune cells include muscularis macrophages (MMs) and ILC2s. By studying the transcriptional profile, gut-innervating sympathetic neurons have been found to polarize MMs towards a protectively M2 phenotype through β 2-AR (52). In murine models of enteric infections, MMs upregulate a neuroprotective program *via* β 2-AR and constrain neuronal death through an arginase 1-polyamine axis (Matheis et al., 2020). ILC2s participate in multiple intestinal physiological processes, including tissue repair, metabolic homeostasis, allergic inflammation and host defense against infections (Cardoso et al., 2017). Research has shown that β 2-AR deficiency results in exaggerated ILC2 responses and type 2 inflammation in the intestine (Moriyama et al., 2018). Another study also demonstrated that sympathetic innervation constrains the effects of innate immune responses on microbes in the gut through the β 2-AR pathway (Willemze et al., 2019). β 2-AR has been proven to mediate negative regulation of ILC2s through the inhibition of cell proliferation and effector function (Moriyama et al., 2018). A recent study reported that colonic sympathetic nerves can also exert an indirect effect on immune cells through endothelial MAdCAM-1. In murine models, activation of local sympathetic nerves decelerated colitis and reduced the abundance of immune cell (Schiller et al., 2021). Hepatic invariant NKT (iNKT) cells are tissue-specific immune cells that primarily reside in the liver (Bendelac et al., 2007). One study showed that the immunosuppressive function of iNKT cells was mediated through NE (59).

In summary, adrenergic signaling regulates a variety of tissue-resident immune cells in the CNS and PNS in which plays an anti-inflammatory and immunosuppressive role (Figure 1, Table 1). Thus, adrenergic regulation is an important neuroendocrine modulating method for tissue-specific immunity.

2.2 Cholinergic regulation

The cholinergic system, which is found in both neuronal and nonneuronal cells, is a network that performs various complex functions in the body. It is composed of acetylcholine (ACh), cholinergic receptors (AChRs), acetylcholinesterase enzyme and choline acetyltransferase enzyme (Halder and Lal, 2021). ACh is the classical neurotransmitter in the cholinergic system. The receptor of ACh is divided into ionotropic nicotinic ACh

receptors (nAChRs) and metabotropic muscarinic ACh receptors (mAChRs).

ACh affects the function of the CNS. AChRs are expressed on microglia in the CNS. mAChR stimulation modulates microglial chemotaxis and phagocytic activity via IFN- γ activation (Pannell et al., 2016). Regarding nAChRs, $\alpha 7$ nAChR is an essential regulator of inflammation (Wang et al., 2003). The anti-inflammatory ACh response in microglia is mediated through $\alpha 7$ nAChR. This response helps to lower inflammatory cytokine levels and microglial activation (Li et al., 2019). Similarly, ACh inhibits LPS-induced IL-1 β and IL-6 elevation and promote IL-4 and IL-10 production through $\alpha 7$ nAChRs to promote the M2 phenotype (Zhang et al., 2017). In addition, ACh stimulation of $\alpha 7$ nAChR in microglia also enhances A β clearance (Hoskin et al., 2019).

Tissue-resident macrophages and ILCs are common tissue-resident immune cells in the periphery. They act in a tissue-specific manner in the liver, lung, gut, where ACh has been shown to modulate these cells *via* ACh-AChR signaling. In the lung, ILC2s are common resident immune cells. The ACh- $\alpha 7$ nAChR axis in ILC2s decreases the synthesis of TNF- α , IL-1, and IL-6 (66). However, ILC2 transcription factor GATA-3 and the inflammatory modulator NF- κ B is diminished. In general, ACh- $\alpha 7$ nAChR signaling in ILC2s helps to promote anti-inflammatory function (Galle-Treger et al., 2016). In the liver, hepatic macrophages are the common resident immune cells. The vagus nerve regulates the secretory and phagocytic activity of resident macrophages *via* cholinergic signaling (Fonseca et al., 2019). ACh-AChR signal-mediated IL-6 production in hepatic macrophages upregulates the expression of FoxM1 in hepatocytes, leading to liver regeneration (Izumi et al., 2018). In the intestine, tissue-specific immune cells include MMs, ILC2s and ILC3s. The vagus nerve regulates the anti-inflammatory effect of intestinal MMs *via* $\alpha 7$ nAChR-mediated JAK2/STAT3 signaling pathway (Matteoli et al., 2014; Yang et al., 2021). The ACh-AChR axis in ILC2s also causes anti-inflammatory effects by promoting ILC2 cytokine production (Chu et al., 2021). Moreover, AChs upregulate the PCITR biosynthetic pathway in ILC3s (Dalli et al., 2017). Besides, the vagus nerve is also reported to modulate anti-inflammatory effect through the $\alpha 7$ nAChR on macrophages in spleen and pancreas (Zhang et al., 2020).

In summary, cholinergic signaling facilitates the behavior of tissue-resident macrophages and promotes the anti-inflammatory function of ILC2s in the nervous system (Figure 1, Table 1). Thus, cholinergic regulation is another important neuroendocrine modulating method for tissue-specific immunity.

2.3 Regulation *via* other neurotransmitters

In addition to NE, epinephrine and ACh, neurotransmitters also include dopamine (DA), serotonin (5-HT) and gamma-

aminobutyric acid (GABA). Research on the neuroendocrine regulation of immune cells by these other neurotransmitters has mainly focused on microglia. Microglia express several receptors for DA, 5-HT and GABA (Younger et al., 2019; Stoloro and Frenkel, 2021).

DA is a neurotransmitter synthesized in both the CNS and PNS. It is mainly distributed in the CNS and has been detected in the liver, spleen, pancreas and gut (Peters et al., 2014; Klein et al., 2019). Dopamine receptors (DRs), including D1R, D2R, D3R, D4R, and D5R, are present on microglia and some other macrophages (Thomas Broome et al., 2020). DA promotes microglial migration, increases NO and ROS production through D1R, and the secretion of proinflammatory cytokines, such as IL-1 β and IL-6 through D2R (75). Also, DA can induce the formation of DNA-based extracellular traps in microglia which participate in immunosurveillance and pathogen clearance (Agrawal et al., 2021) (Figure 1, Table 1).

