



Tissue Adaptations of Memory and Tissue-Resident Gamma Delta T Cells

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Epithelial and mucosal barriers are critical interfaces physically separating the body from the outside environment and are the tissues most exposed to microorganisms and potential inflammatory agents. The integrity of these tissues requires fine tuning of the local immune system to enable the efficient elimination of invasive pathogens while simultaneously preserving a beneficial relationship with commensal organisms and preventing autoimmunity. Although they only represent a small fraction of circulating and lymphoid T cells, $\gamma\delta$ T cells form a substantial population at barrier sites and even outnumber conventional $\alpha\beta$ T cells in some tissues. After their egress from the thymus, several $\gamma\delta$ T cell subsets naturally establish residency in predetermined mucosal and epithelial locations, as exemplified by the restricted location of murine $V\gamma 5^+$ and $V\gamma 3V\delta 1^+$ T cell subsets to the intestinal epithelium and epidermis, respectively. Because of their preferential location in barrier sites, $\gamma\delta$ T cells are often directly or indirectly influenced by the microbiota or the pathogens that invade these sites. More recently, a growing body of studies have shown that $\gamma\delta$ T cells form long-lived memory populations upon local inflammation or bacterial infection, some of which permanently populate the affected tissues after pathogen clearance or resolution of inflammation. Natural and induced resident $\gamma\delta$ T cells have been implicated in many beneficial processes such as tissue homeostasis and pathogen control, but their presence may also exacerbate local inflammation under certain circumstances. Further understanding of the biology and role of these unconventional resident T cells in homeostasis and disease may shed light on potentially novel vaccines and therapies.

Keywords: memory $\gamma\delta$ T cells, resident $\gamma\delta$ T cells, innate $\gamma\delta$ T cells, adaptive $\gamma\delta$ T cells, barrier infections

INTRODUCTION

Epithelial and mucosal tissues form physical barriers separating the body from the outside world. They are constantly exposed to a wide range of stressors such as infectious agents and their toxins capable of damaging barrier tissues. Barrier surface interactions with microorganisms extend far beyond encounters with pathogenic microbes; indeed, these tissues are typically mutualistic ecosystems that maintain beneficial relationships for resident commensal organisms while providing support to the tissue (1). Because of the complexity of these interfaces, the immune system is tightly regulated in order to eliminate invading pathogens while maintaining a robust commensal environment. It is now well established that the microbiota plays a significant role in

educating immune cells and promoting protective anti-infectious responses (2–4). However, the microbiota may also play an important role in aberrant inflammation (5, 6). In addition, pathogenic agents also leave their imprint on the immune system and generate long-lasting memory responses. Protective immunity has mainly been the purview of conventional effector memory (T_{EM}) or central memory (T_{CM}) T cells and B cells. More recently, the discovery of conventional resident memory T cells (T_{RM}) (7, 8), innate immune memory also known as trained immunity (9, 10), and other unconventional memory responses (11, 12) has focused attention on tissue-specific immunity at barrier locations.

$\gamma\delta$ T cells are an unconventional T cell population that display immunologic features common to both the innate and adaptive immune systems (13). This dual nature of $\gamma\delta$ T cell biology is typified by their non-MHC-restricted antigenic specificity while mounting rapid immune responses to a wide range of tissue stressors (14), generally referred to as “lymphoid-stress surveillance” (15). $\gamma\delta$ T cells are the first T cells generated during embryonic development and quickly seed peripheral tissues where specialized subsets are maintained for life in residence. These unconventional T cells are only found at low frequencies in lymphoid tissues and the blood in adult humans and rodents; however, they are enriched in epithelial and mucosal tissues (16–19). Generally, distinct barrier tissues harbor mostly non-overlapping $\gamma\delta$ T cell subsets with non-redundant functions (17). Some tissues contain unique and highly specialized $\gamma\delta$ T cell subsets that are not found elsewhere in the body. For example, $V\gamma 3V\delta 1^+$ skin dendritic epidermal T cells (DETC) reside exclusively in the skin epidermis while $V\gamma 5^+$ T cells reside exclusively in the intestinal epithelium [the Garman nomenclature (20) is used throughout this review for murine $\gamma\delta$ T cells] (21). The development and selection processes that regulate the differentiation of these cells are unique and result in the generation of highly adapted cells that actively survey neighboring cells, sense and respond to stresses of various nature and participate in many tissue processes. Thus, these natural tissue-resident $\gamma\delta$ T cells are programmed sentinels that are also shaped by and highly adapted to their tissue environment.

Because of their preferential location in barrier sites, $\gamma\delta$ T cells are often directly or indirectly influenced by the microbiota or the pathogens that invade these sites. The steady-state microbiota may influence the generation, effector functions, or maintenance of $\gamma\delta$ T cells (22–24). These commensal-induced $\gamma\delta$ T cells adapt to their tissue of residence where they add another level of immune surveillance and may be mobilized in many pathological contexts including inflammation (25–27) and cancer (28, 29). These tissue-resident $\gamma\delta$ T cells are also mobilized during infection to promote anti-pathogen immunity (30) and represent innate first responders during infection. Alternatively, pathogen-induced adaptive $\gamma\delta$ T cells appear to follow a more conventional T cell maturation pathway, resulting in delayed activation and expansion while favoring the establishment of long-lasting memory and heightened protective potential upon pathogen re-exposure. Throughout this review, the term “adaptive” will be utilized to describe $\gamma\delta$ T cells having features consistent with conventional $\alpha\beta$ T cells. This review will focus on the tissue

adaptation of tissue-resident natural $\gamma\delta$ T cells and adaptive $\gamma\delta$ T_{RM} cells in barrier tissues while highlighting their development, maintenance and role in health and disease.

$\gamma\delta$ T CELLS OF HUMANS AND MICE

Murine $\gamma\delta$ T cells are often segregated into different subsets based on their $V\gamma$ T cell receptor (TCR) chain, as it is generally associated with tissue tropism and a bias in effector function (31, 32) (Table 1). It is well established that $\gamma\delta$ T cell ontogeny is temporally controlled and manifested by “waves” of development (76). The factors regulating $\gamma\delta$ T cell development have been recently reviewed (77, 78). Most barrier tissue $\gamma\delta$ T cells develop early during fetal development in the fetal/neonatal thymus with the first thymic wave of $\gamma\delta$ T cells starting at embryonic day 13 and giving rise to DETC characterized by surface expression of an invariant $V\gamma 3V\delta 1$ TCR (16). $V\gamma 3V\delta 1^+$ DETC migrate to the skin epidermis (18, 76, 79) and produce $IFN\gamma$ (80) and other cytokines (81, 82), and growth factors (83, 84). From embryonic day 14 to the perinatal period, the fetal/neonatal thymus generates other innate-like [also called “natural” (85)] $\gamma\delta$ T cells, including the IL-17A biased quasi-invariant $V\gamma 4V\delta 1^+$ T cells which preferentially migrate to the genital tract, the tongue and the lungs (16, 76, 86). Fetal-derived $\gamma\delta$ T cells are typically considered innate-like due to their reduced TCR sensitivity (87) and rapid functional response to innate stimuli like cytokines and pathogen- or danger-associated molecular patterns (72, 88, 89). IL-17A-producing $\gamma\delta$ T cells (referred to as $\gamma\delta 17$ T cells in this review) are characterized by the expression of the transcription factor $ROR\gamma t$ (90), chemokine receptor $CCR6$ (86, 90, 91), scavenger receptor $SCART2$ (92), $CD25$ (93), but lack $CD27$ (86, 90, 94). In contrast, $IFN\gamma$ -producing $\gamma\delta$ T cells express the transcription factor T-bet and surface receptors $NK1.1$ and $CD27$. Consistent with other $IFN\gamma$ producing lymphocytes, they also express high levels of the IL-2/IL-15 receptor β chain $CD122$ (93, 95). It was initially thought that $\gamma\delta 17$ T cells acquired their peripheral effector fate due to a lack of antigenic selection in the thymus; antigen-experienced cells were programmed to make $IFN\gamma$ in the periphery while antigen-inexperienced cells were programmed to make IL-17A (80, 87, 95, 96). However, recent evidence suggests that signaling through the TCR is required for $\gamma\delta 17$ T cells development and that the strength of the signal is the critical factor determining their functional lineage. A strong TCR signal promotes an $IFN\gamma$ -dominant lineage whereas a weak TCR signal promotes an IL-17A-dominant lineage (97–99). An additional level of regulation comes from the thymic cytokine milieu: while signaling through $IL-15R\alpha$ restrains $\gamma\delta 17$ T cell development *in cis* (100), IL-7 promotes their expansion (101). An interesting feature of $\gamma\delta 17$ T cells is their functional plasticity, which allows them to co-produce IL-17A and $IFN\gamma$ under certain circumstances (61, 102). Although $CD27^-$ $\gamma\delta$ T cells have a permissive chromatin state at the *Il17a* and *Ifng* loci, only a handful of situations have been associated with IL-17A and $IFN\gamma$ co-production *in vivo*, including oral *Listeria monocytogenes* (*L. monocytogenes*) infection (61, 62) and peritoneal tumor (102). Post-transcriptional repression of $IFN\gamma$ production has

TABLE 1 | Memory and tissue resident $\gamma\delta$ T cells in infection and disease.

