

REVIEW ARTICLE Local heroes or villains: tissue-resident memory T cells in human health and disease

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Tissue-resident memory T (T_{RM}) cells are increasingly associated with the outcomes of health and disease. T_{RM} cells can mediate local immune protection against infections and cancer, which has led to interest in T_{RM} cells as targets for vaccination and immunotherapies. However, these cells have also been implicated in mediating detrimental pro-inflammatory responses in autoimmune skin diseases such as psoriasis, alopecia areata, and vitiligo. Here, we summarize the biology of T_{RM} cells established in animal models and in translational human studies. We review the beneficial effects of T_{RM} cells in mediating protective responses against infection and cancer and the adverse role of T_{RM} cells in driving pathology in autoimmunity. A further understanding of the breadth and mechanisms of T_{RM} cell activity is essential for the safe design of strategies that manipulate T_{RM} cells, such that protective responses can be enhanced without unwanted tissue damage, and pathogenic T_{RM} cells can be eliminated without losing local immunity.

Keywords: human; T cells; tissue-resident; memory; immunity

Cellular & Molecular Immunology (2020) 17:113-122; https://doi.org/10.1038/s41423-019-0359-1

INTRODUCTION

Improving the quality and breadth of immunity has been an ongoing challenge for the long-term preservation of human health. Much of the focus has been directed at generating immunological memory, a paradigm demonstrated to be effective at protecting against recurrent pathological challenges in an ever-evolving environment. A critical component of this process is a population of non-recirculating lymphocytes, termed tissue-resident memory T (T_{RM}) cells, which are phenotypically and transcriptionally distinct from circulating memory T cells¹ and offer front-line protection against invading microbes and tumor outgrowth.^{2,3} While the majority of studies detailing the identity and differentiation of T_{RM} cells have been performed in mouse models,^{4–8} more recent studies of human tissues describe the association of T_{RM} cell density and phenotype with prognosis in several disease settings.^{9–11} Human T_{RM} cells have heterogeneous developmental and survival requirements, the full extent of which is yet to be completely elucidated, demonstrating a continued need to further dissect fundamental mechanisms of T_{RM} cell biology. Here, we discuss what is known about human $T_{\text{\tiny RM}}$ cells in health and in disease in the context of infection, cancer, autoimmunity, and transplantation, highlighting knowledge gaps and therapeutic opportunities.

AN OVERVIEW OF T_{RM} CELLS: LESSONS FROM MICE

 T_{RM} cells have been investigated across multiple tissues and in various disease settings. Studies from murine models using transplantation, 5,12 parabiosis, $^{13-15}$ and intravascular labeling 15,16

have demonstrated a *bona fide* resident population of memory T cells that are permanently lodged in the tissue. While the majority of studies have focused on CD8⁺ T_{RM} cells, there is increasing evidence that CD4⁺ T_{RM} cells are also present in nonlymphoid tissues in both mice^{17–21} and humans.^{22–25} The defining feature of T_{RM} cells is their commitment to the tissue of residence (as opposed to any particular marker), a key feature being their inability to circulate through the bloodstream or lymphatics. T_{RM} cells lack the lymph node homing molecules CD62L and CCR7,^{6,26} which helps to facilitate tissue residency and downregulate the transcription factor KLF2²⁷ and receptors of sphingosine-1-phosphate (S1P), a chemoattractant produced by endothelial cells that promotes egress from lymph nodes and tissue.²⁸ Moreover, the expression of CD69, which is commonly used to define T_{RM} cells, has a role in antagonizing the expression of the egress receptor S1P receptor 1 (S1PR1) and preventing cells from migrating out of the tissue.^{27,29}

The canonical markers associated with CD8⁺ T_{RM} cells are CD69 and integrin CD103, although T_{RM} cell populations lacking CD103 have also been detected in tissues, including the kidney³⁰ and liver^{31,32} and the small intestine intraepithelial lymphocytes (SI-IELs) and lamina propria.^{33,34} The expression of other surface molecules has been associated with CD8⁺ T_{RM} cells, including CD49a, CD101, PD-1, and CXCR6,^{10,35-37} some of which are dependent on the local tissue. Following entry into nonlymphoid organs, T_{RM} cells acquire several differentiation markers in a process that involves the action of cytokines, including tumor growth factor- β (TGF β) and interleukin-15 (IL-15). Using T cells from mice deficient in cytokines or their receptors, it has been demonstrated that TGF β plays a role

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Received: 14 October 2019 Accepted: 17 December 2019 Published online: 22 January 2020

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in the development of T_{RM} cells in the skin,^{6,7} lung,^{7,38} salivary gland,^{39,40} and SI-IELs^{34,41} and that IL-15 contributes to T_{RM} cell development in the skin, salivary gland, lung, and liver (but not in SI-IELs⁸). Importantly, it has been shown that other tissue-resident cells (including natural killer and natural killer T cells) share a common transcriptional signature regulated by the transcription factors Hobit and Blimp-1, which are distinct from the genetic profile of circulating memory T cells.³¹ Both the Notch family of signaling receptors and the aryl hydrocarbon receptor play a role in the maintenance of mouse T_{RM} cells.⁶⁴² More recently, Runx3 and Bhlhe40 were identified as transcription factors that could regulate T_{RM} cell development and functionality.^{43,44}

The capacity of T_{RM} cells to protect against re-infection and tumor growth has now been shown in numerous settings.⁴⁵ Using experimental systems where circulating memory T cells are depleted, leaving only tissue-resident cells, it has been shown that T_{RM} cells are capable of "sounding the alarm" against recurrent immunogenic challenges.⁴⁶ Upon restimulation, T_{RM} cells are capable of proliferating, secreting effector cytokines, such as interferon- γ (IFN γ), tumor necrosis factor- α (TNF α), and granzyme B, and recruiting other immune cells to the site of challenge; therefore, the mucosal recall response is contributed both by pre-existing T_{RM} cells and those recruited from the circulation.^{47,48} T_{RM} cells prevent and control a wide variety of viral infections.^{14,49–53} Additionally, T_{RM} cell abundance in tumors positively correlates with patient survival,^{11,54–58} and they are able to maintain malignant cells in a state of equilibrium to prevent outgrowth.³ All the above illustrate the role of T_{RM} cells as critical players in mediating long-term immunity.

