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Characterization of the CD4⁺ T Cell Response to Mouse Polyomavirus Infection

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Abstract

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Virus-specific CD4⁺ T cells optimize anti-viral responses by providing help for anti-viral humoral responses and CD8⁺ T cells. However, little is known about the impact of low-level persistent infections on the fate and function of virus-specific CD4⁺ T cells. Using a mouse polyomavirus (MPyV) infection model, we identified two dominant CD4⁺ T cell populations specific for epitopes derived from the nonstructural LT antigen and VP1, the major viral capsid protein. These MPyV-specific CD4⁺ T cells vary in terms of their magnitude, functional profile, and phenotype during acute and persistent phases of infection. Employing a minimally myeloablative mixed bone marrow chimerism approach, we further show that naïve virus-specific CD4⁺ T cells are primed de novo during persistent virus infection.

After clearance of an acute viral infection, memory T cells develop that survive in the absence of antigen and can mount robust recall responses against challenge infection. During chronic high load infections, however, virus-specific CD8⁺ T cells become dependent on antigen for their survival. Whether T cells formed during low-level persistent infections require antigen for their survival is less clear. In this study, we developed a novel approach to ablate MPyV replication during persistent infection. We generated a recombinant MPyV in which genes critical for replication are floxed (A2.Flx). Cre-mediated deletion of A2.Flx leads to reductions in viral levels both in vitro and in mice expressing Cre constitutively. Utilizing mice expressing a tamoxifen-inducible Cre, we found that reduction of viral replication during persistent A2.Flx infection had a variable impact on virus-specific CD4⁺ and CD8⁺ T cells. While some MPyV-specific T cell populations were notably reduced, others were maintained but adopted a more central memory T cell phenotype. Our data suggests that antigen is not necessarily required for survival of MPyV-specific memory T cells and those cells can be redirected toward a phenotype associated with antigen-independent survival following reductions in viral antigen.

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Chapter 1: Introduction

I. Anti-viral immunity and CD4⁺ T cells

Viruses are one of the most prevalent threats faced by mammals. Consisting of either a DNA or RNA genome enclosed within a protein shell that may then be further surrounded by an additional outer lipid envelope, viruses are unable to replicate themselves but must exploit a cell's own DNA/RNA synthesis and protein production machinery to do so. The disruption of normal cell homeostasis and potential tissue destruction can lead to severe and debilitating disease. Thus, it is critical that mammalian hosts are able to defend themselves against this threat. Following initial detection of a viral invasion, the host immune response mounts a sophisticated multi-pronged assault with the objectives of limiting the extent of infection and then launching a counterattack to clear it. As with any combined arms assault, improper coordination and regulation of the immune response can have deleterious consequences for the host including immunopathology and failure to eliminate the targeted pathogen. CD4⁺ T cells play a key role in this command and control, closely interacting with cells of both innate and adaptive arms of immunity.

The innate immune system comprises the front line defense against infection. Dendritic cells (DCs) and macrophages express pattern recognition receptors (PRRs) such as toll-like receptors (TLRs) and retinoic acid-inducible gene I (RIG-I) like receptors (RLRs), which recognize invariant pathogen associated molecular patterns (PAMPs) and provide early warning of infection (1). Engagement of PRRs induces release of proinflammatory cytokines (e.g., IL-1 β) and type I interferons (IFN- α/β), which can induce anti-viral activity in cells at the site of infection and activate incoming natural killer (NK) cells (2, 3). At the same time, PRRs also induce maturation of DCs into antigen presenting cells (APCs) (4). DCs take up viral proteins exogenously by phagocytosis or receptor-mediated endocytosis and endogenously from the cytoplasm if infected themselves, process the proteins into peptides, and load peptides onto either Major Histocompatibility Complex (MHC) class I or MHC class II molecules. In addition, mature

DCs upregulate several surface costimulatory molecules and produce cytokines. They then migrate to secondary lymphoid organs such as the spleen and lymph nodes, where they encounter T cells. DCs are critical for initiation of the adaptive immune response.

The adaptive immune response arises a few days after the initial innate response. B cells and $\alpha\beta$ T cells mount responses that are highly specific for a wide variety of antigens. In addition, a major hallmark of adaptive immunity is the generation of memory B and T cells that are able to rapidly respond to reinfection. Both B and $\alpha\beta$ T cells reside in spleens and lymph nodes as inactive naïve precursors. Following recognition of their cognate antigens, both cell types undergo massive clonal expansion and differentiate into effector cells. B cells are activated after binding specific antigen, either soluble or presented by DCs, macrophages, and follicular dendritic cells (5), through their surface B cell receptor (BCR) and produce antibodies that can neutralize viruses and block infection of new cells. Activation of T cells, however, requires not only recognition of cognate peptide: MHC (pMHC) complexes on DCs by the T cell receptor (TCR) (pMHC I for $CD8^+$ T cells and pMHC II for $CD4^+$), but also a second signal provided through engagement of costimulatory molecules present on DCs (e.g., CD80, CD86) with receptors on T cells (e.g., CD28) (6). In addition, DC-produced cytokines like IL-12, IFN- α/β , and IL-1 provide a “signal 3”, which optimizes differentiation and survival (7). $CD8^+$ T cells differentiate into cytotoxic T lymphocytes (CTLs) that traffic to the periphery and secrete the cytotoxic contents of their lytic granules (e.g., perforin and granzyme) to kill infected cells expressing the cognate pMHC I complex or release cytokines like IFN- γ and TNF- α , which may act noncytolytically to control viral infection (8). $CD4^+$ T cells can also develop into direct effectors, killing or secreting anti-viral effector cytokines directed against infected MHC class II⁺ cells (9-12), but they play by far their most vital role in shaping and providing help to optimize the ongoing immune response.

The importance of CD4⁺ T cells for immune protection is vividly illustrated in individuals with acquired immunodeficiency syndrome (AIDS), who are severely deficient in CD4⁺ T cells and highly susceptible to opportunistic infections. CD4⁺ T cell “help” appears to be especially critical for sustaining function of anti-viral CD8⁺ T cells during chronic infections. For instance, CD8⁺ T cell function progressively deteriorates amidst declining levels of CD4⁺ T cells in HIV/SIV infections progressing to AIDS (13). In mouse models of chronic lymphocytic choriomeningitis virus (LCMV), CD4⁺ T cells are required for sustaining optimal anti-viral CD8⁺ T cell responses and eventual control of infection (14-16). CD4⁺ T cells are also critical for development and/or maintenance of memory CD8⁺ T cells arising after acutely resolved infections, endowing memory CD8⁺ T cells with the ability to mount robust recall responses (17). Furthermore, CD4⁺ T cell “help” for activated germinal center B cells (GC B cells) is required for them to differentiate into memory B cells and plasma cells that can produce affinity matured, class-switched antibodies (18). CD4⁺ T cell help may also be provided at peripheral sites of infection: in a mouse model of HSV infection, CD4⁺ T cells induce secretion of chemokines CXCL9 and CXCL10 required to recruit anti-viral CD8⁺ T cells to the local site of infection (vaginal mucosa) (19); influenza-specific memory CD4⁺ T cells induced production of innate inflammatory cytokines/chemokines in the lung of infected mice that aid early viral control (20).

What is CD4⁺ T cell help?

Help from CD4⁺ T cells is delivered through a multitude of potential surface molecules and secreted cytokines. Engagement of the costimulatory molecule CD154 (CD40L) on activated CD4⁺ T cells with its ligand CD40 plays a critical role in “licensing” (i.e. activating) DCs to prime naïve CD8⁺ T cells (21-23) and is required for formation as well as maintenance of germinal centers, where B cell proliferation and differentiation occur (24). The cytokine IL-2, which drives proliferation of T cells, is produced in abundance by activated CD4⁺ T cells and is critical for programming functional memory CD8⁺ T cells (25); a recent study, however, suggests

that primed CD8⁺ T cells are the source of their own IL-2 and that CD4⁺ T cell help is primarily provided via CD40L (26). CD4⁺ T cells are also the predominant producers of IL-21, which appears to be critical for maintaining the function of virus-specific CD8⁺ T cells and viral control during chronic LCMV infection (27-29). IL-21 also plays major roles in driving optimal GC B cell proliferation and plasma cell differentiation (30-32). Furthermore, the CD4⁺ T cell-produced cytokines impact the antibody isotype produced, which has functional consequences (33): in the mouse, IL-4 induces IgG1 and IgE, IFN- γ induces IgG2a, and IL-21 induces IgG1.

This is only a small survey of the possible mechanisms of CD4⁺ T cell help. One of the challenges for future investigations is to determine which mechanisms are critical and operative in a given scenario. This is often complicated by the fact that CD4⁺ T cells may not be the only expressers of some of these molecules; as mentioned above, CD8⁺ T cells can produce their own IL-2, and CD40L can be expressed by DCs, monocytes, NK cells, and B cells as well (24). An additional complication is that CD4⁺ T cells are phenotypically and functionally diverse, an aspect with implications for the overall immune response.

CD4⁺ T cells come in a variety of flavors...

Effector CD4⁺ T cells are highly heterogeneous and differentiate into lineages or subsets of helper T (T_H) cells distinguished by their effector cytokine profiles, surface molecules, and functions (34). T_H1 cells producing IFN- γ , TNF- α , and IL-2 are critical for control of intracellular infections such as those caused by viruses. T_H2 cells, which produce IL-4, IL-5, and IL-13, control extracellular parasites such as helminthes, while IL-17 producing T_H17 cells are required for defense against fungal infections. In addition, effector CD4⁺ T cells can differentiate into immunosuppressive inducible regulatory T cells (iTregs), which help control ongoing responses and prevent immunopathology. Recently, follicular helper T cells (T_{FH}) have emerged as the subset that provides help for B cells to generate long-lived antibody responses; these cells

predominantly produce IL-21 and IL-4 (some also IFN- γ and IL-17) and express surface molecules like CXCR5, PD-1, and SAP that are critical for their function and localization (33). The predominant subset induced can potentially impact the effectiveness of the anti-microbial immune response. For example, a hurdle to controlling respiratory syncytial virus (RSV) infection, especially after initial immunization with the formalin-inactivated RSV vaccine, is the tendency to generate a T_H2 response, which is marked by severe lung immunopathology associated with eosinophilia and fails to clear virus (35). Likewise, generation of iTregs could limit immune collateral damage (36), but it may also lead to suppression of a desired response. Thus, the regulation of T_H subset differentiation has been an area of intense interest ever since the initial descriptions of T_H1 and T_H2 in 1986 by Mosmann and Coffman (37).

T_H fate is determined by conditions encountered during priming, leading to the expression of “master regulator” transcription factors that, in conjunction with a network of accessory factors, impart distinct differentiation programs (34). For example, expression of T-bet commits a CD4⁺ T cell to a T_H1 phenotype but inhibits T_H2 differentiation, which requires GATA-3. Bcl-6, a transcriptional repressor, was shown to be the master regulator of T_{FH} cells and counteracts Blimp-1, which is expressed by other T_H subsets (T_H1, T_H2, T_H17) (33). The cytokine milieu is a predominant factor in differentiation of T_H cells (34). IL-12 and IFN- γ drive T_H1 differentiation in contrast to IL-4 and IL-2, which polarize cells toward a T_H2 phenotype. TGF- β in the presence of IL-2 induces iTregs but yields T_H17 cells instead when combined with the proinflammatory cytokine IL-6. TCR signaling strength, which is co-determined by affinity for antigen and antigen dose, also has an impact even without cytokines: weak TCR signals induce T_H2 cells while strong signals lead to T_H1 (38, 39) and T_{FH} differentiation (40). Costimulation is yet another regulator of T_H fate as shown by the acquisition of a T_{FH} phenotype (CXCR5^{hi}PD-1^{hi}Bcl-6^{hi}Blimp-1^{lo}) early after activation that required interaction with ICOSL on DCs (41).

Mounting evidence suggests that there is plasticity in T_H fate commitment (42). T_{FH} cells, for instance, can produce modest levels of IL-4, IFN- γ , and IL-17, which impact B cell class switching, typical of T_{H1} , T_{H2} , or T_{H17} cells while expressing a low level of T-bet/GATA-3/ROR γ t. This plasticity has led some to question defining T_{FH} as a separate lineage (33). LCMV-specific T_{H2} cells generated in vitro can be reprogrammed toward a mixed T_{H2+1} profile (GATA-3⁺T-bet⁺/IFN- γ ⁺IL-4⁺) when challenged in vivo with virus, a strong T_{H1} -polarizing regimen (43). T_{H1} memory cells expressing IL-4 following rechallenge under T_{H2} conditions has also been observed (44). The current debate about T_H stability versus plasticity depends on elucidation of the epigenetic mechanisms that dictate CD4⁺ T cell differentiation (42). Understanding CD4⁺ T cell differentiation will allow rationale design of vaccines and therapeutics to shape and manipulate ongoing immune responses for optimal effectiveness.

Why our understanding of virus-specific CD4⁺ T cell responses lags behind that of CD8⁺ T cells

Efforts to understand virus-specific CD4⁺ T cell responses have been hampered by technical hurdles, some of which may stem from intrinsic differences between CD4⁺ and CD8⁺ T cells (45). CD8⁺ T cells only require a short period of stimulation before proliferating and embarking on an autonomous differentiation program. CD4⁺ T cells require a more prolonged period of stimulation (46) but also appear to proliferate far less (47), which may contribute to the much smaller magnitude of response (10-100-fold < CD8⁺ T cells) often observed. It is perhaps not surprising then that a fairly limited range of CD4⁺ T cell-recognized epitopes have been identified. pMHC I tetramers have been useful tools in tracking antigen-specific CD8⁺ T cells, but pMHC II tetramers have proven to be more difficult to construct and use (48). Recent advances in MHC class II tetramer construction have allowed for the tracking of more antigen-specific CD4⁺ T cell populations immediately ex vivo (49).

In Chapter 2, I describe the identification of two MHC class II-restricted epitopes in mouse polyomavirus, a model of low-level persistent infection, recognized by CD4⁺ T cells in C57BL/6 mice. Utilizing MHC class II tetramers complexed to these peptides and intracellular cytokine assays, we were able to follow the evolution of the CD4⁺ T cell response both phenotypically and functionally. Most importantly, we were able to begin to investigate the mechanisms that regulate and maintain virus-specific CD4⁺ T cell populations in the face of persistent antigen.

II. Persistent infection impacts T cell memory and function

Following activation by viral antigen, CD4⁺ and CD8⁺ T cells undergo expansion and differentiation into effectors that control infection through multiple mechanisms. Recently, the quality of the T cell response, a reference to the breadth of effector functions displayed, has been found to correlate with effective control of infection (50). Development of polyfunctional CD8⁺ and CD4⁺ T cells is seen in acutely resolving infections in which virus is completely cleared, such as in vaccinia (smallpox vaccine) (51) and yellow fever virus vaccinated humans (52) and in mice infected with influenza (53) and acutely infecting strains of LCMV (14, 54). After clearance, most effector T cells die and the survivors develop into long-lived memory T cells that can respond rapidly to antigen reencounter (55, 56). However, some viruses have developed mechanisms of immune evasion (57) or actively mitigate anti-viral host immune responses. Failure by the immune system to clear pockets of viral resistance leads to stalemate and persistence of the virus at some level. The situation of continual virus antigen exposure inherent in persistent infection has profound consequences for the fate of responding T cells and their development into long-term protective memory cells (58).

Although polyfunctional T cells initially emerge during persistent infections, they can progressively lose functionality as antigen load and duration of antigen exposure increase. This process is termed exhaustion (58). Exhaustion has been demonstrated in virus-specific CD8⁺ T cells during high load chronic LCMV infection of mice (e.g. DOCILE (59) and strain clone 13),

where effector functions are lost in a hierarchical manner starting with IL-2 production, proliferation, and cytolytic function, then TNF- α production, and finally loss of IFN- γ prior to possible physical deletion (16, 54). Functional impairment is also seen for human anti-viral CD8⁺ T cells in chronic HCV and HIV (58). CD4⁺ T cells too appear to suffer exhaustion during the course of chronic high load infections. In HIV progressors, virus-specific CD4⁺ T cells continue to produce IFN- γ but not IL-2 and do not proliferate (60). Early in infection of mice with the clone 13 strain of LCMV (day 9 post-infection), virus-specific CD4⁺ T cells produce diminished IL-2 and TNF- α compared to their counterparts at the same time point in acute Armstrong strain infected mice (61). The diminished amount of CD4⁺ T cell help may exacerbate CD8⁺ T cell exhaustion (58). However, CD4⁺ T cells appear to be more plastic and heterogeneous than CD8⁺ T cells, and they may respond differently to chronic antigen. Recent reports indicate that virus-specific CD4⁺ T cells during chronic LCMV switch to production of IL-21, which is critical for sustaining CD8⁺ T cells and B cells (27-29), and increasingly acquire a CXCR5⁺ICOS^{hi}Bcl-6^{hi} T_{FH} phenotype (62).

The loss of function by exhausted T cells is accompanied by the sustained expression of inhibitory receptors such as PD-1 (63-66), CTLA-4 (67), LAG-3 (68), and Tim-3 (69); the level of individual receptors and co-expression of multiple receptors correlates with more severe impairment and higher antigen loads (68). Blockade of these inhibitory receptors, either alone or in combination with PD-1 blockade, leads to a restoration of virus-specific CD8⁺ and CD4⁺ T cell functions in chronic LCMV (63, 68) and HIV (64, 65, 67) infections, demonstrating that exhaustion is a reversible state. In contrast to high load infections, during low-level persistent viral infections such as with CMV (mouse and human) (9, 70, 71), polyomaviruses (*vide infra*) (72), and HIV long-term nonprogressors (LTNP) (73), CD4⁺ and CD8⁺ T cells maintain polyfunctionality and may exhibit few obvious signs of dysfunction/exhaustion (74, 75).

In addition to negatively impacting T cell function, persistent viral infections also alter the development and maintenance of T cell memory (58). Memory CD4⁺ and CD8⁺ T cells that develop after resolution of acute infections (“acute memory T cells”) are largely stably maintained long-term and appear not to need antigen to survive (55, 56); instead, survival and self-renewal is driven by the homeostatic cytokines IL-7 and IL-15. In contrast, during chronic viral infection, CD8⁺ T cells that survive into persistence (“chronic memory T cells”) become dependent on antigen (i.e. “antigen addicted”) for their maintenance (58). Virus-specific memory CD8⁺ T cells from mice persistently infected with LCMV clone 13 undergo extensive antigen-driven proliferation when transferred into infection-matched mice but not mice chronically infected with a variant lacking their cognate T cell epitope or when transferred into naïve mice (76, 77); these cells exhibit defects in homeostatic proliferation to IL-7 and IL-15 as a result of lower CD127 and CD122 expression (77).

