



Motility Matters: How CD8⁺ T-Cell Trafficking Influences Effector and Memory Cell Differentiation

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Immunological memory is a hallmark of adaptive immunity that confers long-lasting protection from reinfections. Memory CD8⁺ T cells provide protection by actively scanning for their cognate antigen and migrating into inflamed tissues. Trafficking patterns of CD8⁺ T cells are also a major determinant of cell fate outcomes during differentiation into effector and memory cell states. CD8⁺ T-cell trafficking must therefore be dynamically and tightly regulated to ensure that CD8⁺ T cells arrive at the correct locations and differentiate to acquire appropriate effector functions. This review aims to discuss the importance of CD8⁺ T-cell trafficking patterns in regulating effector and memory differentiation, maintenance, and reactivation.

IMPORTANCE OF TRAFFICKING IN DISTINGUISHING T-CELL SUBSETS

A hallmark of adaptive immunity is defined by the ability of memory T and B lymphocytes to “remember” an initial pathogen encounter, which underlies the success of vaccines to provide long-lived protection against recurrent infections. This review will focus on “cytotoxic” memory CD8⁺ T cells that provide immune surveillance by actively scanning for and killing cells infected with viruses or intracellular bacteria within tissues and the blood, which depends on tissue-specific homing molecules and cell migration. In short, we will discuss how CD8⁺ T-cell priming, function, and cell fates are determined in a spatiotemporal manner during acute infection.

Following pathogen encounter, CD8⁺ T cells expand and acquire cytotoxic effector functions to facilitate pathogen clearance. Upon elimination of infection, the majority of the effector cells die via apoptosis, while some remain to generate various subsets of long-lasting CD8⁺ T memory cells. Foundational work on elucidating the different memory T-cell subsets came from Sallusto et al. (1999), where they subdivided peripheral blood human T cells according to their homing and chemokine receptor expression patterns. Cells that circulate mainly through lymph nodes (LNs) and express CD62L and CCR7, two key molecules necessary for LN homing, were referred to as central memory T (T_{cm}) cells (Sallusto et al. 1999). Instead, cells lacking these receptors with higher effector functions that circu-

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late in blood and express inflammatory chemokine receptors were termed effector memory (Tem) cells. Over time, it has become clear that there is further heterogeneity within the memory T-cell populations; for example, it was later appreciated that a portion of Tem cells actually do not circulate, but rather persist long term in peripheral tissues. These cells became known as tissue-resident memory (Trm) cells (Gebhardt et al. 2009) and express tissue-specific residency markers. Trm cells are found in nearly every tissue and often provide a local first line of defense to reinfection, especially those situated in barrier tissues such as the lungs, skin, and intestine. More recently, another subpopulation of cells referred to as peripheral memory (Tpm) cells was characterized by intermediate levels of CX₃CR1^{int} and their unique ability to enter and survey peripheral tissues and then recirculate back to the blood (Gerlach et al. 2016). Tpm cells are distinguished from longer-lived terminal effector (TE) cells that dwell exclusively in the blood and express the highest amounts of CX₃CR1 and KLRG1. Collectively, these outline unique trafficking patterns between the different subsets of memory T cells that help the cells “divide and conquer” to maximize immune surveillance across a wide range of tissue landscapes.

Herein we will discuss the importance of spatiotemporal regulation of effector and memory CD8⁺ T-cell fate determination, maintenance, and reactivation. We will follow the cascade of events proceeding CD8⁺ T-cell activation and review how their trafficking patterns influence early and late stages of effector and memory cell fate differentiation and key transcriptional changes that drive the functional and anatomical diversification of memory T cells. Finally, we will discuss how tissue-specific environmental factors orchestrate effector and memory CD8⁺ T-cell homing to and maintenance in peripheral tissues.

SPATIOTEMPORAL REGULATION OF CD8⁺ T-CELL PRIMING AND EFFECTOR DIFFERENTIATION

Upon infection, activated CD8⁺ T cells give rise to a heterogeneous pool of effector cells with distinct long-term fates to form the various types of

memory CD8⁺ T cells (Tcm, Tem, Trm, Tpm) described above. We often conceptualize this process as effector CD8⁺ T cells differentiating into multiple cell states along a spectrum. On one end of the spectrum exists “less” differentiated or more stem-like cells that have more memory cell potential, and on the other end cells that progress to more “terminally” differentiated effector states and have lost memory cell potential. Cells in between the two ends tend to have mixtures of effector- and memory-like properties and display dynamic developmental plasticity (i.e., they can interconvert between differentiation states over the course of an immune response) (Kaech et al. 2003; Cui et al. 2009; Rutishauser et al. 2009; Gerlach et al. 2016; Youngblood et al. 2017; Herndler-Brandstetter et al. 2018).

For the purposes of communication and clarity, we will refer to particular subsets of effector and memory CD8⁺ T cells, the differentiation state(s) for which have been well characterized. In several acute viral and intracellular bacterial infections, the majority of activated CD8⁺ T cells acquire a terminally differentiated effector state and are referred to as TE cells, which are characterized by high levels of KLRG1 and CX₃CR1 surface expression (Fig. 1; Joshi et al. 2007; Gerlach et al. 2016). The majority of TE cells die via apoptosis after infection (Kaech et al. 2003; Sanjabi et al. 2009), whereas a minority of effector cells differentiate into memory precursor (MP) cells that express IL-7R and encompass the greatest potential to seed the memory pool (Tem, Tcm, Tpm, and Trm) (Kaech et al. 2003; Mackay et al. 2013; Gerlach et al. 2016). Some MP cells also coexpress KLRG1, but then lose KLRG1 and differentiate into multiple memory cell subsets (Herndler-Brandstetter et al. 2018). One of the most dominant factors that influences CD8⁺ T-cell activation and their stratification into various effector differentiation states is their migration patterns as it dictates the types of cell–cell interactions as well as inflammatory and antigenic signals received. In this section, we will dissect the roles of certain chemokine receptors in regulating effector and memory CD8⁺ T-cell fates during many types of acute viral or bacterial infections.

