

REVIEW

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In response to commensal bacteria: $\gamma\delta$ T cells play a pleiotropic role in tumor immunity

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Abstract

$\gamma\delta$ T cells are a mixture of innate programming and acquired adaptability that bridge the adaptive and innate immune systems. $\gamma\delta$ T cells are mainly classified as tissue-resident V δ 1 or circulating V δ 2 $\gamma\delta$ T cells. In the tumor microenvironment, tumor immunity is influenced by the increased quantity and phenotype plasticity of $\gamma\delta$ T cells. Commensal bacteria are ubiquitous in the human body, and they have been confirmed to exist in various tumor tissues. With the participation of commensal bacteria, $\gamma\delta$ T cells maintain homeostasis and are activated to affect the development and progression of tumors. Here, we summarize the relationship between $\gamma\delta$ T cells and commensal bacteria, the potential protumor and antitumor effects underlying $\gamma\delta$ T cells, and the new developments in $\gamma\delta$ T cell-based tumor therapy which is expected to open new opportunities for tumor immunotherapy.

Keywords: $\gamma\delta$ T cells, Commensal bacteria, Protumor effects, Antitumor effects, Immunity therapy

Background

Commensal bacteria

The human body comprises 10% cells and 90% bacteria. These bacteria reside in the skin, gastrointestinal tract, breast, lung, urinary tract and other regions. They are collectively known as commensal bacteria and have a complex connection with tumor immunity in the body [1]. With the latest developments in 16S rRNA gene sequencing and metagenomic analysis, an increasing number of bacteria have been found in the tumor microenvironment (TME). In an experiment with more than 300 samples of 7 solid tumors the distribution of bacteria was tissue-specific and tumor sub-type specific. One thing in common was that Proteobacteria and Firmicutes phyla account for most of the detected bacterial species, but the ratio of Proteobacteria to Firmicutes seems to vary between tumor types [2].

Cancer patients experience an imbalanced microbiota state called "dysbiosis", which is reflected in a substantial

reduction in bacterial diversity and community stability [3]. Independent of specific bacterial species, dysbiosis promotes the development and progression of tumors [4]. It is mediated by a decrease in tumor necrosis factor alpha (TNF- α) levels in tissues and the blood circulation, leading to reduced expression of tumor endothelial adhesion molecules, especially intercellular adhesion molecule 1 (ICAM-1). The expression of ICAM-1 is reduced by more than 50%, ultimately reducing the anti-tumor effect of CD8⁺ T cells [5, 6]. Dysbiosis also affects the response to chemotherapy, including the traditional chemotherapeutic drug cyclophosphamide [7] and new immune checkpoint inhibitors [8, 9].

$\gamma\delta$ T cells

$\gamma\delta$ T cells are a mixture of innate programming and acquired adaptability that bridge the adaptive and innate immune systems [10, 11]. They are mainly distributed in the skin and mucosal epithelium and account for the majority of tissue-resident T cells. In addition, 1–5% of $\gamma\delta$ T cells are found in peripheral blood [12]. In terms of TCR δ chain usage, V δ 1T cells are mainly located in the skin and mucous membranes and interact with V γ 2, γ 3, γ 4, γ 5 and γ 8 chains to maintain epithelial stability.

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V δ 2V γ 9T cells account for up to 90% of circulating $\gamma\delta$ T cells and can be recruited to the corresponding tissues to perform their functions [13].

It is worth noting that there are some species heterogeneities in gene evolution of TCR between humans and mice. Mice $\gamma\delta$ T cells depends on the specific TCR V γ chain, V γ 1–7. In spite of the discrepancy, $\gamma\delta$ T cells have functional similarity in mice and humans [14].

Most $\gamma\delta$ T cells are CD4⁺ and CD8⁺ cells, and their antigen recognition is not subject to major histocompatibility complex (MHC) restriction. $\gamma\delta$ T cells can also be activated by cytokines independent of their $\gamma\delta$ TCRs and take effect earlier. The activation, expansion, migration and functional plasticity of intratumor $\gamma\delta$ T cells are driven by changes in the TME, and these properties have a significant impact on maintaining mucosal stability and tumor immunity [13, 15].

Here, we review the relationship between commensal bacteria and $\gamma\delta$ T cells as well as the mechanism behind the dual effects of $\gamma\delta$ T cells on tumors harboring commensal bacteria. These findings are expected to identify new targets for tumor immunotherapy.