5-HT, a biogenic amine synthesized from tryptophan, is a well-known neurotransmitter in the CNS which plays a critical roles in mood stability, sleep patterns and pain tolerance. The effects of 5-HT are regulated through 5-HT receptors. It also exist as an important signaling molecule in the periphery, especially in the gastrointestinal tract (Ye et al., 2021). 5-HT plays a role in CNS inflammation and repair. Administering 5-HT to microglia induces inflammatory initiation and IL-6 production (Quintero-Villegas and Valdés-Ferrer, 2019) (Figure 1, Table 1).

GABA is known as a main inhibitory amino acid neurotransmitter in the CNS. The physiological roles of GABA are related to the modulation of synaptic transmission. Two distinct classes of GABA receptors have been identified, including ionotropic receptor GABA_A and metabotropic receptor GABA_B (Ngo and Vo, 2019). Microglia are known to express both GABA_A and GABA_B. GABA has been shown to decrease microglial neurotoxicity and exert an anti-inflammatory effect (Lee, 2013; Crowley et al., 2016) (Figure 1, Table 1).

There are few studies on the role of these neurotransmitters in peripheral tissue-specific immunity. However, there is evidence for their presence in the periphery; for instance, the airway epithelium contains pulmonary neuroendocrine cells filled with 5-HT and GABA neuropeptides (Magnon, 2021). Some peripheral tissue-specific immune cells have been reported to express corresponding neurotransmitter receptors, providing the possibility for neuroendocrine interactions between them.

2.4 Regulation *via* neuropeptides

Neuropeptides are peptide substances produced by neurons that play key roles in modulating cell function by binding to specific receptors. Examples of neuropeptides include neuromedin U (NMU), neuropeptide calcitonin gene-related peptide (CGRP), substance P (SP), neuropeptide TFAA4,

pituitary adenylate cyclase-activating polypeptide (PACAP), vasoactive intestinal peptide (VIP), neuropeptide FF (NPFF), neuropeptide Y (NPY) and somatostatin (SST). Neuropeptides and their receptors have regionally restricted distributions in the nervous system (Hoyer and Bartfai, 2012). Transcriptomic analyses have indicated that immune cells express numerous neuropeptide receptors (Seillet and Jacquilot, 2019). Thus, neuropeptides may play a vital role in mediating tissue-specific immunity.

2.4.1 Neuropeptides secreted by the central nervous system and autonomic nerves

NPFF is a CNS octapeptide that plays a part in pain modulation and opiate tolerance. NPFF has two receptors, NPFF receptor 1 and 2 (NPFFR1, NPFFR2) (Bonini et al., 2000). In peripheral tissues, only NPFFR2 is expressed in ATMs (Waqas et al., 2017). NPFF promotes M2 phenotype and increase the proliferation of ATMs. Specifically, NPFF suppressed the expression of the E3 ubiquitin ligase RNF128, which promote the stability of phosphorylated STAT6 and increased expression of gene related to M2 macrophage. NPFF induced ATM proliferation accompanied with the increase of NDRG2 expression and suppression of MAFB expression (Waqas et al., 2017) (Figure 1, Table 1).

NMU is a neuropeptide widely distributed in the human body and has two receptors, NMU receptor 1 and 2 (NMUR1, NMUR2). NMU mainly functions on ILC2s through NMUR1 (Martinez and O'Driscoll, 2015). NMU stimulates ILC2 activation and promotes type 2 cytokine responses that can induce antimicrobial and inflammatory responses (Klose et al., 2017). In the intestine, NMU increases IL-10 production in intestinal ILC2s. However, the function of ILC2-derived IL-10 in the intestine remains unknown (Bando et al., 2020). NMU can also amplify lung inflammation driven by ILC2s. IL-9 derived from ILC2 plays an important role in increasing the abundance of $\gamma\delta$ T cell and IL-17A production (Wallrapp et al., 2017; Chen et al., 2021).

PACAP and VIP are two highly related neuropeptides widely distributed in organisms and have immunomodulatory actions. The receptors of PACAP and VIP are expressed by numerous immune cell types (Abad and Tan, 2018). The neuropeptide PACAP is an antimicrobial peptide induced in the brain in response to bacterial and fungal infection (Lee et al., 2021). PACAPR1 is a main receptor of PACAP expressed on DC. PACAP induces cutaneous DC functions and promotes the development of contact hypersensitivity through PACAPR1. The expression of CCR7 and CXCR4 of DCs was enhanced by PACAP *in vitro* (Yamamoto et al., 2021).

NPY is a neuropeptide widely distributed in the human body and is secreted mainly by the CNS and sympathetic nerves, where it is co-released with NE. NPY exerts its effects through interacting with NPY receptors (NPYRs), among which NPY1R is the most abundantly expressed NPYR receptor in

immune cells (Dimitrijevic and Stanojevic, 2013). NPY inhibits microglial activation and phagocytosis and affects the direction of migration and phagocytosis. NPY also inhibits cytokine secretion of microglia, especially the secretion of proinflammatory factors (Gonçalves et al., 2012; Pain et al., 2019; Chen et al., 2020). Besides, NPY was reported to attenuate the splenic immune response as well (Yu et al., 2022) (Figure 1, Table 1).

Regarding VIP, intestinal ILC3s and pulmonary ILC2s highly express VIP receptor 2 (VIPR2). In the intestine, VIP activates ILC3s, enhancing the production of IL-22 and the barrier function of the epithelium (Seillet et al., 2020). This dynamic neuroimmune circuit in the intestine is regulated by feeding and circadian mechanisms (Talbot et al., 2020) (Figure 1, Table 1).

SST is a neuropeptide with generally inhibitory function which commonly produced by endocrine cells and the CNS (Weckbecker et al., 2003). SST mediates its biological functions via SST receptors (subtype 1–5), which was found expressing in multiple immune cells (Møller et al., 2003). However, existing studies have shown that SST only affects immune cells in peripheral blood of normal tissues. For instance, SST reduced the secretion of INF- γ from peripheral blood mononuclear cell and inhibit the production of immunoglobulin by B lymphocytes. Also, the chemotaxis of peripheral blood monocytes is inhibited by this peptide (Pintér et al., 2006).