Tissue	Subset(s)	Role	Response	Cytokines	Other features	Context	References
Systemic	V δ 2 ⁻	Protective	Memory?	IFN γ	Stress surveillance against CMV and cancer	CMV	(33–37)
	ND	Protective	Memory?	IFN γ	Antigen specific expansion	Vaccinia	(38)
	V γ 9V δ 2	Protective	Memory	IFN γ	Cross-reactive to HMBPP	Monkeypox	(39)
	V γ 9V δ 2, V δ 1	Protective	Memory?	IFN γ	Late expansion after initial exposure	<i>P. falciparum</i>	(40–43)
	V γ 1.1V δ 6.3	Protective	Memory?	M-CSF, CCL5, CCL3	Oligoclonal expansion	<i>P. chabaudi</i>	(44)
	V γ 9V δ 2	Protective	Memory	IFN γ	Cross-react with <i>M. tuberculosis</i>	BCG	(45, 46)
Lungs	V γ 9V δ 2	Protective	Memory	Granzyme B	Activated by HMBPP	<i>M. tuberculosis</i>	(45–47)
	V γ 1.1 ⁻ , V γ 2 ⁻	Protective	Innate	IL-17A	High expression of IL-1R1, IL-18R, and IL-23R	<i>B. pertussis</i>	(48)
	V γ 2	Protective	RM	IL-17A	<i>B. pertussis</i> -specific	<i>B. pertussis</i>	(48)
Peritoneum	V γ 4	Protective	RM	IL-17A	CD27-CD44+ Effector memory phenotype	<i>S. aureus</i>	(49)
	V γ 1.1, V γ 2	Protective	Innate	ND	Polyclonal response	<i>S. aureus</i>	(49)
Skin	V γ 4V δ 1	Protective	RM	IFN γ , TNF α	TLR2/IL-1 β dependent response	<i>S. aureus</i>	(50)
	V γ 2V δ 4	Pathogenic	RM	IL-17A/F	CCR2-dependent recruitment to tissue	Psoriasis	(25, 26)
	V γ 2	Pathogenic	RM	IL-17A	Constitutive expression of CCR6, ROR γ t, and IL-23R	Dermatitis	(51)
	V γ 9V δ 2, V δ 1	Variable	Memory	IL-17A, IFN γ , TNF α	Pathogenic IL-17A; Protective IFN γ	SCC/Melanoma	(52, 53)
	V γ 3V δ 1	Protective	Innate	IFN γ , KGF-1/2	Immotile; semi-activated	Wound, dermatitis, <i>S. aureus</i> , cancer	(54–58)
Intestine	V γ 9V δ 2	Protective	Memory	IL-17A, IFN γ , IL-4, TNF α	Multifunctional cytokine production	<i>L. monocytogenes</i>	(59, 60)
	V γ 4V δ 1	Protective	RM	IL-17A, IFN γ	Multifunctional cytokine production	<i>L. monocytogenes</i>	(61, 62)
	V δ 1	Pathogenic	Infiltrating	IFN γ	Interacts with colonic fibroblasts	IBD	(63, 64)
	V γ 9V δ 2, V δ 1	Pathogenic	RM	GM-CSF, IL-17A	Pathogenicity dependent on MDSC regulation	CRC	(65)
	V γ 5, others	Protective	Innate	IFN γ , Granzymes	Highly motile; semi-activated	<i>S. enterica</i> , <i>T. gondii</i>	(66–69)
Breast	V γ 2	Pathogenic	RM	G-CSF, IL-17A	Pathogenicity dependent on MDSC regulation	Breast Cancer	(70)
Brain	V δ 2, V δ 1	Protective	Memory	IFN γ , TNF α , Granzyme B	Found in the context of $\gamma\delta$ expansion methodology	Neuroblastoma	(71)
	V γ 2	Pathogenic	Innate	IL-17 cytokines, IL-21	IL-23- and IL-1 β -dependent activation	EAE/MS	(72)
	ND	Pathogenic	Innate	IL-17A	Part of a microbiota-gut-brain axis	Ischemic stroke	(27)
Joints	V γ 1.1, V γ 1.2	Pathogenic	Innate	IL-17A	IL-23- and IL-1 β -dependent activation	CIA	(73)
	ND	Pathogenic	Innate	IL-17A	IL-23-dependent activation	Ankylosing spondylitis	(74)
Eyes	V γ 1.1, V γ 2	Pathogenic	Innate?	IL-17A	Enhanced uveitogenic $\alpha\beta$ T cell development	Uveitis/EAU	(75)
	V γ 2	Protective	Resident	IL-17A	Induced by <i>C. mastidis</i> colonization CD1d- and IL-1 β -dependent	Ocular <i>P. aeruginosa</i> / <i>Candida albicans</i>	(24)
Primate $\gamma\delta$ T cells		Rodent $\gamma\delta$ T cells					

ND, not determined; RM, resident memory; CMV, cytomegalovirus; BCG, *M. bovis* BCG strain; SCC, squamous cell carcinoma; IBD, inflammatory bowel disease; CRC, colorectal cancer; EAE/MS, experimental autoimmune encephalomyelitis/multiple sclerosis; CIA, collagen-induced arthritis; EAU, experimental autoimmune uveitis.

recently been reported in $\gamma\delta 17$ T cells (61); however, whether co-production of IL-17A and IFN γ is regulated by derepression has not been evaluated.

Although most $\gamma\delta 17$ T cells fall into the innate-like category, adaptive-like differentiation of naïve $\gamma\delta$ T cell precursors into mature $\gamma\delta 17$ T cells in peripheral lymphoid organs has also recently been reported in multiple models. After the identification of phycoerythrin (PE) as a $\gamma\delta$ TCR antigen, PE-specific $\gamma\delta$ T cells were shown to transition from a naïve CD44^{lo} CD62L^{hi} to an activated CD44^{hi} CD62L^{lo} phenotype after immunization with PE (103). These $\gamma\delta$ T cells expressed ROR γ t and inflammatory cytokine receptors IL-1R1 and IL-23R which drove production of IL-17A without extensive proliferation (103). Similarly, imiquimod (IMQ)-induced skin inflammation and MOG-induced experimental autoimmune encephalomyelitis (EAE) induced the *de novo* generation of $\gamma\delta 17$ T cells in draining lymph nodes (104, 105). These unrelated models demonstrate that the differentiation of some $\gamma\delta 17$ T cell subsets is optimal with a TCR signal and in the presence of IL-23, reminiscent of the multistep development of naïve CD4⁺ T cells. In contrast to natural $\gamma\delta 17$ T cells, these *de novo* generated cells are often referred to as inducible $\gamma\delta 17$ T cells (14).

$\gamma\delta$ T cell subsets in human and non-human primates are generally divided into two major populations based on the V δ TCR chain: V $\delta 2^+$ and V $\delta 2^-$ $\gamma\delta$ T cells. V $\delta 2^+$ T cells appear to develop almost exclusively in the fetal liver and fetal thymus (106, 107) and form the predominant $\gamma\delta$ T cell population in the peripheral blood of adult humans (108, 109). Most fetal, cord blood and adult V $\delta 2^+$ T cells express the semi-invariant V $\gamma 9$ V $\delta 2$ TCR with a public germline encoded CDR3 γ sequence and a more diverse CDR3 δ sequence (110). Despite their preferential localization in the blood, V $\gamma 9$ V $\delta 2^+$ T cells can also be recruited to inflamed tissues where they can participate in pathogen clearance or promote inflammation (39, 45, 47) (**Table 1**). The TCR combination allows the majority of V $\gamma 9$ V $\delta 2^+$ T cells to recognize prenyl pyrophosphate metabolites (111), broadly referred to as phosphoantigens (PAGs), presented in the context of butyrophilin (BTN)3A1 and BTN3A2 (112–115). PAGs are metabolic intermediates produced by the eukaryotic mevalonate pathway and the microbial 2-C-methyl-D-erythriol 4-phosphate (MEP) pathway, which generates one of the most potent V $\gamma 9$ V $\delta 2^+$ T cell activator (E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate (HMBPP) (111). Fetal V $\gamma 9$ V $\delta 2^+$ T cells express genes found in adult cells and can expand and produce IFN γ in response to HMBPP stimulation (110). By 1 year of age, almost all V $\gamma 9$ V $\delta 2^+$ T cells have acquired a memory phenotype and can rapidly produce IFN γ and cytotoxic molecules (108, 116), similar to circulating adult cells (108, 116, 117). These data suggest that human V $\gamma 9$ V $\delta 2^+$ T cells are preprogrammed fetal-derived effectors with a restricted TCR specificity. Thus, V $\gamma 9$ V $\delta 2^+$ T cells seem to belong to the natural, innate-like population of lymphocytes.

In contrast to V $\gamma 9$ V $\delta 2^+$ T cells, the V $\delta 2^-$ $\gamma\delta$ T cell subset is heterogeneous (106) and preferentially resides in epithelial tissues such as the skin (118) and intestines (119) and appears to form resident populations in the liver (120) (**Table 1**). V $\delta 2^-$ $\gamma\delta$ T cells mainly consist of V $\delta 1^+$ T cells, with fewer V $\delta 3^+$ and

V $\delta 5^+$ T cells. While most antigens recognized by V $\delta 2^-$ $\gamma\delta$ T cells remain unknown, the antigens identified to date suggest a broad reactivity to MHC-like molecules like endothelial protein C receptor (EPCR) (33) and CD1 molecules (33, 121, 122), stress-induced ligands (123) and algal phycoerythrin (103). V $\delta 2^-$ $\gamma\delta$ T cell TCR are highly diverse in cord blood but their TCR repertoire becomes more restricted into adulthood (124). Furthermore, they clonally expand in response to cytomegalovirus (CMV) infection and differentiate into CD45RA⁺ effector memory T (T_{EMRA}) cells (34, 35, 125–127). Thus, the V $\delta 2^-$ $\gamma\delta$ T cell repertoire appears to be shaped by TCR-dependent selection events mediated by microbial encounters throughout life. As V $\delta 2^-$ $\gamma\delta$ T cells can recognize stress antigens, non-infectious events that trigger a response, such as cancer development, may also shape their repertoire (36, 128).

$\gamma\delta$ T cells can provide different physiologic roles depending on the nature and context of the insult, the tissue involved and the $\gamma\delta$ T cell populations mobilized. At steady state, $\gamma\delta$ T cells are involved in many biological processes aiming at maintaining barrier integrity (e.g., by promoting epithelial cell survival and homeostasis) (82–84, 129) and regulating thermogenesis (130). Because of their rapid sensing of stress and recruitment to inflamed sites, $\gamma\delta$ T cells are often involved in shaping early immunologic events. They can promote the activation, maturation, and recruitment of dendritic cells (DC), neutrophils, B cells, and conventional T cells [for a detailed review see (131)]. $\gamma\delta$ T cells are also a direct and potent source of critical inflammatory cytokines like IFN γ , TNF α and IL-17A in many pathological contexts, including infection (59, 111, 132–134), autoimmune disease (25, 26, 72, 135) and cancer (29, 136–138). As such, they are also an integral part of the effector response. At later phases, $\gamma\delta$ T cells can promote the resolution of the inflammation through the production of anti-inflammatory molecules like TGF β (139, 140). Finally, they sustain tissue repair and remodeling after infection or injury (54, 83, 132, 141). Thus, $\gamma\delta$ T cells are critically involved in regulating health during homeostasis and disease.

THE FIRST TISSUE-RESIDENT T CELLS: INTESTINAL AND EPIDERMAL $\gamma\delta$ T CELLS

Many $\gamma\delta$ T cell subsets are constrained to specific tissue locations. DETC and intestinal intraepithelial lymphocytes (IEL) with a $\gamma\delta$ TCR ($\gamma\delta$ IEL) populate the two largest interfaces of the body, the skin and the intestines, respectively. DETC and $\gamma\delta$ IEL are shaped within their respective tissues where they provide adapted support to maintain tissue homeostasis and respond to stresses or invading pathogens. These populations have recently been the focus of an in-depth review (21). Thus, only features relevant to this review will be discussed here.

