Brain-resident memory T cells represent an autonomous cytotoxic barrier to viral infection

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Tissue-resident memory T cells (TRM) persist at sites of prior infection and have been shown to enhance pathogen clearance by recruiting circulating immune cells and providing bystander activation. Here, we characterize the functioning of brain-resident memory T cells (bTRM) in an animal model of viral infection. bTRM were subject to spontaneous homeostatic proliferation and were largely refractory to systemic immune cell depletion. After viral reinfection in mice, bTRM rapidly acquired cytotoxic effector function and prevented fatal brain infection, even in the absence of circulating CD8+ memory T cells. Presentation of cognate antigen on MHC-I was essential for bTRM-mediated protective immunity, which involved perforin- and IFN-γ-dependent effector mechanisms. These findings identify bTRM as an organ-autonomous defense system serving as a paradigm for TRM functioning as a self-sufficient first line of adaptive immunity.

Immunological memory is characterized by a more rapid and efficient response to previously encountered pathogens. Thereby, memory recall responses protect against infections that can otherwise cause disease or even death in immunologically naive hosts. Memory CD8+ T cells (TCM) are instrumental for the rapid detection and eradication of intracellular pathogens. Several subsets of TCM have been identified based on their migration patterns, anatomical location, and functional specialization (Mueller et al., 2013). Historically, memory T cells have been divided into central memory T cells (TCM) and effector memory T cells (TEM; Sallusto et al., 1999). TCM home to secondary lymphoid organs, exhibit high proliferative capacity upon reencountering cognate antigen, and serve as a self-replenishing pool that gives rise to other memory T cell subsets (Graef et al., 2014). Conversely, TEM do not express the homing receptors characteristic of TCM, recirculate through the body, and can provide immediate effector function (Sallusto et al., 1999). Recently, tissue-resident memory T cells (TRM) have been identified as an additional subset of memory T cells that does not recirculate, but persists at sites of previous infection, such as skin and mucosal tissues (Schenkel and Masopust, 2014b; Park and Kupper, 2015), as well as the brain (Wakim et al., 2010). TRM from various organs, including the brain show overlapping transcriptional profiles with a core transcriptional signature (Schenkel and Masopust, 2014a), distinguishing them from circulating TCM (Wakim et al., 2012; Mackay et al., 2013). In most nonlymphoid tissues, TRM outnumber patrolling TEM and constitute the largest component of T cell memory (Steinert et al., 2015). Their persistence in organs is mediated by specific adhesion molecules, such as CD103 (Integrin αE; Gebhardt et al., 2009; Casey et al., 2012; Mackay et al., 2013) and loss of tissue egress receptors from the cell surface (Skon et al., 2013; Mackay et al., 2015a). Bona fide TRM have been described to express CD69, which antagonizes the tissue egress receptor sphingosine 1-phosphate receptor 1 (S1P1; Mackay et al., 2015a). Surface expression of CD103 seems specific for TRM, but not all TRM express the molecule. Long-lived CD103− TRM have been described in secondary lymphoid organs (Schenkel et al., 2014b), in the gut (Bergsbaken and Bevan, 2015), and in the female reproductive tract (Steinert et al., 2015). CD103 expression has been associated with tissue retention (Wakim et al., 2010; Casey et al., 2012; Mackay et al., 2013), epithelial localization (Gebhardt et al., 2009; Sheridan et al., 2014) and function (Wakim et al., 2010; Laidlaw et al., 2014; Bergsbaken and Bevan, 2015), but it remains elusive whether CD103 expression is causally linked to these characteristics. The generation and maintenance of TRM is dependent on IL-7 and IL-15-mediated signals (Mackay et al., 2013; Adachi et al., 2015), however, whether TRM undergo
homeostatic proliferation to maintain a stable population has so far not been demonstrated.

T<sub>RM</sub> accelerate and improve pathogen clearance upon reinfection (Gebhardt et al., 2009; Jiang et al., 2012; Shin and Iwasaki, 2012; Wakim et al., 2012; Sheridan et al., 2014), but the underlying mechanisms remain a subject of ongoing investigation. Reactivation of T<sub>RM</sub> by cognate antigen leads to the production of inflammatory cytokines, such as IFN-γ. Consequently, antiviral genes are induced and additional immune cells are rapidly recruited from the circulation (Schenkel et al., 2013, 2014a; Ariotti et al., 2014). The currently prevailing concept therefore suggests that T<sub>RM</sub> represent a tissue-restricted surveillance system with the capacity to alert circulating T<sub>M</sub> in case of reinfection (Carbone, 2015). Conversely, a potential function of T<sub>RM</sub> as directly cytotoxic antiviral effectors, and thus as an autonomous immunological barrier to viral infection, has so far been mostly dismissed, owing to the small number of T<sub>RM</sub> which persist after primary infection, although reports suggest a direct antiviral function of skin T<sub>RM</sub> (Liu et al., 2010; Jiang et al., 2012; Mackay et al., 2015b).

Here, we studied brain T<sub>RM</sub> (bT<sub>RM</sub>) in established mouse models of viral CNS infection. Antiviral bT<sub>RM</sub> persisted in the CNS for prolonged periods of time, underwent homeostatic proliferation, and served as a potent cellular barrier of antigen-specific immunity, which achieved virus control independently of circulating T cells. Rapid bT<sub>RM</sub>-mediated virus clearance relied on IFN-γ expression and peroxidase-cytotoxicity and protected mice from immunopathological CNS disease. Our findings suggest that bT<sub>RM</sub> can act as an organ-autonomous defense system of the CNS.

