

NEXT GENERATION $\gamma\delta$ T CELL-BASED TUMOR IMMUNOTHERAPY

EDITED BY: Andy Hee-Meng Tan, Alice Cheung and Dieter Kabelitz
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NEXT GENERATION $\gamma\delta$ T CELL-BASED TUMOR IMMUNOTHERAPY

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Editorial: Next generation $\gamma\delta$ T cell-based tumor immunotherapy

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Editorial on the Research Topic

Next generation $\gamma\delta$ T cell-based tumor immunotherapy

The discovery of the $\gamma\delta$ T-cell receptor (TCR) and its ability to confer potent cytotoxic activity in CD3+ cells some 35 years ago sparked the initial proliferation in research that garnered widespread interest in the biology and function of $\gamma\delta$ T cells. The identification of major human $\gamma\delta$ TCR clonotypes, their tissue distributions as well as dynamic changes throughout ontogeny and in disease states have contributed to the appreciation of human $\gamma\delta$ T cell diversity. Despite this, incomplete understanding of mechanisms underlying the complexity of various $\gamma\delta$ T cell subsets in homeostasis, inflammation and malignancy restricted the focus of most early studies to blood circulating V γ 9V δ 2 T cells which could be robustly activated and expanded *ex vivo* using aminobisphosphonates such as zoledronate compared with other $\gamma\delta$ T cell subsets for which activating ligands were then largely unknown. This galvanized attempts to harness the tumoricidal potential of V γ 9V δ 2 T cells in clinical trials. Although these cells exhibited highly promising safety profiles in patients, early trial data revealed suboptimal anti-tumor efficacy. Despite these setbacks, recent breakthroughs in deciphering the unique antigen (Ag) binding modes of $\gamma\delta$ TCR coupled with high dimensional analyses of tissue- and disease-specific $\gamma\delta$ T cell subsets at single cell resolution led to renewed excitement in the development of $\gamma\delta$ T cell-based therapeutics. This Research Topic has compiled a series of nine articles of which five review our hitherto understanding of the multifaceted nature of $\gamma\delta$ T cells and four report original research providing new insights into the molecular and cellular regulation of a diverse repertoire of $\gamma\delta$ T cells, paving the way for next generation $\gamma\delta$ T cell-based tumor immunotherapies.

Despite extensive use of phosphoantigens (pAgs) to activate and expand V γ 9+V δ 2+ T cells, the role of butyrophilins (BTN)s in mediating V γ 9V δ 2 TCR-dependent activation is only gaining recent appreciation. Expression of BTN3A1 and BTN2A1 heterodimers, in complex with pAgs, on the surface of accessory innate immune, infected or tumor cells is an absolute requirement for interaction with the V γ 9V δ 2 TCR. Other BTN and BTN-like (BTNL) molecules are involved in the ontogeny and homeostasis of non-V γ 9+V δ 2+ T cell subtypes as noted by [Herrmann and Karunakaran](#). Their review also emphasized dissection of BTN-associated mechanisms that enhance the effector function to broaden the therapeutic applications of $\gamma\delta$ T cells in disease settings. Extending the role of TCR δ complementarity-determining region 3 (CDR3 δ) in V γ 9V δ 2 TCR-mediated responses, [Vyborova et al.](#) adduced evidence for CDR3 δ determinants in pAg sensing that are significantly correlated with V γ 9V δ 2 TCR affinity and signal strength, contributing to V γ 9V δ 2 T cell repertoire focusing. Furthermore, surface expression of the inhibitory natural killer receptor (NKR) CD94/NKG2A is biased toward while that of activating NKR NKG2D is independent of these CDR3 δ traits, findings which may impact design of high-affinity V γ 9V δ 2 TCR-based therapies.

$\gamma\delta$ T cells manifest substantial plasticity and can be polarised to different cell states in response to environmental stimuli. It is thus not uncommon to identify $\gamma\delta$ T cells with opposing functional properties in different biological contexts. The mini review by [Bhat et al.](#) provides a comprehensive summary of studies highlighting the dichotomous nature of $\gamma\delta$ T cells influenced by diverse pathological milieus, leading to beneficial or detrimental outcomes in the host. For example, IL-17 production by $\gamma\delta$ T cells has been shown to aggravate autoimmune conditions (1, 2) and also be associated with immunosuppression that exacerbate tumour growth (3, 4). Such phenomena attributable to the varied cellular interactions of $\gamma\delta$ T cells can be addressed by appropriate considerations of systems immunology and personalized approaches. In this regard, [Chan et al.](#) provided an updated account of crosstalk between $\gamma\delta$ T cells and a variety of immune cells which collectively coordinates anti-tumor responses. Additionally, the cytokine milieu plays a major role in shaping the fate commitment of $\gamma\delta$ T cells. Consistent with this, [Song et al.](#) discussed how cytokines and their combinations differentially direct the polarization of tissue-resident and tumour-infiltrating $\gamma\delta$ T cells. Such experimental insights will inform strategies to manipulate the cytokine dependencies of $\gamma\delta$ T cells to improve the cytotoxic function and *in vivo* persistence of administered T cells against tumors. [Pei et al.](#) elegantly showed that CD137 costimulation of V γ 9+V δ 2+ T cells using CD137L agonist diminished IL-10 receptor expression and alleviated exhaustion in these cells by mitigating the immunosuppressive tumor microenvironment (TME) mediated by IL-10. This increased V γ 9+V δ 2+ T cell efficacy against Epstein Barr virus (EBV)-transformed B lymphoma in a humanized mouse

model. [Hu et al.](#) examined the immunosuppressive TME of hepatocellular carcinoma (HCC) which the authors showed close correlation with high expression of inhibitory checkpoint molecules, presence of tumor-promoting immune cells and various types of programmed cell death. This is associated with $\gamma\delta$ T cell subtype imbalance characterized by selective depletion of cytotoxic V δ 2+ T cells and enrichment of Treg-like V δ 1+ T cells as well as poorer patient prognosis. These studies underscore the importance of performing greater in-depth analyses of the cellular networks and interplay of cytokines in the TME to accelerate the clinical translation of $\gamma\delta$ T cell therapies.

Over the years, translating $\gamma\delta$ T cell therapies from bench to bedside has encountered tremendous challenges. [Saura-Esteller et al.](#) expertly summarized the evolution of $\gamma\delta$ T cell therapeutic strategies assessed in clinical trials that signifies past progress in $\gamma\delta$ T cell research. With a growing list of companies developing $\gamma\delta$ T cell-based or engaging therapies, the authors noted the high cost of manufacturing $\gamma\delta$ T cell-based products due in part to requirement for multiple cytokines and prolonged *ex vivo* expansion process. Exemplifying continual efforts to reduce $\gamma\delta$ T cell production cost, [Ferry et al.](#) described a one-step protocol utilizing a single cytokine to expand V δ 1+ T cells. In addition, the authors demonstrated that these cells were amenable to high efficiency transduction of chimeric antigen receptors (CARs). Going forward, development of other ways that harness the anti-tumor potency of $\gamma\delta$ T cells, namely bispecific $\gamma\delta$ T cell engagers and advanced $\gamma\delta$ T cell genome-editing, is expected to widen the immuno-oncological applications of these cells.

Author contributions

AT and AC discussed findings of various articles of the Research Topic in broader context of tumor immunotherapy. AT collated contributions and prepared final version of editorial by taking into account suggestions from AC and DK.

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Butyrophilins: $\gamma\delta$ T Cell Receptor Ligands, Immunomodulators and More

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Butyrophilins (BTN) are relatives of the B7 family (e.g., CD80, PD-L1). They fulfill a wide range of functions including immunomodulation and bind to various receptors such as the $\gamma\delta$ T cell receptor ($\gamma\delta$ TCR) and small molecules. One intensively studied molecule is BTN3A1, which binds via its cytoplasmic B30.2 domain, metabolites of isoprenoid synthesis, designated as phosphoantigen (PAg). The enrichment of PAg in tumors or infected cells is sensed by $V\gamma9V\delta2$ T cells, leading to the proliferation and execution of effector functions to remove these cells. This article discusses the contribution of BTNs, the related BTNL molecules and SKINT1 to the development, activation, and homeostasis of $\gamma\delta$ T cells and their immunomodulatory potential, which makes them interesting targets for therapeutic intervention.

Keywords: butyrophilin, immune therapy, T cell receptor, $\gamma\delta$ T cell, BTN3A1, BTN2A1, phosphoantigen, tumor

WHAT ARE BUTYROPHILINS?

Eponymous for the butyrophilin family is butyrophilin 1A1 (BTN1A1 in humans, Btn1a1 in mice). It controls the fat content of milk and is found in membranes of milk-secreting mammary gland epithelial cells and fat droplets (1). Interestingly, it is also expressed in the thymic epithelium (2). The extracellular domains of BTN1A1 and other members of the BTN-family share structural features with the B7 family (**Figure 1**) (5). Its cytoplasmic region contains a juxtamembrane coiled-coiled domain and a B30.2 domain. B30.2 domains are also found in many members of the “tripartite-motif” family (TRIM), known to be involved in innate immune responses and serve as platforms for interaction with other proteins (6). The human *BTN* genes are all part of the gene cluster located at the telomeric end of the *MHC* complex on chromosome 6. It contains protein-encoding genes (7). Four of them; BTN2A1, BTN3A1 (CD277), BTN3A2 and BTN3A3, contribute to $\gamma\delta$ T cell activation (8–13). While BTN3 genes first emerged in placental mammals (14) BTN1 and BTN2 genes co-emerged with the evolution of vertebrates (7).

BUTYROPHILINS AND $\gamma\delta$ T CELL DEVELOPMENT

Some BTN-, Butyrophilin like (BTNL) and the BTN-related Skint (Selection and upkeep of intraepithelial T cells) molecules control the development and function of $\gamma\delta$ T cells (5). $\gamma\delta$ T cells are “non-conventional” T-lymphocytes, which are defined by expression of the $\gamma\delta$ T cell

antigen receptor ($\gamma\delta$ TCR). They can be found in nearly all jawed vertebrates. $\gamma\delta$ T cells differ profoundly from MHC restricted $\alpha\beta$ T cells in antigen-recognition, thymic development and selecting ligand. In contrast to MHC restricted $\alpha\beta$ T cells, whose TCR bind with the CDRs (complementarity determining region) 1, 2 and 3 of both the TCR α and β chains to MHC-peptide complexes, $\gamma\delta$ TCRs do not share specificity for a common class of ligands. The known $\gamma\delta$ TCR antigens are soluble molecules such as Phycoerythrin, various bacterial proteins and stress-induced MHC- and MHC-like molecules (15). $\gamma\delta$ T cells differ from MHC restricted T cells in thymic development, notably that for some populations of $\gamma\delta$ T cells the strength of TCR-ligand interaction during thymic development does not result in classical positive or negative selection, but in programming for differentiation to IFN γ or IL-17-producing cells (16, 17). Furthermore, $\gamma\delta$ TCR rearrangements are typical for certain phases of thymic development and lead to highly specialized $\gamma\delta$ T-cell populations. The most prominent example for such a development is the exclusive homing and functional specialization of the DETC (Dendritic Epidermal T cells) which help to maintain the barrier function of the skin (18). They are the first T cell population to develop in a body and are characterized by their dendritic morphology and a uniform TCR. The discovery of a mouse strain variant devoid of these cells led to the discovery of the butyrophilin-related gene *Skint1* gene (4) which together with *Skint2* is essential for DETC

development (19). Classical DETC has been found so far only in rodents, but interestingly DETC-resembling cells with variable $\gamma\delta$ TCR exist in the crab-eating macaques (*Macaca fascicularis*) which, in contrast to the DETC negative hominids, carry a functional *SKINT1L* (Skint1 like) gene (18).

In humans, most of the circulating $\gamma\delta$ T cells contain a V δ 2-bearing δ chain, while TCR of resident human $\gamma\delta$ T cells are dominated by other V δ (20). Some BTNs and BTNL molecules control $\gamma\delta$ T cell subset homeostasis and activation and bind to their TCR (21).

BTN and BTNL proteins are structurally similar, but the composition and chromosomal location of the gene families varies between species. In humans and mice, activation of $\gamma\delta$ T cells and homeostasis of populations of intestinal epithelial $\gamma\delta$ T cells are under the control of BTN and BTNL molecules. Murine Btl1-Btl6 heterodimers interact with V γ 7 positive $\gamma\delta$ T cells, and human BTNL3-BTNL8 heterodimers bind the TCR of V γ 4 positive cells. In the latter case, direct binding to germline-encoded parts of the γ -chain, especially to its hypervariable region 4 (HV4/CDR4), has been demonstrated, showing similarities to the interaction of some superantigens with V β -gene-encoded regions of $\alpha\beta$ TCRs (22–24). It is likely that differential topologies of TCR-ligands prompt unique modes of signaling, and it has been hypothesized that this superantigen-like type of binding maintains local cell homeostasis, while binding to the CDR3s supports an antigen-specific immune

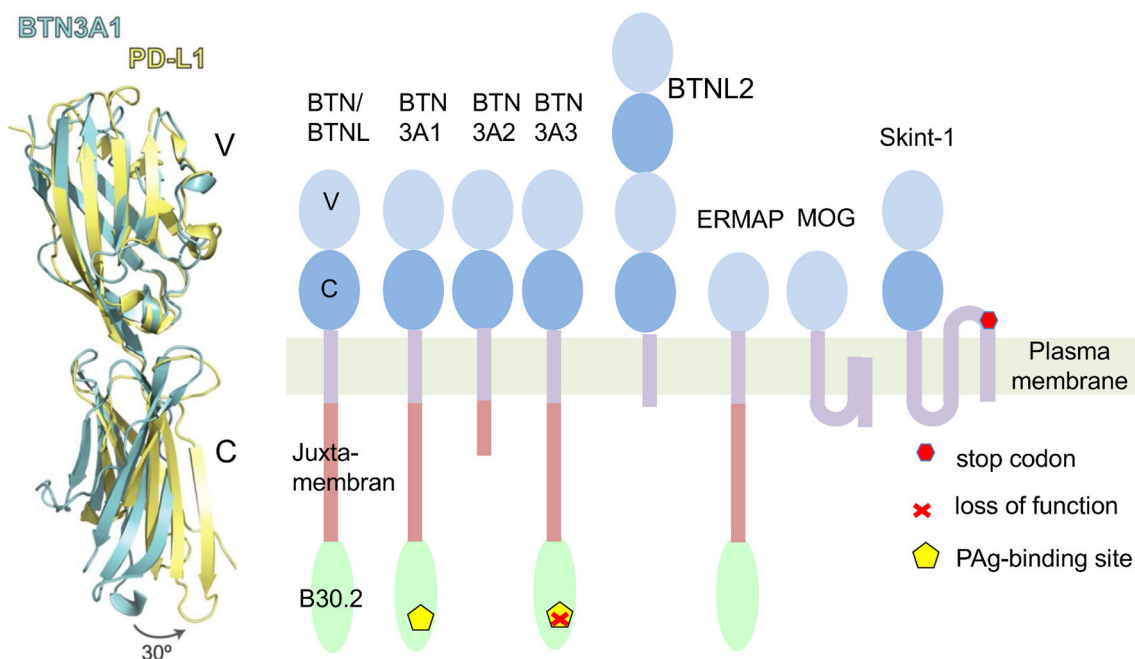


FIGURE 1 | Butyrophilins as members of the B7 family. Left: A comparison of structures of programmed death ligand 1 (PD-L1: yellow) and Butyrophilin 3A1 (BTN3A1: blue). Shown is an overlay of the tertiary structure of both proteins. Differences of the C-domains of both molecules result mainly from a twist in the orientation of V- and C-Ig domains. In an exclusive overlay of V domain alone, similarities in the Ig-V domains would be even more pronounced. Picture is modified from (3). Right: Schematic representation of human BTN/BTNL family members and mouse Skint1. The protein domains are exemplified for BTN3A1. ERMAPP (Erythroblast membrane-associated protein), MOG (Myelin-Oligodendrocyte glycoprotein). Skint 1 (Selection and upkeep of intraepithelial T-cells 1). The indicated Stop codon inactivates the Skint1 function in the DETC deficient FVB/N-Tac mouse strain (4).

response (21). Insights to the physiological significance of BTNL-TCR γ interaction can be expected from a rather frequent copy number variation, which generates a BTNL3*8 fusion product not expected to bind to V γ 4TCRs (25).

PHOSPHOANTIGEN-REACTIVE V γ 9V δ 2 T CELLS AND BUTYROPHILINS

BTN2A1 and BTN3A1 are mandatory for the activation of T cells carrying the eponymous V γ 9V δ 2TCR (10) with a V γ 9JP rearrangement and V δ 2-containing δ -chains. 1-5% of all blood T cells are V γ 9V δ 2 T cells. Usually, V γ 9V δ 2 T cells are cytotoxic cells with a type I cytokine profile, but they also show a remarkable functional plasticity and are activated by pyrophosphorylated metabolites of isoprenoid synthesis, the so-called phosphoantigens (PAGs). One such PAG is isopentenyl diphosphate (IPP), which is found in all organisms. Another well-studied PAG named (E)-4 Hydroxy-3-Methy-but-2-enyl diphosphate (HMBPP) stimulates 10000-fold better than IPP. It is the precursor of IPP in the DOXP metabolic pathway for isoprenoid synthesis, common to many Eubacteria (e.g., *Mycobacteria*), Apicomplexa such *Plasmodium* spp. or *Toxoplasma gondii* and chloroplasts. HMBPP initiates the massive expansion of the V γ 9V δ 2 T cell population during infections with HMBPP-producers, which can end up with up to 50% of human blood T cells becoming V γ 9V δ 2 T cells. In some tumor cells IPP levels are increased and trigger their elimination *via* V γ 9V δ 2 T cells. Increased IPP levels and concomitant V γ 9V δ 2 T cell activation are also induced by amino-bisphosphonates such as zoledronate, drugs commonly used in the treatment of bone metastasis or osteoporosis (26).

A breakthrough for the understanding of PAG-induced V γ 9V δ 2 T cell activation, was the finding that in cultures with peripheral blood mononuclear cells, monoclonal antibodies against BTN3A stimulated V γ 9V δ 2 T cells (agonist) or inhibited their PAG-response (antagonists) (**Figure 1**). This effect was dependent on the monoclonal antibodies binding to BTN3A molecules expressed by antigen-presenting or tumor cells, and not to the BTN3A molecules on the V γ 9V δ 2 T cells (8). PAG does not bind to the V γ 9V δ 2TCR but needs “presentation” by other cells that is initiated by binding to the intracellular B30.2 domain of BTN3A1 (9). The PAG-binding induces a conformational change which leads to the formation of a BTN3A1-BTN2A1 complex and to a not yet understood change at the cell surface, which is recognized by the V γ 9V δ 2 T cells (27). Whether recognition involves direct binding of BTN3A1 to the TCR or a hypothetical counter receptor on the T cells, or both, is unclear, but the key role of both proteins in PAG-stimulation is undisputed. The function of the PAG-non-binding BTN3A2 and BTN3A3 molecules is to increase the efficacy of the BTN3A1 action in PAG-mediated stimulation (23).

Insights into the mechanism of PAG mediated V γ 9V δ 2 T cell activation came from the comparison of species. The alpaca, beside humans and primates, is one of the few mammals with functional *BTN3*, *TCRV γ 9* (*TRGV9*) and *TCRV δ 2* (*TRDV2*) genes (14, 28, 29), and possesses PAG reactive V γ 9V δ 2 T cells (14). Replacing the intracellular region of human BTN3A1 with

that of an alpaca BTN3 results in a chimeric BTN3 molecule which stimulates as efficiently as the complex of the different human BTN3A molecules (14). Sequence comparison and phylogenetic considerations led to the postulation of an Alpaca-like primordial BTN3 which amalgamates the function of the human BTN3A family and can be imagined as a BTN3A3-like molecule with an intact PAG-binding site (15, 29).

Another example of how a comparison of species' differences helps for a better understanding of PAG stimulation, is the comparison of rodent cell lines expressing human BTN3A1 with cell lines carrying single human chromosomes. The comparison showed that, together with BTN3A1, other genes on human chromosome 6 are mandatory for PAG presentation (30). Our strategy to identify the gene(s) was the generation of “radiation hybrids” by fusing irradiated human chromosome 6-bearing rodent cells with other rodent cells (11). The chromosomes of the non-irradiated fusion partner randomly integrate pieces of the chromosomes of the irradiated cells including those of chromosome 6. The hybrids were tested, and it was assumed that only cells carrying the missing (human) genes can present PAGs. Comparison of human genome fragments of the PAG-presenting hybrids led to the identification of a 150 kB fragment at the telomeric end of the HLA complex, which contained the entire *BTN* cluster including *BTN2A1*. The significance of BTN2A1 for PAG presentation was demonstrated by:

1. Co-expression of BTN2A1 and BTN3A1 in rodent cells which rendered the cells PAG-presenters.
2. BTN2A1 inactivation by CRISPR-Cas9-mutagenesis of human 293T cells abolished their PAG-presentation capacity.

The Wilcox group in Birmingham, UK, demonstrated that the V γ 9 part of the TCR binds to BTN2A1 with a similar topology as BTNL3 to V γ 4 (24), which does not involve the TCR δ chain (11). Independently and with another screening system, the groups of Godfrey and Uldrich, at the University of Melbourne, also identified BTN2A1 as a key compound of PAG presentation. Both groups came to very similar conclusions on the interaction of BTN3A1, BTN2A1 and V γ 9V δ 2TCR (11, 12). However, the ligand(s) of the V γ 9V δ 2TCR in PAG-induced activation is still not known, it is speculated that it could be a particular conformation of BTN2A1 and BTN3A1. Our working hypothesis is that apart from BTN2A1 and BTN3A1, other molecules might be involved and that interaction of the TCR with these molecules implies also additional CDR3-binding ligand(s) which leads to different signals than exclusive binding of BTN(L) molecules to the V γ part of the TCR (11) (**Figure 2** 2). In summary, BTN and BTN-like molecules are essential for the development and TCR-mediated activation of many, if not all, $\gamma\delta$ T cells.

OTHER FUNCTION OF BUTYROPHILINS AND IMMUNE THERAPY

BTN2A1 and BTN3A1 fulfill various functions. One function of BTN2A1 is its capacity to bind to DC-SIGN, which depends on the expressing cell type and the degree of its glycosylation state

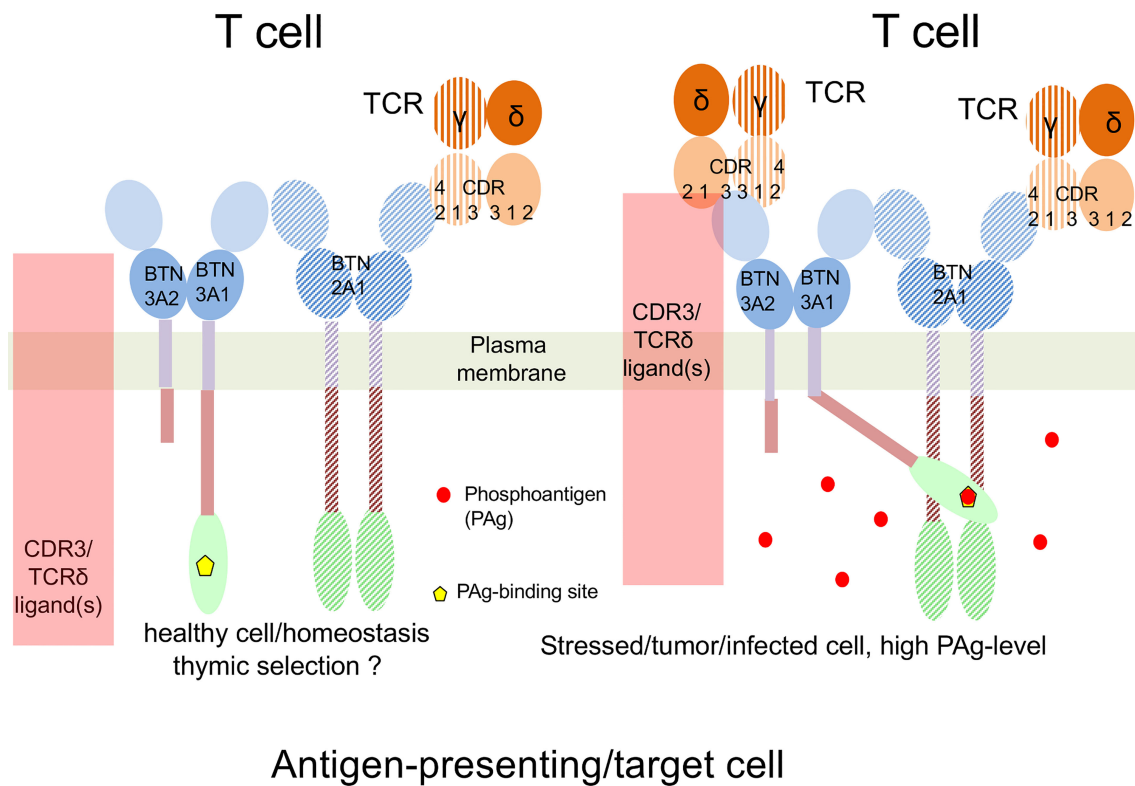


FIGURE 2 | Working hypothesis on PAg-recognition by V γ 9V δ 2 T cells. Left: Under physiological conditions, BTN2A1 binds to the hypervariable region 4 (CDR4 or HV4) of the V γ 9 region of the V γ 9V δ 2TCR. This controls thymic development and homeostasis of V γ 9V δ 2 T cells. Right: Infection or cell transformation increases PAg-levels in the presenting or tumor cell. This leads to PAg-binding to the B30.2 domain of BTN3A1, and subsequent binding of the B30.2-PAg complex to the intracellular domain of BTN2A1. The resulting complex might include additional proteins, which finally bind all CDRs regions of γ and δ chain and trigger V γ 9V δ 2 T cell activation. Please note that so far neither direct binding of the TCR to BTN3A nor existence of an additional ligand recruited by the PAg-binding BTN3A has been demonstrated.

(31). An example of BTN3A1 function is its involvement in the induction of IFN β production by cytoplasmic- or viral nucleic acids (32).

The immunomodulatory function of BTN(L) and using it as a target of immunotherapy is becoming of greater interest. For some time it has been known that BTN(L)-specific monoclonal antibodies can amplify activation of T cells and NK cells (5, 33), while BTN(L) overexpression, soluble BTN(L)-molecules or BTN(L)-Fc constructs often inhibit T-cell activation [e.g. (2, 5)]. However, the involved counter receptors have not been identified and physiological relevance of this suppression is not clear. One of the better-understood examples about the physiological role of BTN(L)s comes from the analysis of BTN2a2-deficient mice. These show an increased $\alpha\beta$ T cell response, and shown by cell transfer experiments, this results from missing Btn2a2 expression of antigen-presenting cells (34). More recently, involvement was also reported in the regulation of ILC2-T cell crosstalk (35) and bone resorption (36) and reduced levels of soluble Btn2a2 in arthritis of in mouse or BTN2A2 in human arthritis (36).

A study which attracted much attention was the analysis of the suppression of tumor-specific T cells by BTN3A1 (37), which

was postulated to be a consequence of BTN3A1-binding to glycosylated CD45 and concomitant disruption of the immunological synapse and TCR-mediated signaling. This immune suppression could be abolished by BTN3A specific monoclonal antibodies *in vitro* and in mouse models. Immunodeficient NGS mice were inoculated with a human ovarian cancer cell line and treated with combinations of human tumor-target specific TCR transductants. $\gamma\delta$ T cells cells with and without BTN3 antibodies showed $\alpha\beta$ and $\gamma\delta$ T cell specific effects, by combining inhibition of BTN3-mediated suppression of the T cell response and agonistic action of agonist on the $\gamma\delta$ T cells. The other model used was BTN3A1-transgenic mice inoculated with an immune suppression inducing ovarian tumor cell line (ID8-*Defb29-Vegf-a*), where the therapeutic effect of the BTN3 specific mAb was even superior to PD1 specific mAb. Interestingly, even in absence of V γ 9V δ 2 T cells, administration of zoledronate had also a beneficial effect (37) which indicates that (partial) reversal of BTN3A1 immunosuppression might also involve PAGs. Another aspect is the interpretation of an ongoing clinical trial with the agonistic BTN3A specific monoclonal antibody ICT01 (ClinicalTrials.gov-Identifier: NCT04243499) where a positive clinical outcome

might not only result from activation of $V\gamma 9V\delta 2$ T cells (38) but also by reconstituting a BTN3-suppressed $\alpha\beta$ T cell.

Very recently a mechanism of immune evasion by expression of BTNL2 on cancer cells was described, where BTNL2 promotes IL-17 production by a local $\gamma\delta$ T cell population which enhances tumor resistance by recruitment of myeloid suppressor cells T cells (39). Blockade of BTNL2 by a monoclonal antibody had a significant therapeutic effect for several mouse tumors and acts synergistically with PD1 blockade. Furthermore, BTNL2 is expressed in multiple human solid cancers and its expression level correlates negatively with patients' survival. Thus, BTNL2 may be a target for therapeutic intervention similar as BTN3 although the mechanism of immune evasion is a different one.

To conclude, BTN(L) molecules fulfill immunological and non-immunological functions of which some affect $\gamma\delta$ T cells and bear therapeutic potential by targeting them with monoclonal antibodies similar to those successfully applied for more conventional B7 family members (40).

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AUTHOR CONTRIBUTIONS

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Apoptosis, Pyroptosis, and Ferroptosis Conspiringly Induce Immunosuppressive Hepatocellular Carcinoma Microenvironment and $\gamma\delta$ T-Cell Imbalance

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Hepatocellular carcinoma (HCC) is highly malignant and prone to metastasize due to the heterogeneous and immunosuppressive tumor microenvironment (TME). Programmed cell deaths (PCDs) including apoptosis, ferroptosis, and pyroptosis routinely occur in the HCC TME and participate in tumorigenesis. However, how apoptosis, ferroptosis, and pyroptosis are involved in constructions of the immunosuppressive TME and their underlying cross-talk remains to be further unveiled. In this work, we deciphered the immunosuppressive landscape of HCC TME, which demonstrated high expressions of inhibitory checkpoint molecules and infiltration of protumor immune cells but low infiltration of antitumor effector immune cells. Further investigations unequivocally revealed that marker genes of apoptosis, ferroptosis, and pyroptosis are closely correlated with expressions and infiltrations of inhibitory checkpoint molecules and immune cells and that higher “-optosis” links to poorer patient prognosis. Notably, such three types of “-optosis” interact with each other at both the gene and protein levels, suggesting that they conspiringly induce the establishment of the immunosuppressive HCC TME. Interestingly, examinations of circulating $\gamma\delta$ T cells in HCC patients revealed a noticeable dysfunction phenotype. The strikingly elevated ratio of the V δ 1⁺ versus the V δ 2⁺ subset suggested that the V δ 1⁺/V δ 2⁺ ratio would be a potential biomarker for the diagnosis and prognosis in HCC patients. Altogether, this work thoroughly decrypted the underlying correlations between apoptosis, ferroptosis, and pyroptosis and the formation of immunosuppressive HCC TME and, meanwhile, indicated that allogeneic V δ 2⁺ $\gamma\delta$ T-cell transfer would be a promising adjuvant strategy for renormalizing circulating $\gamma\delta$ T cell and thus achieving sound clinical efficacy against HCC.

Keywords: apoptosis, pyroptosis, ferroptosis, immunosuppressive HCC TME, $\gamma\delta$ T-cell imbalance

INTRODUCTION

The liver is a major metabolic organ and plays a crucial role in all metabolism processes in the body. In certain circumstances, such as alcohol abuse, virus infection, and drugs, liver inflammation will occur and can deteriorate into hepatic fibrosis, hepatic cirrhosis, and eventually liver cancer. Generally, tumorigenesis is a result induced by complicated events, and one determinant factor is the long-term suppressive or dysfunctional immunity of hosts. Hepatocellular carcinoma (HCC) is well-known for its high relapse rate and poor long-term prognosis. Current routine treatments of HCC rely heavily on chemotherapeutic approaches (e.g., sorafenib) but have unsatisfactory results. Fortunately, immunotherapy strategies (1) including immune checkpoint blockade (ICB) (2) and immune cell therapy (3–5) provide new opportunities for HCC patients. For example, PD1 blockade therapy is now covered for free by the National Healthcare Security System of China and benefits the increasing HCC population. Nevertheless, further decoding of the HCC tumor microenvironment (TME), especially the immune landscape, will benefit the development of immunotherapies. For HCC, how the immunosuppressive microenvironment is triggered and eventually established remains to be further illustrated.

The excessive proliferation nature of cancer cells and the antitumor immunity of the host unavoidably lead to numerous types of cell death, mainly including programmed (e.g., apoptosis) and non-regulated (e.g., necrosis) cell deaths. Currently, intensively investigated programmed cell deaths (PCDs) in HCC TME include apoptosis, ferroptosis, and pyroptosis. Apoptosis belongs to the non-immunogenic cell death and shall not induce detectable immune responses under normal circumstances. On the other hand, immunogenic deaths, ferroptosis, and pyroptosis can result in immune responses due to the release of various intracellular contents, most acting as pro-inflammatory signals. Though the role of ferroptosis and pyroptosis in HCC prognosis had been previously discussed (6, 7), how non-immunogenic apoptosis as well as immunogenic ferroptosis and pyroptosis cross-talk at the gene and protein levels and collaboratively contribute to the development of the immunosuppressive HCC TME remain to be further addressed.

In the HCC TME, there are various types of infiltrated immune cells, including lymphoid and myeloid lineage cells. Among them, $\gamma\delta$ T cell occupies 6.8%–34% CD3⁺ T cell in the liver (8, 9) and plays crucial roles in liver protection from virus infection (10) and tumorigenesis (11, 12). Intra-tumoral $\gamma\delta$ T cell was proposed to be one of the best positive prognosis markers for pan-cancers (13). However, evidence indicated that the two major subsets of $\gamma\delta$ T cell, namely, V δ 1⁺ and V δ 2⁺ subsets, possess contradictory roles in antitumor immunity. The V δ 1⁺ subset tends to perform a Treg-like function in the context of TME, which expresses high levels of inhibitory surface markers like CD73 (14) and CD39 (15), as well as cytokines such as IL10 (15) and TGF β (16). The V δ 2⁺ subset, however, is the early source of IFN γ (17, 18) and performs cytotoxic functions against transformed cells (19). For years, we have mainly focused on the V δ 2⁺ subset; most importantly, we innovatively proved the safety

and efficacy of the allogeneic V δ 2⁺ $\gamma\delta$ T cells in a series of clinical studies (4, 5, 20). Therefore, the primary scientific question we want to illustrate is the performance of the V δ 2⁺ $\gamma\delta$ T cell in the context of HCC TME. Here we not only applied bioinformatics to evaluate the correlations between $\gamma\delta$ T-cell infiltration and three types of cell death (apoptosis, ferroptosis, and pyroptosis) but also statistically evaluated the imbalance of circulating $\gamma\delta$ T-cell subsets in HCC patients.

Together, our present work revealed that the HCC TME is globally immunosuppressive, and three types of “-optosis” (apoptosis, ferroptosis, and pyroptosis) play crucial roles in creating the immunosuppressive TME and lead to the adverse prognosis of HCC patients. Moreover, we found that the proportion of the V δ 1/V δ 2 subsets of circulating $\gamma\delta$ T cell is functionally imbalanced in HCC patients, suggesting that the adoptive transfer of allogeneic V δ 2⁺ $\gamma\delta$ T cells from healthy donors might benefit patients. We further hypothesize that by taking advantage of apoptosis, ferroptosis, and pyroptosis, immune cell-based adjuvant therapy (e.g., V δ 2⁺ $\gamma\delta$ T) might lead to a better prognosis than chemotherapy alone or chemotherapy combined with checkpoint blockade.

METHODS AND MATERIALS

$\gamma\delta$ T-Cell Subset Proportioning in the Healthy Population and Hepatocellular Carcinoma Patients

To reveal the proportional difference in the two subsets of $\gamma\delta$ T cells from peripheral blood mononuclear cells (PBMCs) between the healthy population and HCC patients, the raw immune-phenotyping data of these two populations provided by the Shuangzhi Purui Medical Laboratory Co., Ltd. (Wuhan, China) were obtained and analyzed. The healthy population consisted of 170 disease-free adults (age range, 26–72; gender includes both female and male). The HCC population consisted of 42 patients (age range, 30–71; diagnosis, HCC I to IV including both primary and recurrence; gender includes both female and male). The antibodies used included anti-human CD3, anti-human TCR V δ 1, and anti-human TCR V δ 2 antibodies (BioLegend, San Diego, CA, USA). All examinations were conducted using BD FACSCanto cytometry (BD Biosciences, San Jose, CA, USA).

Online Databases and Bioinformatics Analysis

Tumoral mRNA-sequencing data (level 3) and corresponding clinical information of 371 HCC patients were obtained from The Cancer Genome Atlas (TCGA) dataset (<https://portal.gdc.cancer.gov/>) by following the related guidelines and policies. The mRNA-seq data of 50 paired peri-tumor tissue samples, together with 226 healthy liver tissue samples from the GTEx database (GTEx V8, <https://gtexportal.org/home/datasets>), were used as the control group, which described donors' clinical information including gender, race, age, clinical stages, therapy history, and biospecimen collection. Protein–protein interaction was

analyzed using the online database (<https://string-db.org/>). The R Project for Statistical Computing version 4.0.3 was used for graph plotting and analysis unless specified otherwise. In our analysis, HCC patients were divided into three groups (I, II, and III–IV) according to the clinical stage (pTNM) due to the limited amount of stage IV patients. To analyze the multi-gene correlation, the mRNA-seq dataset from NIH National Cancer Institute (<https://tcga-data.nci.nih.gov/tcga/>) was also included. The R software packages ggstatsplot and pheatmap were respectively used to produce two-gene and multi-gene correlation maps. Spearman's analysis was used to describe the correlation.

As for ferroptosis analysis, the related marker genes were derived from previously published data (21). The marker genes for apoptosis were adopted from <http://biocc.hrbmu.edu.cn/CancerSEA/home.jsp>. The marker genes for pyroptosis were from published work (22). Then R packages ggplot2 and pheatmap were used for data visualization. Based on marker genes of apoptosis, ferroptosis, and pyroptosis, we wanted to know whether samples could be clustered into subgroups. The R packages ConsensusClusterPlus and pheatmap were used to generate clustering heatmaps. Moreover, the Kaplan–Meier survival analysis with log-rank test was used to plot survival curves among groups; p-values and hazard ratio (HR) with 95% CI were generated by log-rank tests and univariate Cox proportional hazards regression. For correlation between single gene and survival, R packages ggrisk, survival, survminer, glmnet, and timeROC were applied for analysis.

To evaluate immune cell infiltration in the context of apoptosis, ferroptosis, and pyroptosis, the R package immunedeconv was applied, which integrates six classes of algorithms, including TIMER, xCell, MCP-counter, CIBERSORT, EPIC, and quanTIseq. Meanwhile, the gene expression of inhibitory checkpoint molecules PDCD1(PD1), CD274(PDL1), PDCD1LG2(PDL2), CTLA4, LAG3, TIGIT, HAVCR2(TIM3), and SIGLEC15 in HCC tissues were intensively inspected. To analyze the correlation between “-optosis” related marker genes and 15 checkpoint molecules, both stimulatory checkpoint molecules (CD27, CD28, CD40, DNAM1, ICOS, and TNFRSF9) and inhibitory checkpoint molecules (CD274, CTLA4, HAVCR2, LAG3, PDCD1, PDCD1LG2, TIGIT, SIGLEC15, and BTLA) were included. To assay ICB among HCC subgroup samples, the potential ICB response was predicted with the Tumor Immune Dysfunction and Exclusion (TIDE) algorithm (23). p-Value <0.05 was considered statistically significant.

RESULTS

Hepatocellular Carcinoma Tumor Microenvironment Is Highly Immune Suppressed

To comprehensively inspect the immune microenvironment of HCC TME, we firstly compared gene expression of immune inhibitory checkpoint molecules between tumor tissues and normal (peri-tumor) tissues, including CD274, CTLA4,

HAVCR2, LAG3, PDCD1, PDCD1LG2, TIGIT, and SIGLEC15. It showed that all inhibitory checkpoint molecules except for CD274 are significantly upregulated in the HCC tumor group (**Figures 1A, B**). Then, 371 HCC samples were divided into 3 groups based on clinical stage (pTNM), and the checkpoint molecules were further compared among the 3 subgroups. It turned out that all checkpoint molecules are not statistically different among subgroups (**Figure 1C**). Further analysis revealed that HCC patients with different clinical stages respond to ICB therapy similarly (**Figure 1D**). We further checked the difference of immune cell infiltration between the HCC and normal groups by CIBERSORT score comparisons. We found that in the HCC group, scores of regulatory T cells (Tregs), resting macrophages M0, resting myeloid dendritic cells (DCs), and activated mast cells are strikingly increased. On the contrary, CIBERSORT scores of infiltrated $\gamma\delta$ T cells, monocytes, macrophages M2, and resting mast cells are all depressed (**Figure 1E**). Furthermore, we inspected tissue infiltration of these immune cells among subgroups according to clinical stages (I, II, III–IV, and normal) and observed a similar pattern (**Figure 1F**) to **Figure 1E**.

Apoptosis Contributes to Establishing the Immunosuppressive Hepatocellular Carcinoma Tumor Microenvironment

Due to the excessive proliferation of HCC tumor cells and corresponding antitumor immunity and because cancer cell apoptosis routinely occurs in the TME, we first checked the expression differences of 63 apoptosis marker genes between HCC and normal tissues. We can see that 48 apoptosis-related marker genes are significantly upregulated in the HCC group (9 downregulated genes highlighted by blue arrows and 6 genes with no statistical difference) (**Figure 2A**). We then analyzed the correlation between each of the 63 marker genes and the overall survival (OS) rate and found that only 22 apoptotic genes are significantly correlated with the OS ($p < 0.05$). Specifically, 21 genes have negative correlations, while only one gene (PPP2R1B) has a positive correlation (**Supplementary Figure 2A**). Afterward, the multi-gene correlation among these 22 genes was calculated, as shown in **Figure 2B**. Moreover, we intensively analyzed those genes that have a better correlation with OS ($p \leq 0.01$), including BCL10, E2F2, BAK1, BCAP31, CASP2, SNW1, and STK4. It shows that higher expressions of these 7 genes lead to poorer prognoses (**Figure 2C**). Further analysis revealed that expressions of these 7 genes among different clinical stages (I, II, and III–IV) are consistently and greatly upregulated as compared with the normal group, and the expression level dramatically increases from stage I to stage III–IV (**Figure 2D**). We then found that six of these seven genes (except BCAP31) are positively correlated with the expression level of checkpoint molecules and immune cell infiltration (**Figures 2E, F; Supplementary Figure 2B**).

Based on the expressions of those 22 genes that are correlated with OS, 371 HCC samples were further divided into 3 subgroups using the R package ConsensusClusterPlus (**Supplementary Figure 2C**), and the clinical information of these 3 groups is

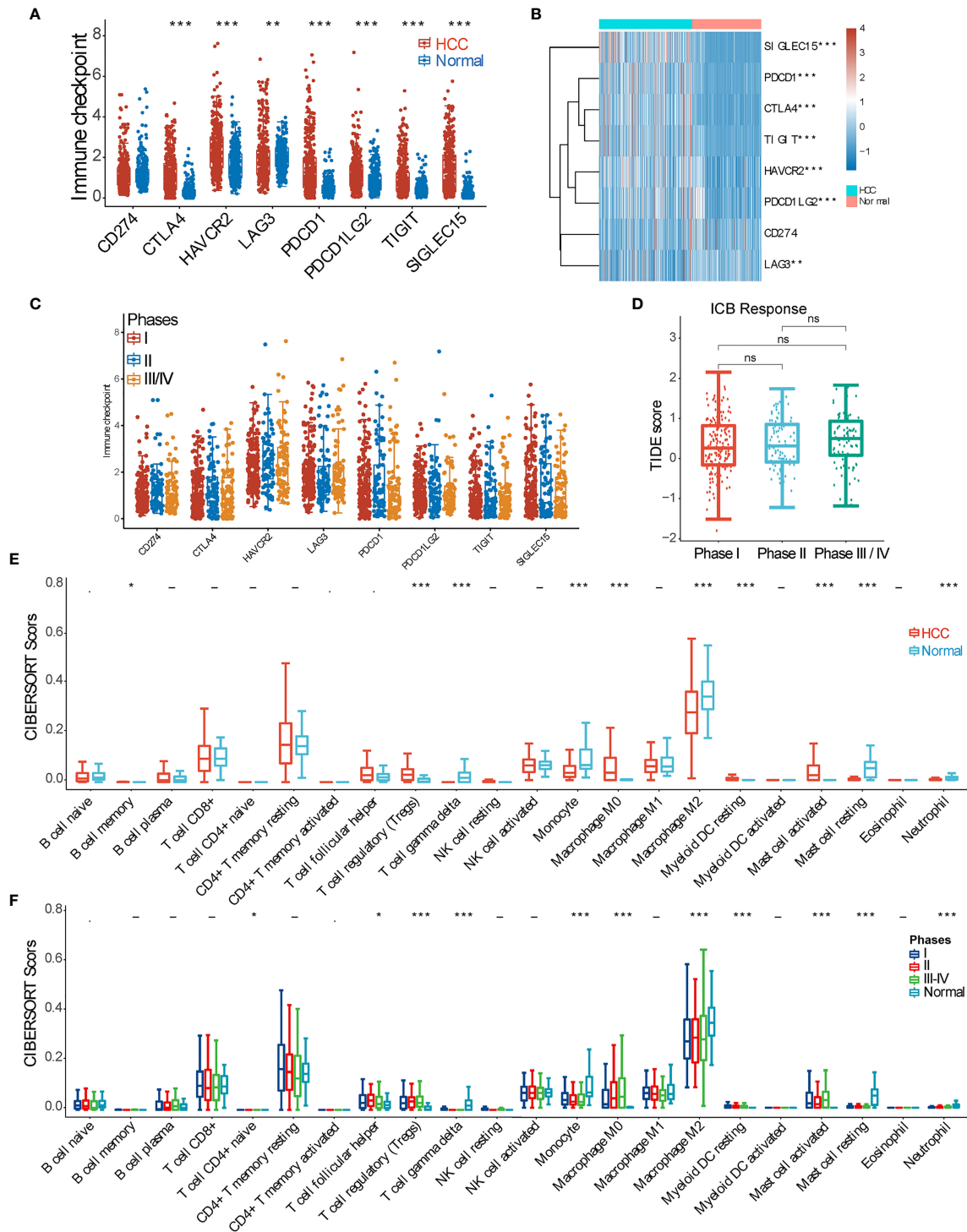


FIGURE 1 | Overview of the immune microenvironment of hepatocellular carcinoma (HCC) tissue. **(A)** Expression difference of inhibitory checkpoint molecules (CD274(PDL1), CTLA4, HAVCR2(TIM3), LAG3, PDCD1(PD1), PDCD1LG2(PDL2), TIGIT, and SIGLEC15) between HCC and normal tissue samples. **(B)** Heatmap of inhibitory checkpoint molecule expression. **(C)** Expression of inhibitory checkpoint molecules in HCC samples of pTNM stages I, II, and III-IV. **(D)** Tumor Immune Dysfunction and Exclusion (TIDE) score analysis was used to predict the responses to immune checkpoint blockade (ICB) of HCC patients at pTNM stages I, II, and III-IV. **(E)** CIBERSORT score of various immune cell infiltrations in HCC and normal tissue samples. **(F)** CIBERSORT score of various immune cell infiltrations among HCC samples of pTNM stages I, II, and III-IV. *p < 0.05; **p < 0.01; ***p < 0.001; -, ns, no statistical significance.

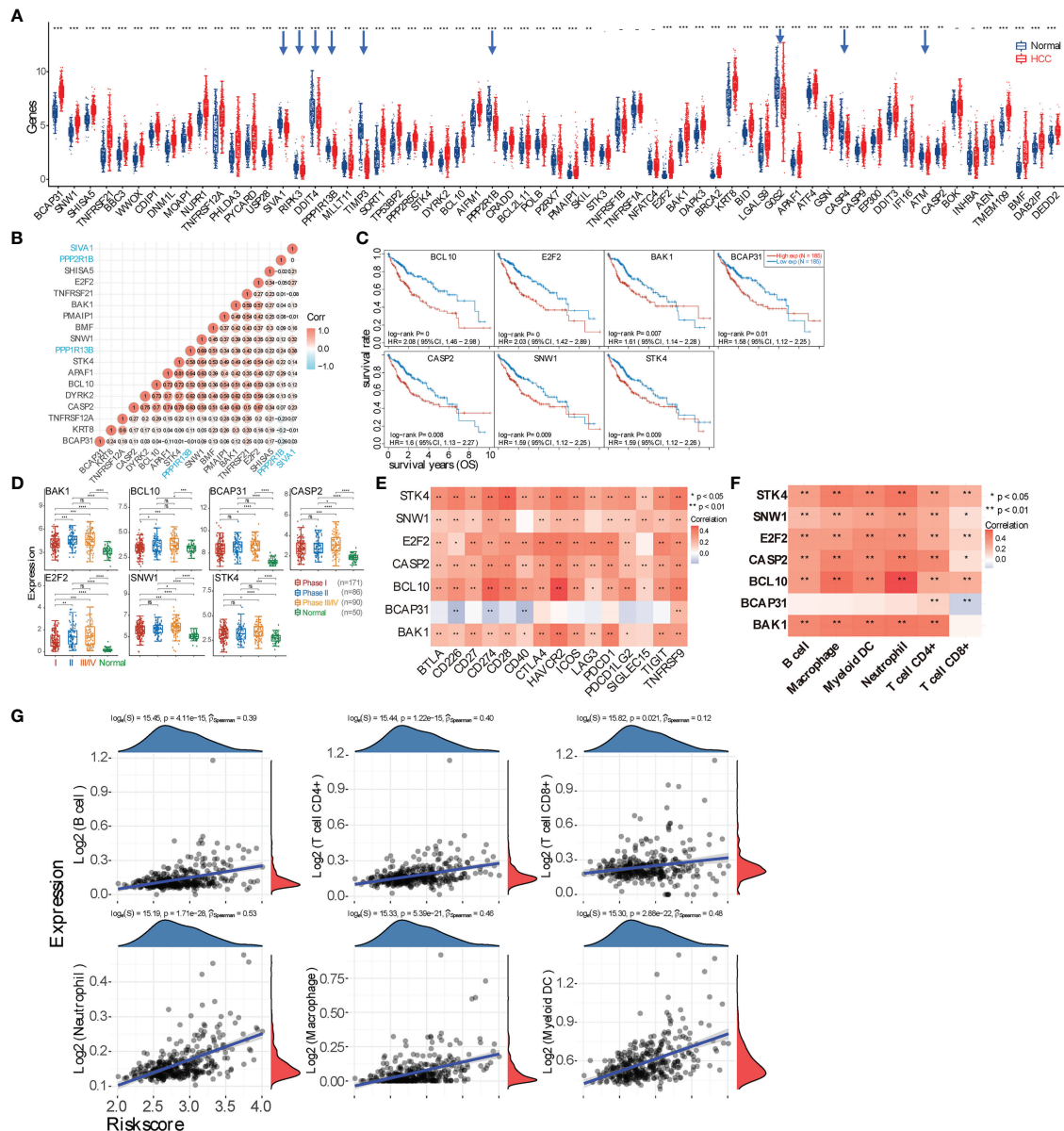


FIGURE 2 | Evaluating the underlying correlation between apoptosis and immune microenvironment. **(A)** Expression spectrum of apoptosis marker genes in hepatocellular carcinoma (HCC) tumor tissue. Downregulated genes are highlighted by blue arrows. **(B)** Multi-gene correlation map generated using the genes with significant ($p < 0.05$) correlation with the overall survival (OS) rate. A positive value represents a positive correlation; otherwise, a negative correlation. The larger correlation value means the better correlation between two genes. The three genes labeled with blue color are downregulated genes in panel **(A, C)** Survival curves of 7 genes (BCL10, E2F2, BAK1, BCAP31, CASP2, SNW1, and STK4) that negatively correlate with prognosis ($p < 0.01$). **(D)** Expression difference of those 7 genes in HCC tumor tissues among patients with stage I, II, or III-IV. **(E)** Correlation analysis between 7 marker genes and checkpoint molecules. Only BCAP31 negatively correlates with checkpoint molecules. **(F)** Correlation between 7 marker genes and major types of immune cell infiltration. **(G)** Spearman's correlation analysis between the risk score of the prognostic model (calculated from the 7 marker genes) and immune score (based on TIMER). The horizontal axis represents the risk score of the prognostic model; the vertical axis represents the immune score. The density curve (red) on the right represents the distribution trend of the immune score, and the dark-blue density curve on the top represents the distribution trend of the risk score. The p-value and correlation coefficient (ρ Spearman) are shown at the top of the respective graph. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$; '-', ns, no statistical significance.

shown in the table. It shows that the expressions of most checkpoint molecules (except SIGLEC15) are significantly elevated in "G2" and "G3" compared with "G1." CIBERSORT scores indicated that infiltrations of naïve B cells, CD8⁺ T cells,

naïve CD4⁺ T cells, resting NK cells, monocytes, macrophage M1, and activated mast cells are statistically different among the three groups ($p < 0.01$). Further TIDE score analysis revealed that "G2" and "G3" have better ICB responses. However, OS probability

shows no statistical difference among the three subgroups. Furthermore, 7 genes with a $p \leq 0.01$ correlation with OS were used to construct a prognostic signature model using the least absolute shrinkage and selection operator (LASSO) Cox regression model. The obtained Riskscore equals $(0.072) * BAK1 + (0.1257) * BCAP31 + (0.0895) * BCL10 + (0.2596) * E2F2 + (0.1424) * SNW1$ (Supplementary Figure 2D). Based on this prognostic model, the correlation between the Riskscore and immune cell infiltration was further visualized (Figure 2G).

Ferroptosis Is Involved in Constructing the Immunosuppressive Hepatocellular Carcinoma Tumor Microenvironment

Given that ferroptosis can be conditionally triggered by chemotherapy or can spontaneously occur under oxidative stress in the HCC microenvironment, we then checked the overall expressions of ferroptosis marker genes between HCC and normal samples. It shows 19 upregulated and 3 downregulated genes in HCC (Figure 3A), and the gene correlation in HCC and normal tissues is shown in Figure 3B and Supplementary Figure 3A. We then calculated how expressions of these genes would affect patient prognosis, and we found that higher expressions of genes SLC1A5, CARS1, SLC7A11, RPL8, and TFRC lead to poorer OS ($p < 0.01$) (Figure 3C and Supplementary Figure 3B). Moreover, the expressions of these 5 genes are gradually enhanced from tumor stage (pTNM) I to III/IV (Figure 3D). Subsequently, the correlation between these 5 genes and checkpoint molecules or immune cells was analyzed, as shown in Figures 3E, F. Moreover, HCC samples were also sub-clustered into 4 groups based on the expression of 22 ferroptosis marker genes, showing the difference in immune cell infiltration as well as expressions of inhibitory checkpoint molecules among subgroups (Supplementary Figure 3C). TIDE score revealed that these 4 subgroups respond to ICB differently, and the OS probability among groups is statistically different ($p < 0.001$). Furthermore, a prognostic signature model was constructed, and the obtained Riskscore equals $(0.1218) * CARS1 + (0.0359) * RPL8 + (0.0095) * TFRC + (0.1585) * SLC7A11 + (0.1652) * SLC1A5$ (Supplementary Figure 3D), which was used to calculate the correlation between the Riskscore and immune cell infiltration (Figure 3G).