Dendritic Epidermal T Cells– DETC

DETC are the first T cells to develop during embryogenesis and by far the most abundant T cell subset present in the mouse skin epidermis (142). Their name stems from the unique DC-like morphology observed during homeostasis. DETC form a

highly uniform population characterized by the expression of a canonical V γ 3V δ 1 TCR with no junctional diversity. The mouse fetal thymus supports the generation of the entire DETC precursor pool between embryonic day 13 and 18, after which mature DETC are maintained life-long in the skin epidermis by self-renewal (18, 76, 79, 143). The narrow developmental window of DETC progenitors may result from the temporally restricted expression of a Btn-like protein, Skint-1, by embryonic medullary thymic epithelial cells (144–146). Expression of Skint-1 is required at various stages of DETC thymic development to regulate their biology. First, Skint-1 promotes the thymic maturation of V γ 3V δ 1⁺ T cell progenitors, without which the skin epidermis would be devoid of mature DETC (144–146). Second, Skint-1 educates DETC precursors by promoting IFN γ production over IL-17A (80), instructing skin-homing (147), and attenuating TCR responsiveness by increasing its activation threshold (87). Similarly, TCR signaling seems required for the maturation of DETC precursors (148–150) and the establishment of a mature population with innate-like properties in the skin epidermis (87, 148–151). It is also indirectly involved in the thymic egress and subsequent migration to the skin of positively selected progenitor cells. Indeed, TCR signaling induced the expression of sphingosine-1-phosphate receptor 1 (S1P1) and the skin-homing chemokine receptor CCR10, which mediates T cell exit from the thymus and migration toward keratinocyte-derived CCL27, respectively (152, 153). Additional molecules like E- and P-selectin ligands and CCR4 may also play a role in the establishment or maintenance of the DETC population in the skin (154).

During homeostasis, mature DETC are maintained in a semi-activated state and constantly survey the epidermis through the extension of motile basal dendrites and by projecting dendrites toward the apical epidermis. These dendrites establish stable synapses at the squamous keratinocyte junctions that allows DETC to survey several surrounding cells simultaneously (155). Each apical dendrite ends with phosphorylated tyrosine-rich aggregates in synapse-like structures enriched with TCR and phosphorylated TCR signaling intermediates. Therefore, mature DETC might receive continuous TCR-mediated signals from neighboring cells residing in the epidermis, which are necessary for their long-term maintenance in the tissue (156). Although healthy skin does not appear to express DETC TCR ligand detectable by soluble V γ 3V δ 1 TCR tetramers (157), exposure of the skin to low grade stresses might sustain basal expression of ligands sufficient for their survival but below the sensitivity of this detection method. Indeed, DETC express basal levels of the type-2 cytokine IL-13 in resting skin, consistent with some level of activation at steady state (82). Absence of DETC-derived IL-13 induces an epithelial cell stress response that disrupts barrier integrity. As such, DETC play a key role in preserving skin homeostasis at steady state.

The skin is constantly exposed to a variety of pathological conditions and stresses. Superficial damage to the epithelium induces a stress response associated with upregulation of the NKG2D ligand Rae-1 and leads to the further activation of DETC (82, 158). Enhanced production of DETC-derived IL-13 induces keratinocyte maturation, which promotes efficient

epithelial cell renewal, restoring tissue integrity (82). Shortly after deep wounding, damaged keratinocytes in close proximity to the lesion quickly and transiently upregulate a yet unidentified stress antigen (156, 157, 159). DETC rapidly become activated in a TCR dependent-manner and their activation is associated with retraction of their dendrites and cellular rounding (54, 155, 159). Full activation of DETC in this context requires engagement of the TCR and costimulation provided by the junctional adhesion molecule JAML (81), CD100 (semaphorin-4D) (160) or NKG2D (161, 162), whose ligands are all upregulated in damaged skin. Activated DETC provide anti-apoptotic signals to keratinocytes and promote their survival through the production of insulin-like growth factor-1 (84). DETC also produce many additional growth factors, including keratinocyte growth factor (KGF)-1 and KGF-2 (54, 83), inflammatory cytokines like IFN γ and TNF α (81, 163) and chemokines (164) that favor epithelial regeneration and wound closure. The important and non-redundant contribution of DETC to wound repair was demonstrated in *Tcrd*^{-/-} mice or animals deficient in DETC costimulatory signals. Lack of DETC or their impaired activation led to a substantially delayed wound healing (54, 81, 160–162). Additional roles of DETC include regulation of aberrant inflammation in a model of contact dermatitis (55) and protection against UV-mediated DNA damage (165), cutaneous infection (56) and development of malignancies (57, 58, 166). Interestingly, DETC may mediate their anti-cancer effect by direct cytolytic activity in a TCR- and NKG2D-dependent manner *in vitro* (57). Additionally, IL-13 production by DETC favors the production of IgE (158), that promotes protective anti-cancer immunity through a yet undetermined mechanism involving tumor infiltrating Fc ϵ RI⁺ cells (166).

Mucosal and epithelial sites are not only patrolled by natural resident cells like DETC, they are also kept under the surveillance of pathogen-induced CD8⁺ and CD4⁺ $\alpha\beta$ T_{RM} cells which provide local long-lived protection against reinfection (7, 8). Natural and induced resident T cells occupy a similar space. Cutaneous infection by herpes simplex virus (HSV) generates CD8⁺ T_{RM} that remain in the basal epidermis around the lesion site (167, 168). Surprisingly, the increased CD8⁺ T_{RM} density at the site of infection inversely correlated with DETC numbers even several months after pathogen clearance. Conversely, distant DETC-rich areas had a reduced CD8⁺ T_{RM} population. One potential explanation for the redistribution of resident T cell subsets is that infection may lead to selective loss of DETC, creating a niche for CD8⁺ T_{RM} cell seeding. Indeed, DETC are rapidly infected by HSV after cutaneous exposure (169). HSV infection of non-neuronal cells is typically lytic and may induce their death. However, alternative mechanisms may also lead to loss of DETC as their redistribution was also observed after intradermal injection of effector CD8⁺ T cells in the absence of infection (168). DETC can also be temporarily displaced by infiltrating NKT cells following acute stress (58), demonstrating that conventional and unconventional $\alpha\beta$ T cells can colonize the skin and create a niche at the expense of DETC. It has been proposed that these cells may compete for maintenance signals like IL-15 or aryl hydrocarbon receptor (AhR) ligands (170), which are necessary for mature DETC

survival in the skin (171–174). Such competition should also occur between $\alpha\beta$ T_{RM} generated by different, non-overlapping infections as both populations would be expected to have similar homeostatic requirements. However, it was recently reported that the generation of new $\alpha\beta$ T_{RM} cells does not result in the replacement of previously established T_{RM} cells (175), suggesting that limited resources like IL-15 may not be responsible for redistribution of DETC and $\alpha\beta$ T_{RM} cells. Identifying the factors involved in the maintenance of natural and induced T cell populations is necessary to better understand their apparent competition and would be beneficial for the design of targeted local therapies.

Intestinal Intraepithelial Lymphocytes– $\gamma\delta$ IEL

The intestinal epithelium is actively patrolled by IEL, a large fraction of which are unconventional $\gamma\delta$ T cells expressing a CD8 $\alpha\alpha$ homodimer in mice (19, 176). The intestine is colonized by $\gamma\delta$ IEL during the perinatal period. In contrast to the essential role of the thymus in the generation other $\gamma\delta$ T cell subsets, its contribution to intestinal $\gamma\delta$ IEL development is more limited. Intestinal $\gamma\delta$ IEL can develop extrathymically in athymic mice but at lower numbers than in euthymic animals (177–180). IL-7 production has been shown to be fundamental for $\gamma\delta$ IEL thymic and extrathymic intestinal development (181, 182). A large fraction of $\gamma\delta$ IEL express the V γ 5 TCR (79, 183). The preferential expression of V γ 5 is controlled at the chromatin level by IL-15-STAT5 signals, which regulate the accessibility of the V γ 5 gene and favor its expression in thymocytes and immature IEL (184). Despite the overrepresentation of the V γ 5 TCR among $\gamma\delta$ IEL, the overall $\gamma\delta$ TCR repertoire in the intestinal epithelium is diverse. Indeed, several mechanisms contribute to the diversity of intestinal $\gamma\delta$ IEL including various V δ and V γ chain pairings, usage of the J δ 1 or J δ 2 segment and addition of non-germline encoded nucleotides (79, 183). Because of their TCR heterogeneity, $\gamma\delta$ IEL have the potential to recognize a wide array of potential antigens or ligands that include host-derived molecules such as nonclassical and nonpolymorphic MHC class Ib molecules T10 and T22 (185). Despite the similarity to MHC class I molecules, T10 and T22 do not present peptide antigens. T10/T22 reactivity is conferred by a specific W-(S)EGYEL CDR3 δ motif, which allows some V γ 5⁺, V γ 1.1⁺ and V γ 2⁺ $\gamma\delta$ IEL to bind T10/T22 (185). To date, the antigenic specificity of the non-T10/T22 reactive $\gamma\delta$ IEL remains obscure.

$\gamma\delta$ IEL precursors do not require S1P1 for their emigration from the thymus (186). However, $\gamma\delta$ thymocytes and unconventional (CD8 $\alpha\alpha$ ⁺) recent thymic emigrants express high levels of the gut homing receptors CCR9 (187, 188) and $\alpha_4\beta_7$ integrin (187–189). Interestingly, CCR9 is preferentially expressed by antigen-inexperienced CD122^{lo} or CD62L^{hi} CD44^{int/lo} thymocytes (189, 190), suggesting they have more potential to home to the gut and that some $\gamma\delta$ IEL did not encounter their antigen prior to their migration into intestinal tissues. This assumption was confirmed by the presence of similar numbers of T10/T22 reactive $\gamma\delta$ T cells in the intestinal epithelium of *B2m*^{-/-} mice, which lack surface expression of

T10/T22 (190). Intestinal $\gamma\delta$ IEL might be selected based on their TCR affinity more than their specificity, as suggested by the inverse correlation between TCR affinity and CCR9 expression (190). This unusual “non-selection” of a diversified $\gamma\delta$ T cells likely reflects the need to maintain a heterogeneous broadly reactive population that can respond appropriately to the wide variety of stresses and antigens encountered in the intestine.

Within the first few weeks of life, V γ 5⁺ T cells expand in the intestinal epithelium and transition from an immature to a mature phenotype (180). Despite the heavy microbial colonization of the gut, $\gamma\delta$ IEL expansion and maturation are independent of the microbiota (66, 178). Instead, expansion and maturation are regulated in a TCR-dependent manner by the BTN-like (Btl)1 and Btl6 heterocomplex expressed on the surface of enterocytes (180), reminiscent of Skint-1-mediated selection of DETC in the thymus (144–146). Upon selection by cells co-expressing Btl1 and Btl6, V γ 5⁺ T cells upregulate CD25 and produce pro-inflammatory cytokines like IFN γ , growth factors like GM-CSF and chemokines like CCL4 (180). The Btl-mediated selection of intestinal $\gamma\delta$ IEL may occur in a similar fashion in humans, with V γ 4⁺ T cells being activated by cells co-expressing BTNL3 and 8 (180). Once established in the tissue, $\gamma\delta$ IEL rely on the production of IL-15 by microbiota stimulated intestinal epithelial cell (IEC) (191–193) and AhR ligands (174) for their maintenance and survival. In return, $\gamma\delta$ T cells participate in the maintenance of tissue homeostasis and barrier integrity. $\gamma\delta$ IEL promote IEC proliferation and maturation through multiple mechanisms that may include production of KGF (83, 129, 141), regulating tight junctions (67), producing anti-microbial peptides in response to pathobiont invasion (68), limiting tissue damage, and promoting epithelial repair after injury (141).