2.4.2 Neuropeptides secreted by sensory nerves

Nociceptor sensory neurons are responsible for the detection of potentially damaging stimuli and elicit defensive behaviors (Chiu et al., 2013). The neuropeptides CGRP and SP are nociceptor mediators that act in the skin, lung and intestine. TAF4A is a neuropeptide secreted by sensory neurons in skin. VIP mentioned above can also be secreted by nociceptors. Tissue-resident macrophages, ILC2s, NK cells, DCs and $\gamma\delta$ T cells are common tissue-resident immune cells reside within epithelial layers of the lung, skin, and gut (Zheng et al., 2013).

CGRP regulates a variety of immune cells which express the receptor, calcitonin receptor-like receptor (CRLR). Broadly speaking, CGRP is a negative regulator of ILC2 responses, which is necessary for suppressing ILC2 expansion and maintaining homeostasis of the type 2 immune machinery (Wallrapp et al., 2019; Xu et al., 2019). Additionally, CGRP in concert with NMU is reported to promote IL-5 but constrain IL-13 expression (Nagashima et al., 2019). In the lung, nociceptors suppress protective immunity through the release of CGRP. Specifically, CGRP suppressed the recruitment and surveillance of neutrophils (Pinho-Ribeiro et al., 2018), and reduced lung $\gamma\delta$ T cell numbers, which act as first responders to infection (Baral et al., 2018). On the contrary, pulmonary neuroendocrine cells (PNECs) are a kind of rare airway epithelial cells that reside near airway branches. CGRP secreted by PNECs enhances ILC2 activity and the production of cytokines (Sui et al., 2018).

In the intestine, precursor and immature NK cells exhibit tissue-resident signatures (Dogra et al., 2020). SP is released from nociceptors after stimulation through the neurokinin receptors NK1R, NK2R and NK3R and has been shown to regulate cell migration and proliferation to generate neurogenic inflammation (Seillet and Jacquilot, 2019). In the airways, lung nociceptor neurons release SP, and amplify T helper 2 cell influx and polarization via NK1R (Crosson et al., 2021). In skin, SP interacts with DCs and mast cells through the Mas-related G-protein coupled receptor member (MRGPR). Sensory neurons release SP, which acts through MRGPRA1 to induce CD301b+ DC migration to the draining lymph node (dLN). Migrated DCs initiate T helper-2 cell differentiation in the dLNs (Perner et al., 2020). One study reported that nociceptors induce the recruitment of neutrophils and monocytes, driving skin inflammation. Nociceptors promote the production of IL-23 by dermal DCs. IL-23 then acts on IL-23R+ $\gamma\delta$ T17 cells to promote the secretion of IL-17F and IL-22 (119). Nociceptors can also amplify skin inflammation by inducing the degranulation of mast cells that are contiguous to the nociceptors and activating MRGPRB2 on the mast cells (Serhan et al., 2019).

TFAA4 is a neuropeptide secreted by sensory neurons in skin. TFAA4 reduce inflammation and cell infiltration by inducing IL-10 production from Tim4+ dermal macrophages (Flayer and Sokol, 2021; Soler Palacios and Gutiérrez-González, 2022). TFAA4 can also affect the inflammatory mechanisms of other macrophage subsets, including CD206+ dermal macrophages and peritoneal macrophages (Hoeffel et al., 2021). In the lung, nociceptors can induce the production of VIP which in turn stimulates ILC2s to promote the occurrence of inflammation (Talbot et al., 2015; Seillet and Jacquilot, 2019).

In a word, sensory nerves function primarily in their widely distributed areas including skin, lung and gut. Neuropeptides secreted by sensory neurons play diverse roles in immune responses against various pathogens (Figure 1, Table 1).

3 Tissue-specific immune effects on nerves

Tissue-specific immune cells regulate nerves by releasing various factors such as cytokines, chemokines, small-molecule peptides and neurotrophic factors.

Among the tissue-specific immune cells, tissue-resident macrophages exhibit a rich regulatory role in different tissues. In adipose tissue, ATM expresses neurotrophic factors to promote white adipose tissue innervation (Xie et al., 2022). Also, ATM reportedly controls brown adipose tissue innervation (Wolf et al., 2017). In subcutaneous fat, a new subset of immune cells called cholinergic adipose macrophages (ChAMs) has been identified. ChAMs secrete ACh to regulate thermogenic activation via β 2-AR (Knights

et al., 2021). ATM can also mediate sympathetic neurons through ROBO1 receptor. Slit3 is a macrophage cytokine secreted by ATM. It binds to the ROBO1 receptor to stimulate Ca^{2+} /calmodulin-dependent protein kinase II signaling and NE release, which enhances adipocyte thermogenesis (Wang et al., 2021). Additionally, MMs regulate peristaltic activity of the colon by secreting bone morphogenetic protein 2 (BMP2), which activates the expression of BMP receptor on enteric neurons. Enteric neurons, in turn, secrete a growth factor required for macrophage development called colony stimulatory factor 1 (CSF1), (Muller et al., 2014). Sympathetic neuron-associated macrophages are another previously undescribed population of resident macrophages that mediate NE clearance via SLC6A2 and MAOA expression (Pirzgalska et al., 2017). A nerve- and airway-associated macrophage (NAM) subset has been identified in the lung. Their closely associated nerves have sympathetic fibers. However, the relationship between NAMs and their associated nerves is unclear (Ural et al., 2020).

In the CNS, microglia perform negative feedback control of neuronal activity. The suppression of neuronal activation depends on the ability to sense and catabolize extracellular ATP of microglia (Badimon et al., 2020). ILC2s also play a part. In the lung, nociceptors can sense IL-5 released by activated immune cells, and IL-5 further induces VIP production. VIP then stimulates ILC2s, creating an inflammatory signaling loop that promotes allergic inflammation (Talbot et al., 2015; Seillet and Jacquilot, 2019). ACh is a broadly distributed signaling molecule that is not only produced by neurons, but also by numerous immune cells. Several immune cell types respond to ACh signaling and can also produce ACh directly (Cox et al., 2020).