FROM MICE TO MEN: INVESTIGATING HUMAN T_{RM} CELLS

The understanding of murine T_{RM} cell biology has driven the investigation of T_{RM} cells in an array of human conditions, including in the context of organ donation and transplantation, infectious diseases, and tumor biology. The persistence of donor HLA-mismatched T_{RM} cells following facial,⁵⁹ lung⁶⁰ and small-bowel^{61,62} transplantation provides strong evidence for non-recirculating T_{RM} cells in human tissue. In one study, organ donors were analyzed over six decades of life, and the frequency of CD4⁺ or CD8⁺ T cells with a CD69⁺ or CD69⁺CD103⁺ phenotype was found to be the greatest in mucosal sites, including the gut and lung, compared to lymphoid tissue.⁶³ Additionally, the administration of anti-CD52 therapeutic antibody (alemtuzumab) to patients with cutaneous T cell lymphoma was found to deplete circulating T cells, but spare those found in skin, illustrating a population of tissue-resident skin cells in disequilibrium with the blood.⁶⁴

While CD69 expression is generally used to identify human CD8⁺ and CD4⁺ T_{RM} cells, it is likely that additional resident T cells exist that do not express this putative marker, as has been reported in mice.¹⁵ For example, while CD69⁺CD103⁻ and CD69⁺CD103⁺ populations of CD8⁺ and CD4⁺ T_{RM} cells have been found in tissues, including healthy human lung⁶⁰ and skin,⁶⁵ T_{RM} cells lacking the expression of both of these markers have been reported in cells from the female reproductive tract,^{50,66} pancreas,⁶⁶ and salivary glands.^{40,67}

Even within the same tissue, the T_{RM} cell pool displays heterogeneity, with distinct transcriptional and phenotypic subsets.²³ For example, skin CD8⁺ T_{RM} cells may be CD49a⁺ or CD49^{-,10} with the expression of CD49a facilitating T_{RM} cell retention through its dimerization with CD29 (integrin β 1) and the binding of collagen IV and laminin.⁶⁸ CD49a⁺ T_{RM} cells have a cytotoxic phenotype based on perforin and IFN γ production, while CD49a⁻ T_{RM} cells can secrete IL-17.^{10,37} Given the unique microenvironment of various organs, local tissue-specific features are likely associated with the differentiation, homeostasis, and protective functions of T_{RM} cells (reviewed in ref. ⁶⁹).

It has been demonstrated that the CD69⁺ memory T cells isolated from human lung tissue share a similar transcriptional

profile to that of mouse T_{RM} cells, with the upregulation of the surface markers *Itgae* (which encodes CD103), *Itga1* (which encodes CD49a), and *Cxcr6* and the downregulation of migration-associated genes such as *S1pr1*, *Klf2*, and *Sell* (encodes CD62L) when compared to CD69⁻ memory T cell compartments from the lung and spleen.²³ The expression of immune checkpoints, including PD-1,^{23,48} on T_{RM} cells indicates that they may be negatively regulated to prevent aberrant activation, a feature that may be critical to the tumor response following treatment with immune checkpoint inhibitors.

Despite the discovery of T_{RM} cells in various human tissues, there is still a lack of complete understanding surrounding T_{RM} cell identification, development, and functionality. Below, we discuss reports on human T_{RM} cells with a focus on CD8⁺ T_{RM} cells in a range of disease settings, highlighting their potential to promote tissue immunity in some contexts and to contribute to tissue damage in others (summarized in Fig. 1).

T_{RM} CELLS IN INFECTIOUS DISEASES

It has been well established that classic circulating effector memory and central memory T cells (T_{EM} cells and T_{CM} cells, respectively) provide critical immune memory to infectious agents and protect against re-infection. Circulating naive T cells migrate through the blood and lymphoid tissue until they encounter a cognate antigen on antigen-presenting cells. This leads to cellular activation of the naïve cell, transformation into a memory T cell, and clonal expansion. A subset of T_{EM} will survive the following memory T cell constriction to become T_{CM} cells; these cells traffic through blood and lymph and provide an augmented effector response upon antigen re-encounter that contributes to the prevention and control of disease (reviewed in refs. 70,71). Two phenomena well described in classic circulating T cells are memory inflation and exhaustion; however, it is unknown whether these phenomena similarly occur in T_{RM} cells. Memory T cell inflation describes the development of expanded, functionally distinct antigen-specific CD8⁺ T cells. These populations occur as the result of restricted contraction, maintain a persisting T_{EM} phenotype without features of exhaustion and have been most characterized in chronic viral infections, including murine and human cytomegalovirus (CMV; reviewed in ref. ⁷²). The repeated antigenic stimulation that occurs in both chronic infection and malignancy leads to an induced hyporesponsiveness of antigenspecific CD8⁺ T cells known as T cell exhaustion. The terminally differentiated exhausted T cells of chronic infection have a PD-1⁺CXCR5⁻TIM3⁺EOMES^{hi}TBET^{lo} phenotype (reviewed in ref.