RESULTS
CD103<sup>+</sup> and CD103<sup>−</sup> bT<sub>RM</sub> persist after cerebral viral infection and accelerate pathogen clearance during infection with a related virus

To study the generation and function of bT<sub>RM</sub>, we infected mice intracerebrally (i.c.) with a genetically engineered, attenuated lymphocytic choriomeningitis virus (LCMV) variant (rLCMV; PinskiChever et al., 2003). As previously shown (PinskiChever et al., 2010), i.c. administered rLCMV rapidly drained to the periphery and triggered a potent peripheral antiviral CD8<sup>+</sup> T cell response, which resolved the brain infection within ten days (Fig. 1 A). Thereafter, T cell numbers in the brain contracted, but a population of T<sub>M</sub> persisted in stable number and frequency from 6 wk after infection onwards (Fig. 1, B and C). At that time point, most persisting T<sub>M</sub> cells expressed CD69, a prototypic T<sub>RM</sub> marker. CD69<sup>+</sup> brain T<sub>M</sub> expressed high Bcl-2 levels, and many were Granzyme B–positive (59 ± 3%), whereas most of them were specific for the immunodominant LCMV epitope NP<sub>396-404</sub> (82 ± 5%). However, only about half of these cells (50 ± 10%) expressed CD103 (Fig. 1 D and Fig. S1). Both CD103<sup>+</sup> and CD103<sup>−</sup> CD69<sup>+</sup> T<sub>M</sub> subsets persisted in stable relative proportions over time (Fig. 1 E). Analogously to the endogenous CD8<sup>+</sup> T cell pool, both CD103<sup>+</sup> and CD103<sup>−</sup> brain T<sub>M</sub> subsets were found in adoptively transferred CD8<sup>+</sup> TCR transgenic P14 or OT-1 cells, respectively, after i.c. infection with rLCMV variants encoding the respective cells’ cognate epitopes (Fig. 1 F). Furthermore, CD103<sup>+</sup> and CD103<sup>−</sup> OT-1 brain T<sub>M</sub> were generated after intrathecal infection with a modified vaccinia virus (MVA; Rothhammer et al., 2014) expressing OVA (Fig. 1 G). CD69 expression correlated with exclusion from staining with i.v. administered fluorescent antibody (Anderson et al., 2014; Fig. 1 H) and extravascular CD8<sup>+</sup> T cells identified by immunostaining on brain sections expressed CD69 (95 ± 3%; n = 3 mice). Furthermore, most brain CD69<sup>+</sup> T<sub>M</sub> cells were refractory to depletion by peripherally administered depleting anti-CD8 antibody (Fig. 1 I). Altogether, this demonstrated that the vast majority of CD69<sup>+</sup> T<sub>M</sub> cells in brain were bona fide T<sub>RM</sub> (from now on referred to as bT<sub>RM</sub>).

To investigate the protective role of bT<sub>RM</sub> upon brain reinfection, we generated rLCMV memory mice by either i.v. or co-infection (i.c. + i.v.; Fig. 2 A). Co-infection was used to assure similar generation of circulating T<sub>M</sub>. Indeed, both infection routes led to similar frequencies of D<sup>β</sup>-NP<sub>396-404</sub> LCMV-specific T<sub>M</sub> in peripheral blood (Fig. 2 B). However, in contrast to bT<sub>RM</sub> generated upon i.c. infection, only limited numbers of T<sub>M</sub> cells were present in the brain after i.v. infection with rLCMV (Fig. 2, C and D). These latter cells were susceptible to depletion by peripherally administered anti-CD8α antibody (unpublished data) demonstrating that T<sub>M</sub> detectable in the brain after i.v. LCMV infection are in equilibrium with the circulation and do not represent bona fide bT<sub>RM</sub>. In addition, brain circulating T<sub>M</sub> generated by i.v. infection failed to up-regulate CD103 and contained a lower percentage of D<sup>β</sup>-NP<sub>396-404</sub>-specific cells than bT<sub>RM</sub> generated by i.c. infection (Fig. 2 E). Next, rLCMV memory mice with bT<sub>RM</sub> (i.e. + i.v. rLCMV co-infection) or without bT<sub>RM</sub> (i.v. rLCMV infection) were i.c. challenged with pathogenic WT LCMV (LCMVwt), which shared the immunodominant NP<sub>396-404</sub> epitope with rLCMV (Fig. 2 F). When analyzed 3 d later, rLCMV memory mice with bT<sub>RM</sub> exhibited significantly lower LCMV virus load in the brain than rLCMV memory mice with only circulating T<sub>M</sub>. This indicated that the generation of bT<sub>RM</sub> provided an advantage during reinfection.

CD103<sup>+</sup> and CD103<sup>−</sup> bT<sub>RM</sub> persist in proximity to anatomical barriers and undergo homeostatic proliferation

We next analyzed the spatial distribution of bT<sub>RM</sub> on brain sections by immunohistochemistry. bT<sub>RM</sub> were preferentially detected at brain surface structures, such as meninges and choroid plexus, around the ventricles or at anatomical borders between different brain regions (Fig. 3 A). Only a small fraction of bT<sub>RM</sub> was in direct contact with vascular endothelium (14 ± 3%; Fig. 3 A), but most bT<sub>RM</sub> localized in close proximity to vessels and brain surface structures, or both (Fig. 3 B). Quantification of CD103<sup>+</sup> and CD103<sup>−</sup> bT<sub>RM</sub> in the measured areas did not reveal a correlation of CD103 expression with...
their localization (Fig. 3 C). Interestingly, a consistent fraction of bT RM expressed proliferation marker Ki-67 (9 ± 1%) long after virus clearance (Fig. 3 D). bT RM at brain surface structures expressed Ki-67 more frequently than bT RM localized in brain parenchyma (Fig. 3 E). Previous studies have shown that IL-7– and IL-15–dependent longevity and homeostatic proliferation are maintaining central memory T cells by Stat5 signaling (Burchill et al., 2003; Willinger et al., 2005; Hand et al., 2010). Indeed, a fraction of brain T cells showed Stat5 phosphorylation (26 ± 7%). Similarly to Ki-67+ T cells, we observed an increased proportion of P-Stat5+ T cells at brain surface structures (Fig. 3 F). Using histocytometry (Fig. S2),
we could confirm that meninges contained a higher frequency of P-Stat5+ T cells than internal brain structures (Fig. 3 G). Altogether, this indicates that Stat5-driven homeostatic proliferation contributes to the maintenance of the long-lived bTRM population preferentially at brain surface structures.