$\gamma\delta$ IEL from specific pathogen-free (SPF) mice constitutively express cytotoxic genes, including granzyme A and B (194), and can lyse target cells directly *ex vivo* (195), consistent with an anti-infectious role of intestinal $\gamma\delta$ IEL. The absence of $\gamma\delta$ T cells in *Tcrd*^{-/-} was associated with enhanced dissemination of enteric bacteria (*Salmonella enterica* serovar Typhimurium) or parasites (*Toxoplasma gondii*), rendering mice more susceptible to systemic infection (67–69). Additionally, $\gamma\delta$ IEL indirectly protect from murine norovirus infection by secreting type I and III interferons and increasing the resistance of IEC to viral infection (196). They are also important in controlling dissemination of commensals that may occur with loss of barrier integrity after pathogen invasion or epithelial injury (197). Thus, $\gamma\delta$ IEL serve multiple functions in regulating immunity at the mucosal interface with the environment.

Intestinal $\gamma\delta$ IEL were initially thought to have limited mobility within the epithelium (188). This view has recently been challenged by two compelling studies that demonstrated that intestinal $\gamma\delta$ IEL are highly dynamic and constantly migrate within the intestinal tissue. During tissue homeostasis, individual $\gamma\delta$ IEL survey a large surface area and contact numerous IEC within a short period of time (66, 198). $\gamma\delta$ IEL mainly remain in the middle region of the intestinal villi, between the basement membrane and the epithelial layer, but they also appear to occasionally migrate to the intercellular space between IEC for

a short period of time (66, 198). Although commensals do not impact $\gamma\delta$ IEL numbers, microbial colonization is required for their normal distribution within the villi and their migratory behavior in the tissue (66), and also promotes their cytotoxic and anti-microbial functions (68, 195). These patterns drastically change upon enteric infection with invasive bacteria or parasites. Shortly after pathogenic exposure, $\gamma\delta$ IEL preferentially localized to pathogen-rich areas and decreased their normal surveillance behavior. Reduced surveillance coverage was associated with increased movement between IEC and the lateral intercellular space in a behavior termed “flossing” (66, 69) that is regulated by the tight junction protein occludin (198). These behavioral and functional changes result from the MyD88-dependent sensing of pathogenic microbes by IEC, and the specific abrogation of MyD88 signaling in IEC severely blunted $\gamma\delta$ IEL responses (66, 68). $\gamma\delta$ IEL at steady-state may also be activated through their TCR as injection of a TCR δ -specific antibody diminished intracellular calcium flux (199). It is therefore conceivable that the IEC- $\gamma\delta$ IEL dialogue could also involve TCR-mediated tissue surveillance. Thus, $\gamma\delta$ IEL continually survey epithelial integrity via cross-talk with IEC which dictates $\gamma\delta$ IEL behavior and leads to their adaptation in the intestinal environment. While the exact function of $\gamma\delta$ IEL flossing remains unclear, its association with pathogen hotspots and the importance of $\gamma\delta$ T cell responses to anti-infection immunity suggests an important role of flossing in controlling intestinal infections or promoting epithelial repair.

Natural tissue-resident $\gamma\delta$ T cells are remarkably adapted to their tissue of residence, where they provide signals necessary to maintain tissue homeostasis and barrier integrity while also providing a rapid front-line defense against infectious assaults continually encountered in epithelial tissues. Both DETC and intestinal $\gamma\delta$ IEL are adapted to efficiently survey their respective tissues, through their placement/migration into the tissue and communication with neighboring epithelial and immune cells. Despite this, natural tissue-resident T cells may have to compete for limited space or nutrients with *de novo* generated conventional T_{RM} cells after local infections. Whether direct competition for resources and space or an undefined crosstalk between these cells regulate tissue colonization is unclear and an area of much interest.

MICROBIOTA-INDUCED $\gamma\delta 17$ T CELLS: DIVERSIFIED EFFECTORS WITH MULTIFACETED ROLES

Almost all tissues exposed to the environment are colonized by established commensal communities, with the exception of the eye for which the presence of a resident microbiome remains a matter of debate (1). The presence of these microorganisms shapes the local immune system and promotes protective anti-infectious immunity, as exemplified by the anti-bacterial, -fungal or -parasitic type-17 and type-1 responses triggered by segmented filamentous bacteria in the intestines (2) or *Staphylococcus epidermidis* (*S. epidermidis*) and other commensals in the skin (3, 4), respectively. However, commensal-specific T cells (especially intestinal T_H17 cells)

can also have detrimental effects at remote sites under certain circumstances, inducing pathological inflammatory responses that lead to the development of diseases like arthritis and autoimmune encephalomyelitis (5, 6).

As for conventional T cells, the microbiota also impacts $\gamma\delta$ T cell responses at many body sites. Interestingly, commensal-induced $\gamma\delta$ T cell responses appear to largely involve IL-17A-producing cells regardless of their tissue distribution among diverse sites such as the skin (4, 200), the liver (22), the oral and peritoneal cavities (23, 201), the eye (24), the lungs (28) and the intestines (29, 197). The generation and activation requirements of microbiota-induced $\gamma\delta$ T cells appear uniquely adapted to the tissue location. First of all, the presence of a microbiota is a prerequisite for the development of some, but not all, tissue tropic $\gamma\delta$ T cells. Indeed, antibiotic-treated SPF or germ-free (GF) mice harbor fewer activated liver-resident (22), pulmonary (28), peritoneal, and small intestinal lamina propria (siLP) $\gamma\delta 17$ T cells (23). In contrast, $\gamma\delta$ IEL numbers are independent of a microbiota (66, 178, 197). Second, few identified microorganisms have been specifically associated to particular $\gamma\delta$ T cell populations: *Corynebacterium mastidis* (*C. mastidis*) colonization with ocular $V\gamma 2^+$ $\gamma\delta 17$ T cells (24), *Corynebacterium accolens* (*C. accolens*) and other bacteria from the *Corynebacterium* genus producing mycolic acid with skin $V\gamma 2^+$ $\gamma\delta 17$ T cells, and *S. epidermidis* with skin $V\gamma 2^-$ $\gamma\delta 17$ T cells (200). The expansion of $V\gamma 2^+$ and $V\gamma 2^-$ $\gamma\delta$ T cell subsets by *C. accolens* and *S. epidermidis* association, respectively, demonstrates that the $\gamma\delta$ T cell responses can adapt within the same niche. In contrast, other $\gamma\delta$ T cell subsets only require the presence of a microbiota without any distinction between bacterial species (22, 28). Lastly, many different signals control the activation and/or expansion of commensal-induced $\gamma\delta 17$ T cells, including lipid presentation by the non-classical molecule CD1d (22), DC-mediated expansion (24, 201) and activation/polarization (27, 29, 200) or MyD88 signaling pathways (23, 197). Cytokines like IL-1 β (23, 24), IL-23 (200) and IL-6 (28), either alone or in combination with other activation signals, also participate in the induction or propagation of IL-17A from microbiota-induced $\gamma\delta$ T cells.

IL-17 family cytokines, including IL-17A, are key regulators of mucosal and epithelial immunity. Over the past decade, a multitude of roles, from the induction of protective anti-infectious responses to the promotion of pathological inflammatory processes, have been attributed to IL-17A (202). Accordingly, the induction of $\gamma\delta 17$ T cells by microbial colonization has also been associated with seemingly contrasting effects. Commensal-induced $\gamma\delta$ T cells can mediate local protection against penetrating commensals (197), pathogenic bacteria or even yeast, as exemplified by the resistance displayed by *C. mastidis* colonized animals to ocular *Candida albicans* infection (24). In this model, induced $\gamma\delta$ T cells were driving the production of antimicrobial peptides such as S100A8 and S100A9 and the recruitment of neutrophils through the production of IL-17A. As IL-17A can elicit these responses in virtually all mucosal and epithelial surfaces, similar broad-spectrum anti-infectious immunity might occur in other $\gamma\delta$ T cell rich tissues. In contrast to their protective effect against infection, microbiota-elicited

$\gamma\delta 17$ T cells may be beneficial (28) or harmful (29) in cancer. Other local detrimental effects attributed to microbiota-induced $\gamma\delta 17$ T cells include the acceleration of nonalcoholic fatty liver disease by liver-resident $\gamma\delta 17$ T cells (22) and the exacerbation of imiquimod-induced skin inflammation following *C. accolens* association (200).

Microbiota-elicited $\gamma\delta$ T cells can also impact distal immune function. They express a plethora of homing receptors that allows them to navigate to distant tissues and impact health or disease. For example, $\gamma\delta$ T cells are recruited to the ischemic penumbra after ischemic stroke in a CCR6-dependent manner (203). There, they contribute to exacerbate brain injury through the production of IL-17A and subsequent recruitment of neutrophils (203–205). In a recent study using a transient middle cerebral artery occlusion mouse model, the $\gamma\delta 17$ T cells recruited to the ischemic brain originated from the small intestine and were dependent on specific commensal species for their maintenance (27). Alteration of the gut microbiota by antibiotic treatment led to a reduction in intestinal $\gamma\delta 17$ T cells and diminished $\gamma\delta$ T cell infiltration to the meninges, limiting injury. Thus, commensal-induced $\gamma\delta$ T cells may have local and distal effects on pathological or physiological tissue processes.

It is now well established that the microbiota is a critical component of human health and disease. In addition to providing many enzymatic and metabolic pathways and colonization resistance to invading pathogens, commensals also participate in the development of and shaping of the immune system (206). Dysbiosis can be sensed by the immune system and has been associated with the development or exacerbation of many diseases in many organ systems. Given their preferential association with epithelial and mucosal tissues, it is not surprising that some $\gamma\delta$ T cell populations are also influenced by the microbiota.