The continued presence of viral antigen could also drive maintenance of memory T cell pools in another way. Mouse polyomavirus (MPyV)-specific CD8⁺ T cells are defective in self-renewal even in the presence of antigen, yet population levels are stably maintained (78). By generating partial bone marrow chimerism in persistently infected mice, Vezys et al. and Kemball et al. demonstrated priming of donor-derived MPyV-specific CD8⁺ T cells (72, 78). Thus, persistent antigen-driven priming of naïve T cells may replenish a continuously deteriorating pool of memory T cells. But how much does *de novo* recruitment of T cells contribute to “chronic memory”? Thymectomy experiments showed a modest reduction of MPyV-specific CD8⁺ T cells (78) but only a transient impact on chronic LCMV-specific CD8⁺ T cell levels (79), indicating *de novo* priming is not required for maintenance. In addition, using an elegant reporter mouse model where granzyme B-expressing effector CD8⁺ T cells are indelibly marked by YFP, Bannard et al. showed that virus-specific CD8⁺ T cells primed during initial infection persisted and continue to proliferate during the latent phase of infection by a mouse γ -herpesvirus (80). More than likely,

maintenance of virus-specific CD8⁺ T cells during persistent infections involves a combination of de novo recruitment of naïve T cells and some antigen-drive self-renewal of existing memory T cells, as suggested by a recent study from Ann Hill's group analyzing epitope-specific memory CD8⁺ T cell inflation in mouse CMV (81).

Memory T cells are heterogeneous in terms of their survival, recall proliferation, functions exhibited, and tissue localization, where local cues may differentially impact memory T cells (82). Based on expression of lymph node homing receptors CD62L and CCR7, memory T cells were originally divided into CD62L^{lo}CCR7^{lo} effector memory (T_{EM}) cells residing primarily in nonlymphoid tissues and spleen or CD62L^{hi}CCR7^{hi} central memory (T_{CM}) cells found mostly in spleen and lymph nodes (83). Although the initial study suggested that T_{EM} expressed immediate effector function, subsequent comparisons of both CD4⁺ and CD8⁺ T_{EM} and T_{CM} demonstrated an equal capacity to display effector functions (IFN- γ , TNF- α , cytotoxicity) after challenge (84, 85); instead, the key differences were in the degree of proliferation and IL-2 production by T_{CM} (83, 85). Studies comparing the protective capacity of virus-specific CD8⁺ T_{EM} and T_{CM} suggested that the larger proliferative burst post-challenge of T_{CM} ultimately makes them more protective on a per-cell basis (85). T_{CM} cells also have the advantage of being longer lived than T_{EM} cells as a result of increased homeostatic turnover in response to IL-7 and IL-15 (55). Indeed, in the case of acutely resolving infections, there appears to be a slow shift toward a largely T_{CM} phenotype perhaps involving conversion of some T_{EM} cells into T_{CM} (55). On the other hand, repetitive antigen stimulation, by either repeated infection or repeated DC immunization, progressively drives memory CD4⁺ and CD8⁺ T cells toward a more T_{EM} phenotype (86, 87). Not surprisingly then, far more T_{EM} than T_{CM} cells have been observed in chronic viral infections (55), consistent with the poor response to IL-7 and IL-15 displayed by “chronic memory” T cells.

The environment of persistent infection is dynamic. Changes in epitope availability and inflammation shape the functional and phenotypic diversity of antigen-specific T cells. In several models of acutely cleared antigen, latecomer CD4⁺ and CD8⁺ T cells primed to low levels of residual cognate antigen (and presumably inflammation) underwent intermediate differentiation and developed into CD62L^{hi} T_{CM}-like memory T cells (88-90). Consistent with this, higher frequencies of virus-specific CD8⁺ T cells recruited de novo during low-level persistent mouse polyomavirus infection are CD27^{hi}CD62L^{hi}, characteristics associated with T_{CM}, the later they are primed; a gradual increase in the proportion of CD27^{hi}CD62L^{hi} cells within the bulk virus-specific CD8⁺ T cell population over time was also observed (78). It remains to be seen whether these late generated antigen-specific CD8⁺ T cells truly behave like “acute memory” T cells.

We are beginning to better understand the behavior and fate of T cells during persistent viral infections. Much of the work has involved models of chronic high load viral infections, exemplified by chronic LCMV, and has provided insights into T cell exhaustion and its molecular regulation. These findings have profound implications for development of effective therapies to combat rapidly disseminating and replicating chronic viral infections in humans like HIV, HCV, and HBV, which cause severe disease and are associated with high morbidity. However, the majority of persisting viruses are clinically silent, primarily causing disease in immunocompromised individuals (57). The continuing scourge of AIDS worldwide along with the increasing effectiveness of immunosuppressive drugs given to transplant/transfusion recipients and sufferers of autoimmune diseases such as multiple sclerosis will assure that we may see ever-increasing incidents of active disease from these pathogens. Thus, it is imperative that we understand how T cells control low-level persistent viral infections under normal circumstances of an intact immune system. The critical role played by CD8⁺ T cells in eliminating viruses, their much larger numbers, and the maturity of the tools to study antigen-specific CD8⁺ T cells ex vivo have made them the focus of many investigations. As their help is

critical for optimal immune responses, it will be important to understand how virus-specific CD4⁺ T cells are impacted by and cope with low-level persistent viral infections. Improvements in development of reagents to study antigen-specific CD4⁺ T cells should make this ever more feasible. While it appears that virus-specific CD4⁺ T cells responding to low-level persistent infections are not functionally exhausted, a critical question is how persistent antigen impacts CD4⁺ T cell differentiation. It also remains to be determined if “chronic memory” CD4⁺ T cell populations are maintained by the same mechanisms CD8⁺ T cells are, namely antigen-driven self-renewal and/or de novo priming. Above all, although T cells with a T_{CM} phenotype can develop and survive despite continual antigen in low-level persistent viral infections, there remains the issue of whether or not these cells are truly like bona-fide memory T cells we see after resolution of acute infections; that is, will they survive if their antigen were removed?

III. Polyomavirus pathogenesis

Polyomaviridae are a family of ubiquitous DNA viruses found in a wide variety of animal species. The founding member of the family was discovered in 1953 when Polish-American physician-scientist Ludwik Gross (1904-1999) discovered that a filterable agent in cell free extracts from leukemic mice induced a constellation of solid tissue tumors in infected neonatal mice (91). Dubbed polyomavirus, mouse polyomavirus (MPyV) was one of the earliest demonstrated links between viruses and cancer. A few years later, a second polyomavirus was discovered in rhesus monkey kidney cells, simian virus 40 (SV40) (92). In 1971, two human polyomaviruses (HuPyV), BKV and JCV, were isolated. BKV was recovered from the urine of a kidney transplant recipient suffering from renal failure, and JCV was isolated from the brain of a patient with progressive multifocal leukoencephalopathy (93, 94). More recently, modern molecular biology screening technology has led to the identification of three new HuPyVs (95-97), including one associated

with Merkel cell carcinomas (MCV), rare but highly aggressive skin cancers. Initial HuPyV infection appears to occur during childhood/early adolescence and persists lifelong. 72-98% of the adult human population is seropositive for JCV and BKV (98); a recent study suggests that seropositivity for the new human polyomaviruses (WUPyV, KIPyV, and MCPyV) in adults is as high as about 50% (99). Although polyomavirus infections are typically subclinical and asymptomatic, they are associated with diseases in immunocompromised individuals. “Reactivation” of BKV in kidney transplant recipients leads to hemorrhagic cystitis and polyomavirus-associated nephropathy (PVAN) then graft rejection (100). Neurotropic JCV is the etiologic agent of progressive multifocal leukoencephalopathy, a typically fatal demyelinating disease with symptoms similar to multiple sclerosis (MS), seen in about 5% of AIDS patients as well as in some individuals taking Natalizumab (anti-VLA-4) or Efalizumab (anti-LFA-1), which inhibit T cell priming and/or trafficking into peripheral tissues, to treat autoimmune diseases such as multiple sclerosis and Crohn’s disease (101). Unfortunately, little is known regarding the mechanisms of pathogenesis and immune control of polyomaviruses. Given the difficulties associated with studying infections in humans and the stringent species specificity of polyomaviruses (98), models utilizing the originally discovered MPyV offers a system to study pathogenesis by this family of viruses in a natural host (102).

MPyV is a nonenveloped virus comprised of a 45 nm icosahedral capsid composed of 3 viral capsid proteins (VP1-3) with VP1 forming the outer capsid; binding of VP1 to cell surface sialic acid enables the virus to potentially infect a variety of host cell types. The virus’ ~5 kb double-stranded DNA plasmid genome encodes 6 genes in two transcripts that are alternatively spliced to generate three mature mRNAs each: the nonstructural small, middle, and large T-antigens, which are expressed in all infected cells, and the 3 capsid proteins expressed only in productively infected cells. Due to its relative simplicity, the MPyV genome is highly amenable to genetic manipulations such as mutagenesis and insertion of new sequences, which we have

taken advantage of to generate recombinant MPyVs encoding epitope tags or model T cell epitopes recognized by TCR transgenic cells (103, 104). Although cytopathic, MPyV establishes a lifelong, silent persistent infection in immunocompetent laboratory mice and is ubiquitous in feral mice (105).

No evidence exists that MPyV is capable of entering a state of latency like herpesviruses do, although some in the literature use the term “reactivating” to denote apparent bursts in viral replication. Instead, MPyV leads to a “smoldering” persistent infection, where viral replication is continuous but below the limit of detection for most viral titer assays. Infectious virus can be readily detected in the urine, saliva, and feces of carrier mice. In addition, the MPyV genome, being an example of packing maximal information into minimal space, does not encode immune evasion genes. Therefore, MPyV is an ideal model for studying the impact of low load persistent viral antigen on generation of an effective immune response.

IV. Adaptive Immunity to mouse polyomavirus

MPyV can cause diverse tumors in some inbred strains of mice when inoculated as newborns as well as immunocompromised mice. $\beta 2m^{-/-}$ mice, which lack functioning CD8⁺ T cells, but not MHC class II^{-/-} mice, which lack CD4⁺ T cells, infected with MPyV are highly susceptible to virus-induced tumors (106, 107). Furthermore, H-2^k mice expressing an endogenous mouse mammary tumor virus (MMTV) superantigen are devoid of T cells expressing the V β 6 and V β 8.1 TCRs including most of the MPyV-specific CD8⁺ T cells, and thus they too are impaired in protection against virus-induced tumors (108). Infection also induces early T-independent as well as later T-dependent production of neutralizing IgG directed against the VP1 major capsid protein (102). However, although antibody may play a critical role in limiting the spread of infection and reducing viral load, the B cell response by itself is insufficient to combat

development of tumors (102). Therefore, virus-specific CD8⁺ T cells are required for effective control of MPyV and resistance to virus-induced disease. Not surprisingly, CD8⁺ T cell responses during MPyV infection have been the focus of our previous studies.

MPyV-tumor resistant C57BL/6 (B6, H-2^b) mice mount a non-coordinately regulated classical MHC class Ia-restricted virus-specific CD8⁺ T cell response directed against epitopes in the nonstructural large and middle T antigens (MT and LT) (72). The epitope-specific CD8⁺ T cell populations displayed notable heterogeneity in magnitude, kinetics of expansion and contraction during acute infection, activation/differentiation phenotype, effector cytokine profile, and functional avidity maturation during persistent infection. Despite these differences, they retained polyfunctionality and did not become exhausted. Furthermore, the expansion and contraction of MPyV-specific CD8⁺ T cells closely parallels the changes in viral replication, with MPyV-specific CD8⁺ T cell populations being stably maintained despite virus persistence. It was previously suggested that persistent antigen is the driving factor behind self-renewal and survival of virus-specific CD8⁺ T cell memory during chronic viral infection (76, 77). However, MPyV-specific CD8⁺ T cells from persistently infected mice exhibit minimal proliferation and survived poorly when transferred into infection-matched recipients (78). Hypothesizing that persistent antigen was instead driving recruitment of new naïve antigen-specific T cells, Lukacher and colleagues developed a novel minimally myeloablative mixed bone marrow chimera approach to demonstrate that de novo priming of virus-specific CD8⁺ T cells occurs during persistent MPyV infection. The critical role of continued recent thymic emigrant priming in MPyV-specific CD8⁺ memory was further emphasized by a modest but statistically significant drop in number of virus-specific cells in thymectomized mice versus shams. “Late-primed” antigen-specific CD8⁺ T cells displayed a CD62L^{hi}CD27^{hi} central memory phenotype that contrasts with the effector/effector-memory CD62L^{lo} phenotype of the bulk population, further demonstrating the impact the level of antigen and inflammation has on T cell differentiation (78). Interestingly, MPyV-infected mice

lacking classical MHC class Ia molecules ($K^{b/-}D^{b/-}$) can control virus and resist virus-induced tumors. Swanson et al. identified a virus specific $CD8^+$ T cell population specific for an epitope in the minor capsid protein VP2 presented on Q9, a non-classical MHC class Ib molecule (109). These virus-specific $CD8^+$ T cells appear to be partially dysfunctional though they have a phenotype consistent with recall-competent memory T cells. They also share a kinetic profile similar to inflationary epitope-specific $CD8^+$ T cells in persistent MCMV infection (70) but can survive despite persistent antigen, which is required for their expansion but not maintenance (110). Capsid protein-specific $CD8^+$ T cells could help keep persistent virus in check, providing critical backup should the more immunodominant T-antigen specific MHC-Ia-restricted $CD8^+$ T cells drive selection of viral epitope escape mutants (109). Altogether, MPyV-specific $CD8^+$ T cells provide multi-faceted and highly flexible protection.

Given the critical role played by $CD4^+$ T cell help for optimal $CD8^+$ T cell and B cell responses (17, 18), Kemball et al. asked what role $CD4^+$ T cells might play in a low-level systemic persistent infection such as ours using MHC class II-deficient mice, which lack $CD4^+$ T cells (107). Similar to acute resolved infections, the primary MPyV-specific $CD8^+$ T cell response was unimpaired in $CD4^+$ T cell-deficient $I-A^{b/-}$ mice but was marked by a significant decline in virus-specific $CD8^+$ T cell populations during the transition to persistent infection compared to wildtype B6 control mice. However, unlike in $CD4^+$ T cell-deficient mice chronically infected with LCMV (14, 16), the surviving MPyV-specific $CD8^+$ T cells were not functionally exhausted. Bone marrow experiments demonstrated that de novo recruitment of MPyV-specific $CD8^+$ T cells was defective in persistently infected $CD4$ -deficient mice. In addition to diminished virus-specific $CD8^+$ T cell levels, significantly lower titers of anti-viral IgG and few antibody-secreting plasma cells in bone marrow were detected in persistently infected MHC class II-deficient mice compared to controls (107). $CD4^+$ T cell help is also critical for both the expansion and maintenance of MHC class Ib-restricted MPyV-specific $CD8^+$ T cells (A.R. Hofstetter, manuscript in preparation). These findings suggest then that MPyV induces a functionally

competent and vital virus-specific CD4⁺ T cell response. However, little has been done so far to identify CD4⁺ T cell epitopes in MPyV, and the tools to track endogenous antigen-specific CD4⁺ T cells *ex vivo* have been lacking until recently. In Chapter 2, I will describe my efforts to identify MHC class II-restricted MPyV epitopes in B6 mice (I-A^b) and to follow the evolution of the virus-specific CD4⁺ T cell response over the course of persistent infection. As CD4⁺ T cells can differentiate into multiple T_H subsets, which can impact the immune response to a given type of pathogen, a key question is what the functional profile of MPyV-specific CD4⁺ T cells, including effector cytokines produced, is and whether it differs during persistent and acute phases of infection (i.e. is it plastic?). I also asked if virus-specific CD4⁺ T cells are stably maintained in the face of persistent MPyV, and if so, whether this is achieved in part by *de novo* recruitment of naïve CD4⁺ T cells.

Another outstanding and unresolved issue in systemic low-level persistent infection with MPyV concerns the role of persistent viral antigen on differentiation and maintenance of virus-specific memory-like T cell pools. Our previous studies suggest a “conveyor belt” scenario, where continual *de novo* recruitment of naïve antigen-specific CD8⁺ T cells is required to replenish a deteriorating pool of virus-specific T cells, but as viral load/inflammation wanes, recently primed cells could acquire a more antigen-independent self-renewing central memory phenotype and assume a larger role in sustaining virus-specific T cell memory (102). However, thymectomy experiments (78) and the persistence of a residual anti-viral CD8⁺ T cell population in CD4⁺ T cell-deficient mice, in which *de novo* recruitment is impaired (107), indicate other mechanisms perhaps including chronic antigen stimulation also contribute to maintenance of “chronic memory” to MPyV.

To answer the question of whether MPyV antigen-independent memory T cells can emerge or if some require chronic antigen stimulation, we need to develop a system in which virus antigen does not persist. Most studies of virus-specific T cells during persistent infection attempt to compare them with those responding to acutely cleared strains. The LCMV mouse

model has benefitted from the availability of both acute and persistent strains, exemplified by the Armstrong (acute) and the clone 13 (chronic) strains. These differ only by two amino acids yet retain the same T cell epitopes (54). Thus, one can transfer virus-specific T cells from persistently infected mice into recipients infected with the acute strain and observe their fates. As acute strains of MPyV have not been identified, this cannot be done with MPyV-specific T cells. In addition, there are no effective direct anti-virals against MPyV, which precludes artificially reducing pathogen loads and observing the reaction of existent anti-microbial T cells. The Cre/lox system has been a useful tool to inducibly delete genes, whose outright deletion would otherwise be embryonically lethal (111). In this system, two 34 bp loxP sequences are inserted in the same orientation flanking the gene of interest; Cre recombinase, which recognizes these sites, deletes the intervening region. Making use of MPyV's ease of genetic manipulation, two loxP sites were inserted flanking the T-antigen genes, which are required for viral replication and persistence (112). Cre-mediated deletion is predicted to terminate viral replication and remove a source of MPyV antigen. In Chapter 3, I will cover the effort to generate and validate this floxed MPyV before unveiling some of our initial findings about what happens to MPyV-specific T cell populations, both CD4⁺ and CD8⁺, when we remove viral antigen during persistent infection.