Pyroptosis Conspires in Creating the Immunosuppressive Hepatocellular Carcinoma Tumor Microenvironment

In addition to ferroptosis, pyroptosis is another type of inflammatory cell death. It is thus interesting to unveil the relationship between pyroptosis and the immune response in the HCC microenvironment. We found that, among 33 marker genes, 21 genes are upregulated, 6 genes are downregulated, and 6 genes have no statistical difference (Figure 4A). Further analysis revealed that only 6 genes (CASP3, GSDME, NLRP6, NOD1, and PLCG1) are statistically correlated with the OS rate of HCC patients ($p < 0.05$) (Figure 4B and Supplementary Figure 4A), and only GSDME, NLRP6, and NOD1 are significantly correlated with the OS ($p < 0.01$). Moreover, genes GSDME and NOD1 expressed higher in

pTNM stage III–IV compared with stages I and II (Figure 4C). Further evaluation revealed that these 6 genes except NLRP6 are all positively correlated with checkpoint molecule expression and immune cell infiltration (Figures 4D, E). Additionally, all HCC samples can be grouped into two subclusters based on pyroptosis marker genes (Supplementary Figure 4B), and then expressions of checkpoint molecules, immune cell infiltration (TIMER and CIBERSORT scores), ICB, and the OS probability between two subgroups were all deciphered (Supplementary Figures 4C, D). The prognostic signature model was also generated by using the genes with $p < 0.01$, and the Riskscore equals $(0.2413) * GSDME + (-0.2142) * NLRP6 + (0.0892) * NOD1$, and the correlation between the Riskscore and immune cell infiltration was obtained (Figure 4F and Supplementary Figure 4E).

Cross-Talk of Apoptosis, Ferroptosis, and Pyroptosis in Hepatocellular Carcinoma Tumor Microenvironment

In the context of HCC TME, apoptosis, ferroptosis, and pyroptosis occur in an interconnecting manner, and their cross-talk may exist at both the gene and protein levels. We thus evaluated those marker genes that have a $p < 0.01$ correlation with the OS rate of HCC patients and found that these three types of “-optosis” genes do show cross-talk at the genomic level (Figure 5A and Supplementary Figure 5A). For example, NOD1 (pyroptosis gene) associates with both apoptosis genes (BCL10, CASP2, STK4, E2F2, and BAK1) and ferroptosis genes (TFRC, SLC1A5, and CARS1), and apoptosis gene BCL10 connects with pyroptosis genes (NOD1 and GSDME) and ferroptosis genes (SLC1A5, TFRC, CARS1, and SLC7A11). The protein–protein correlation analysis (STRING database, <https://string-db.org/>) further supports the analysis at the mRNA level, clearly showing the existing interactions among apoptosis, ferroptosis, and pyroptosis at the protein levels (Figure 5B and Supplementary Figure 5B). Next, we examined the protein–protein interactions between 15 checkpoint molecules and the “-optosis” genes that significantly correlate ($p < 0.01$ and < 0.05 , respectively) with the OS rate (Supplementary Figures 5C, D); the result indicated that only 5 checkpoint molecules (CD27, CD28, CD40, CTLA4, and PDL1) correlate with “-optosis” proteins. Afterward, 15 “-optosis” genes (significantly correlating with the OS rate, $p < 0.01$) were used to construct the prognostic signature model, and the obtained Riskscore (Supplementary Figure 5E) was correlated with immune cell infiltration (Figure 5C), indicating positive correlations with 6 main types of immune cells and specifically relative higher correlations with neutrophils, macrophages, and myeloid DCs ($p_{\text{Spearman}} > 0.4$).

Apoptosis–Ferroptosis–Pyroptosis Collaboratively Induces Immunosuppressive Hepatocellular Carcinoma Tumor Microenvironment

Since cross-talk of apoptosis, ferroptosis, and pyroptosis was demonstrated at both the gene and protein levels, it is interesting to decode whether they conspiringly participate in inducing the

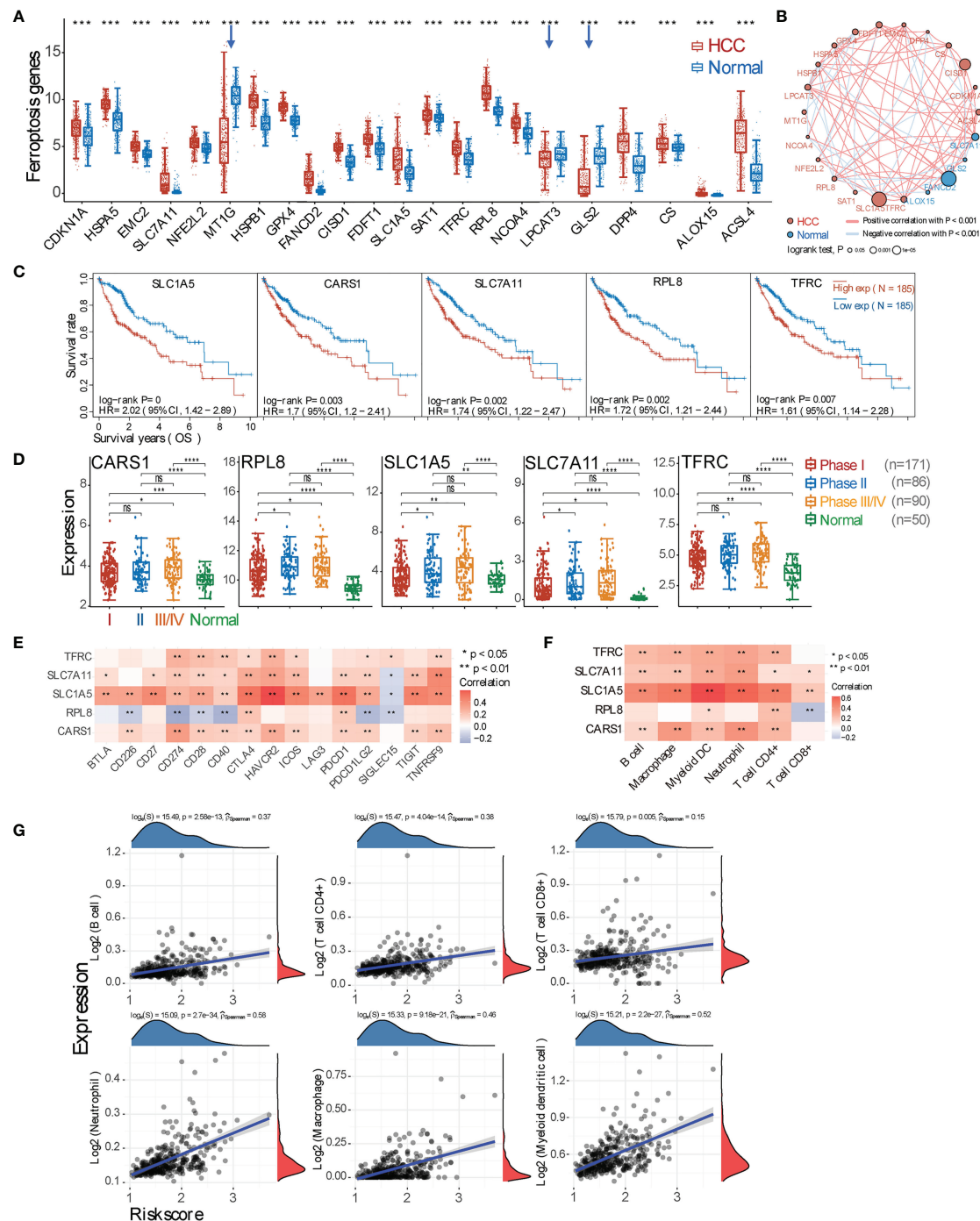


FIGURE 3 | Marker gene expression of ferroptosis and its correlation with tumor microenvironment (TME) immune profile. **(A)** Expression comparison of ferroptosis marker genes between hepatocellular carcinoma (HCC) and normal tissues. The downregulated genes in HCC tissues are highlighted by blue arrows. **(B)** Gene relationship. Each circle represents a gene: the red one means positive, while the blue one represents negative correlation. The different sizes of the circle mean the different log-rank p-value. **(C)** Representative overall survival curves of 5 genes (SLC1A5, CARS1, SLC7A11, RPL8, and TFRC) that are negatively and significantly correlated with prognosis ($p < 0.01$). **(D)** Expression of these 5 marker genes in tumor tissues from pTNM stage I, II, or III-IV patients. **(E)** Correlation analysis between 5 marker genes and checkpoint molecules. **(F)** Correlation between 5 marker genes and major types of immune cell infiltration. **(G)** Spearman's correlation analysis between the risk score of the prognostic model (calculated from the 5 marker genes) and the immune score. The horizontal axis represents the risk score of the prognostic model; the vertical axis represents the immune score. The density curve (red) on the right represents the distribution trend of the immune score, and the dark-blue density curve on the top represents the distribution trend of the risk score. The p-value and correlation coefficient (ρ Spearman) are shown at the top of the respective graph. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$; '-', ns, no statistical significance.

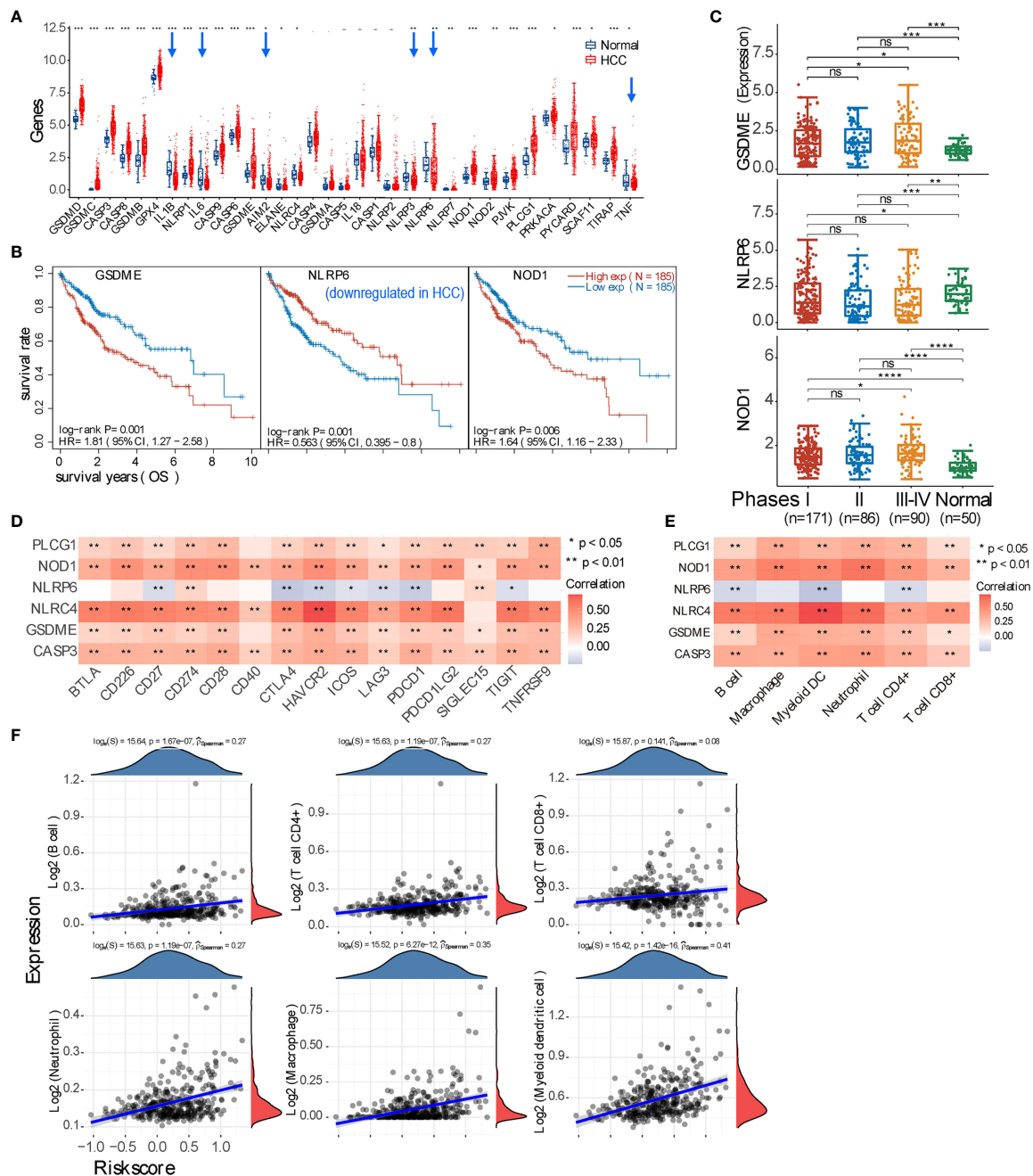


FIGURE 4 | Expression of pyroptosis marker genes and their immune correlation in the context of hepatocellular carcinoma (HCC). **(A)** Expression profile of pyroptosis marker gene in HCC and normal tissue. The downregulated genes in HCC are pointed by blue arrows. **(B)** Three marker genes are significantly correlated with prognosis ($p < 0.01$); specifically, NLRP6 positively correlates with the overall survival of HCC patients. **(C)** Expression comparison of these 3 genes (GSDME, NLRP6, and NOD1) in HCC patients with pTNM stage I, II, or III-IV. **(D, E)** Correlation analysis between all genes that have $p < 0.05$ correlation with prognosis and checkpoint molecules, or immune cell infiltration. **(F)** Spearman's correlation analysis between the risk score of the prognostic model (calculated from the 3 marker genes) and immune score. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$; '-', ns, no statistical significance.

immune-suppressiveness of HCC TME. We thus analyzed how each marker gene ($p < 0.01$ correlation with the OS) correlated with immune cell infiltration (**Figure 5D**). The result unequivocally indicates that tumor-infiltrating Tregs,

macrophage M0, resting myeloid DCs, and activated mast cells are all significantly enriched in the context of expressions of the listed marker genes. Meanwhile, $\gamma\delta$ T cell, monocytes, macrophage M2, resting mast cells, and neutrophils are all

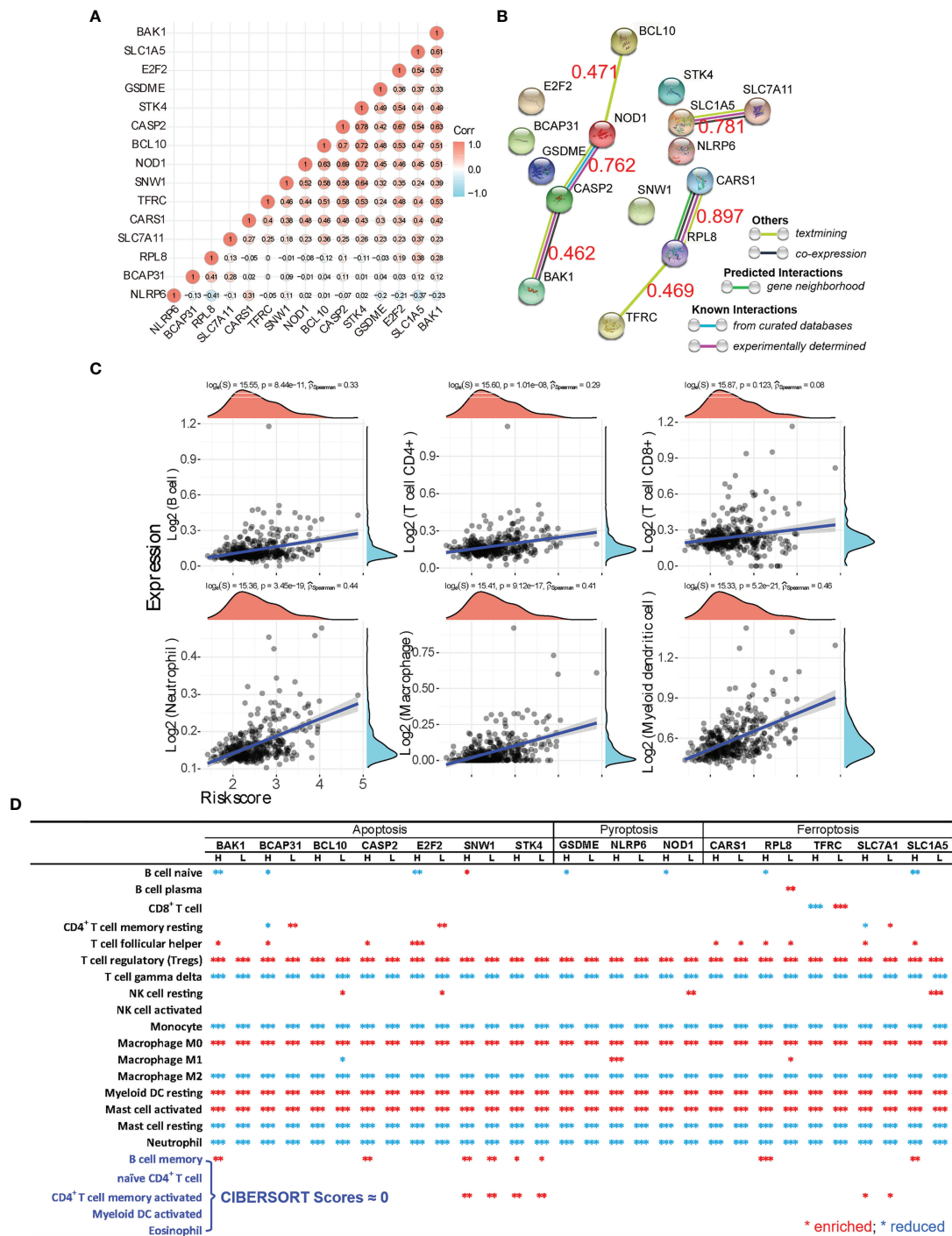


FIGURE 5 | Marker gene cross-talking analysis of apoptosis, ferroptosis, and pyroptosis. **(A)** The gene-gene correlation of all “-optosis” marker genes that have significant correlations with the overall survival (OS) ($p < 0.01$) is analyzed. The correlation coefficient is shown on each circle, and the red circle refers to a positive correlation, while the blue one means a negative correlation. **(B)** Using the analysis tool provided by the STRING database, the interaction of protein corresponding to each “-optosis” marker gene was calculated as well, and the correlation coefficient between genes is marked as red numeric. **(C)** Spearman's correlation analysis between the risk score of the prognostic model (calculated from the 15 “-optosis” marker genes, BCL10, E2F2, BAK1, BCAP31, CASP2, SNW1, STK4, SLC1A5, CARS1, SLC7A11, RPL8, TFRC, GSDME, NLRP6, and NOD1) and immune score. **(D)** Using the CIBERSORT analysis, the comprehensive relationship between the expression of each “-optosis” marker gene ($p < 0.01$ correlating with the OS) and immune cell infiltration is revealed. The red asterisk means enriched infiltration, and the blue one means reduced infiltration of immune cells. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

significantly suppressed. Importantly, both enriched and reduced immune cells significantly ($p < 0.001$) correlate with the “-optosis” marker genes regardless of their high or low expression in HCC tissue compared with normal tissue. Additionally, OS analysis generated by the prognostic signature model shows that higher expressions of marker genes ($p < 0.01$ correlation with the OS) of apoptosis, ferroptosis, and pyroptosis lead to poorer prognosis both individually (Figures 6A–C) and collaboratively (Figure 6D) (Supplementary Figures 2D, 3D, 4E, and 5E). These results again suggest that apoptosis, ferroptosis, and pyroptosis altogether participate in creating the immunosuppressive HCC TME.

Immunosuppressive Hepatocellular Carcinoma Tumor Microenvironment Induces $\gamma\delta$ T-Cell Imbalance

Since the liver is one of the richest sources of tissue-resident $\gamma\delta$ T cells, and our previous works unequivocally proved that adoptive transfer therapy of allogeneic $V\delta 2^+$ $\gamma\delta$ T cells could safely and efficiently help control liver cancer progression or even achieve complete remission (4, 5), we thus focused on exploring how $\gamma\delta$ T cell is repressed in the HCC TME (Figure 5D). We tried to inspect the underlying difference of circulating $\gamma\delta$ T cells between the healthy population and HCC patients. We found that even though the global proportion of $\gamma\delta$ T cells in $CD3^+$ T cells is not statistically different between healthy and HCC populations, the $V\delta 1^+$ subset dramatically elevated, while the $V\delta 2^+$ subset strikingly reduced in the HCC population ($p < 0.0001$) (Figure 6E). This leads to a striking augmentation of the $V\delta 1^+/V\delta 2^+$ ratio in the HCC population. Further analysis revealed the significant reduction of NKG2D expression in the $V\delta 1^+$ subset, but not expressions of PD1, NKP30, and NKP46. For the $V\delta 2^+$ subset, expression of PD1 is greatly increased in the HCC group, implying depressed antitumor immunity of $V\delta 2^+$ $\gamma\delta$ T cells. For other makers, NKG2D, NKP30, and NKP46 show no statistical difference between the healthy and HCC groups (Figures 6F, G).

DISCUSSION

It is commonly recognized that the TME is immunosuppressive, which results from many regulatory factors, including low pH value, hypoxia, nutritional deficiency, metabolic pathways remodeling, inflammation, and others (24, 25). Our focus in this work is to decipher the immune landscape of the HCC TME, facilitating clinical efficacy predictions of immunotherapies. Firstly, our global evaluation of HCC transcriptomic data unequivocally reveals that compared with normal tissue, HCC tissue expresses significantly higher inhibitory checkpoint molecules, including CTLA4, HAVCR2, LAG3, PDCD1, PDCD1LG2, TIGIT, and SIGLEC15. Notably, expressions of these checkpoint molecules are independent of the pTNM stages of patients, therefore clearly suggesting that HCC patients with various pTNM stages will have similar responses to ICB therapy. Then, CIBERSORT evaluation revealed that

HCC TME is indeed immunosuppressive, evident by significantly more infiltration of Tregs, activated mast cells, and M0 macrophages. Meanwhile, HCC TME strikingly suppresses $\gamma\delta$ T-cell infiltration, inhibits the differentiation of macrophages from M0 to M2, dampens the activation of myeloid DCs, and reduces neutrophil infiltration. Importantly, the infiltration of these immune cells shows no statistical difference among samples of different pTNM stages I–IV. Together, we can conclude that HCC TME is highly immunosuppressive, and the patients with different pTNM stages I–IV probably respond to ICB and immune cell therapy similarly.

Inflammation, which causes various types of diseases, is one of the major inducers that closely coordinates with the establishment of the immunosuppressive TME. In HCC TME, inflammation mainly originates from continuous cell death in the context of excessive proliferation of cancer cells. Cancer cell death could be classified into two types, immunogenic and non-immunogenic deaths. Ferroptosis and pyroptosis belong to immunogenic cell death, while apoptosis is a type of non-immunogenic cell death. We thus tried to understand how these three types of PCD (apoptosis, ferroptosis, and pyroptosis) are involved in constructing the immunosuppressive HCC TME. We found that in HCC, most marker genes of the three types of “-optosis” are significantly upregulated, implicating that apoptosis, ferroptosis, and pyroptosis indeed occur routinely in HCC TME. Notably, further inspections indicated that only 7 apoptosis marker genes, 5 ferroptosis marker genes, and 3 pyroptosis marker genes have strong correlations ($p < 0.01$) with the OS rate. This implies that the occurrence of “-optosis” in HCC TME can directly impact the clinical prognosis. Moreover, most of these 15 marker genes are upregulated gradually from pTNM stage I to IV, implying an increasing tendency of “-optosis” from the early to the late stage of liver cancer.

Previously, the gene–gene correlations between checkpoint molecules (both stimulatory and inhibitory) and “-optosis” related marker genes remain largely unknown. After thorough analysis, we found that nearly all “-optosis” marker genes ($p < 0.01$ correlation with the OS) are positively and significantly correlated with expressions of checkpoint molecules except BCAP31, RPL8, and NLRP6 (Figures 2E, 3E, and 4D). This partially explains why the higher expression of “-optosis” marker genes leads to poor prognoses. Even though these marker genes positively correlated with infiltrations of immune cells (B cells, macrophages, myeloid DCs, neutrophils, $CD4^+$ T, and $CD8^+$ T) as well (Figures 2F, 3F, and 4E), further immune cell subsets explorations revealed that the enriched immune cells mainly consist of inhibitory cells (Tregs and activated mast cells) and resting immune cells (resting macrophages and DCs) (Figure 5D). Meanwhile, antitumor effector immune cells are greatly suppressed, including $\gamma\delta$ T cells, monocytes, and neutrophils. Such immune phenotype of HCC TME probably links with checkpoint molecules CD27, CD40, CD28, and CTLA4, which leads to enriched inhibitory cells while depleting effector immune cells, although this hypothesis needs to be validated experimentally. These pieces of evidence altogether indicated that the three types of “-optosis” collaboratively orchestrated the immunosuppressive nature of HCC TME, thus

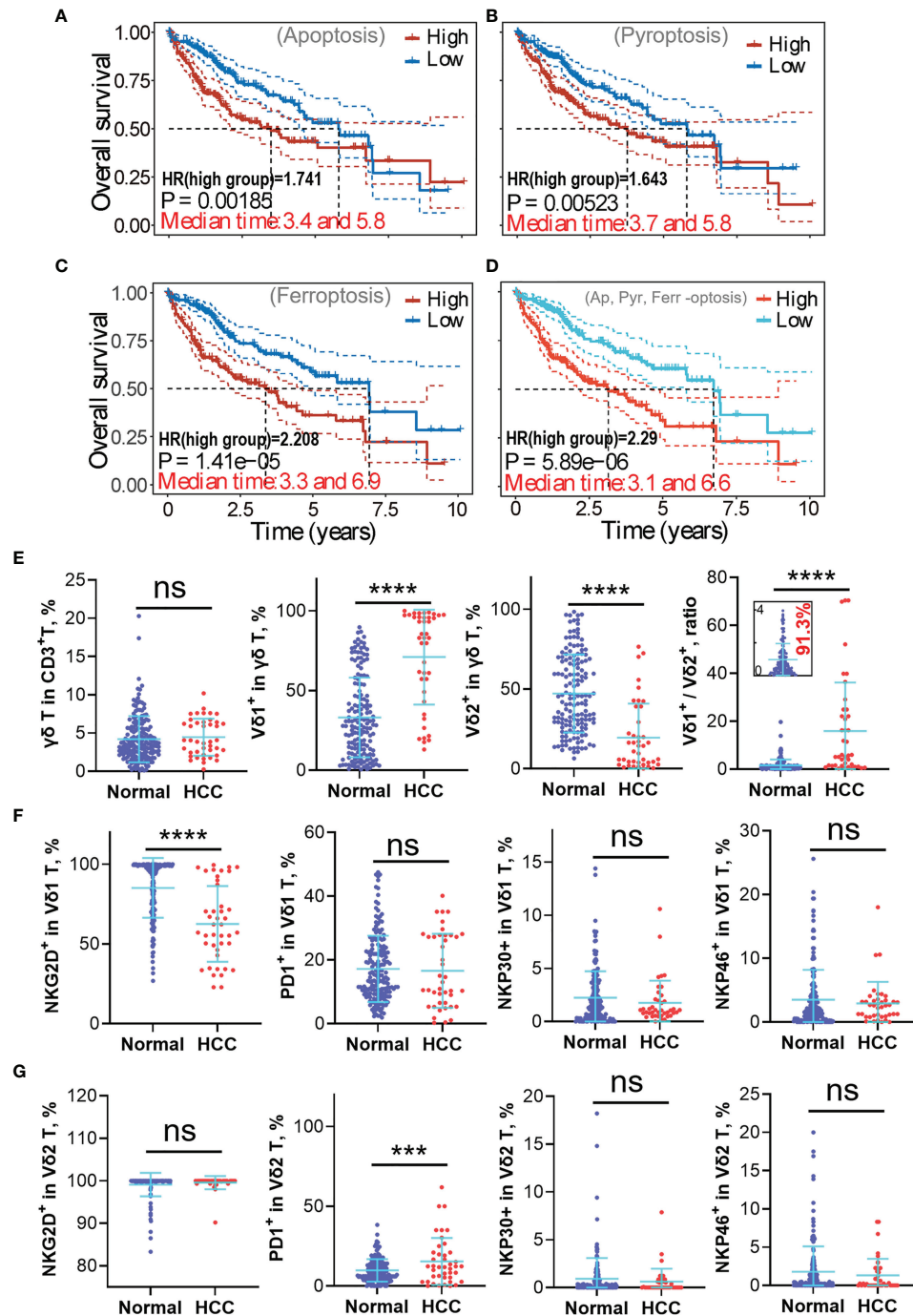


FIGURE 6 | High expressions of apoptosis, ferroptosis, and pyroptosis-related marker genes in hepatocellular carcinoma (HCC) lead to poorer prognosis and implicate $\gamma\delta$ T-cell depletion, particularly V δ 2⁺ $\gamma\delta$ T-cell depletion. **(A–C)** The “-optosis” marker genes were used to create the prognostic signature model using the least absolute shrinkage and selection operator (LASSO) Cox regression model (cited from **Supplementary Figures 2D, 3D, 4E**), the correlations between the Riskscore and overall survival (OS) are graphically shown here. It shows higher expression of marker genes positively correlates with higher risk coefficient (HR > 1), leading to poorer clinical outcome. **(D)** Correlation between the Riskscore (generated using 15 “-optosis” marker genes) and the OS (cited from **Supplementary Figure 5E**). Higher Riskscore leads to a poorer prognosis. **(E)** Circulating $\gamma\delta$ T-cell phenotypes from the healthy population and HCC patients were analyzed using flow cytometry, including the proportion of $\gamma\delta$ T cell in CD3⁺ T cells, V δ 1⁺ subset in $\gamma\delta$ T cell, V δ 2⁺ subset in $\gamma\delta$ T cell, and the V δ 1⁺/V δ 2⁺ ratio. **(F)** Functional phenotypes of circulating V δ 1⁺ $\gamma\delta$ T cell, including expressions of NKG2D, PD1, NKP30, and NKP46. **(G)** Functional phenotypes of circulating V δ 2⁺ $\gamma\delta$ T cell, including expressions of NKG2D, PD1, NKP30, and NKP46. ns, no statistical significance; ***p < 0.001; ****p < 0.0001.

addressing why HCC patients with higher expression of “-optosis” marker genes had poorer responses to ICB therapy.

Since $\gamma\delta$ T cells reside preferentially in the liver and play a key role in preventing liver tumorigenesis, we thus analyzed phenotypic profiles of circulating $\gamma\delta$ T cells in HCC and healthy populations. Universally, $V\delta 2^+$ is dominant over $V\delta 1^+$ subset in the peripheral blood of the healthy population and accounts for over 50% of total $\gamma\delta$ T cells. Under immune-suppressed conditions, the $V\delta 2^+$ subset is slowly depleted in the context of long-term stimulation of phosphoantigens presented by cancer cells and myeloid cells; however, the $V\delta 1^+$ subset can survive, as it is more Treg-like. This interpretation can be supported by results that the $V\delta 1^+$ subset was enriched in HCC patient blood, while the percentage of the $V\delta 2^+$ subset was strikingly decreased. Because the data show that more than 90% of the healthy population has the $V\delta 1^+/V\delta 2^+$ ratio ≤ 4 and more than 63.4% of HCC patients have the $V\delta 1^+/V\delta 2^+$ ratio > 4 , we thus propose that 4 can be used as the threshold value of the $V\delta 1^+/V\delta 2^+$ ratio since higher $V\delta 1^+/V\delta 2^+$ ratio implies more suppressive immunity of the host. Whether or not the proposed

$V\delta 1^+/V\delta 2^+$ ratio can be a predictive factor for discriminating healthy (≤ 4) or sub-healthy conditions (> 4 with no medical abnormalities) and for predicting HCC prognosis (≤ 4 links with better prognosis) needs further validation with a larger scale of clinical samples. Nevertheless, the imbalanced $V\delta 1^+/V\delta 2^+$ ratio has the potential to be used as an indicator in health checkups and clinical prognosis. Additionally, reduced NKG2D expression of the $V\delta 1^+$ population suggests depressed cell activation and probably enhanced survival ability of the $V\delta 1^+$ subset in HCC. In contrast, a significantly higher PD1 expression in the $V\delta 2^+$ population indicated the depressed cytotoxicity of the $V\delta 2^+$ $\gamma\delta$ T cell in the HCC group (Figures 6F, G). Together, we can conclude that in the context of HCC, the $V\delta 1^+$ subset survives and consists of the main $\gamma\delta$ T-cell population, whereas the $V\delta 2^+$ subset is more vulnerable to long-term stimulation of phosphoantigens and is easily depleted or suppressed.

In conclusion, the HCC TME is highly immunosuppressive, leading to high expressions of inhibitory checkpoint molecules and limited infiltrations of antitumor immune cells. Our study revealed that apoptosis, ferroptosis, and pyroptosis conspiringly

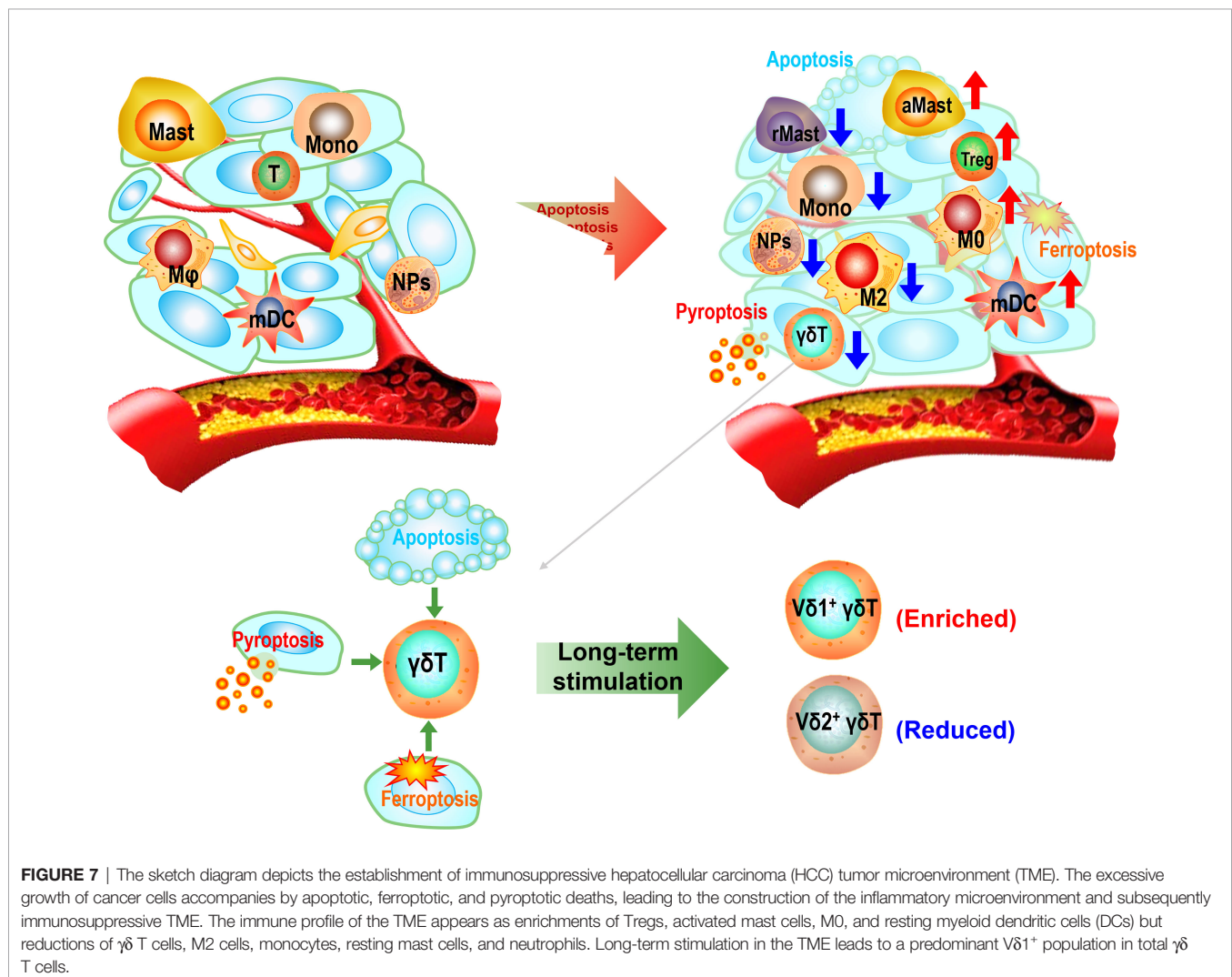


FIGURE 7 | The sketch diagram depicts the establishment of immunosuppressive hepatocellular carcinoma (HCC) tumor microenvironment (TME). The excessive growth of cancer cells accompanies by apoptotic, ferroptotic, and pyroptotic deaths, leading to the construction of the inflammatory microenvironment and subsequently immunosuppressive TME. The immune profile of the TME appears as enrichments of Tregs, activated mast cells, M0, and resting myeloid dendritic cells (DCs) but reductions of $\gamma\delta$ T cells, M2 cells, monocytes, resting mast cells, and neutrophils. Long-term stimulation in the TME leads to a predominant $V\delta 1^+$ population in total $\gamma\delta$ T cells.

induce the establishment of the immunosuppressive HCC TME. The immunosuppressive landscape of the HCC TME was shaped by the high expression of inhibitory checkpoint molecules and enrichments of Tregs, activated mast cells, M0, and non-activated myeloid DCs but low enrichments of antitumor effector cells such as $\gamma\delta$ T cells, M2 cells, monocytes, and neutrophils (Figure 7). Our bioinformatics evidence also showed that the inactivation of the TME infiltrating immune cells might be mediated by checkpoint molecules. Finally, since cytotoxic $V\delta 2^+$ $\gamma\delta$ T cell is selectively depleted whereas Treg-like $V\delta 1^+$ $\gamma\delta$ T cell is upregulated in HCC, the adoptive transfer of allogeneic $V\delta 2^+$ $\gamma\delta$ T cells could be a promising immunotherapeutic strategy for this malignant cancer (4, 5).

DATA AVAILABILITY STATEMENT

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found in the article/Supplementary material.

AUTHOR CONTRIBUTIONS

Work supervision and project design: YH and YW. Experiments: DC, MH, JL, and YJL. Data analysis and bioinformatics: YW and

YH. Data discussion: YW, YH, JH, LL, and ZY. Manuscript drafting, proofreading, and revision: YH and YW. All authors approved manuscript submission.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fimmu.2022.845974/full#supplementary-material>

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Contemplating Dichotomous Nature of Gamma Delta T Cells for Immunotherapy

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$\gamma\delta$ T cells are unconventional T cells, distinguished from $\alpha\beta$ T cells in a number of functional properties. Being small in number compared to $\alpha\beta$ T cells, $\gamma\delta$ T cells have surprised us with their pleiotropic roles in various diseases. $\gamma\delta$ T cells are ambiguous in nature as they can produce a number of cytokines depending on the (micro) environmental cues and engage different immune response mechanisms, mainly due to their epigenetic plasticity. Depending on the disease condition, $\gamma\delta$ T cells contribute to beneficial or detrimental response. In this review, we thus discuss the dichotomous nature of $\gamma\delta$ T cells in cancer, neuroimmunology and infectious diseases. We shed light on the importance of equal consideration for systems immunology and personalized approaches, as exemplified by changes in metabolic requirements. While providing the status of immunotherapy, we will assess the metabolic (and other) considerations for better outcome of $\gamma\delta$ T cell-based treatments.

Keywords: gamma delta T cells, immunotherapy, cancers, infection, neuroimmunology, metabolism, multi-omics

INTRODUCTION

T cells and B cells have emerged as primary lymphocytes lineages throughout 500 million years of evolutionary conservation, mainly generating antigen receptor diversity through somatic recombination (1, 2). The broad range of diversity is achieved by the recombination events occurring on human chromosome 7 for TCR γ and β chain genes, and on human chromosome 14 for TCR α and δ chain genes. TCR γ and δ genes in mice are located on chromosomes 13 and 14, respectively (3, 4). The variable regions of TCR chains comprising of variable (V), diversity (D), and joining (J) elements give rise to the broad range of diversity which enables recognition of foreign molecular patterns (3). Conventionally, TCR α and β chains are rearranged and expressed on the surface to become $\alpha\beta$ T cells (~95% of CD3⁺ T cells in human peripheral blood), while TCR γ and δ chain-expressing cells become $\gamma\delta$ T cells (~5% of CD3⁺ T cells in human peripheral blood). TCR γ and δ chain genes are further classified into subfamilies, consequently, the multiple combinations of these TCR family genes generate many functional $\gamma\delta$ T-cell subsets such as V γ 9⁺V δ 2, V γ 9⁺V δ 1 and V δ 3 which can be paired with various V γ chains. Depending on the ontogeny of the subset, the phenotypic distribution and ligand recognition change dramatically (5). The V δ 1 subset is abundant in the intestine and gut, but it is a minor population in the peripheral blood. This is in contrast to the V δ 2 subset which is a major population in circulation and a minor subset in the mucosa.

The features and functions of both $\alpha\beta$ and $\gamma\delta$ T cells differ remarkably well depending on the thymic and extrathymic origin, as extrathymic T cells are more functionally “innate” immune cells (6, 7). Mouse $\gamma\delta$ T-cell subsets develop through successive but coordinated waves and reside in most of the peripheral tissues. These murine $\gamma\delta$ T cells, classified based on TCR γ chains, are mainly found in two functional states depending on interferon- γ (IFN- γ) or interleukin-17 (IL-17) production (8).

$\gamma\delta$ T cells possess a unique potential of functional plasticity. Within the tumor milieu, $\gamma\delta$ T cells produce cytokines (e.g. IFN- γ or IL-17), which are associated with the prognosis of different kinds of cancers. This dual roles of human $\gamma\delta$ T cells in cancer has been recently reviewed (9). Since $\gamma\delta$ T cells possess a dichotomous nature in cancer, autoimmunity and infections, this review will focus on mechanisms of $\gamma\delta$ T cells in those areas; however, being aware about the fact there are important advances in other fields such as modes of antigen recognition (5, 10), fetal ontology (11, 12), and involvement in hepatic or gastro-intestinal diseases (13–16), which is out of the scope of this review. Apart from the basic understanding of $\gamma\delta$ T-cell subsets and their function in health and diseases, the use of $\gamma\delta$ T cells for immunotherapeutic applications is of great interest. Additionally, other recent technological advances such as single-cell omics, 3D organoid models or humanized mice will facilitate the progress in harnessing the therapeutic potential of human $\gamma\delta$ T cells. In this review, we discuss the pivotal features of $\gamma\delta$ T cells and their potential for therapeutic approaches.

DICHOTOMY OF $\gamma\delta$ T CELLS

$\gamma\delta$ T cells in Cancers – a Double-Edged Sword

Due to their potential of immunosurveillance and anti-tumor response, $\gamma\delta$ T cells are found to be involved in several types of cancer including hematological malignancies (17), glioblastoma (18), gastric (19), colorectal (20) and breast cancer (21). Dysregulated mevalonate metabolism in cancer cells often leads to the accumulation of phosphoantigens (pAg) such as Isopentenyl Pyrophosphate (IPP), which potentiates V γ 9V δ 2 T-cell cytotoxicity (22). IPP can be released to the extracellular space where it is recognized by V δ 2 T cells *via* ATP-binding cassette transporter A1 (ABCA1) and apolipoprotein A-I (apoA-1) (23). Recent studies have shown that phosphoantigens are bound by butyrophilins (BTN), specifically BTN3A1 and BTN2A1, which then interact with the TCR of V δ 2 T cells. Formation of such a signaling complex results in V δ 2 T-cell activation and in the anti-tumor activity (24, 25). Though the molecular details of butyrophilins- $\gamma\delta$ TCR signaling complex is largely unknown, a landmark study showed that BTN3A1 (an isoform of CD277) and its intracellular B30.2 domain are absolutely essential for inside-out signaling to activate V δ 2 T cells (26), which is further modulated by Rho-GTPase (27). Dissecting this molecular complexity further, it was revealed that V γ 9V δ 2 TCR is required initially for T-cell activation and formation of immune synapse

(IS) with CD277 (recruiting BTN3A1 and BTN2A1, independent of pAg), upon which latter provides mandatory coactivation signal and stabilizes IS in a pAg-dependent manner (28).

In addition to the butyrophilins (as mentioned above) and B7 superfamily-like proteins, major histocompatibility class (MHC) - like antigens and immunoglobulin (Ig) -like antigens have also been identified as antigens for $\gamma\delta$ T-cell subsets [extensively reviewed in (5)]. For example, V δ 1 T cells recognize self-derived or foreign lipids bound by the CD1d molecule on the surface of target cells (29, 30). Other interesting examples of MHC-like antigens are MHC-related protein 1 (MR1), ephrin type-A receptor 2 (EphA2) and endothelial protein C receptor (EPCR) (31–33). MR1 is a Vitamin B precursor and known antigen for mucosal associated invariant T cells, but recently shown to be recognized by V δ 1 T cells from healthy individuals and in some diseases (31). EphA2 and EPCR are well known stress-ligands. EPCR serves as a ligand for human V γ 4V δ 5 subset-specific recognition of endothelial cells infected by cytomegalovirus and epithelial tumors (33). Not only EPCR, annexin A2 (an Ig-like antigen) is also recognized by V γ 8V δ 3 subset during cellular stress surveillance (34). Interestingly, non-physiological molecules like red algal protein phycoerythrin have also been reported as antigens for human and murine IL-17-producing $\gamma\delta$ T cells (35). Furthermore, the functional plasticity of $\gamma\delta$ T cells includes a response mediated by CD16 and thus participates in the antibody-dependent cellular cytotoxicity (ADCC). It has been shown to enhance V δ 2 T cell function towards lymphoma cells with the use of anti-CD20 (36, 37). V γ 9V δ 2 T-cell cytotoxicity can also be mediated by the production of cytokines (e.g. IFN- γ and TNF- α), cytotoxic (e.g. granzymes) and apoptotic molecules (e.g. TRAIL), and/or *via* NKG2D receptor-ligand axis (22).

$\gamma\delta$ T cells are highly pleiotropic in function as they possess both anti-tumor and pro-tumor activities in the tumor microenvironment (TME). $\gamma\delta$ T cells are the early producers of IFN- γ during tumorigenesis (38), while IL-2 and IL-15 are the potent inducers of cytotoxic potential (39, 40), which provide an important cancer immunomodulating factor to promote other cytotoxic T lymphocyte responses. Tumor-infiltrating $\gamma\delta$ T cells preferentially produce IFN- γ and are positively associated with better patient outcome in case of colon cancer (20). Also, intracellular IFN- γ expression only after phorbol ester and ionomycin (PMA/Iono) stimulation was remarkable in $\gamma\delta$ T cells from TME of ovarian cancer (41). IFN- γ producing $\gamma\delta$ T cells exert their anti-tumor functions by upregulating MHC class I molecules and CD54, thus further enhancing CD8 T-cell-mediated killing (42). Conversely, $\gamma\delta$ T cells producing IL-17 have been suggested to negatively impact the progression of colon (43), gallbladder (44), and breast cancer (45), either by suppressing immune cell functions, promoting immune cell pro-tumor activity, or by inducing angiogenesis. Hypoxia, which is commonly found in solid tumors, was attributed to reduce cytotoxic activity of $\gamma\delta$ T cells in oral cancer patients (46) and enhance IL-17 production. Furthermore, $\gamma\delta$ T cells provide pro-tumor inflammatory conditions and thus favor tumor

progression, participating in most of the hallmarks of cancer (47, 48).

$\gamma\delta$ T Cells in Autoimmune Disease of the Central Nervous System

Classically, $\gamma\delta$ T cells are known to possess the properties of innate immune cells such as rapid expression of IFN- γ or IL-17 in response to cytokine supplementation without TCR engagement. TME drives IL-17 production in $\gamma\delta$ T cells and hence provide evidence for the $\gamma\delta$ T-cell function as a consequence of (micro) environmental signals. The capacity to produce IL-17 is attributed to epigenetic regulation (49). IL-17 producing $\gamma\delta$ T cells are implicated in autoimmunity and inflammatory conditions. Results from experimental autoimmune encephalomyelitis (EAE), a mouse model of multiple sclerosis (MS), provide evidence that $\gamma\delta$ T cells serve as important source of cytokines IL-17 and IL-23 and consequently amplify IL-17 production by Th17 cells (50). Vice versa, IL-17A is also important for the recruitment of IL-1 β secreting myeloid cells that prime pathogenic $\gamma\delta$ T17 and Th17 cells in EAE (51), suggesting a regulatory loop. One effect of IL-17 producing $\gamma\delta$ T cells is to interfere with regulatory T cells (Treg) development by preventing the conversion of conventional T cells into Foxp3⁺ Treg cells as elicited using IL23R reporter mice (52). This observation was additionally supported by enhanced antigen-specific T cell responses by $\gamma\delta$ T cells. In EAE, V γ 4⁺IL-17 producing $\gamma\delta$ T cells differentiate in the draining lymph nodes, mediated by IL23R and through activation of *Il17* locus, but not *via* IL-1R1 (53).

Those alterations hold also true for MS. Using single-cell RNA-seq and spatial transcriptomics Th17/Tfh cells have been identified as cellular marker of MS disease progression (54). Though EAE is skewed towards IL-17 producing $\gamma\delta$ T cells, studies in human have shown a more remarkable association of MS with IFN- γ producing $\gamma\delta$ T cells. V δ 1 T cells were shown to produce a high amount of IFN- γ in newly diagnosed, untreated MS patients, which was decreased by treatment with natalizumab (55). Contrarily, single or dual expression of IFN- γ and IL-17 by V δ 2 T cells is lower in MS patients compared to healthy controls (56). There is also evidence of direct cytotoxicity towards oligodendrocytes by $\gamma\delta$ T cells (57). $\gamma\delta$ T cells could therefore serve as marker of disease activity. Circulating CCR5⁺ $\gamma\delta$ T cells are decreased during MS relapse in line with higher frequency of IFN- γ ⁺ $\gamma\delta$ T cells, assuming a Th1 profile (58). Hence, beside other nonconventional immune cells, single-cell resolution identified specific $\gamma\delta$ T cell subsets as contributor of MS disease activity with potential as therapeutic target.

$\gamma\delta$ T Cells in Infection

IL-17 production by Th17 cells is usually associated with protection against bacterial and fungal infection through their effector function (59). In 2009, the pivotal role of CCR6⁺ $\gamma\delta$ T cells characterized by IL-17 production, innate receptor expression and recruitment of neutrophils was identified for the first time as first line response to mycobacteria and *Candida albicans* (60). Unlike $\alpha\beta$ T cells, IL-17 producing $\gamma\delta$ T cells are not associated with the engagement of TCR (50, 60, 61). These

observations are highly intriguing, since transcriptionally distinct $\alpha\beta$ - $\gamma\delta$ co-expressing T cells have been discovered, which produce IL-17 upon stimulation by IL-1 β and IL-23 and play a pathogenic role in the CNS autoimmunity in EAE. The characterization of TCR revealed that these hybrid $\alpha\beta$ - $\gamma\delta$ T cells are mainly V γ 4⁺ and TCR β ⁺ and importantly, provide protection against *Staphylococcus aureus* infection (62). This is consistent with findings showing that V γ 6⁺V δ 4⁺ T cells are clonally expanded in skin-draining lymph nodes after *S. aureus* infection in mice. RNA-seq analysis of TRG and TRD sequences revealed the clonal expansion of TRGV5, TRGV6, and TRDV4 (63). In contrast to murine $\gamma\delta$ T cells, human $\gamma\delta$ T cells play a diverse role in infection immunity. Human V δ 2 T cells have been known to respond strongly to phosphoantigens such as (E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate (HMBPP) which is a metabolite produced by microbes *via* the 2-c-methyl-D-erythritol 4-phosphate (MEP) pathway (64). V δ 2 cells are protective in *Plasmodium falciparum* infection (65). Recently, it was shown that $\gamma\delta$ T cells kill infected red blood cells by phagocytosis and opsonization *via* CD16, in addition to the BTN3A1-TCR mediated degranulation process (66). This host defense mechanism adds a new aspect to the $\gamma\delta$ T-cell function and engagement during immune response. Whether the phagocytotic machinery of $\gamma\delta$ T cells is also involved during a response to other pathogens remains to be determined.

For a long time, the role of $\gamma\delta$ T cells in mycobacterial infection has been studied in human and animal models. *Mycobacterium tuberculosis* (Mtb) was one of the first bacteria described to induce $\gamma\delta$ T cell immune responses (67) by recognizing Mtb antigens. Bacillus Calmette-Guérin (BCG) vaccine, the only vaccine protecting against tuberculosis, has been broadly administered worldwide and it has been shown to generate a protective V δ 2 T cell memory response against Mtb infection (68). BCG has been also suggested to provide heterologous protection against infections that are not related to Mtb (69–72). In fact, in the early 90s, it was shown that *in vitro* pre-expanded $\gamma\delta$ T cells with *M. tuberculosis* were able to proliferate in response to re-challenge with unrelated pathogens such as *Listeria monocytogenes*, group A streptococci or *S. aureus* (73). These results indicate that human $\gamma\delta$ T cell responses are not pathogen-specific therefore raising the question, whether BCG-induced $\gamma\delta$ T cells contribute to their cross-protective effect and whether they can develop innate immune cell memory referred to as “trained immunity”. Trained immunity was first described in monocytes and macrophages (which have a shorter half-life) (74, 75). Therefore, those might be less suitable vaccination targets to provide long-term protection. The characterization of trained immunity in long-lived $\gamma\delta$ T cells could potentially open new avenues in designing effective vaccines with cross-protective effects. Whether immune memory responses of $\gamma\delta$ T cells contribute to the protection induced by other vaccines still needs to be explored.

Altogether, it is crucial to broaden the mechanistic knowledge about the role of $\gamma\delta$ T cells in infections using systems immunology approaches such as single-cell multi-omics to provide better therapeutic interventions. This is especially vital

for the development of new generation vaccines, which would not only trigger $\alpha\beta$ T cell memory responses but also harness the therapeutic potential of $\gamma\delta$ T cells.