More recently, the role of non-recirculating T_{RM} cells in the control of infectious diseases has become appreciated. Poised in front-line niches, T_{RM} cells are opportunely placed to protect against pathogen invasion. Human T_{RM} cells have been most studied in the context of viral immunity, but have also been examined in a number of bacterial, parasitic, and fungal infections (reviewed in ref. ⁷⁴). Here, we review the contribution of T_{RM} cells to immunity against common viral infections by summarizing evidence derived from primary human tissue and relevant animal models of disease.

Influenza

Influenza-specific T_{RM} cells have been detected in the respiratory tract of infected patients,^{75–79} and these cells play a role in the control of acute infection and long-term immunity.³⁸ Influenza-specific T_{RM} cells are highly proliferative and polyfunctional,⁸⁰ demonstrating a rapid and robust IFN γ and TNF α response upon ex vivo stimulation.⁸⁰ Prior exposure correlates with protection against re-infection,⁸¹ possibly due to the accumulation of CD8⁺ T_{RM} cells in the lungs.^{77,79} This observation has led to investigation into whether influenza-specific T_{RM} cells play a role in this process and provide long-term heterosubtypic protection.^{22,51,52,78,82} However, while T_{RM} cells in most tissues are thought to be long

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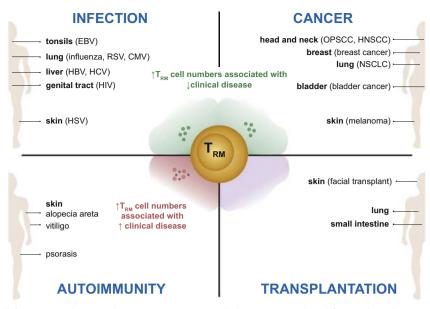


Fig. 1 Overview of T_{RM} cell function in human disease. Human T_{RM} cells have been isolated from a broad range of tissues and assessed for their associations with disease activity in the context of infection, cancer, autoimmunity and transplantation as summarized here. **Infection:** Epstein–Barr virus (EBV)-specific T cells have been identified in the tonsils of infected patients and have shown an increased frequency of CD69 and CD103 coexpression compared to their counterparts in the blood and spleen.¹²⁵⁻¹²⁷ Lung T_{RM} cells from influenza patients¹⁹⁵ as well as liver T_{RM} cells from hepatitis B virus (HBV)-infected patients³³ are capable of producing strong levels of IFN₇ and TNFα ex vivo, and high numbers of these T_{RM} cells were found to correlate with reduced disease severity. This was similarly observed for patients infected with respiratory syncytial virus (RSV),^{33–95} cytomegalovirus (CMV),^{117,118,120-122,124} and hepatitis C virus (HCV),³ whereby increased T_{RM} cells no are able to better control infection.^{131–135} While herpes simplex virus (HSV)-specific T_{RM} cells have shown direct viral control in murine studies,^{103–105} it has also been predicted that a higher density of HSV-reactive T_{RM} cells can correlate with an improved survival rate of patients, including those with oropharyngeal squamous cell carcinoma (DSCC),^{166–168} head and neck squamous cell carcinoma (HNSCC),¹⁵⁴ breast cancer,¹¹¹ nonsmall-cell lung cancer (NSCLC),⁵⁴ bladder cancer,^{56,149} and melanoma.⁵⁵ Moreover, T_{RM} cells with higher levels of perforin, granzyme B, and other effector proteins were noted in cohorts of patients with poor outcomes in psoriasis,¹⁰ vitiligo,¹⁰ and alopecia areata (AA).¹⁸⁷ While an increase in IL-17 production has been shown to be associated with poor outcomes in psoriasis,¹⁰ vitiligo,¹⁰ and alopecia areata (AA).¹⁸⁷ While an increase in IL-17 production has been associated with a reduced incidence of rejection, conflicting studies from facial skin transplant

lived,^{5,6,12} it was also recently demonstrated in a mouse model that influenza-specific lung T_{RM} cells can decline during convalescence and increase their expression of apoptotic proteins.⁸³ It is not known whether human lung T_{RM} cells decay in a similar way to mouse lung T_{RM} cells or whether this contributes to the loss of heterosubtypic immunity against influenza infection. Ex vivo T cell receptor (TCR) analysis of influenza-specific clonotypes in the lung is diverse, but certain sequences can also be found in other tissues, such as blood, spleen, and lymph nodes.⁸⁴ Whether these lymphoid sites act as a source of replenishment for influenzaspecific lung T_{RM} cells is unknown. Certainly, it would be of value to assess whether there are preferred clonotypes that form resident and circulating memory T cells.⁸⁴ The decipherment of clones that favor residency and longevity in human lung T_{BM} cells would provide useful data for vaccine design that could promote the durable protection of lung tissue from repeated exposures through the formation of a persistent influenza-specific lung T_{RM} cell population.⁸⁵ Currently, live attenuated influenza vaccines (LAIVs) are utilized and have been shown to induce IFNyproducing T cells in the blood of children and adults,⁸⁶ and in animal studies, LAIVs provide protection against infection with heterosubtypic strains.^{79,87,88} While the formation of T_{RM} cells has been reported in patients receiving this vaccine, more information about their protective capacity upon re-infection is required.