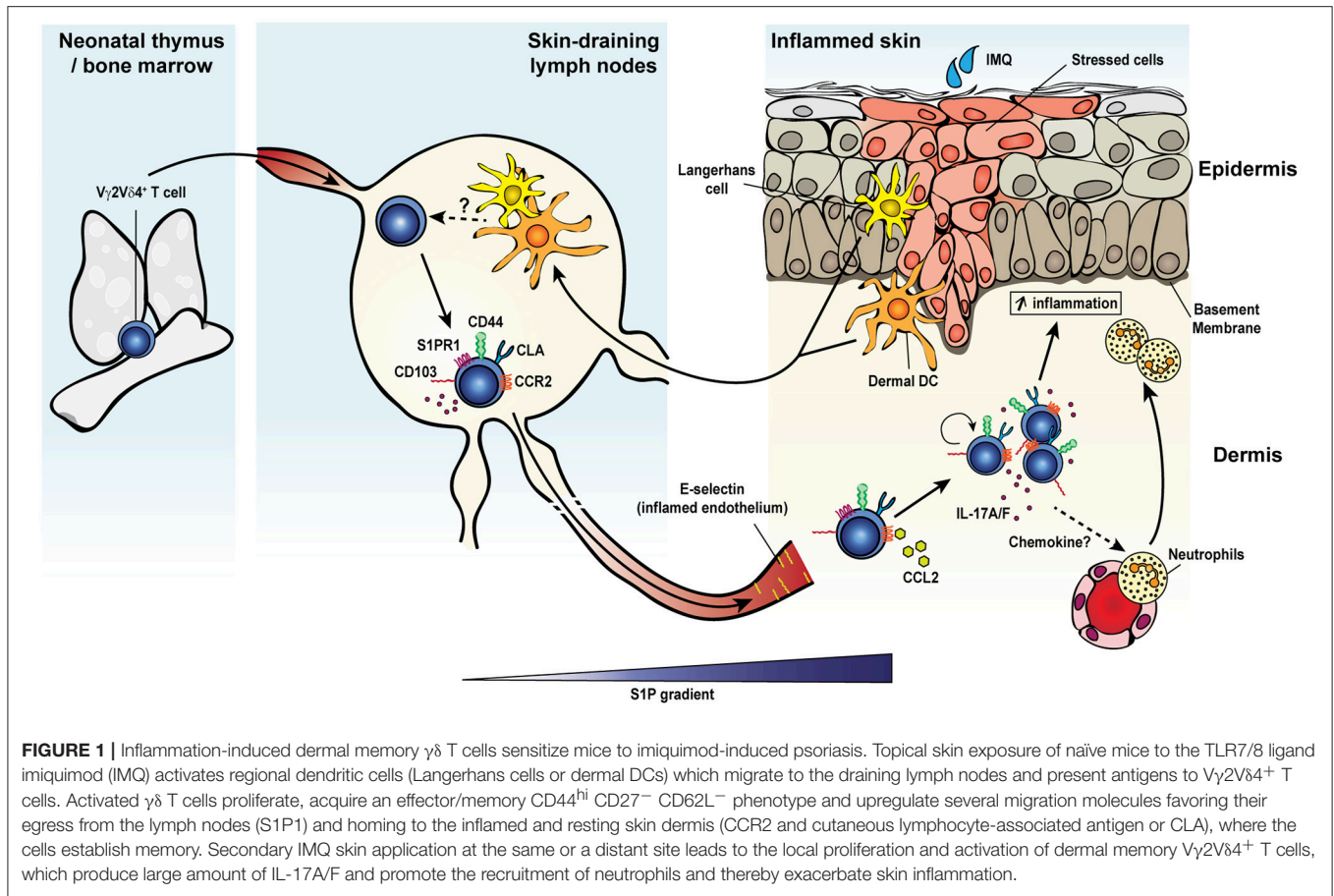
INFLAMMATORY DISEASE AND MEMORY-LIKE $\gamma\delta 17$ T CELL RESPONSE

In addition to $\gamma\delta$ T cell responses to the microbiota or after infection, $\gamma\delta$ T cells have also been implicated in innate responses in inflammatory disease. Inflammatory diseases with $\gamma\delta$ T cell contributions include multiple sclerosis or EAE (72), psoriasis (135), collagen induced arthritis (73), ankylosing spondylitis (74), inflammatory bowel disease (63, 64), and uveitis (75). One factor of inflammatory disease progression attributed to $\gamma\delta$ T cells is IL-17A production, a feature often associated with changes in the microbiota (72, 73, 135). Inflammation-induced tissue damage may allow bacteria to bypass the epithelium leading to a positive feedback inflammatory loop. Interestingly, memory-like $\gamma\delta$ T cell formation has been seen in inflammation of the skin (25, 26, 51, 207). IL-17A-producing $V\gamma 2V\delta 4^+$ T cells initially derive from the neonatal thymus where they are instructed with tissue tropism. IMQ-induced psoriasis-like skin inflammation triggers a potent long-lived $V\gamma 2V\delta 4^+$ T cell response (**Figure 1**) (25, 26). These $V\gamma 2V\delta 4^+$ T cells were phenotypically memory-like with a $CD44^{hi} CD62L^{lo} CD27^{-}$ expression pattern. $V\gamma 2V\delta 4^+$ T cells expanded after primary challenge and migrated from the

draining lymph nodes to both the inflamed and uninfamed skin in a S1P1-dependent manner where they persisted. Migration of $V\gamma 2V\delta 4^+$ T cells from the circulation to the skin may also be influenced by signals including cutaneous lymphocyte antigen (CLA) binding to P- and E-selectins, CD103 interactions with E-cadherin, and C-C chemokine receptor type 2 (CCR2), and CCR6. CCR2 appeared essential for $\gamma\delta 17$ T cell recruitment to inflamed tissues in B16 melanomas and EAE while CCR6 appeared necessary for dermal $\gamma\delta 17$ T cell residence (208). Subsequent IMQ administration on previously untreated skin induced an accelerated and robust re-expansion of skin resident $V\gamma 2V\delta 4^+$ T cells that produced IL-17A/F and exacerbated disease (25, 26). IL-17 production and subsequent neutrophil recruitment for skin disease appeared be partially dependent on an NF κ B-inducing kinase (207). Enhanced inflammation with subsequent exposure was also associated with the $V\gamma 2V\delta 4^+$ T cell recall response but independent of $\alpha\beta$ T cells (26). These findings were also noted in an acute contact dermatitis model using dinitrofluorobenzene where a similar memory $V\gamma 2^+$ $\gamma\delta 17$ T cell population appeared predominately tissue-resident in classical parabiosis experiments (51). Together, these studies suggest that $\gamma\delta$ T cells can modulate inflammatory diseases of the skin by forming long-lived tissue resident memory populations that exacerbate disease through the production of IL-17 family cytokines. While these studies suggest the establishment of long-lived memory T cells, whether this response is driven by a specific antigenic responsiveness or is broadly reactive is unclear.

INFECTION-INDUCED ADAPTIVE $\gamma\delta$ T CELLS: LONG-TERM PLAYERS IN MUCOSAL IMMUNITY

Anamnestic immunity was thought to be mediated solely by conventional $\alpha\beta$ T cells and B cells. The recent identification of several innate and unconventional memory responses challenged this belief and has reshaped our view of immunological memory. $\gamma\delta$ T cells bridge innate and adaptive immunity in many contexts by rapidly responding to stresses such as infections and promoting conventional adaptive immunity. For that reason, most mouse studies focused on $\gamma\delta$ T cell responses in the first few hours to days after pathogen exposure or inflammatory insult. However, mounting evidence in humans, non-human primates and mice demonstrated that $\gamma\delta$ T cells can mount adaptive-like responses. One of the most studied pathogens in that context is CMV. Indeed, the involvement of $\gamma\delta$ T cells in the protective response to CMV infection was first suggested in kidney transplant patients whose $\gamma\delta$ T cells underwent a massive and long-lasting expansion in the blood (34, 209, 210). $\gamma\delta$ T cell expansion to CMV was also observed in the context of immunosuppression or immunodeficiency (35, 36, 126, 211–215), neonatal infection (216) and in otherwise healthy individuals (35, 125). Analysis of the repertoire of CMV-selected $\gamma\delta$ T cells revealed an oligoclonal and in some individuals even monoclonal population (34, 35, 125), which, surprisingly, did not involve circulating $V\gamma 9V\delta 2^+$ T cells but tissue tropic $V\delta 2^{-}$ $\gamma\delta$ T cells. Expanded cells displayed a T_{EMRA}



phenotype, similar to CMV-specific $CD8^+$ T cells (127), and only responded to CMV infection (34, 128). Importantly, the expansion of $V\delta2^- \gamma\delta$ T cells correlated with the resolution of the acute infection in humans (210) and adoptive transfer of murine CMV-expanded $\gamma\delta$ T cells conferred full protection to susceptible immunodeficient mice (217, 218). Thus, CMV-elicited $\gamma\delta$ T cells display many features classically attributed to conventional memory T cells. Another long-lived $\gamma\delta$ T cell response to virus has been reported in the context of vaccinia virus immunization in humans (38) and rhesus macaques (39). Interestingly, vaccinia virus immunized macaques were protected against monkeypox virus challenge infection and this was associated with the expansion of circulating and pulmonary $V\gamma9V\delta2^+$ T cells. Long-lasting adaptive-like $\gamma\delta$ T responses were also reported in the circulation of individuals infected with the protozoan *Plasmodium falciparum* (*P. falciparum*) (40–43) and the circulation and peripheral tissues of animals infected with *Plasmodium chabaudi* (44). Interestingly, $\gamma\delta$ T cell distribution to parasite-targeted tissues raises the possibility that these cells might provide unique functions to control parasite replication during the blood and liver stages. Collectively, these studies provide compelling evidence of adaptive $\gamma\delta$ T cell responses triggered by unrelated pathogens in humans, non-human primates and rodents. However, the chronic or latent nature of the infections and their associated antigen and inflammation

in conjunction with some inherent challenges associated with human studies has hindered conclusive demonstrations of the memory potential and long-term tissue residency of these populations.

Infection-Induced *bona fide* Memory $\gamma\delta$ T cell Responses

Adaptive $\gamma\delta$ T cells survey exposed mucosal and epithelial barriers where they may participate in pathogen clearance or control and have tissue-adapted functions. $\gamma\delta$ T cells are one of the first immune responders in many bacterial infections, where they act concurrently with cells of the innate immune system. However, this innate $\gamma\delta$ T cell response does not preclude the establishment of a subsequent localized memory $\gamma\delta$ T cell response. A mouse model of peritonitis induced by repeated intraperitoneal exposure to *Staphylococcus aureus* (*S. aureus*), induced a rapid $V\gamma1.1^+$ and $V\gamma2^+$ $\gamma\delta17$ T cell response in the peritoneum and the draining mediastinal lymph nodes a few hours after exposure (49). After this early polyclonal innate response, a long-lived predominantly IL-17A-producing $V\gamma4^+$ T cell population emerged in both tissues. Surprisingly, secondary challenge with *S. aureus* of previously exposed but pathogen-free mice induced a conventional memory response of $V\gamma4^+$ T cells. Recalled $V\gamma4^+$ T cells underwent secondary expansion, displayed an activated $CD44^{hi} CD27^-$ phenotype,

and produced elevated levels of IL-17A. Adoptive transfer of purified *S. aureus*-elicited $V\gamma 4^+$ T cells was sufficient to protect naïve recipients against peritonitis and bacterial dissemination to the liver and kidneys (49). In contrast to the fundamental role of IL-1 β in the induction of IL-17A production by naïve $\gamma\delta$ T cells during primary *S. aureus* exposure, memory $V\gamma 4^+$ T cells were IL-1 β -independent suggesting that memory $\gamma\delta$ T cells have an altered ability to respond to unique environmental cues to provide effector functions. Localized *S. aureus* infection of the skin in *Il1b*^{-/-} mice resulted in poor bacterial control during primary infection but protection against reinfection, revealing the potential presence of an additional memory $\gamma\delta$ T cell subset. Indeed, intradermal infection induced the selective expansion of skin resident $V\gamma 4V\delta 1^+$ and $V\gamma 3V\delta 1^+$ T cell clones with conserved CDR3 δ and CDR3 γ motifs that were maintained during the convalescent phase and present after secondary infection of WT and *Il1b*^{-/-} mice (50). Protection during secondary infection was conferred by IFN γ - and TNF α -producing $\gamma\delta$ T cells. Adoptive transfer of purified *S. aureus*-elicited $\gamma\delta$ T cells, but not CD4⁺ T cells, neutrophils or serum from convalescent mice, was associated with bacterial clearance. Thus, different memory $\gamma\delta$ T cell responses can be induced by the same pathogen and local memory $\gamma\delta$ T cell populations may be tissue adapted to provide distinct protective mechanisms.