4 Neuroendocrine tissue-specific immunity axis in cancer

It is generally accepted that tumor innervation correlates with tumor progression across multiple solid tumor types (Albo et al., 2011; Huang et al., 2014; Kappos et al., 2018; Renz et al., 2018). Specifically, autonomic nervous infiltration was discovered to affect the development and dissemination of breast cancer, head and neck carcinoma, prostate cancer, liver cancer, lung cancer, pancreatic cancer, cholangiocarcinoma, colorectal cancer, ovarian cancer, glioma and gastric cancer (Magnon et al., 2013; Zhao et al., 2014; Partecke et al., 2016; Pon et al., 2016; Zahalka et al., 2017; Faulkner et al., 2019; Sha et al., 2019). While sensory neurons were found to play a part in tumor development of melanoma and pancreatic cancer (Saloman et al., 2016; Prazeres et al., 2020). Meanwhile, high intra-tumoral nerve density is associated with poor prognosis and high recurrence in multiple cancers (Silverman et al., 2021). Studies have shown that the mechanism by which tumor

innervation affects cancer can be divided into three parts: direct stimulation of tumor proliferation, promotion of vascularization, and indirect modulation of tumors through immune changes. In this context, we discuss the effect of neuroendocrine regulation on tissue-specific immunity in the TME.

In breast cancer, sympathetic innervation accelerates tumor progression, while parasympathetic innervation decelerates tumor progression in the TME (26). The sympathetic nervous system affects stress-induced cancer behaviors, including initiation, progression and metastasis, by modulating tumor-associated immune cells via the NE- β AR signaling pathway in four ways. First, β -adrenergic signaling represses an effector phenotype of CD8⁺ T cells in the TME. Reducing β -adrenergic signaling induced an immunologically active TME in tumor-bearing animal models (Bucsek et al., 2017). Second, parasympathetic innervation constrains the function of immune checkpoints. Sympathetic nerve denervation and parasympathetic neurostimulation reduced the level of PD-1, PD-L1, and FOXP3 on CD4⁺ or CD8⁺ T cells in murine models of breast cancer. This effect was also proved in human breast cancer samples (Kamiya et al., 2019). Next, the NE- β AR signaling pathway increased the infiltration of macrophages in the TME and induced the differentiation to a prometastatic M2 macrophage phenotype. Stress-induced NE- β AR signaling activation induced a metastasis to distant tissues in mouse breast cancer models (Sloan et al., 2010). Finally, NE- β AR signaling pathway promotes breast cancer metastasis by recruiting myeloid-derived suppressor cells (MDSCs). MDSCs are a population of cells with immunosuppressive phenotype. In murine models of breast cancer, chronic stress led to the elevation of MDSCs, accelerated breast cancer metastasis, and upregulated IL-6 expression and JAK/STAT3 signaling pathways (an et al., 2021). Another study reveals that the expression level of β 2-AR on MDSCs increases with tumor growth. β 2-adrenergic signaling increases oxidative phosphorylation, increase fatty acid oxidation, decreases glycolysis, and also increases autophagy and activates the arachidonic acid cycle (Mohammadpour et al., 2021). A recent study revealed that in brain metastases from breast cancer, neuronal exposure induces synaptic mediators and neurotransmitter signaling in tumors (Deshpande et al., 2022). This research suggests that neuroendocrine regulation in brain metastases seems to be more direct, and whether immune cells in brain metastases TME are regulated by neuroendocrine factors might be the direction of future research.

Likewise, in hepatocellular carcinoma, β -adrenergic signaling promotes tumor growth by mobilizing MDSCs to tumor tissues. In the hepatocellular carcinoma mouse models, stress enhanced tumor progression. Specifically, β -adrenergic signaling changed the spleen structure, and caused a redistribution of MDSCs to tumors. Also, the author found that splenectomy could constrain tumor growth and prevent increase of macrophages in tumor tissues in stressed mice (Jiang et al., 2019). Another study pointed out the possible mechanism of this

mobilization. The recruitment of MDSCs was modulated through β -adrenergic-activated CXCL5-CXCR2-Erk signaling cascades. Chronic stress upregulated the expression of CXCR2 and pErk1/2 in MDSCs, and the expression of CXCL5. *In vitro*, T-cell proliferation was obviously constrained in NE treated medium. *In vivo*, β -adrenergic blockade reversed the acceleration of tumor growth induced by chronic stress and CXCL5-CXCR2-Erk signaling pathway was suppressed (Cao et al., 2021).

Moreover, in prostate cancer, the density of sympathetic fibers in tumors is associated with poor clinical outcomes (Magnon et al., 2013). It was observed that prostate cancer patients with depression showed higher tumor-associated macrophage infiltration. NPY is co-released with NE in sympathetic nerves. Animal experiments revealed that NPY released from NE-treated prostate cancer cells promotes macrophage trafficking and IL-6 release, which subsequently activates the STAT3 signaling pathway (Cheng et al., 2019). Analyses of clinical prostate cancer samples have also suggested that elevated NPY promotes prostate cancer development and is associated with poor prognosis and therapy resistance (Rasiah et al., 2006; Ding et al., 2021). Additionally, NK cells are mobilized by epinephrine through the β -adrenergic signaling pathway, which can reduce the tumor initiation and recurrence. In mouse tumor models, epinephrine induced selective mobilization of IL-6-sensitive NK cells while IL-6 inhibited the infiltration and activation of NK cells in TME (Pedersen et al., 2016).

Yet, different perspectives have been raised in pancreatic cancer. Chronic stress is observed to increase pancreatic cancer progression and can be antagonized by β -AR blockade in some studies (Partecke et al., 2016; Renz et al., 2018). However, a recently published study demonstrated that sympathetic nerves ablation increases tumor growth and spread by increasing intra-tumoral CD163⁺ macrophage numbers. In the mouse model of pancreatic cancer, the sympathetic nerves exert a protective function during the early stage of tumor. The author mentioned that the converse response to sympathectomy in pancreatic cancer may be shaped by the particular TME (Guillot et al., 2022). Otherwise, ablation of sensory neurons of pancreatic cancer reportedly slows initiation and progression of cancer. However, the study did not mention its impact on tumor immunity (Saloman et al., 2016).