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Chapter 2

Heterogeneity among viral antigen-specific CD4⁺ T cells and their de novo recruitment during persistent polyomavirus infection

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Heterogeneity among viral antigen-specific CD4⁺ T cells and their de novo recruitment during
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Abstract

Virus-specific CD4⁺ T cells optimize anti-viral responses by providing help for anti-viral humoral responses and CD8⁺ T cell differentiation. Although CD4⁺ T cell responses to viral infections that undergo complete clearance have been studied extensively, less is known about virus-specific CD4⁺ T cell responses to viruses that persistently infect their hosts. Using a mouse polyomavirus (MPyV) infection model, we previously demonstrated that CD4⁺ T cells are essential for recruiting naïve MPyV-specific CD8⁺ T cells in persistently infected mice. In this study, we defined two dominant MPyV-specific CD4⁺ T cell populations, one directed toward an epitope derived from the nonstructural large T antigen and the other from the major viral capsid protein of MPyV. These MPyV-specific CD4⁺ T cells vary in terms of their magnitude, functional profile, and phenotype during acute and persistent phases of infection. Using a minimally myeloablative mixed bone marrow chimerism approach, we further show that naïve virus-specific CD4⁺ T cells, like anti-MPyV CD8⁺ T cells, are primed de novo during persistent virus infection. In summary, these findings reveal quantitative and qualitative differences in the CD4⁺ T cell response to a persistent virus infection and demonstrate that naïve antiviral CD4⁺ T cells are recruited during chronic polyomavirus infection.

Introduction

CD4⁺ T cells shape and regulate host immune responses to microbial pathogens (1). Virus-specific CD4⁺ T cells drive B cell differentiation to memory B cells and plasma cells bearing isotype-switched, affinity matured antibodies (2, 3). A sizeable body of literature documents the critical contribution of CD4⁺ T cell help for generating memory CD8⁺ T cells capable of mounting strong anamnestic responses (4). CD4⁺ T cells may also elaborate antiviral cytokines (5-7) or directly kill infected MHC class II-expressing cells (8-10). In the setting of acute viral infections that are completely resolved, virus-specific CD4⁺ T cells, like their antiviral CD8⁺ T cell counterparts, give rise to phenotypically and functionally heterogeneous memory T cells that are maintained by Ag-independent self-renewal and are capable of robust recall responses to challenge infection (1, 11, 12).

In the face of high-level persistent virus infection, however, CD4⁺ T cells are handicapped in their effector activities. In viremic individuals, HIV-specific CD4⁺ T cells fail to proliferate or produce IL-2 (13) but upregulate inhibitory receptors that mitigate their functional integrity (14, 15). Using the lymphocytic choriomeningitis virus (LCMV) clone 13 chronic infection mouse model, Brooks et al. recently showed that virus-specific CD4⁺ T cells acquire functional defects early in the course of infection (16). In contrast, antiviral CD4⁺ T cells maintained in the setting of low-level persistent virus infections (e.g., human and mouse CMV and EBV) generally retain their functionality (17-20).

Maintenance of memory virus-specific CD8⁺ T cells in persistent infection, as in acute infection, depends on a functional virus-specific CD4⁺ T cell response, which is affected by the magnitude and duration of infection, and likely, cell types harboring the infection. For LCMV clone 13 infection, functional deterioration and deletion of virus-specific CD8⁺ T cells are exacerbated by the absence of CD4⁺ T cells, with recovery of CD8⁺ T cell numbers and function

associated with resolution of viremia (21-23). For low-level persistent infections, CD4⁺ T cell deficiency likewise dramatically affects the size of the memory antiviral CD8⁺ T cell compartment. Maintenance of stable virus-specific CD8⁺ T cell numbers during persistent viral infection depends on extensive proliferation of memory CD8⁺ T cells and/or de novo priming of naïve virus-specific CD8⁺ T cells (24-26). For persistent mouse polyomavirus (MPyV) infection, virus-specific CD8⁺ T cells fail to divide and suffer rapid attrition, putting the onus for their maintenance on naïve Ag-specific CD8⁺ T cell recruitment (25, 27). Moreover, we recently demonstrated that CD4⁺ T cell help is required for recruitment of naïve antiviral CD8⁺ T cells during persistent MPyV infection (28). Whether MPyV-specific CD4⁺ T cells conserve their effector activities, are stably maintained, and are resupplied via naïve CD4⁺ T cell recruitment during persistent infection are not known.

Efforts to characterize CD4⁺ T cells in persistent infections have been hampered by the small numbers of defined epitopes, the low magnitude of their response, and until recently, few reagents to track Ag-specific populations compared to CD8⁺ T cells. To assess the evolution of the antiviral CD4⁺ T cell response through acute and persistent phases of MPyV infection, we have identified two MPyV-specific CD4⁺ T cell populations in B6 mice, one directed toward an epitope derived from the nonstructural large T (LT) antigen and the other from the major viral capsid protein of MPyV (VP1). These epitope-specific CD4⁺ T cells differ in magnitude, phenotype, functional profile, and TCR repertoire. However, CD4⁺ T cells of both specificities are stably maintained during persistent infection despite exhibiting minimal proliferation. We show in this study that naïve progenitors of each specificity are primed de novo in persistently infected mice. These findings highlight the heterogeneity of the CD4⁺ T cell response during this low-level systemic persistent viral infection and suggest that virus-specific CD4⁺ T cell populations are maintained long-term by recruitment of naïve virus-specific T cells.

Materials and Methods

Mice

C57BL/6NCr (B6) and B6/CD45.1 female mice were purchased from the Frederick Cancer Research and Development Center of the National Cancer Institute (Frederick, MD). Mice were housed and bred in accordance with the guidelines from the Institutional Animal Care and Use Committee and the Department of Animal Resources of Emory University (Atlanta, GA).

MPyV preparation and inoculation

MPyV strain A2 was molecularly cloned and plaque purified, and virus stocks were prepared on primary baby mouse kidney cells as described previously (29). Each mouse received 2×10^6 PFU of virus s.c. Mice were inoculated at 6-12 weeks of age.

Cell isolation and flow cytometry

Spleens were digested in a solution of 125 U/mL collagenase type XI, 60 U/mL hyaluronidase type I-s, and 60 U/mL of Dnase I in RPMI supplemented with 5% FCS plus Ca^{2+} and Mg^{2+} for 1 h at 37°C, then passed through cell strainers followed by RBC lysis.

Allophycocyanin-conjugated I-A^b/LT₆₇₈₋₆₉₀ and I-A^b/VP1₂₂₁₋₂₃₅ tetramers were constructed by the National Institutes of Health Tetramer Core Facility at Emory University (Atlanta, GA). Tetramer staining was performed at 37°C for 1.5 h in RPMI 1640 containing 2% FCS at a concentration of 8 µg/mL per 1×10^6 cells followed by surface staining for CD4, CD44, and other indicated surface markers at 4°C for 30 min. In some experiments, cells were stained with 7-aminoactinomycin D (7-AAD, BD Pharmingen, San Diego, CA) per manufacturer's

instructions. For CTLA-4, Bcl-2, Ki-67, and TCR V β , cells were permeabilized with Cytotfix/Cytoperm buffer (BD Pharmingen) after I-A^b tetramer and surface staining then stained intracellularly for the indicated marker. For Annexin V staining, I-A^b tetramer and surface marker-stained cells were stained with FITC Annexin V (BD Pharmingen) followed by 7-AAD.

The following mAbs were purchased from BD Pharmingen: FITC-conjugated anti-CD44 and anti-Ki-67; allophycocyanin-conjugated anti-IFN- γ ; PE-conjugated anti-CD62L, Bcl-2, IL-2, TNF- α (TN3-19.12), IL-10, IL-17, IL-4; V450-conjugated anti-CD44; and isotype controls; Pacific Blue-conjugated anti-CD4 (RM4-5). PerCP-Cy5.5-conjugated mAb to CD45.1 and CD4 (RM4-5), PE-conjugated mAb to CD27 (LG.7F9), CD127 (A7R34), programmed death 1 (PD-1) (RMP1-30), LAG-3, TIM-3 (RMT3-23), CD154, CTLA-4, ICOS (7E.17G9), OX-40, CD28, and isotype controls were purchased from eBioscience (San Diego, CA). Samples were acquired either on a FACSCalibur or LSR-II (both from BD Biosciences, San Jose, CA). Data were analyzed using FloJo software (Treestar, Inc., Ashland, OR).

BrdU incorporation assay

MPyV-infected B6 mice were administered 1 mg of BrdU (Sigma-Aldrich, St. Louis, MO) i.p. once daily for 7 days. On the day after the last injection of BrdU, mice were sacrificed, and splenocytes were stained with I-A^b/LT₆₇₈ or I-A^b/VP1₂₂₁ tetramers followed by surface staining for CD4 and CD44. BrdU incorporation was then assessed using the FITC BrdU flow kit (BD Biosciences) per manufacturer's instructions.

Intracellular cytokine staining

Cells were stimulated with peptide (10-50 μ M) for 5.5 h in the presence of GolgiPlug (brefeldin A; BD Pharmingen) or GolgiStop (monensin; BD Pharmingen), then surface stained with PerCP-Cy5.5-conjugated anti-CD4 (RM4-5). After washing, cells were permeabilized with Cytotfix/Cytoperm buffer (BD Pharmingen) and stained for intracellular IFN- γ and CD154. For multi-cytokine analysis, cells were stained intracellularly with anti-IFN- γ and PE-conjugated antibodies to IL-2, TNF- α , IL-10, IL-17, or IL-4. Intracellular staining for IL-21 was performed as described by Suto et al. (30).

In vivo programmed death ligand 1 blockade

B6 mice persistently infected by MPyV (35-50 days postinfection [p.i.]) received 200 μ g of rat anti-mouse programmed death ligand 1 (PD-L1) antibody (10F.9G2) or rat IgG control i.p. every 3 days over 2 weeks.

Quantification of MPyV genomes

DNA isolation and TaqMan PCR were performed as described previously (27). MPyV DNA quantity is expressed in genome copies per milligram of tissue and is calculated based on a standard curve of known MPyV genome copy number versus threshold cycle of detection. The detection limit with this assay is 10 copies of genomic viral DNA.

Generation of CD45 congenic bone marrow chimeras

A minimal myeloablation and bone marrow transplantation protocol was performed as previously described, with the following modifications (25, 27). Naïve or persistently MPyV-infected B6

mice were given 600 μg busulfan i.p. (Busulfex; Otsuka America Pharmaceutical, Rockville, MD). 24 h later, these mice received 20×10^6 nucleated cells i.v. from the bone marrow of naïve B6/CD45.1 mice. Establishment of chimerism was confirmed by flow cytometric analysis of whole blood cells for CD45.1 expression (data not shown). We have previously shown that the minimally myeloablative dose of busulfan that we use (25 mg/kg) does not impact the number of MPyV genomes per mg tissue (27). Spleens of chimeric mice were analyzed by flow cytometry > 90 days after bone marrow transplantation.

IFN- γ ELISPOT assay

The single-cell ELISPOT assay was performed as described previously (27).

Statistics

Statistical significance was determined by a two-tailed nonparametric Mann-Whitney *U* test using Prism software (GraphPad Software, La Jolla, CA). A *p*-value < 0.05 was considered statistically significant.

Results

Identification of MPyV-specific CD4⁺ T cell epitopes

As a first step to empirically map MPyV-specific CD4⁺ T cell epitopes, we used IFN- γ ELISPOT assays to screen overlapping synthetic peptides covering sequences for each of the six MPyV proteins for their ability to stimulate spleen cells from acutely infected B6 mice. Overlapping peptides yielding positive wells were then assayed by IFN- γ intracellular staining and CD4 surface staining, and minimum length peptides stimulating optimal responses were determined. From these analyses, one 13-mer and one 15-mer CD4⁺ T cell epitope for MPyV were identified: LT₆₇₈₋₆₉₀ (NEYLLPQTVWARF) from the nonstructural LT antigen; and VP1₂₂₁₋₂₃₅ (GMYPVEIWHDPKKN) from the VP1 major capsid protein. Fig. 1A shows a representative example of LT₆₇₈- and VP1₂₂₁-induced intracellular IFN- γ production by splenic CD4⁺ T cells from B6 mice at day 8 p.i. To facilitate detection of Ag-reactive CD4⁺ T cells, we performed intracellular co-staining for CD154 (CD40L), which is transiently expressed by CD4⁺ T cells following Ag stimulation (31); nearly all of the IFN- γ ⁺ cells co-expressed CD154.

To enumerate and phenotype MPyV-specific CD4⁺ T cells directly *ex vivo*, we used MHC class II tetramers complexed to each of these antigenic peptides. As shown in Fig. 1B, I-A^b/LT₆₇₈ and I-A^b/VP1₂₂₁ tetramers bound Ag-experienced (i.e., CD44^{hi}) splenic CD4⁺ T cells, which were not stained by control I-A^b/hCLIP tetramers; in addition, I-A^b/LT₆₇₈ and I-A^b/VP1₂₂₁ tetramers did not stain CD4⁺ T cells from uninfected B6 mice. Using these tetramers, we found that >2-fold more VP1₂₂₁-specific CD4⁺ T cells than LT₆₇₈-specific cells were detected by tetramers in spleens of day 8-infected mice (Fig. 1C). The larger number of I-A^b/VP1₂₂₁ tetramer⁺ cells was evident as early as 6 days p.i. and continued well into the persistent phase of infection. Notably, both CD4⁺ T cell populations underwent a relatively small contraction and were then maintained at steady levels, response profiles that stand in contrast to the progressive

attrition of memory CD4⁺ T cell populations seen in acute LCMV and *Listeria monocytogenes* infections (32-34).

VP1₂₂₁- and LT₆₇₈-specific CD4⁺ T cells differ in functional competence

In Fig. 1A we noted that fewer VP1₂₂₁-specific CD4⁺ T cells at day 8 p.i. produced IFN- γ than were stained by I-A^b/VP1₂₂₁ tetramers, a difference not seen with the LT₆₇₈-specific CD4⁺ T cells. By peptide titration, we first determined that 50 μ M peptide stimulated maximal intracellular IFN- γ production by both epitope-specific CD4⁺ T cell populations and did not resolve the apparent absence of IFN- γ production by VP1₂₂₁-specific CD4⁺ T cells (data not shown). I-A^b/VP1₂₂₁ and I-A^b/LT₆₇₈ tetramer⁺ cells were also found to express equivalent levels of surface CD3 and slightly higher levels of CD4 than naïve T cells (data not shown), as previously reported for Ag-stimulated CD4⁺ T cells (35). In addition, the frequency of CD4⁺ T cells induced to produce IFN- γ by VP1₂₂₁ peptide stimulation closely approximates those that upregulate CD40L (Fig. 1A and data not shown), suggesting that a proportion of the VP1₂₂₁-specific CD4⁺ T cell population is refractory to T cell activation. We then asked whether this early decline in functionality by VP1₂₂₁-specific CD4⁺ T cells was a transient defect that resolved over time and whether LT₆₇₈-specific CD4⁺ T cells preserved their cytokine effector function during persistent MPyV infection. As shown in Fig. 2A, only 40-50% of the I-A^b/VP1₂₂₁ tetramer⁺ CD4⁺ T cells produce IFN- γ at all acute and persistent infection time points examined, whereas LT₆₇₈-specific CD4⁺ T cells retained function well into persistent infection. Moreover, when one takes into account this selective dysfunction by the VP1₂₂₁-specific CD4⁺ T cells, the numerical advantage of these cells over the LT₆₇₈-specific CD4⁺ T cells nearly vanishes during acute infection and narrows by approximately half of that based on tetramer binding during persistent infection (Fig. 2B). Finally, these analyses reveal that this IFN- γ deficiency by the VP1₂₂₁-specific CD4⁺ T cells

is evident as early as day 6 p.i., suggesting that factors early in acute infection affect the cytokine effector profile or long-term fitness of the CD4⁺ T cell response.

We next asked whether this lack of IFN- γ production by nearly half of the VP1₂₂₁-specific CD4⁺ T cells extended to other effector functions. Using spleen cells from acutely (day 8 p.i.) and persistently (day 60 p.i.) infected mice, we determined the frequency of IFN- γ ⁺ cells that co-produced either TNF- α or IL-2 after stimulation by VP1₂₂₁ or LT₆₇₈ peptides. The data in Fig. 3A show that only a fraction of either the VP1₂₂₁-specific or LT₆₇₈-specific CD4⁺ T cell populations in acutely infected mice co-produce TNF- α and IL-2 along with IFN- γ , although the inability to produce these effector cytokines is greater for the VP1₂₂₁-specific CD4⁺ T cells (especially when taking into account their lack of IFN- γ -producing capability). Moreover, the deficiency in co-producing these cytokines was maintained into the persistent phase of MPyV infection.

We then investigated the possibility that these MPyV-specific CD4⁺ T cells may have modulated their effector cytokine profiles. Although neither the VP1₂₂₁- nor LT₆₇₈-specific CD4⁺ T cell populations produced IL-4 or IL-17 (data not shown), we observed that a fraction of IFN- γ ⁺ cells of each specificity co-produced IL-21 or IL-10 (Fig. 3B). Moreover, in contrast to the stability of IFN- γ /TNF- α /IL-2 co-producers over the course of MPyV infection, for both VP1₂₂₁- and LT₆₇₈-specific CD4⁺ T cells. There was a doubling of those making IL-21 but a halving of those making IL-10 between acute and persistent stages of infection. In addition, <5% of either VP1₂₂₁- or LT₆₇₈-specific CD4⁺ T cells express the regulatory T cell transcription factor Foxp3 in either acutely or persistently infected mice (data not shown). As recently reported for influenza virus-specific CD8⁺ T cells (36), it is tempting to speculate that these virus-specific CD4⁺ T cells may adjust secretion of IL-10 to counter immune-mediated pathology, the potential for which would be higher in acute than persistent infection. The shift toward IL-21 production by

persistent infection-phase MPyV-specific CD4⁺ T cells also fits with recent reports showing that this cytokine contributes to maintenance of virus-specific CD8⁺ T cells during chronic LCMV infection (37-39).