**bTRM autonomously clear pathogenic LCMV challenge independently of circulating TM cells**

To assess the contribution of circulating CD8+ T cells to virus control in the brain, we treated a group of rLCMV memory mice with bTRM and circulating TM contained significantly more T cells in the brain after challenge than mice with only circulating TM (Fig. 4, B and C). As expected (Schenkel et al., 2013), the numbers of brain-infiltrating T cells in the former group were significantly reduced when circulating TM were depleted. This indicated that about half of the brain CD8+ T cells after LCMVwt challenge of nondepleted mice originated from a recruitment of circulating TM, whereas the other half represented bTRM and their progeny. Furthermore, 47 ± 13% of bTRM expressed proliferation marker Ki-67 after LCMVwt i.c. challenge (Fig. 4 D), indicating that a substantial fraction of bTRM entered the cell cycle upon antigen reencounter in the CNS. During LCMV i.c. challenge, both CD103+ and CD103− bTRM expanded in similar proportions and showed equal potential for Ki-67 up-regulation (Fig. 4 E and F). Intriguingly, rLCMV memory mice with bTRM but lacking circulating TM cleared virus from the brain equally efficiently as mice with both bTRM and circulating TM (Fig. 4, C, G, and H). This suggested that recruitment of circulating TM was not required for bTRM-mediated virus clearance from the brain. Conflicting reports exist about TRM dependency on CD4+ T help in different organs (Jiang et al., 2012; Laidlaw et al., 2014). To address the role of CD4+ T cells for the generation and function of bTRM, we depleted CD4+ T cells either during primary i.c. infection with rLCMV or performed a combined depletion of circulating CD4+ and CD8+ T cells during LCMVwt i.c. challenge. bTRM numbers, as well as bTRM-mediated rapid virus clearance during LCMVwt i.c. challenge, was not affected in the absence of CD4+ T cell help during bTRM generation or challenge with LCMVwt (Fig. 5, A–L). Furthermore, to exclude that recruited NK cells contribute to virus clearance, we depleted NK cells in addition to circulating T cells during LCMVwt i.c. challenge. However, virus clearance was unimpaired in animals containing bTRM but not circulating T and NK cells (Fig. 6, A–E), demonstrating that LCMVwt control relied on bTRM.

**bTRM-mediated virus clearance is dependent on presentation of cognate antigen**

Next, we aimed to investigate if presentation of cognate antigen is necessary or if bystander activation and expres-
sion of antiviral genes in surrounding tissue is sufficient for bTM-mediated viral clearance. Therefore, we challenged rLCMV memory mice with a genetically engineered LCMV variant (LCMV-NPN400S), in which the MHC-I anchor residue of the immunodominant epitope NP 396-404 was mutated to abrogate MHC binding (Johnson et al., 2015; Fig. 7 A), thus preventing MHC-I–restricted recognition of this virus by the vast majority of bTM (Fig. 1 D and Fig. 2 E). Accordingly, bTM expansion was reduced when LCMV-NPN400S was used for challenge instead of LCMVwt (Fig. 7, B and C). In further contrast to LCMVwt i.c. challenge, bTM failed to clear the brain from LCMV-NPN400S within 3 d. This was evident in increased numbers of infected cells (Fig. 7, B and D) and heightened LCMV RNA loads (Fig. 7 E). Interestingly, antiviral interferon-induced transmembrane protein 3 (Ifitm3), a marker of bTM-induced antiviral state (Ariotti et al., 2014), was similarly induced after infection with LCMVwt or LCMV-NPN400S, respectively (Fig. 7 F). Furthermore, infection with either of the two viruses induced up-regulation of Granzyme B (Fig. 7, G–H), as well as Ki-67 expression (Fig. 7, G and I) in bTM. This indicated that the capacity of bTM to autonomously clear brain virus infection depended on epitope-specific target recognition. Conversely, the virtually uniform activation of bTM after viral challenge occurred in a largely antigen nonspecific fashion, as Dβ-NP396–404-tetramer+ bTM...
Figure 4. bTRM mediate rapid LCMV clearance independently of circulating Tm cell recruitment. (A) WT mice were infected with rLCMV i.v. (no bTRM) or i.v. + i.c. (bTRM). At least 6 wk later, mice were treated i.p. with anti-CD8a depleting antibody before LCMVwt i.c. challenge or left unchallenged, and brains were analyzed 3 d later. (B) CD8⁺ T cells quantification on immunostained brain sections in relation to the presence of bTRM (+), circulating CD8 depletion (+) and LCMVwt i.c. challenge (+). (C) Representative images of CD8 (top, arrows) or LCMV (bottom, arrows) on immunostained brain sections. Bars: 100 µm; (inset) 20 µm. (D) Representative flow cytometry plot (left) and frequencies (right) of Ki-67–expressing bTRM (CD8⁺CD44⁺CD69⁺) after LCMVwt i.c. challenge (+) or in unchallenged control mice (−). Numbers represent frequencies of positive cells. (E) Frequencies of CD103⁻ expressing bTRM in LCMVwt i.c. challenged (+) or unchallenged (−) mice as in D. (F) Frequencies of Ki-67–expressing CD103⁻ and CD103⁺ bTRM as in D. (D–F) Each symbol represents an individual mouse and bars indicate mean. (G) Quantification of LCMV⁺ cells by immunohistochemistry on brain sections and (H) LCMV RNA by qPCR (normalized to naive mice infected with LCMVwt i.c. = 1) in the brain of mice as in B. Data represent mean ± SEM (n = 3–5 mice for unchallenged controls (−); n = 5–6 for mice challenged with LCMVwt i.c.) *, P < 0.05; **, P < 0.01, one-way ANOVA followed by Sidak’s multiple comparisons test (B, G, and H); unpaired two-tailed Student’s t test (D). One representative out of at least two independent experiments is shown (B–H).
Figure 5. **bTm generation and functionality in the absence of CD4+ T cell help.** (A) WT mice were infected with rLCMV i.c. 11 wk later, mice were treated with anti-CD8a alone or in combination with anti-CD4 depleting antibody i.p., and subsequently challenged with LCMVwt i.c. Naive WT mice infected with LCMVwt i.c. were used as controls. Brains were analyzed 3 d later. (B) Representative images of brain sections immunostained for CD8 (top, arrows) or LCMV (bottom). Quantification of CD8+ T cells (C), LCMV+ cells by immunohistochemistry (D), or LCMV RNA by qPCR (E; normalized to naive mice infected with LCMVwt i.c. = 1). (F) WT mice were treated with anti-CD4 depleting antibody as indicated and were infected with rLCMV i.c. 6 wk later, rLCMV memory mice containing helped or unhelped bTm were treated with anti-CD8a depleting antibody and challenged with LCMVwt i.c. (G) numbers of bTm (CD8+CD44+CD69+) and (H) frequencies of Tm cells (CD127+KLRG1–) among bTm (CD8+CD44+CD69+) were determined by flow cytometry in unchallenged rLCMV memory mice. (I–L) 6 wk after antibody-mediated depletion of CD4+ T cells, rLCMV memory mice, as in F, were challenged with LCMVwt i.c. and analyzed 3 d later. (I) Quantification of CD8+ T cells by immunohistochemistry. (J) Representative images of brain sections immunostained for CD8 (top, arrows) or LCMV (bottom). (G–I) Each symbol represents an individual mouse and bars indicate mean. Quantification of (K) LCMV+ cells by immunohistochemistry (L) LCMV RNA by qPCR (normalized to naive mice infected with LCMVwt i.c. = 1) 3 d after LCMVwt i.c. challenge. Data represent mean ± SEM (where included).
up-regulated GzmB (96 ± 1%) and Ki-67 (42 ± 3%) during i.c. challenge with LCMV-NP$_{N400S}$ (unpublished data).