Respiratory syncytial virus

Respiratory syncytial virus (RSV) is an acute respiratory infection,^{89,90} and unlike influenza, natural RSV infection does not elicit complete strain-specific protection upon re-exposure.⁹¹ It has been reported that RSV-specific CD8⁺ T cells are enriched within the lung compared to the blood,⁷⁹ and these cells remain elevated in tracheal aspirates of children during convalescence following severe RSV infection.⁹² RSV-specific lung CD8⁺ T_{RM} cells coexpress CD69 and CD103; however, they were found to have lower levels of granzyme B and perforin than their blood counterparts.⁵ Higher frequencies of RSV-specific $CD8^+$ T_{RM} cells in the airway correlated with reduced disease severity and viral load. Similarly, low numbers of CD8⁺ T cells in the airway^{94,95} (or an increased proportion of activated T cells in the blood) of hospitalized RSVinfected adults have been associated with more severe human RSV disease.⁹⁶ This may indicate a potential role for lung T_{RM} cells to control and protect against RSV infection,⁹³ as has been demonstrated in animal studies $^{97-100}$ demonstrated in animal studies.⁹

Herpes simplex virus

Herpes simplex virus (HSV) types 1 and 2 are neurotropic herpesviruses that establish latency in dorsal root ganglia. HSV reactivation can be asymptomatic or manifest as painful mucocutaneous ulcerations and rarely as encephalitis.¹⁰¹ Episodes of

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mucocutaneous HSV reactivation are frequent, and effective immune surveillance is required to prevent overt disease.¹⁰² The importance of T_{RM} cells in the control of HSV-1 and HSV-2 reactivation is well established in animal models and human ex vivo studies. Mouse HSV-1 and HSV-2 infection studies have demonstrated that localized T_{RM} cells control viral latency through noncytolytic mechanisms and control viral reactivation by readily producing effector cytokines and initiating local proliferative responses.^{103–105}

In humans, HSV-specific CD4⁺ and CD8⁺ T cells are enriched in the female genital tract compared to the circulation, ¹⁰³ and HSV-2specific CD8⁺ T cells accumulate adjacent to peripheral nerve endings after viral reactivation.¹⁰⁶ In samples from the genital tract of HSV-2-infected women, HSV-specific CD8⁺ T cells expressed the markers of tissue residency, CD69 and CD103.¹⁰⁷ A mathematical model has predicted that the density of HSV-2-specific T_{RM} cells in human skin is critical for successful containment of viral reactivation in cells,¹⁰⁸ and this has been confirmed directly in mouse HSV infection models.⁴⁸

Cytomegalovirus

CMV infects the majority of the world's population and establishes a life-long infection; reactivated CMV can infect many organs, causing retinitis, pneumonitis, colitis, hepatitis, and/or end-organ failure.¹⁰⁹ A significant proportion of the host immune system is devoted to the long-term control of CMV. CMV infection in mice and humans can lead to expanded, sustained effector memory CD8⁺ T cells through the process of memory inflation, which develops in parallel with conventional contracting central memory responses to many epitopes.¹¹⁰ Single-specificity inflationary T cells can constitute up to 30% of the circulating human T cell pool¹¹⁰ and have been shown to provide protection against viral challenge in mouse models.¹¹¹ Inflationary CMV-specific T cells abundantly express CX3CR1, which recognizes the fractalkine expressed by endothelial cells at intermediate (CX3CR1^{int}) and high levels.¹¹² CX3CR1^{int} CD8⁺ memory T cells (termed peripheral memory cells) are associated with enhanced self-renewal, proliferative, and tissue-surveying properties,¹¹³ suggesting that CX3CR1^{int} CMV-specific T cells may be important for the development of memory inflation.¹¹

Mouse infection models have shown a clear role of CMV-specific T_{RM} cells in controlling viral replication. After primary murine CMV (MCMV) infection, virus-specific T_{RM} cells progressively accumulate in mucosal tissues and salivary glands,¹¹⁴ with MCMV-specific T_{RM} cells providing protection against local re-infection.⁴⁰ Lung MCMV-specific T cells are maintained in an antigen-independent manner and are long lived compared to effector memory cells induced by acute respiratory viral infections.¹¹⁵ MCMV-specific CD8⁺ T cells from the gut epithelium show a transcriptome closely linked to a T_{RM} cell phenotype and quite distinct from that of the dominant "inflationary" memory population.¹¹⁶ The capacity of CMV to induce sustained mucosal CD8⁺ T_{RM} cell responses is of interest to vaccine design, and a number of animal studies have demonstrated that intranasal vaccination with an MCMV vector can generate persistent lung T_{RM} cell responses.^{99,117}

CMV-specific T cells have been detected in a variety of human tissues, including lung, spleen, bone marrow, gut, and lymph nodes.¹¹⁸ A discordance in the frequency of CMV-specific CD8⁺ T cells in blood compared with tissues is frequently observed.¹¹⁸⁻¹²⁴ In the lung and spleen, a significant proportion of CMV-specific CD8⁺ T cells express CD69 (but not CD103), whereas influenza-specific and RSV-specific memory CD8⁺ T cells in lung tissue coexpress both CD69 and CD103.⁷⁹ TCR analysis of CMV-specific CD8⁺ T cells revealed scant overlap between clones in paired lymph node and blood samples and that there was little clonal overlap between the effector memory T cell and central memory T cell subsets.¹²⁴ This finding indicates that human CMV-specific CD8⁺ T cells are anatomically compartmentalized; however, their individual contribution to the control of local CMV replication is currently unknown.

Epstein-Barr virus

Epstein-Barr virus (EBV) is a highly prevalent infection that establishes life-long latency. Oropharyngeal exposure to infected saliva leads to transmission with viral replication occurring in epithelial cells and B cells and the clinical presentation of infectious mononucleosis. Following primary infection, EBV establishes latency in the circulating memory B cell pool, and cytotoxic T cells play a major role in controlling EBV-infected cells. EBV is intermittently detected in throat washings of asymptomatic carriers, which has been attributed to the reactivation of EBV in oropharyngeal lymphoid tissue, leading to a lytic oropharyngeal infection.¹²⁵ Studies have shown that EBV-specific T cells preferentially accumulate in tonsils compared to blood and spleen and that a high proportion express CD69 and CD103.¹²⁶⁻¹²⁸ These data suggest that tonsillar T_{RM} cells may play a role in controlling viral replication in oropharyngeal tissue, thereby preventing reactivation. EBV infection is also associated with a range of cancers, including B cell-derived lymphomas, T cell lymphomas, and nasopharyngeal cancer;¹²⁹ however, it is not yet known whether EBV-specific T_{RM} cells contribute to the control of EBVrelated oncogenesis.