TCR repertoire and phenotypic heterogeneity of MPyV epitope-specific CD4⁺ T cells

Differences in efficiency of T cell activation by Ag in vivo have been correlated with changes in the level of clonotypic diversity by the responding T cells (40). We thus asked whether the VP1₂₂₁-specific and LT₆₇₈-specific CD4⁺ T cells might exhibit differences in TCR repertoire diversity early in the course of MPyV infection. By co-staining I-A^b tetramer⁺ CD4⁺ T cells from individual acutely infected (day 8 p.i.) mice with a panel of Vβ mAbs, we observed that the LT₆₇₈-specific T cells express a diverse, and mouse-to-mouse variable, Vβ usage profile. In sharp contrast, 80-90% of the VP1₂₂₁-specific CD4⁺ T cells in individual B6 mice predominantly express TCRs using Vβ8.1/8.2 and Vβ14 domains (Fig. 4). This constrained Vβ expression profile by the VP1₂₂₁-specific CD4⁺ T cells during acute infection is in line with the interpretation that only a subset of the naïve T cells population directed to this epitope is recruited.

T cells maintained in the setting of persistent Ag often express surface receptors that dampen their effector function (15, 41). Recent studies using the LCMV infection model have shown that the extent of T cell dysfunction parallels both the level of expression and diversity of inhibitory receptors expressed by virus-specific CD8⁺ T cells, which correlates with the severity and duration of persistent infection (42). We therefore asked whether differences in cytokine effector function between LT₆₇₈- and VP1₂₂₁-specific CD4⁺ T cells were reflected in differences in the profile and levels of cell surface inhibitory receptors. Of the inhibitory receptors examined (PD-1, CTLA-4, LAG-3, CD160, and TIM-3), only PD-1 and CTLA-4 were expressed by these MPyV-specific CD4⁺ T cells. Moreover, the I-A^b/VP1₂₂₁₋₂₃₅ tetramer⁺ CD4⁺ T cells displayed a

higher geometric mean fluorescence intensity (gMFI) for PD-1 (Fig. 5A) in both acutely and persistently infected mice, with an increase in PD-1 expression between acute and persistent phases of infection; in contrast, CTLA-4 expression levels by CD4⁺ T cells of both specificities declined in persistently infected mice. The higher levels of PD-1 expression on VP1₂₂₁-specific CD4⁺ T cells suggest that these cells more frequently encounter Ag than LT₆₇₈-specific CD4⁺ T cells and that PD-1 receptors might play a role in their partial dysfunction.

To address the possible role of PD-1 in impairing the function of VP1₂₂₁-specific CD4⁺ T cells, we performed in vivo blockade of the PD-1:PD-L1 pathway in persistently infected mice (d35-50 p.i.). Anti-PD-L1-treated B6 mice (n = 3 per each of 2 experiments) showed only a modest increase in the numbers of I-A^b/LT₆₇₈ tetramer⁺ CD4⁺ T cells ($1.1 \times 10^4 \pm 5.8 \times 10^3$ for control rat IgG-treated vs. $1.7 \times 10^4 \pm 4.1 \times 10^3$ for anti-PD-L1-treated mice; $p = 0.065$) and I-A^b/VP1₂₂₁ tetramer⁺ CD4⁺ T cells ($5.9 \times 10^4 \pm 7.9 \times 10^3$ for controls vs. $9.0 \times 10^4 \pm 3.6 \times 10^4$ for anti-PD-L1-treated mice; $p = 0.065$). There was a concomitant small increase in the number of IFN- γ ⁺ VP1₂₂₁-specific CD4⁺ T cells ($1.7 \times 10^4 \pm 3.2 \times 10^3$ for controls vs. $3.0 \times 10^4 \pm 1.0 \times 10^4$ for anti-PD-L1-treated mice; $p = 0.065$) and LT₆₇₈-specific CD4⁺ T cells ($9.5 \times 10^3 \pm 3.5 \times 10^3$ for controls vs. $1.4 \times 10^4 \pm 3.1 \times 10^3$ for anti-PD-L1-treated mice; $p = 0.041$). However, as a fraction of tetramer-binding cells, VP1₂₂₁- and LT₆₇₈-specific CD4⁺ T cell functionality was similar between anti-PD-L1-treated and control mice. In addition, no differences between these groups were seen in the dominant D^b/LT₃₅₉-specific CD8⁺ T cell response or in MPyV viral levels (data not shown). Although PD-1 on its own does not appear to play a role in limiting the function of VP1₂₂₁-specific CD4⁺ T cells, other inhibitory mechanisms may contribute. Thus, it will be of interest in future studies to see whether CTLA-4 blockade singly or in combination with PD-1 blockade bolsters the expansion and function of MPyV-specific T cells and results in a drop of the persistent MPyV infection set point.

The likelihood these two MPyV-specific CD4⁺ T cell populations differentially engage Ag is further supported by other phenotypic differences. Although VP1₂₂₁-specific and LT₆₇₈-specific CD4⁺ T cell populations in persistently infected mice are CD62L^{lo} and express decreased levels of Bcl-2 compared to CD44^{lo}CD4⁺ T cells, indicative of an effector/effector-memory differentiation state, all of the LT₆₇₈-specific CD4⁺ T cells and most of the VP1₂₂₁-specific CD4⁺ T cells are CD127^{hi} and CD27^{hi} (Fig. 5B, 5C). An explanation for this mixed effector-memory/central-memory phenotype may lie in the slower pace for re-expression of surface CD62L than CD127 and CD27 by T cells when cognate Ag is limiting (43). Yet, VP1₂₂₁-specific CD4⁺ T cells also have sizeable CD127^{lo} and PD-1^{hi} populations, whereas LT₆₇₈-specific CD4⁺ T cells are uniformly CD127^{hi} and PD-1^{int} (Fig. 5A, 5B), suggesting that VP1₂₂₁-specific CD4⁺ T cells are more chronically stimulated.

Recruitment of MPyV-specific CD4⁺ T cells during persistent infection

We previously demonstrated by adoptive transfer that MHC class Ia-restricted MPyV-specific CD8⁺ T cells during persistent infection are short-lived (25). However, because of the small frequency of MPyV-specific CD4⁺ T cells in persistently infected mice, we were unable to detect them by tetramer staining and follow their fate after adoptive transfer to infection-matched recipients. Instead, we assessed expression of both the prosurvival molecule Bcl-2 and the apoptotic marker AnnexinV on LT₆₇₈- and VP1₂₂₁-specific CD4⁺ T cells in persistently infected mice (day 60 p.i.). Compared with CD44^{Lo} CD4⁺ cells, both MPyV-specific CD4⁺ T cell populations expressed lower levels of Bcl-2 and higher levels of surface Annexin V staining (Fig. 5C). These data suggest that MPyV-specific CD4⁺ T cells are short-lived.

Because the LT₆₇₈- and VP1₂₂₁-specific CD4⁺ T cell populations are stably maintained during persistent infection (Figs. 1C, 2B), we then asked whether these T cells were capable of

self-renewal and/or were resupplied by de novo priming of naïve Ag-specific T cells. We monitored levels of DNA synthesis of persistent infection-phase LT₆₇₈- and VP1₂₂₁-specific CD4⁺ T cells based on their incorporation of the thymidine analog BrdU. We observed little anti-BrdU co-staining of either I-A^b tetramer⁺ CD4⁺ T cell population in contrast to the strong BrdU co-staining of these cells in acutely infected mice (Fig. 5D). Consistent with this finding, few splenic I-A^b tetramer⁺ CD4⁺ cells from persistently infected mice expressed the nuclear proliferation marker Ki-67 (data not shown).

To explore the possibility that Ag-specific naïve CD4⁺ T cells were primed de novo during persistent MPyV infection, we administered a minimally myeloablative dose of the cytotoxic DNA alkylating drug busulfan to B6 (CD45.2⁺) mice at day 40 p.i., and 24 h later, infused them with 2×10^7 bone marrow cells from naïve CD45.1⁺ congenic donors. Ninety days post-transfer (day 130 p.i.), I-A^b tetramer staining detected both CD45.1⁺ donor-derived LT₆₇₈-specific and VP1₂₂₁-specific CD4⁺ T cells (Fig. 6A). Notably, despite having similar levels of chimerism, individual mice showed variability in the frequency of I-A^b tetramer⁺ CD4⁺ T cells that are donor-derived (Fig. 6B). This mouse-to-mouse variability may be a reflection of differences in frequency of encounter by naïve virus-specific CD4⁺ T cells with low numbers of epitope-expressing MHC-II⁺ cells in persistent MPyV-infected mice; moreover, it is conceivable that the range of viral epitopes presented by APCs during persistent infection may vary among individual mice as a function of those that are productively (i.e., expressing both structural and nonstructural viral proteins) and nonproductively (i.e., expressing only nonstructural viral proteins) infected. Taken together, these data demonstrate that MPyV-specific CD4⁺ T cells are recruited during persistent infection.

Discussion

The natural MPyV provides a valuable model for studying T cell responses to viruses that establish low-level systemic persistent infection. In this study, we defined two I-A^b-restricted viral protein epitopes, one recognized by CD4⁺ T cells directed toward the nonstructural LT antigen and the other toward the VP1 capsid protein. Using MHC class II tetramers and intracellular cytokine assays, we found that virus-specific CD4⁺ T cells to these epitopes differed quantitatively and qualitatively over the course of infection. Most notably, the VP1-specific CD4⁺ T cell response dominated that directed toward LT but differed from the latter in terms of its profound early and sustained effector cytokine dysfunction, which was not offset by blockade of the PD-1:PD-L1 pathway. Despite this difference, the LT-specific and VP1-specific CD4⁺ T cells populations are stably maintained during persistent infection. Data presented in this paper showing that MPyV-specific CD4⁺ T cell populations exhibit little proliferation in persistently infected hosts with a substantial number suffering apoptosis, coupled with the finding that naïve CD4⁺ T cells of both specificities are primed in persistent infection, suggest that de novo recruitment contributes to maintenance of MPyV-specific CD4⁺ T cells in chronically infected hosts.

CD4⁺ T-cell expansion and differentiation are governed by multiple factors, including level and duration of epitope availability, sustained colocalization with APCs, costimulation, and proinflammatory cytokines (44). For persistent viruses that comprise a host's "virome" additional factors merit consideration, such as viral tropism, kinetics of viral gene expression, state of the viral genome during persistent infection, and tactic(s) orchestrated by the virus to evade host surveillance (45). Characterization of MPyV-specific CD4⁺ T cell responses to epitopes from a nonstructural and structural viral protein may offer insights into the relationship between polyomaviruses and their hosts. For example, although MPyV DNA is detectable long term at low levels in select tissues, whether it is maintained latently in an episomal state or if

infectious virus is continuously produced at low yield by semi-permissive cells remains an open question. As VP1 protein production is generally taken as evidence of productive infection, PD-1 and CTLA-4 upregulation by VP1₂₂₁-specific CD4⁺ T cells in persistently infected mice, suggestive of repetitive Ag stimulation, favors the infectious state scenario. This possibility is further supported by evidence in this paper that naïve VP1-specific CD4⁺ T cells are primed de novo during persistent infection.

Differences in functional competence by the LT₆₇₈-specific and the VP1₂₂₁-specific CD4⁺ T cells could stem from differences in availability of MHC class II-restricted epitopes derived from nonstructural and structural viral proteins. Extending from studies showing a positive association between Ag levels and CD8⁺ T cell dysfunction (46, 47), the effector cytokine defect of VP1₂₂₁-specific, but not LT₆₇₈-specific, CD4⁺ T cells suggests more frequent TCR engagement by the former. This functional disparity may lie in differences in the range of potential APCs and the ability of these viral proteins to access the MHC class II processing machinery. Because polyomaviruses bind to sialylated glycolipids and glycoproteins, virions adsorb to a broad array of cells, irrespective of their capacity to support infection (48). Bound virions will thus undergo receptor-mediated endocytosis, which would facilitate shunting of capsid proteins into degradative and MHC class II peptide-loading compartments. In addition, the ratio of infectious to physical particles for MPyV in vitro is ~1:100, raising the possibility that defective virions (including empty capsids) could also contribute VP1-derived epitopes for MHC class II presentation. In contrast, as expression of nonstructural viral T proteins requires synthesis by infected cells, access to MHC class II compartments would most likely be relegated to less efficient nonreceptor-mediated uptake of protein debris from lytically infected cells.

Recent reports detailing Ag-specific CD4⁺ T cell expansion, maintenance, and function to different experimental viral infections highlight variability, but also commonalities, among these responses. For example, infection by acutely resolved LCMV-Armstrong gives rise to virus-

specific memory CD4⁺ T cells that then suffer progressive attrition, but without appreciable functional impairment (32). In contrast, virus-specific CD4⁺ T cells to the persistently infecting mouse CMV are stably maintained during latent infection and retain polyfunctionality (17, 20). Examination of the I-A^b/GP₆₁₋₈₀-specific CD4⁺ T cell response to LCMV clone 13, which establishes high-level persistent infection, revealed functional inactivation of these T cells as early as day 9 of infection (16). Analysis of the MPyV-specific CD4⁺ T cell response yielded a composite of these quantitative and qualitative behaviors, with stable maintenance of virus-specific CD4⁺ T cell populations during persistent infection yet with variations in functional integrity among epitope-specific responses. Reminiscent of the GP₆₁₋₈₀-specific CD4⁺ T cell response to LCMV clone 13 infection, dysfunction of the MPyV VP1₂₂₁-specific CD4⁺ T cell response was also evident during acute infection. Thus, events at the level of priming (e.g., epitope presentation by non-professional APCs) or soon thereafter (e.g., high epitope density and high TCR avidity) may handicap effector differentiation or force premature senescence, respectively, of a sizeable fraction of the VP1₂₂₁-specific CD4⁺ T cell population.

Early dysfunction by the VP1₂₂₁-specific CD4⁺ T cells may also be a consequence of the MPyV life cycle. Because expression of viral capsid proteins is a harbinger for virus-induced cell death, the duration of antigenic stimulation for capsid epitope-specific T cells may be shorter than for T cells recognizing epitopes from nonstructural T antigens, because these are also expressed by abortively infected cells. As a result, naïve VP1₂₂₁-specific CD4⁺ T cells may be suboptimally primed by productively infected APCs, whereas naïve LT₆₇₈-specific CD4⁺ T cells may continue to receive stimulation by nonproductively infected APCs. This alternative scenario may account not only for the early functional deficiencies of the VP1₂₂₁-specific CD4⁺ T cells, but also for their restricted TCR V β usage if only a subset of the naïve T cells having TCRs of sufficiently high avidity are recruited (40). Differences in MHC class II tetramer MFI at optimal concentrations have been taken as a measure of differential TCR binding affinity (49, 50). Thus,

in support of the above possibility, we found that I-A^b/VP1₂₂₁ tetramers stain splenic CD4⁺ T cells from day 8 p.i. mice with significantly higher gMFI than A^b/LT₆₇₈ tetramers, with each population expressing equivalent TCR levels by surface anti-CD3ε staining (data not shown). Stronger TCR signaling by higher affinity VP1₂₂₁-specific CD4⁺ T cells may also account for their higher level of expression of PD-1 and CTLA-4 receptors.

A central finding of this study is that naïve MPyV-specific CD4⁺ T cells are recruited in persistently infected mice. This result is in line with recent reports demonstrating emergence of novel clonotypes of virus-specific CD4⁺ T cells during persistent CMV infection in humans and rhesus macaques and evidence for de novo generation of virus-specific CD4⁺ T cells in baboons persistently infected by baboon CMV and an EBV-like virus (51-53). Given the variability in priming conditions and history of antigenic exposure of individual virus-specific T cells over the course of a persistent infection, it is not surprising that a phenotypic snapshot of these cells in chronically infected hosts reveals heterogeneity in markers indicative of effector/effector-memory/central memory differentiation, as seen for MPyV-specific CD4⁺ and CD8⁺ T cells (Fig. 5) (25). Kinetic profiling of the MPyV-specific CD4⁺ T cell response (Fig. 1C) is notable for its exceedingly shallow contraction phase, suggesting that naïve antiviral CD4⁺ T cells may be vigorously recruited even at this early time point. Because more LT₆₇₈-specific than VP1₂₂₁-specific CD4⁺ T cells bind the Annexin V marker of apoptosis (Fig. 5C), although both populations maintain stable numbers, it is also tempting to speculate that the efficiency for recruitment during persistent infection is higher for the LT₆₇₈-specific CD4⁺ T cells. In addition, our data offers a possible explanation for the deterioration of the memory CD4⁺ T cell pool in mice infected by LCMV-Armstrong (i.e., lack of I-A^b/GP₆₁₋₈₀ Ag for priming naïve CD4⁺ T cells to replenish the virus-specific memory CD4⁺ T cell compartment).

As we recently reported, CD4⁺ T cells, although dispensable for expansion of MPyV-specific CD8⁺ T cells during acute infection, are essential for de novo priming of antiviral naïve

CD8⁺ T cells in persistently infected hosts (28). The low-level inflammatory milieu in persistent infection may shift the burden to CD4⁺ T cells for licensing APCs to drive naïve virus-specific CD8⁺ T cell differentiation. Collectively, our data favor the concept that ongoing recruitment of naïve virus-specific CD4⁺ T cells is linked to priming of naïve antiviral CD8⁺ T cells during persistent infection.

In summary, we have found marked differences between two viral epitope-specific CD4⁺ T cell responses to MPyV infection. Interestingly, despite overall differences in magnitude, which is conventionally used to denote level of immunodominance, the LT₆₇₈ and VP1₂₂₁-specific CD4⁺ T cell responses are nearly co-dominant based on IFN- γ function. Thus, at least with respect to persistent infections, functional rather than numerical attributes may be a more meaningful guide to positioning epitope-specific T cell populations within immunodominance hierarchies. It is also interesting to note that CD4⁺ T cells directed to epitopes in LT and VP1 of the human BK polyomavirus are also detected in seropositive healthy individuals (54). Infections by BK and the related human polyomavirus, JC, are associated, respectively, with kidney transplant rejection and progressive multifocal leukoencephalopathy, a demyelinating disease seen in patients immunocompromised by HIV/AIDS or by agents that block T cell entry into the CNS (55, 56). Another implication of our data, then, is that immunomodulatory regimens designed to interdict T cell priming may interfere with recruitment of virus-specific naïve T cells, shrinking the antiviral effector/memory T cell pool needed to keep otherwise silent persistent viral infections in check.

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FOOTNOTES

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⁴ Abbreviations used in this paper: 7-AAD, 7-aminoactinomycin D; B6, C57BL/6; ICS, intracellular cytokine staining; LCMV, lymphocytic choriomeningitis virus; LT, large T antigen; gMFI, geometric mean fluorescence intensity; MPyV, mouse polyomavirus; PD-1, programmed death 1; PD-L1, PD-1 ligand 1; p.i., postinfection; PD-1, programmed death receptor-1; VP1, major capsid protein of MPyV.