Commensal bacteria participate in the homeostasis of $\gamma\delta$ T cells

The homeostasis of $\gamma\delta$ T cells is affected by commensal bacteria. In dysbiosis or germ-free (GF) mice, the number of $\gamma\delta$ T cells is significantly reduced compared to that in their conventionally housed, specific pathogen-free (SPF) counterparts, as confirmed in the liver, lungs, intestines and peritoneum [16, 17]. The intestinal mucosa can be used as an example. Under normal circumstances, $\gamma\delta$ T cells rely on the communication between aryl hydrocarbon receptors (AhRs) and interleukin (IL)-15 produced by intestinal epithelial cells stimulated by microorganisms [18]. In GF models, Bifidobacteriaceae and Bacillaceae are positively related to intestinal $\gamma\delta$ T cells, while bacteria belonging to the families Rhodospirillaceae, Flavobacteriaceae and Prevotellaceae have the opposite relationship [16]. In the liver, *Escherichia coli* (*E. coli*) transplantation can improve $\gamma\delta$ T cell deficiency, but the *Escherichia coli* population is not irreplaceable [19]. Intraperitoneal injection of neomycin sulfate and vancomycin to kill facultative gram-positive and/or gram-negative organisms may result in lower numbers of $\gamma\delta$ T cells in the peritoneum of the treated group than the control group. However, metronidazole treatment has no effect on the number of $\gamma\delta$ T cells [20].

In general, there are few identified bacteria that are particularly relevant to $\gamma\delta$ T cells. In any case, stability of the commensal bacterial population is important for the homeostasis of $\gamma\delta$ T cells.

Commensal bacteria activate $\gamma\delta$ T cells via different mechanisms

The binding of bacterial pathogen-associated molecular patterns (PAMPs) to Toll-like receptors (TLRs) on $\gamma\delta$ T cells exerts an activating effect through the myeloid differentiation factor 88 (MyD88) pathway [21]. Although the study on TLRs of human $\gamma\delta$ T cells is not sufficient, the current unified conclusion is that $\gamma\delta$ T cells have TLR1~8 [21, 22]. The TLR2 and TLR5 can recognize lipopolysaccharide and flagellin, perceiving commensal bacteria. TLR3 mainly cooperates with TCR to play an antiviral effect [23]. The activation of TLR8 can reverse the immunosuppressive function of $\gamma\delta$ T cells [24]. Other TLRs are poorly expressed and rarely studied. Moreover, phagocytes produce IL-1, an inflammatory factor whose production is stimulated by commensal bacteria. IL-1 can be recognized by $\gamma\delta$ T cells and function through an IL-1R-Vav guanine nucleotide exchange factor 1 (VAV1)-dependent mechanism [20]. V δ 1 TCR has a special affinity for CD1-presented lipid sulfatide, modulated by the complementarity-determining region 3 loop to discriminate different lipid antigens, especially intestinal $\gamma\delta$ T cells [25, 26]. Another study confirmed that $\gamma\delta$ T cells in the liver but not the spleen are uniquely sensitive to lipid antigens derived from *E. coli* [27]. Phosphoantigens, such as bacterial lysate-derived (E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate (HMBPP), are also powerful stimulators of $\gamma\delta$ T cells [28]. As the most potent phosphoantigen known to stimulate $\gamma\delta$ T cells, HMBPP mainly activates circulating V δ 2V γ 9T cells [29]. HMBPP binding to intracellular domain of butyrophilin 3A1 (BTN3A1) leads to the extracellular detection by the V δ 2V γ 9 TCR, which reinforces the efficiency of $\gamma\delta$ T cell activation [30, 31] (Table 1).

Table 1 $\gamma\delta$ T cells activation: ligands and receptors

| Source | Ligand | Receptor | References |
|-------------|--------------------|-----------------|------------|
| Bacterial | PAMP | TLR2/5 | [22] |
| | IL-1 | IL-1R | [20] |
| | Lipid antigen-CD1d | V δ 1TCR | [25, 26] |
| | HMBPP-BTN3A1 | V δ 2TCR | [30, 92] |
| Cancer cell | MICA/B, ULBP | NKG2D | [55, 57] |
| | hMSH2 | NKG2D | [64] |
| | Nectin-like 5 | DNAM-1 | [54] |
| | B7-H6 | NKp30 | [59, 60] |
| | Not known | NKp46 | [58] |
| | F1-ATPase | V δ 2TCR | [61] |
| | annexin A2 | V δ 3TCR | [62] |
| IPP-BTN3A1 | V δ 2TCR | [81, 84] | |