**bTRM-mediated rapid viral clearance depends on IFN-γ and perforin**

T cell–mediated viral clearance from the brain can be achieved by cytolytic, i.e., perforin or Fas-dependent mechanisms, as well as by noncytolytic, cytokine–dependent pathways (Griffin, 2003; Pinschewer et al., 2010; Herz et al., 2015). To investigate cytokine production and cytotoxic potential of bTRM, we depleted memory mice of circulating CD8$^+$ T cells and challenged them with LCMVwt i.c. (Fig. 8 A). We analyzed CD107a cell surface exposure as indicator of degranulation of cytotoxic granule release and production of IL-2, IFN-γ, and TNF upon in vitro peptide stimulation (Fig. 8 B and not depicted). In the absence of LCMVwt challenge and without peptide restimulation, bTRM did not spontaneously produce detectable amounts of cytokines and did not degranulate. After LCMVwt i.c. challenge, bTRM exhibited IFN-γ production (9.7 ± 1.5%) and surface expression of CD107a (9.0 ± 0.5%) in the absence of further ex vivo stimulation. After peptide stimulation, most bTRM produced high amounts of IFN-γ in combination with surface expression of CD107a, which was significantly higher in bTRM from LCMVwt i.c. challenged animals (59.0 ± 2.4%) than from unchallenged controls (36.4 ± 3.1%; Fig. 8 B). In contrast, we detected comparably few bTRM that coproduced IL-2 or TNF, and we failed to detect expression of FasL on bTRM (unpublished data). Thus our analysis identified IFN-γ–producing bTRM with cytotoxic granule release as main effector cell population after LCMVwt i.c. challenge.

Considering IFN-γ as the main effector cytokine expressed by bTRM, we next tested bTRM function in IFN-γ knockout (GKO) mice. Of note, IFN-γ is dispensable for the clearance of primary infection with attenuated rLCMV (Pinschewer et al., 2010) but bTRM generation was not impaired in GKO mice (Fig. 8 C). We depleted circulating CD8$^+$ T cells in IFN-γ–deficient (GKO) and IFN-γ–competent (control) rLCMV memory mice and subsequently challenged them with LCMVwt i.c. (Fig. 8, D–G). Before LCMVwt i.c. challenge, GKO rLCMV memory mice displayed slightly higher bTRM numbers, but the fold expansion of bTRM after virus challenge was similar in GKO and control animals (Fig. 8, D and E). This indicated that the cell-intrinsic reactivation capacity of bTRM was unimpaired in GKO mice. Conversely, the number of infected cells (Fig. 8, D and F) and LCMV RNA loads (Fig. 8 G) 3 d after LCMVwt i.c. challenge were significantly higher in GKO memory mice than in control memory mice.

Based on the notion that bTRM up-regulated the cytotoxic effector molecule Granzyme B after LCMV i.c. challenge (Fig. 7, G and H), we next investigated whether cytolytic effector functions (Kägi et al., 1994) contributed to bTRM-mediated viral clearance. We thus generated perforin-deficient (PKO) rLCMV memory mice and depleted circulating CD8$^+$ T cells (Fig. 8, H–M), as before (Fig. 8 A). Perforin was dispensable for the generation of bTRM (Fig. 8 H). Furthermore, after LCMVwt i.c. challenge, perforin-deficient bTRM showed unimpaired up-regulation of Granzyme B (Fig. 8 I) and secondary expansion (Fig. 8 J and K). Nevertheless, PKO memory mice exhibited significantly higher numbers of infected cells (Fig. 8, J and L) and increased viral RNA loads (Fig. 8 M) than control memory mice. This demonstrated that bTRM cells exert rapid IFN-γ production and perforin-dependent cytotoxicity, both of which made essential contributions to the rapid control of viral infection in the brain.