$\gamma\delta$ T CELLS IN SYSTEMS IMMUNOLOGY – A HOLISTIC APPROACH

The systems approach is defined by the use of a broad strategy for understanding the outcome of a complex set of components (76). Multi-omics methods and systems immunology measures help to investigate changes in the proteome, phenome, transcriptome, epigenome, metabolome, microbiome as well as cell-to-cell communication, all of which shape immune cell responses. A decade ago, these measurements were performed on a bulk cell population. Nowadays, it is possible to use these methods at a single-cell resolution. Such datasets are made publicly available by international consortia such as ImmGen (<https://www.immgen.org>) for mouse immune cells and the cell atlas for humans (<https://www.humancellatlas.org>). Additionally, due to increasing efforts to combine interdisciplinary approaches such as computational biology together with data science and machine learning (77), a comprehensive study of immune cells and their responses is feasible in defining disease severity/progression, therapeutic response, or even vaccine effects. Indeed, a new field of “systems vaccinology” has emerged with the aim to comprehensively analyze the immune response to vaccination and understand potential new mechanisms of protection (78). This will allow immunologists to consider the individual human variation, possibly identifying the reasons driving differential immune responses. This holds specifically true for $\gamma\delta$ T cell responses, which are largely shaped by environmental factors and not genetic control (79). A milestone study for chimeric antigen receptor (CAR) T cells by Melenhorst et al. (2022) shows an impeccable use of single-cell multi-omics and systems immunology methods (80). In this longitudinal study, authors analyzed CD19 chimeric antigen receptor (CAR) T cells in two chronic lymphocytic leukemia patients over 10 years after successful CAR T cell transfer. In the earlier time-points, CD4⁺ CD8⁺ Helios^{hi} CAR T cells in one of these patients were found using cytometry-by-flight (CyTOF) method. Further characterization using 5'cellular indexing of transcriptomes and epitopes by sequencing (CITE-seq) with TCR-seq found that these cells were $\gamma\delta$ CAR T cells with specific TRDV1 and TRGV4 gene expression. However, long-term surviving CAR T cells were predominated by the CD4⁺ T cell population with cytotoxic properties especially at later time points. Yet, the origins and contribution of these cells to the remission remains to be determined. Despite a limited number of patients analyzed, this study is the first to show the potential of systems biology and single cell omics to understand the efficacy of CAR T-cell immunotherapy.

Another good example emphasizing the importance of the systems immunology approach is to evaluate the prognostic significance of immune cells in various cancers using CIBERSORT (a machine learning-based algorithm), where $\gamma\delta$ T

cells have emerged as the most favorable leukocyte with global prognostic association across 25 human cancers (81). Optimizing this computational identification approach further, tumor-infiltrating V γ 9V δ 2 T cells were variably associated with disease outcome due to considerable high inter-individual variation in its abundance (82). A combination of flow cytometry and sequencing results with the help of single sample gene set enrichment analysis (ssGSEA) method has inferred abundance of 24 immune cell types in cancer including $\gamma\delta$ T cells. This algorithm called “Immune Cell Abundance Identifier (ImmuneCellAI)” could accurately predict response to anti-PD1 immunotherapy (83). To a limited extent, we have previously used a comprehensive approach to assess the disease progression and therapeutic response in patients with $\gamma\delta$ T cells malignancies (84, 85). Though the transcriptome and epigenome of $\gamma\delta$ T cells are already available, the focus is now shifted to single-cell studies (Table 1) as it allows to create a compendium of cell types as exemplified in mice (104) and humans (105, 106).

An emerging area in system immunology and single-cell methodology is to decipher the metabolic changes in $\gamma\delta$ T cells during the development and differentiation process. Mechanistic target of rapamycin complex 1 (mTORC1) regulates a distinct metabolic requirement for thymic development of $\alpha\beta$ and $\gamma\delta$ T cells. Interestingly, mTORC1 signaling further coordinates developmental signals with TCR and NOTCH pathways (107). Diving into the details of metabolic requirements at a single-cell level, Single Cell ENergetic metabolism (SCENITH) has been recently developed and used to assess $\gamma\delta$ T cell energy metabolism (108, 109). Consequently, this study found that the metabolic requirements of IL-17⁺ $\gamma\delta$ T cells are imprinted during early thymic development and are maintained in the periphery and tumor of obese mice (109). A distinct metabolic usage by IFN- γ ⁺ versus IL-17⁺ $\gamma\delta$ T cells shows a need for glycolysis versus oxidative metabolism, respectively. Interestingly, glucose supplementation elevated the anti-tumor function of IFN- γ ⁺ $\gamma\delta$ T cells (109). Similarly, altered tumor metabolism also needs to be studied as it is sensed by $\gamma\delta$ T cells (32), which may ultimately implicates $\gamma\delta$ T cell responses in TME causing hypoxia (46, 110) or tumor resistance (111). Moreover, recent reports highlight a crucial role of $\gamma\delta$ T cells in thermogenesis and sympathetic innervation (112, 113). Furthermore, the ketogenic diet has been shown to expand protective $\gamma\delta$ T cells during an infection with influenza virus in the lungs (114) and which restrain inflammation in adipose tissues (97). However, prolonged intake of the ketogenic diet causes obesity and significantly reduces the adipose tissue-resident $\gamma\delta$ T cells (97). Thus, targeting metabolic changes together with transcriptional changes will help to understand the $\gamma\delta$ T-cell differentiation process and its implications in diseases.

$\gamma\delta$ T CELL-BASED IMMUNOTHERAPY: MISSING LINKS AND UNEXPLORED AVENUES

Due to their unique characteristics distinct from conventional $\alpha\beta$ T cells, $\gamma\delta$ T cells are an attractive cellular target for allogeneic transfer as exemplified by the recent phase I clinical trial in 132

TABLE 1 | Summary of single-cell multi-omics datasets from healthy individuals or diseases.

Study	Year	Disease	model organism	Biological source	sc-omics method
Watkin et al. (86)	2020	Allergy	Human	PBMCs from peanut allergic (PA) patients and healthy controls	scRNA-seq
Boufeia et al. (87)	2020	Breast cancer	Human	peripheral blood $\gamma\delta$ T cells from healthy adult donors and from fresh tumor biopsies of breast cancer patients	scRNA-seq
Pizzolato et al. (88)	2019	CMV	Human	PBMC and purified $\gamma\delta$ T cells from CMV ⁺ and CMV ⁻ healthy donors	scRNA-seq
Jaeger et al. (89)	2021	Crohn's disease	Human	IEL T cells sorted from two Crohn's disease patients and two controls	scRNA-seq
10xgenomics	–	Healthy	Human	10k PBMC from a healthy donor (v3 chemistry)	scRNA-seq
Park et al. (90)	2020	Healthy	Human	dissociated cells from human thymus during development, childhood, and adult life	scRNA-seq
Tan et al. (91)	2021	Healthy	Human	$\gamma\delta$ T cells sorted from neonatal and adult blood	scRNA-seq and paired TCR sequencing
Reitermaier et al. (92)	2021	Healthy	Human	CD3 ⁺ T cells FACS-sorted from single-cell suspensions of three fetal skin donors	scRNA-seq
Tan et al. (93)	2019	Healthy	Mouse	FACS-sorted V γ 6 ⁺ T cell, CD4 ⁺ and/or CD8 ⁺ thymocytes	scRNA-seq
Sagar et al. (94)	2020	Healthy	Mouse	Healthy fetal and adult thymus	scRNA-seq
Lee et al. (95)	2020	Healthy	Mouse	total iNKT, MAIT, and $\gamma\delta$ T cells from the pooled thymi of BALB/c mice	scRNA-seq and paired V(D)J sequencing
Alves de Lima et al. (96)	2020	Healthy	Mouse	sorted $\gamma\delta$ T cells from the dural meninges and spleen of 7-d-old (P7) or 8-week-old adult mice	scRNA-seq
Goldberg et al. (97)	2020	Healthy	Mouse	pan-CD45 FACS-sorted tissue-resident haematopoietic cells from white adipose tissue	scRNA-seq
Hu et al. (98)	2021	Healthy	Mouse	sorted hepatic and thymic $\gamma\delta$ T cells	scRNA-seq
Li et al. (99)	2022	Healthy	Mouse	mouse $\gamma\delta$ T cells from peripheral lymph nodes, spleen, and thymus	scRNA-seq and scATAC-seq
Wang et al. (100)	2021	Leukemia	Human	CD45 ⁺ CD3 ⁺ cell populations from B cell-acute lymphoblastic leukemia and healthy controls	scRNA-seq and paired TCR sequencing
Melenhorst et al. (80)	2022	Leukemia	Human	sorted single CD3 ⁺ CAR ⁺ nuclei from patient PBMC	scRNA-seq, CITE-seq and paired TCR sequencing
Gherardin et al. (101)	2021	Merkel Cell Carcinoma	Human	sorted CD3 ⁺ and $\gamma\delta$ ⁺ T cells from dissociated Merkel Cell Carcinomas tumor	scRNA-seq and paired TCR sequencing
Schafflick et al. (102)	2020	MS	Human	CSF and blood from MS and healthy donors	scRNA-seq
Kaufmann et al. (54)	2021	MS	Human	PBMC from MS and healthy donors	scRNA-seq
Cerapio et al. (103)	2021	Ovarian cancer	Human	$\gamma\delta$ T-cell infiltrating lymphocytes from ovarian carcinoma	scRNA-seq

The listed datasets are generated either directly using $\gamma\delta$ T cells or have identified $\gamma\delta$ T cells in their computational approaches. PBMC, peripheral blood mononuclear cells; CMV, cytomegalovirus; FACS, fluorescence activated cell sorting; iNKT, invariant natural killer T cells; MAIT, mucosal associated invariant T cells; MS, multiple sclerosis; CAR, chimeric antigen receptor.

late-stage cancer patients (115) and ongoing clinical trial on patients with solid tumors (<https://clinicaltrials.gov/ct2/show/NCT04765462>). The concept of $\gamma\delta$ T cell-based immunotherapy has been under development for more than a decade. Earlier, the immunotherapy with $\gamma\delta$ T cells for cancer was mainly based on two approaches: *in vivo* activation of $\gamma\delta$ T cells using aminobisphosphonates (e.g. zoledronate) and adoptive transfer of *in vitro* expanded $\gamma\delta$ T cells (116). The approach of *in vivo* activation of $\gamma\delta$ T cells has extended its toolbox. Because of the basic research on $\gamma\delta$ T-cell activation (26), the molecular mediators of activation (e.g. butyrophilins) can be targeted to improve immunotherapy outcome. In an ongoing clinical trial, monoclonal anti-BTN3A1 antibodies (ICT01) are administered alone or in combination with the checkpoint-inhibitor pembrolizumab for hematological cancers (<https://www.clinicaltrials.gov/ct2/show/NCT04243499>). Besides checkpoint inhibitors (117), other immunomodulatory agents that could be used in combination with $\gamma\delta$ T cell-based immunotherapy include epigenetic drugs (118, 119), toll-like receptor ligands

(120), or even bispecific antibodies targeting V γ 9 chains of V γ 9V δ 2 T cells (121). Since most of these modulators have been proposed or shown clinical relevance *in vitro*, many are being tested in a clinical trial. Likewise, the approach of using adoptive transfer of *in vitro* expanded $\gamma\delta$ T cells is now suggested to be supplemented with biomaterials such as cytokines [e.g. TGF- β (122)] or nutrients [e.g. Vitamin C (123)]. Furthermore, engineered cytokines have emerged as an attractive tool to improve T cell immunotherapy by modulating cell expansion, persistence, tumor homing and adaptation to TME (124). As engineered IL-2 and IL-15 are already in clinical trials, their use in $\gamma\delta$ T cell-based therapies might also be beneficial. The use of naturally occurring nutrient supplementation such as Vitamin C could potentially be beneficial too. However, the metabolic requirement and effect of these nutrients need to be considered given the inter-individual variation in $\gamma\delta$ T cell frequency and their subset distribution due to age, gender, and race (125). These needs can be complemented for a more personalized approach to immunotherapy to provide benefit to patients.

$\gamma\delta$ T cell-based immunotherapy has been progressing over the last decades along with the development of T cell-based therapies (Figure 1). The novel first-in-class approach is being exploited to apply genetically modified $\gamma\delta$ T cells in human (138). Previously, the V δ 1 subset of $\gamma\delta$ T cells were designed and applied as a new cellular product called “DOT cells” for adoptive immunotherapy of leukemia patients (17, 139). Further advancing the approach of genetic modifications, CAR $\gamma\delta$ T cell therapy is under investigation (114, 140, 141). The patient-derived xenograft model showed anti-leukemic activity and IL-15-mediated long-term persistence of CD123-CAR-DOTs in acute myeloid leukemia (142). Following the United States Food and Drug Administration (US FDA) approval for ADI-01 in the year 2020, an allogenic CAR $\gamma\delta$ T cell therapy targeting CD20 protein was manufactured at clinical scale. As observed in a preclinical study with B-cell malignancies, CAR $\gamma\delta$ T cell therapy generated an innate and adaptive anti-tumor immune response but no xenogeneic graft-versus-host disease (143). This CD20 CAR $\gamma\delta$ T cell therapy is now in a phase I clinical trial (<https://www.clinicaltrials.gov/ct2/show/NCT04735471>). The interim analysis of the ADI-01 phase I clinical trial showed that 50% patients achieved complete response (CR) while 75% patients achieved objective response rate (ORR) without any ADI-01-related serious adverse events using CD20-CAR $\gamma\delta$ T cell therapy (press release dated on December 6, 2021; <https://www.adicetbio.com>). Furthermore, the ADI-01 therapy has been just granted the Fast Track Designation by the US FDA raising hopes

for even faster implementation of $\gamma\delta$ T cell-based therapies into daily clinical practice (press release dated on April 19, 2022; <https://www.adicetbio.com>). CAR T cell therapy is being broadened towards T cells engineered with $\gamma\delta$ TCR (TEG) (138, 144). With approval by US FDA, genetically modified $\gamma\delta$ T cells might benefit a broad spectrum of cancer patients. In the future, targeting $\gamma\delta$ T cells with tailored immunotherapies might also be a potential new avenue for the treatment of other diseases such as MS and infections.

CONCLUSION

Though neglected for a long time, $\gamma\delta$ T cells have emerged as a key immune cell type, especially in cancer biology and are already investigated in clinical trials. Its pleiotropic role is further being investigated in other disorders including immune diseases such as MS, infections or transplantation. Use of “big data” and integrative multi-omics approaches enable us to more specifically unravel molecular mechanisms. This is complemented by the implementation of new methods such as 3D organoids combined with state-of-the-art technologies such as spatial transcriptomics. However, $\gamma\delta$ T cells still require a clinical testing model for development of immunotherapy. Altogether, targeting $\gamma\delta$ T cells will allow us to more precisely address a broad range of conditions, eventually allowing a $\gamma\delta$ T cell targeted personalized immunotherapy.

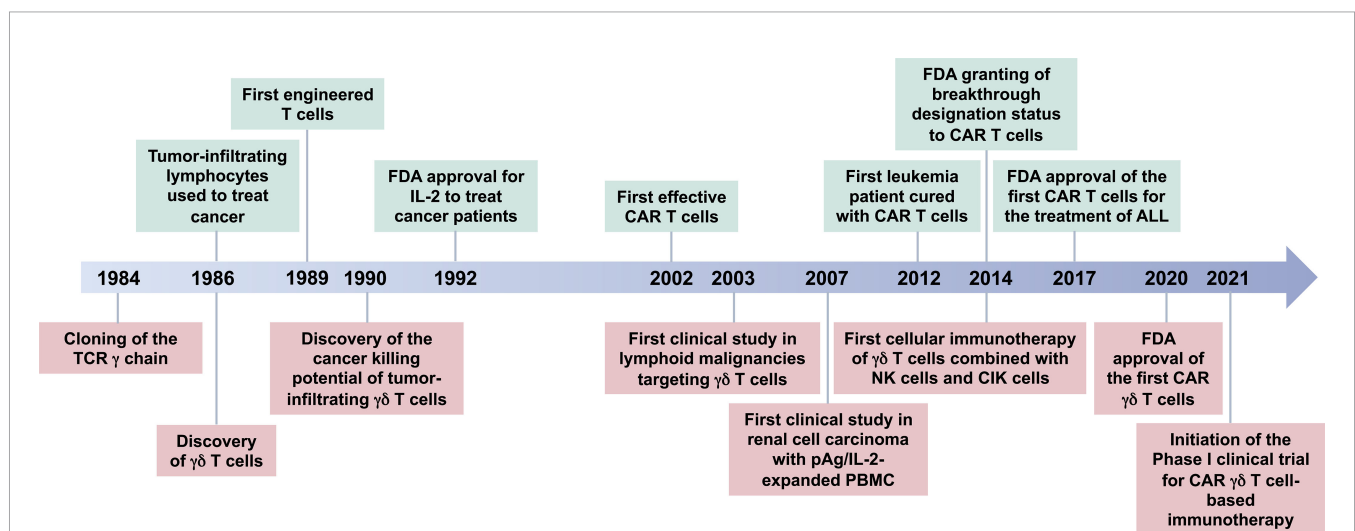


FIGURE 1 | Timeline for $\gamma\delta$ T-cell-based immunotherapy. A brief history of the breakthrough findings that led to the development of $\gamma\delta$ T cell-based immunotherapies. $\gamma\delta$ T cells were discovered in 1986 (126, 127), after accidental cloning of the gamma chain of the T cell receptor (TCR) in 1984 (128). At the same time, Rosenberg's group started to treat cancer patients with their own tumor-infiltrating lymphocytes leading to the first patient to be cured from cancer using this method (129, 130). Fast forward from 1989 to year 2017 (131–137), the FDA approved the first CAR T cells for the treatment of B-cell lymphomas, Kymriah[®] and Yescarta[®] developed by Novartis Pharmaceuticals Corp. (<https://www.hcp.novartis.com/home/>) and Kite Pharma, Inc. (<https://www.kitepharma.com/>), respectively. The first big success came in 2020 for CAR therapy with $\gamma\delta$ T cells, when the FDA cleared an investigational new drug (IND) application and orphan drug designation for GD \times 012 (an allogenic V δ 1 T-cell-based therapy) developed by Lymphact and later GammaDelta Therapeutics (<https://gammadeltatx.com/>). Also, at the same time, the Adicet Bio (<https://www.adicetbio.com/>) received the FDA approval for an IND application ADI-01, an allogenic CAR $\gamma\delta$ T cell therapy targeting CD20 protein in non-Hodgkin lymphomas. In 2021, the first Phase I Clinical Trials of $\gamma\delta$ T-cell-based immunotherapies were initiated. TCR, T-cell receptor; FDA, The United States Food and Drug Administration; IL-2, interleukin-2; CAR, chimeric antigen receptor; pAg, phosphoantigen; PBMC, peripheral blood mononuclear cells; ALL, acute lymphoblastic leukemia; NK cells, natural killer cells; CIK cells, cytokine-induced killer cells.

AUTHOR CONTRIBUTIONS

JB and KP conceptualized and wrote the first draft of manuscript. JB, KP, and SF contributed to the discussion and made final corrections. All authors contributed to the article and approved the submitted version.

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A Simple and Robust Single-Step Method for CAR-V δ 1 $\gamma\delta$ T Cell Expansion and Transduction for Cancer Immunotherapy

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The $\gamma\delta$ T cell subset of peripheral lymphocytes exhibits potent cancer antigen recognition independent of classical peptide MHC complexes, making it an attractive candidate for allogeneic cancer adoptive immunotherapy. The V δ 1-T cell receptor (TCR)-expressing subset of peripheral $\gamma\delta$ T cells has remained enigmatic compared to its more prevalent V γ 9V δ 2-TCR and $\alpha\beta$ -TCR-expressing counterparts. It took until 2021 before a first patient was dosed with an allogeneic adoptive V δ 1 cell product despite pre-clinical promise for oncology indications stretching back to the 1980s. A contributing factor to the paucity of clinical progress with V δ 1 cells is the lack of robust, consistent and GMP-compatible expansion protocols. Herein we describe a reproducible one-step, clinically translatable protocol for V δ 1- $\gamma\delta$ T cell expansion from peripheral blood mononuclear cells (PBMCs), that is further compatible with high-efficiency gene engineering for immunotherapy purposes. Briefly, $\alpha\beta$ TCR- and CD56-depleted PBMC stimulation with known-in-the-art T cell stimulators, anti-CD3 mAb (clone: OKT-3) and IL-15, leads to robust V δ 1 cell expansion of high purity and innate-like anti-tumor efficacy. These V δ 1 cells can be virally transduced to express chimeric antigen receptors (CARs) using standard techniques, and the CAR-V δ 1 exhibit antigen-specific persistence, cytotoxicity and produce IFN- γ . Practicable, GMP-compatible engineered V δ 1 cell expansion methods will be crucial to the wide-spread clinical testing of these cells for oncology indications.

Keywords: gamma delta (gammadelta) T cells, $\gamma\delta$ T cells, $\gamma\delta$ T cells, V delta-1 (V δ 1) cells, CAR-gamma delta T cells, cancer immunotherapy, CAR-V δ 1 cells

INTRODUCTION

Characterized by expression of a T cell receptor (TCR) composed of gamma and delta chains ($\gamma\delta$ TCR), $\gamma\delta$ T cells are an innate-like subset of human T cells representing up to 15% of peripheral CD3-positive cells and up to 60% of intraepithelial lymphocytes in healthy donors. Whilst their physiological role in humans remains an area of active study and debate (1–3), $\gamma\delta$ T cells are a major

area of interest in adoptive cell therapy for oncology indications (4–7). Exome characterisation of >16,000 patient tumors identified infiltrating $\gamma\delta$ T cells as the immune cell species most positively associated with patient survival across all cancers (8). A recent examination of patient brain tumor samples further defined $\gamma\delta$ T cell infiltration as most predictive of patient survival, in unexpected contrast to $\alpha\beta$ T cells, which correlated negatively with survival (9).

Two subsets composed of MHC-unrestricted V γ 9V δ 2-TCR and V γ xV δ 1-TCR-expressing cells (where x denotes one of 6 functional gamma chain genes) dominate the peripheral $\gamma\delta$ T cell compartment. In contrast to the oligoclonal and phosphoantigen-reactive V γ 9V δ 2-TCR population, V γ xV δ 1 cells (referred to hereafter as ‘V δ 1 cells’) express a V δ 1-TCR chain paired with one of various V γ -chains. The peripheral human V δ 1 population has a polyclonal TCR repertoire that is reactive to a range of antigen types including peptides, lipids and various CD1 proteins of self and non-self origin (3, 10).

Adoptive transfer of the V γ 9V δ 2 cell subset has been clinically tested for anti-cancer efficacy for nearly 20 years (11). Several groups have also previously demonstrated methods to expand V δ 1 cells (12–18). 2021 saw publication of data from two first-in-man V δ 1 cell adoptive transfer clinical trials. GammaDelta Therapeutics Ltd are exploring unengineered, allogeneic ‘delta one T’ cell (‘DOT’; ‘GDX012’ product) safety, tolerability, and preliminary antileukemic activity in patients with minimal residual disease-positive acute myeloid leukemia (trial ID: NCT05001451). Adicet Bio Inc are testing the safety and efficacy of ‘ADI-001’ product anti-CD20 CAR-engineered allogeneic V δ 1 cells in adults with B cell malignancies, as a monotherapy or in combination with IL-2 (trial ID: NCT04735471). The discrepancy in the numbers of clinical investigations between V δ 1 and V γ 9V δ 2 $\gamma\delta$ T cell subsets does not stem from a lack of pre-clinical promise of the V δ 1 subset. Indeed, there is literature stretching back decades describing potent V δ 1 cell responses against tumor targets *in vitro* and graft-*versus*-leukemic effects following bone marrow transplantation, hypothesized to be mediated by atypical T cell subsets (19–22).

The discovery that V γ 9V δ 2 cells can be expanded to high numbers and purity using phosphoantigens (e.g. IPP or BrHPP) or phosphoantigen-inducing aminobisphosphonates (e.g. zoledronic acid) enabled high-throughput V γ 9V δ 2 cell pre-clinical exploration, and consequently accelerated clinical translation. A promising two-step multi-cytokine clinical-grade protocol for V δ 1 cell expansion was published and patented by Almeida and colleagues in 2016 (23) (referred to hereafter as the ‘DOT protocol’) and is set for clinical translation in trial NCT05001451. Herein we describe a one-step, single-cytokine gene-engineered V δ 1 cell product manufacturing protocol that utilizes processes and reagents already employed to generate genetically modified $\alpha\beta$ T and V γ 9V δ 2 cell biotherapeutics. We show that V δ 1 cells are readily expandable to high numbers and purity by stimulation of $\alpha\beta$ TCR- and CD56-depleted PBMC with OKT-3 anti-CD3 mAb in the presence of IL-15-supplemented media. Thus-stimulated V δ 1 cells are efficiently

and stably transduced with a chimeric antigen receptor (CAR) using standard viral transduction protocols. The resulting V δ 1-CAR-T cells exhibit innate recognition of targets in addition to antigen-specific boosting of function, and do not exhibit alloreactivity to allogeneic PBMC.

MATERIALS AND METHODS

Ethical Approval

Expansion of T cells from healthy donors was performed under the governance of the following UCL UK research ethics committee approvals: “Establishing cell cultures for pediatric cancers”, IRAS project ID-154668. This ethical approval allows for expansion cell lines from tissue samples following written informed consent or from anonymized blood samples from healthy volunteers. For this study, only anonymized commercially available blood samples or anonymized small samples from healthy volunteers were used.

$\gamma\delta$ T Cell Expansion

PBMC were isolated from purchased whole blood leucocyte cones *via* density gradient centrifugation using Lymphoprep (Stemcell) according to manufacturer’s instruction. PBMC were either cryopreserved in 90% FBS 10% DMSO or re-suspended in complete T cell culture media for further processing. Complete T cell culture media consisted of xeno- and serum-free CTS-OpTmizer (Thermo Fisher) with 10% synthetic serum replacement (Thermo Fisher) and GlutaMAX (Thermo Fisher), all of which are available to research as well as GMP-grade from Thermo Fisher with the following product catalogue numbers: research-grade CTS-OpTmizer (A1048501) and GMP-compatible alternative GMP-grade OpTmizer-CTS (A3705003), synthetic immune cell serum replacement that is compatible with both manufacturing standards (A2596101) and GlutaMAX also compatible with both standards (35050061). If starting with cryopreserved material, PBMC were thawed and rested at 10×10^6 cells/mL in complete pre-warmed media overnight before further processing to avoid over-stressing the lymphocytes and to enhance depletion quality. PBMC at $2\text{--}4 \times 10^6$ cells/mL density were then either stimulated in standard cell culture plates right away or first depleted of $\alpha\beta$ T cells using the TCR α/β Product Line (Miltenyi Biotec) according to manufacturer’s instructions concurrently with depletion of CD56-positive cells using CD56 MicroBeads (Miltenyi Biotec) according to manufacturer’s instructions. Briefly, cells were first labelled with anti-TCR α/β -biotin, then a mix of anti-biotin microbeads and anti-CD56 beads, and then depleted using MACS Cell Separation LD Columns (Miltenyi Biotec). If cultured in G-Rex vessels (Wilson Wolf), depleted PBMC were initiated at $2\text{--}4 \times 10^6$ cells/cm². Thus-prepared PBMC were stimulated with either 1 μ g/mL OKT-3 (Miltenyi Biotec Cat# 130-093-387, RRID : AB_1036144) or 1 μ g/mL PHA (Merck) and various cytokine combinations: (i) 100 IU/mL IL-2 aldesleukin (Proleukin; Novartis), (ii) 70 ng/mL IL-15 (Peprotech), (iii) 20 ng/mL rhIL-7 (Peprotech), or the (iv) ‘DOT protocol’ cytokine

cocktail, which consisted of a first culture in 100 ng/mL rIL-4, 70 ng/mL rIFN- γ , 7 ng/mL rIL-21 and 15 ng/mL rIL-1 β followed by a second culture in 70 ng/mL rIL-15 and 30 ng/mL IFN- γ (all from Peprotech). When comparing the full 'DOT protocol' to test expansion protocols, the methodology described by Almeida and colleagues was used (23), albeit with the omission of a positive selection step using OKT-3 following the alpha beta TCR depletion. Briefly, depleted PBMC were stimulated for a first cytokine culture with 70ng/mL OKT-3, and then a second cytokine culture with 1 μ g/mL OKT-3. Live cells before and during expansion were counted using Trypan Blue exclusion, an automatic cell counter (Invitrogen) and flow cytometry-based Precision Count Beads (Biolegend).

V δ 2 $\gamma\delta$ T Cell Depletion

V δ 2 $\gamma\delta$ T cells were depleted from PBMC at one of three stages of expansion: pre-initiation, at midway split or at harvest. All depletions were done using anti-TCR/V δ 2 mAb clone B6 (BioLegend Cat# 331404, RRID : AB_1089228) at a concentration of 0.5 μ g/10⁶ PBMC. When depleting at initiation V δ 2 cell initiation was incorporated into the $\alpha\beta$ TCR/CD56 depletion process. This was done as follows: PBMC were co-incubated with $\alpha\beta$ TCR-biotin mAb and V δ 2 (clone: B6)-biotin mAb, washed, and then co-incubated with anti-biotin and anti-CD56 microbeads according to manufacturer's protocol, then washed and depleted using Miltenyi LD magnetic column separation, as above and according to manufacturer's protocol. If depleting at midway split or final harvest, expanding cells were harvested, washed and labelled with 0.5 μ g clone B6/10⁶ PBMC, incubated for 20min, washed and incubated and depleted using Miltenyi anti-biotin microbeads and LD columns as above.

Flow Cytometry

The following fluorochrome-antibody conjugates and dyes were used according to manufacturer's instruction in Biolegend Cell Staining Buffer to detect different lymphocyte subpopulations in culture: Zombie Green Viability Dye (BioLegend), Zombie Yellow Viability Dye (BioLegend), LIVE/DEAD Fixable Near IR kit (Thermo Fisher), anti-CD3 PE/Dazzle594 (BioLegend Cat# 980006, RRID : AB_2715768), anti- $\alpha\beta$ TCR APC (BioLegend Cat# 306717, RRID : AB_10612747), anti-TCRV δ 1 APC-Vio770 (Miltenyi Biotec Cat# 130-120-440, RRID : AB_2752099), anti-TCRV δ 2 VioBlue and PE (Miltenyi Biotec Cat# 130-101-152, RRID : AB_2660779), anti-CD69 FITC (BioLegend Cat# 310903, RRID : AB_314838), anti-NKG2D PercP/Cy5.5 (BioLegend Cat# 320817, RRID : AB_2562791) anti-CD56 Alexa Fluor 488 (BioLegend Cat# 318311, RRID : AB_604094), anti-PD-1 APC/Fire750 (BioLegend Cat# 329953, RRID : AB_2616720) and BUV737 (BD Biosciences Cat# 612791, RRID : AB_2870118), anti-LAG-3 PE/Cy7 (BioLegend Cat# 369309, RRID : AB_2629752), anti-TIM-3 BV711 (BioLegend Cat# 345023, RRID : AB_2564045), anti-CD34 QBend10 Alexa Fluor700 (BioTechne), anti-CD34 QBend10 Alexa Fluor488 (Novus Biologicals), anti-NKp44 PerCP/Cy5.5 (BioLegend Cat# 325114, RRID : AB_2616752), anti-NKp30 DyLight 650 (NovusBio, Cat # FAB1849W, clone 210845). When detecting intracellular and cell surface accumulation of

IFN- γ and CD107a, respectively, PBMC were challenged with relevant targets overnight, and incubated at 37°C and 5% CO₂ with anti-CD107a FITC (BioLegend Cat# 328605, RRID : AB_1186058), then 1x monensin (Biolegend) was added followed by incubation for another 4h, stained for cell surface markers, and then permeabilized using Biolegend Intracellular Staining Permeabilization Wash Buffer and stained with anti-IFN- γ Brilliant Violet 605 (BioLegend Cat# 502535, RRID : AB_11125368), anti-IL17a PerCPCy5.5 (BioLegend Cat# 512313, RRID : AB_961397) or anti-Granzyme B Pacific Blue (BioLegend Cat# 372217, RRID : AB_2728384) according to manufacturer's instructions. All expansion and activation samples were analyzed on a BD LSR II flow cytometer using FACSDiva software (BD FACSDiva Software, RRID : SCR_001456), while CAR-V δ 1 proliferation was analyzed on a Beckman Coulter CytoFlex using CytExpert software (CytExpert Software, RRID : SCR_017217). For setting of gates in analysis of panels we employed fluorescence minus one (FMO) controls. Post-acquisition data processing was carried out using FlowJo software (FlowJo, RRID : SCR_008520). T-SNE analysis on flow cytometry data was performed using FlowJo software and concatenated using R language Statistical Computing (RRID : SCR_001905).

Retroviral Production and T Cell Transduction

293T cells (ATCC Cat# CRL-3216, RRID : CVCL_0063) were plated at 1.5x10⁶ cells per 10cm² plate (Corning) in 10mL 10% fetal bovine serum (FBS)-supplemented Gibco IMDM (Thermo Fisher). At 70% confluence, 293T cells were transfected using GeneJuice (Merck) according to manufacturer's protocol. Triple plasmid transient transfection was carried out using SFG-gammaretroviral vectors (RRID : Addgene_22493). The anti B7H3 CAR-T was synthesized within SFG and contains the following components: IL-2 signal peptide, TE9 ScFv, CD8 hinge and transmembrane, CD28 endodomain, CD3zeta. The CAR was co-expressed with the RQR8 sort suicide gene allowing detection with anti-CD34 antibody.

The B7H3-CAR (second generation with CD28 and 325 CD3-zeta endodomains synthesized in our laboratory), gag+pol 326 (RRID : Addgene_8449) and RD114 envelope (RRID : 327 Addgene_17576) plasmids were added at an equimolar ratio. Retroviral supernatant was harvested at 48 and 72 hours following transfection and used immediately for T cell transduction. Briefly, non-tissue culture treated 24 well plates (Costar) were coated with RetroNectin (Takara) in PBS (final concentration of 1mg/mL) and incubated at 4°C for 24 hours. The retronectin was removed and 1.5 mL of retroviral supernatant was added to each retronectin coated well. Following this, 3x10⁵ stimulated T cells in 500 μ L was added and plates were centrifuged at 1000 x g for 40 minutes, at room temperature before incubation in complete T cell culture media at 37°C, supplemented with IL-15 to a final concentration of 70ng/mL (~140 IU/mL). Transduced T cells were harvested after three days, washed and re-suspended for expansion in specified cytokine-supplemented complete T cell culture medium.

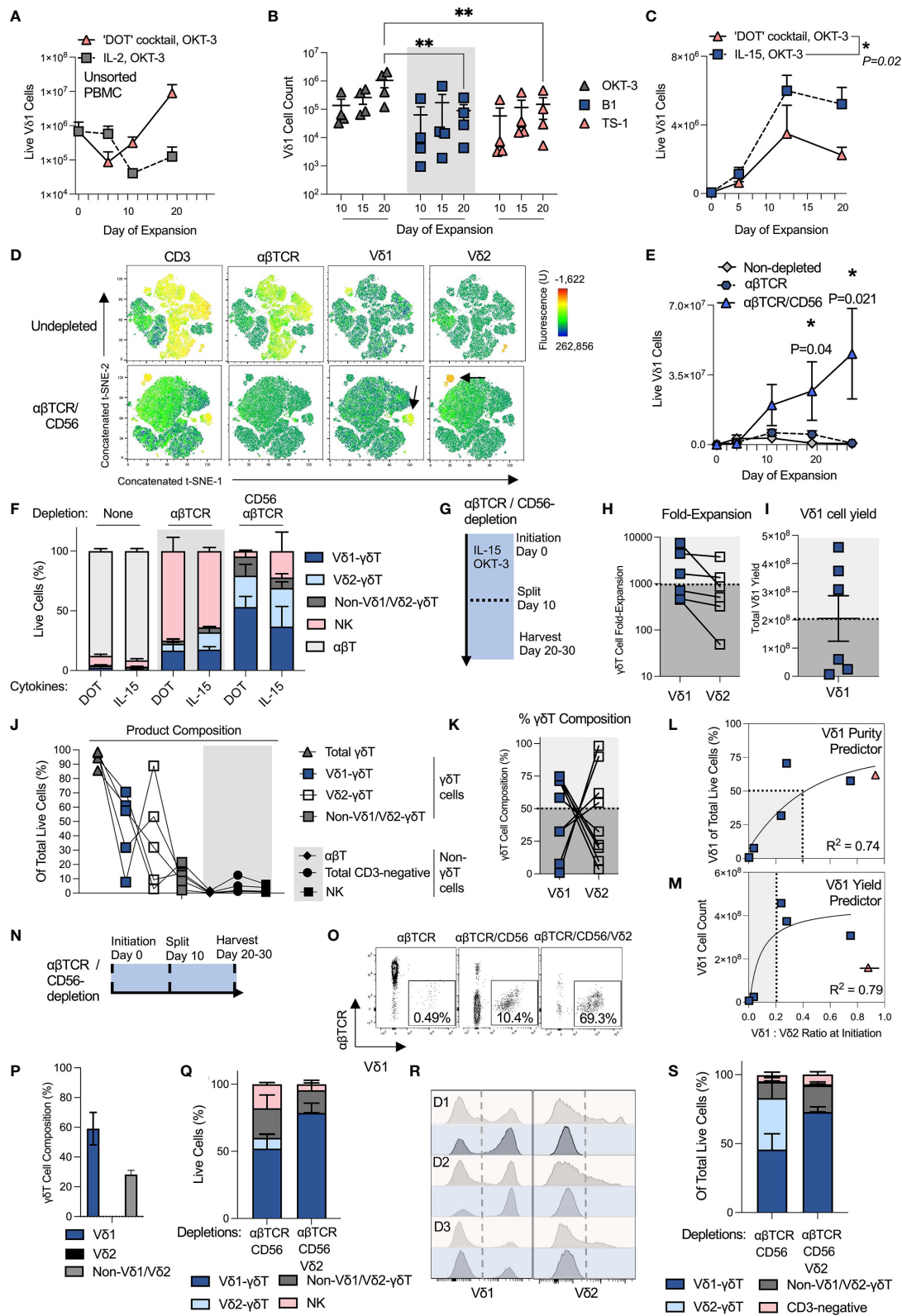


FIGURE 1 | Continued

FIGURE 1 | OKT-3 and IL-15 stimulation of $\alpha\beta$ TCR- and CD56-depleted PBMC leads to robust and reproducible V δ 1 cell expansion. All experiments used separate and independent donors except where indicated they were from the same donors. **(A)** V δ 1 cell yield was compared when expanding PBMC with either the 'DOT' cocktail of cytokines or IL-2 (N=2; mean \pm standard error mean (SEM)). **(B)** $\alpha\beta$ T-depleted PBMC were expanded with the 'DOT' cocktail of cytokines and a single stimulation with 1 μ g/mL of either anti-CD3 mAb clone OKT-3, anti- $\gamma\delta$ TCR mAb clone B1 or V δ 1-TCR clone TS-1. (N=4; mean \pm SEM; statistical significance was determined by two-way ANOVA with Sidak's multiple comparisons test). **(C)** $\alpha\beta$ T-depleted PBMC were expanded with either the 'DOT' cocktail of cytokines or IL-15. Expansion was measured over a period of 20 days, and compared at day 20 post-stimulation (N=3; mean \pm SEM; statistical significance was determined by two-way ANOVA with Sidak's multiple comparisons test). V δ 1 cell numbers in the starting material ranged from 40e3 – 80e3/well. **(D)** Three separate donor PBMC were stained for flow cytometry analysis of population composition before and after $\alpha\beta$ TCR/CD56 depletion and visualized using a t-SNE algorithm. The three donor t-SNE data was concatenated using 'R'. The black arrows on the bottom row indicate V δ 1 and V δ 2 cells among the depleted PBMC. **(E)** V δ 1 cells were expanded using OKT-3 and IL-15 from PBMC either unmanipulated, depleted only of $\alpha\beta$ T cells, or depleted of $\alpha\beta$ T cells and CD56-positive cells (N=3; mean \pm SEM; statistical significance was determined by ordinary two-way ANOVA with Sidak's multiple comparisons test). V δ 1 cell numbers in the starting material ranged from 7e3 – 80e3/well. **(F)** Day 20-harvested expansate composition was compared after culture in either the 'DOT' cocktail of cytokines or IL-15 alone, from either undepleted, $\alpha\beta$ TCR single-depleted or $\alpha\beta$ TCR/CD56-double depleted PBMC at initiation (N=3). **(G)** To achieve optimal 20 day expansion, expanding T cell cultures were split 1:4 at day 10 of expansion to avoid overconfluence. **(H)** Matched V δ 1 cell expansions using OKT-3 and IL-15 from $\alpha\beta$ TCR/CD56-depleted PBMC in 6-well G-Rex vessels were compiled from six different donors and two separate experimental repeats and compared in terms of fold-expansion and **(I)** absolute cell yield. **(J)** A further five donors were initiated for G-Rex culture in a third $\alpha\beta$ TCR/CD56-depleted OKT-3/IL-15 manufacturing run. Day 20 expansates were analyzed for product composition (N=5). **(K)** G-Rex expansion donor data was pooled to examine the V δ 1/V δ 2 cell composition of total product $\gamma\delta$ T cells (N=11). **(L)** The effect on $\alpha\beta$ TCR/CD56-depleted IL-15/OKT-3-expanded V δ 1 cell purity of pre-depleted, pre-stimulation PBMC V δ 1:V δ 2 ratio was determined (N=6; statistical significance was determined by a non-linear least squares model). Purity in this context denotes V δ 1 cells of total live cells in the product at day 20. **(M)** The effect on $\alpha\beta$ TCR/CD56-depleted IL-15/OKT-3-expanded V δ 1 cell yield of pre-depleted, pre-stimulation PBMC V δ 1:V δ 2 ratio was determined (N=6; statistical significance was determined by a non-linear least squares model; one data point indicated in red and crossed out was not included in the statistical analysis of the data). **(N)** Three potential timepoints (shown with black, dotted lines) were identified for testing V δ 2 cell depletion from V δ 1 cell product: at initiation, at midway split or at harvest. **(O)** Initiation V δ 2 depletion: V δ 1 cell purity of total T cells (CD3-positive cells) were compared in single ($\alpha\beta$ TCR), double ($\alpha\beta$ TCR/CD56) or triple ($\alpha\beta$ TCR/CD56/V δ 2)-depleted freshly-isolated PBMC at initiation. Shown are representative dot plots from one donor. **(P)** Initiation V δ 2 depletion: Three donor triple $\alpha\beta$ TCR/CD56/V δ 2-depleted PBMC OKT-3/IL-15 expansates were harvested at day 10 of expansion to examine $\gamma\delta$ T cell subset composition (N=3). **(Q)** Midway V δ 2 depletion: $\alpha\beta$ TCR/CD56-depleted PBMC were expanded with OKT-3/IL-15, then depleted of V δ 2 cells at day 10 and plated for another 10 days' expansion until day 20. Resulting day 20 PBMC composition was analyzed and compared in V δ 2-depleted ($\alpha\beta$ TCR/CD56/V δ 2) or undepleted ($\alpha\beta$ TCR/CD56) expansates (N=3). **(R)** Harvest V δ 2 depletion: Expansate depletion of V δ 2 cells was tested at day 20 harvest of cell cultures. Shown are three donor (D1, D2, D3) PBMC pre- (red) and post- (blue) depletion, in which V δ 1 and V δ 2 cells was measured (N=3). **(S)** Harvest V δ 2 depletion: Expansate product composition was characterized following day 20 product V δ 2-depletion (N=3). * means $P < 0.05$; ** means $P \leq 0.01$.

Transduction efficiency was assessed by flow cytometric detection of the CD34 marker gene (26).

Cytotoxicity Assays

Cytotoxicity was determined either by staining for cell surface accumulation of CD107a as above where indicated, or by four-hour chromium (^{51}Cr)-release assay. Briefly, 1×10^6 target cells were labelled with 20 μL ^{51}Cr amounting to 3.7 MBq (PerkinElmer) for 60 minutes at 37°C . Following this, target cells were co-cultured with effector CAR T cells at range of effector: target (E:T) ratios (10:1, 5:1, 2.5:1 and 1.25:1) for four hours at 37°C in 96 well U bottom plates (Grenier). After incubation, the plates were centrifuged at 1500RPM for 5 minutes and 50 μL of the supernatant was transferred to 96 well OptiPlate-96 HB (PerkinElmer). 150 μL of scintillation fluid was added per well and the plates were sealed and incubated at room temperature overnight. ^{51}Cr release from lysed target cells was counted on 1450 MicroBeta Trilux Scintillation Counter (PerkinElmer). The scintillation counts from wells with only targets (without effectors) were used as spontaneous release controls and target cells lysed with 1% Triton X-100 (ThermoFisher) were used as a maximum ^{51}Cr release control.

Proliferation Assay

Proliferation of expanded and harvested V δ 1 cells following repeated stimulation was evaluated to determine CAR-V δ 1 persistence in the presence of an antigen-expressing target cell line. Briefly, CAR-V δ 1 cells were labelled with CellTrace Violet proliferation dye (ThermoFisher) according to manufacturer's instructions for 20 minutes at 37°C . Once labelled, CAR-V δ 1

cells were plated at 5×10^5 per well of a 48-well plate (Corning) and co-cultured at a 1:1 E:T ratio with irradiated tumor targets, either B7H3-negative Jurkat wild type cells (Jurkat-WT) or isogenic Jurkat cells transduced to express high levels of B7H3 (Jurkat-B7H3). Plates were incubated at 37°C and 5% CO_2 for 6 days, without exogenous cytokine supplementation. Freshly irradiated target cells were fed every two days following co-culture and proliferation was evaluated by flow cytometry.

Cell Lines

Jurkat (ATCC Cat# TIB-152, RRID : CVCL_0367), HeLa (ATCC Cat# CCL-2.2, RRID : CVCL_0058), NOMO-1 (DSMZ Cat# ACC-542, RRID : CVCL_1609), K562 (ATCC Cat# CCL-243, RRID : CVCL_0004) and U87 (ATCC Cat# HTB-14, RRID : CVCL_0022) cell lines were all acquired from ATCC and cultured as recommended by the supplier. LAN-1 cell line (DSMZ Cat# ACC-655, RRID : CVCL_1827) was acquired from DSMZ and cultured as recommended by the supplier. Cell lines were screened monthly for mycoplasma contamination. Briefly, Jurkat, K562 and NOMO-1 cells were grown in 10% FBS-supplemented RPMI1640 (Sigma Aldrich) suspension culture and kept at $<1 \times 10^6/\text{mL}$ density. LAN-1, HeLa and U87 cell lines were grown in 10% FBS-supplemented DMEM (Thermo Fisher) adherent culture and split regularly at around 80-90% confluency using trypsin (Thermo Fisher)-based disaggregation, to avoid overgrowth.

Production of B7-H3 Positive Jurkat Cells

A truncated B7-H3 (T-B7-H3) in an SFG γ -retroviral expression cassette was a gift from Karin Straathof (UCL). A 4Ig-B7-H3

isoform of B7-H3 was purchased (Sinobiological) and cloned into a γ -retroviral expression cassette. Retroviral transduction was used to stably transduce Jurkat cells with 4Ig-B7-H3.

Statistical Design

Data was analyzed with GraphPad Prism (GraphPad Prism, RRID : SCR_002798). Data are displayed at mean \pm SEM unless otherwise stated. For normally distributed numerical data, parametric tests were used to determine significance of difference between groups. Analysis of variance (ANOVA) was used, unless otherwise stated. Significance is represented by: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

Calculation of Earth Mover's Distance (EMD)

EMD describes change in signal strength based on difference in probability distribution, with a higher EMD denoting a larger change. The use of EMD to describe changes in protein accumulation allows multiple biological replicates to be characterized with a high degree of consistency, without collapsing the data to mean or median values at the expense of interpretability (24). EMD was computed between bulk CAR-transduced T cell culture versus non-transduced culture. Samples were time- and donor-matched. EMD was calculated between T cell populations that had undergone the same processing. The Python (Python Programming Language, RRID : SCR_008394) module 'wasserstein_distance', which is a component of 'scipy.stats', was used to calculate EMD between samples.

RESULTS

OKT-3 and IL-15 Stimulation of $\alpha\beta$ TCR- and CD56-Depleted PBMC Leads to Robust and Reproducible V δ 1 Cell Expansion

Benchmarking our efforts to the two-step and multi-cytokine 'DOT protocol' [described in detail by Almeida and co-workers (23)], we compared its ability to expand V δ 1 cells with canonical *ex vivo* T cell expansion methodology, consisting of a single step PBMC stimulation with clone OKT-3 anti-CD3 mAb and IL-2 at 100 IU/mL. Briefly, the 'DOT protocol' entails a first 10 day culture in OKT-3 with IL-4, IFN- γ , IL-21 and IL-1 β , followed by a second culture in OKT-3 with IL-15 and IFN- γ . Over 20 days of expansion, the 'DOT' cocktail of cytokines yielded a mean 100-times more V δ 1 cells than culture in IL-2 following activation of unsorted PBMC with a single dose of OKT-3 at initiation (**Figure 1A**). The inferiority of IL-2 monoculture to the 'DOT' cocktail of cytokines is consistent with what was reported in the original 'DOT' protocol publication (23). In pursuit of an allogeneically-applicable expansion protocol that generates a product without potentially alloreactive $\alpha\beta$ T cells, we then depleted the starting PBMC of $\alpha\beta$ T cells using a standard and GMP-compatible $\alpha\beta$ TCR-biotin and anti-biotin bead-based protocol from Miltenyi. Aside from removing contaminating $\alpha\beta$ T cells, $\alpha\beta$ TCR-depletion further enhanced the yield of V δ 1

cells following 20 day culture in the 'DOT' cocktail of cytokines with a single dose of OKT-3 at initiation (**Supplementary Figures 1A, B**). This may be at least in part be due to the removal of $\alpha\beta$ T cell competition for cytokines.

We then investigated, in the context of the DOT cocktail of cytokines, whether we could expand V δ 1 cells more efficiently by using a more specific $\gamma\delta$ TCR stimulus, such as an anti- $\gamma\delta$ TCR mAb (clone: B1) or specific anti-V δ 1-TCR mAb (clone: TS-1). A single stimulating 1 μ g/mL mAb dose at initiation has been previously reported to be effective for TS-1/B1 mAb-driven V δ 1 cell expansion (25). Anti-CD3 OKT-3 stimulation led to an order of magnitude higher V δ 1 cell expansion from non-depleted PBMC than either $\gamma\delta$ T cell-specific clone (**Figure 1B**). Moreover, specific anti- $\gamma\delta$ TCR stimulation applied to non-depleted PBMC failed to prevent expansion of contaminating $\alpha\beta$ T cells in culture (**Supplementary Figure 1C**). V δ 1 cell numbers in DOT cytokine cocktail culture were evaluated and found equivalent between single stimulation with OKT-3 at initiation or repeated OKT-3 stimulation at 5 day intervals over the course of expansion, suggesting that a single OKT-3 administration is sufficient for optimal T cell expansion (**Supplementary Figure 1D**). As a result, $\alpha\beta$ TCR-depletion and a single stimulation with OKT-3 anti-CD3 mAb were progressed for further study.

We next evaluated V δ 1 cell expansion in this culture setup using either the two-step DOT cocktail of cytokines or continuous culture in 70ng/mL (corresponding to \sim 140 IU/mL) of IL-15 alone, it also being a component of the latter half of the DOT protocol regimen. Having discarded IL-2 alone as an optimal milieu, IL-15 was chosen as the second most commonly-employed GMP-compatible T cell manufacturing mitogen. Unexpectedly, IL-15 monoculture yielded at least equivalent or higher V δ 1 cell numbers to the DOT cocktail of cytokines (**Figure 1C**). We next examined whether IL-15-driven V δ 1 cell expansion could be improved by further depleting competition for cytokine from NK cells. We first confirmed that freshly-isolated PBMC V δ 1 cells do not express canonical NK cell-marker, CD56, while CD3-negative freshly-isolated PBMC and some V δ 2 cells do (**Supplementary Figure 1E**). We then combined the $\alpha\beta$ TCR-biotin and anti-biotin depletion step with GMP-compatible Miltenyi anti-CD56 magnetic beads according to manufacturer's protocol. Three donor concatenated t-SNE analysis of culture initiation material demonstrates the difference between undepleted and $\alpha\beta$ TCR/CD56-depleted freshly-isolated PBMC (**Figure 1D**). The double-depleted material is predominantly CD3-negative, though with enriched V δ 1 and V δ 2 composition relative to undepleted PBMC.

Undepleted, $\alpha\beta$ TCR- and $\alpha\beta$ TCR/CD56-depleted PBMC starting material was then compared for its ability to expand V δ 1 cells when stimulated with IL-15 and OKT-3. Double-depleted PBMC yielded not only substantially greater V δ 1 cell numbers, but also purity (**Figures 1E, F**). Of note, no substantive differences in product composition from any of the starting materials could be found when comparing IL-15 monoculture with culture in the DOT cocktail of cytokines (**Figure 1F**). We, therefore, progressed a single-step OKT-3 + IL-15-based

$\alpha\beta$ TCR/CD56-depleted V δ 1 expansion protocol for further optimization. We note that in this setup, a majority of donor $\alpha\beta$ TCR/CD56-depleted PBMC initially plated at 1×10^6 cells/cm² approached over-confluence by day 10 of culture (**Supplementary Figure 1F**). We, therefore, opted for a 1:4 culture split midway through the protocol (**Figure 1G**). While feasibly the cells can be cultured for shorter or longer periods as per desired product specification, we progressed a 20-day expansion period with a midway split for further analysis.

We benchmarked our OKT-3 and IL-15-based single step protocol against other published single step V δ 1 expansion methods that utilize phytohemagglutinin (PHA) instead of anti-CD3 mAb (16–18). We stimulated $\alpha\beta$ TCR- and CD56-depleted PBMC with OKT-3 and IL-15, or PHA with either IL-2 (16, 17) or IL-7 (18). OKT-3 with IL-15 outperformed both PHA-based protocols in terms of V δ 1 yield in all donors tested (**Supplementary Figures 2A–D**). The choice of anti-CD3 stimulation was further re-enforced by data indicating that, at harvest, OKT-3-stimulated V δ 1 cells expressed higher activation marker levels with concurrently lower exhaustion markers than PHA-stimulated V δ 1 cells, all the while expressing more NKG2D and CD56 receptors, indicative of favorable functional phenotype (**Supplementary Figure 2E**). Indeed, PHA-stimulated V δ 1 cells expressed higher apoptotic markers than CD3-stimulated V δ 1 cells at harvest (**Supplementary Figure 2F**).