Figure Legends

FIGURE 1. Identification of MPyV epitope-specific CD4⁺ T cells. A, Splenic LT₆₇₈⁻ and VP1₂₂₁-specific CD4⁺ T cells from B6 mice at day 8 p.i. are detected by intracellular IFN- γ staining assays. Splenocytes were stimulated with the indicated peptide (50 μ M) for 5.5 h, then surface-stained for CD4 and co-stained intracellularly for IFN- γ and CD154. Plots are gated on CD4⁺ cells. B, Splenic LT₆₇₈⁻ and VP1₂₂₁-specific CD4⁺ T cells from B6 mice are detected by I-A^b tetramer staining at day 8 p.i. but not in uninfected mice. Splenocytes were stained with the indicated I-A^b tetramers then stained for CD4 and CD44. Tetramer plots are gated on CD4⁺ 7-AAD⁻ cells. Values indicate percentage of gated cells that co-stain with IFN- γ and CD154 (A) or I-A^b tetramer and CD44 (B). Plots are representative of 3 experiments with 3 mice apiece. C, Time course of MPyV-specific CD4⁺ T cell numbers in spleen as assessed by I-A^b/LT₆₇₈ and I-A^b/VP1₂₂₁ tetramer staining, with background staining by I-A^b/hCLIP tetramers subtracted. Values for each time point represent the mean \pm SD of 6-9 mice from 2-3 independent experiments.

FIGURE 2. Differences in functional competence between LT₆₇₈-specific and VP1₂₂₁-specific CD4⁺ T cells. A, Comparison of the frequency of I-A^b tetramer versus intracellular IFN- γ staining of LT₆₇₈⁻ and VP1₂₂₁-specific CD4⁺ T cells over time p.i. At each time point, splenocytes were stained directly ex vivo with I-A^b/LT₆₇₈ and I-A^b/VP1₂₂₁ tetramers or stimulated with the indicated peptides and stained intracellularly for IFN- γ as in Fig. 1A. Differences between frequency of IFN- γ ⁺ and I-A^b tetramer⁺ CD4⁺ T cells is statistically significant by the nonparametric Mann-Whitney U test ($p < 0.05$) at each time point for VP1₂₂₁-specific CD4⁺ T cells and days 10 and 100 p.i. for LT₆₇₈-specific cells. B, Enumeration of splenic LT₆₇₈⁻ and VP1₂₂₁-stimulated IFN- γ ⁺ CD4⁺ T cells (with background intracellular IFN- γ staining by CD4⁺ T

cells in absence of peptide subtracted) over the course of MPyV infection. Numbers and frequencies are of CD4⁺ T cells that are I-A^b tetramer⁺CD44^{hi} or IFN- γ ⁺CD154⁺. Values for each time point represent the mean \pm SD of 6-9 mice from 2-3 independent experiments.

FIGURE 3. Variations in effector cytokine profiles of LT₆₇₈-specific and VP1₂₂₁-specific CD4⁺ T cells over the course of MPyV infection. At acute (day 8 p.i.) and persistent (day 60 p.i.) infection time points, splenocytes were stimulated with LT₆₇₈ or VP1₂₂₁ peptides for 5.5 h then stained for surface CD4 followed by co-staining for intracellular IFN- γ and TNF- α , IL-2, IL-10 or IL-21. A, Representative plots of IFN- γ /TNF- α or IFN- γ /IL-2 (*left panels*) and frequency of IFN- γ ⁺ CD4⁺ cells that express TNF- α or IL-2 (*right graphs*). B, Frequency of IFN- γ ⁺ CD4⁺ cells that express IL-10 or IL-21. Data in all graphs represent mean \pm SD of 6 mice in 2 independent experiments. The *p* values were calculated using the nonparametric Mann-Whitney U test.

FIGURE 4. LT₆₇₈-specific and VP1₂₂₁-specific CD4⁺ T cells differ in TCR repertoire. V β TCR chain repertoire analysis of LT₆₇₈- and VP1₂₂₁-specific CD4⁺ T cells at day 8 p.i. (*upper and lower graphs*, respectively). Splenocytes were stained with either I-A^b/LT₆₇₈ or I-A^b/VP1₂₂₁ tetramers and then intracellularly with indicated V β TCR mAb. Each bar of same pattern shows the percentage of tetramer⁺ cells from an individual mouse expressing the indicated V β TCR.

FIGURE 5. Phenotypic differences between LT₆₇₈-specific and VP1₂₂₁-specific CD4⁺ T cells during persistent MPyV-infection. A, Representative histograms showing PD-1 and CTLA-4 expression by I-A^b/LT₆₇₈ and I-A^b/VP1₂₂₁ tetramer⁺ CD4⁺ T cells (black line) compared with naïve CD44^{lo} CD4⁺ cells (gray filled) from spleens of day 8 and 60 p.i. mice (*upper panels*) and

gMFI of staining by Abs for each of these receptors on tetramer⁺ cells from individual mice at each of these time points (*lower panels*). CD62L, CD127, and CD27 (B), and Bcl-2 and Annexin V (C, gray line, isotype control) expression on I-A^b/LT₆₇₈ and I-A^b/VP1₂₂₁ tetramer⁺ CD4⁺ T cells (black line) from spleens of day 60 p.i. mice compared with CD44^{lo} CD4⁺ cells (gray filled). For Annexin V, plots are gated on live (7AAD⁻) CD4⁺ I-A^b tetramer⁺ CD44^{hi} cells. D, Comparison of BrdU incorporation by LT₆₇₈- and VP1₂₂₁-specific CD4⁺ T cells given daily i.p. injections of BrdU from days 33-40 p.i. (*upper panels*) or from days 0-7 p.i. (*lower panels*). Black line, tetramer⁺ CD44^{hi} CD4⁺ T cells; gray filled, CD44^{lo} CD4⁺ T cells. Data are representative of 2 independent experiments of 3 mice each.

FIGURE 6. Naïve MPyV-specific CD4⁺ T cells are primed de novo during persistent infection. Persistently infected (day 40 p.i.) busulfan-treated B6 (CD45.2⁺) mice received 2 x 10⁷ bone marrow cells from naïve B6/CD45.1 mice. A, At 90 days post-transplant (d130 p.i.), splenocytes were analyzed by I-A^b tetramer staining. Donor (CD45.1⁺)- and host (CD45.1⁻)-derived I-A^b/VP1₂₂₁ (*top row*) and I-A^b/LT₆₇₈ (*middle row*) tetramer⁺ CD4⁺ T cells. Control I-A^b/CLIP tetramer staining of donor and host CD4⁺ T cells (*bottom row*). All plots are gated on CD4⁺CD45.1⁺ (donor) or CD4⁺CD45.1⁻ (host) cells and numbers represent the percentage of gated cells that are tetramer⁺CD44^{hi}. Data are representative of 2 experiments with 2-3 mice each. A total of 63.3 ± 24.0 % (mean ± SD) of splenic CD4⁺ T cells were of donor origin (CD45.1⁺). B, Frequency of I-A^b/LT₆₇₈ tetramer⁺ or I-A^b/VP1₂₂₁ tetramer⁺ CD4⁺ T cells that are donor-derived.