Commensal bacteria play an important role in the migration of $\gamma\delta$ T cells

Similar to $\alpha\beta$ T cells, $\gamma\delta$ T cells are highly dynamic. Both tissue-resident and circulating $\gamma\delta$ T cells can rapidly migrate and be recruited to the effector site. Many studies have focused on gut-resident cells. Epithelium-mediated microbial sensing is part of an important mechanism [32]. $\gamma\delta$ T cells actively respond to bacterial signals and migrate from the basal to the apical surface of the epithelium, which is in direct contact with bacteria. This process occurs via a mechanism dependent on occluding, which is expressed by $\gamma\delta$ T cells [33, 34]. IL-15 is also engaged in that mechanism [35]. Vertical displacement of $\gamma\delta$ T cells is reduced in mice devoid of a microbiota [36], which reemphasizes the importance of bacteria. In addition, V δ 2T cells highly express C-X-C chemokine receptor 3 (CXCR3), C-C motif chemokine receptor 5 (CCR5) and, to a lesser extent, CCR2, guiding the recruitment of $\gamma\delta$ T cells from blood to tissues [37].

Classification of intratumoral $\gamma\delta$ T cells

Hinging on the TME, $\gamma\delta$ T cells undergo functional plasticity and differentiate into different phenotypes [38]. The actions of $\gamma\delta$ T17 cells are indispensable within the tumor and are the main producers of IL-17 in tumor tissues [20, 39, 40]. Unlike mice, there has been some evidence that human $\gamma\delta$ T17 cells are not pre-programmed in the thymus, but acquire IL-17 expression bias from the periphery under the stimulation of stable commensal bacteria and the participation of many cytokines [41, 42]. Tumor-associated myeloid cells sense microbial stimulation via MyD88 and TIR-domain-containing adaptor inducing interferon- β (TRIF) pathways and secrete IL-1 and IL-23, which are key inducers of $\gamma\delta$ T17 cells [43, 44]. In addition, IL-7 has been proven to be a more rapidly responsive IL-17 stimulator in solid tumors [45, 46]. IL-7 preferentially activates STAT3 in $\gamma\delta$ T cells rather than STAT5 in Th17 cells, significantly expanding the $\gamma\delta$ T17 cells, in both humans and mice [47]. Retinoic acid-related orphan nuclear receptor gamma t (ROR γ t) is also related to the polarization of $\gamma\delta$ T17 cells. This characteristic is specifically manifested as the induced expression of the gene encoding IL-17 by ROR γ t when $\gamma\delta$ T cells are

stimulated with transforming growth factors (TGF- β) and IL-6 [48]. TGF- β also promotes the polarization of Foxp3⁺ regulatory $\gamma\delta$ T ($\gamma\delta$ Treg) cells with cooperation from IL-15 in vitro [49, 50]. Cytotoxic helper $\gamma\delta$ T1 ($\gamma\delta$ Th1) cells are also found in the TME and their properties are selectively acquired upon stimulation with IL-2 or IL-15 [51, 52] (Table 2).

The dual effects of $\gamma\delta$ T cells on tumors

Antitumor effect (Fig. 1)

A meta-analysis of 18,000 human tumor samples clarified that intratumoral $\gamma\delta$ T cells participate in the formation of the most favorable cell population for cancer prognosis [53]. $\gamma\delta$ T cells express multiple natural killer receptors, including natural killer, group 2, member D (NKG2D); the DNAX accessory molecule-1 (DNAM-1) receptor; and the natural cytotoxicity receptor (NCR) [54–56]. MHC class I-related chains A/B (MICA/B) and UL16-binding proteins (ULBP) are upregulated ligands in cancer cells that are recognized by NKG2D and exert cytotoxic effects in cooperation with $\gamma\delta$ TCR [55, 57]. DNAM-1 and nectin-like-5 have been demonstrated to interact on V δ 2V γ 9T cells in hepatocellular carcinoma [54]. NCRs, especially NKp46, which is negatively correlated with the risk of metastasis in colorectal cancer, are abundantly expressed on V δ 1T cells [58]. The ligand for NKp30 on V δ 1T cells is B7-H6, which is common in lymphoma and leukemia [59, 60] (Table 1).