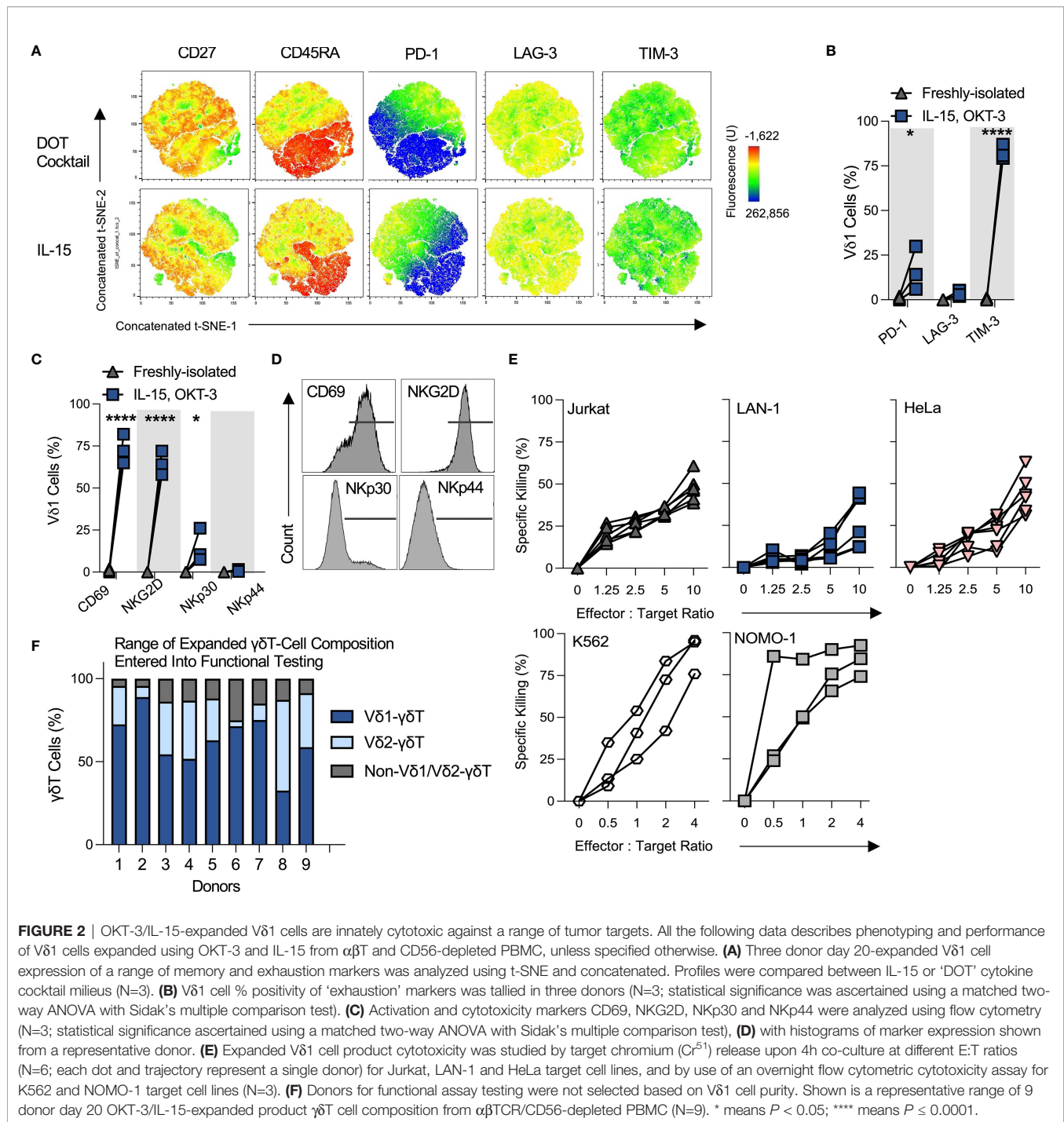
Encouragingly for clinical practicality, OKT-3 with IL-15 expanded not only freshly-isolated PBMC, but also V δ 1 cells from thawed cryopreserved PBMC that were $\alpha\beta$ TCR-/CD56-depleted following an overnight rest upon resuscitation (**Supplementary Figures 3A, B**). We note that an overnight PBMC ‘rest and recovery’ step in complete media at standard culture conditions enabled retention of a pre-cryopreservation V δ 1/V δ 2 cell ratio (**Supplementary Figure 3C**), and substantially increased the quality of $\alpha\beta$ TCR-/CD56-depletions as well as V δ 1 cell expansion. Resting was carried out at a high cell density (10^6 PBMC/mL) in complete expansion media, without cytokine supplementation.

To simulate a potential manufacturing process, we compiled expansion data of six arbitrarily chosen healthy donor cryopreserved leukapheresate-derived PBMC from two experimental runs, each of which consisted of PBMC thaw and overnight rest in complete media, followed by $\alpha\beta$ TCR/CD56-depletion and OKT-3/IL-15 stimulation the following day, as described above, except that in this iteration V δ 1 cells were cultured in 6-well G-Rex (as opposed to standard cell culture) vessels. Expansions were split into new wells at a 1:4 culture surface area ratio on day 10 of expansion and harvested at day 20 for analysis. Out of six donors tested, three achieved >1,000-fold V δ 1 cell expansion, and all achieved >400-fold expansion (**Figure 1H**). While in every donor examined V δ 1 cell expansion rate was greater than that of V δ 2 cells, in five out of six donors the difference was minimal suggesting a relatively unbiased $\gamma\delta$ T subset expansion by OKT-3/IL-15 (**Figure 1H**). The total V δ 1 cell yield per harvested 6-well G-Rex well was $>2 \times 10^8$ V δ 1 cells per 4×10^6 PBMC initiated in three out of six donors tested, delineating apparent ‘good’ and ‘poor’ expanders

(**Figure 1I**). These donors further clustered by product composition. While all yielded 80–100% pure $\gamma\delta$ T cells, $\gamma\delta$ T cell composition varied greatly (**Figure 1J**). $\alpha\beta$ T cell contamination was negligible, though some CD3-negative cells (mostly NK cells) persisted (**Figure 1J**). We investigated $\gamma\delta$ T cell product composition further and found that in all G-Rex-expanded donor products, an apparently inverse relationship existed between high purity V δ 1-donors and V δ 2-donors (**Figure 1K**). Given the relatively unbiased subset expansion by OKT-3/IL-15 we observed, we interrogated whether a high-purity (or ‘good’) V δ 1-donor could be predicted by examining the undepleted leukapheresates of donors entered for expansion.

The pre-depletion donor PBMC V δ 1:V δ 2 ratios were compared in six donors and correlated to V δ 1 cell purity and total V δ 1 cell count after 20 day stimulation of $\alpha\beta$ TCR/CD56-depleted PBMC with OKT-3 and IL-15. In these donors, a pre-initiation V δ 1:V δ 2 ratio of greater than 0.4:1 was associated with at least 50% V δ 1 cell purity at harvest ($R^2 = 0.74$) (**Figure 1L**). The relationship between V δ 1:V δ 2 ratio and absolute V δ 1 cell yield was also investigated. We observed, however, that with excluding one donor from analysis for yield (indicated in red in **Figures 1L, M**), high V δ 1:V δ 2 ratio at initiation correlated with high V δ 1 cell yield at harvest in this small sampling of independent donors. A minimum pre-initiation V δ 1:V δ 2 ratio of 0.2:1 was associated with harvests of $>2 \times 10^8$ V δ 1 cells per 4×10^6 PBMC initiated ($R^2 = 0.79$) (**Figure 1M**). We hypothesize, therefore, that a high V δ 1:V δ 2 ratio at initiation of expansion may serve as a biomarker for high ultimate V δ 1 cell yield and purity at harvest, though more donor material screening is required to substantiate this observation.

We next examined whether $\alpha\beta$ TCR/CD56-depleted OKT-3/IL-15-stimulated product can be further enriched for V δ 1 cells by depleting contaminating V δ 2 cells. To this end, we identified three potential depletion points during the manufacture: at initiation concurrently with $\alpha\beta$ TCR/CD56-depletion, midway at the split, or at harvest (**Figure 1N**). First examining the initiation depletion strategy, we compared the following depletions for V δ 1 cell purity among freshly-isolated PBMCs, (i) $\alpha\beta$ TCR, (ii) $\alpha\beta$ TCR/CD56, and (iii) $\alpha\beta$ TCR/CD56/V δ 2. The triple depletion was performed as follows: PBMC were co-incubated with $\alpha\beta$ TCR-biotin mAb and V δ 2 (clone: B6)-biotin mAb, washed, and then co-incubated with anti-biotin and anti-CD56 microbeads according to manufacturer’s protocol. Each depletion step further increased V δ 1 cell purity among the initiation T cell compartment (**Figure 1O**). Not only was the clone B6 V δ 2-depletion highly effective at the outset, it also prevented re-growth of V δ 2 cells during expansion (**Figure 1P**). Though, it also encouraged non-V δ 1/V δ 2 $\gamma\delta$ T cell expansion, resulting in a V δ 1: non-V δ 1/V δ 2 $\gamma\delta$ T cell ratio of ~ 2:1. Product V δ 2 depletion midway was highly efficacious; at harvest it yielded a ~77% pure V δ 1 cell product, with a ~17% non-V δ 1/V δ 2 $\gamma\delta$ T cell presence (**Figure 1Q**). Product depletion at harvest yielded a similar purity of ~72% V δ 1 cells and ~20% non-V δ 1/V δ 2 $\gamma\delta$ T cells (**Figures 1R, S**). Non- $\gamma\delta$ T cell content was ~10% in all methods tested and was largely CD3-negative. A majority of these were NK cells (CD3-negative/CD56-positive PBMC)



(Supplementary Figure 4B), that we hypothesize either escaped initial depletion or upregulated CD56 during expansion. We note that, while initially negative, also 50-70% of V δ 1 cells upregulated CD56 upon expansion (Supplementary Figure 4C), negating the possibility of a CD56-based contaminant depletion at harvest.

Of the V δ 2 cell depletion strategies tested, we hesitate to recommend the best, nor indeed whether it is required at all - as

optimal product specifications in terms of γ δ T cell subset purity for maximal therapeutic efficacy are yet to be determined. It is not necessarily the case that the purest V δ 1 cell product is the most efficacious against cancer, and it is feasible that other γ δ T cell subsets in the product will synergize rather than suppress V δ 1 cell anti-cancer functionality. Substantial further study in this area is required. Other factors that will impact the decision on V δ 2 cell depletion include post-harvest processing, such as

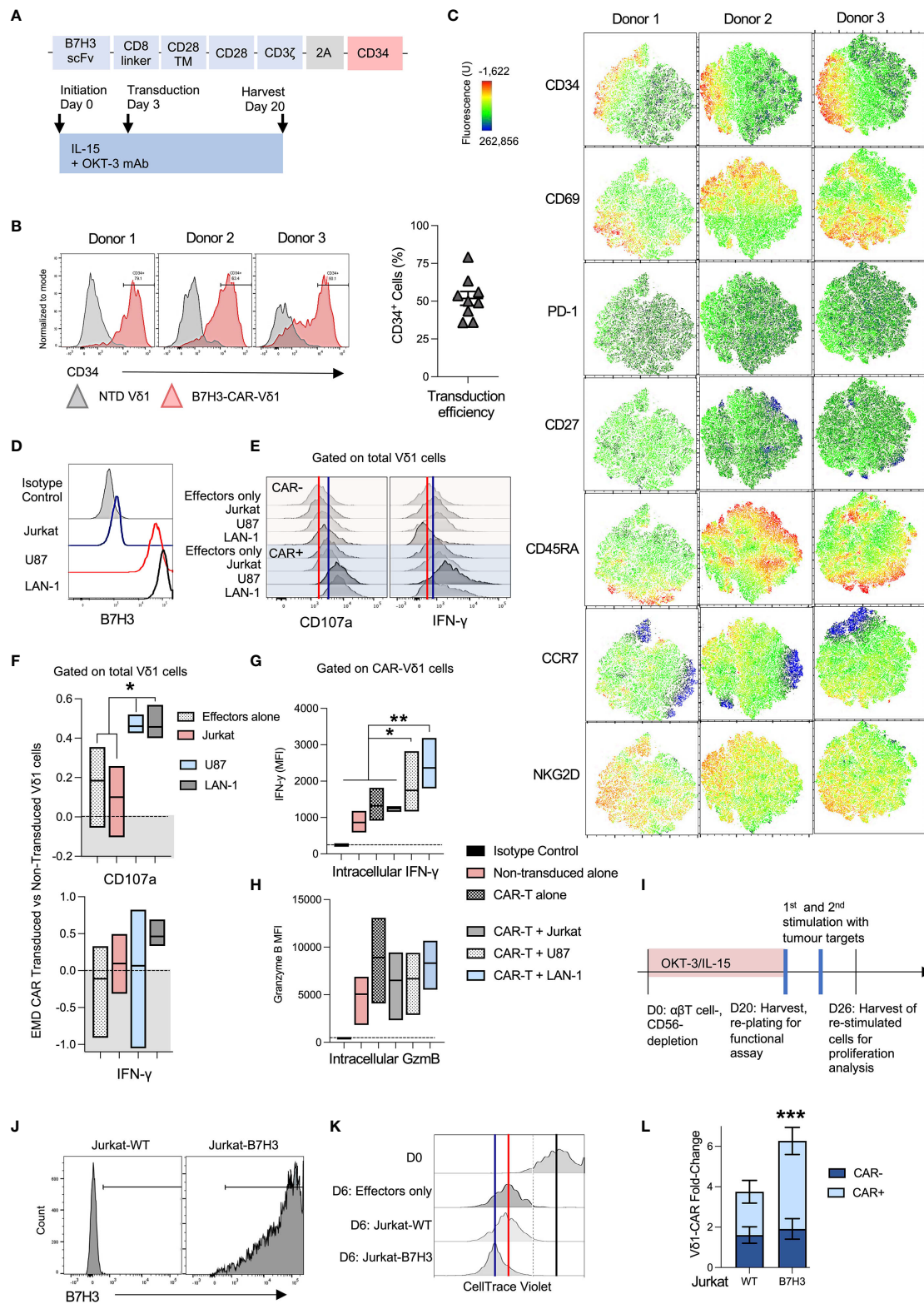


FIGURE 3 | Continued

FIGURE 3 | OKT-3/IL-15-expanded V δ 1 cells are readily transducible with chimeric antigen receptors (CAR). **(A)** V δ 1 cells were transduced with an SFG retroviral vector encoding a B7H3-28 ζ -CAR and a CD34 marker gene separated with a T2A cleavage sequence at day 3 post-activation. **(B)** Three representative donor V δ 1 cell CD34 marker gene expression is shown (left panel), along with a compilation of 9 different donor transduction efficiencies 5 days post-transduction (right panel). **(C)** V δ 1 cell activation and memory markers were characterized in a whole population of CAR-transduced cells. t-SNE data is shown for three individual donor day-20 harvested PBMC, gated on live V δ 1 cells. **(D)** A panel of B7H3-positive and negative target cell lines was selected. **(E)** V δ 1 cell accumulation of intracellular IFN- γ and cell surface CD107a was measured after overnight co-culture with targets followed by a 4h culture in monensin-supplemented media. Marker accumulation was measured in CAR-transduced and non-transduced V δ 1 cells. Shown are representative histograms of marker expression from a representative donor. The red line indicates median fluorescence intensity (MFI) of CAR-negative effectors alone, while the blue line indicates MFI of CAR-positive effectors alone. **(F)** IFN- γ and CD107a expression histogram data from 3 separate donors was converted to earth mover's distance (EMD) values that compared marker expression between CAR-transduced versus non-transduced cells. A score of '0.0' indicates no difference and is indicated by the dotted line (N=3; mean and distribution indicated). **(G)** The same data was analyzed using MFI measurements, compared in stratified CAR-positive (CD34+) and non-transduced (CD34-) V δ 1 cells in the same culture (N=3; mean and distribution indicated; statistical significance ascertained using one-way ANOVA). **(H)** V δ 1 cells in the same culture were similarly analyzed for intracellular granzyme B levels (N=3; mean and distribution indicated). **(I)** To test expanded CAR-V δ 1 persistence and proliferation, expanded cells were harvested and challenged twice at a 1:1 E:T ratio with **(J)** irradiated B7H3 antigen-positive and negative Jurkat targets. **(K)** CAR-V δ 1 CellTrace Violet dye dilution was measured after 6 day co-culture. One representative donor matched data is shown. The black line indicates the edge of undiluted dye at day 0 of the assay, the red line indicates dye MFI of CAR-V δ 1 only at day 6 indicative of background proliferation, while the blue line indicates dye MFI of CAR-V δ 1 in co-culture with antigen-positive targets. **(L)** To account for ongoing background proliferation, V δ 1 cells were counted pre and post-co-culture using flow cytometric counting beads, and V δ 1 fold-change was normalized to effectors alone (N=3; mean \pm SEM; statistical significance was ascertained using a two-way ANOVA with Sidak's multiple comparison). * means $P < 0.05$; ** means $P \leq 0.01$; *** means $P \leq 0.001$.

intention to cryopreserve, etc. The remainder of the functional data in this study is presented on V δ 1 cell products derived from double (α BTCCR/CD56)-depleted PBMC.

We note that the above depletions could be reproduced to GMP-standard by replacing research-grade α BTCCR and CD56 depletion reagents with GMP-grade alternatives from Miltenyi Biotec (CliniMACS TCR α / β Product Line cat nr: 200-070-407; CliniMACS CD56 Product Line cat nr: 170-076-713) and carried out on either CliniMACS *Plus* or CliniMACS *Prodigy* hardware. We note the lack of commercially-available GMP-compatible clone B6 V δ 2-biotin products, though anticipate that those could be obtained from suppliers through custom manufacture.

OKT-3/IL-15-Expanded V δ 1 Cells Are Innately Cytotoxic Against a Range of Tumor Targets

20-day-expanded OKT-3/IL-15 V δ 1 cells exhibited a similar memory and exhaustion profile to DOT cytokine cocktail counterparts. As indicated in concatenated t-SNE plots of various markers, V δ 1 cells were broadly positive for CD27, with a subpopulation brightly expressing CD45RA. While a proportion of CD27+/CD45RA- cells expressed PD-1, few V δ 1 cells bound anti-LAG-3 antibody above isotype control (**Figures 2A, B**). Nearly all V δ 1 cells were dimly but universally TIM-3-positive. OKT-3/IL-15-expanded V δ 1 cells further upregulated activation marker CD69 as well as cytotoxic differentiation marker NKG2D, but not NKP44 (**Figures 2C, D**). A small subpopulation of expanded V δ 1 cells consistently upregulated NKP30.

Functionally, OKT-3/IL-15-expanded V δ 1 cells exhibited highly consistent innate cytotoxicity against a range of hematological and solid tumor targets, including T cell leukemia Jurkat cells, cervical cancer HeLa cells, neuroblastoma LAN-1 cells, chronic myelogenous leukemia K562 cells and acute myeloid leukemia NOMO-1 cells (**Figure 2E**). This is of note, as donors were not specifically selected for only high V δ 1 cell purity, but rather represented a range of γ DT-subset compositions (a range of harvested α BTCCR/CD56-depleted PBMC-derived products is illustrated in **Figure 2F**). This suggests that maximal V δ 1 cell

purity does not uniquely determine the cytotoxic potential of the OKT-3/IL-15-expanded product.

OKT-3/IL-15-Expanded V δ 1 Cells Are Readily Transducible With Chimeric Antigen Receptors (CAR)

To assess the suitability of this expansion protocol for generating genetically-modified immunotherapeutics, we evaluated V δ 1 cell retroviral transduction with an anti-B7H3 2nd generation 28 ζ chimeric antigen receptor (CAR) (**Figure 3A**). A consistent ~50% transduction efficiency (ranging from 35.8% - 79.1%) was achieved transducing nine different donors in three experimental runs (**Figure 3B**).

We queried the impact of viral transduction with an ITAM-containing CAR on OKT-3/IL-15 V δ 1 cell product by comparing expression of a range of memory, exhaustion and functional markers within the transduced cell population. Cells were transduced on day 3 following initiation, and thereafter expanded for an additional 17 days until harvest at day 20. Anti-CD34 staining was used to detect expression of the RQR8 CAR marker gene (26) in the transduced cell product. Unexpectedly, none of the activation, memory or exhaustion markers we tested mapped neatly onto CAR(CD34+)-V δ 1 cells (**Figure 3C**). The closest matches were increased expression of NKG2D and a dim but consistent association of CD34 with PD-1 expression in CAR-V δ 1 compared to unmodified V δ 1 cells. Curiously, there was little association between CD69 and CD34 in any of the donors tested, suggesting that the V δ 1 cell product was highly activated regardless of CAR expression. The most notable difference between CAR-transduced V δ 1 cells as a whole compared to OKT-3/IL-15 V δ 1 cells that were never exposed to retrovirus (**Figure 2A**) was the downregulation of CD27 in virus-exposed compared to non-exposed cells. Most other queried markers were similar between both populations.

CAR-V δ 1 were then tested against a range of antigen-positive and negative hematological and solid tumor targets: B7H3-negative Jurkat cells, and B7H3-positive cell lines U87 (originating from glioblastoma) and LAN-1 cells (**Figure 3D**). Intracellular IFN- γ and cytotoxic degranulation cell surface

marker CD107a accumulation was compared in CAR-transduced *versus* unmodified V δ 1 cells using flow cytometry (**Figure 3E**). The red line in **Figure 3E** indicates marker median fluorescence intensity (MFI) of unmodified target-free V δ 1 cells, while the blue line indicates the MFI of target-free CAR-V δ 1 cells. These measures are included to account for the innate, B7H3-independent reactivity of V δ 1 cells, as well as potential baseline activation mediated by CAR-transduction. Differences between histograms were quantified using the statistical analysis tool Earth Mover's Distance (EMD), which quantifies the dissimilarity between two dimensional distributions whilst respecting the single-cell nature of the dataset; a greater value of EMD indicates greater difference (see methods). EMD scores were generated measuring the difference between bulk V δ 1 cell IFN- γ or CD107a accumulation when either unmodified or transduced with a B7H3-28 ζ -CAR and challenged with different tumor targets. An EMD score of 0 indicates no relative change between transduced and non-transduced V δ 1 cells. Interestingly, while CAR-V δ 1 CD107a-mediated cytotoxic degranulation was significantly higher upon challenge with antigen-positive U87 and LAN-1 targets than without challenge or challenge with antigen-negative Jurkat cells, IFN- γ production was less consistently impacted by the presence of target antigen and highly variable on a donor-donor basis (**Figure 3F**). This inconsistency was caused not by the inability of CAR engagement to mediate IFN- γ production, but rather high innate and non-CAR-dependent IFN- γ production in some of the donors. All donor V δ 1 cells demonstrated intracellular IFN- γ with and without CAR transduction. A significant, antigen-dependent upregulation of intracellular IFN- γ could be observed when gating on specifically CAR-positive V δ 1 cells, rather than bulk V δ 1 cells in culture (**Figure 3G**). IFN- γ production correlated positively with V δ 1 cell CAR marker gene, CD34, expression when challenged with antigen-positive but not negative targets (**Supplementary Figure 5**). Consistent with a high and sustained cytotoxic potential, granzyme B levels were at least as high or higher in matched unmodified V δ 1 cells compared to CAR-V δ 1 cells before and after challenge with targets (**Figure 3H**).

To test proliferative and persistence capacity, CAR-V δ 1 were harvested post-expansion, plated with no exogenous cytokine and challenged twice at a 1:1 E:T ratio at three day intervals with irradiated B7H3-negative Jurkat wild type cells (Jurkat-WT) or isogenic Jurkat cells transduced to express B7H3 (Jurkat-B7H3) (**Figures 3I, J**). Expansion was monitored *via* dilution of CellTrace Violet proliferation dye, as well as cell counts performed using Precision Count beads and flow cytometry. While all CAR-V δ 1 were highly activated and continued low-grade proliferation after re-plating, more proliferation was seen upon challenge with Jurkat-B7H3 compared to no targets or Jurkat-WT (**Figure 3K**). The black line in **Figure 3K** indicates the CellTrace Violet MFI of V δ 1 cells at plating, the red line of effectors only after 6 days in culture, and the blue line – of effectors co-cultured with antigen-positive targets. Normalized to effectors only, V δ 1 cells expanded more when expressing a CAR but only in response to antigen-positive Jurkat cells (**Figure 3L**).

Unmodified V δ 1 cells expanded ~2-fold over target-free matched effectors, likewise CAR-V δ 1 in response to Jurkat-WT. In response to Jurkat-B7H3, meanwhile CAR-V δ 1 cells expanded 4-fold.

DISCUSSION

We set out to develop a single-step, GMP-compatible CAR-V δ 1 cell expansion and transduction protocol that utilizes standard T cell therapy expansion reagents already employed in the CAR-T field. To that end, we focused on pan-T cell stimulating anti-CD3 mAb, clone OKT-3, and the classic T cell cytokine expansion milieu of IL-2 and IL-15. While OKT-3 with IL-2 failed to support sufficient V δ 1 cell expansion, OKT-3 with IL-15 led to substantial V δ 1 cell expansion that was further boosted by depletion of CD56-positive cells. The additive effect of CD56-positive cell depletion was likely at least in part mediated by decreasing competition for IL-15 from CD56-expressing PBMC, such as NK cells. Given the pan-T cell stimulatory nature of both OKT-3 and IL-15, stringent $\alpha\beta$ T cell depletion prior to initiation was obligate for achieving V δ 1 cell yield and purity. $\alpha\beta$ TCR/CD56-depleted OKT-3/IL-15-stimulated V δ 1 cells were highly tumor-reactive in their own right and amenable to transduction to high efficiency with a second generation B7H3-28 ζ CAR using standard retroviral protocols. CAR-V δ 1 cells retained innate tumor responsiveness while also engaging in CAR-directed reactivity. Upon challenge with targets, B7H3-28 ζ -V δ 1 exhibited antigen-specific persistence, cytotoxicity and IFN- γ production. Taken together, we have described a fully GMP-compatible CAR-V δ 1 manufacturing protocol that utilizes reagents and processes well practiced in the CAR-T field.

We further examined the additional purification of V δ 1 cell product with V δ 2 cell depletion. V δ 2 cells were effectively removable using anti-V δ 2TCR mAb clone B6 conjugated to biotiny, magnetically removed with anti-biotin microbeads. These depletions could be successfully carried out at initiation of culture with a triple $\alpha\beta$ TCR/CD56/V δ 2 depletion, midway through depletion at culture split or at harvest. We reserve judgement as to the best approach in this instance, or whether V δ 2 cell depletion is required at all. We hypothesize that an ultra-pure V δ 1 cell product may not exhibit improved efficacy over a product that contains other $\gamma\delta$ T cell populations. Though, this warrants substantial further investigation with a range of donors. Indeed, it will be difficult to assess optimal product composition until such products are tested clinically. As the debate for “which $\gamma\delta$ T cell subset is best?” pervades the immunotherapy field, we expect that only clinical testing and conscientious and scientific clinical trial design will shed light on these questions. Ultimately, it may be that no single subset is superior, but rather that a correct balance of the different subsets is optimal for anti-cancer targeting.

In developing the optimized protocol described herein we used the “DOT protocol” cytokine cocktail described by Almeida and colleagues (23) as a comparator, investigating whether we can design a simplified process. V δ 1 cell yield and phenotype

were broadly similar between cells expanded with either OKT3/IL-15 or the “DOT protocol” cocktail of cytokines. There are four main modifications in our process compared to the published “DOT protocol”: (1) a simultaneous $\alpha\beta$ TCR- and CD56-bead depletion step replaces the $\alpha\beta$ TCR-depletion only, (2) the “DOT protocol” employs a second OKT-3-based CD3 positive selection step while our protocol adds OKT-3 to the depleted product without the need for a second selection step, 3) the multi-cytokine cocktail of the “DOT protocol” is replaced by IL-15 alone, 4) a second OKT-3 stimulation in the “DOT protocol” midway through expansion is omitted in our protocol. Together these changes represent a considerable simplification of the V δ 1 cell expansion process, and a reduction in cost. It was beyond the scope of the current study to perform a detailed side-by-side comparison in terms of *in vitro* and *in vivo* effector function. Further studies are warranted to compare the long-term effector function between these approaches.

We anticipate an increase of pre-clinical and clinical gene-engineered V δ 1 cell investigations for oncology indications in what is a rapidly evolving immunotherapeutic landscape. With the clinical success of canonical autologous CAR- $\alpha\beta$ T for a range of B cell malignancies, a role may be carved out for allogeneic non-canonical cell therapies. This includes $\gamma\delta$ T cells of V δ 1 and V γ 9V δ 2 subsets, as well as NK cells, for the targeting of solid tumor indications and CAR- $\alpha\beta$ T refractory hematological cancers. Allogeneic approaches of this type may further play an important role in democratizing access to a new generation of gene-engineered cell therapy drugs that can be manufactured in bulk from healthy donor material, with accompanying reductions in price and supply chain complexity, as well as possible improvement in product clinical efficacy.

An important area of ongoing research remains the identification of ‘optimal’ donors for allogeneic cell therapy products. It remains unclear whether high product yield during manufacture is a sure indicator of maximum therapeutic performance, or as recent data from the CAR- $\alpha\beta$ T field suggests (5) – that cell ‘quality’, including memory and exhaustion status, is a more predictive metric than quantity. The elucidation of the factors that govern $\gamma\delta$ T cell product ‘quality’ will be crucial to sustained clinical success. V δ 1 cells expanded with this one-step IL-15/OKT-3 process expressed high CD27 and CD45RA, in a pattern that is consistent with naïve and central memory in $\alpha\beta$ T cells and was diminished upon transduction with B7H3-28 ζ -CAR. It is unclear whether this marker expression profile correlates with $\alpha\beta$ T-like memory phenotypes in V δ 1 cells. Indeed, relatively little is known of $\gamma\delta$ T cell memory, and less still how such cell surface marker phenotypes correlate with anti-tumor functionality. Expanded and CAR-transduced V δ 1 cells weakly upregulated PD-1 and strongly upregulated TIM-3 ‘exhaustion’ markers, the significance of which on $\gamma\delta$ T cells is little understood. It is unclear whether their presence is indicative of true T cell exhaustion, activation or something other still.

These properties may further vary between the types of indications targeted and gene engineering applied. Intelligent clinical trial design and study of adoptively transferred $\gamma\delta$ T

cells pre- and post-infusion into patients will be crucial in elucidating the specific qualities of cells that confer the greatest therapeutic benefit.

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 author/s.

ETHICS STATEMENT

Ethical approval was granted by the UCL UK research ethics committee under IRAS project ID-154668.

AUTHOR CONTRIBUTIONS

MB and JA designed the experiments and wrote the manuscript. GF, CA, MF, and SD performed the data-generating experiments for this paper. JF provided data analysis. KC co-supervised CA. All authors contributed to the article and approved the submitted version.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fimmu.2022.863155/full#supplementary-material>

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Targeting Cytokine Signals to Enhance $\gamma\delta$ T Cell-Based Cancer Immunotherapy

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$\gamma\delta$ T cells represent a small percentage of T cells in circulation but are found in large numbers in certain organs. They are considered to be innate immune cells that can exert cytotoxic functions on target cells without MHC restriction. Moreover, $\gamma\delta$ T cells contribute to adaptive immune response via regulating other immune cells. Under the influence of cytokines, $\gamma\delta$ T cells can be polarized to different subsets in the tumor microenvironment. In this review, we aimed to summarize the current understanding of antigen recognition by $\gamma\delta$ T cells, and the immune regulation mediated by $\gamma\delta$ T cells in the tumor microenvironment. More importantly, we depicted the polarization and plasticity of $\gamma\delta$ T cells in the presence of different cytokines and their combinations, which provided the basis for $\gamma\delta$ T cell-based cancer immunotherapy targeting cytokine signals.

Keywords: $\gamma\delta$ T cell, cytokine, cancer, immunotherapy, cellular therapy

CHARACTERISTICS AND ANTIGEN RECOGNITION OF $\gamma\delta$ T CELLS

Although $\gamma\delta$ T cells share the same progenitors with conventional $\alpha\beta$ T cells and develop in the thymus, they are considered as innate immune cells due to their major histocompatibility complex (MHC) unrestricted antigen recognition, as well as the expressions of Natural Killer Receptors (NKR) and Toll-like Receptors (TLRs) along with rapid cytokine production. The majority of $\gamma\delta$ T cells are negative for CD4 and CD8. In both human and mice, $\gamma\delta$ T cells account for 5% of total peripheral T cells.

Based on the TCR δ chain usage, human $\gamma\delta$ T cells can be subtyped to V δ 1, V δ 2, V δ 3 and V δ 5 cells (Table 1). V δ 1 and V δ 2 are the major subsets, which are of great interest among human $\gamma\delta$ T cells. Human V δ 2 cells are generally paired with T cell receptor (TCR) γ 9, also named as V γ 9V δ 2 cells. V γ 9V δ 2 cells are the dominant $\gamma\delta$ T subset in human peripheral blood mononuclear cells (PBMCs). V γ 9V δ 2 TCRs recognize phosphoantigens (PAGs) such as isopentenyl pyrophosphate (IPP), which is accumulated in tumor cells, and (E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate (HMBPP) that is produced during microbial infections (Figure 1A). Interestingly, although $\gamma\delta$ T cells bind PAGs in the MHC independent manner, PAGs-mediated activation of V γ 9V δ 2 requires butyrophilin (BTN) and BTN-like molecules (1). Recent studies reported that BTN2A1 associated with BTN3A1 to initiate antigen-presentation to V γ 9V δ 2 T cells (2, 3). Besides TCR-associated antigen recognition, V γ 9V δ 2 T cells also express NK receptors including NKG2D and DNAM1, which recognize

TABLE 1 | $\gamma\delta$ T subsets and distribution in human and mouse.

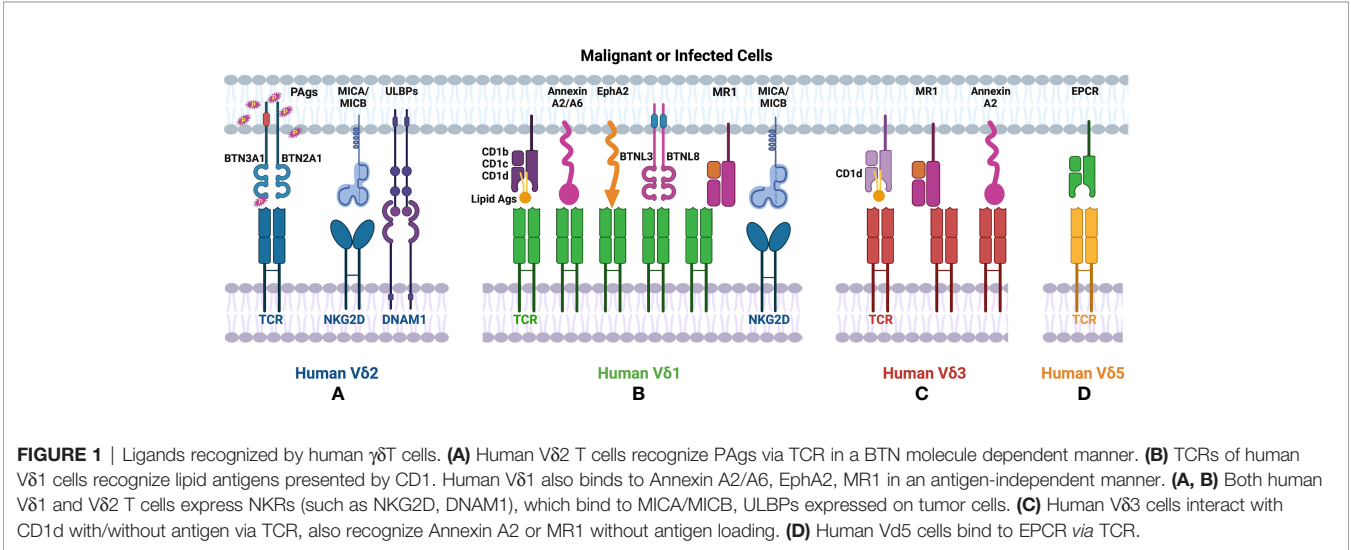
Species	δ Chain	γ Chain	Distribution
human	V δ 1	V γ 2, V γ 3, V γ 4, V γ 5, V γ 8, and V γ 9	dermis, gut, thymus, liver, and other epithelial tissues, PB
	V δ 2	V γ 9, V γ 8, V γ 4	PB, liver
	V δ 3	various γ chains	liver, gut, PB
	V δ 5	V γ 4	PB
	V γ 1	high diversity	spleen, blood, lymph node, liver, lung, dermis
mouse	V γ 4	high diversity	spleen, blood, lymph node, liver, lung, dermis
	V γ 5	V δ 1	dermis
	V γ 6	V δ 1, V δ 4	reproductive mucosa, skin
	V γ 7	V δ 4, V δ 5, V δ 6	gut

MHC class I chain-related molecules (MICA, MICB), ULBP-binding proteins (ULBPs) and Nectin-like-5 that are broadly expressed on tumor cells (4).

Human V δ 1 cells are mainly distributed in epithelial tissues, such as skin, gut, spleen, and liver. Human V δ 1 cells constitute only up to 15% of human $\gamma\delta$ T cells in PBMCs (5), but they exhibit fast and marked expansion during CMV infections (6). $\gamma\delta$ T cell compartment involved in HCMV-specific response is non-V γ 9V δ 2 T cells with the TCRV δ 1⁺ lymphocytes representing the prominent non-V γ 9V δ 2 $\gamma\delta$ T cell subset (7–9). Furthermore, these V δ 1 cells display a mixed CD27⁺/CD45RA⁺ or CD27⁺/CD45RA⁺ phenotype that is identified as cytotoxic effector/memory populations in CMV⁺ individuals (10). These findings indicated the potential immune surveillance function of V δ 1 cells. Whereas the TCR γ chains paired with V δ 1 display high diversity and the antigens recognized by V δ 1 cells are not well revealed, it has been shown that CD1 molecules with or without loaded lipid antigens can specifically activate V δ 1 cells. The direct interactions between V δ 1 and CD1b, CD1c, or CD1d have been identified by CD1 tetramers, mutagenesis experiments and crystal structures (11–15). In addition to CD1-associated recognition, V γ 4V δ 1 cells have been reported to respond to BTNL3 and BTNL8 expressing cells *via* V γ 4 chain (Figure 1B) (16). Annexin A2 and Annexin A6 that are known as stress-induced phospholipid-binding proteins and involved in

tumorigenesis also stimulated the proliferation and the production of TNF- α in V γ 4V δ 1 cells (17). Another newly identified stress-induced antigen that is recognized by V δ 1 TCR is ephrin type-A receptor 2 (EphA2) (Figure 1B), which is upregulated upon AMP-activated protein kinase (AMPK)-dependent metabolic reprogramming of cancer cells. It can be recognized co-ordinately by ephrin A to govern the activation of V γ 9V δ 1 cells (18). The involvement of EphA2 in V δ 1-mediated tumor cell lysis was demonstrated by reduced susceptibility to killing by EphA2 blocking (19). Human V δ 1 cells from peripheral blood and tissues exhibit autoreactivity to the monomorphic MHC-related protein 1 (MR1) without binding with any ligands, indicating MR1 as a ligand of V δ 1 $\gamma\delta$ TCR (20). Similar to V δ 2 cells, V δ 1 cells also mediate tumor cell lysis through recognizing ULBP3 and MICA by NKG2D (Figures 1A, B) (21–23).

V δ 3 cells account for ~0.2% of lymphocytes in PBMCs from healthy donors but are enriched in the liver and gut and can be expanded in patients with CMV activation and B cell chronic lymphocytic leukemia (24, 25). Human V δ 3 cells were identified as CD1d-restricted T cells and can mediate specific killing against CD1d⁺ cells (Figure 1C). Different from V δ 1 cells, V δ 3 cells can not recognize other CD1 molecules (such as CD1b,CD1c) (26). Annexin A2 was identified as the direct ligand of V γ 8V δ 3 TCR (Figure 1C) (17). Recently, human V δ 3 cells have also been shown to bind to MR1 in an antigen-independent manner (Figure 1C). Another notable population of human $\gamma\delta$ T cells is V δ 5 subset. Human



development in mice and patients with lung cancer (41, 42). Additionally, activated $\gamma\delta$ T cells also express death induced ligands CD95L (also known as FasL) and TNF-related apoptosis-inducing ligand (TRAIL), which engage with death receptor CD95 (Fas) and TRAIL receptor, and apoptosis of infected or malignant cells (43–45). Similar to NK cells, the majority of $\gamma\delta$ T cells in peripheral blood express CD16. CD16 acts as an activation site triggering antibody dependent cellular cytotoxicity (ADCC) (**Figure 2**: top right) (46). A recent study showed that exosomes derived from human V γ 9V δ 2T cells ($\gamma\delta$ T-Exos) efficiently induced the apoptosis of tumor cells through death receptor ligation (**Figure 2**: top right) (47, 48).

In addition to the direct killing against tumor cells, $\gamma\delta$ T cells can exert the indirect anti-tumor function by regulating other immune cells in the tumor microenvironment (**Figure 2**: bottom right). Human V δ 2 T cells are described as professional antigen-presenting cells, which can process antigens and provide co-stimulatory signals to induce the proliferation and differentiation of $\alpha\beta$ T cells (49). It is also reported that human $\gamma\delta$ T-APCs efficiently cross-present soluble antigens to CD8⁺T cells *via* MHC-I (50, 51). The high expression levels of APC-associated molecules and tumor antigen presenting capability of *in vitro* expanded human V γ 9V δ 2 T cells were also detected during the early stage of differentiation (52). Activated human $\gamma\delta$ T cells boost NK cell mediated killing of tumor cells through CD137L (53).

Besides ligand-receptor interactions, cytokine production is the pivotal pathway to regulate other immune cells. Like conventional T cells, $\gamma\delta$ T cells can be polarized to different subsets based on the secreted cytokines, including IFN- γ -producing $\gamma\delta$ T cells ($\gamma\delta$ T-IFN or $\gamma\delta$ T1), IL-4-producing $\gamma\delta$ T cells ($\gamma\delta$ T2), IL-17-producing $\gamma\delta$ T cells ($\gamma\delta$ T17) and Foxp3⁺ regulatory $\gamma\delta$ T cells ($\gamma\delta$ Treg). These cytokine-producing $\gamma\delta$ T cells exist in both human and mouse and can regulate other immune cell functions *via* their signature cytokine productions (**Figure 2**: bottom right). For instance, activated $\gamma\delta$ T1 cells promoted the maturation of DCs *via* IFN- γ dependent manner in mouse (54). Human freshly isolated $\gamma\delta$ T1 cells also induced the upregulation of HLA-DR, CD86, CD83 and release of IFN- γ , IL-6, and TNF- α of monocyte-derived DCs through the production of TNF- α and IFN- γ (55, 56). Both human V δ 2 and V δ 3 cells can promote B cell differentiation, antibody maturation and cytokine production (25, 55). IL-4 producing mouse V γ 1V δ 6 T cells can drive the proliferation and IgA secretion of Germinal Centre (GC) B cells (57). In additions, $\gamma\delta$ T17 cells promoted the infiltration of CTLs within the tumor bed *via* IL-17 production after chemotherapy (58).

Although the anti-tumor functions of $\gamma\delta$ T cells have been shown in many murine models and in cancer patients, the pro-tumor activities of $\gamma\delta$ T cells were also reported in numerous studies (**Figure 2**: left). Co-inhibitory molecules can be upregulated on human and murine $\gamma\delta$ T cells in tumors, which can bind to the co-inhibitory receptors expressed on $\alpha\beta$ T cells to restrain their activation, infiltration, and anti-tumor efficiency (59). The expressions of PD-1, TIM3 and TIGIT also induced the exhaustion and dysfunction of $\gamma\delta$ T cells in AML and MM patients (60). Moreover, co-inhibitory receptors on $\gamma\delta$ T cells

contribute to the tumor immune escape by interaction with immunosuppressive molecules (**Figure 2**: top left) (61). Meanwhile, hypoxic tumor microenvironment induced by metabolic status of cancer cells is a critical factor in mediating immunosuppression. The anti-tumor function of $\gamma\delta$ T cells can be inhibited by hypoxia *via* the downregulation of NKG2D and CD107a expressions (62, 63). Over the past decade, IL-17-producing $\gamma\delta$ T cells have been found to associate with enhanced tumor growth and metastasis. $\gamma\delta$ T is one of the major sources of IL-17 in the tumor microenvironment and reduced tumor burden was observed in IL-17-producing V γ 4-depleted and IL-17-deficient mice (64). $\gamma\delta$ T17 cells recruit myeloid-derived suppressor cells (MDSCs) to the tumor site, which can suppress CD8⁺T cell responses (64, 65). Consistently, this is also demonstrated in human colorectal cancer (66). In addition, IL-17-producing $\gamma\delta$ T cells can accelerate tumor progression by promoting angiogenesis and mobilizing pro-tumor macrophages (67, 68). $\gamma\delta$ Treg cells were found to impair DC maturation and function and CD8⁺T cell-mediated anti-tumor function in cancer patients *via* TGF- β , IL-6 or IL-10 dependent or independent manner (69, 70). Moreover, CD39⁺ $\gamma\delta$ Tregs were implicated in the immunosuppressive environment *via* producing adenosine in human colorectal cancer (71). The IL-6-adenosine positive feedback loop between CD73⁺ $\gamma\delta$ Tregs and cancer-associated fibroblast (CAF) was also involved in tumor progression in breast cancer patients (72).

The role of $\gamma\delta$ T cells during tumor development is still controversial. Their functions could be cancer type specific. For example, human V δ 1 cells exhibit potent cytotoxicity against colon cancer cells and B-cell chronic lymphocytic leukemia (73, 74), whereas V δ 2 cells are shown to kill a wide variety of tumors including acute myeloid leukemia, multiple myeloma and lung cancer (60, 75). On the other hand, some $\gamma\delta$ T subsets may exert different functions in the same type of cancer under different treatment conditions/environment. $\gamma\delta$ T17 cells promoted CTL infiltration into colon cancer after chemotherapy (58), whereas they have been reported to inhibit anti-tumor immune response *via* promoting the recruitment, proliferation, and survival of MDSCs in colorectal cancer and hepatocellular carcinoma (66). Therefore, $\gamma\delta$ T cell function during tumor development may be greatly influenced by the cytokines present in the tumor microenvironment under specific conditions.

CYTOKINE-MEDIATED REGULATION OF $\gamma\delta$ T CELL FUNCTION

IL-2 is the commonly used cytokine for expanding human and murine $\gamma\delta$ T cells. IL-2 is identified as T cell growth factor and is necessary for the proliferation and differentiation of naïve T cells into effector T cells (76). However, $\gamma\delta$ T cells produce relatively less IL-2 than $\alpha\beta$ T cells (77). Due to the PAg recognition of human V γ 9V δ 2 T cells, the combination of IL-2 with synthetic PAg, such as Zoledronate (Zol) and BrHPP, was widely used for the generation of human V γ 9V δ 2 T cells from PBMCs for $\gamma\delta$ T cell-based immunotherapy (**Figure 3**). Adoptive transfer of pamidronate-expanded V γ 9V δ 2 cells alone effectively

prevented EBV-induced B cell lymphoproliferative disease (EBV-LPD) in mouse and the injection of pamidronate significantly controlled the development through specific activation and expansion of V γ 9V δ 2 cells in humanized mice (78). The adoptive transfer of IL-2/PAGs *ex vivo* expanded V γ 9V δ 2 cells from autologous or allogeneic hosts exhibited potent anti-tumor effects in a variety of cancer patients, such as gastric cancer, osteolytic breast cancer, prostate cancer, and colorectal cancer and so on (79–81). The *in vivo* administration of pamidronate/Zol and low-dose IL-2 also triggered the proliferation of $\gamma\delta$ T cells in clinical trials and engaged the anti-tumor response without appreciable toxicity in patients (82–84).

IL-15, another proinflammatory cytokine in IL-2 superfamily, has been shown to contribute to the effector functions and maintain the survival of human NK cells *via* IL-15-AKT-XBP1s signalling pathway (Figure 3) (85). It is also a promising candidate for enhancing the expansion and cytotoxicity of $\gamma\delta$ T cells. With the stimulation of IL-2 or IL-15, human V δ 1 cells were selectively induced to express Nkp30, Nkp44 and Nkp46 in a PI3K/AKT dependent manner. The expression of NCRs is associated with increased production of granzyme B and improved cytotoxicity against tumor cells (86, 87). Although low IL-2 and additional IL-15 did not affect NKR expression level on human V γ 9V δ 2 cells, IL-15 significantly increased the expressions of perforin, granzyme B, granulysin and T-bet, which led to enhanced cytotoxic capacity of V γ 9V δ 2 cells. A recent study showed that IL-15 and vitamin C (VC) promoted the proliferation and differentiation and reduced the apoptosis of human V γ 9V δ 2 T cells *in vitro* (88). Moreover, these cells possessed improved cytotoxicity, both *in vitro* and in

humanized mouse model. The adoptive transfer of IL-15+VC expanded V γ 9V δ 2 T cells prolonged the survival of patients with late-stage lung cancer or liver cancer (89). IL-15 receptor α signalling limited the development of IL-17-producing $\gamma\delta$ T cells in a mouse model (90). A global increase of $\gamma\delta$ T17 cells was found in IL-15R α -KO mice, but only modest dysregulation of IL-17 production was observed on $\gamma\delta$ T cells from IL-15-KO mice (90).

Other members of IL-2 cytokine family, including IL-4, IL-7, and IL-21, can also act on $\gamma\delta$ T cells (Figure 3). IL-4 was demonstrated to negatively regulate the anti-tumor function of $\gamma\delta$ T cells *via* inhibiting the expression of NKG2D and promoting the IL-10 production from V δ 1 cells, which in turn suppressed IFN- γ production and the proliferation of V δ 2 cells (91). IL-7 was used to expand V δ 1 cells from PBMCs in the presence of PHA *in vitro*. These expanded V δ 1 cells exhibited great anti-tumor function and prolonged the survival of human colon carcinoma xenografted mice *via* expressing high levels of cytotoxicity-related molecules, chemokine receptors and NCRs (73). However, IL-7 selectively promoted the IL-17 production of human V δ 1, V δ 2 from cord blood and murine CD27- $\gamma\delta$ T cells (92). The combination of IL-2 and IL-21 directly enhanced the cytotoxicity of human $\gamma\delta$ T cells to hepatocellular carcinoma cells *in vitro* (93). In the presence of IL-21, PAGs-expanded V γ 9V δ 2 T cells expressed high level of CXCR5, which enhanced their potential to support antibody production by B cells (94). On the other hand, IL-21-stimulated V γ 9V δ 2 T cells can differentiate to CD73⁺ $\gamma\delta$ Treg cells, which exert immunosuppressive function *via* inhibiting T cell responses (95).

The synergistic function of IL-12 and IL-18 in inducing the IFN- γ production of T cells and NK cells has been demonstrated

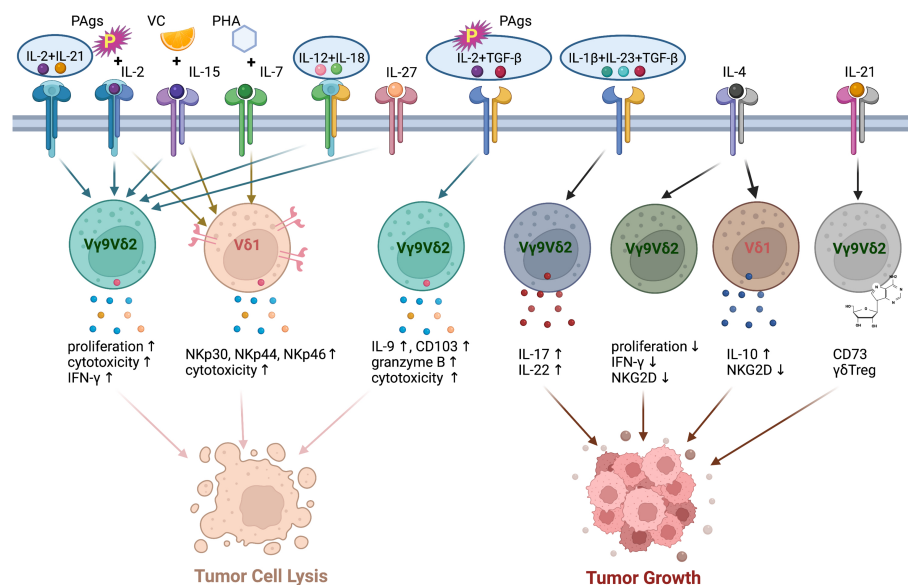


FIGURE 3 | The polarization of human $\gamma\delta$ T cells induced by different cytokine combination. PAGs and IL-2 with the addition of VC and IL-15, IL-12+IL-18, IL-27, IL-21+IL-2 enhance the cytotoxicity of human V γ 9V δ 2 T cells. IL-2 or IL-15 induces the expressions of Nkp30, Nkp44, Nkp46 on human V δ 1 cells. PHA and IL-7 enhance the cytotoxic capacity of human V δ 1 cells. TGF- β increases the anti-tumor cytotoxicity of human V γ 9V δ 2 T cells in the presence of PAGs and IL-2. The combination of IL-1 β , IL-23 and TGF- β promotes the differentiation of V γ 9V δ 2 T cells to IL-17-producing $\gamma\delta$ T cells. IL-4 reduces the proliferation, NKG2D expression and IFN- γ production of V γ 9V δ 2 T cells *via* promoting IL-10 secretion of V δ 1 cells. IL-21 alone induces V γ 9V δ 2 T cell differentiation to CD73⁺ $\gamma\delta$ Treg cells, which promote tumor growth.

(96–99). Similarly, IL-12 and IL-18 also induced the production of IFN- γ and increased cytotoxicity in $\gamma\delta$ T cells in an antigen-independent manner (**Figure 3**) (100, 101). However, the combination of IL-12 and IL-18 led to the upregulation of TIM3 on $\gamma\delta$ T cells (102). That might indicate the exhaustion or dysfunction of $\gamma\delta$ T cell under the treatment of IL-12/18. IL-27 is a heterodimeric cytokine of IL-12 cytokine family. The expression of IL-12R on T cells can be induced by IL-27 (103). The expression of IL-27R was also detected on human V γ 9V δ 2 cells. As expected, IL-27 enhanced the cytotoxicity of human V γ 9V δ 2 T cells by promoting the production of cytotoxic molecules (**Figure 3**) (104).

In addition to cytokines inducing IFN- γ production in $\gamma\delta$ T cells, IL-17-inducing cytokines are responsible for the polarization of $\gamma\delta$ T17 cells. It is well known that combination of IL-1 β , IL-6, IL-23 and TGF- β induce Th17 differentiation in mouse (105). In human, IL-1 and IL-23 but not TGF- β and IL-6 serve as a rheostat tuning the magnitude of Th17 development (106). The stimulation of IL-1 and IL-23 also promoted ROR γ t, IL-17, IL-21, and IL-22 expression by $\gamma\delta$ T cells without the engagement of T cell receptor in mouse (107, 108). TGF- β was found to play a key role in the generation of murine $\gamma\delta$ T17 in thymus during the postnatal period (109). In adults, IL-1 β , TGF- β and IL-23 are required for the commitment of human V γ 9V δ 2 T cells to IL-17-producing $\gamma\delta$ T cells, which also produce IL-22 (110). The function of IL-6 during the differentiation of $\gamma\delta$ T17 is uncertain. However, the cocktail of cytokines (IL-1 β , TGF- β , IL-6 and IL-23) was used to selectively generate IL-17⁺ V γ 9V δ 2 T cells *in vitro* (111). These expanded IL-17⁺ V γ 9V δ 2 T cells produce IL-17 but neither IL-22 nor IFN- γ . The expressions of granzyme B, TRAIL, FasL and CD161 on IL-17⁺ V γ 9V δ 2 T cells indicated that they contributed to host immune responses against infectious microorganisms. By contrast, TGF- β surprisingly augmented the cytotoxic activity of human V δ 2 T cells when they were stimulated with PAgS and IL-2 or IL-15 in the presence of TGF- β . TGF- β enhanced the migration and anti-tumor function of V δ 2 T cells through upregulating the expressions of CD54, CD103, IFN- γ , IL-9 and granzyme B (112, 113).