**bTRM cells protect from fatal immunopathological CNS disease in an antigen–dependent manner**

i.c. infection of naive immunocompetent mice with LCMV–wt results in fatal choriomeningitis, which is the result of antiviral CD8$^+$ T cell–mediated immunopathology (Cole et al., 1972). T$_{RM}$ have been shown to amplify immune responses in nonlymphoid tissues during rechallenge with cognate antigen (Schenkel et al., 2013, 2014a). Here, we observed analogous findings in the brain (Fig. 4 B), raising the possibility that bTRM could enhance immunopathological consequences of brain virus infection (Oehen et al., 1991). We therefore investigated how the presence of bTRM impacts the disease after LCMVwt i.c. challenge. For that, we depleted LCMV-specific circulating TM in rLCMV memory mice using anti-CD8 antibody 6 wk before LCMVwt i.c. challenge (Fig. 9 A). This timing enabled the reconstitution of the peripheral compartment with naive CD8$^+$ T cells before LCMVwt challenge (unpublished data). Analogous to the experiment in which anti-CD8 depletion and challenge had been performed simultaneously (Fig. 4, B and D), the presence of bTRM resulted in enhanced T cell numbers in the brain when circulating memory CD8$^+$ T cells were present (Fig. 9, B and C). However, irrespective of the presence or absence of circulating memory CD8$^+$ T cells, brain LCMV loads as assessed 3 d after LCMVwt i.c. challenge were significantly reduced in mice with bTRM compared with mice with only circulating TM (Fig. 9, B, D, and E). As expected (Oehen et al., 1991), mice with only circulating TM did not develop disease, demonstrating that the observed peripheral virus–specific TM recall response can afford antiviral protection (Fig. 9 F). Furthermore, circulating TM$^+$–depleted rLCMV memory mice without bTRM developed fatal choriomeningitis, which had kinetics comparable to unimmunized control mice. Most importantly, six out of seven rLCMV memory
mice with bTRM were protected from disease even though circulating T
M cells had been depleted. This underscored the self-sufficient nature of bTRM-mediated antiviral protection. Next, we investigated whether bystander activation of bTRM (Fig. 7) was sufficient to protect animals from fatal immunopathology. We therefore depleted rLCMV memory mice of circulating T
M and challenged them with either LCMVwt or LCMV-NP400S i.c. after reconstitution of circulating CD8+ T cells. As expected, mice challenged with LCMV-NP400S i.c. did not mount a Dβ-NP396-404-specific CD8+ T cell response, but developed a CD8+ T cell response specific for the Dβ-GP33-41 epitope (data not shown), to which they had not been previously exposed (rLCMV does not encode for LCMV-GP33-41). Unlike rLCMV memory mice challenged with LCMVwt i.c., challenge with LCMV-NP400S i.c. resulted in the development of fatal choriomeningitis with disease kinetics comparable to unimmunized control mice (Fig. 9 G). Altogether, this demonstrated that bTRM immunity was antigen-specific and provided rapid autonomous elimination of virus-infected cells from the brain and thereby protected from fatal immunopathological disease.

DISCUSSION

The identification of T
RM as a separate lineage of long-lived memory T cells has fundamentally reshaped our concepts of cell-mediated immunity to infection. With this study, we establish bTRM as an autonomous first line of adaptive immune defense against viral infection of the brain. bTRM were found after acute infection with rLCMV or a replication-deficient modified vaccinia virus strain in mice, attesting to the general validity of our findings. bTRM showed strong proliferative potential and protected against fatal viral infection in an organ-autonomous manner, independent of the recruitment of circulating CD8+ memory T cells.
Similar to other nonlymphoid organs (Steinert et al., 2015), CD69+ bT RM represented 90% of CD8+ T cells in the brain. Contrary to brain infection with vesicular stomatitis virus (Wakim et al., 2010), we found in two independent models that CD103 was expressed only on a proportion of bT RM. This may be a result of differences in isolation and quantification methods, as has been described for other organs (Steinert et al., 2015). We do not exclude the possibility that CD103+ and CD103− bT RM may be functionally different; however both subsets persisted in stable proportions over time, exhibited an analogous preference for retention at surface-lining structures of the brain, and showed equal proliferative capacity upon reactivation. Although bT RM show very limited survival and proliferative capacity in vitro (Wakim et al., 2010), they seem to possess self-renewing capacity in vivo and exhibit high proliferative capacity after reactivation. Similar to central memory T cells (Burchill et al., 2003; Willinger et al., 2005; Hand et al., 2010), the population of long-lived bT RM seems to be maintained by Stat5-driven homeostatic proliferation, preferentially at brain surface structures, such as meninges and periventricular areas. However, the exact nature of a supposed T RM maintaining microenvironment near
Figure 8. bTRM-mediated rapid virus clearance depends on IFN-γ and perforin. (A) Mice were infected with rLCMV i.c. to generate bTRM. At least 6 wk later, mice were treated with anti-CD8a depleting antibody i.p. before LCMVwt i.c. challenge or left unchallenged. Brains were analyzed 3 d later. (B, left) Representative flow cytometry plot of IFN-γ production and degranulation as measured by surface exposure of CD107a in bTRM (CD8+CD44+CD69+) of unchallenged (bTRM) or LCMVwt i.c.-challenged (bTRM + LCMVwt i.c.) WT mice with (+) or without (−) in vitro NP396-404 peptide stimulation. Numbers indicate frequencies (%) of cells in corresponding gates. (B, right) Frequencies (mean ± SEM) of IFN-γ-positive (black bars), CD107a positive (gray bars), and double-positive (blue bars) bTRM with (+) or without (−) LCMVwt i.c. challenge and with (+) or without (−) in vitro NP396-404 peptide stimulation (n = 3–4 mice per group). (C–G) IFN-γ-competent (control)- or GKO-rLCMV memory mice were generated and treated as in A. (C) Frequencies of TM cells (CD127+KLRG1−) among bTRM (CD8+CD44+CD69+) as determined by flow cytometry in unchallenged IFN-γ-competent (control) and GKO mice. Each symbol represents an individual mouse and bars indicate mean (n = 4 mice per group). (D) Representative images of immunostained brain sections for CD8 (top, arrows) or LCMV (bottom). (E) Quantification of CD8+ T cells, (F) LCMV+ cells, or (G) LCMV RNA by qPCR (normalized to naive mice infected with LCMVwt i.c. = 1) in brains of GKO and control mice with (+) or without (−) LCMVwt i.c. challenge. Data represent mean ± SEM (n = 3–10 mice per group). (H–M) Perforin-competent (control)- or PKO-rLCMV memory mice were generated and treated as in A. (H) Frequencies of TM cells among bTRM (as in C) in unchallenged perforin-competent (control) and PKO mice. Each symbol represents an individual mouse and indicates mean (n = 4 mice per group). (I) Frequencies of GzmB-expressing cells among bTRM as determined by flow cytometry 3d after LCMVwt i.c. challenge of control or PKO mice. Each symbol represents an individual mouse, and bars indicate mean (n = 4–6 mice per group). (J) Representative images of immunostained brain sections for CD8 (top, arrows) or LCMV (bottom). (K) Quantification of CD8+ T cells, (L) LCMV+ cells, or (M) LCMV RNA by qPCR (normalized to naive mice infected with LCMVwt i.c. = 1) in brains of PKO and control mice with (+) or without (−) LCMVwt i.c. challenge. Data represent mean ± SEM (n = 4–6 mice per group). *, P < 0.05; **, P < 0.01, asterisk colors represent multiple comparisons performed, two-way ANOVA with Tukey’s multiple comparisons (B), one-way ANOVA with Sidak’s multiple comparisons test (I), unpaired two-tailed Student’s t test (C, F, G, H, L, and M). One representative (B–F and J–M) or pool (G) of two independent experiments is shown. (H and I) Experiments were performed once. Bars, 100 µm; (inset) 20 µm.
tissue surfaces that was also observed in other organs, i.e., in the skin (Gebhardt et al., 2009), remains to be investigated.