Sensory innervation was reported to constrain melanoma progression. Ablation of sensory nerves lead to worse outcomes in melanoma-bearing mice (Prazeres et al., 2020). In a recent study, Costa et al. (2021) informs that sensory neuron activity may slow the melanoma progression by inducing tumor immunosurveillance. Specifically, in sensory neuron-overactivated melanoma mice, the number of MDSCs and neutrophils significantly decreased, while tumor-infiltrating DCs, CD8⁺ T cells, CD4⁺ T cells, $\gamma\delta$ T cells and NK cell was detected to increase. The expression of immune checkpoint

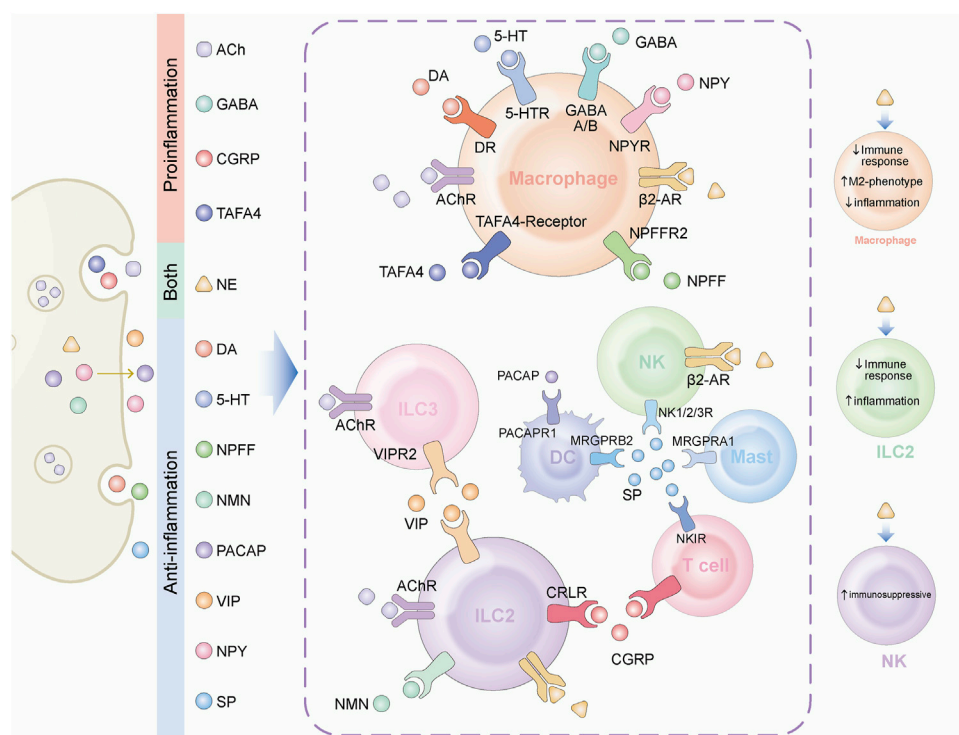


FIGURE 1

Neuroendocrine factors play various role in tissue immune regulation. A variety of neuroendocrine factors play regulatory roles in tissue-resident immune cells. The target cells and their receptors for different factors are displayed in the figure. On the left, neuroendocrine factors are classified according to their function. ACh, GABA, CGRP and TAF4 mainly play a pro-inflammatory function. DA, 5-HT, NPFF, NMU, PACAP, VIP, NPY, and SP mainly play an anti-inflammatory function. NE plays different roles in different target cells. On the right side of the figure, we marked the functions of NE.

molecules such as PD-1 and CTLA-4 decreased. And it induces a Th17-immune response in the melanoma microenvironment. Furthermore, the author validated these results in a large human melanoma cohort. They found that SCN10A (encoding Nav1.8), a key gene of sensory neurons, has higher expression in patients with better prognosis. The enrichment of tumor-infiltrating immune cells showed an increase of DCs, CD8 + T cells, CD4 + T cells and NK cell in patients with better prognosis. Conversely, an earlier published study by Keskinov et al. (2016) reported that the dorsal root ganglia (DRG) of sensory nerves contribute to melanoma progression by recruiting MDSCs which help to create an oncogenic TME. Experimental results suggested that, *in vitro*, melanoma cells can activate DRG neurons and increase the expression of chemokines that attract MDSC. *In vivo*, in the presence of DRG cells, tumor growth was accelerated and the number of MDSC increased. To sum up, for sensory neuron modulation, Costa et al. (2021) used a designer drug to selectively activate or inhibit sensory neurons within the tumor *in vivo*, whereas Keskinov et al. (2016) used DRG cells injection in mice. Besides, Costa et al. (2021) focused on multiple kinds of cells involved in tumor immunity including T cells, DCs, and MDSCs, while Keskinov et al. (2016) focused

only on the alteration of MDSCs. Furthermore, Costa et al. (2021) proved their findings through *in vivo* assays and bioinformatic validations, while Keskinov et al. (2016) validated through *in vitro* and *in vivo* assays. In our opinion, there are several possible reasons for the opposite results produced by the two studies. First, the nerve fibers at work are different. It speculates that it is inappropriate to choose DRG cells as a representation of sensory neurons. The DRG is an enlargement of the dorsal root that houses somata of sensory neurons. But DRGs can also receive signals from the autonomic nervous system by connecting to the sympathetic nerve via rami communicantes nerves (Esposito et al., 2019). Consequently, the tumor-promoting effects of DRGs mentioned in the study of Keskinov et al. (2016) is likely to be partially mediated by the autonomic nerves. The oncogenic role of the autonomic nervous system in multiple cancers has been mentioned above. Apart from that, the neuroendocrine factors at work are different. Signals from sensory neurons in normal tissues can be transmitted to immune cells through various factors such as CGRP, SP, and VIP. But neither study involved exploration on factors that signal between neurons and immune cells. Although Costa et al. (2021) observed an elevation of CGRP level after

TABLE 1 Summary of central and peripheral neuroendocrine factors regulating tissue specific immunity.