In conclusion, $\gamma\delta$ T cells display high functional plasticity depending on the cytokine environment (**Figure 3**). In view of the cytokine-dependent polarization of $\gamma\delta$ T cells, it is crucial to understand the roles of various cytokines regulating $\gamma\delta$ T cell function, which can guide the effective $\gamma\delta$ T cell-based cancer immunotherapy.

CURRENT $\gamma\delta$ T CELL-BASED CANCER IMMUNOTHERAPIES

Currently, the majority of the preclinical and clinical studies on $\gamma\delta$ T cell-based cancer immunotherapy focus on adoptive transfer of expanded $\gamma\delta$ T cells and its combination with other treatments (**Table 2**, **Figure 4**: top left and bottom left). Due to the feasible expansion of human V γ 9V δ 2 T cells using PAgS or aminobisphosphonates, Zol has been used to expand human $\gamma\delta$ T cells for adoptive transfer or directly injected to induce the proliferation of human $\gamma\delta$ T cells *in vivo* for cancer immunotherapy (115, 136).

Due to the successful application of chimeric antigen receptor (CAR) technology in $\alpha\beta$ T cells, it has also been applied in $\gamma\delta$ T cell therapy (**Figure 4**: bottom right). The study of allogeneic CAR-V δ 1 T cells targeting CD20 antigen exhibited strong anti-tumor activity and minimum xenogeneic graft-versus-host diseases (GVHD) post transplantation (137). This result further supports the clinical evaluation of ADI-001, an allogeneic CD20-CAR-V δ 1 T cell-associated clinical trial (NCT04735471). CAR-V δ 2 T cells also showed promising results in clearing tumor *in vivo* (138). Mucin 1 (MUC1) with the Tn epitope is a tumor associated antigen that is highly expressed on the surface of a variety of cancer cells. MUC1-Tn CAR-modified V γ 9V δ 2 T cells exhibited similar or stronger anti-tumor effect against breast cancer cell and gastric cancer cell *in vitro* compared with CAR- $\alpha\beta$ T cells. MUC1-Tn-CAR-V γ 9V δ 2 T cells more effectively suppressed tumor growth than V γ 9V δ 2 T cells in a xenograft murine gastric cancer model (138).

Many recent studies focus on antibody-induced $\gamma\delta$ T cell activation (**Figure 4**: top right). Fab fragment of anti-CD3e antibody UCHT1 could bind to $\gamma\delta$ TCR and enhance the tumor killing of V γ 9V δ 2 T cells (139). Aude De Gassart et al. constructed a humanized antibody, ICT01, that could activate V γ 9V δ 2 T cells (140). This antibody activated $\gamma\delta$ T cells that could kill various tumor cell lines and primary tumor cells but not normal healthy cells. Rajkumar Ganesan et al. designed a bispecific antibody, anti-TRGV9/anti-CD123, that could simultaneously bind to the V γ 9 chain of V γ 9V δ 2 T cells and AML target antigen, CD123, then induce the recruitment and activation of V γ 9V δ 2 T cells to target AML blasts (141). Recently, it is demonstrated that tribody activated $\gamma\delta$ T cells efficiently. Hans H Oberg et al. reported that tribody [(HER2)2 X CD16] is more effective than anti-HER2 monoclonal antibodies in enhancing $\gamma\delta$ T cell killing against HER2-expressing cancer cells (142). Similarly, tribody of (Her2)2X V γ 9 targets human V γ 9 T cells and HER2-expressing tumor cells to induce $\gamma\delta$ T cell-mediated tumor killing (143).

The combination therapy of $\gamma\delta$ T cells with chemotherapy, monoclonal antibody, immune checkpoint blockade or surgery can exert better anti-tumor efficacy than monotherapy (**Figure 4**: bottom left). The combination of $\gamma\delta$ T cells with locoregional therapy enhanced clinical efficacy (134). The study using rituximab combined with obinutuzumab and daratumumab activated $\gamma\delta$ T cells expanded the therapeutic potential of distinctive tumor-antigen-targeting mAbs induced ADCC by $\gamma\delta$ T cells (144). Targeting the costimulatory signals such as CD137 agonist antibody may promote the anti-tumor functions of V γ 9V δ 2 T cells (145). $\gamma\delta$ T cell therapy enhanced chemotherapy-induced cytotoxicity to advanced bladder cancer cells (146). Chemotherapeutic agent temozolomide (TMZ) may promote the anti-tumor efficacy of the adoptively transferred *ex vivo* expanded $\gamma\delta$ T cells for malignant glioblastoma (147). A few studies demonstrated that nanoparticles could also enhance $\gamma\delta$ T cells function. In a recent work, it was found that selenium nanoparticles (SeNPs) pre-treatment strengthened the anti-tumor cytotoxicity of V γ 9V δ 2 T cells by increasing the expression of cytotoxicity related molecules, such as NKG2D, CD16, and IFN- γ (148). Chitosan nanoparticles (CSNPs) also exhibited the role of enhancing anti-

TABLE 2 | Clinical trials of $\gamma\delta$ T cell-based immunotherapy.

Cell types	Cancer type	Phase	Stimulation	Ref
Both V δ 1 and V δ 2 cells	Lymphoma	I	Anti- $\gamma\delta$ T-cell receptor (TCR) antibody combine with IL-2 <i>in vitro</i> expanded	(114)
V γ 9V δ 2	Renal cell carcinoma	I/II	Zoledronate and IL-2 <i>in vivo</i>	(115)
V γ 9V δ 2	Renal cell carcinoma, Colon cancer, Oesophagus carcinoma, Gastric cancer, Ovarian cancer, Breast cancer	I	Bromohydrin pyrophosphate (IPH1101) combine with IL-2 <i>in vivo</i>	(116)
V γ 9V δ 2	Metastatic renal cell carcinoma	I	Bromohydrin pyrophosphate (IPH1101) combine with IL-2 <i>in vivo</i>	(117)
V γ 9V δ 2	Non-Hodgkin lymphoma (NHL) or Multiple myeloma (MM)	Pilot study	IL-2 combine with pamidronate	(84)
V γ 9V δ 2	Renal cell carcinoma	Pilot study	IL-2 <i>in vivo</i>	(118)
V γ 9V δ 2	Breast cancer	II	Neoadjuvant letrozole (LET) plus zoledronic acid	(119)
V γ 9V δ 2	Colorectal cancer	Unknown	Zoledronate and IL-2 <i>in vitro</i> expansion	(120)
V γ 9V δ 2	Myeloma	II	Zoledronate and IL-2 <i>in vivo</i>	(121)
V γ 9V δ 2	Neuroblastoma	I	Zoledronate and IL-2 <i>in vivo</i>	(82)
V γ 9V δ 2	Leukaemia	Pilot study	Zoledronate and IL-2 <i>in vivo</i>	(122)
V γ 9V δ 2	Renal cell carcinoma [RCC], Malignant melanoma, and Acute myeloid leukemia	I/II	Zoledronate and IL-2 <i>in vivo</i>	(123)
V γ 9V δ 2	Renal cell carcinoma	Pilot study	Zoledronate and IL-2 <i>in vivo</i>	(124)
V γ 9V δ 2	Breast cancer	II	zoledronic acid <i>in vivo</i>	(125)
V γ 9V δ 2	Non-small cell lung cancer	I	Zoledronate and IL-2 <i>in vitro</i> expansion	(126)
V γ 9V δ 2	Non-small cell lung cancer	I	Zoledronate and IL-2 <i>in vitro</i> expansion	(127)
V γ 9V δ 2	Breast cancer	I	Zoledronate and IL-2 <i>in vivo</i>	(128)
V γ 9V δ 2	Various solid tumors	Unknown	zoledronic acid <i>in vitro</i>	(129)
V γ 9V δ 2	Breast cancer	Unknown	zoledronic acid <i>in vivo</i>	(130)
V γ 9V δ 3	Multiple myeloma	Pilot study	Zoledronate and IL-2 <i>in vitro</i> expansion	(131)
$\gamma\delta$ T	Pancreatic cancer	I	Combination of gemcitabine (GEM) and autologous $\gamma\delta$ T-cell therapy	(132)
$\gamma\delta$ T	Locally advanced pancreatic cancer	II	Irreversible electroporation plus allogeneic $\gamma\delta$ T cells	(133)
$\gamma\delta$ T	Hepatocellular carcinoma (HCC) and intrahepatic cholangiocarcinoma (ICC).	I/II	Locoregional therapy followed by adoptive transfer of allogeneic $\gamma\delta$ T cells	(134)
$\gamma\delta$ T	Non-muscle invasive bladder cancer	II	Rapamycin and BCG instillations	(135)

tumor immune responses of $\gamma\delta$ T cells (149). Immune checkpoint blockade using anti-PD-1 mAb promoted V γ 9V δ 2 T cell cytotoxicity against PC-2 tumors in immunodeficient NSG mice (150). Furthermore, combination of Tim-3 blocking antibody and bispecific antibody MT110 (anti-CD3 and anti-EpCAM) enhanced the anti-tumor efficacy of the adoptively transferred $\gamma\delta$ T cells (151). However, autologous $\gamma\delta$ T cells combined with gemcitabine therapy for patients with curatively resected pancreatic cancer revealed no significant difference compared with those receiving gemcitabine alone (132), suggesting better understanding of the mechanism of action during different treatment is required to achieved effective combination treatment outcome with $\gamma\delta$ T cells. Cytokine combinations promoting $\gamma\delta$ T cell function revealed in pre-clinical studies are yet to be evaluated in clinical trials.

CHALLENGES AND POTENTIAL STRATEGIES TARGETING CYTOKINE SIGNALS TO IMPROVE $\gamma\delta$ T CELL-BASED IMMUNOTHERAPY

$\gamma\delta$ T cell-based immunotherapy mainly faces three challenges in achieving improved outcomes for cancer patients. The first challenge is the *in vitro* generation/expansion of activated $\gamma\delta$ T cells with superior cytotoxicity. Although adoptive transfer or *in vivo* expanded human V γ 9V δ 2 T cells exhibited good safety profile, it did not achieve clinical benefit in some patients (123). To boost the

cytotoxicity of expanded $\gamma\delta$ T cells and overcome the immune suppressive tumor microenvironment, cytokine stimulated allogeneic V γ 9V δ 2 cells or V δ 1 cells have been used for clinical trials. A recent study on 132 late-stage cancer patients confirmed the safety and efficacy of IL-15 and VC activated allogeneic V γ 9V δ 2 T cells (89). The addition of IL-15 resulted in the activation, proliferation and increased cytotoxic capacity of $\gamma\delta$ T cells (152). To activate cytokine signals, expanded V δ 1 T cells were engineered with a GPC-3 CAR and secreted IL-15 (sIL-15) which significantly controlled tumor growth without inducing GVHD. Moreover, GPC-3-CAR/sIL-15 V δ 1 T cells displayed greater proliferation and stronger anti-tumor responses when compared with GPC-3-CAR V δ 1 T cells lacking sIL-15, suggesting IL-15 signal was critical for CAR V δ 1 T cell function (153). The adoptive transfer of IL-7-expanded human V δ 1 cells also displayed improved cytotoxicity and prolonged the survival of human colon carcinoma xenografted mice (73).

Secondly, rapid exhaustion is a big challenge for maintaining survival and durable anti-tumor functions of $\gamma\delta$ T cells. Persistent stimulation of human $\gamma\delta$ T cells with PAgS often induces $\gamma\delta$ T cell exhaustion (154). It was demonstrated that CD137 costimulation promoted the proliferation and prolonged the survival of V γ 9V δ 2 T cells *in vitro* and *in vivo* (145). Moreover, Endogenous IL-15 acted as a potential factor to support the survival of human V γ 9V δ 2 T cells *in vivo* in the absence of exogenous IL-2 (120). The dysfunction of T cells is also associated with the immunosuppressive tumor microenvironment which will be discussed in the following session.

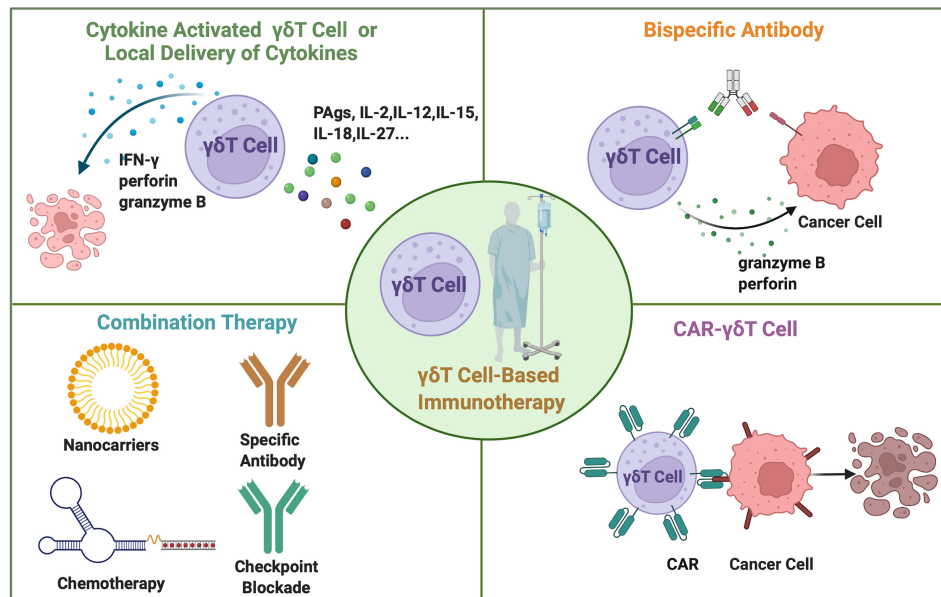


FIGURE 4 | The current approaches for $\gamma\delta$ T cell-based cancer immunotherapy. The adoptive transfer of cytokine-activated $\gamma\delta$ T cells *in vitro* or locally administration of cytokines *in vivo*. Combination therapy includes $\gamma\delta$ T cell transfer combined with specific antibody therapy, immune checkpoint blockade, chemotherapy, and nanoparticles. Bispecific antibodies simultaneously bind to $\gamma\delta$ T cells and cancer cells. Gene modified CAR- $\gamma\delta$ T cells directly recognize the cancer cells and mediate cancer cell lysis.

The third challenge is the immunosuppression mechanisms in cancer patients that can impair the anti-tumor functions of the infused/activated $\gamma\delta$ T cells. The lack of IL-2 and IL-21 in HCC patients was associated with the PD-1 expression and reduced cytotoxicity of human $\gamma\delta$ T cells (93). In a murine HCC model, IL-23 overexpression in the liver induced the polarization of $\gamma\delta$ T cells to IL-17-producing $\gamma\delta$ T cells (155). Then $\gamma\delta$ T17 cells promoted tumor growth *via* recruiting immunosuppressive myeloid-derived suppressor cells (MDSCs). TGF- β is a pivotal immunosuppressive cytokine that secreted by immunosuppressive cell subsets (such as MDSCs and Treg) and tumor cells (156). Mouse Foxp3⁺ $\gamma\delta$ T cells can be induced by TGF- β and inhibit T cell activation (157). To avoid $\gamma\delta$ T cell exhaustion and circumvent tumour immunosuppressive microenvironment, it is a feasible approach to target cytokine signals *via* administering exogenous stimulating cytokines or blocking the immunosuppressive cytokines. As systemic administration of cytokines usually induces toxicity in patients (158, 159), local delivery of cytokine can limit the systemic toxicity and offer an approach to benefit from the therapeutic effects of the activating cytokines. The local delivery of mRNAs encoding interleukin-12 (IL-12) single chain, interferon- α , granulocyte-macrophage colony-stimulating factor, or IL-15 sushi led to robust anti-tumor immune responses and tumor regression in multiple murine models (160). These findings provided preclinical evidence for modifying the tumor microenvironment *via* local administration of cytokines. It is possible to induce highly cytotoxic $\gamma\delta$ T cells through modulations of tumor microenvironment through the induction or delivery of cytokines that can specially promote the anti-tumor functions of $\gamma\delta$ T cells (Figure 4: top left).

CONCLUSION AND FUTURE DIRECTIONS

Taken together, $\gamma\delta$ T cells are promising cellular products for adoptive cancer immunotherapy. $\gamma\delta$ T cells mediate anti-tumor effects by direct killing and indirect immune regulatory function to other immune cells. $\gamma\delta$ TCR can recognize specific molecules often in an antigen-independent manner. $\gamma\delta$ T cells can differentiate into various subsets producing signature cytokines, which can have anti-tumor or pro-tumor functions. In the meantime, this differentiation is greatly influenced by the cytokines present in the microenvironment. $\gamma\delta$ T cell-based cancer immunotherapy has a good safety profile in the clinical trials but its clinical efficacy needs further improvement. Combination therapies involving $\gamma\delta$ T cells have had some clinical successes, including chemotherapy, CAR therapy, and checkpoint blockade therapy. IL-2 and IL-15 have been explored for their functions to activate $\gamma\delta$ T cells in clinical trials. However, other cytokines and combinations that can activate $\gamma\delta$ T cells are yet to be evaluated in clinical trials. First, cytokines or cytokine combinations can be used to expand, activate, and polarize $\gamma\delta$ T cells *ex vivo* to generate potent cellular products for adoptive therapy. Cytokine signals can also be modulated to prolong the survival of the transferred $\gamma\delta$ T cells *in vivo*. Second, cytokine can be incorporated into CAR $\gamma\delta$ T cell therapy to facilitate CAR $\gamma\delta$ T cell function and prolong their survival *in vivo via* autocrine mechanism, which can avoid the toxicity induced by systemic cytokine treatment. Third, cytokine signal on $\gamma\delta$ T cells can be triggered *via* antibody binding in the form of bi-specific or tri-specific antibody targeting tumor antigens. The additional cytokine signal can facilitate $\gamma\delta$ T cell function and survival. Thus, detailed understanding of the effects of cytokines and cytokine combinations

on $\gamma\delta$ T cell anti-tumor function is critical for designing effective therapeutic strategies to incorporate cytokine signals into various $\gamma\delta$ T cell-based cancer immunotherapy to achieve superior clinical efficacy.

AUTHOR CONTRIBUTIONS

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

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Gamma Delta T-Cell Based Cancer Immunotherapy: Past-Present-Future

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$\gamma\delta$ T-cells directly recognize and kill transformed cells independently of HLA-antigen presentation, which makes them a highly promising effector cell compartment for cancer immunotherapy. Novel $\gamma\delta$ T-cell-based immunotherapies, primarily focusing on the two major $\gamma\delta$ T-cell subtypes that infiltrate tumors (*i.e.* V δ 1 and V δ 2), are being developed. The V δ 1 T-cell subset is enriched in tissues and contains both effector T-cells as well as regulatory T-cells with tumor-promoting potential. V δ 2 T-cells, in contrast, are enriched in circulation and consist of a large, relatively homogeneous, pro-inflammatory effector T-cell subset. Healthy individuals typically harbor in the order of 50-500 million V γ 9V δ 2 T-cells in the peripheral blood alone (1-10% of the total CD3⁺ T-cell population), which can rapidly expand upon stimulation. The V γ 9V δ 2 T-cell receptor senses intracellular phosphorylated metabolites, which accumulate in cancer cells as a result of mevalonate pathway dysregulation or upon pharmaceutical intervention. Early clinical studies investigating the therapeutic potential of V γ 9V δ 2 T-cells were based on either *ex vivo* expansion and adoptive transfer or their systemic activation with aminobisphosphonates or synthetic phosphoantigens, either alone or combined with low dose IL-2. Immune-related adverse events (irAE) were generally mild, but the clinical efficacy of these approaches provided overall limited benefit. In recent years, critical advances have renewed the excitement for the potential of V γ 9V δ 2 T-cells in cancer immunotherapy. Here, we review $\gamma\delta$ T-cell-based therapeutic strategies and discuss the prospects of those currently evaluated in clinical studies in cancer patients as well as future therapies that might arise from current promising pre-clinical results.

Keywords: gamma delta T-cell, cancer, immunotherapy, phosphoantigens, aminobisphosphonates, adoptive cell transfer, bispecific t-cell engager, chimeric antigen receptor

INTRODUCTION

In humans, $\gamma\delta$ T-cells represent 1 to 10% of total CD3⁺ T-cells (1, 2), and express a combination of either of 7 different V γ TCR chains (V γ 2, 3, 4, 5, 8, 9, and 11), paired with either of 4 V δ (V δ 1, 2, 3, and 5) chains (2–4). $\gamma\delta$ T-cells are considered to bridge the innate and adaptive immune systems (3). Activated $\gamma\delta$ T-cells display strong cytotoxic activity through the release of granzyme B and perforin, by membrane bound TRAIL and Fas (CD95) ligands or production of IFN γ or TNF α to

amplify the immune response (12), thereby counteracting tumor development. Using $\gamma\delta$ T-cell-deficient mice in a cutaneous carcinogenesis model, $\gamma\delta$ T-cells were first shown to prevent malignancy formation (5). High $\gamma\delta$ T-cell frequency in tumor infiltrates from cancer patients correlates with better clinical outcome in different malignancies (6–10) and $\gamma\delta$ T-cells were identified as the prognostically most favorable immune cell subset in tumor infiltrates from 18,000 tumors across 39

malignancies (11). A more recent study confirmed the relative abundance of V γ 9V δ 2 T-cells in TILs and their association with improved patient outcome (12). These results highlight the relevance of $\gamma\delta$ T-cells in tumor control and their potential for cancer therapy. $\gamma\delta$ T-cells express several receptors shared with natural killer (NK) cells that participate in enhanced tumor cell recognition of which Fc γ RIIIa (CD16a), DNAM-1, and NKG2D are a few examples (13) (**Figure 1A**).

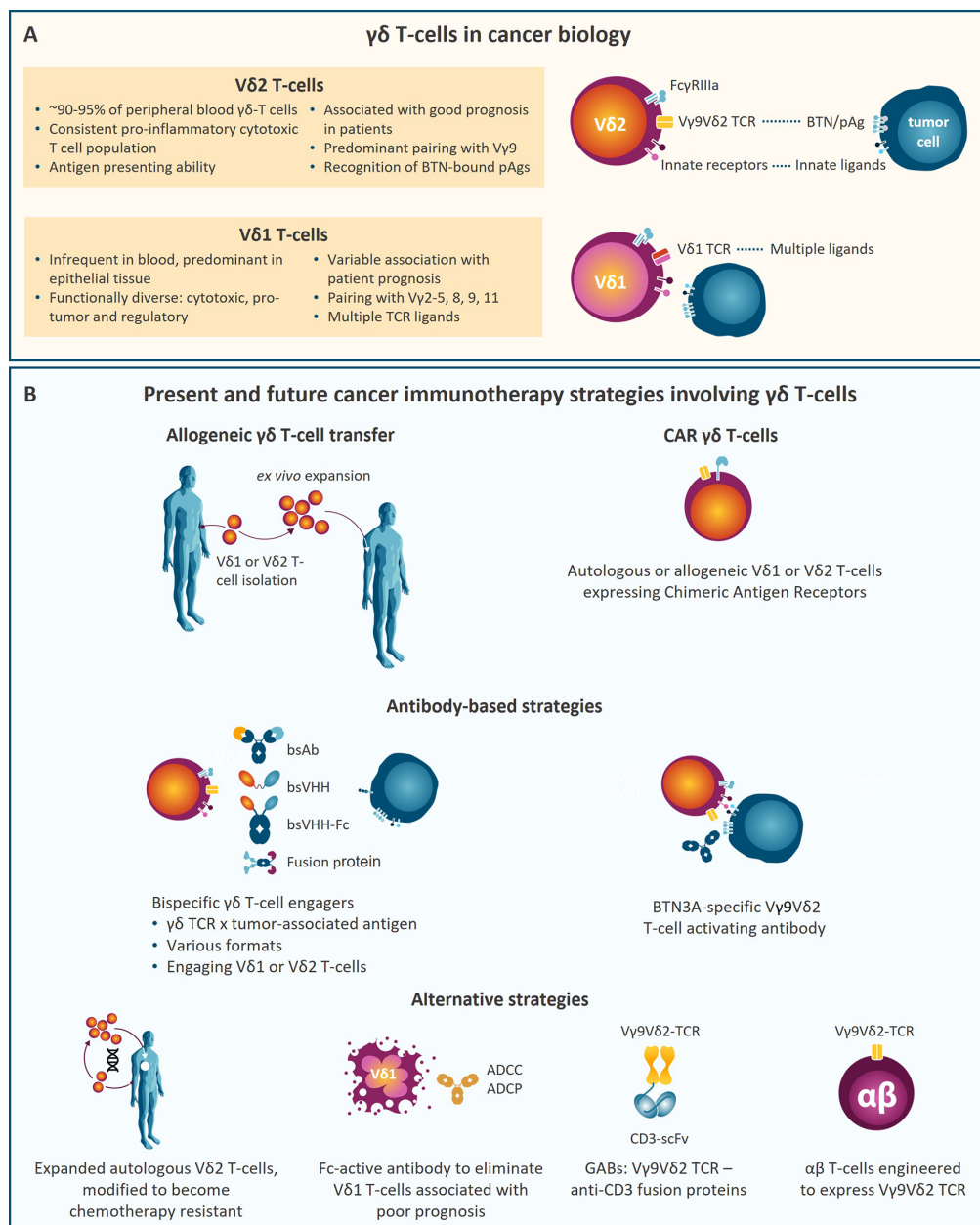


FIGURE 1 | (A) Key characteristics of the two main $\gamma\delta$ T-cell subsets, V δ 2 and V δ 1 T-cells, in cancer biology. **(B)** Schematic representation of therapeutic strategies involving $\gamma\delta$ T-cells that are currently being developed. ADCC, Antibody-dependent cellular cytotoxicity; ADCP, antibody-dependent cellular phagocytosis; bsAb, bispecific antibody; bsVHH, bispecific variable domain of heavy-chain only antibody; BTN, Butyrophilin; CAR, chimeric antigen receptor; pAg, phosphoantigen; scFv, single-chain variable fragment.

The complete repertoire of antigens recognized by $\gamma\delta$ -TCRs and the specificity of each $\gamma\delta$ T subset is still not fully understood. V γ 9V δ 2 T-cells represent the predominant $\gamma\delta$ T-cell subset (95%) in peripheral blood (14). V γ 9V δ 2 T-cells participate in the defense against malignant cells by sensing small phosphorylated metabolites (phosphoantigen (pAg) molecules) produced in cholesterol synthesis [isopentenyl pyrophosphate (IPP)] or by pathogens [e.g. (E)-4-hydroxy-3-methyl-but-2-enyl-pyrophosphate (HMBPP)] (5, 15–19). Unlike conventional $\alpha\beta$ T-cells, ligand recognition by V γ 9V δ 2 and most $\gamma\delta$ T-cells does not involve antigen presentation by human leukocyte antigen (HLA) molecules (15, 20). Ligand recognition by V γ 9V δ 2 T-cells requires butyrophilin (BTN) 3A1 (21) and BTN2A1 (22–24). Intracellular pAg levels are increased under stress conditions like infection or malignant transformation or by aminobisphosphonates (ABP) (16, 17, 25–27). V γ 9V δ 2 T-cells sense increased intracellular pAg levels causing their activation and target cell killing. Recent studies show that pAg-bound BTN3A1 associates with BTN2A1 which directly interacts with non-variable regions of the V γ 9 chain on $\gamma\delta$ T-cells. Besides V γ 9V δ 2 T-cell recognition of pAgs, some subsets of V δ 1 and V δ 3 T-cells detect pathogenic and self-lipids presented by CD1d through their TCR (28, 29). V δ 1 T-cells are less abundant in circulation than V γ 9V δ 2 T-cells, but they are enriched in epithelia (30) and among tumor infiltrating lymphocytes (TILs). While cultured V δ 1 T-cells may have higher cytotoxic capacity than V γ 9V δ 2 T-cells, V δ 1 T-cells can be pro-tumoral in certain malignancies (6, 31, 32) (**Figure 1A**).

In this review we discuss $\gamma\delta$ T-cell-based therapeutic strategies with a focus on recent developments of bispecific $\gamma\delta$ T-cell engagers (bsTCEs) and chimeric antigen receptor (CAR) $\gamma\delta$ T-cells, and point towards approaches that may develop into therapies in the near future (**Figure 1B**).

PAST CLINICAL STUDIES WITH V γ 9V δ 2 T-CELLS

In the year 2000, ABP drugs, already approved to treat patients with excessive bone resorption, were shown to cause systemic V γ 9V δ 2 T-cell stimulation and to increase their antitumor activity in a preclinical study (26). Following this observation, studies explored ABP treatment as a systemic $\gamma\delta$ T-cell stimulant or as an *ex vivo* tool to expand them for subsequent adoptive cell transfer (ACT) for cancer immunotherapy.

The ABPs pamidronate (PAM) and zoledronate (ZOL), and synthetic pAg analogues, mainly bromohydrin pyrophosphate (BrHPP) and 2-methyl-3-butenyl-1-pyrophosphate (2M3B1PP), have been used alone or in combination with IL-2 to activate V γ 9V δ 2 T-cells (33, 34). ABP treatment has been evaluated in cancer patients (e.g. with multiple myeloma (MM), non-Hodgkin lymphoma (NHL), acute myeloid leukemia (AML), prostate cancer, renal cell carcinoma, colorectal cancer, breast cancer, melanoma or neuroblastoma) (33, 35–39). Additionally, *ex vivo* expansion of autologous $\gamma\delta$ T-cells with ABPs or synthetic pAg followed by ACT has been tested in a wide range of malignancies (e.g. in MM, renal cell carcinoma, non-small cell lung cancer, gastric cancer, hepatocellular carcinoma,

melanoma, ovarian cancer, colon cancer and pancreatic cancer) (40–51). While these approaches were well tolerated, clinical responses typically were found to be infrequent and not long-lasting, though sporadic meaningful responses were achieved (52–54). The overall moderate clinical antitumor effect of systemic $\gamma\delta$ T-cell activation with ABP or synthetic pAg and of autologous $\gamma\delta$ T transfer, negatively impacted further development of these V γ 9V δ 2 T-cell-directed cancer immunotherapeutic approaches.

PRESENT AND FUTURE STUDIES INVOLVING $\gamma\delta$ T-CELLS

$\gamma\delta$ T-Cell-Based Cellular Strategies Allogeneic $\gamma\delta$ T-Cell Transfer

As mentioned above, most $\gamma\delta$ T-cells recognize target cells independently of HLA antigen presentation, suggesting that allogeneic donor derived $\gamma\delta$ T-cells can be relatively safe for ACT due to low risk of graft-versus-host disease (GvHD). Taking advantage of this, current strategies exploring the use of *ex vivo* expanded $\gamma\delta$ T-cell infusion have shifted towards allogeneic origin (**Table 1**). Increased frequency of $\gamma\delta$ T-cells in leukemia patients that underwent $\alpha\beta$ -depleted allogeneic stem cell transplantation from partially HLA-mismatched donors, was associated with a higher 5-year and overall survival (OS) (55, 56). A single infusion of allogeneic V γ 9V δ 2 T-cells, expanded *ex vivo* with ZOL plus IL-2, is being administered in a clinical trial (NCT03533816) to maximize antitumor response and reduce GvHD, after allogeneic hematopoietic cell transplant (alloHCT) and cyclophosphamide for hematologic malignancies. Moreover, allogeneic V γ 9V δ 2 T-cell infusion after lymphodepletion is being tested independently of alloHCT for hematologic malignancies and solid tumors. Some of these studies have already been completed with no major adverse effects reported, highlighting the safety of V γ 9V δ 2 T-cell transfer (57, 58). Importantly, patients receiving V γ 9V δ 2 T-cell infusion had increased OS compared to control patients and repeated V γ 9V δ 2 T-cell infusions resulted in higher OS when compared to single infusion. Future approaches are based on allogeneic $\gamma\delta$ T-cells derived from healthy donors, either unmodified or CAR-transfected (see below) (**Table 2**).

Application of non-V γ 9V δ 2 T-cell subsets, like V δ 1 T-cells, is of interest but lagged behind because of lack of proper expansion protocols. In 2016, Almeida *et al.* described a 3 week culture protocol based on stimulation of $\gamma\delta$ T-cells from healthy donors or CLL patients with a combination of cytokines and anti-CD3 monoclonal antibody (mAb) clone OKT-3, resulting in 2000-fold expansion and 60–80% enrichment of V δ 1 T-cells (59). Expanded cells expressed the NK receptors NKp30 and NKp40, displayed cytotoxic activity, produced IFN γ , TNF α and no IL-17. Application of this protocol led to the development of different “delta one T” (DOT) cell products. Gamma Delta Therapeutics initiated a first-in-human phase I clinical trial in AML patients after lymphodepletion with fludarabine and cyclophosphamide (NCT05001451) (**Table 1**). This study will analyse safety and

TABLE 1 | Ongoing clinical trials based on $\gamma\delta$ T-cells.

Title	Intervention	Malignancy	Organization	Phase	Initial Date	Status	Study Identifier
Allogeneic $\gamma\delta$ T-cell transfer							
TCR $\alpha\beta$ -depleted Progenitor Cell Graft With Additional Memory T-cell DLI, Plus Selected Use of Blinatumomab, in Naive T-cell Depleted Haploidentical Donor Hematopoietic Cell Transplantation for Hematologic Malignancies	HPC-A Infusion (TCR α/β^+ and CD19+ depleted)	ALL, AML, MDS, NK-CL, HL, NHL, JMML, CML	St. Jude Children's Research Hospital	II	January 31, 2019	Recruiting	NCT03849651
Ex-vivo Expanded $\gamma\delta$ T Lymphocytes in Patients With Refractory/Relapsed Acute Myeloid Leukaemia	Ex-vivo expanded allogeneic $\gamma\delta$ T-cells from blood of related donors	AML	Wuhan Union Hospital and Jinan University, China	I	September 1, 2019	Recruiting	NCT04008381
Expanded/Activated Gamma Delta T-cell Infusion Following Hematopoietic Stem Cell Transplantation and Post-transplant Cyclophosphamide	EAGD T-cell infusion	AML, CML, ALL, MDS	University of Kansas Medical Center and In8bio Inc.	I	January 31, 2020	Recruiting	NCT03533816
Allogeneic "Gammadelta T Cells ($\gamma\delta$ T Cells)" Cell Immunotherapy in Phase 1 Hepatocellular Carcinoma Clinical Trial	Ex-vivo expanded allogeneic $\gamma\delta$ -T cells from related donors	HCC	Beijing 302 Hospital	I	August 15, 2020	Recruiting	NCT04518774
Gamma Delta T-cell Infusion for AML at High Risk of Relapse After Allo HCT	AlloHCT + AAPC-expanded donor T-cells	AML	H. Lee Moffitt Cancer Center and Research Institute	I/Ib	August 13, 2021	Recruiting	NCT05015426
Study of GDX012 in Patients With MRD Positive AML	GDX012. Allogeneic cell therapy enriched for V δ 1+	AML	GammaDelta Therapeutics Limited	I	August 13, 2021	Recruiting	NCT05001451
Allogeneic $\gamma\delta$ T Cells Immunotherapy in r/r Non-Hodgkin's Lymphoma (NHL) or Peripheral T Cell Lymphomas (PTCL) Patients	Ex-vivo expanded allogeneic $\gamma\delta$ T-cells from related donors	NHL, PTCL	Institute of Hematology & Blood Diseases Hospital	I	January 6, 2021	Recruiting	NCT04696705
Safety and Efficiency of $\gamma\delta$ T Cell Against Hematological Malignancies After Allo-HSCT	Ex-vivo expanded $\gamma\delta$ T-cell infusion	AML, ALL, MDS	Chinese PLA General Hospital	I/II	September 2021	Recruiting	NCT04764513
$\gamma\delta$ CAR-T-cells							
Immunotherapy With CD19 CAR $\gamma\delta$ T-cells for B-Cell Lymphoma, ALL and CLL	Allogeneic $\gamma\delta$ CAR-T-cells (anti-CD19)	RR ALL, CLL, B-NHL	Beijing Doing Biomedical Co., Ltd.	I	October 2017	Active, not recruiting	NCT02656147
Haplo/Allogeneic NKG2DL-targeting Chimeric Antigen Receptor-grafted $\gamma\delta$ T Cells for Relapsed or Refractory Solid Tumour	Haploidentical or allogeneic V δ 2 CAR-T-cells (anti-NKG2DL) (CTM-N2D)	RR solid tumors of different types	CytoMed Therapeutics Pte Ltd.	I	December 1, 2019	Active, not recruiting	NCT04107142
A Study of ADI-001 in B Cell Malignancies (GLEAN-1)	Lymphodepletion + ADI-001 (Anti-CD20 $\gamma\delta$ CAR-T-cells) in monotherapy and combined with IL-2	B-NHL	Adicet Bio, Inc	I	March 4, 2021	Recruiting	NCT04735471
Antibody-based strategies							
First-in-Human Study of ICT01 in Patients With Advanced Cancer (EVICTION)	ICT01. monoclonal antibody targeting BTN3A	Solid Tumor, Adult Hematopoietic/Lymphoid Cancer	ImCheck Therapeutics	I/II	February 10, 2020	Recruiting	NCT04243499
Trial With LAVA-051 in Patients With Relapsed/Refractory CD1d (Cluster of Differentiation (CD)1d)-Positive CLL, MM, AML	LAVA-051. Bispecific $\gamma\delta$ T-cell engager	CLL, AML, MM	Lava Therapeutics	I/II	July 12, 2021	Recruiting	NCT04887259
Trial of LAVA-1207 in Patients With Therapy Refractory Metastatic Castration Resistant Prostate Cancer	LAVA-1207. Bispecific $\gamma\delta$ T-cell engager	Prostate Cancer	Lava Therapeutics	I/IIa	January 31, 2022	Recruiting	NCT05369000

(Continued)

TABLE 1 | Continued

Title	Intervention	Malignancy	Organization	Phase	Initial Date	Status	Study Identifier
Alternative γδ T-cell-related strategies							
Safety of TEG001 in patients with r/r AML, high-risk MDS or MM	TEG001	RR AML, high-risk MDS, MM	Gadeta B.V.	I	June 01, 2017	Recruiting	NTR6541
Novel Gamma-Delta (γδ) T Cell Therapy for Treatment of Patients With Newly Diagnosed Glioblastoma	DRI γδ T-cells modified to be resistant to TMZ + TMZ	Glioblastoma multiforme	University of Alabama at Birmingham and IN8Bio Inc.	I	February 11, 2020	Recruiting	NCT04165941
A Study to Investigate the Safety and Efficacy of TEG002 in Relapsed/Refractory Multiple Myeloma Patients	TEG002	RR MM	Gadeta B.V.	I	May 13, 2021	Recruiting	NCT04688853

AAPC, Artificial antigen presenting cell; ALL, acute lymphocytic leukemia; AlloHCT, Allogeneic hematopoietic cell transplantation; AML, Acute myeloid leukemia; B-NHL, B cell Non-Hodgkin lymphoma; CAR, Chimeric antigen receptor; CLL, Chronic lymphocytic leukemia; CML, Chronic myeloid leukaemia; DLI, Donor lymphocyte infusion; DRI, Drug resistant immunotherapy; EAGDT, Expanded/Activated γδ T-cell; HCC, Hepatocellular carcinoma; HL, Hodgkin lymphoma; HPC-A, Hematopoietic progenitor cells apheresis; HSCT, haematopoietic stem cell transplantation; JMML, Juvenile myelomonocytic leukemia; MM, Multiple myeloma; MDS, Myelodysplastic syndrome; NHL, Non-Hodgkin lymphoma; NKCL, Natural killer cell leukemia; PBMC, peripheral blood mononuclear cell; PTCL, peripheral T cell lymphoma. RR, Relapsed/Refractory; TMZ, temozolomide. Initial date, Date of first patient enrolment.

maximum tolerated dose of GDX012 and its effect on minimal residual disease, progression free survival (PFS) and OS.

Chimeric Antigen Receptor γδ T-Cells

Another therapeutic approach to harness the potent anti-tumor effects of γδ T-cells consists of adoptive transfer of γδ CAR-T-cells (60). CARs are chimeric antigen-recognition receptors, consisting of an ectodomain, which binds a tumor specific cell surface receptor, and endodomains, consisting of CD3ζ as the

signaling domain with co-stimulatory domains to provide robust activation (e.g. CD28, 4-1BB, or ICOS) (61). In recent years, CAR-T-cell therapy has been extensively investigated in preclinical and clinical studies, primarily focused on conventional αβ T-cells (62–64). These autologous CAR-T-cells have triggered encouraging remission rates in patients refractory to standard treatments against, in particular, B-lymphoid malignancies. This resulted in FDA approvals of CAR-T-cell therapies for the treatment of B-cell NHL, ALL,

TABLE 2 | Companies developing γδ T-cell-based or γδ T-cell-engaging therapies.

Organization	γδ T-cell subtype	Approach
γδ T-cell-based therapy		
Acepodia	information not available	Allogeneic mAb-conjugated γδ-cells
Adicet Bio	Vδ1	Allogeneic γδ CAR-T-cells
Expression Therapeutics	Vδ2	Allogeneic γδ CAR-T-cells
GammaDelta Therapeutics (acquired by Takeda)	Vδ1	Allogeneic unmodified or engineered Vδ1 ⁺ T-cells
Immatics	information not available	Allogeneic γδ CAR-T-cells
IN8bio (previously Incysus Therapeutics)	Vδ2	Expanded γδ T-cells engineered to achieve drug resistant immunotherapy (DRI)
Kiomic BioPharma	information not available	Allogeneic γδ CAR-T-cells genetically engineered using ABBIE non-viral gene editing technology
PersonGen BioTherapeutics	information not available	Allogeneic universal CAR (UCAR) based γδ-cells
TC BioPharm	Vδ1/Vδ2	Allogeneic unmodified γδ-cells or engineered γδ CAR-T-cells
One Chain Immunotherapeutics	Vδ1	Expanded allogeneic Vδ1 ⁺ T-cells for ACT
Beroni group	information not available	Allogeneic γδ ACT
γδ T-cell-based antibody therapy		
Organization	γδ T-cell subtype	Approach
Adaptate Biotherapeutics (acquired by Takeda)	Vδ1	Vδ1 bispecific T-cell engagers
ImCheck Therapeutics	Vδ2	mAbs targeting BTN isoforms to modulate γδ T-cell activation
LAVA Therapeutics	Vδ2	Vδ2 bispecific T-cell engagers
PureTech Health	Vδ1	mAb against Vδ1 to induce pro-tumoral Vδ1 T-cell killing
Shattuck Labs	Vδ2	Recombinant proteins containing heterodimeric BTN extracellular domains and a tumor targeting scFv
Other γδ T-cell-based therapies		
Organization	γδ T-cell subtype	Approach
American Gene Technologies	Vδ2	Lentivirus to increase pAg levels in tumor cells

ACT, Adoptive cell transfer; bsTCE, bispecific T cell engager; bsVHH, bispecific Variable Heavy chain-only antibody; BTN, Butyrophilin; CAR, Chimeric antigen receptor; mAb, monoclonal antibody; pAg, phosphoantigen; scFv, Single chain variable fragment.

and MM (65–69). The remarkable success of CAR-T-cell therapy revolutionized the field of adoptive cell therapy for treating hematologic malignancies and resulted in numerous ongoing clinical trials. However, CAR-T-cell therapy can be complicated by severe, potentially life-threatening, toxicities such as cytokine release syndrome (CRS), immune effector cell-associated neurotoxicity syndrome (ICANS) and other ‘on-target off-tumor’ toxicities (70). Moreover, in contrast to the results seen in hematologic malignancies, only limited antitumor effects have been obtained in patients with solid tumors.

It was hypothesized that the efficacy of CAR-T-cells could be improved and its side effects mitigated by harnessing the innate properties of $\gamma\delta$ T-cells as a backbone for CAR. CAR-modified $\gamma\delta$ T-cells were first described by Rischer *et al.* (71), demonstrating specific *in vitro* tumor cell lysis using ZOL-expanded V γ 9V δ 2 T-cells with CD19- or GD2-directed CARs, followed by other studies confirming these findings using $\gamma\delta$ T-cells containing CARs against a variety of targets (72–77). Interestingly, CAR-modified V γ 9V δ 2 T-cells maintained their ability to cross-present tumor antigens to $\alpha\beta$ T-cells *in vitro*, which may prolong the anti-tumor efficacy (76). Furthermore, $\gamma\delta$ T-cells bearing a CD19-CAR, unlike standard CD19- $\alpha\beta$ CAR-T-cells, had reactivity against CD19-positive and negative tumor cells *in vitro* and *in vivo*, an effect that was enhanced by ZOL (78), suggesting that CD19-directed $\gamma\delta$ CAR-T-cells may target leukemic cells also after antigen loss and retain pAg specificity *via* their TCR. More recently, Wallet *et al.* described the generation of induced pluripotent stem cell-derived $\gamma\delta$ CAR-T-cells ($\gamma\delta$ CAR-iT) (79). They demonstrated sustained *in vitro* tumor cell killing by $\gamma\delta$ CAR-iT-cells in the presence of IL-15, with markedly less IFN- γ and other inflammatory cytokines being produced compared to conventional $\alpha\beta$ CAR-T-cells, potentially resulting in lower risk of CRS. Moreover, a single dose of $\gamma\delta$ CAR-iT-cells resulted in potent tumor growth inhibition in a xenograft mouse model (79). **Table 2** summarizes the companies currently developing $\gamma\delta$ CAR-T-cells.

Pre-clinical research on $\gamma\delta$ CAR-T-cell based therapy initially focused on V γ 9V δ 2 T-cells, due to their dominant frequency in blood and their unique pAg response that allowed the specific expansion of this subset (80). Makkouk *et al.* recently showed the first example of genetically modified V δ 1 T-cells. They expanded PBMC-derived V δ 1 T-cells using an agonistic anti-V δ 1 antibody and genetically modified them to express a GPC-3 targeted CAR and to secrete IL-15 (81). In a HepG2 mouse model, these allogeneic V δ 1 CAR-T-cells primarily accumulated in the tumor and a single dose efficiently controlled tumor growth without evidence of xenogeneic GvHD. ADI-001 consists of CD20-targeting V δ 1 CAR-T-cells generated by a similar procedure by Adicet Bio (82) and is currently being used in a phase I clinical trial (NCT04735471). Recently reported interim data from this dose-escalation study showed complete responses in two and a partial response in one out of four evaluable patients already with low doses (30×10^6 cells) of ADI-001, indicating that relatively low amounts of $\gamma\delta$ T-cells may suffice for activity (press release). To date, no dose-limiting toxicities, GvHD, or grade 3 or higher CRS has been reported. These encouraging first results

underscore the potential of V δ 1 CAR-T-cell therapy in the clinic. A complete overview of the ongoing clinical trials evaluating CAR-modified $\gamma\delta$ T-cells is listed in **Table 1**.

Antibody-Based Strategies

Imcheck develops ICT01, a V γ 9V δ 2 T-cell activating humanized IgG1 with a silent Fc that binds to all three BTN3A isoforms to trigger V γ 9V δ 2 T-cell activation and increased cytotoxicity against BTN3A⁺ tumor cell lines from diverse origin (21). However, this approach is not tumor specific as BTN3A is broadly expressed and could also be hampered by soluble BTN3A molecules potentially acting as decoy receptors (83). In immunodeficient NSG mice, treatment with ICT01 resulted in *in vivo* activation of adoptively transferred human V γ 9V δ 2 T-cells and delayed outgrowth of the AML cell line MOLM14 (84). The EVICTION trial is a Phase I/IIa clinical trial currently testing the effect of ICT01 in relapsed/refractory advanced-stage hematologic malignancies as a monotherapy and in a broad range of solid tumors as monotherapy or in combination with pembrolizumab (NCT04243499). Preliminary results show a good safety profile with activation of V γ 9V δ 2 T-cells and increased tumor infiltration in one melanoma patient. Stable disease has been achieved in 31% of patients treated with ICT01 as a monotherapy and in 62% in combination with pembrolizumab (84).

BsTCEs have emerged as a promising therapeutic approach for immune-oncology (85) and consist of a tumor antigen binding antibody linked to a T-cell engaging antibody fragment aiming to crosslink tumor cells and T-cells to elicit T-cell-mediated anti-tumor cytotoxicity (86, 87). Most efforts to generate bsTCEs have made use of CD3 as a T-cell engaging domain due to its role in T-cell activation. For CD3-based TCEs, proteins that are uniquely expressed or specifically overexpressed by tumor cells are the most attractive candidates for targeting, as this reduces on-target off-tumor toxicity. After approval of the CD19-CD3 bsTCE blinatumomab (88), multiple CD3-directed TCEs have been developed (89), but in many cases development has been complicated by the occurrence of adverse events such as on-target off-tumor toxicity, CRS or ICANS, highlighting the need for more tumor-selective targeting (90–92). Considering the clinical safety observed following systemic $\gamma\delta$ T-cell activation and $\gamma\delta$ T ACT, specific engagement of $\gamma\delta$ T-cells using $\gamma\delta$ bsTCEs might have an improved safety profile due to their tumor selectivity compared to CD3-bsTCEs. By avoiding detrimental co-activation of regulatory CD3⁺ T-cells observed with CD3 pan T-cell engagers (93) and their ability to bridge and engage components of both the innate and adaptive immune system, $\gamma\delta$ bsTCEs could potentially result in increased antitumor activity.

Several $\gamma\delta$ T-cell engaging formats are being developed and evaluated preclinically. V γ 9-TCR specific engagers directed against Her2 (94–96) and CD123 (97) were shown to cause killing of Her2 expressing cell lines and AML cell lines, respectively. The GADLEN platform (Shattuck Labs) consists of fusion proteins containing BTN heterodimers, to engage and activate V γ 9V δ 2 T-cells, bound to a tumor targeting scFv

domain through an Fc linker (98). V δ 1 bsTCEs are also being developed by Adaptate Biotherapeutics. Heavy chain only antibodies occur naturally in camelids (99). Their antigen-binding fragments or variable heavy chain-only antibodies (VHH), are small, stable and with low inherent immunogenicity (100, 101). Lava Therapeutics' Gammabody™ platform combines V δ 2-specific and tumor-targeting VHHs as modules to generate bsTCE (102–105). In pre-clinical studies, Gammabody™ molecules targeting CD40, CD1d and EGFR efficiently engage V γ 9V δ 2 T-cells to kill tumor cells expressing these antigens (102–105). Two Gammabody™ molecules, are currently evaluated in clinical trials. LAVA-051, a Gammabody™ targeting CD1d is tested in a Phase I/IIa clinical trial (NCT04887259) in patients with therapy-refractory CLL, AML or MM. Preliminary data of the first 3 cohorts from this study showed a thus far good safety profile with no dose-limiting toxicities or CRS. In addition, LAVA-1207, a Gammabody™ targeting PSMA is tested in a phase I/IIa clinical trial (NCT05369000) in patients suffering from therapy-refractory metastatic castration-resistant prostate cancer. **Table 2** summarizes companies developing antibody-based $\gamma\delta$ T-cell therapies, and **Table 1** contains clinical trials involving antibody-based $\gamma\delta$ T-cell approaches.

Alternative $\gamma\delta$ T-Cell-Related Strategies

A new $\gamma\delta$ T-cell based approach being tested in clinical trials is DeltEx drug-resistant immunotherapy (DRI). IN8Bio's first DeltEx DRI product, INB-200, consists of expanded autologous V γ 9V δ 2 T-cells genetically modified to express a methylguanine DNA methyltransferase (MGMT). MGMT confers them resistance to temozolomide (TMZ) allowing for simultaneous treatment with TMZ and immunotherapy (106). TMZ, which is the current standard of care for glioblastoma multiforme (GBM) together with radiotherapy after resection, might sensitize tumor cells to $\gamma\delta$ T-cell recognition through upregulation of NKG2D ligands but it also causes lymphocytopenia that is avoided by MGMT expression (107). An ongoing clinical trial (NCT04165941) is testing intracranial administration of INB-200 to the tumor site after surgical resection, followed by TMZ treatment (**Table 1**). All 4 GBM patients enrolled in this study have been reported to exceed the expected PFS for TMZ alone treatment. This technology is based on expansion and modification of autologous $\gamma\delta$ T-cells, however, other DeltEx DRI based on allogeneic $\gamma\delta$ T-cells (INB-400) and $\gamma\delta$ CAR-T-cells (INB-300) are being developed.

Interestingly, although V δ 1⁺ T-cells have cytotoxic capacity, V δ 1⁺ TIL associate with poor prognosis in certain malignancies, possibly through production of IL-17 (6, 32). LYT-210 is a mAb directed towards the V δ 1⁺ TCR with the aim of eliminating these pathogenic cells (**Table 2**). Gamma-delta TCR bispecific molecules (GABs) combine the extracellular domain of the V γ 9V δ 2 TCR fused with a CD3 binding domain, allowing conventional T-cells to recognize the presence of pAg on tumor cells (108). In the presence of GABs, $\alpha\beta$ T-cells recognized and killed the squamous cell carcinoma cell line SCC9 in a pAg dependent manner and produced increased

amounts of IFN γ when exposed to patient-derived AML blasts but not with healthy hematopoietic cells indicating preferential recognition of tumor cells.

Two phase I dose-escalation clinical trials (NCT04688853; NTR6541) initiated by Gadeta are assessing the safety and tolerability of $\alpha\beta$ T-cells engineered to express a defined V γ 9V δ 2 TCR (TEGs) in relapsed/refractory AML, MM, and high-risk myelodysplastic syndrome patients. These T-cells combine the tumor specificity of $\gamma\delta$ T-cells with the tumor cell killing potential of $\alpha\beta$ T-cells and show promising antitumor reactivity both *in vitro* and *in vivo*. Furthermore, chimeric PD-1 receptor (chPD1) $\gamma\delta$ T-cells, turn PD-1 immune suppression into T-cell activation (109). The chPD1 $\gamma\delta$ T-cells selectively killed PD-L1⁺ tumor cells in a xenograft murine model, without lysis of normal PD-L1⁺ cells or significant elevation of CRS-related cytokines. The authors reported that chPD1 $\gamma\delta$ T-cell therapy will be assessed in a phase I/II clinical trial.