Hepatotropic viruses

Hepatitis B virus (HBV) and hepatitis C virus (HCV) are hepatotropic viruses that can cause chronic infection in the liver, leading to cirrhosis and hepatocellular cancer. In contrast to acute and resolving viral infections (e.g., influenza), the immune response to chronic viral infections is a continuous effort. This requirement may lead to different characteristics of virus-specific T_{RM} cells in chronic infections compared with acute infections. Higher numbers of CD69-expressing CD8⁺ T cells were observed in the liver of patients with partial immune control of HBV and chronic HCV infection.^{35,130} In HBV infection, these cells can be distinguished by high expression of the exhaustion markers PD-1 and CD39, but are capable of producing high levels of IL-2, IFNy, and TNFa upon ex vivo stimulation with HBV epitopes.³⁵ Liver T_{RM} cells obtained from patients with chronic HBV expressed higher levels of granzyme B than those obtained from control patients,¹³⁰ but whether this contributes to the immunopathology of cirrhosis and hepatocellular cancer is yet to be determined.

Human immunodeficiency virus

Human immunodeficiency virus (HIV) is a chronic noncurable infection that results in acquired immunodeficiency syndrome (AIDS) if left untreated. Although combination anti-retroviral therapy has reduced the incidence of AIDS, HIV/AIDS continues to cause significant morbidity and mortality worldwide. Most HIV replication occurs in tissues, particularly mucosal and lymphoid tissue, and CD8⁺ T cells are critical for effective immune control. T_{RM} cells are generated in response to HIV infection in multiple locations, including the gastrointestinal tract, female reproductive tract, and lymphoid tissue.^{131–135} HIV-specific CD8⁺ T_{RM} cells are found in high frequencies and exhibit robust polyfunctional responses in the gastrointestinal and lymphoid tissue of individuals who naturally control HIV infection ("elite controllers"), suggesting that T_{RM} cells may play an important role in limiting HIV replication.¹³³ Because HIV is frequently transmitted through sexual intercourse, the generation of HIV-specific T_{RM} cells in the genital tract through vaccination is a desirable goal. Several studies have reported success in generating genital HIV (or simian immunodeficiency virus)-specific $T_{\rm RM}$ cells in animals, $^{136-138}$ offering hope for similar translational studies in humans.

T_{RM} CELLS IN CANCER

The immune system plays important roles in controlling and eliminating malignant cells through tumor surveillance. The

current model of the tumor immunity cycle suggests that dendritic cells loaded with tumor antigen are presented to naive CD8⁺ T cells in the lymph node. This results in the activation and expansion of a tumor-specific T_{EM} population that traffics back to tumor sites and engages in cell-mediated tumor lysis.¹³⁹ How successful tumor-specific memory CD8⁺ T cells are in penetrating the tumor carries important prognostic value. Memory CD8⁺ T cells that accumulate at the peripheral margins of tumors are denoted as infiltrated-excluded and are characterized as poorly immunogenic. In contrast, memory CD8⁺ T cells that further penetrate the tumor are classified as infiltrated-inflamed and are associated with superior responses to therapy (reviewed in ref.¹⁴⁰). Similar to chronic viral infection, repeated exposures of memory T cells to their cognate antigen lead to the upregulation of immune checkpoint molecules during the process of T cell exhaustion, and these cells have been successfully targeted by immune checkpoint inhibitor therapies.¹

 $T_{\rm RM}$ cells are located in tissues where solid tumors arise, and mounting evidence indicates that CD8⁺ $T_{\rm RM}$ cells play a role in the inhibition of cancer progression and metastasis. The growing understanding in this field provides an opportunity to improve upon current immunotherapies for solid tumors.

Tumors have distinct microenvironments that host heterogeneous populations, including macrophages, natural killer cells, innate lymphoid cells (ILCs), IELs, $\gamma\delta T$ cells, and group 1 ILCs. Many studies have shown that a proportion of tumor-infiltrating lymphocytes (TILs) have a T_{RM} cell-like phenotype, defined by surface staining and/or molecular signature.^{55,142–144} For the purpose of this review, we denote these cells as "T_{RM}-like TILs," a population that makes up 25–75%¹⁴² of all TILs.

In human studies, T_{RM} -like TLs are found in several cancers, including melanoma;^{55,143,144} non-small-cell lung cancer (NSCLC);^{54,145} and breast,^{11,146} colorectal,^{147,148} bladder,^{56,149} ovarian,^{57,150,151} and cervical cancer.¹⁵² However, the *bona fide* residency of these CD69⁺CD103⁺ TLs remains to be determined. CD69 expression may be induced by cognate antigen stimulation or oxygen deprivation, and CD103 expression can be induced on circulating CD8⁺ T cells that recognize antigen in the presence of TGF β ,^{153,154} all of which are factors that are present in the tumor microenvironment. Whether the expression of CD69 and CD103 induced by the tumor microenvironment is analogous to the formation of T_{RM} cells in nonmalignant tissue is an area of current investigation.