In addition, tumor cells express a variety of specific surface proteins, which are of great significance to the functional activation of $\gamma\delta$ T cells (Table 1). The mitochondrial F1-ATPase-related structure has been detected on the surface of tumor cells. With binding to the delipidated form of apolipoprotein A-I (apo A-I), F1-ATPase shows the characteristic of being actively recognized by V δ 2V γ 9 TCR [61]. In recent years, annexin A2 was identified to be a ligand for V δ 3 TCR [62]. Annexin A2 is a phospholipid-binding protein in the cytoplasm and is exposed on the membrane in response to oxidative stress [63]. In general, tumor-specific surface proteins could constitute danger signals for $\gamma\delta$ T cells recognition, reducing the possibility of immune shielding.

Table 2 The phenotypes, stimulators and effects of intratumoral $\gamma\delta$ T cells

| Phenotype | Stimulator | Effect | References |
|----------------------|--|--|----------------------|
| $\gamma\delta$ T17 | IL-7; IL-1, IL-23; TGF- β , IL-6 | Recruit PMN-MDSC and TAN, increase VEGF, express anti-apoptotic genes | [43, 44, 47, 70, 75] |
| $\gamma\delta$ Treg | TGF- β , IL-15 | Increase adenosine, inhibit $\gamma\delta$ Th1 | [49, 80] |
| $\gamma\delta$ Th1 | IL-2, IL-15 | Secret IFN- γ | [51, 52] |
| $\gamma\delta$ T-APC | PAMP | Regulate CD4 ⁺ or CD8 ⁺ T cells, induce mucosa to release calprotectin | [67, 68] |