CONCLUSION

Past clinical trials have demonstrated that systemic activation of V γ 9V δ 2 T-cells or adoptive transfer of autologous V γ 9V δ 2 T-cells were well tolerated and could trigger antitumor immunity. These studies have been followed by a number of trials based on V γ 9V δ 2 and the first study with V δ 1 allogeneic T-cell transfer, which would allow for donor-derived therapies. Up to this date, these trials have not resulted in major adverse effects. Most strategies that are currently under evaluation profit from the safety of $\gamma\delta$ T-cell activation and incorporate tumor-targeting mechanisms, *e.g.* CARs or bsTCEs, which might be key to obtain more robust and consistent clinical responses. Initial results from these targeted approaches, both cell and antibody-based, show great promise and confirm the safety of V γ 9V δ 2 and V δ 1 T-cell-based strategies. However, cell-based products present challenges that are not shared by antibody-based therapies, such as high cost, difficulty of production or need of specialized facilities, and preparatory lymphodepleting chemotherapy regimens. In the near future, the results obtained by the trials described in this review will determine whether the potential of $\gamma\delta$ T-cells can be translated into clinical benefit.

AUTHOR CONTRIBUTIONS

JS-E and MJ wrote the manuscript. HV co-wrote and reviewed the manuscript. LK, PP, EE, BW and TG reviewed the manuscript. All authors contributed to the article and approved the submitted version.

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CD137 Costimulation Enhances the Antitumor Activity of V γ 9V δ 2-T Cells in IL-10-Mediated Immunosuppressive Tumor Microenvironment

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Although $\gamma\delta$ -T cell-based tumor immunotherapy using phosphoantigens to boost $\gamma\delta$ -T cell immunity has shown success in some cancer patients, the clinical application is limited due to the rapid exhaustion of V γ 9V δ 2-T cells caused by repetitive stimulation from phosphoantigens and the profoundly immunosuppressive tumor microenvironment (TME). In this study, using a cell culture medium containing human and viral interleukin-10 (hIL-10 and vIL-10) secreted from EBV-transformed lymphoblastoid B cell lines (EBV-LCL) to mimic the immunosuppressive TEM, we found that the antitumor activity of V γ 9V δ 2-T cells was highly suppressed by endogenous hIL-10 and vIL-10 within the TME. CD137 costimulation could provide an anti-exhaustion signal to mitigate the suppressive effects of IL-10 in TME by suppressing IL-10R1 expression on V γ 9V δ 2-T cells. CD137 costimulation also improved the compromised antitumor activity of V γ 9V δ 2-T cells in TME with high levels of IL-10 in Rag2^{-/-} γ c^{-/-} mice. In humanized mice, CD137 costimulation boosted the therapeutic effects of aminobisphosphonate pamidronate against EBV-induced lymphoma. Our study offers a novel approach to overcoming the obstacle of the hIL-10 and vIL-10-mediated immunosuppressive microenvironment by costimulating CD137 and enhancing the efficacy of $\gamma\delta$ -T cell-based tumor therapy.

Keywords: CD137, $\gamma\delta$ -T cells, antitumor activity, IL-10, immunotherapy

INTRODUCTION

Epstein-Barr virus (EBV) is a predominant type of human herpesviruses. It infects over 95% of the population by adulthood (1, 2). EBV infection is highly correlated with several human malignancies (1–3). As the first known human tumor virus, the carcinogenesis of EBV has been identified in various hematopoietic and epithelial cell cancers, including EBV-associated tumors and lymphoproliferative disorder (1, 2, 4). Current therapeutic approaches for EBV-associated tumors are restricted by undesirable side effects and ineffectiveness for refractory or relapsed

diseases (5, 6). It was reported that EBV-specific CTL-based therapy is effective in the control of EBV-associated malignancy (5, 6). However, its clinical application is hampered due to insufficient quantity of EBV-specific CTL generated *ex vivo* (7).

As a major subset of human $\gamma\delta$ -T cells, V γ 9V δ 2-T cells have been extensively demonstrated to have promising anti-tumor effects (8–13). V γ 9V δ 2-T cells can be activated specifically by phosphoantigens from isoprenoid biosynthesis in an MHC-unrestricted manner. Aminobisphosphonates pamidronate (PAM) and zoledronate (ZOL) are commonly used pharmacological phosphoantigens for osteoporosis and Paget's disease treatment (11, 14). Previously, we demonstrated that direct administration of PAM could expand V γ 9V δ 2-T cells *in vivo* and thus control EBV-induced lymphoma in humanized mice, suggesting that V γ 9V δ 2-T cell-based immunotherapy is promising for treating EBV-associated tumors (15). A recent meta-analysis of about 18,000 human cancers revealed that tumor-infiltrating $\gamma\delta$ T cells are the most favorable cancer-wide prognostic marker (16). However, the clinical application was limited by the rapid exhaustion of V γ 9V δ 2-T cells caused by the repetitive stimulation from phosphoantigens *in vivo* (17) and the profoundly immunosuppressive tumor microenvironment (TME) (18–20).

Interleukin (IL)-10, as a major immunosuppressive cytokine in TME secreted by tumor cells, can help tumor cells escape immunological recognition and destruction (21–24). Current evidence indicates that EBV codes a homologue of human IL-10 (vIL-10) with immunosuppressive properties to evade immunity and establish persistent/latent infections (25–28). EBV-LCL also express and release various amounts of human IL-10 (hIL-10) (29, 30). hIL-10 and vIL-10 are crucial for B cell transformation of B cell (31, 32) and oncogenesis of EBV-associated tumors (33). However, whether the antitumor activity of V γ 9V δ 2-T cells was suppressed by IL-10 in TME remained largely unknown.

CD137 (4-1BB), a membrane-bound receptor, is a costimulatory molecule expressed in many lymphocytes (34–36). Recently, we demonstrated that CD137 costimulation enhanced the activation and cytolytic activity of V γ 9V δ 2-T cells against virus-infected cells (37). Importantly, boosting cancer immunotherapy with agonistic CD137 antibodies has been demonstrated to be a promising therapeutic strategy for different tumors (38, 39). However, the roles of CD137 signaling for human V γ 9V δ 2-T cells in the immunosuppressive TME remained to be determined.

In this study, we aim to clarify whether IL-10 in the TME is responsible for the exhaustion of V γ 9V δ 2-T cells and determine whether targeting CD137 can enhance the antitumor activity of V γ 9V δ 2-T cells compromised by the immunosuppressive TME.

MATERIALS AND METHODS

V γ 9V δ 2-T Cell Cultures

hPBMC were isolated from buffy coats by Ficoll-Hypaque gradient centrifugation of EBV⁺ healthy donors after informed

consents were obtained. PAM-expanded V γ 9V δ 2-T cells were prepared according to the protocol we established before (40). Briefly, hPBMC were cultured in RPMI1640 medium with 10% fetal bovine serum (FBS) in the presence of PAM from day 0 to day 3 at a concentration of 9 μ g/ml. Recombinant human IL-2 was added to medium from day 3 to day 14 at a concentration of 500 IU/ml. After 2 weeks, the $\gamma\delta$ -T cells were purified by positive selection with α -TCR γ/δ MicroBead (Miltenyi Biotec).

Cytotoxic Assay

Purified V γ 9V δ 2-T cells were cultured with IL-10^{low} or IL-10^{high} conditioned medium for 24h, RPMI 1640 with 10% FBS medium (plain medium, PM) as a control. The pretreated V γ 9V δ 2-T cells (effector cells, E) were cocultured with autologous EBV-LCL (target cells, T) at an E: T ratio of 10:1 for 4 to 6 h in the IL-10^{low/high} CM or PM, and then the death of target cells was analyzed with flow cytometry. Cells were stained with anti-CD3 to identify V γ 9V δ 2-T cells and propidium iodide (PI) was used to identify dead cells. The death of EBV-LCL was shown as the percentage of PI⁺ cells in the CD3⁺ population (40). In some experiments, neutralizing antibody against IL-10 (abcam) was added to block IL-10 mediated pathways. To confirm the suppressive role of IL-10 in the CM, recombinant hIL-10 (Peprotech) or recombinant vIL-10 (R&D systems) was added to culture medium at the indicated concentration.

Establishment of EBV-LCL

EBV-secreting cell lines B95-8 and B95.8EBfaV-GFP were cultured and EBV-containing supernatants were collected for the following infection. hPBMC were incubated with EBV-containing supernatants, and then cultured in the RPMI 1640 medium containing 15% FBS with the addition of cyclosporine-A (1 μ g/ml) as we describe before (15).

Collection of EBV-LCL Conditioned Medium

EBV-LCL were cultured in RPMI1640 medium for 24 h. The conditioned medium (CM) was collected, centrifuged at 5000 rpm at 4°C for 10 min to remove cell debris and then frozen at –80°C in aliquots. Stored CM was passed through a 0.22- μ m syringe filter (Millipore) before use. Plain medium (PM) collected from complete medium without cell incubation under the same experimental conditions served as the control for CM.

Determination of hIL-10 and vIL-10 Levels

For hIL-10, the concentrations in conditioned medium were measured by ELISA. The procedures for human IL-10 ELISA kits (Biolegend, San Diego, CA, USA) were performed based on the manufacturer's instructions. For vIL-10, the concentrations in conditioned medium were measured according to the method described before (41). The conditioned medium was concentrated by Amicon-Ultra centrifugation filters (Millipore) following the manufacturer's instructions. Then, the concentrated conditioned medium was used for performing Western blot assay. Mouse monoclonal antibody against vIL-10 (R&D) was used as primary antibody for incubating transferred membranes at 4°C overnight. Horseradish peroxidase

conjugated goat anti-mouse secondary antibody (R&D) was used as secondary antibody for detecting vIL-10 levels. The bands of Western blot were quantified by “Gels” analysis tool of ImageJ. Recombinant vIL-10 was used as a standard to quantify the vIL-10 level in conditioned medium.

Establishment and Treatment of EBV-Associated Lymphoma in Mice

All animal studies were approved and performed in compliance with the guidelines for the use of experimental animals by the Committee on the Use of Live Animals in the Teaching and Research, the University of Hong Kong. Rag2^{-/-} γ c^{-/-} mice were bred in Centre for Comparative Medicine Research of the University of Hong Kong. Humanized mice were generated according to the protocol we established before (14, 15). Rag2^{-/-} γ c^{-/-} or humanized mice were inoculated with EBV-LCL expressing high or low level of IL-10 (0.1×10^6 /mouse) by subcutaneous injection to establish the EBV-associated lymphoma model. For Rag2^{-/-} γ c^{-/-} mice, PAM-expanded V γ 9V δ 2-T cells (5×10^6 /mouse) with or without the addition of SA-hCD137L (5 μ g/mouse) were adoptively transferred intravenously into EBV-associated lymphoma murine model at indicated time. For humanized mice, PAM (5mg/kg body weight) and SA-hCD137L (15 μ g/mouse) were injected intraperitoneally at the indicated time. The mice treated with an equivalent volume of PBS or SA were used as controls. The tumor volume and mice survival were monitored every day and calculated at the indicated time. Mice were counted as dying when their subcutaneous tumor diameter was larger than 17 mm and thus sacrificed according to the regulation of Centre for Comparative Medicine Research of the University of Hong Kong. Otherwise, mice were monitored for 100 days before being sacrificed. The tumor tissues were reserved for immunohistochemical evaluation.

Preparation of the Recombinant SA-hCD137L Protein

Recombinant SA-hCD137L proteins were generated as described before (37). Briefly, the DNA sequences were synthesized encoding the extracellular domain of human CD137L (a.a. 58–254) and the core streptavidin (SA; a.a. 16–133) with an N-terminal 6 \times His tag. The recombinant SA-hCD137L protein was expressed in *E. coli* by inserting the SA-hCD137L DNA fragments into the pETH expression vector and transforming into competent cells. After purifying with Ni-nitrilotriacetic acid affinity chromatography (QIAGEN, Germany), the recombinant SA-hCD137L protein was filtered and quantitated by BCA Protein Assay Kit (Pierce, USA).

Flow Cytometric Analysis

Cells were stained for surface molecules with the following antibodies: α IL10R (Miltenyi Biotec, clone REA239), α CD3 (Biolegend, clone HIT3a), α TCR γ 9 (Biolegend, clone B3), α TCRV δ 2 (Biolegend, clone B6), and α CD137 (Biolegend, clone 4B4-1). All samples were performed with a FACS LSR II (BD). The results were analyzed with FlowJo software.

Histological Staining and Immunohistochemical Assays

The tumor tissues were fixed with 10% formalin for 24 h and maintained in 70% ethanol. Fixed tumor tissues were embedded in paraffin and sectioned. The tumor sections were performed immunohistochemistry staining with α IL-10 antibody (abcam) (42).

Statistics

Data are shown in the form of mean \pm standard error of the mean (SEM). All data were tested by Shapiro-Wilk test to verify the normality. For data that did not meet normal distribution, Mann-Whitney U test was used for analysis. For data that met normal distribution, one-way analysis of variance (ANOVA) with Bonferroni correction was used for analysis. For multiple variables, two-way ANOVA was used. Kaplan-Meier log-rank test was used for comparing survival among different groups. Two-tailed test was used for all analyses. $P < 0.05$ was regarded as significant.

RESULTS

Antitumor Activity of V γ 9V δ 2-T Cells Was Inhibited by IL-10 Secreted From EBV-LCL *In Vitro*

To investigate the effects of IL-10 in TME on the antitumor activity of V γ 9V δ 2-T cells, conditioned medium (CM) was obtained by collecting the supernatant of EBV-LCL culture for modeling TME *in vitro*. As shown in **Figure 1A**, CM from EBV-LCL culture established from different donors contained distinct levels of IL-10, and vIL-10 accounted for about $9.56 \pm 5.74\%$ of total IL-10. CM collected from EBV-LCL1 and EBV-LCL6, which contained the lowest and highest concentrations of IL-10, was used as IL-10^{low} CM and IL-10^{high} CM, respectively, in the following experiments. Importantly, the cytotoxic activity of IL-10^{high} CM-treated V γ 9V δ 2-T cells against EBV-LCL was significantly lower than IL-10^{low} CM- or PM-treated V γ 9V δ 2-T cells (**Figure 1B**). To verify the immunosuppressive role of IL-10 in the CM, an IL-10 neutralizing mAb was applied to block IL-10 signaling during V γ 9V δ 2-T cells exposed to IL-10^{high/low} CM. The reduced cytotoxicity of V γ 9V δ 2-T cells against EBV-LCL was significantly abrogated when blocked with the IL-10 neutralizing mAb (**Figure 1C**). Furthermore, both hIL-10 and vIL-10 recombinant proteins showed dose-dependent inhibitions in the cytotoxicity of V γ 9V δ 2-T cells against EBV-LCL in the PM (**Figures 1D, E**). Taken together, our data indicate that the antitumor activity of V γ 9V δ 2-T cells against EBV-LCL was suppressed by both the hIL-10 and vIL-10 in the CM from EBV-LCL *in vitro*.

Antitumor Activity of V γ 9V δ 2-T Cells Against EBV-Induced Lymphoma Was Decreased Under IL-10^{high} TME *In Vivo*

To determine whether the therapeutic effects of V γ 9V δ 2-T cells on EBV-induced B cell lymphoma were inhibited by IL-10 within the TME, EBV-LCL1 expressing low levels of IL-10 (IL-10^{low} LCL) and EBV-LCL6 expressing high levels of IL-10 (IL-10^{high} LCL) were inoculated into Rag2^{-/-} γ c^{-/-} mice, respectively

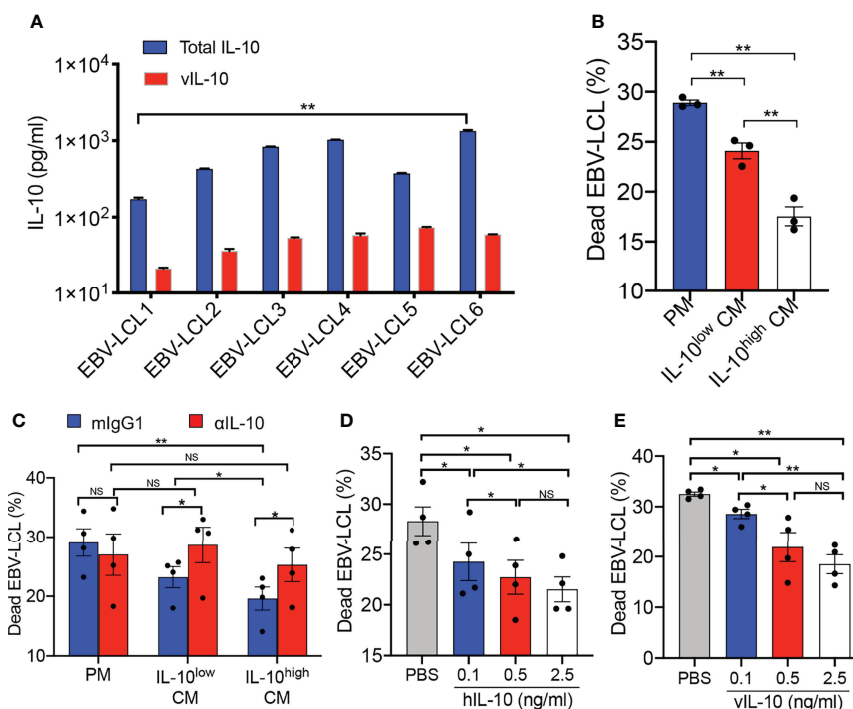


FIGURE 1 | Antitumor activity of V γ 9V δ 2-T cells was inhibited by IL-10 secreted from EBV-LCL *in vitro*. **(A)** The concentration of vIL-10 and total IL-10 in conditioned medium (CM) collected from EBV-LCL established from different donors were detected. **(B)** Purified V γ 9V δ 2-T cells were pretreated in the IL-10^{low} CM and IL-10^{high} CM separately for 24 h, RPMI 1640 with 10% FBS medium (plain medium, PM) as a control. Pretreated V γ 9V δ 2-T cells then cocultured with autologous EBV-LCL at an effector: target (E:T) ratio of 10:1 for 4–6 h in the IL-10^{low/high} CM and PM, respectively. Cytotoxicity was calculated as the proportion of dead EBV-LCL (CD3⁺PI⁺). **(C)** Purified V γ 9V δ 2-T cells were pretreated with IL-10^{low} CM, IL-10^{high} CM or PM in the presence of a neutralizing anti-IL-10 mAb (α IL-10, 5 μ g/ml) or isotype control (mlgG1, 5 μ g/ml), then cocultured with autologous EBV-LCL at an E:T ratio of 10:1 for 4–6 h in the IL-10^{low/high} CM and PM respectively. Cytotoxicity was calculated as the proportion of dead EBV-LCL (CD3⁺PI⁺). **(D, E)** Purified V γ 9V δ 2-T cells were pretreated with recombinant hIL-10 **(D)** or vIL-10 **(E)** at different concentration, then cocultured with autologous EBV-LCL at an E:T ratio of 10:1 for 4–6 h. The proportion of dead EBV-LCL (CD3⁺PI⁺) were detected by flow cytometry. All data are shown as mean \pm SEM and representative of three independent experiments. * p < 0.05; ** p < 0.01; ns, no significant difference.

(Figure 2A). After 21 days, large subcutaneous tumors developed in all the mice as detected by *in vivo* imaging (Figures 2B, C). The expressions of IL-10 in the tumor tissues generated from IL-10^{low} LCL and IL-10^{high} LCL were detected by immunohistochemistry (Figure 2D). Consistent with our previous results (15), V γ 9V δ 2-T cell treatment constrained tumor growth and prolonged the survival of tumor-bearing mice in contrast with the mice treated with PBS as the control (Figures 2E, F). Importantly, V γ 9V δ 2-T cells showed less efficacy in controlling EBV-induced lymphoma developed from IL-10^{high} LCL compared with that developed from IL-10^{low} LCL, along with larger tumor volume and lower survival rates (Figures 2E, F). These results suggest that the decreased antitumor activity of V γ 9V δ 2-T cells against EBV-induced lymphoma may be associated with IL-10^{high} TME *in vivo*.

CD137 Costimulation Suppressed IL-10R1 Expression and Restored the Antitumor Activity of V γ 9V δ 2-T Cells

IL-10 mediates its biological effects mainly through a heterodimeric membrane receptor composed of IL-10R1 and

IL-10R2 (43). Since IL-10R2 is shared by more than five IL-10 family cytokines (44), we investigated the expression of IL-10R1 on V γ 9V δ 2-T cells exposed to the IL-10^{high} CM upon $\gamma\delta$ -TCR activation *in vitro*. Importantly, we found that following activation, IL-10R1⁺ V γ 9V δ 2-T cell subset expressed high levels of CD137 compared with IL-10R1^{-/lo} V γ 9V δ 2-T cell subset in the IL-10^{high} CM, indicating that CD137 could be an effective costimulatory signaling to restore the antitumor activity of V γ 9V δ 2-T cells compromised by the IL-10 in TME (Figures 3A, B).

To determine whether CD137 costimulation could provide an anti-exhaustion signal to mitigate the inhibiting effects mediated by IL-10 in TME, a recombinant SA-hCD137L protein containing a core streptavidin (SA) molecule with the extracellular domains of human CD137L (hCD137L) was generated as we reported previously (37). We found that the addition of the recombinant SA-hCD137L protein significantly inhibited the surface expression of IL-10R1 in total and CD137⁺ V γ 9V δ 2-T cells in IL-10^{high} CM in terms of both percentage and expression level (MFI) changes (Figures 3C–E). These results indicate that CD137 costimulation suppressed IL-10R1

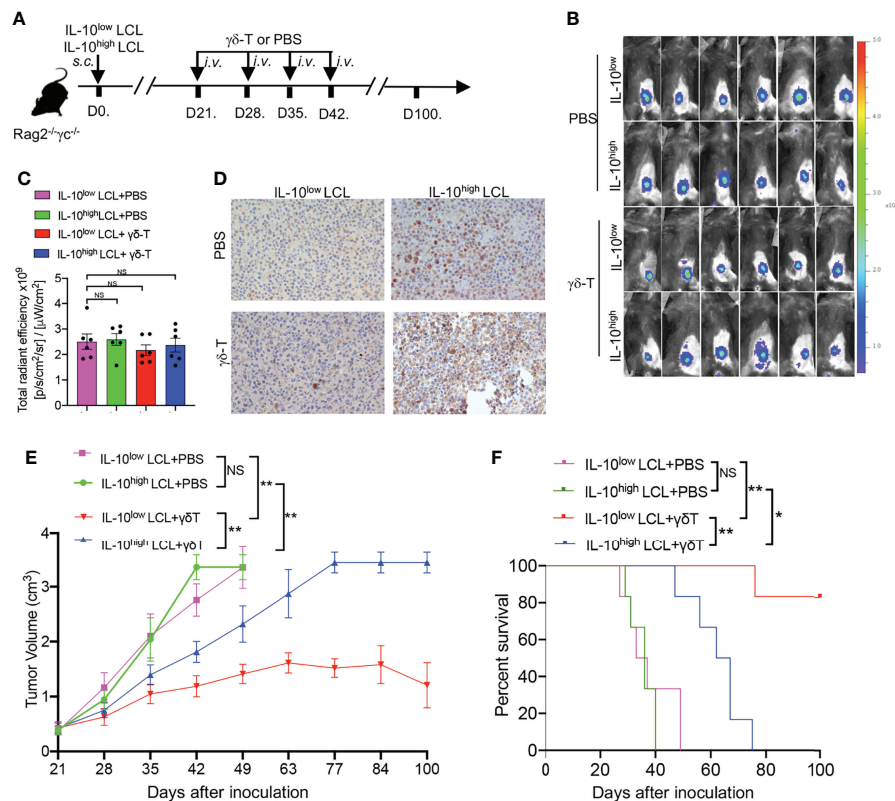


FIGURE 2 | Antitumor activity of V γ 9V δ 2-T cells against EBV-induced lymphoma was decreased under IL-10^{high} TME *in vivo*. **(A)** IL-10^{low} LCL and IL-10^{high} LCL were injected s.c. in Rag2^{-/-} γ c^{-/-} mice separately. After 21 days, mice that had developed subcutaneous tumor were randomly divided into two groups respectively followed by the treatment with allogeneic V γ 9V δ 2-T cells or PBS at indicated time (six mice per group). **(B, C)** Whole-body fluorescence images **(B)** and total radiant efficiency **(C)** of mice before treatment with V γ 9V δ 2-T cells or PBS. **(D)** Representative histology of IL-10 in tumor sections that developed from IL-10^{low} LCL and IL-10^{high} LCL. **(E, F)** The tumor volume **(E)** and mouse survival **(F)** were determined at the indicated time. The tumor volume was compared using two-way ANOVA analysis, and mice survival was compared using Kaplan-Meier log-rank test. Data are representative for three independent experiments. * $p < 0.05$; ** $p < 0.01$; ns, no significant difference.

expression in CD137⁺ V γ 9V δ 2-T cells, and thereby was able to reduce their sensitivity to endogenous IL-10 in the immunosuppressive TME.

To determine whether CD137 costimulation could rescue the impaired antitumor efficacy of V γ 9V δ 2-T cells in suppressive TME, the recombinant SA-hCD137L protein was added to the coculture of V γ 9V δ 2-T cells with EBV-LCL in IL-10^{high} CM for mimicking the tumor milieu. As shown in **Figure 3F**, the SA-hCD137L protein significantly increased the cytotoxicity of V γ 9V δ 2-T cells against EBV-LCL under both the immunosuppressive and normal microenvironments mimicked by the IL-10^{high} CM and the PM. Importantly, CD137 costimulation not only completely restored the reduced cytotoxicity of V γ 9V δ 2-T cells in the IL-10^{high} CM to normal levels, but also had a better effect to enhance the cytotoxic activity of V γ 9V δ 2-T cells in IL-10^{high} CM than that in PM (**Figure 3F**). These data demonstrate that CD137 engagement enables V γ 9V δ 2-T cells to withstand the hostile environment mediated by endogenous IL-10, resulting in the increase of the antitumor activity of V γ 9V δ 2-T cells *in vitro*.

CD137 Costimulation Enhanced the Compromised Antitumor Activity of V γ 9V δ 2-T Cells With IL-10^{high} TME in Rag2^{-/-} γ c^{-/-} Mice

Previously we have demonstrated that V γ 9V δ 2-T cells could control EBV-inducing lymphoma (15), and their antitumor activity in controlling EBV-induced lymphoma developed from IL-10^{high} LCL was lower than that developed from IL-10^{low} LCL (**Figures 2E, F**). To further elucidate the roles of CD137 costimulation in the compromised antitumor activity of V γ 9V δ 2-T cells in IL-10^{high} TME *in vivo*, EGFP-expressing IL-10^{high} LCL was inoculated in Rag2^{-/-} γ c^{-/-} mice, s.c. (**Figure 4A**). Twenty-one days later, mice bearing subcutaneous tumors were randomly divided into three groups as detected by *in vivo* imaging (**Figure 4B**). No significant differences were found in fluorescent density from tumor cells among the three groups after 21 days of tumor cell inoculation (**Figure 4C**). PAM-expanded V γ 9V δ 2-T cells were adoptively transferred to one group of the tumor-bearing mice with the recombinant SA-hCD137L protein weekly from day 21 to day 42. The other two groups of mice were adoptively

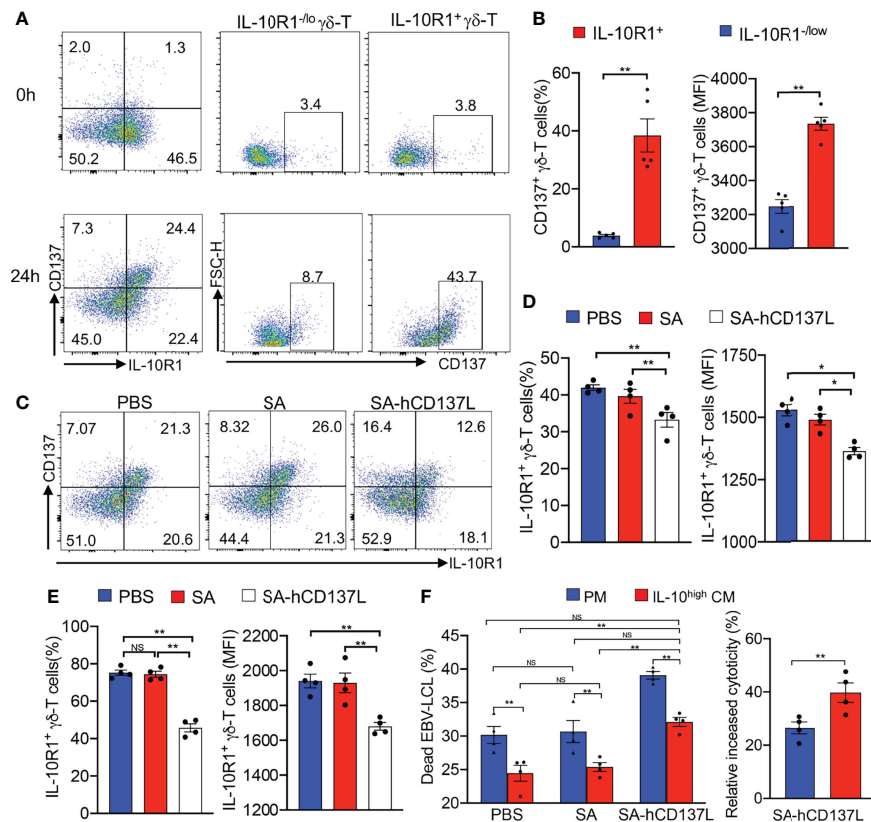


FIGURE 3 | CD137 costimulation suppressed IL-10R1 expression and restored the antitumor activity of V γ 9V δ 2-T cells. **(A)** The expression of CD137 on IL-10R1^{-/-} and IL-10R1⁺ V γ 9V δ 2-T cells before (0h) and after stimulation with anti- $\gamma\delta$ -TCR mAb for 24h (24h) in IL-10^{high} CM. **(B)** The percentages and expression levels (mean fluorescence intensities, MFI) of CD137 on IL-10R1^{-/-} and IL-10R1⁺ V γ 9V δ 2-T cells upon stimulation for 24h in IL-10^{high} CM. **(C, E)** The FACS patterns of CD137 and IL-10R1 expressions **(C)**, surface expression of IL-10R1 in total V γ 9V δ 2-T cells **(D)** and in CD137⁺ V γ 9V δ 2-T cells **(E)** upon stimulation by anti- $\gamma\delta$ -TCR mAb supplemented with SA-CD137L (500ng/ml), PBS and SA in IL-10^{high} CM for 24h were detected by flow cytometry after surface staining of IL-10R1. **(F)** Purified V γ 9V δ 2-T cells were pretreated with SA-hCD137L (500ng/ml), PBS or SA for 24 h in the PM and IL-10^{high} CM, and then cocultured with autologous EBV-LCL at an E: T ratio of 10:1 for 4-6h. The proportions of dead EBV-LCL (CD3⁻ PI⁺, left), and the relative increase of cytotoxicity after being treated with SA-hCD137L (right) are shown. All data are shown as mean \pm SEM and representative of three independent experiments. * p < 0.05; ** p < 0.01; ns, no significant difference.

transferred with V γ 9V δ 2-T cells in the presence of PBS or SA as the controls. Importantly, V γ 9V δ 2-T cells in combination with SA-hCD137L treatment significantly limited tumor growth (**Figure 4D**) and improved mouse survival (**Figure 4E**) compared to treatments of V γ 9V δ 2-T cells with PBS or SA. These data indicate that the costimulation of CD137 efficiently enhanced the antitumor activity of V γ 9V δ 2-T cells in the highly immunosuppressive microenvironment mediated by IL-10 *in vivo*.

CD137 Costimulation Improved the Therapeutic Effect of PAM in Controlling EBV-Induced Lymphoma With IL-10^{high} TME in Humanized Mice

Previously we had demonstrated that PAM could expand V γ 9V δ 2-T cells *in vivo* to control EBV-induced lymphoma in humanized mice with functional hPBMC (15). We then investigated the role of CD137 costimulation on the therapeutic effect of PAM in controlling EBV-induced lymphoma with IL-10^{high} TME in humanized mice. EBV-induced lymphoma with IL-10^{high} TME model was generated by

inoculation *s.c.* of IL-10^{high} EBV-LCL in humanized mice (**Figure 5A**) (15). All humanized mice developed subcutaneous tumors after IL-10^{high} EBV-LCL inoculation for 28 days with similar fluorescent density from tumor cells as detected by *in vivo* imaging (**Figures 5B, C**). PAM, SA-hCD137L, or the combination of these two agents were injected intraperitoneally (*i.p.*) at days 28, 35, 42, and 49 after IL-10^{high} EBV-LCL inoculation (**Figure 5A**). PBS- and SA-treated mice were controls. As a result, PAM administration alone decreased the tumor volume significantly and extended the survival of the tumor-bearing humanized mice compared with the treatment with PBS, SA, or SA-hCD137L protein alone, respectively (**Figures 5D, E**). Importantly, the combination treatment of PAM with SA-hCD137L was more potent than PAM alone to control the development of EBV-induced lymphoma with IL-10^{high} TME in humanized mice, in terms of tumor growth and survival (**Figures 5D, E**).

Humanized mice reconstituted with V γ 9V δ 2-T-cell-depleted hPBMC were also used to confirm whether the effect of SA-hCD137L costimulation on the control of EBV-induced

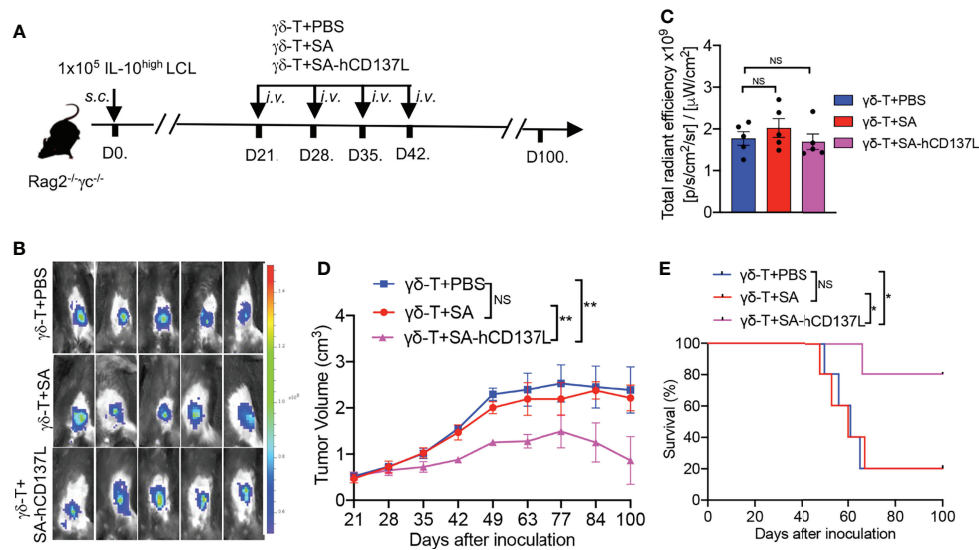


FIGURE 4 | CD137 costimulation enhanced the antitumor activity of V γ 9V δ 2-T cells with IL-10^{high} TME in Rag2^{-/-} γ c^{-/-} mice. **(A)** Protocol for evaluation of the synergistic therapeutic effect of V γ 9V δ 2-T cells and SA-hCD137L on EBV-induced lymphoma in Rag2^{-/-} γ c^{-/-} mice (five mice per group). **(B, C)** Whole-body fluorescence images **(B)** and total radiant efficiency **(C)** of mice before treatment with PAM, SA-hCD137, SA, and PBS. **(D, E)** The tumor volume **(D)** and mouse survival **(E)** were determined at the indicated time. The tumor volume was analyzed by two-way ANOVA test, and mice survival was analyzed by Kaplan-Meier log-rank test. Data are representative for three independent experiments. *p < 0.05; **p < 0.01; ns, no significant difference.

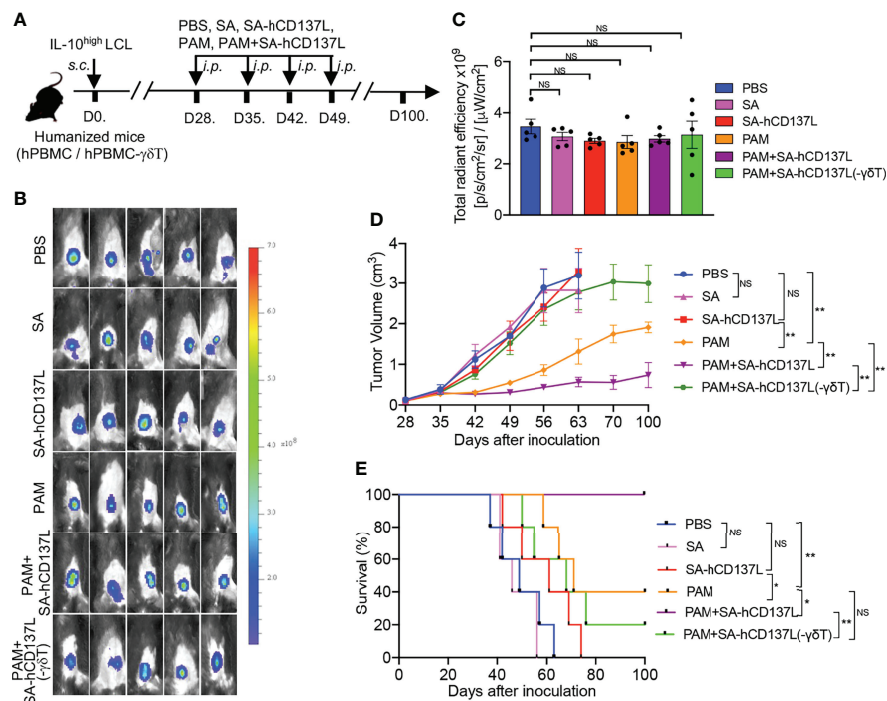


FIGURE 5 | CD137 costimulation improved the therapeutic effect of PAM in controlling EBV-induced lymphoma with IL-10^{high} TME in humanized mice. **(A)** The evaluation protocol of the synergistic therapeutic effect of PAM and SA-hCD137L on EBV-induced lymphoma in humanized mice (five mice per group). **(B, C)** Whole-body fluorescence images **(B)** and total radiant efficiency **(C)** of mice before treatment with PAM, SA-hCD137, SA and PBS. **(D, E)** The tumor volume **(D)** and mouse survival **(E)** were determined at the indicated time. The tumor volume was analyzed by two-way ANOVA test, and mice survival was analyzed by Kaplan-Meier log-rank test. Data are representative for three independent experiments. *p < 0.05; **p < 0.01; ns, no significant difference.

lymphoma with IL-10^{high} TME was mediated by V γ 9V δ 2-T cells (**Figure 5A**). As shown in **Figures 5D, E**, there were no therapeutic effects by the combination treatment of PAM with SA-hCD137L in humanized mice reconstituted with V γ 9V δ 2-T-cell-depleted hPBMC. These data demonstrate that the recombinant SA-hCD137L protein had a synergistic effect with PAM to overcome the barriers of IL-10^{high} TME *in vivo* and this synergistic effect was mainly mediated by V γ 9V δ 2-T cells.

DISCUSSION

In this study, we demonstrated that the antitumor activities of V γ 9V δ 2-T cells against EBV-LCL were inhibited by both hIL-10 and vIL-10 *in vitro* and *in vivo*. Importantly, we found that IL-10R1 was highly expressed on CD137⁺ V γ 9V δ 2-T cells compared to CD137^{-lo} V γ 9V δ 2-T cells following activation. CD137 engagement significantly suppressed IL-10R1 expression in V γ 9V δ 2-T cells, therefore reducing the V γ 9V δ 2-T cells' sensitivity to IL-10 in the TME. We further demonstrated that SA-hCD137L in a tetrameric form of human CD137L protein obviously enhanced the therapeutic effects of adoptive transfer of *ex vivo* expanded V γ 9V δ 2-T cell in Rag2^{-/-} γ c^{-/-} mice and direct administration of PAM in humanized mice for the treatment of EBV-induced lymphoma with IL-10^{high} TME.

IL-10 is important as an immunoregulatory cytokine to suppress inflammatory responses. However, its effects on tumorigenesis and development are controversial (45). IL-10 can inhibit the process of antigen presentation by downregulating the expression of MHC-II in APCs (46) and MHC-I in tumor cells (47). Thus, IL-10 can facilitate tumor escape by contributing to an immunosuppressive environment. A meta-analysis of 1788 cancer patients also revealed that the elevated serum IL-10 can predict poor prognosis (48). Paradoxically, it was reported that IL-10 can also induce immune-dependent antitumor effects (15, 49–51). Therefore, the roles of IL-10 on tumor development are dependent on the local environment and physiopathological states. The inhibitory role of IL-10 on APCs, CD8⁺ T cells, and CD4⁺ T cells has been clearly defined, but its impact on V γ 9V δ 2-T cells remains unclear. In this study, our data supported that hIL-10 and vIL-10 derived from tumor cells and EBV significantly inhibited the cytotoxicity of V γ 9V δ 2-T cells, which substantially limits the antitumor efficacy of V γ 9V δ 2-T cells.

EBV has evolved to express vIL-10, thereby providing a suitable microenvironment for itself to evade immunity and cause tumorigenesis (52, 53). The structurally homologous viral and human IL-10 perform similarly in several biological properties, including inhibition of IFN- γ production, suppression of T cell proliferation in response to antigens and mitogens, and stimulation of B cell growth (54). This similarity has raised the possibility that EBV might have captured the IL-10 gene during evolution. Furthermore, IL-10 has been shown to be involved in the pathogenesis of lymphoid disorders (55, 56). Elevated IL-10 levels are correlated with shorter survival and

adverse disease features in patients with EBV-associated tumors (33, 57). Thus, we reasoned that hIL-10 and vIL-10 may be associated with the suppression of V γ 9V δ 2-T cells' antitumor activity. Such an interaction would provide a suitable microenvironment for viruses to evade immunity and cause tumorigenesis. Here, our *in vitro* data revealed that vIL-10 derived from EBV and hIL-10 derived from EBV-LCL were the dominant factors for inhibiting the antitumor activity of V γ 9V δ 2-T cells in TME. Our *in vivo* data also suggested that the reduced antitumor activity of V γ 9V δ 2-T cells against EBV-induced lymphoma may be associated with IL-10^{high} TME. Further study using IL-10 neutralizing mAb or IL-10 knockout mice is required to determine the exact role of IL-10 in antitumor activity of V γ 9V δ 2-T cells *in vivo*. Of note, additional factors in the CM might also contribute to suppressing V γ 9V δ 2-T cells activity because a smaller extent of cytotoxicity reduction after treatment with recombinant hIL-10 and vIL-10 proteins was observed when compared with IL-10^{high} CM (**Figure 1**).

Recently, clinical trials utilizing bisphosphonates, such as PAM and ZOL, to expand $\gamma\delta$ -T cell *in vivo* in combination with IL-2 therapy or adoptive transfer of *ex vivo* cultured $\gamma\delta$ -T cells were performed in patients with tumors and virus infections (11, 15, 58, 59). Administration of bisphosphonates with IL-2 and the transfer of expanded autologous V γ 9V δ 2 T-cells have been demonstrated to be safe with limited adverse events (60). However, there is only a modest efficacy in the treatment of some tumors (61, 62). One drawback of $\gamma\delta$ -T cell-based immunotherapy is the rapid exhaustion of proliferation and effector responses due to repeated phosphoantigen treatments (17). Another drawback of this therapy is the impaired antitumor activity of $\gamma\delta$ -T cells caused by the tumor immunosuppressive microenvironment (18, 63).

CD137 is a promising costimulatory immunologic target for enhancing antitumor immune responses (39). CD137 costimulation, known as “stepping on the accelerator,” is believed to be a compelling complement for “removing the brakes” *via* blocking inhibitory signaling. Importantly, it is now appreciated that CD137 signaling not only works as an “accelerator” to provide costimulation, but also breaks and reverses the established anergy in cytotoxic T lymphocytes (CTLs) (64, 65). However, the role of CD137 signaling in V γ 9V δ 2-T cells within the context of IL-10-mediated TME is not clear. Here, we revealed that IL-10R1⁺ V γ 9V δ 2 T-cell subset expressed high levels of CD137. Moreover, CD137 costimulation suppressed IL-10R1 in V γ 9V δ 2-T cells, suggesting that CD137 engagement possessed the potential to ameliorate the exhaustion and dysfunction of V γ 9V δ 2-T cells.

Ligation of CD137 is correlated with effective antitumor responses; however, the application of anti-CD137 agonistic antibodies in patients is limited by a variety of side effects (66). The natural CD137 ligand is an alternative to the CD137-specific antibodies to stimulate antitumor T cell responses. Shirwan lab reported that a streptavidin-conjugated murine CD137L (SA-mCD137L) complex could induce effective antitumor immune responses (67, 68). SA-mCD137L induces less pathological side effects than anti-CD137 agonistic antibody therapy, suggesting a

higher therapeutic index of SA-mCD137L. Previously, we demonstrated that recombinant SA-hCD137L enhanced the cytotoxic effect of V γ 9V δ 2- T cells against influenza virus infection (37). Here, we further found that SA-hCD137L restored the antitumor activity of V γ 9V δ 2-T cells compromised by the IL-10-mediated TME. These data indicate that SA-hCD137L can provide an alternative to anti-CD137 agonistic for anti-tumor therapy.

There are no V γ 9V δ 2-T cells in mice, thus it is impossible to study these cells in mouse models (69). Previously, we successfully established humanized mice with a similar proportion of V γ 9V δ 2-T cells in murine peripheral blood to that in humans (12, 14, 70, 71). Importantly, here the synergistic effect of PAM and recombinant SA-hCD137L V γ 9V δ 2-T cells was verified in humanized mice.

In conclusion, our study further elucidates the role of CD137 in the antitumor activity of human V γ 9V δ 2-T cells in the IL-10-mediated immunosuppressive TME. The combination of a phosphoantigen and CD137 agonist also provides a novel strategy for treating EBV-induced tumors by avoiding V γ 9V δ 2-T cell exhaustion and enhancing the efficacy of V γ 9V δ 2-T cell-based therapy.

AUTHOR CONTRIBUTORS

YP, WT, and YL conceived and designed the study, interpreted the results, wrote and edited the manuscript; YP, KW, ZX, CT, XW, YZ, and XM designed and performed the experiments,

analyzed the results. WT supervised this study. All authors contributed to the article and approved the submitted version.

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 author.

ETHICS STATEMENT

The studies involving human participants were reviewed and approved by the institutional review board of The University of Hong Kong/Hospital Authority Hong Kong West Cluster. The patients/participants provided their written informed consent to participate in this study. The animal study was reviewed and approved by the Committee on the Use of Live Animals in Teaching and Research, The University of Hong Kong.

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$\gamma\delta$ T-Cell Expansion and Phenotypic Profile Are Reflected in the CDR3 δ Repertoire of Healthy Adults

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$\gamma\delta$ T cells fill a distinct niche in human immunity due to the unique physiology of the phosphoantigen-reactive $\gamma\delta$ TCR. Here, we highlight reproducible TCR δ complementarity-determining region 3 (CDR3 δ) repertoire patterns associated with $\gamma\delta$ T cell proliferation and phenotype, thus providing evidence for the role of the CDR3 δ in modulating *in vivo* T-cell responses. Features that determine $\gamma\delta$ TCR binding affinity and reactivity to the phosphoantigen-induced ligand *in vitro* appear to similarly underpin *in vivo* clonotypic expansion and differentiation. Likewise, we identify a CDR3 δ bias in the $\gamma\delta$ T cell natural killer receptor (NKR) landscape. While expression of the inhibitory receptor CD94/NKG2A is skewed toward cells bearing putative high-affinity TCRs, the activating receptor NKG2D is expressed independently of the phosphoantigen-sensing determinants, suggesting a higher net NKR activating signal in T cells with TCRs of low affinity. This study establishes consistent repertoire–phenotype associations and justifies stratification for the T-cell phenotype in future research on $\gamma\delta$ TCR repertoire dynamics.

Keywords: human $\gamma\delta$ T cells, CDR3 δ , adult V δ 2 repertoire, differentiation profile, public clonotypes, NKG2D, CD94/NKG2A(B)

INTRODUCTION

From generation onward, the T-cell receptor repertoire accumulates footprints of selection and clonotypic expansion that reduce its diversity and lead to skewing. As a result, the repertoire of antigen-experienced T cells represents only a modest fraction of the repertoire of their newly generated naïve precursors, limited to the antigenic specificities relevant to the individual's immunological history [reviewed in (1)]. A $\gamma\delta$ TCR is notably different from an $\alpha\beta$ TCR, as it senses the accumulation of intracellular phosphorylated non-peptide antigens (phosphoantigens or pAgs) through modification of surface butyrophilin family members BTN3A1 and BTN2A1, orchestrated by interaction with the small GTPase RhoB, rather than sensing peptide–MHC complexes (2–6). Nevertheless, despite the unique antigen specificity and recognition mode, the $\gamma\delta$ TCR repertoire equally acquires imprints of selection and expansion throughout the human lifetime (7, 8), starting with a wave of polyclonal expansion immediately after birth (9, 10) and

ultimately leading to a characteristic “selected,” highly private pAg-reactive γδ2TCR repertoire in adults [reviewed in (11)]. While the TCRγ chain harbors motifs that are critical for binding the non-polymorphic BTN ligand, the TCRδ2 chain contains the yet unresolved clue to pAg reactivity (4, 12), possibly through the influence of the CDR3δ on the γδ2TCR binding affinity in this multiple-ligand system (13, 14). Therefore, the most dramatic repertoire changes are seen in the CDR3δ repertoire from T-cell generation to maturity.

Phenotypic maturation in T cells parallels repertoire maturation and eventually reaches terminal differentiation defined by the dominance of cytotoxic responses over the proliferative, acquisition of natural cytotoxicity markers and reduced TCR signaling (15, 16). γδ2T cells mature across a similar continuum of transcriptional, phenotypic, and functional changes as αβT cells do (17, 18). The CD27+CD28+ T cells (“early-stage differentiation profile,” proliferative, characteristic of T cells isolated from cord blood or thymus) or CD27-CD28-CD16+ cells (“late-stage differentiation profile,” readily cytotoxic, seen in selected healthy adults) dominate the two distinct poles of the continuum. Unlike αβT cells, however, γδT cells are characterized already at the fetal stage of T-cell development by a prominent natural killer receptor (NKR) signature, present independently of other differentiation markers (19), and continuing to distinguish γδT cells from their αβ counterparts during adulthood (20, 21).

In early infancy, massive γδ2T cell expansion and phenotypic maturation are evidently reflected by enrichment of the γδ2TCR repertoire in features that underpin recognition of the pAg-driven changes in BTN2 and BTN3, such as TRGJP rearrangements in the γ chain and a hydrophobic amino acid at position 5 of the CDR3 of the δ chain, suggestive of the key role of these γδ2TCR traits in the effector responses of the γδ2T cells at that developmental stage (10). As to already highly selected adult γδ2TCR repertoires, a clonotypic bias in association with T-cell expansion and differentiation profile has been reported (7); however, it remains unclear whether any distinct TCR features explain this bias. In addition, the expression of certain NKRs has been associated with a CDR3δ bias (22). Considering the growing interest in γδT cells and their TCRs as therapeutics (23), and in reliance on a model in which the γδ2TCR diversity is assumed to underpin a range of ligand-binding affinities (13, 14), the question of whether the repertoire changes are related to the phenotypic changes is particularly relevant, since it clears the way for isolating the TCRs with the highest affinity to the antigen and the T-cell populations most potent for therapeutic use (14, 24). In this study, we deconstruct the adult CDR3δ repertoire in relation to the phenotype of the γδ2T cells in an attempt to understand the functional role of the γδ2TCR diversity in adults.

MATERIALS AND METHODS

Isolation of Peripheral Blood Mononuclear Cells and Cell Phenotyping

Buffy coats were obtained from Sanquin blood bank (Amsterdam, The Netherlands). Peripheral blood mononuclear cells (PBMCs) were isolated from buffy coats using Ficoll-Paque

PLUS gradient centrifugation (GE Healthcare, Chicago, IL, USA). The cells at the interface were harvested, washed 4× with phosphate-buffered saline (PBS) (Sigma-Aldrich, St. Louis, MO, USA), and further stained with the following monoclonal antibodies (mAbs): CD3 (CD3-PB Clone UCHT1, BD Biosciences, San Jose, CA, USA; cat. no. 558117), TCR panγδ (TCR panγδ-PE-Cy7 Clone IMM510, Beckman Coulter, Brea, CA, USA; cat. no. B10247), Vδ2 (TCR Vδ2-FITC Clone B6, BioLegend, San Diego, CA, USA; cat. no. 331406), CD8a (CD8a-PerCP-Cy5.5 Clone RPA-T8, BioLegend; cat. no. 301031), CD4 (CD4-APC Clone RPA-T4, BioLegend; cat. no. 300514), CD27 (CD27-APC-eF780 clone O323, eBioscience, San Diego, CA, USA; cat. no. 47-0279-42) and isotype control (IgG1-APC-eF780 Clone P3.6.2.8.1, eBioscience; cat. no. 47-4714-80), CD45RA (CD45RA-BV650 Clone HI100, BD Horizon, Franklin Lakes, NJ, USA; cat. no. 563963), CD28 (CD28-BV605 Clone CD28.2, BD Horizon; cat. no. 562976), CD16 (CD16-PE Clone eBioCB16, eBioscience; cat. no. 12-0168-41), CD16-BV785 Clone 3G8, BioLegend; cat. no. 302046), CCR7 (CCR7-APC Clone G043H7 Sony Biotechnology, San Jose, CA, USA; cat. no. 2366070), NKG2D (NKG2D-PE clone 1D11, eBioscience; cat. no. 12-5878-42), CD94 (CD94-PE clone HP-3B1, Beckman Coulter; cat. no. IM2276), NKG2A (human CD159a (NKG2A)-APC/Fire™ 750 clone S19004C, BioLegend; cat. no. 375115), and NKG2C (CD159c(NKG2C)-AF700clone 134591, R&D Systems, Minneapolis, MN, USA; cat. no. FAB138N-025).

Live/dead aqua stain (LIVE/DEAD stain kit Aqua fluorescent, Life Technologies, Carlsbad, CA, USA; cat. no. L34957) was used to exclude dead cells.

Cell phenotyping was performed on BD Fortessa and BD Canto, and all fluorescence-activated cell sorting (FACS) processes were performed on BD ARIALL. Sorted T-cell subpopulations were collected in equal numbers in at least duplicates, which were further processed separately as independent biological replicates. We sorted 50,000 cells per population for the late-stage profile donors; for the early-stage donors, there were 12,000–30,000 cells. Cells were collected in ice-cold Roswell Park Memorial Institute (RPMI) medium (Gibco, Grand Island, NY, USA) supplemented with 20% fetal calf serum (FCS) and spun down; cell pellets were resuspended in RLTplus buffer (Qiagen, Valencia, CA, USA; art 1053393) supplemented with fresh β-mercaptoethanol (Life Technologies; art 11528926) (10 μl of βME per 1 ml of RLTplus) for 2 min for lysis at RT and stored at –80°C until RNA isolation.