In naive hosts, the task of rapidly detecting invading pathogens and alerting the adaptive immune defense generally falls to the innate immune system (Iwasaki and Medzhitov, 2015). The resulting secretion of antiviral effector cytokines, such as type I interferons, is crucial to limiting virus spread until adaptive immune responses are induced and can accomplish viral clearance (McNab et al., 2015). TRM from peripheral organs other than the brain have been described to subserve a similar immunological function, i.e., to alert circulating T cell subsets to invading pathogens and to induce...
antiviral genes in the tissue surrounding the site of initial infection (Ariotti et al., 2014; Schenkel et al., 2014a). These functions were reported to be largely dependent on inflammatory cytokines, such as IFN-γ. Similar to T_{RM} from other organs, we show here that bT_{RM} share the capacity to secrete IFN-γ upon antigen reencounter. However, they largely do that in combination with the release of cytotoxic granules, and perforin-mediated cytotoxicity was essential for rapid bT_{RM}-mediated virus control. One may thus speculate that IFN-γ–deficient bT_{RM} fail to provide sufficient noncytolytic antiviral function, or fail to prepare the site of infection for lytic effector function as a result of impaired up-regulation of MHC I expression on infected cells (Bergmann et al., 2003). Whereas both possibilities are not mutually exclusive and can contribute to the observed outcome, our data strongly suggest that a direct interaction of bT_{RM} with infected cells rather than a generalized antiinflammatory state is necessary for bT_{RM}-mediated rapid viral elimination. This conclusion is based on our observation that bT_{RM} can be activated in a bystander manner, i.e., in the absence of cognate antigen and solely as the result of the inflammatory environment (Kohlineier et al., 2010; Soudja et al., 2012; Raüé et al., 2013), yet under such circumstances fail to rapidly control the virus. This does not, however, exclude the possibility that bystander activation may contribute to a viral load reduction in the brain. Furthermore, depending on the pathogen type and infection scenario, bT_{RM}-driven induction of IFN-γ response genes may be sufficient to limit early pathogen spread or even to cleanse viruses from nonrenewable cells such as neurons (Griffin, 2003; Herz et al., 2015).

Neurotropic viruses of hematogenous origin frequently infect the CNS secondary to systemic infection. Neuroinvasion typically occurs through the brains outer or inner linings (McGavern and Kang, 2011), namely the meninges or the ependyma, to subsequently spread into the brain parenchyma. The resulting inflammation manifests as meningitis or even encephalitis and can be life-threatening (Gilden et al., 2007). Our model of intracranial rLCMV immunization recapitulates the spread from the brain linings into the parenchyma albeit it does not reproduce neuroinvasion secondary to systemic infection. Conversely, its attenuated behavior enabled us to study solid bT_{RM} immunity without the caveats of life-threatening complications from primary brain infection.

Although we noted a protective function of bT_{RM} in infection, T_{RM}-mediated activation and recruitment of inflammatory cells to the site of infection can, however, also have detrimental effects such as those described in the context of skin contact hypersensitivity (Gaide et al., 2015). In organs with limited regenerative capacity, such as the CNS, excessive inflammation can induce collateral damage (immunopathology). In this regard, severe immunopathological disease is one of the most dangerous complications of viral infections in the brain, and depending on pathogen loads, circulating T_{M} can even accentuate disease rather than prevent it (Oehen et al., 1991). Therefore, not only infections of the CNS but also the resulting immune responses must be tightly controlled. The functioning of bT_{RM} as a border patrol, which rapidly detects and autonomously eliminates the first few virus-infected cells, thus bypasses the need for antigen drainage to lymph nodes and reactivation of T_{M} cells inside secondary lymphoid organs. It has been shown for other organs that T_{RM} cells use a continuous migratory behavior, enabling few cells to survey large organ structures and readily detect their cognate antigen (Ariotti et al., 2012). The positioning and preferential maintenance of bT_{RM} at surface-associated brain structures and in proximity to vessels as described in this study therefore matches the specific immunological challenge and need of the brain to limit viral spread from the circulation and brain linings into the parenchyma and to rapidly eliminate the initially infected cells. Thereby, bT_{RM} can balance pathogen control against excessive inflammation.