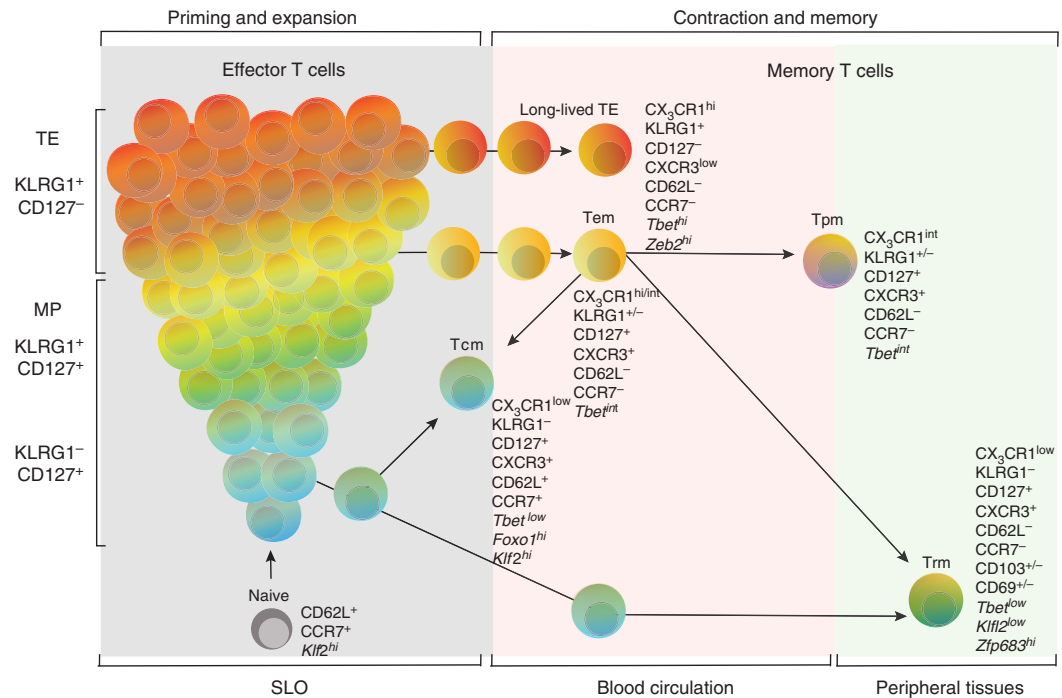


Figure 1. CD8⁺ T-cell effector and memory differentiation. Effector and memory differentiation of CD8⁺ T cells. During many acute infections, activated CD8⁺ T cells form a heterogeneous effector population with distinct developmental trajectories. The majority of activated CD8⁺ T cells acquire a terminally differentiated effector state known as terminal effector (TE) cells. After clearance of infection, most of the KLRG1⁺ cells die, while a small subset survives as long-lived TE cells. Additionally, surviving effector cells that also express IL-7R α (CD127) seed the effector memory T-cell (Tem) pool, and some of these cells even lose KLRG1 expression and develop into various memory T-cell subsets (Herndler-Brandstetter et al. 2018). In contrast, a smaller fraction of effector cells differentiates into memory precursor (MP) cells, which encompass the greatest potential to develop into long-lived memory cells and are characterized by increased amounts of CD127 (Kaech et al. 2003). After resolution of infection, the MP cells seed most of the memory pool, giving rise to the various memory T-cell subsets (Tem, Tcm, Tpm, and Trm).

Trafficking Patterns that Influence CD8⁺ T-Cell Priming and Effector Cell Formation

Secondary lymphoid organs ([SLOs], i.e., spleen, LNs, and Peyer's patches) are specialized organs that are highly compartmentalized into distinct regions (Fig. 2) to enable efficient priming and activation of CD8⁺ T cells (von Andrian and Mempel 2003; Bajénoff et al. 2007). Naive T cells express CD62L and CCR7, which recognize endothelial peripheral node addressin and the chemokines CCL19 and CCL21, respectively, to facilitate their entry into the T-cell zones within SLOs (Luther et al. 2000; Stein et al. 2000). While naive CD8⁺ T cells in mice that lack CCR7 ligands

(*plt/plt* mice) have defective T-cell zone trafficking, surprisingly, following infection or immunization, CD8⁺ T cells in these mice only show delayed kinetics in activation and effector cell development, a result that was also supported later by CCR7 knockout (KO) CD8⁺ T cells (Mori et al. 2001; Jung et al. 2002; Jung et al. 2016). These experiments highlight that CD8⁺ T-dendritic cell (DC) encounters can occur outside of the T-cell zones of LNs. In fact, several studies using immunization or infection with vaccinia virus (VV), vesicular stomatitis virus (VSV), and *Toxoplasma gondii* showed that optimal CD8⁺ T-cell priming occurs via multiple interactions with distinct DC subsets in diverse regions of LNs (Hick-