Figure 1

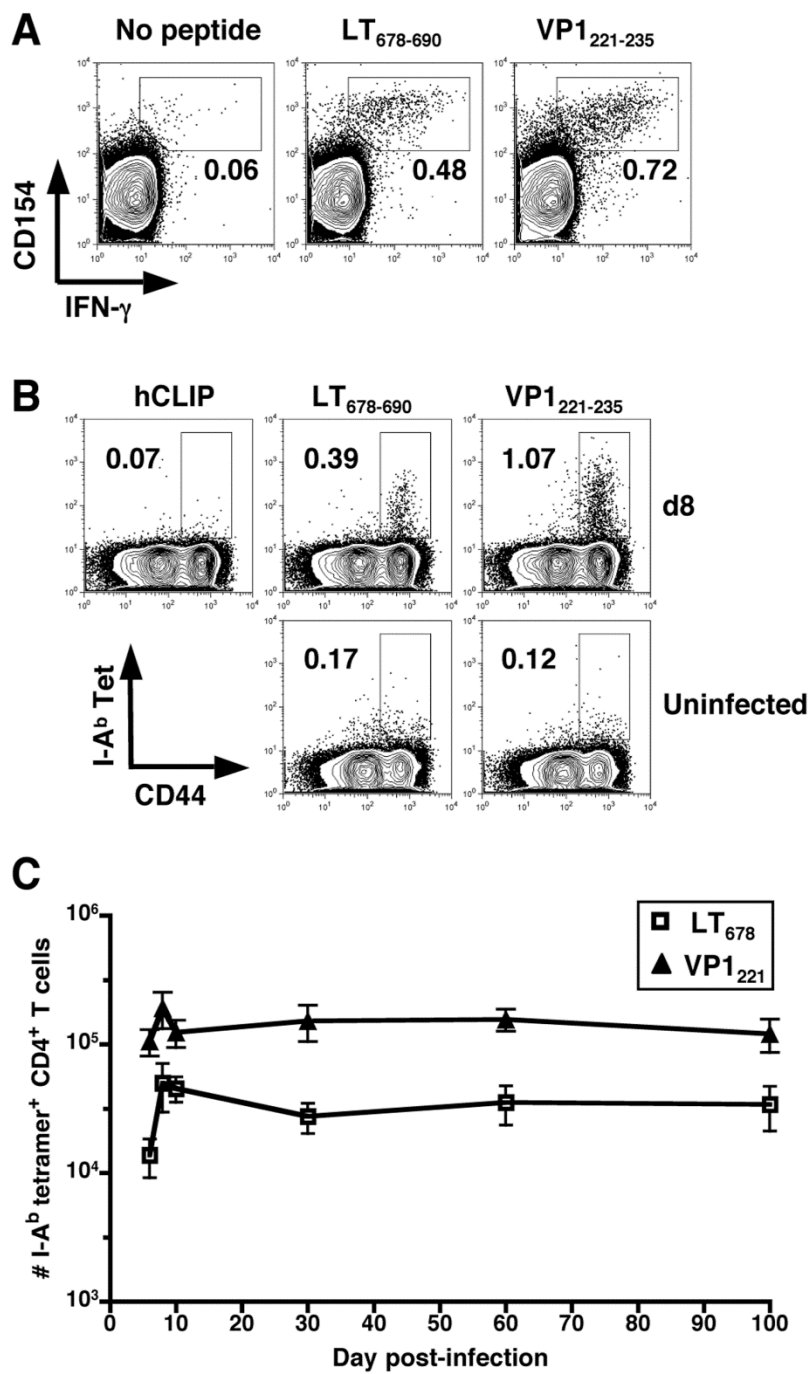


Figure 2

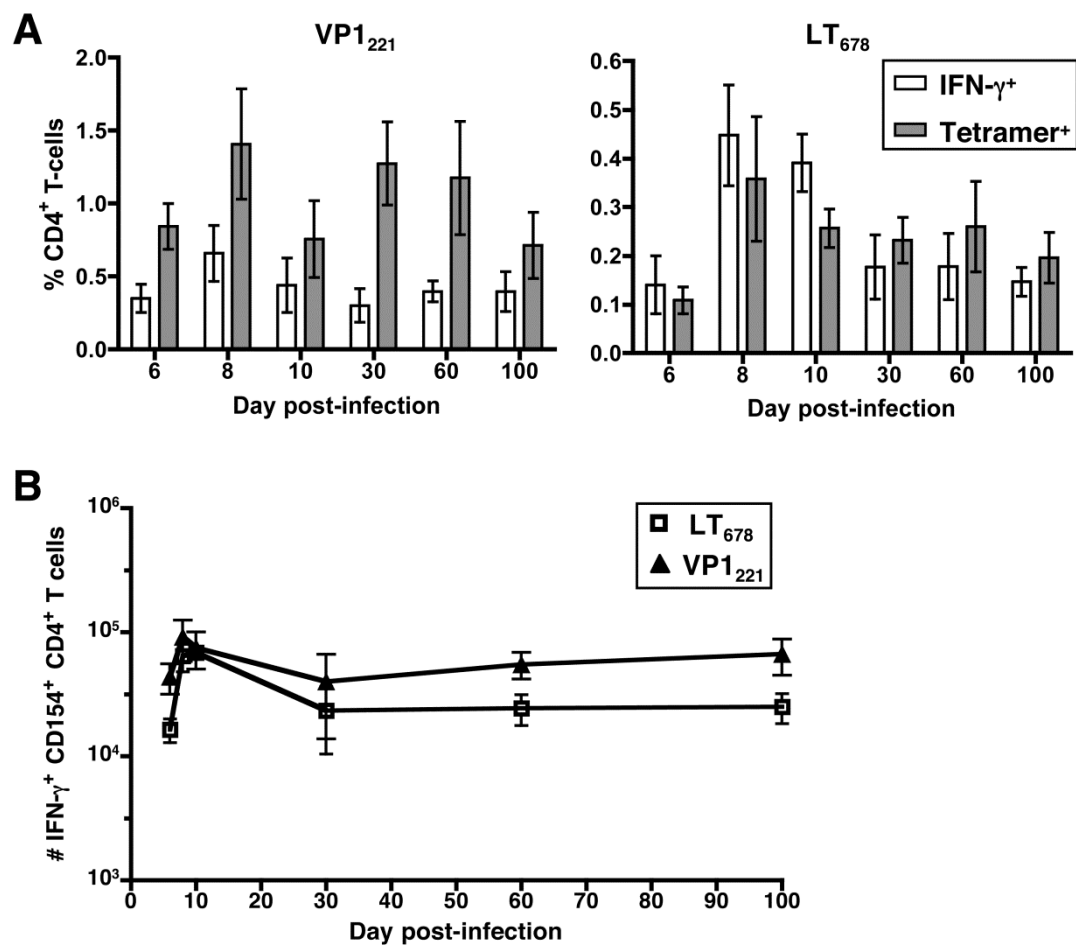


Figure 3

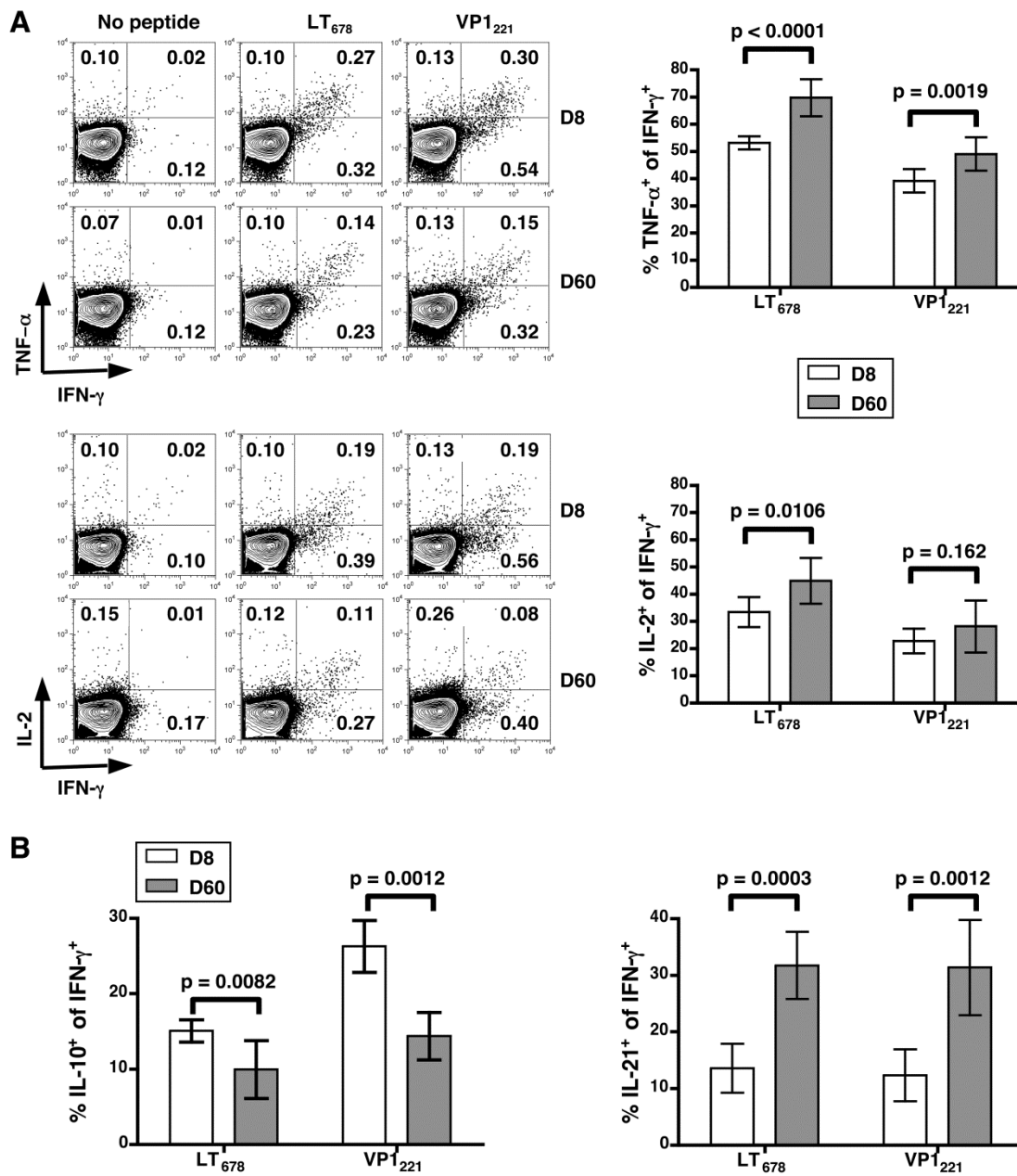


Figure 4

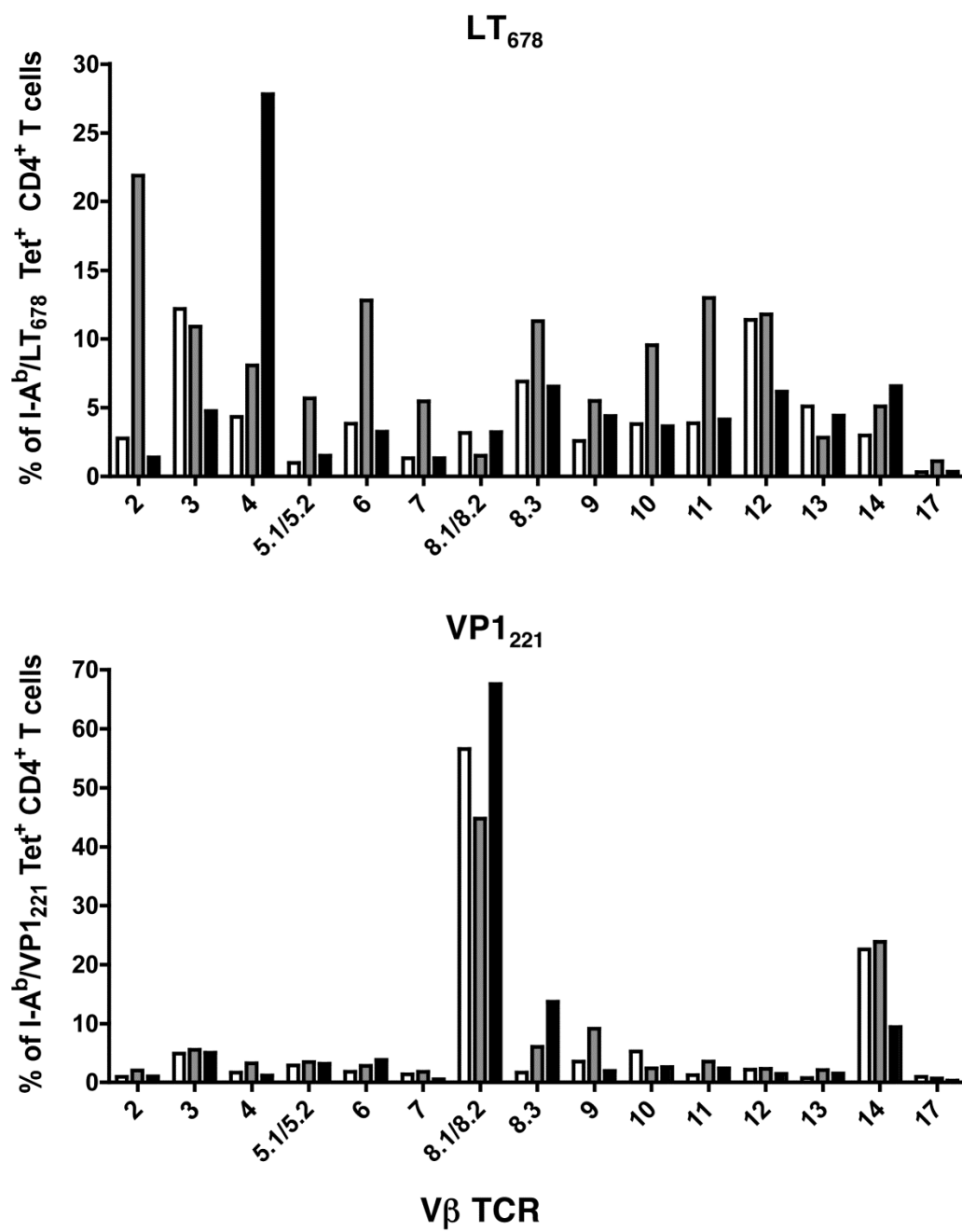


Figure 5

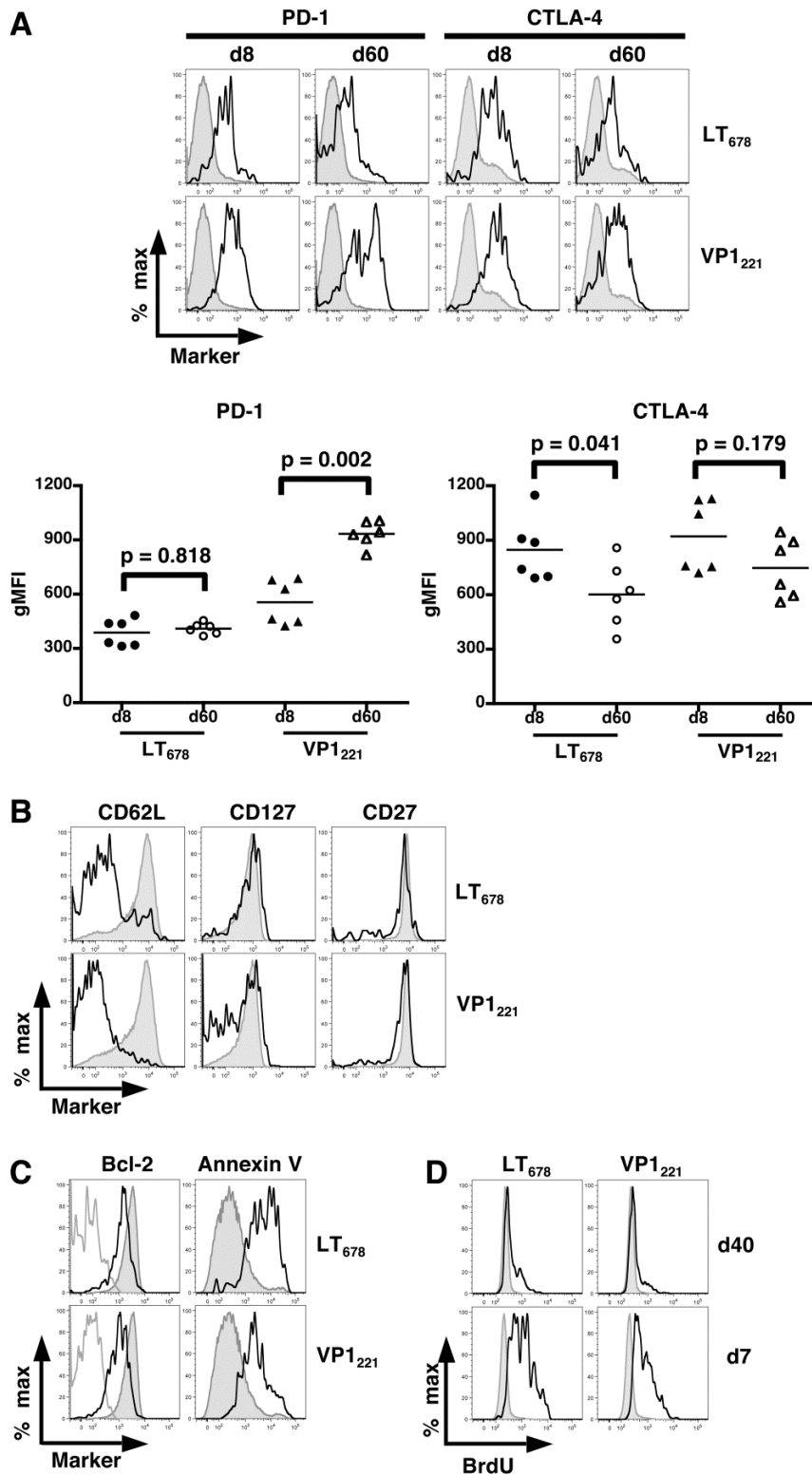
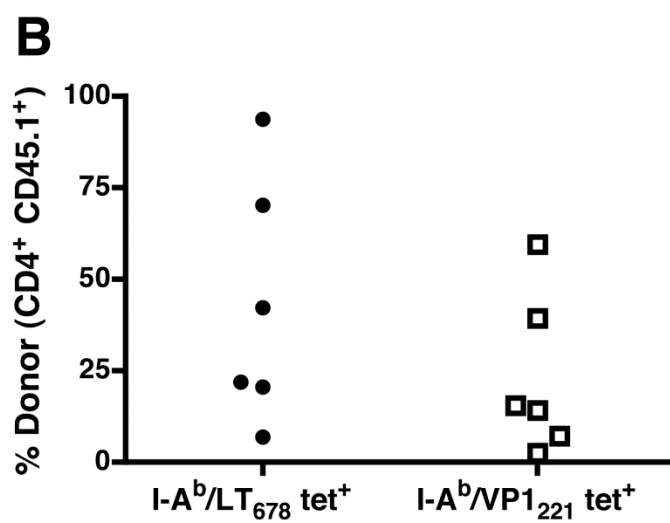
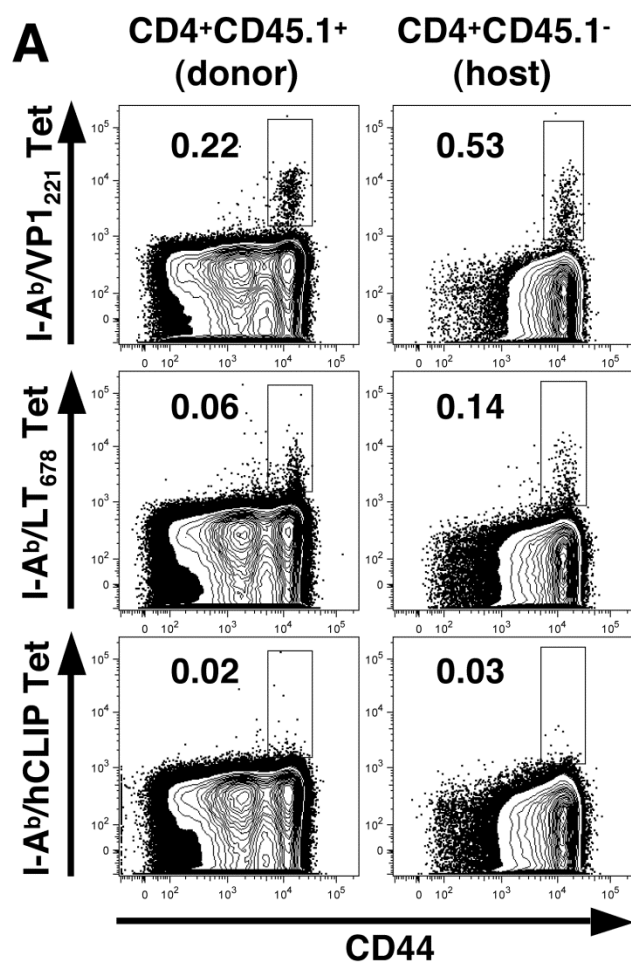


Figure 6



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Chapter 3

Assessing the impact of persistent infection on polyomavirus-specific T cells

All figures in Chapter 3 are based on data generated by the Ph.D. candidate

Abstract

After clearance of an acute viral infection, stable memory T cell populations develop that are maintained independently of antigen by cytokine-driven homeostatic turnover. In contrast, memory CD8⁺ T cells during chronic high load infections require persistent antigen for their self-renewal and fail to respond to homeostatic cytokines. Whether memory T cells formed during low-level persistent infections require antigen for their survival is less clear. Here we describe the development of a novel approach to ablating virus replication during persistent infection with mouse polyomavirus (MPyV). We generated a recombinant MPyV in which genes critical for replication are floxed (A2.Flx). Viral levels are reduced following Cre-mediated deletion in vitro and in mice expressing constitutive Cre. Utilizing mice expressing a tamoxifen-inducible Cre, we found that reduction of viral replication during persistent A2.Flx infection has an epitope-dependent effect on virus-specific CD4⁺ and CD8⁺ T cells. While major viral capsid protein VP1-specific CD4⁺ T cells and nonstructural large T protein (LT)-specific CD8⁺ T cells significantly decreased, LT-specific CD4⁺ T cells displayed a shift toward CD62L^{hi} central memory phenotype cells with less apparent loss. Our data suggests that antigen is not necessarily required for survival of MPyV-specific memory T cells and that cells can be redirected toward a phenotype associated with antigen-independent central memory T cells following reduction in replication.

Introduction

Following complete resolution of an acute viral infection, highly functional memory T cells gradually emerge from effector T cells that have survived the contraction phase (1, 2). Both CD4⁺ and CD8⁺ memory T cells are maintained long-term independently of antigen via slow homeostatic turnover driven by the cytokines IL-7 and IL-15 (3). Upon rechallenge infection, memory T cells mount rapid and robust recall responses marked by immediate elicitation of effector function and enhanced accumulation of antigen-specific secondary effectors compared to primary naïve responses (1, 2). However, during persistent viral infections, memory T cell homeostasis is greatly altered, and the memory-like T cell populations depend on persistent antigen for survival and maintenance (4). Virus-specific CD8⁺ T cells during chronic lymphocytic choriomeningitis virus (LCMV) infection do not respond to IL-7 or IL-15 as they express low levels of the receptors CD127 (IL-7R α) and CD122 (IL-15R β) (5). Instead these “chronic memory” cells are maintained by antigen-driven proliferation and do not survive in an antigen-free environment be it in naïve mice or mice chronically infected with an epitope variant (5, 6). Further support for antigen-dependent self-renewal comes from an elegant study that tracked virus-specific effector CD8⁺ T cells indelibly marked by YFP during acute infection with murine herpesvirus 68 (MHV68), a model of latent infection, and showed that these cells persisted and continued to proliferate for several months (7). By contrast, in persistent mouse polyomavirus (MPyV) infection, virus-specific chronic memory CD8⁺ T cells exhibit minimal proliferation and appear to survive poorly (8). Partial bone marrow chimera experiments showed that MPyV-specific CD8⁺ T cells could be primed de novo during persistent infection (8, 9). Thus, de novo recruitment of virus-specific T cells could be a mechanism to replenish a continually deteriorating memory T cell population. The relative importance of de novo recruitment to chronic memory T cell maintenance compared to antigen-driven turnover remains unclear. However, as shown with mouse cytomegalovirus (MCMV)-specific memory T cell inflation, where populations display

short half-lives despite intermittent antigen-driven proliferation, both mechanisms can contribute (10).

In addition to alterations in maintenance of memory T cell populations, persistent viral infection also leads to changes in memory cell heterogeneity. Based on expression of lymphoid homing receptors CCR7 and CD62L, memory T cells can be divided into CCR7^{hi}CD62L^{hi} central memory T (T_{CM}) cells, which tend to reside in lymph nodes as well as spleen, and CCR7^{lo}CD62L^{lo} effector memory T (T_{EM}) cells that reside in the spleen and nonlymphoid tissues such as lung or gut (11). Although both are capable of making effector cytokines like IFN- γ and TNF- α upon restimulation (12, 13), T_{CM} produce more IL-2, proliferate more robustly to antigen, and express higher levels of CD127, which correlate with increased homeostatic proliferation in response to IL-7 and improved survival, than T_{EM}, which are more terminally differentiated (14). Accumulating evidence suggests that T_{CM} cells ultimately correlate with superior protection compared to T_{EM} against infections and tumors (1). The memory T cell population generated after acutely resolved infections gradually but progressively shifts toward more T_{CM} cells (1). In contrast, chronic memory T cell populations tend to display a CD62L^{lo} T_{EM} phenotype consistent with repetitive antigen stimulation (15, 16). Despite this, CD62L^{hi}CD127^{hi} T_{CM}-like cells can emerge during some persistent viral infections by MPyV and MHV68 (8, 17). Development and survival of these cells may reflect the stimulation conditions that they encountered during priming or later as persistent infection progresses.

The level/strength of antigen:TCR signals and inflammation along with costimulation during priming critically influence the activation/differentiation of T cells. CD4⁺ T cells require prolonged stimulation for their optimal expansion and differentiation (18). Increasing intraclonal competition for antigen and cytokines like IFN- γ by transferring larger numbers of antigen-specific CD4⁺ T cell receptor (TCR) transgenic cells results in development of partially dysfunctional effector CD4⁺ T cells and impaired memory formation or survival (19-21). Even in

cases in which intraclonal competition is not an issue, stronger TCR signaling during the primary response, as might be provided with greater antigen availability and/or higher TCR avidity, appears critical for optimal differentiation into CD4⁺ memory T cells that survive long-term after resolution of acute infection (22). On the other hand, CD8⁺ T cells can embark on expansion and an autonomous differentiation program with a shorter period of stimulation. Reducing the amount of stimulation to CD8⁺ T cells, either by curtailing infection or increasing intraclonal competition, diminishes expansion but accelerates memory CD8⁺ T cell generation, with the balance tilted toward more CD62L^{hi}CD127^{hi}T_{CM} cells (23-25). However, excess antigen and/or inflammatory signals leads to development of short-lived terminally differentiated effector T cells. Increased exposure to the proinflammatory cytokine IL-12, for instance, pushes LCMV-specific CD8⁺ T cells to develop into KLRG-1^{hi}CD127^{lo}T-bet^{hi} short-lived effector cells (SLECs) rather than KLRG-1^{lo}CD127^{hi}T-bet^{lo} memory precursor effector cells (MPECs) (26). Additional evidence that the level of antigen or inflammation impacts memory T cell differentiation comes from studies of latecomer CD4⁺ and CD8⁺ T cells, which encounter less antigen and inflammation than cells primed earlier, expand less but differentiate into memory T cells with an intermediately-differentiated T_{CM} phenotype (27-30). During persistent infections, antigen and inflammatory signals continue to impact virus-specific T cell differentiation, leading to altered memory development and degradation of T cell functionality with increasing viral/antigen loads (4). A major question is whether fates of chronic memory T cells are fixed or if the cells retain some plasticity so that removal of persistent viral antigen leads to a restoration of the bona-fide memory T cell characteristics of antigen-independent, homeostatic cytokine-dependent maintenance.

We asked this question utilizing a model of systemic low-level persistent infection with MPyV. In our previous studies, we demonstrated that MPyV-specific CD8⁺ and CD4⁺ T cells mount polyfunctional responses and form stable chronic memory populations during persistent

infection (8, 9, 31). MPyV-specific chronic memory CD4⁺ and CD8⁺ T cells exhibited defects in self-renewal and survival, but de novo recruitment of naïve antigen-specific CD4⁺ and CD8⁺ T cells could be a critical mechanism for sustaining continually deteriorating chronic memory T cell pools. However, we have not fully ruled out the possibility that T cells primed earlier during the acute phase of infection could contribute through antigen-driven self-renewal. In addition, the different stimulation histories of cells primed earlier and more recently could account for the observed phenotypic heterogeneity of MPyV-specific CD8⁺ T cells, including the emergence of T_{CM}-like cells late during the persistent phase of infection (8). We have now developed a novel recombinant MPyV in which genes critical for viral replication and persistence are “floxed”. This floxed MPyV (A2.Flx) allows us to temporally ablate viral replication and reduce antigen load following Cre recombinase induction. Utilizing Cre/Esr mice, which expressing a tamoxifen-inducible Cre, we test the hypothesis that persistent MPyV antigen is required for the maintenance of virus-specific CD4⁺ and CD8⁺ T cell memory.