TCRδ Chain Sequencing and Data Analysis

RNA isolation, cDNA synthesis, PCR of the TCRδ chain, library preparation, high-throughput sequencing, and analysis of the raw sequencing files were performed at the University Medical Center Utrecht as described earlier (13). In-house R scripts were used for repertoire analysis; data were filtered to include clonotypes with a frequency higher than one read/clonotype. The tcr package (25) was used as the framework of the repertoire analysis pipeline.

All head-to-head comparisons of quantitative repertoire features, such as diversity, were made on samples with equal numbers of sorted cells.

Sequences were annotated as public if they were shared among at least 2 donors in the current study. In order to reduce the uncertainty intrinsic to the detection of low-frequency sequences, which might impair the robust detection of rare public clonotypes, we analyzed only the nucleotides that had been detected at least in two samples from the same donor. When analyzing public AA clonotypes, multiple (both private and public) nucleotides encoding for the same AA sequence were collapsed to a single entry with a read count equaling the total of the read counts of all nucleotides. Several previously published datasets containing high-throughput TCRδ chain sequencing data were used to identify highly common public Vδ2 CDR3 sequences in healthy individuals (9, 10, 26–28).

Analysis of the number of N insertions was performed using the IMGT Junction Analysis tool (29).

Cells and Cell Lines

Daudi and Phoenix-Ampho cells were obtained from ATCC (Manassas, VA, USA). The TCRβ^{−/−} Jurkat76 cell line was a kind gift from Miriam Heemskerk (LUMC, Leiden, the Netherlands).

Retroviral Vector Generation

The γ chain of the TCR clone 5 cloned into a pBullet-IRES-neomycin vector *via* 5' *Nco*I and 3' *Bam*HI restriction sites was previously available (30). Public and private CDR3δ chain retroviral plasmid vectors were generated based on the previously available retroviral vector encoding the δ chain of the TCR clone 5 (30) by introducing the new CDR3δ sequence using overlap extension PCR as described earlier (13). For the overhang primer pairs encoding the target CDR3δ NT sequences, see **Supplementary Table 3**.

Retroviral Transduction of T Cells

All public and private TCR δ2 chains were paired with clone 5 TCRγ chain and were transduced into TCR-deficient T-cell line Jurkat76.

For the generation of transduced Jurkat76 cells, Phoenix Ampho cells were transfected with the pBullet retroviral constructs containing TCRγ and TCRδ using FuGENE HD (Promega, Madison, WI, USA). Next, Jurkat76 cells were transduced with the viral supernatants in the presence of polybrene (4 μg/ml; Sigma-Aldrich). The transduced Jurkat76 cells were magnetic-activated cell sorting (MACS)-selected using anti-CD3 microbeads (Miltenyi, Bergisch Gladbach, Germany) and cultured for at least 5 days before functional assay.

CD69 Upregulation Assay

10⁵ transduced Jurkat76 cells were cocultured overnight in a 1:1 ratio with Daudi cells as a target, with or without 100 μM of pamidronate treatment. The cells were then stained with the following antibody mix for 30 min on ice: Vδ2-FITC clone B6 (BioLegend), CD69-APC clone FN50 (Sony Biotechnology; cat. no. 2154550), and CD20-eFluor450 clone 2H7 (eBioscience; cat.

no. 48-0209-42). After being washed, the cells were fixed using 1% paraformaldehyde and analyzed with BD FACS Canto II (BD Biosciences). Readouts were analyzed using FlowJo software.

Statistical Analysis

Statistical analysis was performed using R Studio. The two-sided Wilcoxon rank-sum test was used to calculate the median difference between two independent groups (31) and its significance.

Code Availability

Details of the code can be requested from the corresponding author.

RESULTS

Clonotypic Expansion Involves Concentration of the CDR3δ Phosphoantigen-Sensing Determinants

As a framework for the study of the repertoire fingerprints of the T-cell expansion, we used the publicly available repertoire data of healthy preterm infants and young children in whom γδ2T cells are actively proliferating (10), focusing in this study on the TCRδ chain. Intending to define the CDR3δ features associated with *in vivo* expansion, we classified clonotypes according to their abundance, or clonotype frequency *f* into non-expanded (*f* < 0.1%), expanded (0.1% ≤ *f* < 1%), and hyperexpanded (*f* ≥ 1%) and further analyzed their qualitative traits. Clonotypic expansion associated unambiguously with J1 region usage, and the presence of the “invariant T” nucleotide (invT) (32), or, more generally, a hydrophobic amino acid at position 5 (hAA5) of the CDR3δ (position 109 according to IMGT) (12), features that define the transition from poorly reactive neonatal (8, 19) to adult-type highly pAg-reactive repertoires (7, 9–11, 32) (**Supplementary Figure 1A**). Next to these well-defined pAg-sensing determinants, we noted a marked enrichment in shorter CDR3δ sequences in expanding clones, seen most clearly in the J1-rearranged subrepertoires (**Supplementary Figures 1B, C**). As clonotype frequency might be determined not solely by the expansion of a T-cell clone upon antigen encounter but by generation biases such as short-homology-repeat recombination (33–36) or convergent recombination [reviewed in (11)], we performed a separate analysis of the infant repertoires at the moment of postnatal “γδ2T cell burst” (3–5 weeks of age) (10) while splitting the data according to the possible origin of bias. We analyzed independently the germline-encoded sequences (no N insertions) and the sequences with N insertions, thus segregating the effect of the short-homology-repeat recombination. A separate analysis of the sequences shared between the subjects (public sequences) and private sequences allowed to account for the effect of convergent recombination since the generation of most if not all public clonotypes relies on this mechanism [(11); see **Supplementary Table 1**]. Although the highly prevalent “hyperexpanded” clonotypes at this developmental stage are almost exclusively germline-encoded and public, emphasizing the recombination effect on clonotype frequency, enrichment in sequences featuring

hAA5 and in shorter sequences with increased clonotype frequency remained equally evident in all independent analyses (**Supplementary Figures 1D, E**), suggesting that both features have a functional implication in T-cell proliferation and do not solely reflect a production bias.

Similar to the proliferative burst seen in early childhood, a marked γ 9 δ 2T cell expansion associated with loss of CD27 expression has been occasionally noted in adults, resulting in γ 9 δ 2TCR repertoires focused on a few (hyper)expanded clones (7). We wondered whether CDR3 δ features that are associated with expansion in infant repertoires similarly underpin clonotypic expansion and T-cell maturation in adults. Therefore, we sorted V δ 2^{pos}CD27^{pos} and V δ 2^{pos}CD27^{neg} populations in a cohort of 9 adult donors (**Supplementary Figure 2A**) and performed high-throughput sequencing of the TCR δ chain of the sorted subsets, first focusing the analysis on the phenotypically younger CD27^{pos} cells. The gating strategy at sorting did not include an antibody directed against the V γ 9 chain (**Supplementary Figure 2A**); however, we confirmed that V γ 9^{neg}V δ 2^{pos} cells represented less than 3.5% (median 1.75%) of the total V δ 2^{pos} sorted cells and less than 10% (median 6.8%) of the V δ 2^{pos}CD27^{pos} subset. V γ 9^{neg}V δ 2^{pos} cells were mainly V δ 2^{dim} cells, a population gated out during sorting (**Supplementary Figure 2B**). As seen with the infant and the child repertoires, in the CD27^{pos} cells of the healthy adults, clonotype frequency was positively associated with rearrangement to the J1 region, the invT nucleotide, and the hAA5 (**Figures 1A–C**); however, the effect sizes observed were smaller in comparison to changes seen in early ontogeny. Within the dominant subset of clonotypes rearranged to the shorter J1 region, a far less notable but still discernible enrichment in shorter sequences was seen with increased clonotype frequency, largely due to the fact that none of the long (>20 AA) sequences reached f of 1% (**Figures 1D, E**). Not

surprisingly, as parts of the variable stretch between the conserved motifs of the CDR3 δ are encoded by N nucleotides, we saw a similar decrease in the average number of the N insertions (**Figure 1F**). Germline-encoded sequences and public sequences are fewer in number and occupied space in adult repertoires compared to the infant ones (**Supplementary Figures 2C, D**); nevertheless, we repeated the analysis of private subrepertoires and subrepertoires generated with N insertions to account for the possible generation bias in these phenotypically “young” cells. We obtained overall similar trends for enrichment in J1 rearrangements, invT, and hAA5 (**Supplementary Figure 2E**) and equally in the shorter sequences, despite an overall shift toward slightly greater mean CDR3 lengths after sorting out the public sequences (**Supplementary Figures 2F, G**; see **Figure 3** and the corresponding text for the characteristics of the public sequences).

Thus, CDR3 δ features postulated as determinants of sensing pAg-driven changes in BTN2 and BTN3 likely underpin the *in vivo* clonotypic expansions seen in infancy and adulthood, although the enrichment patterns are less pronounced in adult repertoires that are nearly saturated with pAg-reactive clones. Clonotypic expansion is further associated with a narrowing range of CDR3 δ lengths. Enrichment in shorter sequences in expanded clones, translating, in part, from fewer N insertions, is readily apparent at the time of active T-cell expansion in infants and, as a reminiscence of the patterns seen in infancy, is still discernible in the repertoires of CD27^{pos} cells in adults.

Phenotypic Maturation Reflects Repertoire Focusing, Which Is Independent of the CDR3 δ Traits

We next focused on the repertoire traits associated with phenotypic maturation. Assuming that the phenotype shifts

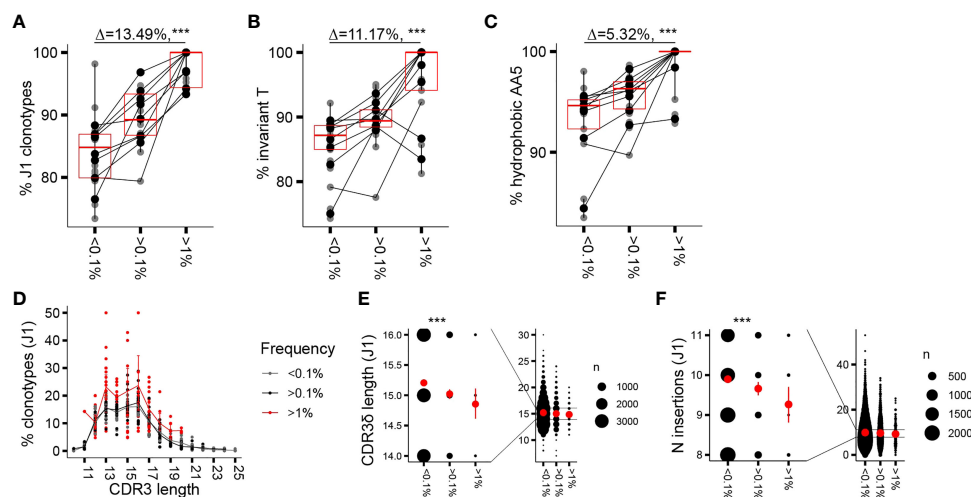


FIGURE 1 | Clonotypic expansion involves concentration of the CDR3 δ pAg-sensing determinants. (**A–C**) Proportion of sequences featuring the determinants of pAg reactivity: rearrangement to J1 region (**A**), the invT (**B**), and a hAA5 (A/V/L/I/P/W/F/M) (**C**) among clonotypes with increasing f in the CD27^{pos} cells. Lines connect the average of the replicates in each donor. Bars represent median values and interquartile range (IQR). The median difference and the p-values were obtained using Wilcoxon rank-sum test. (**D**) CDR3 δ length distribution among J1-rearranged clonotypes in the CD27^{pos} cells. Sequences were classified by f . Lines connect the mean abundances of clonotypes of each respective length within the frequency category. (**E, F**) CDR3 δ length (**E**) and number of N insertions (**F**) in clonotypes rearranged to J1 region. Mean values and error bars representing 95% CI for the mean are shown in red *** $P \leq 0.001$ (Wilcoxon rank-sum test).

result from an antigenic trigger in the periphery (37), we thus aimed to identify CDR3δ traits underlying peripheral repertoire selection. As adult donors are extremely heterogeneous with respect to the proportions of cells at distinct stages of differentiation (17), we concentrated on the part of the cohort in which a sizable fraction of the Vδ2+ compartment has completed differentiation to CD27–CD28–CD45RA++CD16+ phenotype, designated here as late-stage differentiation profile donors ($n = 6$ of the 20 donors phenotyped, cells from 4 out of 6 donors sorted, and repertoires sequenced; see **Supplementary Figure 2A**, an example of a healthy donor (HD) 94, and **Supplementary Figure 3A**). The rest of the cohort ($n = 14$, cells from 5 donors sorted and repertoires sequenced) was collectively characterized by the dominance of CD27^{pos} cells (**Supplementary Figure 2A**, example of HD101), as well as by a less-differentiated state of the sorted CD27^{neg} population, and was categorized here as belonging to the early-stage differentiation profile (**Supplementary Figure 3A**). Late-stage profile donors had a higher proportion of Vδ2TCR+ T cells among CD3+ cells (**Figure 2A**), and the expression of each differentiation marker in the cohort correlated positively (CD16) or negatively (CD27, CD28) with the percentage of Vδ2TCR+ T cells among total T cells (**Figure 2B**). The CD27^{neg} population showed a markedly lower CDR3δ repertoire diversity (estimated here using Shannon entropy) compared to the CD27^{pos} cells (**Figure 2C**). This resulted from a lower number of clonotypes in the CD27^{neg} subset, suggesting a selection process as cells mature from “young” CD27^{pos} to terminally differentiated CD27^{neg} phenotype (**Figure 2D**), as well as from lower evenness, indicating a greater degree of clonotypic expansion in the terminally differentiated cells (evenness was estimated using D75, the percentage of unique clonotypes that occupy 75% of the sample library, **Figure 2E**). The same metrics in early-stage profile individuals showed less profound and less consistent demarcation between the populations sorted according to CD27 expression (**Supplementary Figures 3B–D**). In general, cells with larger distances in phenotype showed more CDR3δ repertoire dissimilarity. Thus, the TCRδ repertoire in phenotypically differentiated cells is shaped by both selection of clonotypes and clonotypic expansion, the latter arguably effectuating the observed inflation of the Vδ2+ compartment as a whole in the late-stage profile donors.

We then analyzed the qualitative repertoire traits that could denote repertoire selection, performing first a head-to-head comparison of the entire repertoires of the sorted subsets. Only a marginal enrichment in the pAg reactivity determinants (**Supplementary Figures 4A–C**) a slight shift towards longer CDR3 length (**Supplementary Figure 4D**) and no change in the number of N insertions (**Supplementary Figure 4E**) characterized the transition from CD27^{pos} to CD27^{neg} phenotype at the level of the complete repertoires. Considering the extreme focusing in the CD27^{neg} compartment (median D75 of 9.43%), we were particularly interested in the characteristics of the high-frequency clonotypes. The “hyperexpanded” repertoires of the CD27^{neg} cells appeared to be permissive to occasional J3 rearrangements, and sequences featuring “non-invT encoded”

amino acids, mostly alanine and glycine (**Figures 2F–H**). Further, the CDR3δ length distribution that was centered around the 13 and 16 AA in the CD27^{pos} subset here peaked at 14 and 17 AA (**Figure 2I**). Thus, although terminally differentiated cells harbor a TCR repertoire slightly more “saturated” in sequences sensing the pAg-driven ligand than cells of CD27^{pos} phenotype, the extreme clonotypic expansions that skew the CDR3δ repertoires in the late-stage donors to near oligoclonality do not strictly rely on the pAg-sensing determinants, and therefore non- or poorly pAg-reactive T-cell clones may take prominent positions in the repertoire.

Public Delta Clonotypes Expand *In Vivo*, But Their Number Diminishes Upon Maturation

CDR3δ clonotypes shared between unrelated subjects (public δ clonotypes) have been shown to play a prominent role in the first wave of postnatal expansion of the γδ2T cells in newborns (9, 10). However, their number decreases with advancing age in children (10) and decreases even further in adults, possibly as a result of peripheral repertoire selection (7, 27), changes in thymic output after birth (36), or both. Here we aimed to explore the expansion potential and the evidence for peripheral selection of the public sequences in adults, by tracing the sequences shared between at least two individual donors in the current study. The proportion of public clonotypes increased with increasing f in the CD27^{pos} population in the majority of the donors (**Figure 3A**). More widely shared clonotypes were encoded by larger numbers of nucleotides, emphasizing that convergent recombination is the foundation of publicity (**Figure 3B**); however, we detected no tendency toward more common clonotypes having higher frequencies (**Figure 3C**), unlike the observations made for the public sequences of fetal origin in infants (10). We then narrowed the analysis down to public sequences with a high degree of sharing, i.e., sequences detected in >50% of the donors included in this study and present in multiple published studies (**Table 1**; see **Supplementary Table 1** for the encoding nucleotides). We looked at the impact of peripheral repertoire selection on the maintenance of the public sequences, again using the model of transition from the CD27^{pos} phenotype to terminal differentiation in the late-stage profile donors. We observed a loss of the highly common public sequences as the cells evolve from CD27^{pos} to the CD27^{neg} phenotype (**Figures 3D, E**), suggesting their deletion in the periphery as cells mature. Thus, public TCRδ clonotypes persist in the repertoires of healthy adults and expand *in vivo* but are only partly maintained when cells undergo terminal differentiation.

Public Delta Clonotype Function: The Beauty of Brevity

The published evidence for the expansion of public Vδ2 clonotypes in infants (10), our current data on their persistence into adulthood, the high degree of sharing and *in vivo* proliferation in adults made us wonder whether these sequences may share properties that would confer high TCR affinity to the pAg-driven ligand. We first characterized the

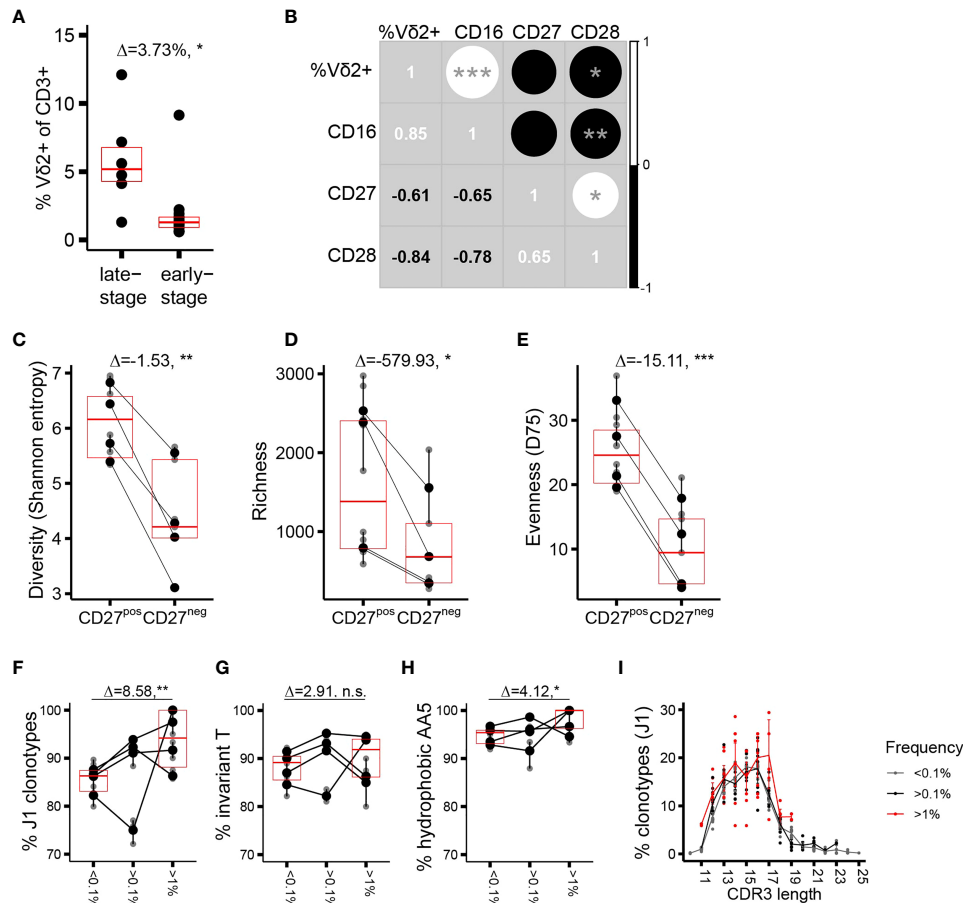


FIGURE 2 | Phenotypic maturation reflects repertoire focusing which is independent of the CDR3δ traits. **(A)** Proportion of Vδ2TCR+ T cells among CD3+ cells in the donors of different phenotypic profiles. **(B)** Correlation matrix showing Spearman's correlation coefficients for the proportion of Vδ2+ T cells among CD3+ T cells, and the proportion of CD27+, CD28+, or CD16+ T cells among Vδ2+ T cells, measured in an independent set of 10 healthy donors. **(C–E)** Measures of diversity: Shannon entropy **(C)**, repertoire richness (number of individual clonotypes), **(D)**, and repertoire evenness, defined as D75 **(E)** in the late-stage profile donors ($n = 4$). **(F–H)** Proportion of sequences featuring the determinants of pAg reactivity: rearrangement to J1 region **(F)**, the invT **(G)**, and a hydrophobic AA5 **(H)** among the clonotypes with increasing frequency f in the CD27^{neg} cell population of the late-stage donors. Bars represent median values and IQRs. The median difference and the p-values were determined using Wilcoxon rank-sum test. * $p < 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$. **(I)** CDR3δ length distribution among J1-rearranged clonotypes in the CD27^{neg} cells. Sequences were classified by f . Lines connect the mean abundances of clonotypes of each respective length within the frequency category.

qualitative features of adult public CDR3δ sequences, looking for distinct traits that could potentially underpin their functionality. Public sequences were most notable for their short average length, which peaked at 12AA for the most common public clonotypes versus 16AA for the private sequences (**Figure 3F**), and the underlying low number of N insertions (**Figure 3G**). Public and private sequences did not differ in J region usage (**Figure 3H**), while the CDR3δ AA5 was exclusively hydrophobic in common public sequences, with relative enrichment in non-invT-encoded amino acids A and W (**Figures 3I, J**).

In order to assess the impact of the public and private TCRδ chain properties on TCR functionality, we selected four common public CDR3δ sequences present in this study, as well as in previously published repertoire studies (9, 10, 26–28) (**Table 1**), which all have 12AA length, and expressed them alongside a fixed γ chain of the TCR clone 5 (30). A set of private sequences

of various lengths (median length 16AA), all rearranged to the J1 region and all harboring a hAA5, was taken along as a control (**Supplementary Table 2**). All constructs were transduced into TCR-deficient Jurkat76 (J76) cells, yielding similar $\gamma\delta$ TCR surface expression levels (**Supplementary Figure 5A**), and CD69 upregulation by J76 cells upon co-culture with the tumor cell line Daudi, was used as a marker for TCR-mediated T-cell activation. We saw higher T-cell activation with the short public δ sequences in the condition without N-amino biphosphonate (NBP), while NBP treatment eliminated the difference (**Figure 3K**). There was no confounding effect of the TCR surface expression level on the observed differences (**Supplementary Figure 5B**). In summary, a shorter length of public CDR3δ sequences, in addition to the consistent positivity for hAA5, is associated with a higher functional avidity, as demonstrated in the TCR gene transfer experiment.

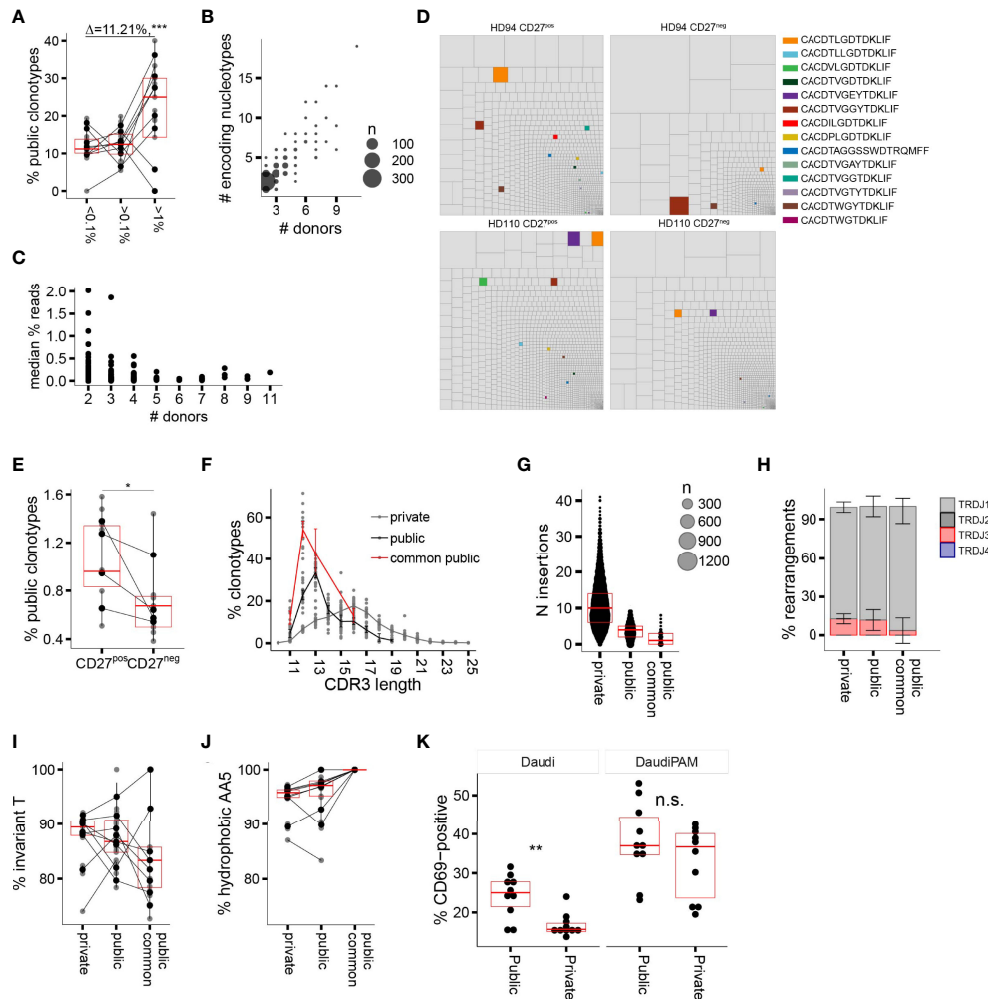


FIGURE 3 | Public delta sequences; persistence in the adult repertoire, qualitative traits, and functionality. **(A)** Percentage of public AA CDR3 δ sequences among clonotypes with increasing f . **(B)** Number of individual nucleotides encoding for individual public AA sequence in relation to the sequence “publicity” (number of individual donors sharing a given sequence). **(C)** The relationship between the number of donors sharing a public sequence and the median f (all donors pooled together; each dot represents an individual sequence). **(D)** Representative treemaps of the repertoires of CD27^{pos} and CD27^{neg} populations of two late-stage profile donors. Public AA clonotypes are highlighted in color; private sequences are shown in gray. **(E)** Percentage of highly common public AA CDR3 δ sequences in the repertoires of CD27^{pos} and CD27^{neg} populations in the late-stage profile donors ($n = 4$). **(F)** CDR3 δ length distribution of private vs. public AA sequences; the highly common public clonotypes are shown separately in red. **(G)** Number of total N insertions in private vs. public AA sequences. **(H–J)** J region usage **(H)**, invT **(I)**, and hAA5 **(J)** in private versus public AA sequences. **(K)** Percentage CD69^{pos} TCR-transduced Jurkat76 cells upon overnight incubation with target cell line Daudi without or in the presence of 100 μ M of PAM. In all panels horizontal bars represent median values and IQRs. The median differences and the p-values were determined using Wilcoxon rank-sum test. * $p < 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$. Panels **(A, C, F–J)** refer to the CD27^{pos} cell populations.

Surface NKG2D Expression Declines With T-Cell Maturation and Is Independent of TCR Clonality

Despite the general trend for preferential *in vivo* expansion of putative high-affinity CDR3 δ clones containing the traits associated with sensing pAg-driven changes in BTN2 and BTN3, we occasionally witnessed (hyper)expanded clonotypes harboring polar, or even charged amino acids at position 5 of the CDR3 δ (**Figure 4A**), which according to the existing experimental evidence are non- or poorly pAg-reactive (13, 14). We hypothesized that pAg-unrelated stimuli could trigger

in vivo proliferation of such T-cell clones and that poorly pAg-reactive TCRs could possibly benefit from the expression of non-clonally restricted activating receptors. In exploring this hypothesis, we focused on NKG2D, the best-studied activating NKR on $\gamma\delta$ T cells, previously reported to play both an autonomous stimulatory role (38–40) and a co-stimulatory role next to a $\gamma\delta$ TCR (41, 42).

We found the absolute majority of the V δ 2+ T cells in adult blood to express NKG2D (**Supplementary Figure 6A**). NKG2D expression correlated with T-cell differentiation phenotype within a donor, as, in general, more differentiated CD27^{neg}CD28^{neg} T cells

TABLE 1 | Public clonotypes shared among >50% of donors in this study and their occurrence in other published repertoire studies.

Public CDR3 δ clonotypes	CDR3 δ length	Nucleotides		# donors in this study	Adult repertoires			Infant and child repertoires	
		Public	Private		(27)	(26)	(28)	(10)	(9)
CACDTLGDTDKLIF*	12	6	13	11	+	+	+	+	+
CACDTLLGDTDKLIF	13	5	9	9	+	+	–	+	+
CACDVLGDTDKLIF*	12	2	4	9	+	+	+	+	+
CACDTLGVYTDKLIF	13	1	8	9	–	–	+	+	+
CACDTVGDYTDKLIF*	12	2	8	8	+	+	+	+	+
CACDTVGEYTDKLIF	13	2	5	8	+	+	+	+	+
CACDTVGGYTDKLIF	13	3	11	8	+	+	–	+	+
CACDILGDTDKLIF	12	2	3	7	+	+	+	+	+
CACDPLGDTDKLIF	12	2	10	7	–	+	+	+	+
CACDTAGGSSWDTRQMFF	16	2	4	7	–	+	+	+	+
CACDTVGGTDKLIF	12	3	6	7	–	+	+	+	–
CACDTVGTYTDKLIF	13	0	8	7	+	+	+	+	–
CACDTWGTDKLIF	11	1	6	7	+	+	+	+	+
CACDTWGYTDKLIF*	12	2	3	7	+	+	+	+	+

Sequences used for the TCR transfer experiment (see below) are marked with an asterisk.

expressed less surface NKG2D (**Supplementary Figure 6B**). The trend for declining surface expression with T-cell maturation was in line with lower NKG2D mRNA expression levels in more differentiated populations, detected in an independent dataset that we extracted from the study by Ryan et al. (17) (**Supplementary Figure 6C**). Conversely, gating on NKG2D^{bright} vs. NKG2D^{dim/neg} cells (**Supplementary Figure 6D**) revealed an overall “younger” phenotype of the NKG2D^{bright} cells in the majority of donors, with notably higher expression of CCR7, CD27, and TCR $\gamma\delta$ (**Supplementary Figures 6E, F**), with the NKG2D^{intermediate} population lying between two extremes (**Supplementary Figures 6G, H**).

To examine the repertoire characteristics of V δ 2+ T cells in the context of NKG2D expression, we sorted NKG2D^{dim/neg} and NKG2D^{bright} V δ 2+ T cells as shown in **Supplementary Figure 6D** and again performed sequencing of the TRDV2 repertoires as described above. Unlike the T-cell differentiation profile, the NKG2D expression level did not denote any change in the TCR diversity metrics (**Figures 4B–D**). When we looked into the set of qualitative CDR3 δ features that could define the unique clonotypes, we detected no difference between the NKG2D^{neg/dim} and NKG2D^{bright} cells, except for a bias in J1 region usage in the low-frequency clones (**Figure 4E**), which, however, did not translate into a shorter average CDR3 δ length (**Supplementary Figure 6I**).

Thus, although the expression level of the activating receptor NKG2D in adult $\gamma\delta$ 2T cells shows a discernible relation to the T-cell differentiation status, it is not associated with a bias toward putative low-affinity or pAg-unreactive TCRs.

Expression of Inhibitory NKR CD94/NKG2A(B) Associates With a Bias Toward Putative High-Affinity $\gamma\delta$ 2TCRs

The net total of the inhibitory and activating signals from the environment will direct the $\gamma\delta$ 2T cell effector functions (43). Although we did not find compelling evidence for skewing in NKG2D expression toward putative pAg-unreactive clones, there could be still an effect of the signal strength through the $\gamma\delta$ TCR,

generally considered “signal one” (44), on the landscape of the remaining NKRs and thus on the net NKR signal. We therefore aimed to investigate the TCR repertoire features in the context of surface expression of CD94/NKG2A(B), an inhibitory C-type lectin receptor broadly expressed on the $\gamma\delta$ 2T cells and recently reported to identify a highly pAg- and tumor-reactive $\gamma\delta$ 2T cell subset (45).

We sorted V δ 2+ T cells from peripheral blood based on CD94 expression into a CD94^{bright} subpopulation, in which CD94 is known to heterodimerize with NKG2A(B) (22, 46), and a CD94^{neg} subpopulation (**Supplementary Figures 6J, K**), and performed a similar comparative CDR3 δ repertoire analysis. CD94^{bright} cells were collectively characterized by a higher percentage of sequences featuring an invT-encoded or generally hydrophobic AA5 in the repertoire (**Figure 4F**), in line with an earlier low-throughput sequencing study (22). CDR3 δ bias according to the invT/hAA5 as one of the strong predictors of the TCR reactivity is further exemplified here by the differential clonotypic expansion of a single pAg-unreactive clonotype (**Figure 4G**). Moreover, we observed a trend toward enrichment in shorter CDR3 δ sequences in CD94^{bright} cells (**Supplementary Figure 6L**).

In summary, the CDR3 δ features known to underpin pAg-sensing and $\gamma\delta$ 2TCR signal strength appear to impact the surface expression of an inhibitory NKR CD94/NKG2A(B), with the putative high-affinity CDR3 δ sequences being accompanied by high CD94/NKG2A(B) surface expression, while low-affinity TCR-bearing clones remained predominantly CD94-negative.

DISCUSSION

The discovery of the germline region-mediated interactions at the basis of the mechanism of antigen recognition by a $\gamma\delta$ 2TCR (2, 4) provides a rationale for the observed *in vitro* (47) and *in vivo* (9, 10) polyclonal $\gamma\delta$ 2T cell responses to antigenic stimuli, fostering the paradigm of the $\gamma\delta$ 2TCR as a pattern recognition

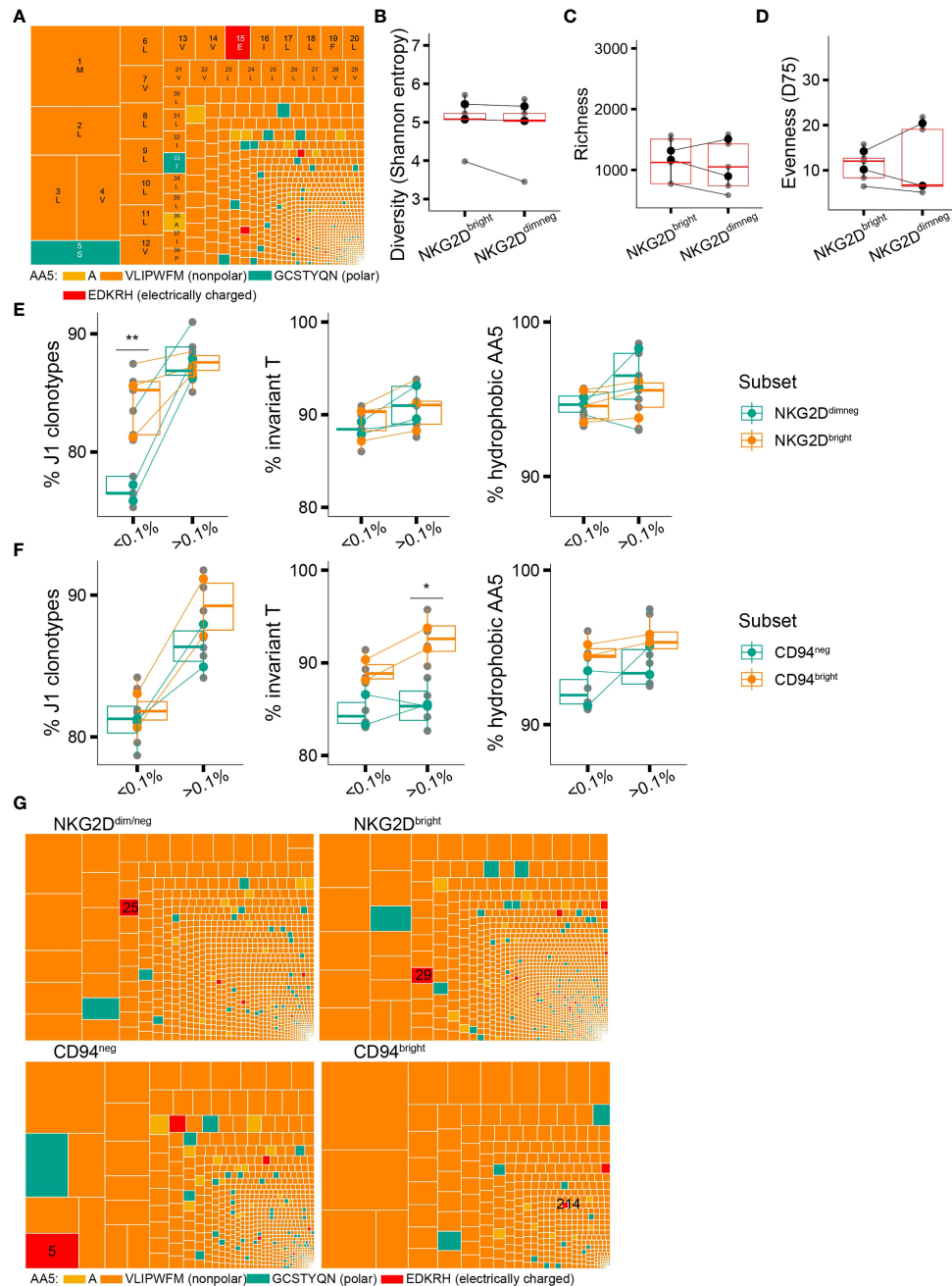


FIGURE 4 | Non-clonally restricted NKG2D expression versus a CDR3 δ bias in surface expression of CD94/NKG2A(B). **(A)** An example of a repertoire of a healthy donor where a putative non-pAg-reactive clonotype occupies a prominent position (position 16, CACDTEGTPTLIF). **(B–D)** TCR repertoire diversity of the NKG2D^{dim}neg and NKG2D^{bright} cell populations estimated with Shannon entropy **(B)**, species richness **(C)**, and evenness(D75) **(D)** ($n = 3$ donors). y-Axis limits are set equal to those in **Figures 2C–E**. **(E)** Qualitative features of the repertoires of the NKG2D^{dim}neg and NKG2D^{bright} cells in relation to clonotype frequency: proportion of sequences rearranged to J1 region and proportion of sequences featuring the invT or a hAA5. **(F)** Qualitative features of the repertoires of the CD94^{neg} and CD94^{bright} cells in relation to clonotype frequency: proportion of sequences rearranged to J1 region and proportion of sequences featuring the invT or a hAA5 ($n = 2$ donors). **(G)** Treemaps showing the CDR3 δ repertoires of the NKG2D^{dim}neg, NKG2D^{bright}, CD94^{neg}, and CD94^{bright}-sorted populations in the same healthy donor as in **(A)** Position of the putative non-pAg reactive clonotype CACDTEGTPTLIF is indicated. **(B–F)** Bars represent median values and interquartile range (IQR) (Wilcoxon rank-sum test, * $p < 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$).</sup></sup></sup></sup></sup></sup></sup></sup></sup></sup>

receptor. The absence of a known polymorphic ligand leaves the role of the highly diverse CDR3 regions currently undefined. Nevertheless, particularly in the case of the CDR3 δ repertoire, a distinct evolution pattern seen during ontogeny (11) hints at the

still significant role of the CDR3 δ in antigen recognition. Here we expand the evidence on the role of CDR3 δ in $\gamma\delta$ 2TCR-mediated responses. We show that *in vivo* $\gamma\delta$ 2T cell expansion and phenotypic maturation are associated with repertoire

enrichment in the CDR3 δ determinants of sensing pAg-induced changes (12, 48, 49), presumably equating to the concentration of the $\gamma\delta$ 2TCRs with higher binding affinity and signal strength (13, 14). We find that the number of the highly common public TCR δ sequences that combine all known pAg reactivity features, known to diminish with the transition from infant to adult repertoires, diminishes even further within an individual upon T-cell maturation, despite optimal signaling. Lastly, we detect skewing in the inhibitory NKR CD94/NKG2A(B) surface expression toward cells expressing putative high-affinity TCRs. In contrast, expression of the activating NKR NKG2D emerges as independent of CDR3 δ traits, suggesting possibly higher net NKR activating signal in T cells with low $\gamma\delta$ 2TCR affinity.

Prevalence of a clonotype in the repertoire, especially in the repertoires of infants and of the “younger” CD27^{pos} cells in adults, had the most apparent association with the features of the V δ 2 chain known as “sensors” of the pAg-induced changes in the target. Such features include rearrangement to the J1 region, a hydrophobic AA5, and, notably, an optimal (shorter) CDR3 δ length. Although generation biases such as short-homology-repeat recombination (33–36) and convergent recombination (11) play a role in shaping the repertoire, especially that of the immature cells, the above-described enrichment patterns remained evident in the analysis of subrepertoires generated by either mechanism, suggesting the true implication of the pAg-sensing features in T-cell proliferation, and not solely a reflection of a generation bias. The enrichment was less pronounced in adult repertoires, compared to the repertoires of infants, presumably as a result of the switch from the fetal-type to adult-type thymic output (36), which is nearly saturated with pAg-reactive clones.

Analysis of the CD27^{pos} and CD27^{neg} populations in the late-stage profile donors allowed us to correlate distances in phenotype to CDR3 δ repertoire dissimilarity. A change in phenotype from young CD27^{pos}CD28^{pos} cells to a mature CD27^{neg}CD28^{neg}CD16^{pos} profile was associated with extreme repertoire focusing, suggesting a major proliferation event preceding maturation, or, alternatively, expansion of the already mature cells (20). Such inflation remained visible at the level of the entire V δ 2 compartment in these donors, and both the visible inflation and mature phenotypes of these cells suggested preceding antigenic triggers rather than possible generation bias. Although the enrichment in putative high-affinity clonotypes was equally evident with increasing clonotype frequency in the mature CD27^{neg}CD28^{neg}CD16^{pos} cells, the hyperexpanded clonotypes in the terminally differentiated subpopulation occasionally encompassed sequences that in theory mediate submaximal pAg reactivity.

Earlier studies of the $\alpha\beta$ T cells highlighted the mechanistic differences between homeostatic proliferation with the maintenance of the T-cell memory phenotype that depends on the strength of tonic TCR signaling, in comparison to massive expansion with differentiation to the effector phenotype as a result of antigenic stimulation [reviewed in (37)]. We suggest the possibility of a similar disparity here: while expansion in the “young” (naïve and central memory) cells, defined here as

CD27^{pos}, clearly showcases the enrichment in the CDR3 δ traits associated with TCR binding affinity, the repertoire of the terminally differentiated CD27^{neg} population might reflect additional imprints of the stimuli other than BTNs/pAgs, which bypass signaling through the TCR. Another argument supporting the hypothesis of critical (co-)stimulants involved in massive oligoclonal proliferation seen in late-stage profile donors is the maintenance of the once-established profile over long time periods, even under repetitive NBP stimulation (17). Likewise, *in vitro* stimulation with pAg or NBPs could not induce such massive oligoclonal outgrowth from PBMCs (47); however, the latter study did not specify the phenotype of the cells used for stimulation experiments.

Sequences that universally possess the key pAg reactivity features are the (near-)germline public TCR δ sequences of high generation probability (50) shared between the repertoires of multiple unrelated individuals. The repertoire studies published to date (7–10, 27, 28, 36, 47) define public sequences at the AA rather than at the NT level, to highlight the functionality of a sequence rather than its generation probability, and to account for convergent recombination (11). Thus, public V δ 2 clonotypes have recently been shown to expand *in vivo* shortly after birth (9, 10) and *in vitro* after stimulation with NBP of cord blood-derived $\gamma\delta$ 2 T cells (47). The more common sequences appear to take more prominent positions in the infant repertoires, pointing to the functional relevance of the public sequences at this stage of development (10). Here we found highly common sequences seen in children across continents, back in the adult repertoires, whether due to persistence from early childhood or *de novo* thymic synthesis at a later stage. The more common sequences had a higher number of encoding individual nucleotides, emphasizing the role of convergent recombination in sequence sharing. However, we did not find the most common public sequences to occupy more repertoire space in adults, suggesting that recombination bias, while explaining occurrence in multiple unrelated donors, does not necessarily govern repertoire focusing in an individual donor. Being uniformly positive for a hAA5, and except for an occasional J3-rearranged sequence distinguished by a short length of 11–13 AA, the highly common public δ sequences appeared to confer higher functional avidity when expressed alongside a fixed γ chain, as demonstrated by the TCR transfer experiment, suggesting their functional advantage. However, high-dose pamidronate treatment minimized the difference between the shorter public δ chains and the longer private ones, supposedly through conjugation enhancement and stabilization of the immunological synapse in case of putative low-affinity TCRs (13). Remarkably, as the cells differentiate to effector phenotype in the periphery, public sequences are partly disappearing. Thus, a decline in the number of public clonotypes set by the switch in thymic production from the neonatal to adult-type, more private output (36), is extended further, due to negative selection in the periphery.

Collectively, our results support the role of the specific features of the CDR3 δ as a $\gamma\delta$ 2TCR signaling modulator by demonstrating their steady enrichment associated with

clonotypic expansion, and to a lesser extent with the peripheral repertoire selection *in vivo*. In addition, our results corroborate the paradigm of the orderly evolution of the CDR3δ repertoire, rather than its use for random barcoding. *In vivo* T-cell homeostatic proliferation is related to J region usage, hAA5, and, no less critically, CDR3δ length. At the same time, antigen-driven outgrowth might result in the endorsement of putative low-affinity sequences at the prominent positions in the repertoire and the loss of the high-affinity public sequences.

The expression of NK receptors on terminally differentiated CD8+ αβT cells has been associated with defective TCR signaling and a shift from TCR-mediated to NKR-mediated effector functions, including NKG2D-mediated responses (15, 16, 51). Surprisingly, in the majority of the donors, we found NKG2D expression to decline as γ9δ2T cells mature. NKG2D surface expression could not point to clonotypes with supposed weak γ9δ2TCR signaling, substantiating the notion of its constitutive expression that is uncoupled from the γ9δ2TCR signal strength. In contrast, we observed a bias toward high-affinity CDR3δ features in the surface expression of CD94/NKG2A(B), corroborating the results of the earlier low-throughput study (22). The skewed expression of CD94/NKG2A(B) found here is in line with the activation-inducible expression of this inhibitory NKR in CD8+ αβT cells (52) and its low expression on γ9δ2T cells at the early stages of development, compared to relatively high NKG2D expression already *in utero* (19). We consider the observed CDR3δ bias a likely explanation for the recently reported high antitumor responses of the NKG2A^{Pos} γ9δ2T cells (45).

From the translational standpoint, with the advancing field of γδT cell- and γδTCR-based therapies in mind, the repertoire-phenotype associations explored in this study are crucial. Researchers exploring these areas should consider the fact that donors with the highest numbers of γ9δ2T cells in the periphery, which are likely to be selected for *in vitro* experiments, as it is easy to get sufficient cell numbers, will frequently harbor cells whose phenotype is largely skewed toward terminal differentiation and whose repertoire, in turn, will be skewed to near-oligoclonality, where potentially poorly pAg-reactive clonotypes may take prominent positions. Concerning the design of the high-affinity γ9δ2TCR-based therapies (14, 24), CDR3δ features such as the AA5 and CDR3 length are essential, while J1 region usage might reflect an advantage of the shorter length. Lastly, as a high-affinity γ9δ2TCR will influence the net NKR signaling through upregulation of inhibitory receptors, it is worth modifying this second signal in favor of the activating arm.

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DATA AVAILABILITY STATEMENT

FASTQ files of the TRD sequences are deposited and available under the Sequence Read Archive (SRA) accession code PRJNA851385 (<http://www.ncbi.nlm.nih.gov/bioproject/851385>).

ETHICS STATEMENT

Ethical review and approval was not required for the study on human participants in accordance with the local legislation and institutional requirements. Written informed consent for participation was not required for this study in accordance with the national legislation and the institutional requirements.

AUTHOR CONTRIBUTIONS

AV, AJ, DB, and JK designed the experiments. AV, AJ, LG, AY, SD, and FK performed the experiments and analyzed the data. AV, AJ, and JS generated and analyzed the high-throughput sequencing data. AV and JK wrote the manuscript. DB, TS, ZS, and JK supervised the work. All authors provided critical reviews.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fimmu.2022.915366/full#supplementary-material>

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Conflict of Interest: JK reports grants from Gadeta, Novartis, and Miltenyi Biotech and is the inventor of patents dealing with $\gamma\delta$ T cell-related aspects, as well as the co-founder and shareholder of Gadeta. AV, AJ, DB, and ZS are inventors of patents dealing with $\gamma\delta$ T cell-related aspects.

The remaining 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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$\gamma\delta$ T Cells in the Tumor Microenvironment—Interactions With Other Immune Cells

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A growing number of studies have shown that $\gamma\delta$ T cells play a pivotal role in mediating the clearance of tumors and pathogen-infected cells with their potent cytotoxic, cytolytic, and unique immune-modulating functions. Unlike the more abundant $\alpha\beta$ T cells, $\gamma\delta$ T cells can recognize a broad range of tumors and infected cells without the requirement of antigen presentation *via* major histocompatibility complex (MHC) molecules. Our group has recently demonstrated parts of the mechanisms of T-cell receptor (TCR)-dependent activation of V γ 9V δ 2⁺ T cells by tumors following the presentation of phosphoantigens, intermediates of the mevalonate pathway. This process is mediated through the B7 immunoglobulin family-like butyrophilin 2A1 (BTN2A1) and BTN3A1 complexes. Such recognition results in activation, a robust immunosurveillance process, and elicits rapid $\gamma\delta$ T-cell immune responses. These include targeted cell killing, and the ability to produce copious quantities of cytokines and chemokines to exert immune-modulating properties and to interact with other immune cells. This immune cell network includes $\alpha\beta$ T cells, B cells, dendritic cells, macrophages, monocytes, natural killer cells, and neutrophils, hence heavily influencing the outcome of immune responses. This key role in orchestrating immune cells and their natural tropism for tumor microenvironment makes $\gamma\delta$ T cells an attractive target for cancer immunotherapy. Here, we review the current understanding of these important interactions and highlight the implications of the crosstalk between $\gamma\delta$ T cells and other immune cells in the context of anti-tumor immunity.

Keywords: $\gamma\delta$ T cells, $\alpha\beta$ T cells, B cells, dendritic cells, macrophages, monocytes, natural killer cells, neutrophils

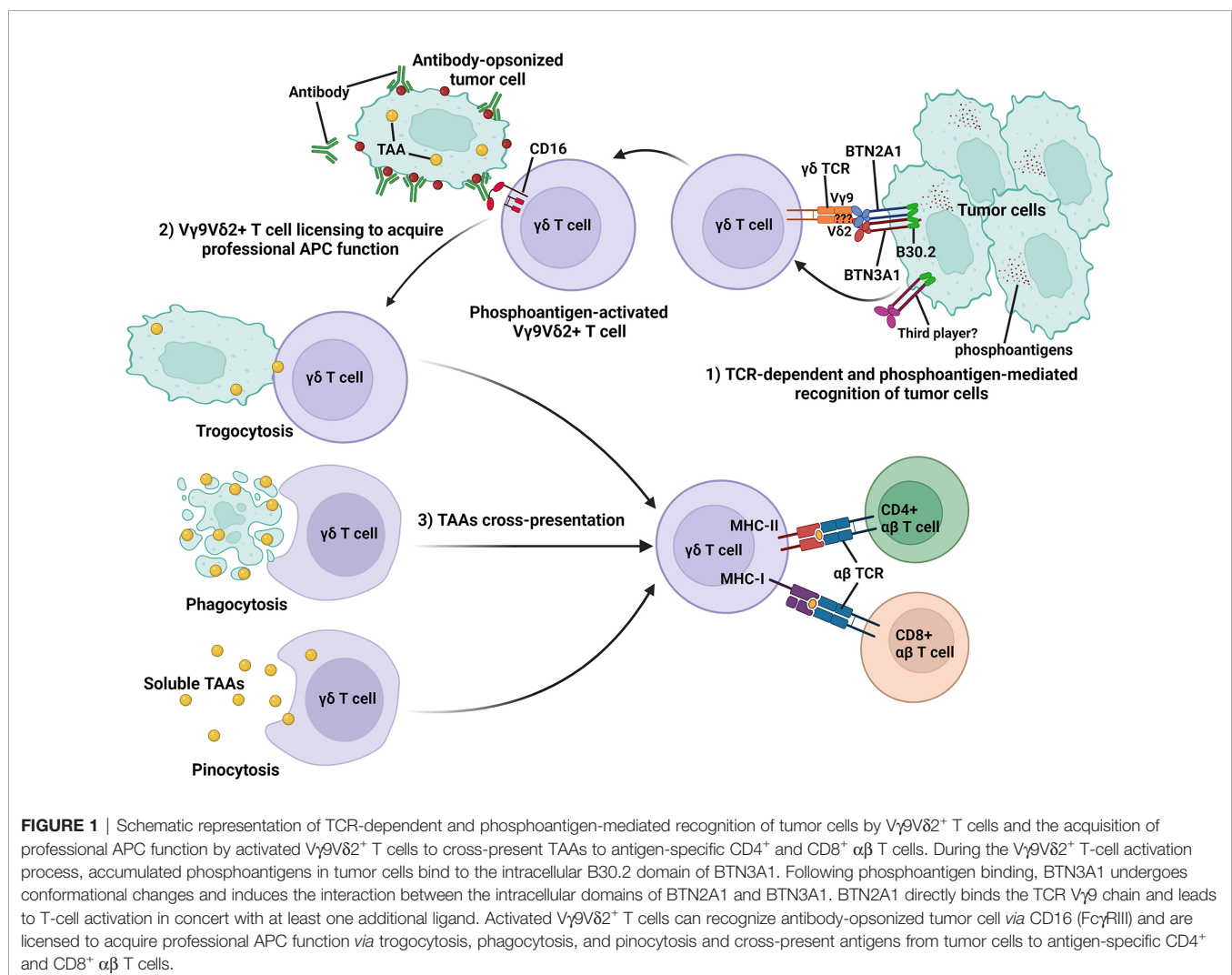
INTRODUCTION

For the past 37 years, since the first isolation of the TCR γ gene segment (1, 2), the knowledge accumulated about the $\gamma\delta$ T-cell lineage has grown exponentially and received strong clinical interest, especially for cancer immunotherapy development (3–15). Similar to the other two lineages of lymphocytes in the jawed vertebrates that utilize somatically recombined receptors for immunosurveillance (B cells and $\alpha\beta$ T cells) (16), TCR heterodimers of $\gamma\delta$ T cells are generated through somatic rearrangements of genes encoding for TCR δ chain variable (V), diversity (D), joining (J), and constant (C) gene segments, and TCR γ chain V, J, and C gene segments at the thymus (17, 18). Hypothetically, such diverse gene rearrangements can result in a total of 10¹⁷

possible distinct $\gamma\delta$ TCRs (19). Despite the diverse theoretical $\gamma\delta$ TCR repertoire, human $\gamma\delta$ T cells can be classified into two major subsets according to their TCR V δ chain usage: V δ 2⁺ populations that are usually paired with V γ 9 chain, and V δ 2⁻ populations with diversified V γ chain usage (6, 20). Among all 8 TCR V δ gene segments, V δ 1, V δ 2, and V δ 3 are three commonly used segments for δ chain rearrangement (21, 22).