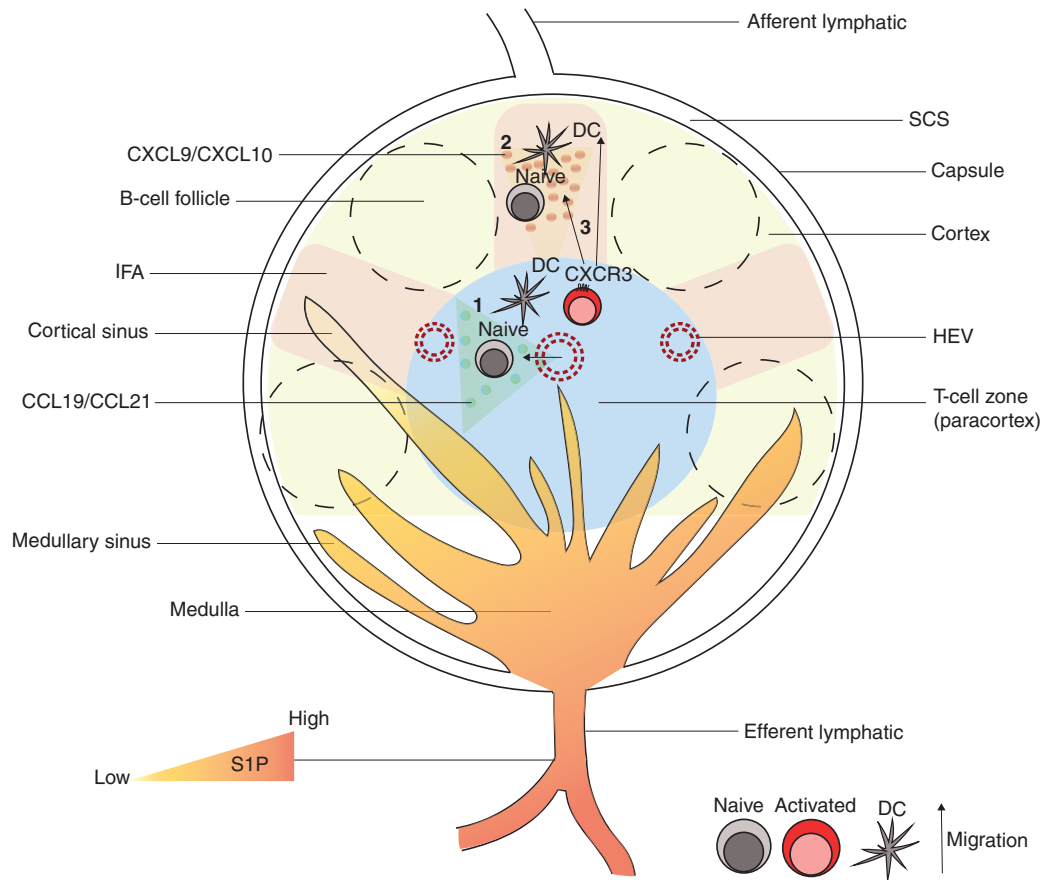


Figure 2. Lymph node (LN) architecture and CD8⁺ T-cell priming. A schematic representation of the major regions of an LN and CD8⁺ T-cell priming sites. The main regions of LNs consist of the subcapsular sinus (SCS), B-cell follicles, interfollicular areas (IFAs), T-cell zone (paracortex), and the medulla. Lymph enters LN from afferent lymphatics and flows through the SCS. IFAs lie beneath the SCS and between B-cell follicles and are considered the inflammatory hotspots of LN as they contain innate immune cells that secrete various inflammatory molecules. Naive T cells enter LNs via high endothelial venules (HEVs) and locate to T-cell zones by responding to chemokines CCL19 and CCL21, where they get primed and activated by DCs (1). Alternatively, naive CD8⁺ T cells can also get activated in the IFA and SCS of LNs (2). Activated CD8⁺ T cells express CXCR3, which enables their migration toward the IFA, SCS guided by CXCL9 and CXCL10 gradients (3). Effector CD8⁺ T cells use sphingosine-1-phosphate (S1P) gradients in cortical and medullary sinuses to leave LNs via the efferent lymphatics.

man et al. 2008; John et al. 2009; Gerner et al. 2012, 2015; Eickhoff et al. 2015). For instance, during VV infection, early priming of CD8⁺ T cells occurred in the interfollicular area (IFA) and subcapsular sinus (SCS) of the LN by VV-infected CD11b⁺ classical DC (cDC), and subsequent contacts occurred in the paracortex with cross-presenting XCR1⁺ DCs (Eickhoff et al. 2015). These intranodal interactions are guided

by diverse chemokine receptors such as CXCR3 (Hickman et al. 2008; Ozga et al. 2016), CCR5, and CCR4 (Semmling et al. 2010). Notably, CCR5 and CCR4 facilitate CD8⁺ T-cell migration toward CCL3- and CCL4-producing cDCs that have been “helped” by CD4⁺ T cells, which not only enhances priming and expansion of effector CD8⁺ T cells but also aids in their memory cell development (Castellino et al. 2006).



One of the best-studied chemokine receptors involved in effector CD8⁺ T-cell development is CXCR3, which permits homing to CXCL9, CXCL10, and CXCL11 (Groom and Luster 2011a). *Cxcr3* is rapidly induced upon T-cell receptor (TCR) activation and its expression is influenced by TCR-peptide major histocompatibility complex (pMHC) affinity and inflammatory cytokines such as IL-12 and type I and II interferons (IFNs) (Groom and Luster 2011a,b; Ozga et al. 2016). High-affinity interactions allow prolonged CD8⁺ T-DC contacts and augment *Cxcr3* and *Il2ra* (CD25) expression, enhancing CD8⁺ T-cell expansion (Zehn et al. 2009; Ozga et al. 2016). Temporally, CXCR3 has two main roles on CD8⁺ T-cell trafficking: (1) early on, it promotes migration of antigen (Ag)-specific CD8⁺ T cells to inflamed regions such as the IFA and SCS in LNs and marginal zones of spleens within SLOs, which promotes T-cell activation, expansion, and effector differentiation. (2) Later, it functions to steer effector cells in the circulation toward infected peripheral tissues to help clear infection. Indeed, in multiple infections, it has been shown that *Cxcr3*-deficient effector CD8⁺ T cells that are unable to localize to such areas are impaired in generating TE-like CD8⁺ T cells and preferentially form more MP-like cells (Hu et al. 2011; Kurachi et al. 2011). Moreover, when CD8⁺ T cells are forcefully sequestered in T-cell zones by overexpression of CCR7, MP fates are favored over TE fates (Unsoeld et al. 2004; Hu et al. 2011). These studies demonstrate that CXCR3 permits CD8⁺ T cells to access environments in infected tissues that promote TE cell development, and cells that are shielded from these environments are better able to maintain memory cell potential.