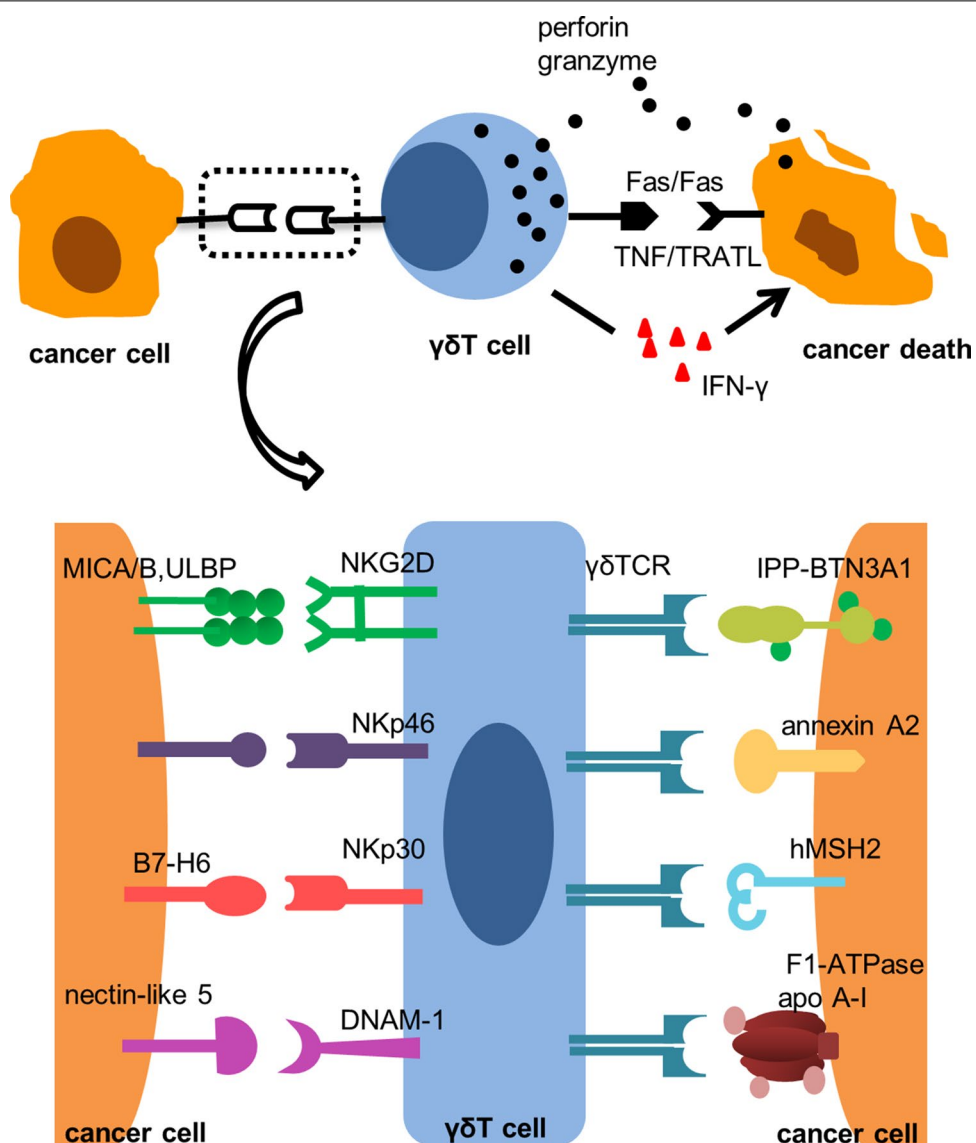


Fig. 1 Antitumor effects of $\gamma\delta$ T cells. $\gamma\delta$ T cells inhibit tumor growth through receptor-ligand interactions. MHC class I-related chains A/B (MICA/B) and UL16-binding protein (ULBP) are upregulated in cancer cells and are recognized by natural killer, group 2, member D (NKG2D), which exerts cytotoxic effects in cooperation with $\gamma\delta$ TCR. DNAX accessory molecule-1 (DNAM-1) and nectin-like-5 have been proven to interact on V δ 2V γ 9T cells in hepatocellular carcinoma. Natural cytotoxicity receptors (NCRs), especially NKp46, which is negatively correlated with the risk of metastasis in colorectal cancer, are abundantly expressed on V δ 1T cells. The ligand for NKp30 on V δ 1T cells is B7-H6, which is common in lymphoma and leukemia. Tumor surface protein: hMSH2, F1-ATPase-related structure and annexin A2 could constitute danger signals for $\gamma\delta$ T cells recognition, reducing the possibility of immune shielding. Like natural killer cells, $\gamma\delta$ T cells kill cancer cells indirectly by releasing interferon-gamma (IFN- γ), thereby exhibiting a Th1 cell-like phenotype, or directly via the death receptor signal factor associated suicide ligand (FasL) and TNF-related apoptosis-inducing ligand (TRAIL), secreting cytotoxic molecules such as granzyme and perforin

Similar to natural killer cells, $\gamma\delta$ T cells can kill cancer cells indirectly by releasing abundant amounts of interferon-gamma (IFN- γ) thereby displaying a Th1 cell-like phenotype. $\gamma\delta$ T cells can also kill cancer cells directly via the death receptor signal factor associated suicide ligand (FasL) and TNF-related apoptosis-inducing ligand (TRAIL), secreting cytotoxic molecules such as

granzyme and perforin [54]. Human MutS homologue 2 (hMSH2) is an ectopic nuclear protein associated with a variety of epithelial tumor cells. Both $\gamma\delta$ TCR and NKG2D participate in the recognition of hMSH2, stimulating the proliferation of V δ 2V γ 9T cells and enhancing IFN- γ mediated antitumor activity [64]. In addition, an increase in the number of V δ 1 T cells expressing

CCR2, which produce IFN- γ , has been observed in melanoma and hepatocellular carcinoma [65, 66]. $\gamma\delta$ T cells with antigen presentation function ($\gamma\delta$ T-APCs) regulate CD4⁺ or CD8⁺ T cells, which initiate the adaptive immune response [67]. $\gamma\delta$ T-APC induces the mucosa

to secrete calprotectin, which plays a role in the defense against intestinal mucosal inflammation [68].