In addition to the memory responses involving $V\gamma 4^+$ T cells, a long-lasting protective response of $V\gamma 2^+$ T cells was observed after pulmonary *Bordetella pertussis* (*B. pertussis*) infection (Figure 2) (48). After an early innate response dominated by IL-17A-producing $V\gamma 1.1^- V\gamma 2^- \gamma\delta$ T cells, effector memory CD44⁺ CD27⁻ $V\gamma 2^+$ T cells started accumulating from day 14 and were

maintained long-term in the lungs. The later emergence of $V\gamma 2^+$ T cells coincided with the expansion of T_{RM} precursors and T_{EM}-like CD4⁺ T cells in the lungs (219). Expanded pulmonary $V\gamma 2^+$ T cells share several features with *B. pertussis*-specific memory CD4 T cells: (i) they reside in the lungs for a prolonged period of time after bacterial clearance and rapidly and locally proliferated in response to secondary pulmonary challenge, (ii) a considerable fraction expresses the T_{RM} marker CD69 and some also co-express CD103, (iii) they have a strict reactivity to *B. pertussis*, (iv) they are biased toward IL-17A production, and (v) they contribute to enhanced bacterial clearance after challenge (48, 219). Thus, *B. pertussis*-elicited memory $\gamma\delta$ T cells closely resemble conventional T_{RM} cells. In contrast to the reported displacement of skin DETC by virus-specific CD8⁺ T_{RM} (168), CD4⁺ T_{RM} and memory $\gamma\delta$ T cells were able to coexist in the lungs of infected mice and both subsets expanded after infection and participated in conferring protection, suggesting that they may reside in distinct niches within the tissue or do not compete for space or survival factors.

Microorganisms producing PAg are potent activators of human and non-human primate $V\gamma 9V\delta 2^+$ T cells. Mycobacteria, including *Mycobacterium bovis* BCG strain and *Mycobacterium tuberculosis* (*M. tuberculosis*), produce HMBPP (220–222), the most potent $V\gamma 9V\delta 2^+$ T cell activator. Correspondingly, intravenous (i.v.) BCG vaccination of macaques triggered a drastic expansion of these circulating cells in the blood, but also in the lungs and the intestines (45). Pulmonary *M. tuberculosis* infection led to a similar expansion of mucosal but not circulating $V\gamma 9V\delta 2^+$ T cells (47), demonstrating tissue-adapted responses by adaptive $\gamma\delta$ T cells that may be

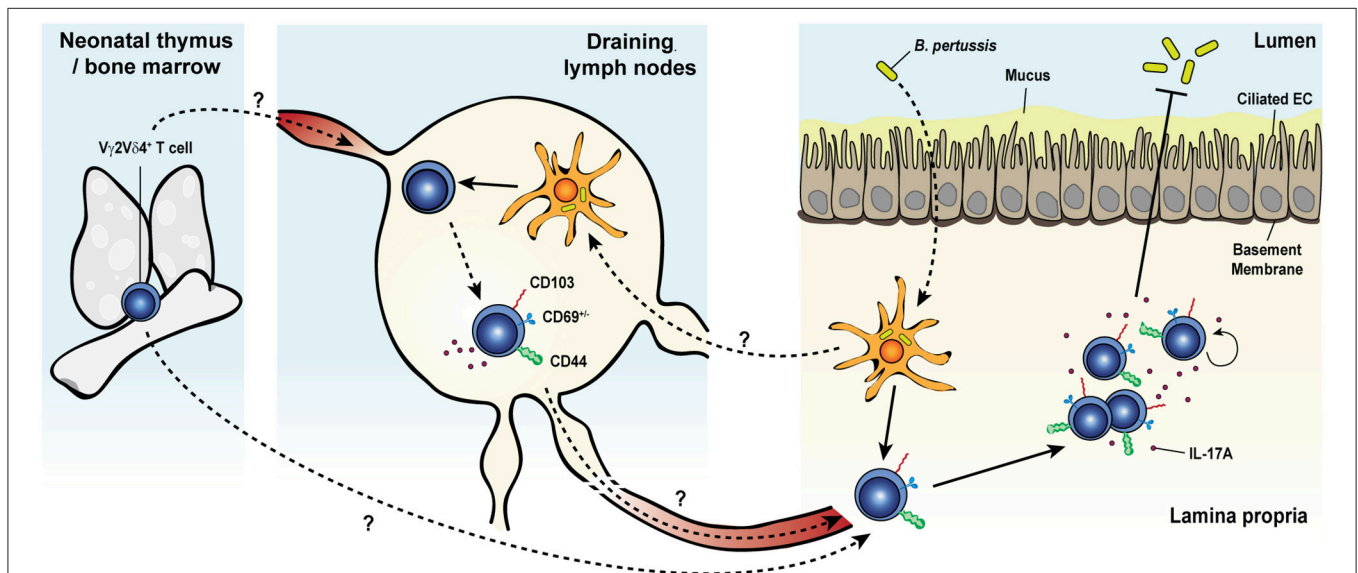


FIGURE 2 | Memory $\gamma\delta$ T cell response to pulmonary *Bordetella pertussis* infection. Upon primary intranasal infection with *Bordetella pertussis* (*B. pertussis*), $V\gamma 2V\delta 4^+$ T cells are activated by *B. pertussis* antigen-presenting dendritic cells either in the draining lymph nodes or directly in the lung tissue. Activated $\gamma\delta$ T cells expand, display a CD44⁺ and CD103⁺CD69^{+/-} activated resident memory phenotype and remain at an elevated number in the lungs after bacterial clearance. Secondary exposure to *B. pertussis* induces a recall expansion of memory $V\gamma 2V\delta 4^+$ T cells in the lung tissue and a protective and robust IL-17A response leading to an enhanced pathogen clearance.

predicated on immunization route. BCG challenge of vaccinated monkeys induced a more rapid and robust clonal expansion of $V\gamma 9V\delta 2^+$ T cells but no other $\gamma\delta$ T cell subsets. Thus, $V\gamma 9V\delta 2^+$ T cells are capable of forming long-lived clonally-expanded memory responses (45). Interestingly, direct contact with antigen presenting cells was required for the recall-like expansion of $V\gamma 9V\delta 2^+$ T cells (46). The recall response of $V\gamma 9V\delta 2^+$ T cells in BCG immunized macaques was associated with enhanced clearance of challenge infection and protection against fatal tuberculosis (45). In line with these findings, $V\gamma 9V\delta 2^+$ T cells induced in BCG vaccinated volunteers that were previously unexposed to any *mycobacteria* showed an enhanced responsiveness to *M. tuberculosis ex vivo* (223), suggesting that BCG vaccination also primes $\gamma\delta$ T cells to respond to *M. tuberculosis* in humans. Although human and monkey $V\gamma 9V\delta 2^+$ T cells share many features, including a memory-like response to *mycobacteria*, it remains to be established whether human $\gamma\delta$ T cells, like their non-human primate counterparts, are maintained in peripheral tissues following BCG immunization to confer some protection against *M. tuberculosis* infection.

Multifunctional Memory $\gamma\delta$ T Cells to *L. monocytogenes*

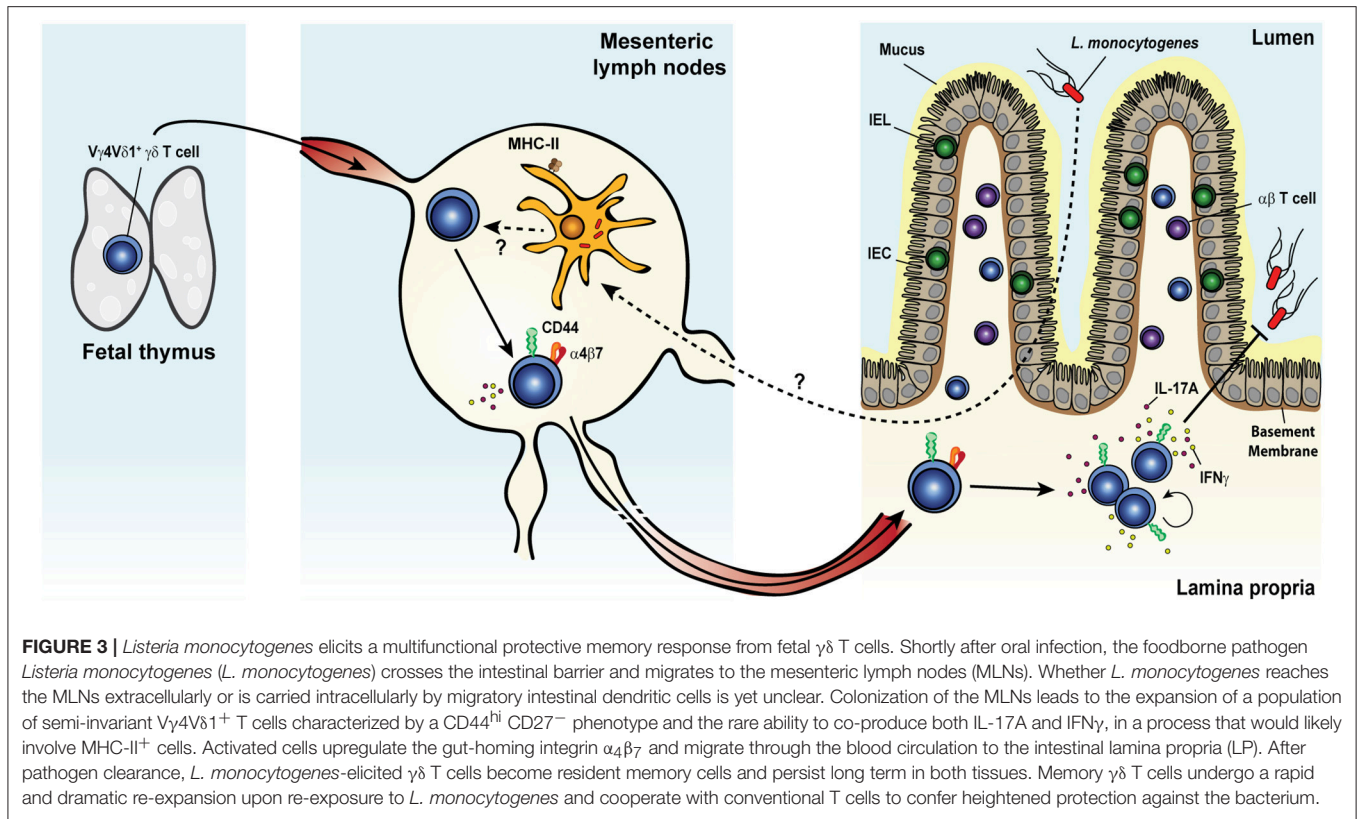
L. monocytogenes is known to be a potent inducer of $\gamma\delta$ T cell responses. In humans, expansion of $V\gamma 9V\delta 2^+$ T cells has been detected in the blood of pregnant women, newborns, infants and the elderly early after *L. monocytogenes* exposure (224, 225). These $\gamma\delta$ T cells displayed an activated (HLA-DR⁺) and memory (CD45RO⁺) phenotype. Consistent with a predetermined innate response, stimulation of PBMC from healthy donors with heat-killed *L. monocytogenes* (225), listeria lysate or culture supernatant (226) led to rapid proliferation of $V\gamma 9V\delta 2^+$ T cells.