Ligand	Target tissue	Target cell	Receptor	Effect
NE	CNS	Microglia	β 2-AR	\uparrow A β clearance (Kong et al. (2010))
				\downarrow Microglia response (Lechtenberg et al. (2019))
	Adipose tissue	ATM	β 2-AR	\downarrow Inflammation (Tang et al. (2015))
				\downarrow Extracellular fatty acid (Petkevicius et al. (2021a))
	Intestine	ILC2	β 2-AR	Indirect effect through ASC (Cardoso et al. (2021); Shan et al. (2021))
		MM	β 2-AR	\uparrow M2 phenotype (Gabanyi et al. (2016))
		ILC2	β 2-AR	\uparrow Neuroprotection (Matheis et al. (2020))
				\downarrow Innate immune response (Willemze et al. (2019))
	liver	Immune	β 2-AR	Indirect effect through endothelium (Schiller et al. (2021))
		iNKT	β 2-AR	\uparrow Immunosuppressive function (Bendelac et al. (2007); Wong et al. (2011))
ACh	CNS	Microglia	mAChR	\uparrow Chemotaxis and phagocytosis (Pannell et al. (2016))
			α 7nAChR	\downarrow Inflammation (Wang et al. (2003); Li et al. (2019))
				\uparrow M2 phenotype (Zhang et al. (2017))
				\uparrow A β clearance (Hoskin et al. (2019))
	Llung	ilc2	α 7nAChR	\downarrow Type 2 inflammation (Galle-Treger et al. (2016); Pavón-Romero et al. (2021))
	Liver	Macrophage	AChR	\uparrow Phagocytosis and secretion (Fonseca et al. (2019))
				\uparrow FoxM1, \uparrow liver regeneration (Izumi et al. (2018))
	Intestine	MM	α 7nAChR	\downarrow Inflammation (Matteoli et al. (2014); Yang et al. (2021))
		ILC2	AChR	\downarrow Type 2 inflammation (Chu et al. (2021))
		ILC3	AChR	\uparrow PCTR biosynthetic pathway (Dalli et al. (2017))
	Spleen, pancreas	Macrophage	α 7nAChR	\downarrow Inflammation (Zhang et al. (2020))
DA	CNS	Microglia	D1R	\uparrow Microglial migration (Stolero and Frenkel (2021))
			D2R	\uparrow ROS and NO (Stolero and Frenkel (2021))
			DR	\uparrow Inflammation (Stolero and Frenkel (2021))
				\uparrow Extracellular trap in microglia (Agrawal et al. (2021))
5-HT	CNS	Microglia	5-HTR	\uparrow Inflammation \uparrow IL-6 (Quintero-Villegas and Valdes-Ferrer, 2019)
GABA	CNS	Microglia	GABA _A /GABA _B	\downarrow Microglial neurotoxicity (Lee (2013); Crowley et al. (2016))
				\downarrow Inflammation (Lee (2013); Crowley et al. (2016))
NPFF	Adipose tissue	ATM	NPFFR2	\uparrow M2 phenotype (Waqas et al. (2017))
				\uparrow ATM proliferation (Waqas et al. (2017))
NMU	Lung	ILC2	NMUR1	\uparrow Type 2 inflammation (Wallrapp et al. (2017); Chen et al. (2021))
				\uparrow $\gamma\delta$ T cell, \uparrow IL-17A (Wallrapp et al. (2017); Chen et al. (2021))
	Intestine	ILC2	NMUR1	\uparrow Type 2 inflammation (Klose et al. (2017))
				\uparrow IL-10 (Bando et al., 2020)
PACAP	Skin	DC	PACAPR1	\uparrow Contact hypersensitivity (Yamamoto et al., 2021)
VIP	Lung	ILC2	VIPR2	\uparrow CCR7, \uparrow CXCR4 (Yamamoto et al., 2021)
				\uparrow Type 2 inflammation (Talbot et al. (2015); Seillet and Jacquilot (2019))
	Intestine	ILC3	VIPR2	\uparrow IL-22, \uparrow barrier function of the epithelium (Seillet et al. (2020); Talbot et al. (2020))

(Continued on following page)

TABLE 1 (Continued) Summary of central and peripheral neuroendocrine factors regulating tissue specific immunity.

Ligand	Target tissue	Target cell	Receptor	Effect
NPY	CNS	Microglia	NPYR	↑ Inflammation, ↓ microglial activation and phagocytosis (Gonçalves et al. (2012); Pain et al. (2019); Chen et al. (2020))
	Spleen	Immune	NPYR	↓ Immune responses (Yu et al. (2022))
CGRP	Skin, lung and intestine	ILC2	CRLR	↓ Type 2 inflammation (Wallrapp et al. (2019); Xu et al. (2019))
				↑ IL-5, ↓ IL-13 (Nagashima et al. (2019))
	Lung	T cell	CRLR	↓ protective immunity (Baral et al. (2018); Pinho-Ribeiro et al. (2018))
				↓ γδ T cell number (Baral et al. (2018); Pinho-Ribeiro et al. (2018))
CGRP (PNEC)	Lung	ILC2	CRLR	↓ Neutrophil (Baral et al. (2018); Pinho-Ribeiro et al. (2018))
				↑ Type 2 inflammation (Sui et al. (2018))
				↑ ILC2 activity (Sui et al. (2018))
SP	Intestine	NK cell	NK1R/NK2R/NK3R	↑ Inflammation (Talbot et al. (2015); Seillet and Jacquelot (2019))
	Lung	T cell	NK1R	↑ T helper 2 cell influx and polarization (Crosson et al. (2021))
	Skin	DC	MRGPRA1	↑ DC migration, ↑ T helper 2 cell differentiation (Perner et al. (2020))
				↑ IL-23, ↑ neutrophil, ↑ monocytes (Riol-Blanco et al. (2014))
		Mast cell	MRGPRB2	↑ Inflammation (Riol-Blanco et al. (2014))
				↑ Mast cells degranulation (Serhan et al. (2019))
TAF4A	Skin	Macrophage	unknown	↑ Inflammation (Serhan et al. (2019))
				↑ IL-10, ↓ inflammation (Hoeffel et al. (2021))