Protumor effects (Fig. 2)

$\gamma\delta$ T cells exert unexpected protumor effects. The tumor-promoting functions are mainly due to IL-17-producing

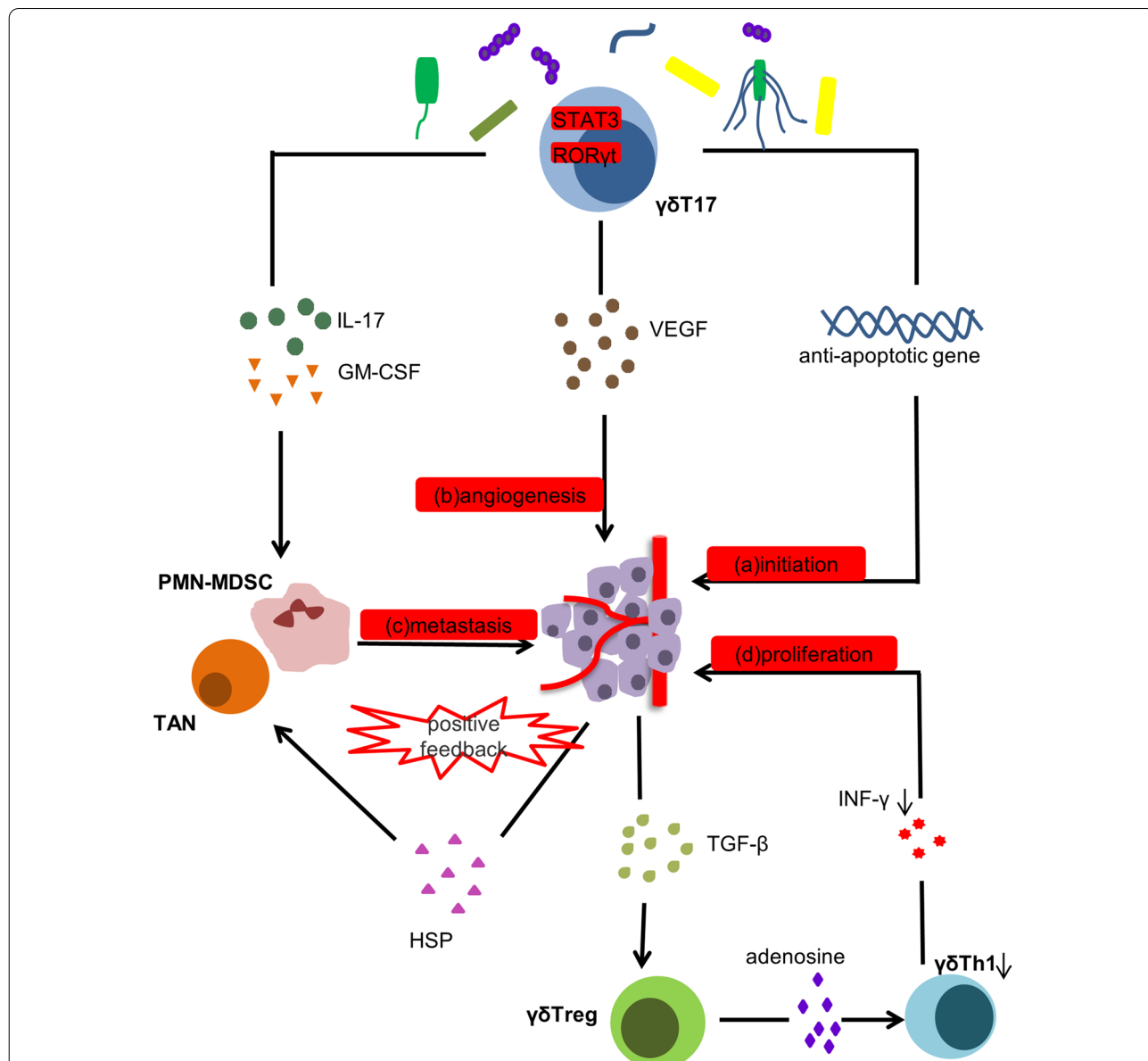


Fig. 2 Protumor effects of $\gamma\delta$ T cells. $\gamma\delta$ T cells are activated and recruited to tumor sites under stimulation by commensal bacteria. Signal transducer and activator of transcription 3 (STAT3) and orphan nuclear receptor gamma t (ROR γ t) are essential transcription factors for $\gamma\delta$ T17 cells. a $\gamma\delta$ T17 cells express antiapoptotic genes, such as Bcl-2, Mcl-1 and Survivin, promoting the growth of cells with tumorigenic potential and imparting the possibility for tumor initiation. b $\gamma\delta$ T17 cells increase the concentration of vascular endothelial growth factor (VEGF), which promotes tumor angiogenesis. c Secretion of IL-17 is accompanied by production of granulocyte–macrophage colony-stimulating factor (GM-CSF), leading to accumulation of polymorphonuclear myeloid-derived suppressor cells (PMN-MDSCs) and tumor-associated neutrophils (TANs), which is conducive to tumor metastasis. PMN-MDSCs can also sense heat shock proteins (HSPs) released by cancer cells and play a further immunosuppressive role. d In addition, $\gamma\delta$ Tregs can inhibit the secretion of interferon γ (INF- γ) from $\gamma\delta$ Th1 cells by increasing the amount of adenosine in the tumor microenvironment, resulting in excessive tumor proliferation