Interestingly, while CXCR3 is critical for acquiring TE cell states, TE cells actually down-regulate CXCR3 and up-regulate CX₃CR1 and sphingosine-1-phosphate receptor 5 (S1PR5) as they form (Jung et al. 2010; Hu et al. 2011). This change in trafficking receptors on TE cells presumably enables their egress from the inflamed tissues back to the blood, where sphingosine-1-phosphate (S1P) and CX₃CL1 is enriched (Cyster and Schwab 2012). During resolution, the vast

majority of TE cells undergo apoptosis as they are exposed and sensitized to molecules that may induce cell death such as TGF-β (Sanjabi et al. 2009) and certain resolvins (i.e., resolvin E1) (Vassiliou et al. 2008; El Kebir et al. 2012) that are highly concentrated at sites of tissue repair as infection resolves, while those that egress back into the blood may circumvent cell death. Therefore, it would be interesting to speculate whether overexpression of CXCR3 would enhance tissue retention and apoptosis of TE cells during contraction. In contrast to TE cells, MP cells maintain high levels of CXCR3 and some express intermediate amounts of CX₃CR1 (Kaech and Wherry 2007; Gerlach et al. 2016). CXCR3 likely aids in MP cell retention in tissues, facilitating their exposure to tissue-specific signals and tailoring the type of memory T cells they will become. MP cells are also intrinsically wired in such a way that exposure to environmental factors like TGF-β can enable vastly different outcomes than TE cells. For example, CXCR3-dependent exposure to TGF-β drives CD103⁺ Trm cell formation in the skin epidermis (Mackay et al. 2013) and in the intestinal epithelium (Sheridan et al. 2014).

Whereas CXCR3 critically influences the formation of effector cells, other chemokine receptors also impact CD8⁺ T-cell trafficking and differentiation patterns to varying degrees. Among them, CXCR6 is also expressed by activated CD8⁺ T cells and responds to CXCL16, which is constitutively expressed and up-regulated upon an inflammatory insult in the splenic red pulp (RP), liver, lung, and various other tissues (Matloubian et al. 2000; Kim et al. 2001; Sato et al. 2005; Wein et al. 2019). Interestingly, while a study using graft versus host disease observed reduction of CXCR6 KO CD8⁺ T-cell infiltration into inflamed liver (Sato et al. 2005), other studies using malaria and VV infections did not observe migration differences between CXCR6 KO and wild-type (WT) effector CD8⁺ T cells to livers. These differences may indicate that the requirement for CXCR6 in liver homing may be dependent on the inflammation status of the liver or possibly the differentiation status of the T cells (and other chemokine receptors they express) (Tse et al. 2014). In support of

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this, as effector cells transition to memory cells following infection, CXCR6 becomes important for the formation and/or maintenance of memory cells in liver, skin, and lung (Tse et al. 2014; Zaid et al. 2017; Wein et al. 2019).

Tissue Is the Issue: How Migratory DCs from Draining Tissues Influence CD8⁺ T-Cell Differentiation and Trafficking Patterns

To locate infected tissues and clear infection, CD8⁺ T cells need to exit LNs and join the circulation. Initially, early activated CD8⁺ T cells up-regulate CD69 expression, which down-regulates S1PR1 allowing tissue retention (Shiow et al. 2006; Bankovich et al. 2010; Mackay et al. 2015a). Following successful priming and activation, CD8⁺ T cells become temporarily unresponsive to pMHC (Bohineust et al. 2018) and down-regulate CD69, which results in up-regulation of S1PR1, leading to CD8⁺ T-cell egress from LNs via efferent lymphatics (Cyster and Schwab 2012). Interestingly, low-affinity pMHC interactions cause accelerated up-regulation of S1PR1 expression on CD8⁺ T cells that results in early egress from the LNs (Ozga et al. 2016). Once in circulation, guided by their newly expressed chemokine receptors, effector CD8⁺ T cells traffic into inflamed tissues, where they locate infected cells through chemotactic gradients and perform effector functions to suppress intracellular pathogen spread.

How do T cells know which tissues to migrate to after leaving the SLOs and enter circulation? Evidence indicates that T cells receive these instructions (or zipcodes) from the migratory DCs emigrating from the infected tissues at the time of DC priming. For example, in skin-draining LNs, vitamin D derivatives are metabolized and presented to CD8⁺ T cells by Ag-presenting DCs. This results in the up-regulation of CCR4 or CCR10 together with P- and E-selectin ligands on CD8⁺ T cells, which bias their migration toward skin (Reiss et al. 2001; Sigmundsdottir et al. 2007). Similarly, in gut-draining mesenteric LNs and Peyer's patches, the vitamin A derivative retinoic acid enables DCs to imprint gut homing molecules $\alpha 4\beta 7$ and CCR9 on effector CD8⁺ T cells (Stagg et al.

2002; Mora et al. 2003; Iwata et al. 2004), demonstrating that draining LNs of specific tissues can influence the trafficking patterns of effector CD8⁺ T cells toward where these cells are primed. Interestingly, a recent study showed that activation of TGF- β by skin-draining migratory DCs imprints an epidermal Trm cell fate on naive CD8⁺ T cells by epigenetically programming *Itgae* (CD103) expression (Mani et al. 2019), indicating that imprinting of trafficking and residency molecules on CD8⁺ T cells can occur at multiple stages throughout the life span of the cell. Interestingly, imprinting of naive cells only occurred in draining LNs and not in the spleen, signifying that organ-specific differences exist even within functionally related tissues (Mani et al. 2019).