While a high proportion of total TILs is associated with improved cancer survival, the proportion of T_{RM} -like TILs may also be of importance (reviewed in ref. 155). The abundance of T_{RM} -like TILs in the tumor epithelium positively correlates with disease-free and/or overall survival in NSCLC⁵⁴ and breast, 11 melanoma, 55 bladder, 146 ovarian, 57 and endometrial cancer. 58 Additionally, the accumulation of T_{RM} -like TILs has been used to predict the clinical response to immune checkpoint inhibitors. 11,55

Although CD103⁺CD8⁺ T_{RM}-like TILs often have a high expression of immune checkpoint molecules, including PD-1, TIM-3, and LAG-3, in comparison with CD103⁻ TILs, their ability to produce cytotoxic molecules and effector cytokines is maintained.^{11,54,143,145,152,156} T_{RM}-like TILs exhibit enhanced cytotoxic potential and effector functions compared with CD103⁻ TILs, suggesting that they potentially mediate superior tumor surveillance compared to circulating tumor-specific T cells.¹⁵⁷ As expected, T_{RM}-like TILs were capable of mediating a melanoma-immune equilibrium in mouse skin.³ In vitro, CD103⁺ T_{RM}-like TILs were more efficient at lysing NSCLC cells than their CD103⁻ counterparts, possibly due to these cells being able to form more stable synapses with target cells and to direct cytotoxic granules in a polarized fashion.^{145,158} Similarly, CD39⁺CD103⁺CD8⁺ T_{RM}-like TILs had the highest tumor reactivity in vitro in tumor specimens obtained from patients with melanoma, lung cancer, HNSCC, ovarian cancer, and rectal cancer.¹⁵⁴

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A significant proportion of TILs may be T_{RM} -like and potentially do not recirculate, which has implications for divergent treatment responses in metastatic disease.¹⁴² TILs are established in each metastasis early, and the TCR repertoires are distinct between individual metastatic sites. The interlesion diversity of TCRs is mostly accounted for by T_{RM} -like TILs,¹⁴³ even with apparent equal exposure to neoantigens. This suggests that the interlesional diversity of tissue-resident T cells may differentially affect the outcome of checkpoint inhibitor therapy at each site.¹⁴³

A more comprehensive understanding of the characteristics of tumor-residing T_{RM} cells in different cancer types may reveal novel targets for therapeutic intervention.¹⁵⁹ The role of T_{RM} -like TILs in organ-specific malignancies, as elucidated in primary human tissues and animal models of disease, is discussed further below and summarized in Fig. 1.

Melanoma

Mouse models have provided strong evidence that T_{RM} cells mediate effective antitumor responses to melanoma and suppress tumor growth,^{3,160} providing a basis for translational studies in humans. Indications that T_{RM} cells play a role in human melanoma are suggested from reports demonstrating improved survival in patients with greater proportions of T_{RM}-like TILs and the increased expression of tissue residency genes, including Cd69, Itgae, and Cd244.⁵⁵ T_{RM}-like TILs had significantly higher levels of PD-1 (~75% of CD8⁺ T cells) than their CD69⁻CD103⁻ counterparts, and the potential significance of this observation was sustained by longitudinal data that demonstrated that these PD-1⁺CD69⁺CD103⁺ T cells expand early during anti-PD-1 therapy compared to baseline values.⁵⁵ In the same study, the authors also associated the level of II-15 transcripts with patient outcome, where improved survival rates were directly proportional to the expression of IL-15 in the tumor.⁵⁵ While skin T_{RM} cells are known to require IL-15 for their development and longevity, an evaluation of whether this cytokine in the local tumor microenvironment can directly affect T_{RM}-like TILs to promote cancer regression is yet to be determined. An understanding of the contribution of T_{RM} cells in melanoma has the potential to direct the design of anti-melanoma vaccines for long-term protection, which has shown promise in animal models.¹⁰

Non-small-cell lung cancer

NSCLC is the most common form of lung cancer¹⁶² and is a setting in which the characterization of lung T_{RM} cells is being investigated. Reports have noted the presence of tumor-specific CD103⁺ T_{RM} -like TILs in NSCLC tissue, and the transcriptional signature of these cells was similar to that of infection-induced lung T_{RM} cells, including a high expression of *Itgae*, *Cxcr6*, and *Ctla4* with the downregulation of *Klf2*.⁵⁴ Moreover, T_{RM} -like TILs had increased levels of genes associated with cell cycling, proliferation, and toxicity.⁵⁴ Patients with high proportions of TILs had reduced mortality rates, and the risk was further reduced in patients with higher proportions of T_{RM} -like TILs,⁵⁴ suggesting the potential cytotoxic response of lung T_{RM} cells for controlling NSCLC.

Bladder cancer

The successful use of the therapeutic intravesical bacillus Calmette-Guerin in bladder cancer demonstrates the capacity to stimulate a localized T cell-mediated antitumor response.¹⁶³ T_{RM}-like TILs were found in local tissue from patients with bladder urothelial cancer,⁵⁶ and these cells had high expression of perforin, granzyme B, and PD-1 compared with CD8⁺ T cells from the peripheral blood of healthy volunteers,¹⁴⁹ corroborating the licensed use of anti-PD-1 and anti-PDL1 checkpoint inhibitors for the treatment of this cancer.¹⁶⁴ An abundance of T_{RM}-like TILs has been associated with improved prognosis in bladder urothelial cancer,⁵⁶ and T_{RM}-like TILs were the dominant T cell subset of TILs

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in patients with early (stage I) disease, suggesting a role in disease control.¹⁴⁹ In this setting, T_{RM} -like TILs demonstrated a methylation of the perforin gene that was two-fold lower than that in CD8⁺ T cells from the peripheral blood of healthy volunteers, and this was associated with a corresponding higher perforin protein expression,¹⁴⁹ suggesting a potential T_{RM} -like TIL contribution to the control of bladder cancer.