Based on the present observations, we propose to adapt the concept of immunological privilege of the brain. With identification of the bT_{RM} compartment, the brain undoubtedly maintains powerful immunological forces to fight recurrent microbial intruders. This observation stands in stark contrast to the several layers of immunomodulatory mechanisms, including constitutively low expression of MHC molecules (Neumann et al., 1995), which are in place to limit inflammation in the brain (Galea et al., 2007). Thus, pathogens that have previously invaded the brain appear to be specifically excluded from this immunological privilege and are instead rapidly and efficiently eliminated by bT_{RM}. It is tempting to speculate that bT_{RM} immunity must be particularly potent because the blood–brain barrier prevents antibody access to the brain, and thus is largely excluding this organ from protection by the humoral arm of immunological memory.

**MATERIALS AND METHODS**

**Mice.** C57BL/6 WT, IFN-γ–deficient (GKO; Dalton et al., 1993), perforin-deficient (PKO; Kägi et al., 1994), OT-1 TCR transgenic (Hogquist et al., 1994), and P14 TCR (Pincher et al., 1989) transgenic mice were bred and lodged under P2 conditions in the animal facilities of the University Medical Centre of Geneva and Munich. Sex- and age-matched mice between 6 and 12 wk of age were used for experiments. All animal experiments were authorized by the cantonal veterinary office of Geneva and performed in agreement with the Swiss law for animal protection.

**Virus infection.** Recombinant LCMV strains were generated according to established methods (Pinschewer et al., 2003). The following virus strains were used: recombinant LCMV encoding for the glycoprotein of vesicular stomatitis virus (VSV) instead of its own glycoprotein (rLCMV/INDG, abbreviated rLCMV throughout); rLCMV encoding for a chimeric glycoprotein of VSV containing the leader sequence of LCMV glycoprotein with the GP33 epitope of LCMV (rLCMV-GP33); and recombinant LCMV encoding for OVA (rLCMV-OVA). Genetically engineered WT
LCMV (LCMVwt, Armstrong strain) and LCMV mutant virus (LCMV-NP<sub>N400S</sub>) lacking the CTL-specific epitope NP<sub>396-404</sub> were generated as described previously (Johnson et al., 2015). Viruses were produced, titrated, and administered to mice as previously described (Flatz et al., 2006). For transient virus infection in the brain, 10<sup>5</sup> PFU rLCMV was administered i.c. i.v. infected control animals were injected i.c. with vehicle. Memory and naive mice were challenged with 10<sup>3</sup> PFU LCMVwt (Armstrong strain) i.c. Incidence of choriomeningitis was determined by occurrence of general malaise and hind limb cramps, and severely diseased animals were immediately sacrificed. Brain virus load was analyzed by quantitative RT-PCR for LCMV-NP (McCausland and Crotty, 2008). Brain total RNA was isolated from deparaf-finized tissue sections using RNeasy Mini kit (QIAGEN), cDNA was synthesized using iScript cDNA synthesis kit (Bio-Rad Laboratories), and relative expression of LCMV S segment was determined against GAPDH as housekeeping gene (QIAGEN) using iQ SYBR Green Supermix (Bio-Rad Laboratories).

Replication-deficient MVA-OVA was generated as described previously (Staib et al., 2004). 2 x 10<sup>5</sup> IU MVA-OVA was administered intrathecally (i.th.) as previously described (Rothhammer et al., 2014). In some experiments, OT-1 or P14 TCR transgenic CD<sup>8</sup> T cells were adoptively transferred into naive C57BL/6 mice 24 h before i.c. or i.th. infection.

**Antibody-mediated depletion.** For depletion of peripheral CD4<sup>+</sup> T cells, CD8<sup>+</sup> T cells, or NK cells, mice were treated i.p. twice over a 3-d interval with 250 µg anti-CD4 antibody (YTS191), 450 µg anti-CD8a depleting antibody (clone YTS169.4), or 500 µg anti-NK1.1 depleting antibody (clone PK136), respectively. Depletion of T cells or NK cells was confirmed by flow cytometry showing T cell or NK cell frequencies <0.1% during LCMVwt i.c. challenge. After antibody-mediated CD<sup>8</sup> T cell depletion and subsequent reconstitution by naive CD<sup>8</sup> T cells, frequencies of D<sup>∆</sup>NP<sub>396-404</sub>-specific CD8<sup>+</sup> T cells in rLCMV memory mice were reduced from 1.4 ± 0.3% to 0.06 ± 0.02%, which was not significantly above technical background in uninjected naive control mice (0.005 ± 0.004%).

**Intravascular staining of CD8<sup>+</sup> T cells.** Mice were injected i.v. with 3 µg PE-labeled anti-CD8b (YTS156.7.7) according to previously described protocols (Anderson et al., 2014). 3 min later, peripheral blood samples were taken, and mice were anesthetized and perfused with PBS. Brains were dissected and processed immediately (<10 min after antibody injection) for leukocyte isolation (see Flow cytometry).

**Immunohistochemistry.** For immunohistochemical bright field staining of mouse tissue, brains and spleen were prepared and fixed in Hepes-glutamic acid buffer-mediated organic solvent protection effect (HOPE, DCS Innovative) fixative as previously described (Bergthaler et al., 2007) and embedded in paraffin. Upon inactivation of endogenous peroxidases, tissue sections were incubated with rat anti-mouse CD8a (YTS169.4) or rat anti-LCMV NP (VL-4; Battegay et al., 1991). Bound primary antibodies were visualized with biotin-labeled anti-rat antibody and streptavidin-peroxidase staining method using polymerized 3,3′-diaminobenzidine (all reagents from Dako; haemalaun counterstaining of nuclei).