Whereas it is clear that DCs can stamp a zipcode onto CD8⁺ T cells and influence tissue-trafficking, distinct DC subsets can also influence the types of memory CD8⁺ T cells that form. For example, in the lung-draining mediastinal LN, interactions with migratory CD103⁺ DCs induce lung-homing effector CD8⁺ T cells that eventually differentiate into Tem cells, whereas interactions with migratory CD11b^{hi} DCs preferentially induce Tcm cell formation (Kim et al. 2014). Similarly, priming by DNGR-1⁺ migratory DCs in skin-draining LN is essential for skin-resident Trm cell differentiation, but dispensable for the formation of circulating memory CD8⁺ T cells following VV infection (Iborra et al. 2016). Non-DC cell types have also found to play roles in Trm cell development; for instance, pulmonary monocytes, intestinal macrophages, and vaginal tissue macrophages can help to establish Trm cells in the lungs, lamina propria, and vagina, respectively (Iijima and Iwasaki 2014; Bergsbaken et al. 2017; Dunbar et al. 2020).

In addition to environmental differences between distinct organs that affect CD8⁺ T-cell fate, there also exists macroanatomical heterogeneity within a given organ creating more inflammatory or tolerogenic zones that produce different types of T-cell responses. For example, Esterházy and colleagues demonstrated that LNs draining upper parts of the intestines are tolerogenic in nature, while colon-draining LNs show more of an inflammatory signature (Esterházy

et al. 2019). Similar observations have been made in the liver-draining LNs, in which the portal LN results in more tolerogenic immune responses than those in the celiac LN (Yu et al. 2017); however, the signals that induce such qualitatively distinct types of immune responses are yet to be discovered.

SPATIOTEMPORAL REGULATION OF CD8⁺ T-CELL MEMORY CELL MAINTENANCE AND REACTIVATION

As mentioned earlier, following the resolution of infection, the remaining effector cells undergo further differentiation into memory subsets with diverse migratory patterns. Here we will discuss how the trafficking patterns of memory cells facilitate their maintenance at steady state and reactivation upon subsequent exposure to antigen.

Involvement of Trafficking Patterns on Maintenance of CD8⁺ T-Cell Memory Subsets

If the goal of adaptive immunity is to provide protection against future infection, then memory cells per se must be equipped with the capacity to survive for long periods of time while remaining poised to differentiate and reacquire effector functions. Memory T-cell survival is largely mediated via IL-7 and IL-15 signaling that support the bioenergetic needs for survival and self-renewal (Schluns et al. 2000; Becker et al. 2002; Goldrath et al. 2002). IL-7 is mainly secreted by stromal cells of the SLOs and bone marrow (BM) (Hara et al. 2012; Onder et al. 2012; Miller et al. 2013), whereas IL-15 is predominantly produced and *trans*-presented by hematopoietic cells via IL-15R α to T cells (Schluns and Lefrançois 2003). Interestingly, IL-15 is important for CD62L up-regulation on CD8⁺ T cells (Obar and Lefrançois 2010) and its *trans*-presentation by DCs is essential for Tcm cell maintenance, whereas *trans*-presentation of IL-15 by macrophages supports both Tem and Tcm cells (Mortier et al. 2009; Obar and Lefrançois 2010).

Studies in mice and humans demonstrated that Tcm cells undergo a remarkably slow homeostatic turnover rate with an estimated mitotic

event every 50 and 450 d (Choo et al. 2010; Akondy et al. 2017), respectively. Indeed, migration of Tcm cells into lymphoid organs is critical for the accession of prosurvival signals that promote longevity and capacity to self-renew, and the BM appears to be the predominant tissue-supporting memory T-cell homeostatic proliferation (Becker et al. 2005; Chaix et al. 2014). Memory T-cell migration into the BM is dependent on CXCR4 as CXCR4-deficient Tcm cells display reduced BM migration and rates of homeostatic proliferation (Becker et al. 2005; Mazo et al. 2005; Chaix et al. 2014). In contrast, CCR7-deficient memory CD8⁺ T cells have impaired trafficking into SLOs but display enhanced migration into the BM and homeostatic turnover rates (Jung et al. 2016). Likely, the CCR7-deficient memory CD8⁺ T cells compensate for reduced access to IL-7-rich stromal niches within the SLOs by enhancing their homing to IL-15-rich niches (such as in the BM) for their survival, which induces more proliferation. Niches like the BM may also provide unique organ-specific cues that support the metabolic needs of memory cells. Along this line, a recent study demonstrated that under conditions of caloric restriction in mice, memory CD8⁺ T cells are depleted in circulation, but accumulate in the BM in a CXCR4-CXCL12- and S1P-S1PR-dependent fashion (Collins et al. 2019). The BM acts like a metabolic reservoir by providing lipids as a key energy source for memory CD8⁺ T-cell fatty acid oxidation and survival (Collins et al. 2019). Perhaps caloric restriction dampens mTORC2 signaling in CD8⁺ T cells, which leads to increased CXCR4 expression and BM trafficking (Arojo et al. 2018).

Whereas comparatively less is understood about how Tem cell trafficking influences access to prosurvival signals and growth factors, a recent study showed that GPR18, a chemokine receptor that recognizes *N*-arachidonyl glycine and resolvin D2, was critical for the formation and maintenance of KLRG1-expressing Tem cells (Sumida and Cyster 2018). Although the conversion of Tem to Tcm cells in mice is generally considered a unidirectional lineage relationship (Wherry et al. 2003), Tcm cells that traffic through the liver, but not the lung, can down-regulate CD62L and adopt Tem-like qual-

ities. This highlights the importance of tissue-derived signals in influencing cell fates.