Breast cancer

A high frequency of TILs in breast cancer is a strong predictor for improved patient survival, particularly in triple-negative and HER-2-overexpressing tumors.¹¹ Recently, an in-depth transcriptional analysis of TILs within primary, triple-negative human breast cancer tissue was performed and demonstrated a previously unappreciated level of heterogeneity of T cell subsets within tumors.¹¹ Tumors with a high number of TILs contained CD103⁺CD8⁺ T cells with a T_{RM}-like phenotype, and these cells expressed high levels of PD-1 and effector proteins. A CD8⁺ T_{RM}-like gene signature was significantly associated with improved relapse-free and overall survival following chemotherapy and provided better prognostication than CD8 expression alone.¹¹ These data support the notion that authentic T_{RM} cells exist within tumor microenvironments and contribute to breast cancer immune surveillance.

Oropharyngeal, head and neck cancer

The recent rise in the incidence of oropharyngeal, head and neck cancers has been attributed to high-risk strains of human papilloma virus (HPV), such as HPV16.165 Interestingly, oropharyngeal squamous cell cancer (OPSCC) that occurs independently of HPV infection has a worse prognosis than HPV-associated OPSCC, and it has been postulated that the dense infiltration of CD4⁺ and CD8⁺ T cells evident in the latter disease can contribute to a strong antitumor response.^{166,167} HPV-specific CD4⁺ T cells were found at a higher concentration in the pro-inflammatory tumor microenvironment of HPV16⁺ OPSCC than in that of HPV16⁻ OPSCC, and these cells expressed a type 1 T helper (Th1) and type 17 T helper (Th17) phenotype and high levels of CD38, PD-1, and the C-type lectin CD161.¹⁶⁸ Improved survival was positively associated with the proportion of CD4⁺CD161⁺ TILs as well as greater frequencies of T_{RM} -like TILs.¹⁶⁸ The expression of CD161 on T_{BM} cells has been noted in the colon,¹⁶⁹ and while its exact function in the setting of malignancy is currently unknown, it may provide an additional correlative marker of patient outcomes.¹⁷⁰

In patients with primary head and neck squamous cell carcinoma (HNSCC), a low frequency of $CD39^+CD103^+$ $CD8^+$ T_{RM} -like TILs was associated with more advanced disease, and those with a high frequency of $CD39^+CD103^+$ $CD8^+$ T_{RM} -like TILs had better survival at 3 years than those with a low frequency (86% survival versus 58%).¹⁵⁴ Taken together, many independent studies on diverse cancer types corroborate the consistent observation that improved patient outcomes are strongly correlated with increased frequencies of T_{RM} -like TILs. It is postulated that the enhanced cytotoxic and functional potential of T_{RM} -like TILs, compared with nonresident T cell counterparts, including the increased proficiency of tumor cell lysis, forms the basis of the reported patient survival benefits.

T_{RM} CELLS IN AUTOIMMUNITY

Recent studies indicate that T_{RM} cell populations residing in the same tissue are highly heterogeneous with distinct phenotypic and functional profiles.^{65,171,172} This heterogeneity is evident in human disease, and while T_{RM} cells are beneficial against infection and cancer, they may also contribute to the pathology of autoimmune and inflammatory diseases.¹⁷³ While T_{RM} cells have been implicated in the pathogenesis of multiple sclerosis,¹⁷⁴ type

, and evidence is the strongest¹⁷⁷ and has been derived both from animal models and primary human tissue (Fig. 1). Psoriasis

The observation that psoriatic skin lesions reoccur at the same location led to speculation that T_{RM} cells could be the mediator of this site-specific response.¹⁷⁸ The pathogenesis of psoriasis is a complex interplay of dysregulated immune cells and cytokines, including IL-17, IL-12, IFNy, TNFa, and IL-23 (reviewed in ref. ¹⁷⁹). Recent investigations have focused on infiltrating CD4⁺ and/or CD8⁺ T cells and skin-resident T cells as the drivers of the abnormal regulation of the IL-23/IL-17 axis.^{10,180} The first indication that T_{RM} cells may have a role in the pathogenesis of psoriasis was the finding that the inhibition of T cell migration from the blood to the skin (by E-selectin blockade) was an ineffective treatment.¹⁸¹ The transfer of nonlesional skin grafts from patients with psoriasis to immunodeficient mice resulted in psoriatic lesions on the mice, indicating that autoreactive pathogenic T cells were present in healthy-appearing skin and that psoriatic skin lesions can develop without the recruitment of cells from blood.¹⁸² TCR gene sequencing showed that resolved psoriatic lesions retain IL-17-producing oligoclonal T cell populations, suggesting a mechanism by which disease can reoccur at the same site.¹⁸³ Subsequent studies demonstrated that IL-22secreting CD4⁺ T cells and IL-17-secreting CD8⁺ T cells remained resident in healed psoriatic skin after treatment with a number of therapies.^{183,184} Furthermore, the lack of CD49a expression on CD8⁺ T_{RM} cells from psoriasis lesions defines a T_{RM} cell subset producing IL-17.¹⁰ Biological treatments targeting TNFa, IL-17, or IL-23 have revolutionized the treatment of psoriasis and have helped to demonstrate the centrality of T cells to the disorder.¹⁷⁸ It is currently unknown whether T_{RM} cells directly contribute to the exacerbation of psoriasis, and the determination of whether T_{RM} cell-mediated cytokine secretion plays a role in disease pathogenesis may encourage the advent of novel therapies aimed at dislodging pathogenic T_{RM} cells while preserving protective counterparts.