For immunofluorescence staining of mouse tissue, cryosections were fixed with 2% PFA for 5 min and unspecified binding blocking (PBS/1% BSA/2% FCS). Sections were incubated with FITC-labeled Armenian hamster anti–mouse CD103 (2E7) and rat anti–mouse CD8a (YTS169.4), followed by rabbit anti–FITC (Invitrogen) antibody. Bound antibodies were visualized with Alexa Fluor 488–labeled goat anti–rabbit and Cy3-labeled goat anti–rat secondary antibodies (Jackson ImmunoResearch Laboratories). Nuclei were stained with DAPI (Invitrogen).

For immunofluorescence staining of paraffin embedded tissue, mice were transcardially perfused with 4% PFA. After antigen retrieval and unspecified binding blocking (PBS/10% FCS), sections were incubated with rat anti–human CD3 (CD3-12), rat anti–mouse CD8 (clone 4S15), goat anti–mouse CD69 (AF2386), rabbit anti–VWF (ab6994), rabbit anti–Ki-67 (ab6155), and rabbit anti–phospho-Stat5 (tyr694, C71E5). Bound antibodies were visualized with Alexa Fluor 488 or Alexa Fluor 568 goat anti–rabbit tyramide signal (TSA) amplification (Thermo Fisher Scientific), Cy2- or Cy3-labeled goat-anti–rat, or Cy5-labeled goat anti–rabbit secondary antibodies (Jackson ImmunoResearch Laboratories). Nuclei were stained with DAPI (Invitrogen).

Immunostained sections were scanned using Panoramic Digital Slide Scanner 250 FLASH II (3DHISTECH) in 200× magnification. Quantifications were performed manually using Panoramic Viewer software (3DHISTECH) blinded to the experimental setup of histological samples. For representative images, white balance was adjusted and contrast was linearly enhanced using the tools levels, curves, brightness, and contrast in Photoshop CS6 (Adobe). For histocytometry analysis, fluorescence-immunostained brain sections were scanned using a high-dynamic range camera (16 bit).

For histocytometry and density plots, CD3<sup>+</sup> or CD8<sup>+</sup> cells, respectively, were detected on scanned slides applying a custom-programmed script in Cognition Network Language (Definiens Developer XD software). For analysis of distance, a grayscale distance map was computed to encode the closest distance of each detected CD3<sup>+</sup> or CD8<sup>+</sup> cell to the brain surface and vessels (detected by von-Willebrand Factor staining) and mean values of distance maps were extracted. For histocytometry, each CD3<sup>+</sup> cell size (area), as well as mean and max grayscale values for CD3, P-Stat5, and DAPI signals, were extracted. The resulting CSV files were converted to .fcs format using an open source program (FlowJo). The converted file was analyzed using FlowJo X. Co-staining of anti-CD3 and anti–phospho–Stat5 was gated based on control staining without primary P-Stat5 antibody.
Flow cytometry. For staining, the following antibodies were used: anti–Bcl-2 (BCL/10C4), anti–CD3ε (145–2C11), anti–CD8α (53–6.7), anti–CD11a (M17/4), anti–CD11b (M1/70), anti–CD44 (IM7), anti–CD45.1 (A20), anti–CD45.2 (104), anti–CD45R/B220 (RA3–6B2), anti–CD49a (HMα1), anti–CD49b (DX5), anti–CD49d (9C10), anti–CD69 (H1.2F3), anti–CD107α (2E7), anti–CD107a (1D4B), anti–CD127 (A7R34), anti–E–Cadherin (36/E–Cadherin), anti–FaSL (MFL3),–Granzyme B (GB11), anti–IFN-γ (XMG1.2), anti–IL–2 (JES6–5H4), anti–Integrinβ7 (FIB27), anti–Ki–67 (SolA15), anti–KLRG1 (2F1), anti–NK1.1 (PK136), and anti–TNF (MP6–XT22). For detection of virus–specific CD8+ T cells, D3–NP,996–904–tetramer (TCmetrix) or K1–B8R,20–27–tetramer (provided by D.H. Busch, Institute of Medical Microbiology, Immunology and Hygiene, Technical University Munich, Munich, Germany) were used.

Peripheral blood samples and splenocytes were collected in FACS–Buffer (10% FCS, 10 mM EDTA, and 0.01% NaN3 in PBS). Peripheral blood erythrocytes were lysed using BD FACS lysing solution (BD). For the preparation of brain leukocytes, mice were anesthetized and transcardially perfused with PBS. Brains were minced, digested with Collagenase/DNaseI (Roche), and homogenized using 70–µm cell strainers (BD). Leukocytes were separated using a discontinuous Percoll gradient (30%/70%). Surface staining was performed with directly labeled antibodies and tetramers in FACS buffer. Isolated CD8+ T cell numbers were quantified using BD FACS, while differences between single comparisons were assessed using Student’s t test was used, whereas differences between groups with multiple measurements, two–way repeated–measures ANOVA was performed followed by Dunnet’s multiple comparisons test against control group. For comparison of disease incidence, Log rank (Mantel–Cox) test was used. P < 0.05 was considered significant, and P < 0.01 was considered highly significant, whereas P > 0.05 was considered statistically not significant.

Online supplemental material. Fig. S1 shows the gating strategy used for analysis of brain–derived leukocytes. Fig. S2 shows the histocytometry data processing and the gating strategy. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20151916/D1.

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Statistical analysis. Analysis was performed using GraphPad 6.0 (Prism). To assess significant differences between single measurements of two groups, unpaired or paired two–tailed Student’s t test was used, whereas differences between single measurements of more than two groups was assessed by one–way ANOVA, followed by post hoc analyses of selected pairs of datasets using Sidak’s multiple comparisons test or all pairs of datasets using Tukey’s multiple comparisons test to control for multiple comparisons. To assess significant differences between groups with multiple measurements, two–way repeated–measures ANOVA was performed followed by Dunnet’s multiple comparisons test against control group. For comparison of disease incidence, Log rank (Mantel–Cox) test was used. P < 0.05 was considered significant, and P < 0.01 was considered highly significant, whereas P > 0.05 was considered statistically not significant.

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