Whereas the inherent motile nature of circulating memory cells allows for access to diverse homeostatic cues in various tissues, Trm cells by contrast have a limited range of motility and thus require unique trafficking capabilities to access tissue-specific prosurvival signals and maximize their potential for long-term survival while continuously scanning for antigen (Ariotti et al. 2012). One seemingly universal feature of CD8⁺ Trm cells is the loss of surface S1PR1 and the gain of CD69, which abrogates tissue egress and enables residency within the parenchyma of solid tissues (Skon et al. 2013). The α E integrin subunit (CD103) is another defining feature of some Trm cells, particularly those that localize to the E-cadherin-expressing epithelium, and is critical for promoting tissue retention; fewer Trm cells are found and the cells display faster migration within in barrier tissues in *Itgae* (CD103) KO mice (Wakim et al. 2010; Casey et al. 2012; Mackay et al. 2013; Zaid et al. 2017). CD103 expression is regulated by TGF- β and Notch signaling in the lungs (Lee et al. 2011; Hombrink et al. 2016) and more generally by TGF- β in diverse epithelial sites like the epidermis, salivary glands, and small intestine (Casey et al. 2012; Mackay et al. 2013; Zhang and Bevan 2013; Hirai et al. 2019). However, in Trm cells in many tissues like the gut lamina propria (Bergsbaken et al. 2017) and liver (McNamara et al. 2017), the Trm cells largely lack CD103 expression. Instead, CD103⁻ Trm cells in liver and lungs use other integrins such as LFA-1 or α 1 β 1 (VLA-1) to help with retention (Ray et al. 2004; McNamara et al. 2017). In addition to adhesion, CD103 may also help the Trm cells sense local survival factors, like IL-15, which is important for Trm cell survival in some tissues like the skin, intestinal epithelium, and liver (Mackay et al. 2013, 2015b; Zhang and Bevan 2013; Holz et al. 2018). However, Trm cell survival in other organs such as the pancreas, small intestine, female reproductive tract, and thymus is IL-15 independent (Schenkel et al. 2016). Additionally, IL-15-deficient mice appear to have an accumulation of Trm cells in LNs, suggesting that mechanisms of Trm cell maintenance in SLOs are distinct from Tem and Tcm cells (Schenkel

et al. 2014a). More work is needed to better understand the manner by which Trm cells adapt to the tissue-specific cues to persist and inhabit distinct anatomical niches.

Anatomical Control of Memory CD8 T-Cell Reactivation

Similar to the priming events, homing molecules and chemokine receptors are also critical for memory CD8⁺ T-cell recall responses. Both Tem and Tcm cells play critical roles in protection against reinfection, but they differ qualitatively by how they functionally respond. For example, Tem cells show immediate cytotoxicity following reinfection (Olson et al. 2013; Ruiz et al. 2014), while Tcm cells display enhanced proliferative capacity and greater IL-2 production. In LNs, Tcm cells are localized within the paracortex, while CX₃CR1⁺ Tem cells are located in the IFA and SCS region of the LNs close to SCS macrophages (Böttcher et al. 2015; Nikolova et al. 2020); but following reinfection, however, Tcm cells rapidly localize in a CXCR3-dependent manner to SCS and IFA where infected cells are first emerging and CXCL9 and CXCL10 are produced (Sung et al. 2012; Kastenmüller et al. 2013).

Because memory T cells are rather mobile and viruses often infect multiple cell types (Sung et al. 2012), one may predict that memory T cells could be reactivated by a variety of cell types; but actually, many studies have shown that following secondary challenges with multiple viruses or *Listeria monocytogenes*, memory T-cell reactivation depends on CD11c⁺ or XCR1⁺ DCs (Zammit et al. 2005; Dorner et al. 2009; Alexandre et al. 2016). However, there do appear to be exceptions to this because XCR1⁺ DCs are dispensable for memory T-cell recall responses to murine cytomegalovirus (MCMV) infection (Alexandre et al. 2016). Our laboratory recently showed that following secondary influenza infection the CD8⁺ memory T cells in the draining LNs were, as predicted, dependent on CD11c⁺ XCR1⁺ DCs for reactivation; however, the Trm cells in the lungs were not (Low et al. 2021). Rather, lung Trm cells were efficiently reactivated in infected lungs by various types of antigen-presenting cells (APCs) in situ. These findings indi-



cate that the mechanisms of reactivation of memory T cells are distinct in different tissues and reshape the paradigm of how memory T-cell responses are triggered upon reinfection. Moreover, this greater promiscuity in APC partners offers an explanation for how Trm cells may be able to protect more rapidly at the site of infection in peripheral tissues (Ariotti et al. 2012) by not only deploying antiviral functions, but also facilitating the activation of innate immune cells and infiltration of circulating immune cells into the infected tissue. For example, local Trm cell IFN- γ production induces more rapid expression of integrins ICAM-1 and VCAM-1 and chemokines CXCL9 and CXCL10 and extravasation of circulating memory CD8⁺ T cells into the infected tissues (Parr and Parr 1999; Schenkel et al. 2013, 2014b; Ariotti et al. 2014). The anatomical distribution, tissue-specific adaptations, and specialized functions of each memory T-cell subset synergize with the others to provide systemic protection against invading pathogens.