A similar mobilization of circulating $\gamma\delta$ T cells during *L. monocytogenes* infection has also been reported in rhesus macaques. In a model of disseminated *L. monocytogenes* infection, $V\gamma 9V\delta 2^+$ T cells increased in the blood of rhesus macaques infected with an attenuated *L. monocytogenes* strain through an intramuscular, and to a lesser extent i.v. route (59). These cells were also elevated in bronchoalveolar lavages and rectal biopsies suggesting that they actively traffic to and seed mucosal tissues during infection. More interestingly, *L. monocytogenes* challenge of immunized animals led to a rapid and robust re-expansion of $V\gamma 9V\delta 2^+$ T cells that correlated with the resolution of infection (59). One peculiar feature of *L. monocytogenes* is its ability to use both the classical mevalonate and the alternative MEP pathways for isoprenoid synthesis (227). Both primary and recall-like responses of $V\gamma 9V\delta 2^+$ T cells have been shown to rely on the bacteria's ability to co-produce mevalonate-derived isopentenyl pyrophosphate and MEP-derived HMBPP, the latter being much more efficient at inducing primary and secondary expansion of primate $V\gamma 9V\delta 2^+$ T cells and promoting their differentiation into CD27⁺ CD45RA⁻ CD28⁻ memory cells (60). *L. monocytogenes*-elicited $\gamma\delta$ T cells displayed various effector functions after secondary

challenge, including production of IFN γ , IL-4, IL-17A, and TNF α (59). Surprisingly, a substantial portion of these cells were multifunctional and simultaneously produced IFN γ and IL-17A, IFN γ and IL-4, or TNF α and perforin in response to HMBPP (59, 60). Expanded $V\gamma 9V\delta 2^+$ T cells were also potent bactericidal effectors capable of efficiently lysing *L. monocytogenes*-infected DC and restraining intracellular bacterial growth in macrophages *ex vivo*. Thus, *L. monocytogenes* infection elicits a multifunctional circulating $\gamma\delta$ T cell response in non-human primates. Because this response is accompanied by the colonization of epithelial tissues, infection-elicited mucosal $\gamma\delta$ T cells may also have distinct effector functions that provide tissue-adapted responses.

A large body of evidence has convincingly demonstrated the involvement of $\gamma\delta$ T cells in the early phase of the primary immune response to systemic *L. monocytogenes* infection of mice (228–244) and rats (245, 246). More recently, our group reported a *bona fide* memory $\gamma\delta$ T cell response in mice after food-borne infection with a mouse-adapted *L. monocytogenes* capable of intestinal epithelial cell invasion (Figure 3) (62, 134, 247). Food-borne infection induced a long-lived $V\gamma 4V\delta 1^+$ T cell population in the gut draining mesenteric lymph node (MLN) with a CD44^{hi} CD27⁻ phenotype (62). By 7 days after infection, these cells were mobilized into the blood, up-regulated the gut-homing integrin $\alpha 4\beta 7$ and trafficked to the intestinal lamina propria similarly to conventional *L. monocytogenes*-specific CD8⁺ (248) and CD4⁺ (249) $\alpha\beta$ T cells. Like *L. monocytogenes*-induced CD4⁺ and CD8⁺ $\alpha\beta$ T_{RM} cells, *L. monocytogenes*-elicited $\gamma\delta$ T cells established residency in MLN and intestinal lamina propria where they were maintained long term in the absence of further antigenic stimulation (62, 134). The generation of this $\gamma\delta$ T cell subset was restricted to tissues associated with the gastrointestinal system and was induced by food-borne (62) but not i.v. infection (232, 233). *L. monocytogenes*-elicited $\gamma\delta$ T cells demonstrated enhanced anamnestic response upon *L. monocytogenes* challenge infection and were fully competent for immunologic boosting upon tertiary exposure (62). Although *L. monocytogenes*-elicited $\gamma\delta$ T cells appeared to share a similar anatomical niche as *L. monocytogenes*-specific CD4⁺ and CD8⁺ $\alpha\beta$ T cells (248, 249), all populations expanded robustly after infection and were maintained without any apparent competition for limiting resources or anatomic space.

Memory $\gamma\delta$ T cells cooperated with $\alpha\beta$ T cells to confer optimal protection in the MLN and the small intestine during food-borne *L. monocytogenes* challenge infection. Indeed, only the concomitant antibody-mediated depletion of $\alpha\beta$ T cells (both CD8⁺ and CD4⁺) and forced internalization of the $\gamma\delta$ TCR resulted in the complete loss of protection afforded to immunized mice, whereas the sole removal of $\alpha\beta$ T cells only partially impaired *L. monocytogenes* control (62). One striking feature of *L. monocytogenes*-elicited $\gamma\delta$ T cells was their ability to produce IFN γ and IL-17A during each stage of the immune response. Moreover, subsets within the CD44^{hi} CD27⁻ $\gamma\delta$ T cell population co-produced both cytokines during the primary and secondary responses (62), reminiscent of the multifunctional response described in rhesus macaques after



secondary challenge (59). During the recall response, the majority of IL-17A was derived from reactivated memory $\gamma\delta$ T cells in the MLN. This production of IL-17A was a critical component of anti-listerial immunity as it mediated the formation of *L. monocytogenes*-containing immune cell clusters composed of memory $\gamma\delta$ T cells and $IL-17RA^{+}$ inflammatory monocytes and neutrophils (134).

Collectively, these studies demonstrate that systemic and food-borne *L. monocytogenes* infection generates long-lived multifunctional memory $\gamma\delta$ T cells in rhesus macaques and mice, respectively. Thus, a population of pathogen-elicited $\gamma\delta$ T cells appears to behave very similarly between mice and primates, and this may suggest a conserved biology among mucosal $\gamma\delta$ T cells. These studies also highlight the important influence of infection route and models that mimic natural infection on understanding the $\gamma\delta$ T cell response. Interestingly, amongst the memory and memory-like responses described to date, *L. monocytogenes* is the only agent known to induce multifunctional $\gamma\delta$ T cells in two distinct species. Although $\gamma\delta 17$ T cells are known to have a permissive chromatin state for $IFN\gamma$ expression (102), other memory $\gamma\delta$ T cell populations reported in mice only produce IL-17A (25, 26, 48, 49). Conversely, only $IFN\gamma$ was shown to be produced by virus-activated memory-like $V\gamma 9V\delta 2^{+}$ T cells (39). miR-146a has recently been shown to negatively regulate $IFN\gamma$ production by murine $\gamma\delta 17$ T cells, including during oral *L. monocytogenes* infection (61). Elucidating the mechanisms by which *L. monocytogenes* partially breaks miR-146a-mediated inhibition of $IFN\gamma$ production by $\gamma\delta 17$ T cells

and understanding why other pathogens do not would provide important clues about the fine regulation of $\gamma\delta 17$ T cell functions and might open new avenues for the manipulation of these cells.

ANTI-TUMOR MEMORY $\gamma\delta$ T CELLS IN CANCER

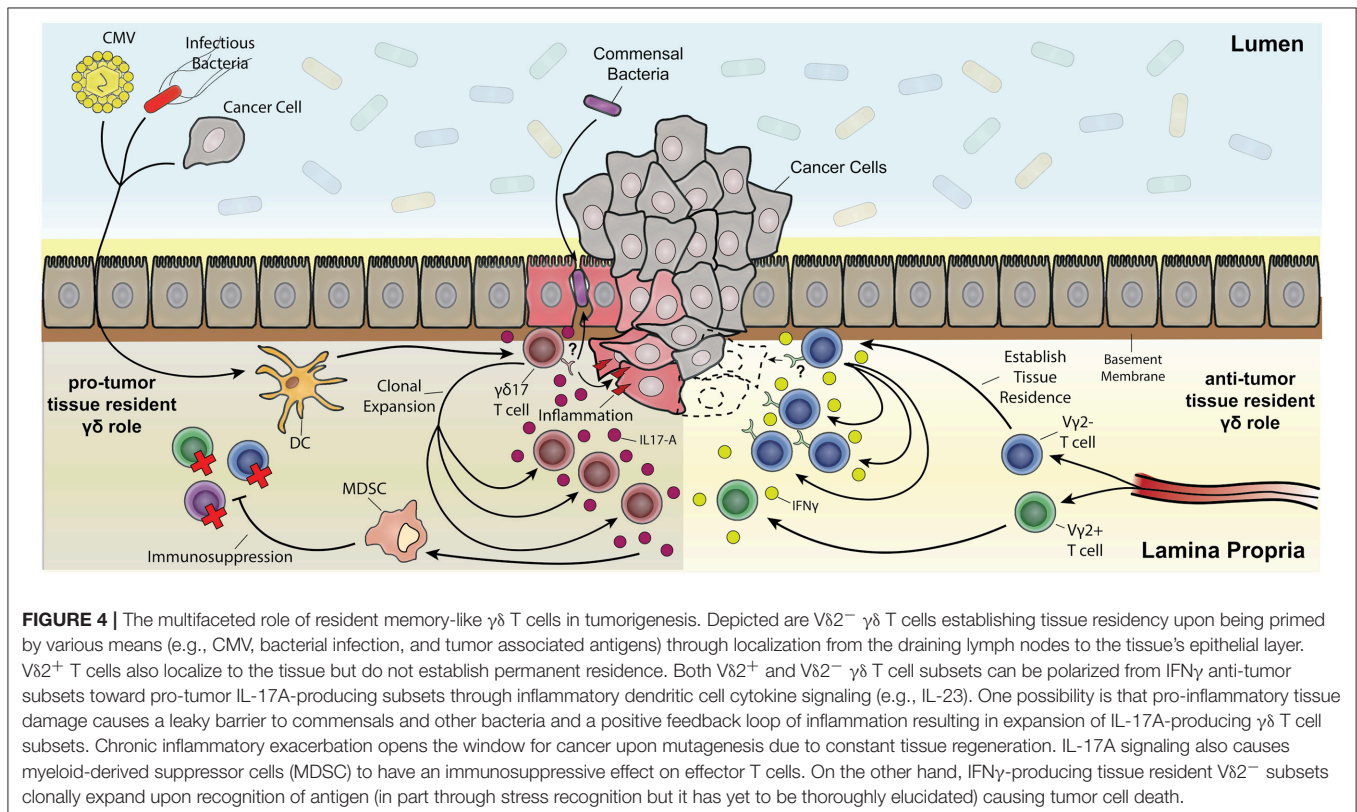
A substantial body of research has focused on the beneficial nature of $\gamma\delta$ T cells in anti-cancer immunity and their potential as a targetable therapeutic since a landmark study demonstrated that $\gamma\delta$ T cells in the epithelial compartment play a substantial role in prevention of cutaneous carcinogenesis (57). Indeed, the presence of an intra-tumoral $\gamma\delta$ T cell gene signature was associated with the single most favorable prognostic indicator of patient outcome for a wide range of cancers (250). $\gamma\delta$ T cells can have a wide range of effects ranging from reshaping the tumor microenvironment (251, 252), being integral in promoting a diverse cancer protective IgE repertoire through NKG2D stress surveillance (166), or $IFN\gamma$ production (52). Substantial effort has focused on resolving the anti-tumor activity of $V\gamma 9V\delta 2^{+}$ T cells, the predominant $\gamma\delta$ T cell population in human PBMC, in multiple cancers (253–257). Tissue resident $V\delta 2^{-}$ $\gamma\delta$ T cells may also substantially contribute to anti-tumor immunity. $V\delta 2^{-}$ $\gamma\delta$ T cells typically predominate over $V\delta 2^{+}$ T cells within tumors (52, 65) as well as in tissues from healthy individuals (120). This $V\delta 2^{-}$ $\gamma\delta$ T cell population is principally composed of $V\delta 1^{+}$ T