1 diabetes mellitus,¹⁷⁵ and inflammatory bowel disease,¹⁷⁶ here

we focus on the emerging role of pathogenic T_{RM} cells in

mediating common autoimmune diseases of the skin, where the

Alopecia areata

Alopecia areata (AA) is a chronic immune-mediated disease that results in nonscarring hair loss.¹⁸⁵ The pathogenesis of AA is only partially understood, but it is thought that genetic and environmental factors cause an autoimmune reaction in hair follicles.¹⁸⁶ MHC class II is normally absent in hair follicle root sheaths and hair matrix, but increased MHC class II expression and the upregulation of adhesion molecules occurs in AA.¹⁸⁷ Skin Th1 cells produce IFNy, which triggers the infiltration of cytotoxic $CD8^+$ T cells to the perifollicular area, leading to hair cycle arrest.¹⁸⁷ Early evidence that skin T_{RM} cells may play a pathogenic role in AA was suggested by a study in which T cells isolated from AA scalp explants were injected into severe combined immunodeficiency (SCID) mice, and hair growth and clinical parameters were monitored. When compared to mice that had not received T cells (or had been injected with peripheral blood mononuclear cells), mice with AA skin-derived T cells demonstrated hair loss as a result of fewer hair follicles and presented histological evidence of AA.¹⁸⁸ Transcriptional profiling of AA skin revealed gene signatures suggestive of cytotoxic effector CD8 $^+$ T cells¹⁸⁷ and higher transcripts of Itgae.¹⁸⁹ Inhibitors of the Janus kinase (JAK) signaling pathway (e.g., tofacitinib), which predominantly produces IFN γ , have shown promise in treating AA.¹⁹⁰ Lesional T cell clones do not completely disappear after tofacitinib administration,¹⁹¹ leading to the relapse of disease after treatment cessation. However, it is yet to be confirmed whether T_{RM} cells are the main source of IFNy in AA and (if so) the effect of tofacitinib on T_{RM} cell functionality.

Vitiligo

Vitiligo is a disease characterized by the apoptosis of melanocytes or the lack of melanin production, which results in depigmented skin.¹⁹² CD8⁺ T_{RM} cells expressing the cytotoxic molecules perforin and granzyme B are present in the skin of active and stable vitiligo lesions and are responsive to IL-15 stimulation,¹⁰ a cytokine with a role in T_{RM} development and survival in skin.⁷ Both human and mouse T_{RM} cells express the CD122 subunit of the IL-15 receptor, and keratinocytes upregulate CD215, the subunit required to display the cytokine on their surface to promote the activation of T cells.¹⁹³ In mice, the targeting of IL-15 signaling with an anti-CD122 antibody reversed vitiligo, and the effects of such treatment remain to be confirmed in humans.¹⁹³ Further work is also needed to determine whether the ablation of IL-15 signaling in T_{RM} cells can directly affect disease outcomes in vitiligo.

T_{RM} CELLS IN TRANSPLANTATION

Donor-derived lymphocytes are transferred within the allograft during solid organ transplantation. The close association between donor-derived T_{RM} cells and host cells may determine whether allografts undergo acute or chronic rejection (Fig. 1).^{59,194,195} It has been shown that donor-derived CD4⁺ and CD8⁺ IELs were dominant in an intestinal allograft for ~400 days post transplant, after which recipient-derived T cells (which adopted a T_{RM} cell phenotype) then outnumbered donor-derived cells.^{61,62} During rejection, host-versus-graft reactive T cell clones accumulated in the graft, and the infiltration of recipient T cells was accelerated and was associated with a reduced proportion of donor-derived cells. However, in the absence of overwhelming cellular and antibody-mediated rejection, donor-derived T_{RM} cells persisted and even expanded in the graft, delaying complete repopulation by recipient T cells and possibly reducing the risk of rejection.⁶¹

While the persistence of donor-derived T_{RM} cells has been associated with a reduced incidence of rejection in both intestinal⁶¹ and lung⁶⁰ transplants, T_{RM} cells have conversely also been implicated in driving allograft rejection. Following a facial transplant, donor-derived CD8⁺ T cells were predominantly skinresident (CD8⁺ CD69⁺CD103⁺CLA⁺) phenotypes, and histological analysis revealed that these donor cells were associated with areas of damaged vasculature and epithelium.⁵⁹ The results of this report suggest that donor-derived T cells may also play a role in tissue injury that results in graft rejection. Overall, the contribution of tissue-resident cells to the field of transplantation is in its infancy, and more studies are needed to clarify the contribution of T_{RM} cells to graft rejection and stability.

CONCLUDING REMARKS AND FUTURE DIRECTIONS

The importance of human T_{RM} cells is increasingly recognized in a wide array of tissue-specific diseases. Progress has been made in identifying surface markers and transcriptional profiles of human T_{RM} cells, although unique human T_{RM} cell phenotypes and signatures still remain to be elucidated. Human studies have shown the beneficial roles of T_{RM} cells in controlling infections, and T_{RM} cells are being targeted in the rational design of T cell vaccines. Additionally, T_{RM} cells appear to play an important role in the control of malignancies and will prove a likely target of cancer immunotherapies. However, given the potentially harmful contribution of T_{RM} cells in autoimmune diseases, understanding both the protective and pathogenic human T_{RM} cell roles is crucial for the safe design of approaches that allow for their manipulation. Many critical questions remain to be answered. For example, do T_{RM} cells contribute to pathology in a direct or indirect manner? What signaling pathways regulate T_{RM} cell differentiation and longevity? How can these processes be manipulated to enhance or eliminate T_{RM} cells in a tissue-specific manner? Much work is required to understand the breadth of T_{RM} cell heterogeneity and

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function in human tissues, such that adverse effects can be predicted and controlled for; however, there appears enormous potential to harness T_{RM} cells for novel T cell-based vaccines and immunotherapies for a broad range of diseases.

ACKNOWLEDGEMENTS

S.C.S. is supported by an Oxford-Celgene Postdoctoral Fellowship. C.L.G. is supported by an NHMRC Early Career Fellowship (GNT 1160963). P.K. is supported by an Oxford and NIHR Senior Fellowship (WT10966MA). L.K.M. is a Senior Medical Research Fellow supported by the Sylvia and Charles Viertel Charitable Foundation.

ADDITIONAL INFORMATION

Competing interests: The authors declare no competing interests.

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