Materials and Methods

Generation and propagation of A2.Flx

The genome of the mouse polyomavirus (MPyV) strain A2 was used as the backbone for construction of A2.Flx. Recombinant A2.Flx was generated by insertion of loxP sequences at a unique BglII site in the noncoding region upstream of the T antigen start site and at the unique BlnI site in frame with the large T antigen (LT Ag). LoxP was inserted at the BlnI site by PCR with high-fidelity *Taq* polymerase (Invitrogen, Carlsbad, CA) using an overhanging forward primer that incorporated a BlnI recognition site (5'-

GTGTTGCTGAGCCCATCACTTCGTATAATGTATGCTATACGAAGTTATATGACAGCAT
ATC-3') and a reverse primer encoding an EcoRI site (5'-TCAGAATTCGGGCCTGAACTTCC-3') (restriction sites underlined and loxP in bold italics). In order to retain the reading frame of LT, we made a single base pair substitution replacing a G in LT with the final T in loxP. The resulting PCR product was cloned into the BlnI/EcoRI restriction site of A2 SF-pUC19b, where the small fragment of BamHI/EcoRI-digested MPyV A2 genome was subcloned into a modified pUC19 vector in which the BglII site has been mutated. This clone, MPyV llox SF, was used as template for a second PCR to insert loxP at the BglII position using a forward primer incorporating the BglII site (5'-

TGGCGCCTTGGAGGCATCACTTCGTATAATGTATGCTATACGAAGTTATGCTGTGGGG
CCAC-3') and the same reverse primer used above. This PCR product was then cloned into the BglII/EcoRI site of A2 SF-pUC19b to generate A2.Flx SF-pUC19b. A2.Flx SF was excised from pUC19b by BamHI/EcoRI digestion and ligated with the large fragment generated by BamHI/EcoRI digestion of the MPyV A2 genome. The ligation product was then cloned into BamHI-digested pUC19 to generate full length A2.Flx cloned into pUC19. Following DNA sequencing verification, A2.Flx was excised by BamHI digestion and the ends religated to generate full length circular MPyV DNA, which was used for transfections of Balb/c A31

fibroblast cell lines by Lipofectamine 2000 (Invitrogen, Carlsbad, CA). The resulting A2.Flx virus was subsequently propagated in primary baby mouse kidney cells and titered as previously described (32) .

In vitro assay of Cre-mediated deletion of A2.Flx

Subconfluent layers of nMuMG mouse mammary epithelial cell lines (ATCC, Manassas, VA) were infected with replication-deficient adenovirus expressing Cre recombinase (AdCre), a kind gift from Dr. Daniel Kalman (Emory University), at an MOI of 10 followed by infection 24 hrs later with wildtype MPyV strain A2 or A2.Flx at an MOI of 5. Forty-eight hours later, DNA was isolated according to the cell culture isolation protocol for the QIAamp DNA mini kit (Qiagen, Valencia, CA). Cre-mediated deletion of A2.Flx was assessed by PCR using A2floxed-F (5'-TCTCCACCCAGGCCTAGAATGTTT-3') and A2floxed R (5'-TGGCGTTGCATTGAATGAGCTCTG-3') primers, which flank the region that is floxed.

Mice

C57BL/6Ncr (B6) female mice were obtained from the National Cancer Institute's Frederick Cancer Research and Development Center (Frederick, MD). B6.C-Tg (CMV-Cre) 1 Cgn/J (CMV-Cre) mice were purchased from Jackson Laboratories (Bar Harbor, ME). B6.Cg-Tg (CAG-Cre/Esr1*) 5 Amc/J (Cre/Esr) mice are originally from Jackson Laboratories and were obtained from Dr. David G. Harrison (Emory University). Cre/Esr mice express a fusion protein of Cre recombinase and a mutated ligand binding domain from mouse estrogen receptor (CreERTM) under the control of a chimeric promoter consisting of a modified chicken β -actin promoter/enhancer and cytomegalovirus (CMV) immediate-early enhancer (33). CreERTM

translocates to the nucleus in the presence of tamoxifen, thereby allowing Cre-mediated recombination. Cre/Esr mice were genotyped by PCR of DNA from tail clippings isolated according to manufacturer's protocol using the E.Z.N.A. Tissue DNA Kit (Omega-Biotek, Norcross, GA). PCR for Cre was performed using primers Cre For (5'-GCGGTCTGGCAGTAAAACTATC-3') and Cre Rev (5'-GTGAAACAGCATTGCTGTACTT-3'). All mice were housed and bred in accordance with the guidelines of the Institutional Animal Care and Use Committee, and the Department of Animal Resources of Emory University.

Mouse infections and tamoxifen administration

Mice at ages 7-12 weeks received $3-6 \times 10^4$ PFU of A2.Flx intraperitoneally (i.p.) or subcutaneously (s.c.) in the hind footpads. For experiments involving tamoxifen injection, tamoxifen free base (Sigma-Aldrich, St. Louis, MO) was dissolved in a 10% ethanol in corn oil solution at a concentration of 10 mg/mL. 2 mg of tamoxifen per 30 g mouse was injected i.p. once daily for 5-10 consecutive days. Cre negative littermates or B6 mice given tamoxifen were used as controls.

Cell isolation and flow cytometry

Splenocytes were isolated as previously described (31). In brief, spleens were digested in a solution of collagenase, hyaluronidase, and Dnase I prior to passage through cell strainers and red blood cell lysis.

Staining with allophycocyanin (APC)-conjugated D^b/LT₃₅₉₋₃₆₈, I-A^b/LT₆₇₈₋₆₉₀, and I-A^b/VP1₂₂₁₋₂₃₅ tetramers was performed as previously described (9, 31). All tetramers were

constructed by the National Institutes of Health Tetramer Core Facility at Emory University (Atlanta, GA). In some experiments, 7-actinomycin D (7-AAD, BD Pharmingen, San Diego, CA) was used to stain cells after I-A^b tetramer and surface marker staining. For CTLA-4 and Bcl-2 staining, cells were first stained with tetramers and for surface markers CD8 α or CD4 and CD44. They were then permeabilized with Cytofix/Cytoperm buffer (BD Pharmingen) prior to staining with antibodies for CTLA-4 or Bcl-2. For intracellular cytokine staining assays, cells were stimulated for 5.5 hr with 10 μ M LT₆₇₈₋₆₉₀, 50 μ M VP1₂₂₁₋₂₃₅, or 1 μ M LT₃₅₉₋₃₆₈ peptide in the presence of brefeldin A (Golgi-Plug, BD Pharmingen) prior to staining as described in earlier work (9, 31). LT₆₇₈₋₆₉₀ and VP1₂₂₁₋₂₃₅ stimulated cells were stained for CD4, IFN- γ , IL-2, and CD154, whereas LT₃₅₉₋₃₆₈ stimulated cells were stained for CD8, IFN- γ , and IL-2.

All mAbs and isotype controls used for staining were purchased from BD Pharmingen or Ebiosciences (San Diego, CA) unless otherwise indicated: FITC-conjugated anti-CD44 (IM7), CD4 (RM4-5), CD8 α (53-6.7), CD62L, CD27 (LG.7F9), IFN- γ ; PE-conjugated anti-CD127 (A7R34), PD-1 (RMP1-30), CD154, CTLA-4, Bcl-2, CD43 (Biolegend, San Diego, CA), and KLRG-1 (Southern Biotech, Birmingham, AL); Per-CP-conjugated mAb for CD8 α ; PerCP-Cy5.5-conjugated anti-CD4 and IL-2; V450-conjugated mAb for CD44; and V500-conjugated anti-CD4. Samples were acquired using a BD Biosciences LSR-II, and data analyzed using FloJo software (Treestar, Ashland, OR).

Quantification of MPyV genomes

DNA isolation and TaqMan quantitative real-time PCR (qPCR) were performed as described (9) except for a modified TaqMan probe. The TaqMan probe 5'-AGACGAAATCCTTGTGTTGCTGAGC-3' corresponds to nt 1061-1085 of wildtype MPyV strain A2 (Genbank Acc. # J02288.1) and lies immediately upstream of the B1pI restriction site.

MPyV DNA quantity is expressed in genome copies per milligram of tissue and is calculated based on a standard curve of known MPyV genome copy number vs. threshold cycle of detection. The detection limit with this assay is 10 copies of genomic viral DNA.

Statistics

Statistical significance was determined by a two-tailed nonparametric Mann-Whitney *U* test using Prism software (GraphPad Software, La Jolla, CA). A *p*-value < 0.05 was considered statistically significant.

Results

Development of A2.Flx

As no approved effective direct anti-MPyV drugs are available, we created a novel recombinant MPyV that would allow us to make use of the Cre/lox system (34) to temporally ablate viral replication and reduce viral antigen. The genome of MPyV consists of a 5 kb circular double-stranded DNA plasmid that has been fully mapped (35-37), attributes permitting use of standard molecular DNA techniques to generate mutants and insert short sequences such as epitopes. The nonstructural T-antigens small, middle, and large T (ST, MT, LT), which are encoded within a single alternatively-spliced mRNA transcript, are critical for viral replication and persistence (38). Utilizing PCR, we inserted two directly repeated 34 bp loxP sites into the genome of wildtype MPyV strain A2, one at the BglI site in the noncoding region upstream of the T-antigen start site and a second at the BlnI site, which was inserted in frame with LT through a single base pair substitution (Fig 1A). The BlnI restriction site is located within sequence shared by MT and LT. This region was shown to tolerate a 66 bp deletion without impacting viral pathogenesis in vitro (39). We thus expected that loxP sequences inserted at these sites would minimally impact virus replication. Permissive A31 mouse fibroblast cell lines were transfected with DNA for this floxed MPyV (A2.Flx) and an initial batch of virus isolated. The stock of A2.Flx was further amplified in primary baby mouse kidney (BMKs) cells. Despite serial rounds of amplification, we observed titers that were ~2 logs less than typically seen for wildtype virus (data not shown), indicating that this virus is attenuated.

Nonetheless, we first tested whether these loxP sites were functional in vitro. NMuMG mouse mammary gland cell lines were infected with A2.Flx or wildtype MPyV in the presence or absence of co-infection with a replication-deficient adenovirus expressing Cre recombinase (AdCre). Cre-mediated deletion was assessed by PCR using primers flanking the floxed region

(Figure 1A). As shown in Figure 1B, the floxed region in A2.Flx was deleted only in cells co-infected with AdCre, whereas wildtype MPyV was unaffected by its presence. Yet there still remained residual DNA corresponding to intact MPyV from the A2.Flx/AdCre co-infected cells, which was similar in size to that detected from cells infected with A2.Flx alone. That band in turn is clearly larger than the band from wildtype-infected cells. Furthermore, sequencing of the A2.Flx stock used and DNA from cells infected with that virus alone revealed the presence of only DNA from A2.Flx. Thus, we believe that the residual intact MPyV band does not indicate contamination by wildtype MPyV and instead corresponds with intact A2.Flx that was not targeted perhaps because of insufficient amounts of Cre or inefficient recombination. In line with the Cre-mediated deletion results, measuring viral genome copies by quantitative real-time PCR (qPCR) of LT showed a nearly two-fold drop in MPyV levels in cells co-infected with A2.Flx and AdCre compared to those infected with just A2.Flx (Figure 1C). These in vitro experiments demonstrate the feasibility of using the Cre-mediated recombination approach to intentionally ablate MPyV replication.

A2.Flx induces MPyV-specific CD8⁺ and CD4⁺T cell responses despite constitutive Cre expression

To ensure that A2.Flx could induce an anti-viral immune response, we infected wildtype B6 mice. B6 background CMV-Cre mice, which constitutively express Cre under the control of a human CMV minimal promoter (40), were also infected with A2.Flx. We hypothesized that expression of Cre would prevent establishment of an infection and generation of a T cell response as the viral genome would be immediately targeted upon entry into the nucleus of an infected cell. Contrary to expectations, A2.Flx was still able to establish an infection in CMV-Cre mice. However, assessment of viral levels by qPCR at d20 post-infection (p.i.) showed nearly half as many copies

of MPyV DNA in the spleens of CMV-Cre mice compared with B6 (Figure 2A). Thus, it appears that we can also blunt A2.Flx replication in vivo in Cre-expressing mice.

Despite the decrease in viral levels, the impact on the H-2^b-restricted MPyV-specific T cell response varied by epitope (Figure 2B and C). While the frequency of D^b-restricted LT₃₅₉-specific CD8⁺ T cells and I-A^b-restricted LT₆₇₈-specific CD4⁺ T cells showed no change between B6 and CMV-Cre mice, there were nearly two-fold less VP1₂₂₁-specific CD4⁺ T cells in CMV-Cre than B6 control mice regardless if detected by tetramer or IFN- γ production (Figure 2C). We previously reported that VP1₂₂₁-specific CD4⁺ T cells appear to be partly dysfunctional as there were only ~50% as many IFN- γ -producing as tetramer⁺ cells; the frequency of cells upregulating CD154 (CD40L), which is transiently upregulated by recently antigen-activated CD4⁺ T cells (41), was similar to IFN- γ (31). However, we detected no shift in the overall ratio of IFN- γ ⁺ or CD154⁺ VP1₂₂₁-responding cells to I-A^b/VP1₂₂₁ tetramer⁺ cells (Figure 2C and data not shown). As viral levels were only reduced by half in CMV-Cre mice, it is possible that the residual VP1 antigen may still be high enough to impair T cell function. Alternatively, the dysfunction may be an effect of factors during initial priming and not a reaction to continued antigen stimulation. Nonetheless, as VP1 expression is associated with productive replication, the decrease in VP1₂₂₁-specific CD4⁺ T cells in the Cre⁺ compared with B6 mice could be interpreted as an indicator of reductions in viral replication.

Persistent viral antigen is critical for maintenance of MPyV-specific chronic memory T cells

To determine the impact of depleting MPyV antigen during persistent infection on virus-specific CD8⁺ and CD4⁺ chronic memory T cell populations, we infected Cre/Esr mice, which express tamoxifen-inducible Cre recombinase, and transgene negative littermate controls with A2.Flx then waited until persistent infection (~d35 p.i.) before administering tamoxifen (Figure 3A). We

reasoned that the lower level of virus during persistent infection would make Cre deletion more efficient. As these mice are backcrossed onto a C57BL/6 background for >5 generations, we were able to monitor the fate of D^b-restricted LT₃₅₉-specific CD8⁺ T cells as well as I-A^b-restricted LT₆₇₈- and VP1₂₂₁-specific CD4⁺ T cells in these mice. One month after the last dose of tamoxifen, we detected a modest approximately two-fold decrease in the number of tetramer⁺ LT₃₅₉-specific CD8⁺ T cells and VP1₂₂₁-specific CD4⁺ T cells in Cre/Esr mice compared with littermates, although the difference in LT₆₇₈-specific CD4⁺ T cells is less evident (Figure 3B). Similar epitope-specific decreases were evident when comparing the antigen-specific CD4⁺ and CD8⁺ T cells by IFN- γ production (Figure 4A). Despite the diminished number of virus-specific CD4⁺ T cells, the immunodominance hierarchy was not altered and remained VP1₂₂₁>LT₆₇₈ based on tetramer. Unfortunately, no discernible differences in viral levels as assessed by qPCR for LT was observed in the spleens, kidneys, hearts, or lungs of Cre/Esr versus littermate control mice, with several mice in both groups having nearly undetectable MPyV genome copies (Figure 3C and data not shown). However, extending from the finding of reduced viral levels and numbers of VP1-specific CD4⁺ T cells in the CMV-Cre compared with B6 mice, the significant decrease in VP1₂₂₁-specific CD4⁺ T cells in Cre/Esr mice compared with littermate controls suggests that there may indeed be less MPyV replication and antigen in the Cre/Esr mice.

Epitope variable impact of persistent antigen reduction on MPyV-specific T cell phenotype and function

As progressive functional exhaustion of T cells, often starting with a diminished ability to produce IL-2, is associated with increasing levels of persistent antigen (4), we asked whether the presumed diminishment of MPyV antigen led to improvements in functional competence of virus-specific T cells. As shown in Figure 4A, the functional competence of VP1₂₂₁-specific

CD4⁺ T cells did not improve in mice with activated Cre; functionality of LT₃₅₉-specific CD8⁺ T cells and LT₆₇₈-specific CD4⁺ T cells remained unaltered as well. In addition, there was no change in the overall ability of any of these MPyV-specific T cells to co-produce IL-2 with IFN- γ (Fig 4B). Measurement of functional avidity of LT₃₅₉-specific CD8⁺ T cells also failed to uncover any differences (data not shown).

We also wondered if there might be an accelerated shift toward development of virus-specific T cells with a central memory T cell (T_{CM}) phenotype as opposed to that of the more prevalent effector memory T cells (T_{EM}). While the relative proportion of CD62L^{hi}CD127^{hi} T_{CM}, CD62L^{lo}CD127^{hi} T_{EM}, and CD62L^{lo}CD127^{lo} effector T (T_{Eff}) cells was similar in Cre/Esr mice and littermates for the VP1₂₂₁-specific CD4⁺ T cells, there appeared to be a significant increase in the proportion of T_{CM} phenotype LT₆₇₈-specific CD4⁺ T cells and a significant drop in the frequency of antigen-specific T_{EM} cells in the mice with tamoxifen-induced Cre (Figure 5A). The proportion of T_{CM} cells making up the D^b/LT₃₅₉ tetramer⁺ CD8⁺ T cell population did not noticeably increase in Cre/Esr mice, but the frequency of T_{EM} cells was reduced nearly 3-fold. Looking at just CD127 expression, we did not observe a change in the frequency of cells expressing CD127 in any population, which correlated with a lack of difference in expression of the pro-survival molecule Bcl-2 (Fig 5B and data not shown). We also did not observe variation in expression of other markers associated with the effector-memory transition such as CD27, CD43, and the senescence marker KLRG-1, which is expressed on CD8⁺ SLECs as well virus-specific CD8⁺ T cells in several persistent infections (data not shown). Thus, with the possible exception of I-A^b/LT₆₇₈-specific CD4⁺ T cells, there was no appreciable shift toward a higher ratio of T_{CM} to T_{EM} cells despite the presumed decrease in viral antigen in Cre/Esr mice.

Discussion

During high load chronic infections such as with chronically infecting strains of LCMV, the function of virus-specific T cells is degraded, and memory T cells develop that appear to require antigen for their self-renewal and survival (4). Whether memory T cells to low-level persistent infections become fully dependent on antigen for their maintenance is less clear. Natural mouse polyomavirus (MPyV) provides an excellent model to study the response of virus-specific T cells to low-level persistent infection. As reported here, we have taken advantage of the virus' ease of genetic manipulation and knowledge about regulation of its replication to develop recombinant MPyVA2.Flx, in which genes critical for replication and persistence are floxed. We show that Cre-mediated deletion of the floxed region leads to a decrease in viral DNA levels in vitro, which also occurs in vivo in A2.Flx-infected Cre-expressing mice. Utilizing transgenic mice engineered to express a tamoxifen-inducible Cre, we find that targeting viral replication during persistent infection has an epitope-dependent impact on virus-specific chronic memory CD4⁺ and CD8⁺ T cells. Both CD8⁺ T cells specific for nonstructural large T (LT) antigen and viral capsid (VP)-specific CD4⁺ T cells were notably reduced. Although a decrease in LT-specific CD4⁺ T cells was less obvious, there appeared to be a shift toward more cells bearing a central memory T cell phenotype. These results suggest that some MPyV-specific T cells are dependent on MPyV antigen for their persistence, whereas others retain the potential to differentiate into cells with phenotypes associated with bona fide memory cells capable of antigen-independent survival and robust recall responses.