cells but also contain a significant population of $V\delta 3^+$ T cells. Due to $V\delta 2^-$ $\gamma\delta$ T cell prevalence in tumor microenvironment, it is likely that this subset also substantially contributes to anti-tumor activity.

$V\gamma 9V\delta 2^+$ T cells were previously delineated based on expression of CD45RA and CD27 as naive ($CD45RA^+ CD27^+$) cells or effector and memory T_{CM} ($CD45RA^- CD27^+$), T_{EM} ($CD45RA^- CD27^-$), and T_{EMRA} ($CD45RA^+ CD27^-$) cells (117). While naive T cells and T_{CM} cells primarily reside in secondary lymphoid tissues, T_{EM} and T_{EMRA} migrate to inflammatory sites to perform effector functions. These latter populations have been investigated in multiple cancers including squamous cell carcinoma (SCC) (52), CRC (65), neuroblastoma (71), and melanoma (53) due to their proliferative capacity and tendency to migrate toward inflammatory sites. Substantial effort has also sought to leverage the anti-tumor properties of $V\gamma 9V\delta 2^+$ T cells using approaches like *in vitro* expansion of patient-derived $\gamma\delta$ T cells and chimeric antigen receptor T cells for potential adoptive immunotherapies (258, 259). $V\gamma 9V\delta 2^+$ T cells can be selectively activated through PAgS or amino bisphosphonates such as zoledronic acid (zoledronate) in combination with various growth factors, cytokines, or costimulatory molecules (260). While various adoptive transfer methods have been primarily explored in a number of pre-clinical studies (261–267), to date, clinically favorable outcomes appear limited to prostate cancer (137). However, challenges remain in the rapid and robust generation of the large numbers of cells that would be necessary for successful adoptive immunotherapies (268). Zoledronate also

has various indirect effects on $\gamma\delta$ T cells by independently impacting the tumor microenvironment (251, 269, 270), which can provide a pro-tumor or anti-tumor outcome (271, 272). As such, it will be important to assess the contribution of $\gamma\delta$ T cells and the impact of any therapies in individual tumor types.

A protective role of tissue resident $\gamma\delta 17$ T cells has been readily described in the context of infectious disease, but they have also been implicated in exacerbating chronic inflammatory diseases like psoriasis. Chronic inflammatory disease is a risk factor and clinical precursor to a number of cancers including pancreatic cancer (273), skin cancer (274) and CRC (275). A growing body of literature has also demonstrated a $\gamma\delta$ T cell response that promotes tumor growth. This pro-tumor outcome of some $\gamma\delta$ T cell responses appears predominately a consequence of IL-17A production that is often associated with the up-regulation of proliferation pathways in cancerous lesions (276) (Figure 4). These apparent anti- and pro-tumor discrepancies are likely due to the dichotomous functional outcomes associated with type-1 or type-17 $\gamma\delta$ T cell responses. A pro-tumor role of IL-17A-producing $\gamma\delta$ T cells is evident in a number of cancers such as SCC (52), CRC (29), and metastatic breast cancer (70). In human SCC, tumor infiltration of IL-17A-producing $V\delta 1^+$ and $V\delta 2^+$ T cells was associated with a negative prognosis, in contrast to a more favorable outcome associated with tumor-infiltrating IFN γ -producing $\gamma\delta$ T cells (52). Similar results were seen in human CRC where a predominately $V\delta 1^+$ IL-17A-producing $\gamma\delta$ T cell population positively correlated with a more advanced tumor stage. This correlation was attributed



to an inflammatory DC - $\gamma\delta 17$ T cell - MDSC regulatory axis (29). Interestingly, tissue resident memory $V\gamma 2^+$ T cells were also seen in a metastatic mouse model of breast cancer. These $V\gamma 2^+$ T cells produced IL-17A and G-CSF, which promoted the establishment of immunosuppressive intratumoral MDSC (70). Collectively, these studies implicate tissue resident $V\delta 1^+$ and $V\gamma 2^+$ T cells as tumor growth promoting through IL-17A-mediated MDSC recruitment and immunosuppression in cancer. More importantly, these findings segregate deleterious $\gamma\delta$ T cell responses from those which may have a beneficial outcome.

On the other hand, $V\delta 2^-$ $\gamma\delta$ T cells are not limited to pro-tumor effects and effort has been invested into their therapeutic benefits. Intrahepatic $V\delta 1^+$ and $V\delta 3^+$ T cells express a $CD45RA^+ CD27^-$ and $CD45RA^- CD27^-$ phenotype that is nearly absent from the blood. Intrahepatic $CD45RA^- CD27^- V\delta 1^+$ and $V\delta 3^+$ T cells were competent producers of $IFN\gamma$ and $TNF\alpha$ and also expressed receptors for early activation and tissue retention, such as CD69, that have also been noted in both liver resident NK and $CD8^+ \alpha\beta$ T cell populations (120, 277). CMV infection has notably been one of the drivers of hepatic $V\delta 2^-$ $\gamma\delta$ T cell expansion and memory formation, and these factors appear to have a protective effect against tumor formation. CMV-seropositive patients (infected pre- or post-transplantation) have a reduced risk of skin cancer development and leukemia relapse after kidney or bone marrow transplant, respectively (36, 37). $V\delta 2^-$ $\gamma\delta$ T cells from CMV-infected kidney transplant patients were capable of killing HT29 colon cancer cells *in vitro* (128) and CMV-induced $V\delta 2^-$ $\gamma\delta$ T cells had anti-tumor activity against primary and metastatic tumors in a HT29 xenograft mouse model (278, 279). The characterization of the antigenic specificity of one highly expanded $\gamma\delta$ T cell clone from a CMV-seropositive transplant patient revealed that its recognition of stressed (infected or transformed) cells was mediated by the direct binding of the TCR to EPCR, independently of its cargo (33). Similarly, Annexin A2 is upregulated at the surface of stressed cells and can activate another $V\delta 2^-$ $\gamma\delta$ T cell clone (123). However, regardless of which epitope is being recognized, TCR sequencing of intrahepatic $V\delta 2^-$ $\gamma\delta$ T cell populations has revealed that CMV infection can induce expansion, memory phenotypes, and tumor reactivity in a clonally expansive manner (120). Overall, these studies suggest that $V\delta 2^-$ $\gamma\delta$ T cells form T_{RM} cell populations that can clonally expand and cross-react with tumor epitopes to provide anti-tumor immunity.

Knowledge of resident $\gamma\delta$ T cell biology is integral for future cancer therapies. Despite intra-tumoral $\gamma\delta$ T cell gene signatures being regarded as a favorable prognostic, there is a delicate balance between becoming pro-tumor and anti-tumor $\gamma\delta$ T cells (Figure 4). Pro-tumor populations are characterized by $\gamma\delta 17$ T cells and their indirect immunosuppressive activity through MDSC (29). On the other hand, anti-tumor populations are characterized by $IFN\gamma$ producing $\gamma\delta$ T cells (52). Notably, IgE response mediated by DETC stress surveillance can have

anti-tumor effects (166) as well as potential autoimmune effects (280). A better understanding of how signals in tumor microenvironment shape and potentially polarize $\gamma\delta$ T cell cytokine production and signal to other cells would be of great benefit.

CONCLUDING REMARKS

The roles of $\gamma\delta$ T cells in response to pathogens and commensals and in inflammatory disease and cancer have been an area of expanding interest over the last decade generating significant advances in knowledge. However, our basic understanding of $\gamma\delta$ T cell biology is still largely incomplete and lags far behind our understanding of their $\alpha\beta$ T cell counterparts, particularly in the area of anamnestic responses. $\gamma\delta$ T cells are adapted to their tissue environment which in turn shapes the immune landscape of that environment. Like most cells of the immune system, $\gamma\delta$ T cells can appear duplicitous under certain circumstances. On one hand, they can provide beneficial outcomes to the host by conferring anti-pathogen and anti-tumor immunity. On the other hand, they can lead to negative outcomes or exacerbated disease in some inflammatory disorders and cancers. Regardless of their impact, it is now clear that $\gamma\delta$ T cell responses encompass both innate inflammatory responses and more traditional adaptive memory responses that provide substantial opportunities for therapeutic targeting. Memory $\gamma\delta$ T cell responses may advance a new arm of rationale vaccine design that has broad implications for boosting anti-pathogen or anti-tumor immunity. Vaccines that elicit broadly reactive long-lived circulating or tissue-resident memory $\gamma\delta$ T cells may provide protection against a wide range of cancers and infections. Similarly, innate inflammatory or adaptive effector responses may be targeted to enhanced therapeutic modalities with far ranging implications. In the context of a detrimental impact on human health, $\gamma\delta$ T cell responses may be blunted or, in the context of cancer, diverted to a lineage that promotes tumor eradication. Thus, memory and tissue-resident $\gamma\delta$ T cells represent a lineage of the adaptive immune system that necessitate greater understanding to facilitate the generation of novel therapeutics to promote human health and reduce disease.

AUTHOR CONTRIBUTIONS

CK wrote the first draft of the manuscript. THC wrote sections of the manuscript. All authors contributed to manuscript revision, read and approved the submitted version.

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

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