V γ 9V δ 2⁺ T cells are the most abundant V δ cell population found in peripheral blood and are activated by phosphorylated non-protein metabolites called phosphoantigens *via* the BTN2A1/BTN3A1 complexes in a TCR-dependent manner (3, 11, 23, 24). Phosphoantigens are derived from the mevalonate pathway as an intermediate metabolite known as isopentenyl pyrophosphate (IPP) (25), or are generated in the microbial non-mevalonate isoprenoid synthesis pathway as (E)-4-hydroxy-3-methyl-but-2-enyl-pyrophosphate (HMBPP) (26). Following phosphoantigen binding to the intracellular B30.2 domains of BTN3A1 in tumor or pathogen-infected cells (27), BTN3A1 undergoes a conformational change (28–30) and promotes the interaction between BTN2A1 and BTN3A1 intracellular

domains (31). Subsequently, the germline-encoded regions of the TCR V γ 9 chain directly bind to BTN2A1 on tumor cells (3, 32, 33), as described by us and confirmed later by others (34–36). An additional but yet to be identified ligand is likely to bind to a separate region within the complementarity-determining region 2 δ (CDR2 δ) and CDR3 γ of the V γ 9V δ 2 TCR for phosphoantigen-mediated V γ 9V δ 2⁺ T-cell activation (3, 33). In concert with BTN2A1, the phosphoantigen-induced conformational change of BTN3A1 then leads to V γ 9V δ 2⁺ T-cell activation (31, 33–36) (**Figure 1**). Accordingly, dysregulation of the mevalonate pathway in tumors was shown to cause activation of V γ 9V δ 2⁺ T cells *via* IPP accumulation (37) and induced $\gamma\delta$ T-cell chemotaxis toward tumor cells (38, 39). Activated V γ 9V δ 2⁺ T cells are capable of inducing cytotoxicity *via* secretion of Th1 cytokines such as tumor necrosis factor- α (TNF- α) and interferon- γ (IFN- γ), pro-apoptotic protease granzyme B, and cytolytic granules containing pore-forming perforin molecules (40–44). Therefore, many clinical studies used aminobisphosphonates (e.g., zoledronate and pamidronate) to inhibit farnesyl pyrophosphate synthase in the



mevalonate pathway to promote accumulation of IPP in cells, or synthetic phosphoantigen analogues such as bromohydrin pyrophosphate (BrHPP) and 2-methyl-3-butenyl-1-pyrophosphate (2M3B1PP), to activate $V\gamma 9V\delta 2^+$ T cells in cancer patients (19, 45–47). In recent years, however, agonist antibodies against BTN3A such as clone 20.1 (48–51), CTX-2026 (52), and ICT-01 (53) have been explored as a phosphoantigen-independent approach to activate $V\gamma 9V\delta 2^+$ T cells for targeted cell killing. Moreover, $V\gamma 9V\delta 2^+$ T cells can be activated by other ligands including human MutS homolog 2, stress-induced MHC class I chain-related antigens A and B (MICA/MICB), UL16-binding proteins (ULBPs), nectin-like-5, staphylococcal enterotoxins (SEs), toxic shock syndrome toxin 1 (TSST-1), and F1-ATPase-apolipoprotein-AI through surface receptors, natural killer group 2D (NKG2D), and DNAX accessory molecule-1 (DNAM-1) (12, 13, 17, 19, 54, 55). Other than

direct targeted cell killing, activated $V\gamma 9V\delta 2^+$ T cells have been implicated to directly or indirectly interact with a range of immune cells: $\alpha\beta$ T cells (56–63), B cells (64–72), natural killer (NK) cells (73–75), monocytes (76–78), macrophages (79–82), neutrophils (78, 83–86), monocyte-derived dendritic cells (moDCs) (87–93), and DCs (72, 76, 94–96), and influence the outcome of the immune responses. The underlying mechanisms of such $\gamma\delta$ T-cell crosstalk with other immune cells are summarized in **Table 1** and will be thoroughly discussed in the following sections.

The non- $V\delta 2$ $\gamma\delta$ T cells are mostly identified with $V\delta 1^+$ or $V\delta 3^+$ TCR chain usage and are localized in the skin, large intestine, spleen, and liver (6, 12, 54). Several studies have shown that $V\delta 1^+$ $\gamma\delta$ T cells recognize CD1c-phosphomycoketide (110), CD1d- α -GalCer (111), CD1d-sulfatide (112, 113), R-phycoerythrin (PE) (114), ephrin receptor A2 (EphA2) (115), and MHC-related

TABLE 1 | Summary of distinct $\gamma\delta$ T-cell subset interactions with other immune cells.

$\gamma\delta$ T-cell subset	Crosstalk target	Comments	References
Pan- $\gamma\delta$	CD4 ⁺ and CD8 ⁺ $\alpha\beta$ T cells	Activated $\gamma\delta$ T cells were capable of professional phagocytosis to mediate presentation of antigens to CD4 ⁺ and CD8 ⁺ $\alpha\beta$ T cells	(62, 97, 98)
	CD4 ⁺ and CD8 ⁺ $\alpha\beta$ T cells; CD4 ⁺ CD25 ⁺ Treg cells	Tumor-activated $\gamma\delta$ T cells induced proliferation and differentiation of CD4 ⁺ and CD8 ⁺ $\alpha\beta$ T cells, mediated cytotoxic function of CD8 ⁺ $\alpha\beta$ T cells and inhibited immunosuppression effect by CD4 ⁺ CD25 ⁺ Treg cells on CD4 ⁺ CD25 ⁺ $\alpha\beta$ T cells	(99)
	B cells	Phosphoantigen-activated $\gamma\delta$ T cells provided B-cell help for the downstream production of IgA, IgG, and IgM antibodies	(68)
	NK cells	IPP-activated $\gamma\delta$ T cells upregulated CD137L expression and co-stimulated CD25 ^{hi} , CD54 ^{hi} , CD69 ^{hi} , CD137 ^{hi} NK cells <i>via</i> CD137/CD137L (4-1BB/4-1BBL) interactions to promote NK cell-mediated cytotoxicity against tumors	(73, 75)
	NK cells	IPP-activated $\gamma\delta$ T cells expressed ICOS and co-stimulated NK cell activation through ICOS/ICOS-L interactions, leading to increased CD137/CD137L signaling and acquisition of NK cell-mediated DC editing function	(100, 101)
$V\delta 1^+$	CD4 ⁺ and CD8 ⁺ $\alpha\beta$ T cells; DCs	Activated $V\delta 1^+$ $\gamma\delta$ T cells suppressed proliferation and IL-2 production by both CD4 ⁺ and CD8 ⁺ $\alpha\beta$ T cells and impaired the maturation and function of DCs. The suppressive activity of activated $V\delta 1^+$ $\gamma\delta$ T cells was mediated by TLR8 signaling pathway	(102)
	DCs	Tumor-derived CXCL10 increased the expansion of $V\delta 1^+$ $\gamma\delta$ Treg cells that infiltrated solid tumors and either induced immune-senescence in DCs or killed DCs	(102–107)
$V\delta 2^+$	CD4 ⁺ $\alpha\beta$ T cells	IPP-activated $V\gamma 9V\delta 2^+$ T cells acquired professional APC functions by upregulating expression of co-stimulatory (CD40, CD80, and CD86), MHC class II and lymph node-homing CCR7 receptors, presented exogenous antigen and induced naïve autologous CD4 ⁺ $\alpha\beta$ T cells to proliferate and differentiate into T helper, Th1 subset	(56)
	CD8 ⁺ $\alpha\beta$ T cells	IPP-activated HLA-A2 ⁺ $V\gamma 9V\delta 2^+$ T cells could uptake soluble antigens, processed and cross-presented immunodominant or subdominant HLA-A2-restricted peptides and primed naïve CD8 ⁺ $\alpha\beta$ T cells for proliferation and effector cell function	(57–61)
	CD8 ⁺ $\alpha\beta$ T cells	IPP-activated $V\gamma 9V\delta 2^+$ T cells upregulated CD36 expression to mediate apoptotic and live tumor cells uptake, cross-presentation, and induction of TAA-specific CD8 ⁺ $\alpha\beta$ T-cell response	(108)
	B cells	$V\gamma 9V\delta 2^+$ T cells promoted the development of antibody-producing B cells <i>via</i> immunoglobulin class switching	(65–67, 69)
	B cells	Activated $V\gamma 9V\delta 2^+$ T cells with functional CCR7 expression induced transient lymph node-homing and clustering within B-cell zones of germinal centers in lymphoid tissues	(64, 68)
	NK cells	IPP-activated $V\delta 2^+$ $\gamma\delta$ T cells induced cytotoxicity against CD56 ⁺ DC-like cells and prematurely terminated NK cell response	(74)
	Monocytes	IPP- or HMBPP-activated $V\delta 2^+$ $\gamma\delta$ T cells induced downregulation of CD14, and upregulation of CD40, CD86, and HLA-DR on monocytes	(76, 77)
	Macrophages	Macrophages recruited $V\delta 2^+$ $\gamma\delta$ T cells to the site of infection <i>via</i> IP-10 and CXCR3; once there they were able to drive the local cytotoxic response <i>via</i> granzyme and perforin release or Fas ligand binding	(79–82)
	Neutrophils	IPP- or HMBPP-activated $V\gamma 9V\delta 2^+$ T cells can induce neutrophil recruitment, migration, adhesion, activation, phagocytosis, and degranulation	(78, 83, 86)
	Neutrophils	TNF- α secretion by $\gamma\delta$ T cells induces reactive oxygen species, arginase-1, and serine protease production from neutrophils, which subsequently inhibits CD25 and CD69 expression, IFN- γ production, and cell proliferation of $V\delta 2^+$ $\gamma\delta$ T cells	(84–86)
$V\delta 3^+$	DCs	Activated $V\gamma 9V\delta 2^+$ T cells secreted IFN- γ and TNF- α and promoted maturation of antigen-expressing immature moDCs in circulation	(87–91, 93)
	DCs	Activated $V\delta 3^+$ $\gamma\delta$ T cells induced immature moDCs to upregulate APC markers CD40, CD83, CD86, and HLA-DR and secreted IL-10 and IL-12. $V\delta 3^+$ $\gamma\delta$ T cell-mediated moDC maturation involved CD1d recognition but not CD40/CD40L interaction. $V\delta 3^+$ $\gamma\delta$ T cell-matured moDCs induced activation of naïve allogeneic T cells.	(109)

protein 1 (MR1) (116) ligands, and play a crucial role for anti-tumor responses (117–124). Similar to $V\delta 2^+$ $\gamma\delta$ T cells, the NKG2D-expressing $V\delta 1^+$ $\gamma\delta$ T cells can be activated by stress-inducible MICA/MICB and ULBP1–6 family proteins, which are frequently upregulated in tumor cells (8, 11). Ligand-bound NKG2D induces cytolytic functions of $\gamma\delta$ T cells *via* granzyme B and perforin secretion to mediate tumor cell killing (125). Several studies have utilized $V\delta 1^+$ $\gamma\delta$ T-cell populations for adoptive cancer immunotherapy (8, 10, 126), but the clinical outcome so far was limited. The less frequent $V\delta 3^+$ $\gamma\delta$ T cells were shown to recognize and kill CD1d⁺ target cells (109) and are activated by annexin A2 ligands on tumor cells that are upregulated under oxidative stress conditions (127). Interestingly, the binding affinity of the $V\delta 1^+$ and $V\delta 3^+$ $\gamma\delta$ TCR ligands identified thus far falls within the range of 3 to 150 μ M (55, 128), comparable to the well-studied $\alpha\beta$ TCR binding affinities for the peptide–MHC complex (129, 130), suggesting a possible shared TCR docking footprint on the bound ligand (131). With the increasing numbers of non- $V\delta 2$ $\gamma\delta$ T-cell ligands uncovered so far (8, 55, 116, 132), different strategies have been developed to utilize activated non- $V\delta 2$ $\gamma\delta$ T cells for cancer immunotherapy (10, 19, 128). Of note, activated non- $V\delta 2$ $\gamma\delta$ T cells have also been implicated to modulate other immune cells (Table 1) including $\alpha\beta$ T cells (102), B cells (133–135), DCs (89, 102–107, 109, 136, 137), macrophages (70, 138), and neutrophils (139).

Human $V\delta 2^+$ $\gamma\delta$ T cells represent ~0.5% to 10% of all circulating T lymphocytes in healthy adults and can undergo rapid expansion of up to 60% in the periphery during infections, and form between 20% to 30% of total infiltrating CD3⁺ T cells in the early stage of disease onset (11, 17). Activated $V\delta 1^+$ and $V\delta 2^+$ $\gamma\delta$ T cells upregulate various C-C chemokine receptor (CCR) such as CCR1 and CCR8 (140), CCR2 (141), CCR5 (142), and C-X-C chemokine receptor 3 (CXCR3) (107) to mediate infiltration into the tumor microenvironment (TME). Additionally, tumor cells and tumor-derived fibroblasts express chemokine ligand 2 (CCL2) (141), IFN- γ -inducible protein 10 (IP-10) (107), monocyte chemoattractant protein 1 (MCP-1), macrophage inflammatory protein 1 α (MIP-1 α), MIP-1 β , and regulated on activation, normal T cell expressed and secreted (RANTES) to promote recruitment of activated $V\delta 1^+$ and $V\delta 2^+$ $\gamma\delta$ T cells to the TME (140). Once recruited into the TME, tumor-infiltrating $V\delta 1^+$ and $V\delta 2^+$ $\gamma\delta$ T cells can eliminate tumor cells *via* TNF-related apoptosis-inducing ligand (TRAIL) (143), Fas/Fas ligand pathway (144), induction of antibody-dependent cellular cytotoxicity (ADCC) on antibody-opsonized tumor cells through CD16 (Fc γ RIII) (60, 145, 146), perforin/granzymes, IFN- γ /TNF- α secretion, and NKG2D-mediated cytotoxicity (13, 147). As a result of the complex interplay between TME and tumor-infiltrating $\gamma\delta$ T cells, activated $\gamma\delta$ T cells can be functionally polarized to become the anti-tumor Th1 and follicular Th (Tfh) cells or the pro-tumor Th17 and T regulatory (Treg) cells (12, 132). For example, IPP-activated $V\gamma 9V\delta 2^+$ T cells can be polarized into three distinct subsets based on the presence of different cytokines in the microenvironment: Th1 [interleukin-12 (IL-12) and anti-IL-4 antibody] (148), Th2 (IL-4 and anti-IL-12 antibody) (148), and

Th17 [IL-1 β , transforming growth factor β (TGF- β), IL-6 and IL-23] (149). Recent reviews on the topic of $\gamma\delta$ T-cell polarization has provided comprehensive insight into the different role of $\gamma\delta$ Th1, Th2, Th17, Tfh, and Treg cells, and we refer readers to these excellent publications (7, 8, 11, 54, 150–153).

Importantly, the presence of tumor-infiltrating $\gamma\delta$ T cells was shown to be the most favorable prognostic marker for overall cancer patients survival in 25 different cancer types and solid tumors (non-brain tumor) (4). Their role in cancer immunosurveillance was clearly evidenced and validated in many tumor models and clinical studies including cutaneous carcinoma (154), melanoma (119, 155, 156), lymphoma (157–159), leukemia (44, 117, 160, 161), gastric (162), colorectal (43, 163, 164), kidney (41), prostate (165, 166), and pancreatic (143) cancers. The ability of $\gamma\delta$ T cells to produce large quantities of cytokines and chemokines rapidly and their tendency to reside in blood circulation or in non-lymphoid tissues (e.g., skin, intestines, and lungs) (8, 16, 17), helps to provide the first line of immunosurveillance against aberrant cell growth and infectious diseases, and bridges the innate and adaptive immune responses. Thus, it is important to understand the crosstalk between $\gamma\delta$ T cells and other immune cells in the TME and to harness this knowledge for effective cancer immunotherapy development.

CROSSTALK BETWEEN $\gamma\delta$ T CELLS AND $\alpha\beta$ T CELLS

The role of antigen processing and presentation to $\alpha\beta$ T cells is mostly associated with the classical professional antigen-presenting cells (APCs) like DCs, macrophages, and B cells (167, 168). However, with the unexpected discovery by Brandes et al., it was shown that activated but not resting human $V\gamma 9V\delta 2^+$ T cells were also capable of acquiring professional APC functions (56). Indeed, activated $V\gamma 9V\delta 2^+$ T cells isolated from both healthy individuals and cancer patients' peripheral blood mononuclear cell (PBMC) exhibited potent APC functions to stimulate robust antigen-specific $\alpha\beta$ T-cell responses (169).

During the activation process, human $V\gamma 9V\delta 2^+$ T cells can rapidly gain APC functions by upregulating co-stimulatory (CD40, CD80, and CD86), MHC class I and II molecules (56, 57, 61, 62, 97, 108, 169), and transiently expressed lymph node-homing markers, chemokine receptor CCR4 and CCR7 (62, 68, 97). This allows recruitment of activated $\gamma\delta$ T cells from the peripheral sites to secondary lymphoid tissues for antigen presentation and bridges the early phase of rapid innate-like $\gamma\delta$ T-cell response to microbial or tumor antigens with the later phase of adaptive immune response involving the antigen-specific CD4⁺ and CD8⁺ $\alpha\beta$ T cells (14, 15, 17, 168, 170). In a study by Himoudi et al., it was shown that activated human $V\gamma 9V\delta 2^+$ T cells were “licensed” to acquire their APC functions through recognition of antibody-opsonized tumor cells, mediated targeted cell killing by their innate cytotoxicity, and subsequently helped to release tumor-

responses in naïve $CD4^+ \alpha\beta$ T cells (56). Activated $V\gamma9V\delta2^+$ T cells were also able to cross-present antigens to $CD8^+ \alpha\beta$ T cells with a higher efficiency and reproducibility (57), and induced less $CD4^+ CD25^{hi}$ FoxP3⁺ Treg cell expansion than moDCs (59). Similar results were seen under pathological condition, when it was shown that $\gamma\delta$ T cells isolated from gastric cancer patients can acquire APC functions upon activation with cells derived from autologous tumor tissues (99). These clinically relevant tumor-activated $\gamma\delta$ T cells induced strong antigen-specific $CD4^+$ and $CD8^+ \alpha\beta$ T-cell responses and prevented immunosuppression mediated by $CD4^+ CD25^+$ Treg cells (99) (**Figure 2**). Of note, Muto et al. showed that resting $V\gamma9V\delta2^+$ T cells can significantly upregulate the expression of scavenger receptor CD36 during activation and that this was mediated by a key transcription factor, CCAAT/enhancer-binding protein α (C/EBP α), that supports acquisition of APC functions in activated $V\gamma9V\delta2^+$ T cells (108). In contrast, resting $\alpha\beta$ T cells expressed a low level of CD36 and did not upregulate it upon activation (108). In DCs and macrophages, the CD36 receptor was shown to facilitate the uptake of apoptotic cells and cross-presentation (173, 174), potentially explaining the induction of a stronger antigen-specific $\alpha\beta$ T-cell response by activated $V\gamma9V\delta2^+$ T-cell APC.

The ability to migrate to the tumor site and cross-present TAAs to $\alpha\beta$ T cells was also retained when $V\delta1^+$ and $V\delta2^+$ $\gamma\delta$ T cells were engineered to express tumor-specific chimeric antigen receptors (CARs) and resulted in an increased cytotoxic level against tumor cells (175). Hence, activated $V\gamma9V\delta2^+$ T cells can process and present antigens and provide critical co-stimulatory signals to prime and induce naïve $CD4^+$ (56) and $CD8^+$ (57) $\alpha\beta$ T cells for proliferation, differentiation, and cytokine production and to mediate cytotoxic responses against tumors and pathogen-infected cells (176–179). This remarkable ability of $\gamma\delta$ T cells to uptake and present antigens and prime $\alpha\beta$ T cells has been highlighted by Vantourout et al. (168), and the accumulated data so far have illustrated the potential of harnessing the APC functions of $\gamma\delta$ T cells to crosstalk with $\alpha\beta$ T cells for immunotherapy development.

Given their natural tropism for TME (14, 119, 175, 180–182), activated $\gamma\delta$ T cells could hence be utilized to prolong the intratumoral immune response by cross-presenting TAAs to other tumor-infiltrating lymphocytes and provide an early source of IFN- γ to expand and increase immunogenicity of TAA-specific $\alpha\beta$ T cells within the TME (155, 183, 184), and to upregulate expression of MHC class I and II on tumor cells (185, 186) for $\alpha\beta$ T cell-mediated killing (**Figure 2**). The presence of tumor-infiltrating $\gamma\delta$ T cells within the TME as revealed by genomic data analysis in over 18,000 human tumors has uncovered a strong correlation to good prognosis (4). In the context of cancer immunotherapy, the capability of activated $\gamma\delta$ T cells to cross-present TAAs to $\alpha\beta$ T cells could be further boosted through the “licensing” pathway (60, 187) by using therapeutic monoclonal antibodies against tumor cells, e.g., rituximab (anti-CD20) and trastuzumab (anti-HER2/neu) (145, 188, 189). Such combination treatment could greatly improve the outcome of $\gamma\delta$ T-cell cancer immunotherapy.

Activated $V\gamma9V\delta2^+$ T cells can also modulate $\alpha\beta$ T-cell activity indirectly by co-stimulating NK cells *via* inducible T-cell co-stimulator (ICOS)/ICOS-L and CD137/CD137L engagements to enhance IFN- γ and TNF- α production (100, 101), which, in turn, helps to support $\alpha\beta$ T-cell activation (190). Another study has shown that activated $V\gamma9V\delta2^+$ T cells can induce B-cell and DC maturation and subsequently leads to alloreactive stimulation of $\alpha\beta$ T-cell proliferation and IFN- γ production by mature B cells and DCs (72). The interactions between $\gamma\delta$ T cells and other immune cells (B cells, DCs, and NK cells) will be discussed later in this review.

Despite their ability to exert positive immune modulation functions on $\alpha\beta$ T cells, activated $\gamma\delta$ T cells can also negatively regulate $\alpha\beta$ T-cell response by upregulating an immune checkpoint inhibitory ligand, programmed cell death 1 ligand 1 (PD-L1) (11, 151, 191). The suppressive phenotype of activated $V\delta2^+$ $\gamma\delta$ T cells on autologous $\alpha\beta$ T cells was shown to be mediated by the PD-1/PD-L1 interactions and correlated well with the strength of $V\delta2^+$ $\gamma\delta$ TCR signaling during the activation process but was independent of TGF- β and FoxP3 expression (192) (**Figure 2**). Daley et al. showed that tumor-infiltrating $\gamma\delta$ T cells with high expression levels of checkpoint inhibitory ligands PD-L1 and Galectin-9 could inhibit $\alpha\beta$ T-cell activation through checkpoint receptor ligation (193). The immunosuppressive effect can also be mediated by the interaction between CD86 on activated $V\delta2^+$ $\gamma\delta$ T cell and cytotoxic T lymphocyte-associated antigen 4 (CTLA-4) on activated $\alpha\beta$ T cells (191). Such $\gamma\delta$ T cell-mediated immunosuppression of $\alpha\beta$ T cells, however, can be significantly reduced by disrupting PD-1/PD-L1 and CTLA-4/CD86 interactions with blocking antibodies (191, 192). Furthermore, Peng et al. identified tumor-infiltrating $V\delta1^+$ $\gamma\delta$ T cells that could suppress naïve/effector $\alpha\beta$ T-cell proliferation and IL-2 production through the Toll-like receptor (TLR) 8 signaling pathway and may lead to tumor immune escape (102). The immunosuppressive activity of $V\delta1^+$ $\gamma\delta$ T cells can be reversed using TLR8 ligands, and this signaling involved the myeloid differentiation primary response 88 (MyD88), TNFR-associated factor 6 (TRAF6), IKB kinase α (IKK α), IKK β , and mitogen-activated protein kinase 14 (MAPK14), but not transforming growth factor- β -activated kinase 1 (TAK1), Jun N-terminal kinase (JNK), and extracellular signal-regulated kinase (ERK) molecules in $V\delta1^+$ $\gamma\delta$ T cells (102). It was also reported that $\gamma\delta^+$ NKG2A⁺ intraepithelial lymphocytes (IELs) can mediate suppression of $CD8^+ \alpha\beta^+$ IEL cytotoxic responses (IFN- γ and granzyme B) in patients with celiac disease through TGF- β secretion (194). The immunosuppressive effect on $CD8^+ \alpha\beta^+$ IELs can be further enhanced upon $\gamma\delta^+$ IELs NKG2A receptor ligation with the cognate ligand, human leukocyte antigen-E (HLA-E) (194). This immunosuppressive effect can be reduced by blocking NKG2A/HLA-E interaction and TGF- β with blocking antibodies (194). Therefore, it is important to consider these negative immunomodulatory roles of $\gamma\delta$ T cells when designing novel immunotherapeutics.

Apart from the PD-1/PD-L1 and CTLA-4/CD86 immune checkpoint axes, other non-conventional checkpoint

receptors [killer Ig-like inhibitory receptors (KIRs), Ig-like transcript 2 (ILT-2), and NKG2A] can be expressed on $V\gamma9V\delta2^+$ T cells, inhibit their cytotoxic function, and prevent tumor cell lysis upon recognition of specific HLA class I ligands on tumor cells (195–203). In this context, the presentation of HLA class I molecules on tumor cells can be a double-edged sword. On one hand, it facilitates the presentation of antigenic peptides to activate $CD8^+ \alpha\beta$ T cells, but at the same time, it can also inhibit the activation of $V\gamma9V\delta2^+$ T cells. Such inhibitory signals on immune cells mediated by KIRs, ILT-2, or NKG2A can be blocked using monoclonal antibodies targeting KIRs (lirilumab and IPH4102), ILT-2 (anti-ILT-2, anti-HLA-G1, anti-FasL), or NKG2A (monalizumab) (204, 205). In a study by André et al., treatment with monalizumab indeed led to enhanced anti-tumor immune responses elicited by T and NK cells (206). As a type 2 inhibitory membrane receptor, NKG2A carries cytoplasmic immunoreceptor tyrosine-based inhibitory motifs (ITIMs) and forms heterodimers with CD94 to recognize non-classical HLA-E molecule (207). Many human tumors have been shown to express HLA-E including in the colon, cervical, endometrial, head and neck, liver, lung, pancreas, ovarian, and stomach (206). Moreover, a majority of $V\gamma9V\delta2^+$ T cells in healthy individuals express NKG2A/CD94 (197, 198, 200, 208), and the expression levels can be induced by IL-15 and TGF- β (209, 210). Therefore, treatments targeting these non-conventional checkpoint receptors on $V\gamma9V\delta2^+$ T cells (KIRs, ILT-2, and NKG2A) to disrupt the interactions with their respective HLA class I ligands on tumor cells (HLA-C, HLA-G, and HLA-E) may help to enhance the effectiveness of $V\gamma9V\delta2^+$ T cell-based tumor immunotherapy.

Recent work by Payne et al. suggests that BTN3A, itself part of the molecular complex required for phosphoantigen-mediated activation of $V\gamma9V\delta2^+$ T cells, can also inhibit tumor-reactive $CD8^+ \alpha\beta$ T cells when bound to N-mannosylated residues of CD45 by preventing its segregation from the immunological synapse (52). In this study, the suppression of $\alpha\beta$ T-cell activation was shown to involve BTN3A1 but not BTN2A1, and the immunosuppressive effect could be blocked by BTN3A1-specific monoclonal antibodies such as clone 20.1, 103.2, and CTX-2026 (52). Targeting BTN3A1 with the agonistic antibody CTX-2026 induced BTN3A1 switching from immunosuppressive to immunostimulatory conformations and promoted coordinated $V\gamma9V\delta2^+$ and $CD8^+ \alpha\beta$ T-cell anti-tumor responses against BTN3A1⁺ tumors (52). Hence, BTN3A1 may be an attractive immune target for intervention to orchestrate effective and coordinated $\gamma\delta$ and $\alpha\beta$ T-cell anti-tumor responses.

CROSSTALK BETWEEN $\gamma\delta$ T CELLS AND B CELLS

$\gamma\delta$ T cells have been previously reported to interact with B cells and modulate their immune functions (5, 8, 168, 211, 212).

$V\gamma9V\delta2^+$ T cells can adopt a role similar to T follicular helper (Tfh) cells and provide B-cell help, thereby regulating B-cell maturation. Specifically, a subset of $CXCR5^+$ $V\gamma9V\delta2^+$ T cells present in circulation and in tonsil tissue expresses co-stimulatory molecules (ICOS and CD40L) upon antigen stimulation and secrete cytokines (IL-2, IL-4, and IL-10), which can promote the development of antibody-producing B cells *via* immunoglobulin class switching [including immunoglobulin A (IgA), IgE, IgG1, IgG2, IgG3, and IgG4] (8, 213, 214) in the extra-follicular or within germinal centers (65–67, 69) (Figure 2). Furthermore, upon stimulation with IL-21 and HMBPP, activated tonsillar $V\gamma9V\delta2^+$ T cells can express CXCL13 receptor, CXCR5, induce lymphoid-homing phenotype and clustering in germinal centers, and sustain the production of germinal centers (70, 71). Similarly, IPP-stimulated $V\delta2^+$ $\gamma\delta$ T cells with functional CCR7 expression can also induce transient lymph node-homing, migration, and clustering of $V\delta2^+$ $\gamma\delta$ T cells within B-cell zones of germinal centers in lymphoid tissues (64, 68).

Phosphoantigen-activated $V\delta2^+$ $\gamma\delta$ T cells can additionally induce the expression of B-cell co-stimulatory molecules (CD40L, OX40, CD70, and ICOS) and affect the downstream production of circulating IgA, IgG, and IgM antibodies by B cells (68). In patients with specific mutations (*RAG1* and *CD3D*) that impair $\alpha\beta$ T-cell function, $\gamma\delta$ T cells are responsible for hyper-IgE syndromes or the elevated production of circulating IgA, IgG, and IgM (215, 216). $\gamma\delta$ T cells can also suppress antibody responses *via* the induction of $CD4^+$ Foxp3⁺ Treg cells (217). Conversely, some B cells can express BTN2A1 and BTN3A1, required for $V\gamma9V\delta2^+$ T-cell activation (33–35), thereby directly influencing $V\delta2^+$ $\gamma\delta$ T-cell activation (218, 219) as shown by early studies using Daudi cells, a B-cell malignancy cell line (Burkitt's lymphoma) (220–226). $V\gamma9V\delta2^+$ T cells can directly engage BTN2A1 expressed on B cells *via* the TCR $V\gamma9$ chain (3, 32–36, 227), and in concert with BTN3A1, this results in $V\gamma9V\delta2^+$ T-cell activation and expansion (101, 212). Hebbeler et al. showed that the $V\gamma9V\delta2^+$ T cells activated and expanded by phosphoantigen or Daudi B lymphoma cells use public TCR $V\gamma9$ clonotypes, and elicit comparable cytotoxic responses against tumor cells (228). Further investigations revealed that the germline-encoded region between TCR $V\gamma9$ CDR2 and CDR3 is responsible for contacting BTN2A1 on target cells (33, 34). Such findings indicate the inherent property of TCR $V\gamma9$ to recognize diverse range of cell types that express BTN2A1 including B cells (212, 227–229). In addition to BTN2A1 and BTN3A1, B cells also express other closely related BTN molecules such as BTN3A2 (in naïve or germinal center B cells), BTN3A3 (in memory B cells), BTN1A1, and BTN2A2 (3, 50). The contribution of these other BTN molecules in B cells for $\gamma\delta$ T-cell activation remains elusive. Similarly, circulating activated $B7^+$ $CD39^+$ B cells can stimulate $V\delta1^+$ $\gamma\delta$ T-cell proliferation (133, 134). The $V\delta1^+$ $\gamma\delta$ T-cell stimulatory ligand is upregulated in B cells upon activation and can induce polyclonal $V\delta1^+$ $\gamma\delta$ T-cell responses (133). This B cell-mediated immunostimulatory effect on $V\delta1^+$ $\gamma\delta$ T cells can be blocked with antibodies against B7 and CD39 (133, 212).

In summary, $V\gamma9V\delta2^+$ T cells can regulate B-cell maturation during development or initiation of an immune response, sustain the production of germinal centers within secondary and possibly tertiary lymphoid structures, and affect the production of circulating (auto)antibodies for humoral immunity (168, 211, 212), while B cells can activate $V\delta1^+$ and $V\gamma9V\delta2^+$ T cells (230).

CROSSTALK BETWEEN $\gamma\delta$ T CELLS AND NK CELLS

Human NK cells are important innate immune subset for controlling early tumor growth and metastasis through cell-mediated cytotoxicity and show broad reactivity to tumors that escaped immunosurveillance by loss or aberrant MHC class I expression (14, 231, 232). Being a specialized group of innate lymphoid cells (ILCs), NK cell functions are closely regulated by a range of cytokines such as IFN- γ , TNF- α , IL-2, IL-12, IL-15, IL-18, and IL-21 (233, 234). These effector molecules are important for the initiation of anti-viral and anti-tumor immune responses (235–238). However, more established tumors can evade NK cell surveillance by developing resistance to NK cell-mediated cytotoxicity, leading to tumor immune escape (239).

In order to overcome NK-resistant tumors, Maniar et al. showed that activated human NK cells ($CD25^{hi}$, $CD54^{hi}$, $CD69^{hi}$, and $CD137^{hi}$) increased surface expression of natural NKG2D receptors to promote tumor cytolysis and death (73). NKG2D is a lectin-like type 2 transmembrane receptor mostly expressed by human NK cells and binds to MHC-related ligands such as ULBPs, MICA, and MICB, which are highly expressed in tumor cells but rarely in healthy cells (231, 240). IPP-activated $V\delta2^+$ $\gamma\delta$ T cells upregulate CD137L (4-1BBL), engage with $CD137^+$ NK cells, and can in turn lead to enhanced NKG2D expression and NK cell-mediated cytotoxicity against tumors (73) (**Figure 2**), highlighting a potential key role for $\gamma\delta$ T cells in this process. CD137 or 4-1BB is a member of the tumor necrosis factor receptor superfamily (TNFRSF) and is expressed by a range of immune cells (190). Expression of CD137 on NK cells is induced by IL-2 and IL-15, and following CD137 signaling, it promotes NK cell proliferation and production of IFN- γ , which, in turn, can support NK tumor effector functions (101, 190). This finding was further corroborated by Liu et al., and they demonstrated that in the context of liver fibrosis, $\gamma\delta$ T cells engaged with conventional and liver-resident NK cells through CD137/CD137L interactions to promote NK cell-mediated cytotoxicity against activated hepatic stellate cells and conferred immune protection (75).

Similar to NK and $CD8^+$ $\alpha\beta$ T cells, human $\gamma\delta$ T cells also express NKG2D to detect stress-inducible ligands on tumors and pathogen-infected cells (125, 241–245). Several studies have shown that NKG2D ligation to its cognate ligand can co-stimulate $V\gamma9V\delta2^+$ T-cell activation (CD25 and CD69 upregulation) and promotes the release of IFN- γ , TNF- α , and cytolytic granules to mediate killing of NKG2D ligand-

expressing tumors (163, 246–251). In the context of leukemia and lymphoma cell recognition by $V\gamma9V\delta2^+$ T cells, it was reported that tumor-expressed ULBP1 was a strong marker for tumors susceptible to $V\gamma9V\delta2^+$ T cell-mediated cytotoxicity (252). Similarly, it was shown that ULBP1 overexpression in tumor cells can lead to enhanced killing by $V\gamma9V\delta2^+$ T cells (253). Hence, blocking NKG2D-mediated $V\gamma9V\delta2^+$ T-cell recognition of tumor cells with anti-NKG2D and anti-MICA/B monoclonal antibodies inhibits tumor cell killing to varying degrees (247, 249, 253). $V\delta1^+$ $\gamma\delta$ T cells can also recognize and kill NKG2D ligand-expressing tumors *via* NKG2D receptor (8, 11, 245, 254). The number of $V\delta1^+$ $\gamma\delta$ T cells and ULBP3 expression level are negatively correlated with disease progression in chronic lymphocytic leukemia patients (254). A study reported by Kamei et al. demonstrated a longer overall survival in gastric cancer patients with high expression levels of NKG2D and ULBP1 (255). Hence, upregulation of stress-inducible NKG2D ligand in tumor cells and NKG2D receptor in tumor-infiltrating immune cells can help to orchestrate concerted NKG2D-mediated NK, $CD8^+$ $\alpha\beta$, and $\gamma\delta$ T-cell anti-tumor responses within the TME. Of note, several anti-cancer drugs have been found to induce expression of NKG2D ligand in tumor cells, including the proteasome inhibitor bortezomib and the alkylating agent temozolomide, and these can help to promote tumor cell lysis by NK and $\gamma\delta$ T cells (256, 257). Therefore, it is feasible to target NKG2D and its ligands for $\gamma\delta$ T cell-based immunotherapy development.

It was later shown that IPP-activated $V\gamma9V\delta2^+$ T cells can upregulate ICOS and signal NK cells *via* ICOS/ICOS-L engagement to promote CD69 and CD137 expression, which then leads to enhanced production of IFN- γ , TNF- α , MIP-1 β , I-309, RANTES, and soluble Fas ligand by activated NK cells (100). Such ICOS/ICOS-L-mediated crosstalk enables NK cells to acquire the “license” to kill mature DCs that may play a role in inflammation and tumor growth (100). These studies have uncovered the immunomodulatory role of IPP-activated $V\gamma9V\delta2^+$ T cells to circumvent NK-resistant tumors and to promote NK-mediated DC editing function by modulating NK cell cytotoxicity through CD137/CD137L and ICOS/ICOS-L engagements (73, 101) (**Figure 2**). Such findings will provide an alternative strategy for $\gamma\delta$ T cell-based immunotherapy development against difficult-to-treat solid tumors or to prevent metastasis (239, 258, 259).

However, NK cell activity can also be negatively regulated by $\gamma\delta$ T cells. Zoledronate-activated $V\delta2^+$ $\gamma\delta$ T cells not only can co-stimulate early NK cell activation for IFN- γ production but also lead to premature ending of the response by inducing cytotoxicity against $CD56^+$ DC-like cells (74). In the absence of activated $V\delta2^+$ $\gamma\delta$ T cells, $CD56^+$ DC-like cells survived (74) and maintained NK cell activity through secretion of NK cell-activating cytokines such as IL-1 β and IL-18 (260, 261). Therefore, further studies will help to provide a better understanding of the immunosuppressive role of $V\delta2^+$ $\gamma\delta$ T cells on NK cells.

CROSSTALK BETWEEN $\gamma\delta$ T CELLS AND MONOCYTES/MACROPHAGES

$\gamma\delta$ T cells share many of their innate functions with other immune cell subsets, including NK cells, monocytes, and macrophages (56, 98, 262, 263). These are integral to the innate inflammatory response against infectious pathogens and tumors, which, in turn, activates a strong and targeted adaptive immune response (170). While the hallmark of $V\gamma9V\delta2^+$ T cell is recognition of phosphoantigens produced by bacteria-infected or tumor cells (25, 264), monocytes are adept at potentiating this process by taking up and accumulating phosphoantigen for subsequent presentation to $\gamma\delta$ T cells (262, 263). Conversely, the prototypical roles of myeloid cells, such as phagocytosis and MHC class II presentation, are also shared by $V\gamma9V\delta2^+$ T cells, which can act as professional APCs (56, 98). The close interconnection between these cell types and partial redundancy in functional properties denotes multiple implications for tumor immunity.

$V\gamma9V\delta2^+$ T cells have been shown to activate monocytes, induce adhesion and aggregation, and increase their survival (76, 265). This occurs *via* production of inflammatory molecules including IFN- γ , TNF- α , granulocyte-macrophage colony stimulating factor (GM-CSF), lymphocyte function-associated antigen 1 (LFA-1), and CCL2 (76, 78). In turn, this leads to changes in monocyte markers such as downregulation of CD14, and upregulation of CD40, CD86, and HLA-DR (76, 77) (**Figure 2**). Bidirectionally, zoledronate- or HMBPP-primed monocytes can activate $V\gamma9V\delta2^+$ T cells through phosphoantigen accumulation and presentation, leading to $\gamma\delta$ T-cell proliferation and bacterial pathogen killing (76, 263). However, *in vitro*, it has also been reported that in the presence of zoledronate, monocytes and $V\delta2^+$ $\gamma\delta$ T cells can negatively regulate each other by inducing apoptosis (266, 267). It is interesting to note that the contact-dependent stimulation of $V\gamma9V\delta2^+$ T cells by monocytes *via* the intercellular adhesion molecule 1 (ICAM-1)/LFA-1 engagement can be disrupted by blocking CD11a with monoclonal antibody (78). In contrast to these *in vitro* results, *in vivo* treatment with zoledronate or other aminobisphosphonates has shown varying effects, with some studies reporting an increase in circulating monocyte numbers, while others found no difference (77, 268). This suggests that the relationship between these cells may be more nuanced and context-dependent than first thought and will require further investigation.

The crosstalk between $\gamma\delta$ T cells and macrophages has not yet been thoroughly elucidated; however, the effects are again cell subtype- and context-dependent. Macrophages have been demonstrated to recruit $V\gamma9V\delta2^+$ T cells to the site of infection *via* IP-10 and CXCR3 receptor–ligand interactions (80). Once this occurs, $V\delta2^+$ $\gamma\delta$ T cells can drive the local cytotoxic response *via* granzyme and perforin release or Fas ligand binding (79, 81, 82). Both $V\delta1^+$ cells and $V\delta2^+$ cells have been shown to produce CCL3, CCL4 (MIP-1 α and MIP-1 β), and CXCL10, which find their respective cognate receptors expressed by macrophages (70, 138). *In vitro*, the supernatant of cultured $\gamma\delta$ T cells has been shown to induce macrophage activation *via* IFN- γ , TNF- α , and GM-CSF production, arguing for a tightly regulated and

balanced interplay between these immune cell populations (265). This was further demonstrated by studies showing that IFN- γ and TNF- α released by activated $V\gamma9V\delta2^+$ T cells can induce cyclooxygenase-2 (COX2) expression and prostaglandin E2 (PGE2) release by both macrophages (**Figure 2**) and tumor cells, and this downregulates the cytotoxic response of $\gamma\delta$ T cells (269, 270) and plays a major role in tumor immune escape (271, 272). Furthermore, galectin-9 on both $\gamma\delta$ T cells and pancreatic tumor cells has been shown to bind dectin-1 on tumor-infiltrating macrophages, leading to M2 macrophage polarization and subsequent downregulation of IFN- γ and TNF- α production by $\gamma\delta$ T cells (273, 274).

CROSSTALK BETWEEN $\gamma\delta$ T CELLS AND NEUTROPHILS

Neutrophils are another immune cell population with complex interactions with $\gamma\delta$ T cells at peripheral sites of inflammation and in the TME. Zoledronate-activated $V\gamma9V\delta2^+$ T cells release cytokines and chemokines such as IFN- γ , TNF- α , IL-6, and MCP-2, and these have been demonstrated *in vitro* to induce neutrophil migration, activation, phagocytosis, degranulation, and release of α -defensins (83). In a differing context using a bacterial phosphoantigen, HMBPP-activated $V\gamma9V\delta2^+$ T cells produce CXCL8 and TNF- α , which together mediate neutrophil recruitment, induce CD11b upregulation and prevent apoptosis, and downregulate CD62L, allowing neutrophil adhesion (78). This finding was further corroborated by Sabbione et al., showing that HMBPP-activated $V\delta2^+$ $\gamma\delta$ T cells can stimulate CD11b expression and myeloperoxidase production by neutrophils (86), all of which imply a stimulatory role of $\gamma\delta$ T cells towards these granulocytes. In another study, tissue-resident $V\delta1^+$ $\gamma\delta$ T cells were shown to regulate the recruitment of neutrophils to the site of bacterial infection *via* IL-17 secretion (275). In the absence of $V\delta1^+$ $\gamma\delta$ T cells, the production of IL-17 is reduced and leads to lower numbers of neutrophil recruitment to the site of infection (275).

Interestingly, activated neutrophils can inhibit CD25 and CD69 expression, IFN- γ production, and cell proliferation of $V\delta2^+$ $\gamma\delta$ T cells either spontaneously or in response to HMBPP (86). This is dependent on initial TNF- α production by $\gamma\delta$ T cells, which then induces reactive oxygen species (ROS) secretion from neutrophils (86) (**Figure 2**). These processes can be independent of cell–cell contact; however, the inhibition is more potent if cells are allowed to interact and form conjugates (86). Neutrophils can take up zoledronate, and despite also expressing BTN2A1 and BTN3A1, they do not have the capability of activating $V\gamma9V\delta2^+$ T cells, which may be due to their extremely limited production and accumulation of IPP (276–278). Rather, these zoledronate-activated neutrophils inhibit TNF- α and IFN- γ production and proliferation of $V\gamma9V\delta2^+$ T cells *via* ROS, arginase-1, and serine protease production. Some serine proteases are also able to downregulate BTN3A1 expression on PBMCs, which has

downstream consequences for BTN-mediated activation of $V\delta 2^+$ $\gamma\delta$ T cells (84, 85). Furthermore, $V\delta 1^+$ $\gamma\delta$ T cells have been shown to exhibit reduced proliferation in the presence of hydrogen peroxide as well as decreased glutathione production, which may be indicative of ROS-dependent neutrophil inhibition (139). In some instances, however, neutrophils that have phagocytosed HMBPP-producing bacteria subsequently release HMBPP, which is then able to activate $V\gamma 9V\delta 2^+$ T cells. This results in CD25, CD69, LFA-1, IFN- γ , and TNF- α production and is crucial for initiating an immediate anti-inflammatory response (78).

Functionally, pancreatic tumor cell killing by $\gamma\delta$ T cells within a PBMC context is decreased in the presence of neutrophils, in both unstimulated and zoledronate-activated conditions (279). However, when pancreatic tumor cells are co-cultured with purified, expanded $\gamma\delta$ T cells and neutrophils, tumor cell lysis is increased compared to co-culture with $\gamma\delta$ T cells alone, which can be attributed to elevated granzyme B and IFN- γ production. These conflicting observations may be explained by differences in immune cell subpopulation crosstalk within PBMCs, or by differing polarization of neutrophils: N1 neutrophils are tumor suppressive while N2 neutrophils have a pro-tumoral phenotype (280). It is worth noting that a higher neutrophil-to-lymphocyte ratio in a cohort study of 1,714 cancer patients treated with immune checkpoint inhibitors was recently reported to significantly correlate with low progression-free survival, poor response rates, and low clinical benefit (281). Considering the immunosuppressive functions of activated neutrophils on $\gamma\delta$ T-cell activation as discussed above, this may partly contribute to the poor outcomes in cancer patients with higher neutrophil-to-lymphocyte ratios.

CROSSTALK BETWEEN $\gamma\delta$ T CELLS AND DENDRITIC CELLS

DCs are professional APCs, and consist of classical or conventional DCs (cDCs), including cDC1 (CD11c $^+$ and CD141 $^+$) and cDC2 (CD11c $^+$ and CD1c $^+$), and plasmacytoid DCs (pDCs, CD11c $^-$, CD123 $^+$, and CD303 $^+$) (282, 283). Their key role in anti-tumor immunity is well described, but the interactions between DCs and $\gamma\delta$ T cells is lacking behind. It has been shown that upon recognition of bacteria-infected or tumor cells, activated $V\gamma 9V\delta 2^+$ T cells can aid DC maturation through cytokine secretion (IFN- γ and TNF- α) (87, 88), and promote maturation of antigen-expressing immature DCs (monocyte-derived) in circulation *via* contact-dependent mechanisms (Fas/FasL, CD40/CD40L, and TCR/CD1) independent from TLR signaling (89–91, 93) (Figure 2). These $V\gamma 9V\delta 2^+$ T cell-matured DCs upregulate HLA-DR, CD25, CD40, CD80, CD83, and CD86, and are capable of cytokine production (TNF- α , IL-12, and IL-15, but not IL-10), antigen presentation, and stimulation of naïve CD4 $^+$ $\alpha\beta$ T cells (76, 87, 89, 92, 284–288). In addition, $V\gamma 9V\delta 2^+$ T cell-derived cytokines (IFN- γ and TNF- α) can also enhance TLR-dependent DC maturation, upregulate CCR7 (lymph node-homing receptor), and facilitate their migration to lymphoid tissues for CD4 $^+$ $\alpha\beta$ T-cell priming (289, 290).

In contrast, the tumor-derived chemokine ligand CXCL10 can promote the expansion of $V\delta 1^+$ $\gamma\delta$ Treg cells that infiltrate solid tumors and induce immune senescence in DCs, and prevent DC maturation (by inhibiting CD80, CD83, CD86, and HLA-DR expression), DC function (decreased IL-6 and IL-12 production), and DC phenotype (inability to stimulate naïve T-cell proliferation) *via* the TLR8 signaling pathway or by killing of DCs through a perforin-mediated pathway (102–107) (Figure 2).

In turn, DCs can mediate $V\gamma 9V\delta 2^+$ T-cell activation by sensing/presenting HMBPP and induce $\gamma\delta$ T-cell proliferation in the presence of IL-2, IL-15, and IL-21 (76, 94–96). Immature DCs can enhance the ability of $V\gamma 9V\delta 2^+$ T cells to secrete inflammatory cytokines necessary for $\gamma\delta$ T-cell maturation (TNF- α) in part due to the ability of DCs to upregulate and/or sense phosphoantigens (88). Mature cDCs and pDCs (monocyte-derived) can secrete cytokines (IL-1 β , IL-12, IL-18, IFN- γ , and TNF- α) that activate $V\gamma 9V\delta 2^+$ T cells, enhancing their proliferation and cytotoxic function (IL-18-mediated cytotoxicity against tumor cells) (287, 291–296). In the presence of phosphoantigen, IL-15-producing DCs (monocyte-derived) can also activate $\gamma\delta$ T cells in a contact-dependent manner (CD86) and induce secretion of IFN- γ (284, 297, 298). Zoledronate-treated immature and mature DCs (monocyte-derived) can induce phosphoantigen-mediated activation and expansion of effector $V\gamma 9V\delta 2^+$ T cells capable of co-stimulatory and cytotoxic functions *via* the expression of CD40L (299–303).

In summary, different $\gamma\delta$ T-cell subsets can either aid and promote or inhibit DC maturation and function (7, 13, 304, 305), while DCs can activate and expand $V\gamma 9V\delta 2^+$ T cells (7, 13, 304–307). The crosstalk between $\gamma\delta$ T cells and DCs can thus have downstream anti- or pro-tumoral effects with therapeutic potential, albeit warranting further investigation using DCs that are not monocyte-derived (8, 150, 308).

OUTLOOK AND FUTURE PERSPECTIVE

Our understanding on $\gamma\delta$ T cells continues to expand and their contributions in bridging the innate and adaptive anti-tumor immune responses are becoming more evident. Multiple studies are now highlighting their role in interacting with and orchestrating a variety of other immune cell subsets as reviewed here. Traditionally, $\gamma\delta$ T cell-based cancer immunotherapies have been focused on assessing the efficacy of activated $\gamma\delta$ T cells alone in mediating tumor clearance (41–46, 145, 157, 163, 165, 309). Although these past clinical trials have shown that $\gamma\delta$ T cell-based immunotherapies were safe and well tolerated in patients, given the limited success to date (8, 10, 19, 101, 310–312), more innovative strategies aiming to overcome the challenges and immunosuppression within the TME should be thoroughly explored. Notably, with the ever-increasing numbers of studies demonstrating the intricate network of immune interactions within the TME, it is high time to deeply explore some of these interactions and to gain valuable insights into the unique immunomodulatory functions of $\gamma\delta$ T cells in the context of cancer immunotherapy. Such acquired knowledge can be fully

harnessed to develop a multipronged $\gamma\delta$ T cell-based immunotherapy focusing on $\gamma\delta$ T cells' capability to influence the activities of other tumor-infiltrating immune cells *via* rapid cytokine and chemokine secretion, expression of various co-stimulatory molecules, and the professional APC functions in cross-priming and presenting antigens to $\alpha\beta$ T cells.

For example, we are now armed with several potent therapeutic agents including the agonist antibodies against BTN3A1 (clone 20.1, CTX-2026, and ICT-01) and BTN2A1 (ICT-0302) that are capable of activating and enhancing the immunomodulatory functions of V γ 9V δ 2⁺ T cells (48–53, 227, 313, 314). Treatment targeting BTN3A1 (CTX-2026) can induce coordinated V γ 9V δ 2⁺ and $\alpha\beta$ T-cell responses for tumor cell killing and represents a promising therapeutic approach that could be combined with other immune checkpoint inhibitors targeting PD-1/PD-L1 (nivolumab and pembrolizumab), CTLA-4/CD86 (ipilimumab and tremelimumab), KIRs (lirilumab and IPH4102), ILT-2 (anti-ILT-2, anti-HLA-G1, anti-FasL), and NKG2A (monalizumab) to circumvent potential immunosuppression in TME (11, 204, 205). These anti-tumor responses could potentially be further enhanced by inducing the expression of NKG2D ligands in tumor cells using a proteasome inhibitor (bortezomib) and an alkylating agent (temozolomide) to promote orchestrated NKG2D-mediated tumor cell lysis by tumor-infiltrating NK, CD8⁺ $\alpha\beta$, and $\gamma\delta$ T cells (240, 256, 257). Moreover, CD137 (4-1BB) co-stimulation with recombinant human CD137L can boost the therapeutic effect of V γ 9V δ 2⁺ T cell-based immunotherapy and lead to heightened NK cell-mediated cytotoxicity (73, 75, 101, 315). Taken together, such combined therapeutic treatment will be a powerful approach to elicit concerted anti-tumor responses in different tumor-infiltrating

immune cells and help to maximize the efficacy of future $\gamma\delta$ T cell-based immunotherapy treatments in cancer patients.

AUTHOR CONTRIBUTIONS

KFC, JDGD, SO, and AB wrote and prepared the manuscript draft. KFC prepared the figures. All authors contributed to the article and approved the submitted version.

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