$\gamma\delta$ T cells. Current studies believe that tissue-resident V δ 1T cells are more inclined to differentiate into $\gamma\delta$ T17 cells, a finding seen in skin squamous cell carcinoma [69], colorectal cancer [70], breast cancer [71] and lung cancer [72]. Signal transducer and activator of transcription 3 (STAT3) is an indispensable transcription factor for IL-17 and it is also a target of antiapoptotic genes [73, 74]. The expression of genes such as Bcl-2, Mcl-1 and Survivin promotes the growth of cells with tumorigenic potential [74]. Secretion of IL-17 by $\gamma\delta$ T cells is accompanied by upregulation of the expression of granulocyte-macrophage colony-stimulating factor (GM-CSF), which leads to accumulation of polymorphonuclear myeloid-derived suppressor cells (PMN-MDSCs) [70] and tumor-associated neutrophils (TANs) [75] at tumor sites. Accumulation of PMN-MDSCs and TANs at tumor sites establishes an immunosuppressive network in the TME, such that local and distant tumor metastasis becomes possible [76]. Also, PMN-MDSCs respond to heat shock proteins (HSPs) in tumor exosomes to exert further immunosuppressive effects [77]. Furthermore, high expression of IL-17 by $\gamma\delta$ T cells is associated with a high microvessel density. IL-17 also increases the concentration of vascular endothelial growth factor (VEGF) to promote tumor angiogenesis and has a unique tumor-promoting effect in human colorectal [78] and gallbladder cancers [79].

The CD39⁺ $\gamma\delta$ T cells are a new type of $\gamma\delta$ Treg found in human colorectal cancer reported in 2020 by Hu et al. [80]. The phenotype of $\gamma\delta$ T cells is plastic, such that it is normal for different types of $\gamma\delta$ T cells to have functional crossover. CD39⁺ $\gamma\delta$ T cells express high levels of FOXP3 and secrete IL-17 and GM-CSF. In addition to attracting PMN-MDSCs, CD39⁺ $\gamma\delta$ Tregs can also inhibit the functions of $\gamma\delta$ Th1 cells by increasing the concentration of adenosine in the TME, which allows cancer cells to further escape immune attack. Unexpectedly, CD39⁺ $\gamma\delta$ T cells were found to exhibit more potent immunosuppressive activity than conventional CD4⁺ Tregs [80].

Clinical implication

At present, tumor therapy based on $\gamma\delta$ T cells has received increasing attention, as a satisfactory response has been achieved in combination with chemotherapy and immunotherapy. Zoledronate can upregulate the expression of isopentenyl pyrophosphate (IPP) in cancer cells [81]. V δ 2V γ 9T cells exposed to a large number of phosphoantigens can rapidly develop amplified antigen sensitivity and tumor recognition [82, 83]. Solid cancer cells pretreated with low concentrations of zoledronate can be quickly killed by V δ 2V γ 9T cells in vitro [84]. A combination of chemotherapeutic drugs, zoledronic acid and V δ 2V γ 9T cells has shown promising results in

clinical trials [84]. In addition to V δ 2V γ 9T cells, research focused on V δ 1T cells has also showed promising results [85]. Afonso et al. in 2016 [86] defined a V δ 1-enriched (>60%) and NKG2D-upexpressing cytotoxic cell type, namely DOT cells. By designing a two-step method with distinct IL-4 expansion and IL-15 differentiation stages, a large number of (>2500-fold) DOT cells can be amplified in vitro to show special cytotoxicity against the MEC-1 cell of chronic lymphocytic leukemia, but not healthy autologous leukocytes [86].