TRANSCRIPTIONAL REGULATION OF CD8⁺ T-CELL EFFECTOR AND MEMORY DIFFERENTIATION

Transcription Factors Governing Circulating Memory T-Cell Trafficking and Function

Functional diversity and trafficking patterns are key distinguishing features of various effector and memory T-cell subtypes, but how are those features regulated transcriptionally and how does a single CD8⁺ T cell give rise to functionally diverse progeny with distinct migratory dispositions? Extracellular signaling inputs are major drivers of transcription factor (TF) expression and the establishment of complex transcriptional networks, and there has been extensive work in the field to describe how certain TFs both guide effector differentiation patterns and preserve the survival and function of long-lived memory cells. Herein, we describe how this transcriptional response controls the spatiotemporal programming of effector and memory CD8⁺ T-cell differentiation.

As discussed above, Tcm cells bear a remarkably similar trafficking pattern to naive cells, and

perhaps not unsurprisingly express a similar set of TFs to regulate this process, including *Klf2* (Carlson et al. 2006; Sebzda et al. 2008; Weinreich et al. 2009), *Foxo1* (Kerdiles et al. 2009; Lou et al. 2012; Utzschneider et al. 2018), *Eomes* (Pearce et al. 2003; Intlekofer et al. 2005, 2008), *Tcf7* (Zhou et al. 2010), and *Zeb1* (Guan et al. 2018). *Klf2* maintains the expression of S1PR1 and *Sell* (CD62L) in naive and Tcm cells (Carlson et al. 2006) while repressing expression of “inflammatory” chemokine receptors found in effector T cells such as CXCR3 and CCR5 (Sebzda et al. 2008; Weinreich et al. 2009). *Foxo1* lies upstream of *Klf2* and T-cell deficiency of *Foxo1* results in reduced expression of *Klf2* and *Sell* (Kerdiles et al. 2009), which consequently impairs the capacity of naive and Tcm cells to home to LNs (Kerdiles et al. 2009; Utzschneider et al. 2018). FOXO1 also programs naive and Tcm cell responsiveness to prosurvival signals through the coordinated expression of IL-7R α and CCR7 (Kerdiles et al. 2009; Utzschneider et al. 2018), which will drive the cells toward IL-7- and CCL19/21-producing fibroblastic reticular cells (FRCs) (Luther et al. 2000; Hara et al. 2012; Onder et al. 2012). Indeed, deletion of *Foxo1* results in the rapid loss of *Il7r*, *Sell*, and *Ccr7* expression in these cells in vivo, and late inducible deletion impairs the capacity of Tcm cells to access LNs, undergo homeostatic turnover, and mount a productive secondary recall response (Kerdiles et al. 2009; Utzschneider et al. 2018). FOXO1 is typically inactivated by phosphoinositide-3-kinase (PI3K) and protein kinase B ([PKB], also known as AKT) signaling and thus, cytokines like IL-2, IL-12, and IL-15 inactivate FOXO1 to enhance effector differentiation (Kelly et al. 2002; Kim et al. 2012; Rao et al. 2012). In contrast, IL-7 is a relatively weak activator of PI3K and AKT signaling (Wofford et al. 2008), and perhaps this permits IL-7 to sustain memory CD8⁺ T-cell survival without overtly inducing more effector-like differentiation states.

During the initial expansion phase in response to an acute infection, the transition from naive→effector→TE states is coupled to microanatomical sites in tissues. Synergistic exposure to IL-2 and type I IFNs or IL-12 during priming induces *Tbx21* (T-bet) and *Prdm1* (Blimp-1) (Rutishauser et al. 2009; Jung et al.

2010; Xin et al. 2016) expression, which, in addition to *Zeb2* (Dominguez et al. 2015; Omilusik et al. 2015) and *Id2* (Omilusik et al. 2018), program various overlapping and distinct aspects of the cytotoxic and trafficking programs for encountering and combatting infected cells (Jung et al. 2010; Schenkel et al. 2014a) in addition to promoting TE differentiation. T-bet, which is transcriptionally induced by inflammatory signals like IL-12, IFN- γ , and type I IFNs, is a predominant TF involved in determining the ultimate fate of differentiation effector cells (Joshi et al. 2007). Indeed, high T-bet levels specify TE fates, while low T-bet levels are needed by MP cells to program optimal IL-15 responsiveness and ensure memory CD8 T-cell longevity (Joshi et al. 2007). High levels of T-bet and Blimp-1 suppress FOXO1-dependent genes *Ccr7* and *Il7ra* while inducing CXCR3 expression; this simultaneously restricts effector cell access to FRC-derived IL-7 in the splenic white pulp (Lord et al. 2005; Joshi et al. 2007; Jung et al. 2010; Zhu et al. 2010; Hara et al. 2012) and guides them to sites of infection and inflammation like the IL-15-rich RP (Cui et al. 2014). Intrinsic rewiring of IL-7 signaling also contributes to the short-lived nature of TE cells, as forced *Il7ra* (IL-7R) expression could not rescue them from terminal differentiation and death in vivo despite intact immediate downstream STAT5 signaling (Hand et al. 2007). Thus, by regulating both cell-intrinsic and -extrinsic aspects of effector cell responsiveness to environmental signals, T-bet and Blimp-1 constitute a transcriptional rheostat that fine-tunes effector and memory cell potential in differentiating cytotoxic T lymphocytes (CTLs), ultimately resulting in an effector cell pool with heterogeneous cytotoxic capacity and long-lived potential for optimized host protection.

Graded TF expression, as a mechanism to maintain functional diversity, also exists among circulating memory cells, where the relative level of T-bet controls trafficking potential in Tem cells by tuning chemokine receptor expression. Circulating Tem cells with high T-bet levels express high levels of CX₃CR1 but lose expression of CXCR3 and circulate exclusively in blood (Slütter et al. 2013; Laidlaw et al. 2014; Gerlach et al.