DC, dendritic cell; ILC, innate lymphoid cell; CNS, central nervous system; NE, norepinephrine; AR, adrenergic receptor; ATM, adipose tissue macrophage; ASC, adipose stem cell; MM, muscularis macrophage; iNKT, invariant natural killer T; ACh, acetylcholine; mAChR: metabotropic muscarinic ACh, receptor; nAChR: ionotropic nicotinic ACh, receptor; 5-HT: serotonin; GABA, gamma-aminobutyric acid; DA, dopamine; DR, dopamine receptor; 5-HT: 5-HT, receptor; NMU, neuromedin U; SP, substance P; CGRP, calcitonin gene-related peptide; PNEC, pulmonary neuroendocrine cell; PACAP, pituitary adenylate cyclase-activating polypeptide; VIP, vasoactive intestinal peptide; NPY, neuropeptide Y; CRLR, receptor calcitonin receptor like receptor; MRGPR, Mas-related G-protein coupled receptor member.

sensory nerve activation, this mechanism has not been confirmed. Whether sensory nerves also interact with immune cells through these substances in the melanoma microenvironment might be a direction of future research. We believe that further explorations of neuroendocrine factors involved in immune regulation in melanoma may answer the reasons for the opposite conclusions of the two studies above.

An analysis of clinical samples reveals that GABA is associated with poor prognosis in lung cancer and colon adenocarcinoma (Huang et al., 2022). GABA is reported to have an anti-tumor immunity function through two different pathways. One study informed GABA promotes the differentiation from monocyte to anti-inflammatory macrophages that secrete IL-10. GABA also inhibit CD8⁺ T cell killer function (Zhang et al., 2021). Another study suggested GABA activates the GABA_B receptor to stimulate tumor cell proliferation and suppress CD8⁺ T cell infiltration in TME. In mouse models, targeting GABA_B overcame resistance to anti-PD-1 immune checkpoint blockade therapy (Huang et al., 2022).

Regarding neuropeptides, a systematic review found evidence that the elevation of SP and NK-1R are oncogenic events in head and neck carcinogenesis and probably act in the early stages of

tumorigenesis (Gonzalez-Moles et al., 2021). Proline rich polypeptide 1, (PRP-1) is a neuropeptide secreted by the brain neurosecretory cells which causes inhibition of chondrosarcoma cell growth (Galoyan, 2000; Galoian et al., 2009). A study proves that PRP-1 functions via toll like receptor family TLR1/2, TLR6 and mucin MUC5B which are responsible for innate immunity pattern recognition. This result suggests that the anti-tumor effect of PRP-1 might be related to immune cells in TME. But the author also suggested that the receptors predominantly located in the tumor nucleus (Galoian et al., 2018). Another research demonstrated that PRP-1 can also inhibit cancer stem cell proliferation in chondrosarcoma (Granger et al., 2020). In addition, somatostatin analog (SSA) is the analog of SST which is now widely used in the treatment of neuroendocrine neoplasms. Long-acting repeatable of SSA decrease the level of total regulatory T cells and MDSCs, as well as the expression of PD1, CTLA4 and ENTPD1 in neuroendocrine neoplasms which exert an anti-tumor immunosurveillance function (von Arx et al., 2020). SSA was also reported to decrease cell proliferation and tumor growth in multiple cancers, such as lung cancer, breast cancer, colon carcinoma and endometrial carcinomas (Kahán et al., 1999; Engel et al., 2005; Treszl et al., 2009; Hohla et al., 2010). However, if these oncogenic effects are associated with tumor-

associated immune cells has not yet been discussed. The function of neuropeptides in tumor-specific immunity requires further research.

In brief, under the regulation of neuroendocrine factors, some components of TME play the role of immunosurveillance, such as effective T cells, NK cells, and the immune checkpoint molecules produced by them. Yet some other components play the opposite pro-tumor effects including MDSCs, regulatory T cells and tumor-associated macrophages. Immunosurveillance effects are negatively regulated by β -adrenergic signaling in breast, prostate and liver cancers. In lung and colon cancer, immunosurveillance is negative regulated by sensory nerves. Pancreatic cancer immunosurveillance is positive regulated by β -adrenergic signaling, however negative regulated by sensory nerves. Melanoma is mainly mediated by sensory nerves, but the direction of regulation is controversial. Lastly, immunosurveillance in neuroendocrine neoplasm is positive regulated by SST.

From the perspective of therapy, there are also many researches emerged in recent years. Since tumor innervation plays an active role in cancer initiation and progression, neuron ablation emerged as a treatment strategy mentioned a lot. Some studies demonstrate that surgical or pharmacological denervation attenuate tumor growth in a tissue-specific manner. For instance, sensory neuron ablation is proved to favor melanoma progression, but slows the initiation and progression of pancreatic cancer (Saloman et al., 2016; Prazeres et al., 2020). And denervation suppresses gastric and breast tumorigenesis (Zhao et al., 2014). Although method to manoeuvre intra-tumoral innervations is not yet mature for clinical treatment, it provides a promising new avenue for anti-cancer therapy (Prazeres et al., 2020).

Apart from neuron ablation, antagonize β 2-AR seems to be a more mature approach to block the neuroendocrine signal. Propranolol is a nonselective beta blocker used for cardiovascular indications for decades (Srinivasan, 2019). However, in recent years, propranolol has been applied in the treatment of some kinds of tumors successfully, such as angiosarcoma (Wagner et al., 2018). Retrospective studies have observed a correlation between β blocker usage and increased overall survival among cancer patients (Nagaraja et al., 2013). Blockade of β -AR reduces tumor progression and upregulates the response to anti-CTLA4 therapy contributes to the formation of an immunosuppressive TME. In mouse fibrosarcoma models, propranolol increased the number of T cells, reduced the number of intra-tumoral MDSCs and altered the gene expression profile of tumor-associated macrophages significantly in the TME. Similar phenomenon was observed in murine models of colon cancer (Fjæstad et al., 2022). Specifically, one study demonstrates that NE- β AR pathway helps to maintain the level and the suppressive function of MDSCs. In murine breast cancer models, β 2-adrenergic signaling modulated the expression of

immunosuppressive molecules such as arginase-I and PD-L1 and suppressed the proliferation of T cells. Also, the author pointed out that the regulatory functions of β 2-AR signaling in MDSCs is activated by STAT3 phosphorylation. The β 2-AR-mediated increase in MDSC is dependent on Fas-FasL interactions. Besides, the immunosuppressive function of MDSCs can be decelerated by β -AR antagonists (Mohammadpour et al., 2019). Propranolol was also reported to reduce stress-induced elevation of regulatory T cells in breast cancer patients (Zhou et al., 2016). Another study report that β 2-adrenergic signaling contributes to an exhausted phenotype in T cells and induce metabolic dysfunction in the TME. In mouse melanoma and colon cancer models, it is observed that by using propranolol, tumor growth rate was slowed accompanied by a significantly decrease of tumor-infiltrating T cells that express exhaustion related genes and an increase in progenitor exhausted T cells. Also, β -AR blockade in mice increases oxidative phosphorylation and glycolysis in tumor-infiltrating lymphocyte (Qiao et al., 2021). Therefore, β -AR antagonists such as propranolol could be a potentially efficacious therapy approach of tumors in the future.