Autologous chimeric antigen receptor (CAR)-T cell therapy has emerged as a star component of tumor immunotherapy in recent years. Specifically, CAR-T cell therapy has remarkable efficacy in the treatment of hematological tumors [87]. In spite of this success, CAR-T cell therapy based on $\alpha\beta$ T cells has not yet achieved a breakthrough in the treatment of solid tumors. The application space of CAR-T therapy is also limited by difficulty in applying the therapy in allogeneic cells. $\gamma\delta$ T cells make it possible to use allogeneic CAR-T cells from donors due to their MHC-independent characteristics, and this method may be more convenient and economical than existing methods [88]. Based on this assumption, Utrecht University have validated CAR-T cells expressing given V δ 2V γ 9 TCR clone 5 (TEG001) in condition of a good manufacturing practice [89]. These heterozygous T cells are called T cells engineered with defined $\gamma\delta$ TCRs (TEGs) [90], and have undoubtedly brought light to this therapeutic idea. Corporation Lava is developing a type of bispecific antibody that connects cancer cells and $\gamma\delta$ T cells separately, improving the precision of targeting and prevents immune silencing of $\gamma\delta$ T cells [91]. In-depth research on butyrophilin has provided a very effective target for the development of small molecule drugs based on $\gamma\delta$ T cell therapy [92].

Conclusion

Crosstalk between commensal bacteria and $\gamma\delta$ T cells increases the complexity and uncertainty of the tumor immune microenvironment. During the initiation of the tumor, $\gamma\delta$ T cells are triggered by bacteria and migrate to the effector sites. The function of the aggregated $\gamma\delta$ T cell population is further amplified, and $\gamma\delta$ T cells can directly kill tumor cells or indirectly inhibit tumor growth through receptor-ligand interactions. However, the presence of $\gamma\delta$ T17 cells is an unfavorable factor, and the immunosuppressive state created by these cells allows cancer cells to escape immune surveillance.

At present, there is no definite relationship between the structure and functional subsets of $\gamma\delta$ T cells. Both V δ 1 and V δ 2 $\gamma\delta$ T cells have potential use in immunotherapy against cancer. Reprogramming $\gamma\delta$ T cells to transform towards an antitumor phenotype through precise regulation is a hot

research topic. As an impressive candidate for adoptive cellular therapy, $\gamma\delta$ T cells have broad therapeutic prospects.

Abbreviations

AhRs: Aryl hydrocarbon receptors; apo A-I: Apolipoprotein A-I; BTN3A1: Butyrophilin 3A1; CAR: Chimeric antigen receptor; CCR: C–C motif chemokine receptor; CXCR: C–X–C chemokine receptor; DNAM-1: DNAX accessory molecule-1; *E. coli*: *Escherichia coli*; FasL: Factor associated suicide ligand; GF: Germ-free; GM-CSF: Granulocyte–macrophage colony-stimulating factor; HMBPP: (E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate; hMSH2: Human MutS homologue 2; HSPs: Heat shock proteins; ICAM-1: Intercellular adhesion molecule 1; IFN- γ : Interferon-gamma; IL: Interleukin; IPP: Isopentenyl pyrophosphate; MHC: Major histocompatibility complex; MICA/B: MHC class I-related chains A/B; MyD88: Myeloid differentiation factor 88; NCR: Natural cytotoxicity receptor; NKG2D: Natural killer, group 2, member D; PAMPs: Pathogen-associated molecular patterns; PMN-MDSCs: Polymorphonuclear myeloid-derived suppressor cells; ROR γ t: Acid-related orphan nuclear receptor gamma t; SPF: Specific pathogen-free; STAT3: Signal transducer and activator of transcription 3; TANs: Tumor-associated neutrophils; TGF: Transforming growth factors; TLRs: Toll-like receptors; TME: Tumor microenvironment; TNF- α : Tumor necrosis factor alpha; TRAIL: TNF-related apoptosis-inducing ligand; TRIF: TIR-domain-containing adaptor inducing interferon- β ; ULBP: UL16-binding proteins; VAV1: Vav guanine nucleotide exchange factor 1; VEGF: Vascular endothelial growth factor; $\gamma\delta$ T-APCs: $\gamma\delta$ T cells with antigen presentation function; $\gamma\delta$ Th1: Helper $\gamma\delta$ T1; $\gamma\delta$ Treg: Regulatory $\gamma\delta$ T.

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Authors' contributions

YTL and HS designed and drafted the manuscript; YH and SZ wrote figure legends and revised the article; YTL and YH drew the figures. All authors read and approved the final manuscript.

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Ethics approval and consent to participate

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Consent for publication

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Competing interests

The authors declare that they have no competing interests.

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