2016), while intermediate T-bet expression identifies a subset of Tem that maintains low CX₃CR1 but high expression of CXCR3, and broadly traffics throughout blood, lymph, and tissues. How T cells “sense” the relative level of T-bet is not entirely clear, but evidence suggests that *Zeb2* may serve as an “interpreter” that modifies the activity of T-bet to fine-tune effector and KLRG1⁺ Tem cell differentiation. In fact, T-bet overexpression in *Zeb2*-deficient cells was unable to induce expression of *Cx3cr1* or suppress *Cxcr3*, suggesting that the cooperative action of T-bet and *Zeb2* are required for appropriate specification of effector fates (Dominguez et al. 2015). A close cousin of T-bet, *Eomes* also plays an equally fundamental and often complementary role to T-bet in shaping circulating and tissue-resident memory T-cell identity (Intlekofer et al. 2008) and programming responsiveness to IL-15 (Pearce et al. 2003; Intlekofer et al. 2005). However, there are certain states where T-bet functions reciprocally with *Eomes*, for example, when T-bet expression increases to its highest levels in TE cells it begins to repress *Eomes* and CXCR3 expression (Dominguez et al. 2015; Gerlach et al. 2016). Together these results suggest that in addition to the functional redundancy of T-bet and *Eomes* in promoting core effector and memory cell processes, the relative ratio of the two TFs in Tem cells is a critical determinant of differentiation states and trafficking potential.

Tissue-Specific Regulation of Memory Cell Formation and Function

Trm cells across multiple tissues express a “core” set of TFs that optimize their ability to survive and persist in tissues. Notably, *Zfp683* (Hobit) and *Runx3* are universally necessary for the establishment of residency in diverse tissues (Mackay et al. 2016; Milner et al. 2017). The *Klf2* locus becomes less accessible and is down-regulated early upon entrance into tissues, resulting in the loss of *Slpr1* expression (Milner et al. 2017). Blimp-1 also plays an important role in instructing Trm cell identity, possibly by coordinating with Hobit to repress *Klf2* (Mackay et al. 2016). Both *Eomes* and *Tbx21* are down-regulated by Trm in the skin and gut, and

the residual expression of T-bet releases its transcriptional repression of *Itgae* (encoding CD103), which in turn is promoted through concurrent exposure to epithelial tissue-derived TGF- β (Laidlaw et al. 2014). On the other hand, low levels of T-bet are also needed for Trm cell survival by maintaining *Il2rb* expression and IL-15R signaling (Mackay et al. 2015b).

The BM is a major reservoir for both Tem and Tcm cells likely due to its preponderance of IL-7 and IL-15 that support survival and homeostatic proliferation (Becker et al. 2005). Migration into the BM from the circulation depends on a combination of *Eomes*-dependent CXCR4 (Banerjee et al. 2010) and other Gq α -dependent receptors for homing and extravasation into the tissue (Mazo et al. 2005). CXCR4 likewise plays a critical role in positioning cells within the BM in proximity to stromal cells, which are major producers of both IL-7 and IL-15 (Cui et al. 2014).

In addition to the core set of genes that define Trm cells broadly, unique environmental cues facilitate tissue-specific transcriptional programs regulating metabolism, effector functions, and tissue-remodeling and healing responses. In the lung, Notch signaling promotes the maintenance of Trm cells, both by regulating expression of *Itgae* as well as metabolite transporters like *Aqp3* and other solute carrier proteins (Hombrink et al. 2016). Recent work has revealed tissue-specific expression of unique fatty acid-binding protein (FABP) isoforms in Trm cells (Frizzell et al. 2020); and given the specificity of FABPs for unique lipid ligands, these expression patterns likely represent metabolic adaptations to distinct anatomical niches regulated by tissue-specific cues. However, the transcriptional regulators governing these particular tissue-specific programs remain to be discovered.

SUMMARY

Immunological memory is a hallmark of the adaptive immune system and the foundation of vaccines, which is entirely dependent upon the formation of a large pool of functionally diverse memory cells. However, designing vaccines is clearly not a “one-size-fits-all” approach,

as there are still human endemic diseases for which traditional antibody-based vaccines have not been successful, as with HIV (Burton 2019) and malaria (Wilson et al. 2019). Ideally, memory T cells protect the host at portals of entry like mucosal surfaces, but also systemically in the blood and internal organs—a feat that is currently only achieved through natural infection. Therefore, a greater understanding of the spatial and temporal dynamics of memory cell formation is needed if protective-induced immunity is to be achieved.

Although this review has largely focused on the trafficking patterns of CD8⁺ T cells that influence their responses to acute pathogens, the concepts described certainly apply to other disease settings like autoimmunity and cancer. In fact, CD8⁺ T-cell infiltration into tumors has been identified as a major prognostic for favorable outcomes in multiple tumor types (Galon et al. 2006; Gooden et al. 2011; Mahmoud et al. 2011; Tumeh et al. 2014). However, a major challenge in cancer immunotherapy is understanding the mechanisms by which antitumor T cells traffic into tumors and the methods that immunologically “cold” tumors use to prevent proper immune cell trafficking. Several studies in mice have demonstrated the utmost importance of CXCR3 in driving chemotactic migration of CD8⁺ T cells into tumors (Mikucki et al. 2015) and enabling the antitumor response after PD-1 blockade in models of colon carcinoma (Chow et al. 2019). Similarly, pre- and posttreatment levels of the CXCR3 ligands in melanoma patient plasma and tumor biopsies correlated with response to immune checkpoint blockade (Ji et al. 2012; Chow et al. 2019).

Developments in single-cell omics technologies have significantly advanced our understanding of immune cell functional diversity. Combining these methodologies with spatial omics will be instrumental for further elaborating upon the spatiotemporal dynamics of CD8⁺ T-cell differentiation, trafficking, and memory cell maintenance in situ. Understanding how these dynamics are transcriptionally regulated by environmental signals will certainly aid in the design of vaccines that induce protective im-

munity against emerging pathogens in the form of both tissue and circulating memory T cells.

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