In traditional Chinese medicine, moxibustion, a treatment modality with a long history, has been used to treat cancer-related symptoms in clinical practice for years. However, few people have explored its mechanism of action. Interestingly, a recent study informed that grain-sized moxibustion significantly reduced tumor growth in lung cancer. Grain-sized moxibustion performed at the acupoint of Zusanli promotes anti-tumor immunity of NK cell by inhibiting adrenergic signaling. The acupoint of Zusanli is an important acupoint involved in the interaction between neuroendocrine systems and immune cells (Zhang et al., 2018). *In vitro*, grain-sized moxibustion increased the proportion, infiltration and activation of NK cells, yet it didn't affect T cells. Additionally, the grain-sized moxibustion mediated NK cells activation can be reduced by β -blocker treatment (Hu et al., 2021). To sum up, we describe the role of moxibustion in neuroendocrine regulation of lung cancer, which indicated that traditional Chinese medicine is still an ancient but promising therapeutic regimen for cancers.

5 Conclusion

Many studies have shown that tumor innervation is associated with tumor initiation, progression and a worse prognosis, and neuroendocrine regulation is the main mechanism by which nerves modulate tumor cells and other non-nerve cells. Several studies have focused on the neuroendocrine regulation of tumor cells; however, immune cells are also a vital part of the TME. Various tumor-associated immune cells have complex functions that can greatly impact tumor development, prognosis and treatment. Therefore, this review discusses the existing research on the neuroendocrine regulation of tissue-specific immunity. The

regulatory mechanisms of different immune cell types in various tissues were summarized according to the classification of regulatory factors. Adrenergic and cholinergic signaling are two common regulatory pathways. In central and peripheral tissues, sympathetic nerves mainly modulate tissue-resident immune cells through the NE- β 2A pathway, exerting anti-inflammatory and immunosuppressive roles. The parasympathetic nervous system regulates resident macrophages and ILCs mainly by secreting ACh from the vagus nerve to promote macrophage activity and anti-inflammatory effects. Other neurotransmitters are secreted primarily in the CNS and regulate microglia activity. Neuropeptides are another type of neuroendocrine factor that is secreted by central, autonomic and sensory neurons. These neuropeptides have various functions in tissues. Furthermore, many tissue-resident immune cells secrete cytokines and other factors to regulate nerves. We also summarized the available studies on neuroendocrine immunomodulatory regulation in different kinds of tumors. Some studies focused on autonomic nervous regulation in cancers and have helped to explain why chronic stress promotes tumor development from an immune aspect. Yet, many tumors are also regulated by sensory nerves and other factors. After that we discuss the neuroendocrine regulation of tumor immunity from the perspective of immune cell function and tumor therapy.

There are still knowledge gaps in the field of neuroendocrine regulation of immune cells in the TME. Many receptors of neuroendocrine factors are expressed on macrophages, T cells, and other cells that play important roles in tumor immunity. Some regulatory pathways have been studied in nontumor tissues, while their roles in tumors have not been studied. Moreover, a variety of cancers have been reported to be affected by tumor innervation, but the neuron-immune interactions in most cancers remain unclear. Thus, we also covered some articles that only discussed neuroendocrine regulation from the perspective of TME. Although they did not mention the neuroendocrine regulation of immune cells, we believe that some of them can provide ideas for the following research.

Due to the tissue specificity of immune cells, individualized immunotherapy in tumors may bring greater benefits to patients. For example, some studies have found that β 2-AR blockade can inhibit NE-mediated tumor progression, but it has not been applied clinically in most kinds of tumors. Therefore, enriching

the research focusing on these aspects may provide new insights for personalized tumor immunotherapy.

Author contributions

QW, BL, and S-QL are responsible for collecting and collating documents. S-QL and BL are responsible for writing this review, while QW and S-RS are responsible for the revision, and J-JL and SS are responsible for editing and submission. 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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Glossary

TME tumor microenvironment	5-HTR 5-HT receptor
DC dendritic cell	NMU neuromedin U
ILC innate lymphoid cell	SP substance P
TRM tissue-resident memory T cell	CGRP calcitonin gene-related peptide
CNS central nervous system	PACAP pituitary adenylyl cyclase-activating polypeptide
PNS peripheral nervous system	VIP vasoactive intestinal peptide
NE norepinephrine	NPFF neuropeptide FF
AR adrenergic receptor	NPY neuropeptide Y
NGF nerve growth factor	CRLR receptor calcitonin receptor like receptor
TEM effective memory T cell	PNEC pulmonary neuroendocrine cell
ATM adipose tissue macrophage	MRGPR Mas-related G-protein coupled receptor member
ASC adipose stem cell	dLN draining lymph node
MM muscularis macrophage	ChAM cholinergic adipose macrophage
iNKT invariant natural killer T	BMP2 bone morphogenetic protein 2
ACh acetylcholine	CSF1 colony stimulatory factor
mAChR metabotropic muscarinic ACh receptor	SAM Sympathetic neuron-associated macrophage
nAChR ionotropic nicotinic ACh receptor	NAM nerve- and airway-associated macrophage
5-HT serotonin	MDSC myeloid-derived suppressor cell
GABA gamma-aminobutyric acid	DRG dorsal root ganglia
DA dopamine	PRP-1 proline rich polypeptide 1
DR dopamine receptor	SST somatostatin
	SSA somatostatin analog

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