Drugs have been used in several model systems to reduce or eliminate pathogen load and inflammation. Treatment with ribavirin of mice early in infection with a chronic strain of LCMV, an RNA virus, resulted in blunted viral titers and a rescue in CD4⁺ T cell effector cytokine functionality (42). More recently, the Tarleton group used benznidazole to cure mice of persistent infection by *T. cruzi*, the causative agent of Chagas disease, and found that a stable, antigen-

independent central memory CD8⁺ T cell population emerged, which could mount a robust protective recall response (43). Our rationale for developing the floxed MPyV A2.Flx stems from the lack of available drugs having a demonstrable direct effect against polyomaviruses. We find that Cre-mediated deletion of floxed genes essential for viral replication appears to be a viable alternative for reducing levels of MPyV both in vitro and in vivo. However, a caveat is that although we did not believe insertion in a noncoding region and a region reported to tolerate a 66 bp deletion (39) would significantly impact viral growth, we found that A2.Flx is highly attenuated compared to wildtype MPyV even when propagated on highly permissive baby mouse kidney cells. This may account for the difficulties we see in detecting viral DNA by Taqman qPCR in tissues in B6 or Cre negative control mice later in persistent infection (e.g. d60 p.i.). Our group typically measures MPyV levels using Taqman qPCR for LT, but due to the disruption of the normal LT-specific Taqman probe by the downstream loxP site near the BlnI restriction site (Figure 1A), we had to design a new LT-specific probe that hybridized upstream of the BlnI site. This probe is far less efficient at detecting even wildtype viral DNA compared with the normal probe (unpublished data) and probably compounds the problem. We have recently acquired qPCR primers specific for the major viral capsid VP1 from one of our collaborators (E. Szomolanyi-Tsuda, UMass Medical School), and it remains to be seen if these will improve our detection of A2.Flx in vivo since VP1 is untouched.

Attenuation of A2.Flx could stem from defects in the functions of LT, which is required for initiation of MPyV DNA replication and plays critical roles in controlling viral gene transcription including activating transcription of viral capsid genes (44). Replication and transcription are controlled from the noncoding region (NCR) between the coding sequences for T antigens (early genes) and viral capsid proteins (late genes). The NCR consists of a core origin of replication (ori), promoter elements, and enhancer elements (45-49). LT binds to sequences within these regulatory elements with the consensus motif of G(A/G)GGC (50) and recruits the

host cell transcriptional and DNA replication machinery (44). In addition, LT binding of the retinoblastoma protein (pRb) inactivates it and promotes the G1 → S transition (51). Based on DNA and protein sequence analysis, the BlnI site at which we inserted one loxP sequence does not encode residues critical for LT function, but it lies between the nuclear localization signal and a pRb binding site (44). By substituting one base to insert the 34 bp loxP sequence in frame with LT, we added 11 extra amino acids and changed an aspartate (D) into a tyrosine (Y). Those additions could possibly alter folding of LT and negatively impact activity of functional domains. Interestingly, although they did not observe a significant difference in viral replication based on in vitro growth curves, Bendig et al. reported that their mutant with the 66 bp deletion in the region where the BlnI site is located synthesized 60% as much viral DNA as wildtype (39). Thus, changes at this site are not as innocuous as previously thought. It is also possible that the attenuation of A2.Flx may also be due to disruptions of key cis-regulatory elements in the NCR. However, the loxP site inserted adjacent to the BglI site does not disrupt any LT binding sites, although one is in the BglI recognition sequence and another is immediately downstream (50). Even if there was a disruption of these sites, this alone would not be enough to account for the severe attenuation of A2.Flx we have observed. In addition, this site does not include any replication or transcription control elements. Therefore, it appears unlikely that this loxP insertion is detrimental to MPyV replication. Nonetheless, we did not test whether any one of these insertions alone could attenuate the virus.

The severe attenuation of A2.Flx, especially in vivo, is a glaring defect in the system that needs to be rectified. We need to redesign floxed polyomavirus so that it is far less attenuated and more detectable in normal, persistently infected mice. If the current placement of loxP at the BglI site in the NCR indeed does not significantly impair MPyV replication, that site could be left alone. To avoid disruption of protein coding sequence, the second loxP site could be inserted in the NCR but on the late gene side, where the viral capsid proteins are encoded. However, we

would need to be cautious and ensure the loxP site does not disrupt the late gene promoter sequences that lie in the enhancer (45) or the mRNA processing signals, including the mRNA leader sequence (52, 53). This leaves a stretch of 10-15 bp between the transcription start sites for the viral capsid genes and the end of the leader sequence as a potential site to insert a second loxP. Due to a lack of a nearby unique restriction enzyme site, this loxP may have to be inserted using methods other than the one we utilized to generate the original A2.Flx. We could make use of the sequence and ligation independent cloning (SLIC) method with mixed PCR inserts developed by Li and Elledge (54). If we can generate an A2.Flx v2 virus that is far less attenuated, we could splice out nearly the entire NCR following Cre recombination, which would terminate both replication and transcription.

Even if we could demonstrate that Cre activation during persistent infection ablates A2.Flx replication, the question remains as to why MPyV epitope-specific T cells did not react the same way. Our group previously observed that MPyV-specific chronic memory CD8⁺ T cells poorly self-renew and survive despite the presence of persistent antigen, which puts an onus on de novo recruitment of antigen-specific CD8⁺ T cells during persistent infection for maintenance (8). MPyV-specific CD4⁺ T cells during persistent infection also appeared to display this behavior (31). Thus, during persistent MPyV infection, virus-specific T cell populations comprise a hodge-podge of cells primed under different antigenic/inflammatory conditions and having a different history of persistent stimulation. T cells primed early during high antigen and inflammation conditions will tend to be more terminally differentiated, short-lived effector/effector-memory T cells, whereas de novo primed naïve antigen-specific T cells encounter less antigen/inflammation and differentiate toward a central memory T cell phenotype (8, 9) as has been shown for latecomer T cells (27-30). However, this occurs under the shadow of repetitive antigen stimulation, which has been shown to increase T cell differentiation toward a more CD62L^{lo} effector/effector-memory T cell phenotype, diminishes cytokine production especially of IL-2,

increases expression of senescent markers such as KLRG-1 (on CD8⁺ T cells), and eventually degrades proliferative potential (15, 16). How much repetitive stimulation impacts epitope-specific T cells may depend on differences in the strength of antigenic signaling. Both LT₃₅₉-specific CD8⁺ T cells and VP1₂₂₁-specific CD4⁺ T cells display a more activated phenotype than LT₆₇₈-specific CD4⁺ T cells during early to middle persistent infection with wildtype MPyV (d30-60 p.i.) as evidenced by a notable frequency of cells with low expression of CD127 and higher amounts of inhibitory receptors like PD-1 (VP1₂₂₁) or KLRG-1 (LT₃₅₉) (8, 31). As a result of less stimulation, the LT₆₇₈-specific CD4⁺ T cells may retain some plasticity and acquire a central memory phenotype after a fall in antigen. On the other hand, more stimulated and earlier primed VP1₂₂₁- and LT₃₅₉-specific T cells die, leaving residual populations of presumably more recently primed cells for which the fate is currently unclear. These cells could continue to decline or develop into stable, antigen-independent memory T cells. Transfer of sorted cells into naïve or MPyV-infected mice could provide an answer.

Admittedly, the changes in the number of virus-specific T cells we detect are fairly modest. The LT₃₅₉-specific CD8⁺ T cells and VP1₂₂₁-specific CD4⁺ T cells only decreased about 2 fold in Cre/Esr mice compared to littermates, while LT₆₇₈-specific CD4⁺ T cells appeared to decrease less obviously (Figure 3B). The residual intact A2.Flx DNA we detect in our in vitro Cre-mediated recombination assays (Figure 1B) suggests that the ratio of Cre to target DNA is critical in determining the efficiency of the Cre reaction. The stoichiometry of Cre recombination has been calculated to be 4 molecules of Cre per recombination event (34). An increase in the ratio of Ad-Cre versus A2.Flx per infected cell may lead to more Cre-mediated deletion and a larger drop in MPyV replication. Increasing Cre induction in Cre/Esr mice by administering more tamoxifen may also result in effects that are more visible (33). An experiment is currently underway in which Cre/Esr and littermate mice persistently infected with A2.Flx (d35 p.i.) have been given 10 rather than the 5 consecutive injections of tamoxifen initially used (Figure 3A).

Even if a more dramatic effect on chronic memory MPyV-specific T cells is detected, we are still left with the question of whether the loss in cells was due to an inability to de novo prime naïve antigen-specific cells or the death of T cells primed earlier that required antigen for their self-renewal and survival. In addition, residual T cells would themselves still consist of cells with varying antigen stimulation experiences. To better control the timing of T cell priming, we have recently constructed an MPyV in which the D^b-restricted LT₃₅₉ epitope was mutated by single base substitutions to the highly homologous D^b-restricted LT₂₀₆₋₂₁₄ epitope from SV40 LT antigen, for which TCR-1 TCR transgenic CD8⁺ T cells are specific (55). We are currently in the process of constructing an MPyV that would combine features of this MPyV.LT206 virus with A2.Flx. This MPyV.Flx.LT206 virus will enable us to adoptively transfer TCR-1 cells at different time points post infection into Cre/Esr and littermates then administer tamoxifen at differing times post transfer to reduce viral replication. We can thereby better test the hypothesis that less stimulated MPyV-specific T cells can develop into bona-fide memory T cells imbued with the ability to persist independently of antigen and mount a robust, protective recall response.

Figure Legends

Figure 1. Cre-mediated deletion of A2.Flx impacts viral replication in vitro. (A) Schematic depicting genome of A2.Flx compared to wildtype MPyV strain A2. Result of Cre-mediated recombination of A2.Flx is also depicted. Black dot indicates origin of replication. Arrows above the DNA indicate PCR primers flanking the floxed region, which were used to determine the extent of deletion. (B) PCR of DNA from nMuMG cells following infection with wildtype (WT) MPyV or A2.Flx with or without AdCre co-infection. nMuMG cells were first infected with AdCre for 24 hrs prior to infection with MPyV. PCR was run on DNA isolated from cells 48 h p.i. with A2.Flx or WT MPyV. (C) Copies of MPyV genome in A2.Flx infected compared with A2.Flx/Ad-Cre co-infected nMuMG as measured by qPCR. Infections done as discussed in (B). Data are from 2 independent experiments.

Figure 2. MPyV-specific CD4⁺ and CD8⁺ T cell responses to A2.Flx are mounted in B6 mice and mice constitutively expressing Cre (CMV-Cre). (A) QPCR assay for copies of MPyV genome in spleen and kidney at d20 p.i. (B) Frequency of LT₃₅₉-specific CD8⁺ T cells in spleen at d20 p.i. as measured by D^b/LT₃₅₉ tetramer (*left*) or intracellular IFN- γ staining assay following direct ex vivo LT₃₅₉₋₃₆₈ peptide stimulation (*right*). (C) Splenic LT₆₇₈-specific (*left graph*) and VP1₂₂₁-specific (*right graph*) CD4⁺ T cells at d20 p.i. Frequencies are of CD4⁺ T cells that are I-A^b tetramer⁺CD44^{hi} (*left side of graphs*) or IFN- γ ⁺CD154⁺ following direct ex vivo stimulation with indicated peptides (*right side of graphs*).

Figure 3. Loss of virus-specific chronic memory T cells following ablation of A2.Flx during persistent infection. (A) Experimental set-up. Cre/Esr or transgene negative littermate controls were infected with A2.Flx. Tamoxifen was administered starting at d35 p.i. and given once daily

for 5 days. 30 days after the last tamoxifen injection, mice were sacrificed and MPyV-specific T cell responses assessed. (B) Comparison of the numbers of MPyV-specific CD8⁺ and CD4⁺ T cells in Cre/Esr versus Cre negative controls. Number of LT₃₅₉-specific CD8⁺ T cells as assessed by D^b/LT₃₅₉ tetramer staining (*left*). Number of CD4⁺ T cells specific for LT₆₇₈₋₆₉₀ and VP1₂₂₁₋₂₃₅ as assessed by I-A^b tetramer staining (*right*). (C) qPCR assay for MPyV genomic DNA in spleen and kidney. Data in all graphs represent mean of 5-6 mice per group in two independent experiments. P values calculated using the nonparametric Mann-Whitney U test.

Figure 4. Functional competence of MPyV-specific T cells is unaltered by reduction in A2.Flx replication during persistent infection. (A) Comparison of the frequency of tetramer versus intracellular IFN- γ staining of (from left to right) LT₃₅₉-specific CD8⁺ T cells, LT₆₇₈-specific CD4⁺ T cells, and VP1₂₂₁-specific CD4⁺ T cells in Cre/Esr mice versus littermates. Splenocytes were stained directly ex vivo with D^b/LT₃₅₉, I-A^b/LT₆₇₈, or I-A^b/VP1₂₂₁ tetramers. Alternatively, they were stimulated ex vivo with the respective peptides and stained intracellularly for IFN- γ , CD154 (LT₆₇₈- or VP1₂₂₁-stimulated only), and IL-2. (B) IL-2 co-production with IFN- γ . Data shown is from the same mice depicted in Figure 3.

Figure 5. Epitope-specific impact of persistent antigen on phenotype of MPyV-specific chronic memory CD4⁺ and CD8⁺ T cells. (A) Frequency of tetramer⁺CD44^{hi} CD4⁺ and CD8⁺ T cells that are CD62L^{hi}CD127^{hi} central memory (T_{CM}), CD62L^{lo}CD127^{hi} effector memory (T_{EM}), or CD62L^{lo}CD127^{lo} effector (T_{eff}) cells. Splenocytes were stained directly ex vivo with the indicated tetramers and for CD4, CD8, CD44, CD62L, and CD127. (B) Level of Bcl-2 expressed by MPyV-specific CD4⁺ and CD8⁺ T cells from spleen as measured by geometric mean fluorescence

intensity (gMFI) of staining by antibody for Bcl-2. Data are from the same mice shown in Figure

3. P values calculated using the nonparametric Mann-Whitney U test.

Figure 1

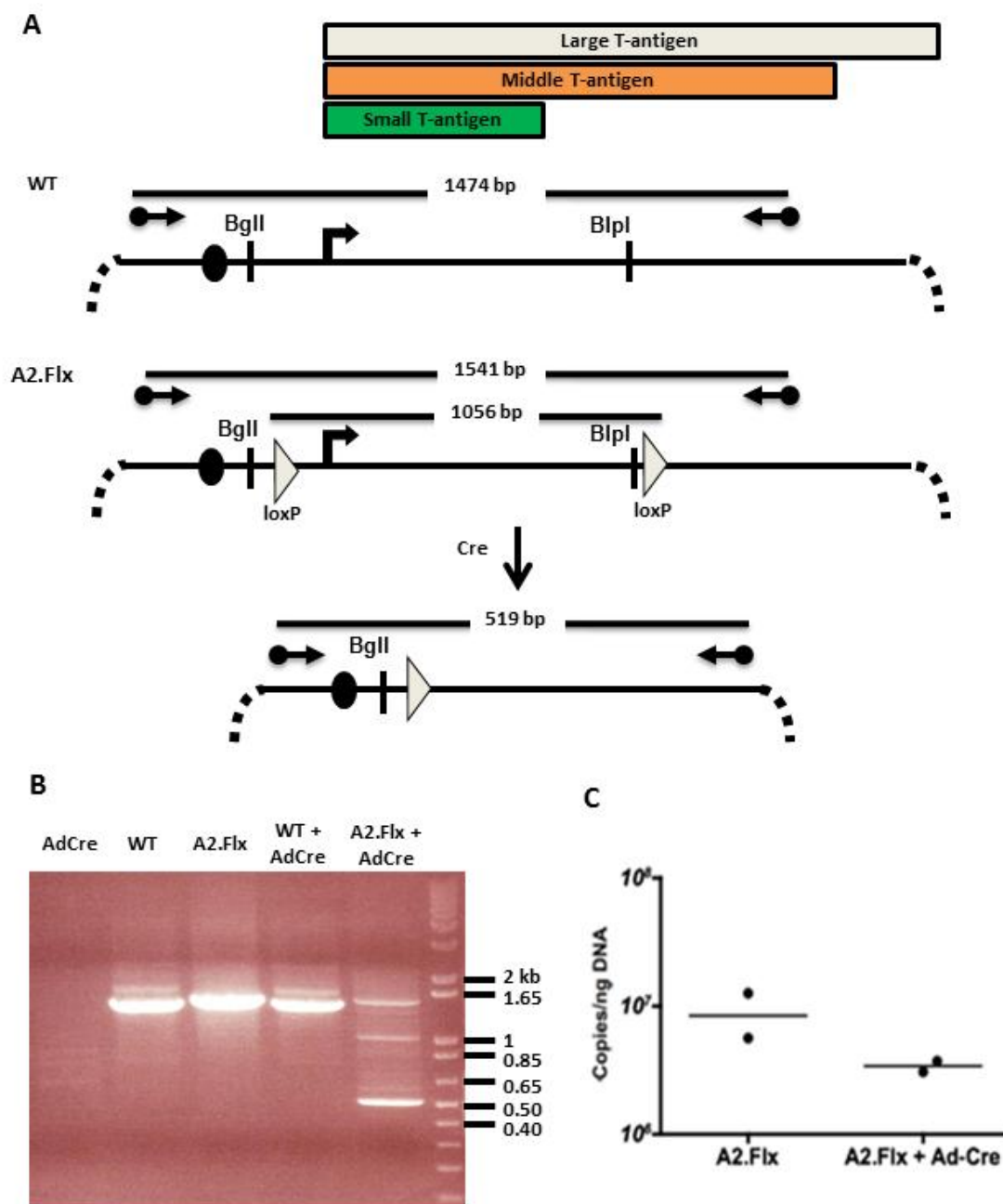


Figure 2

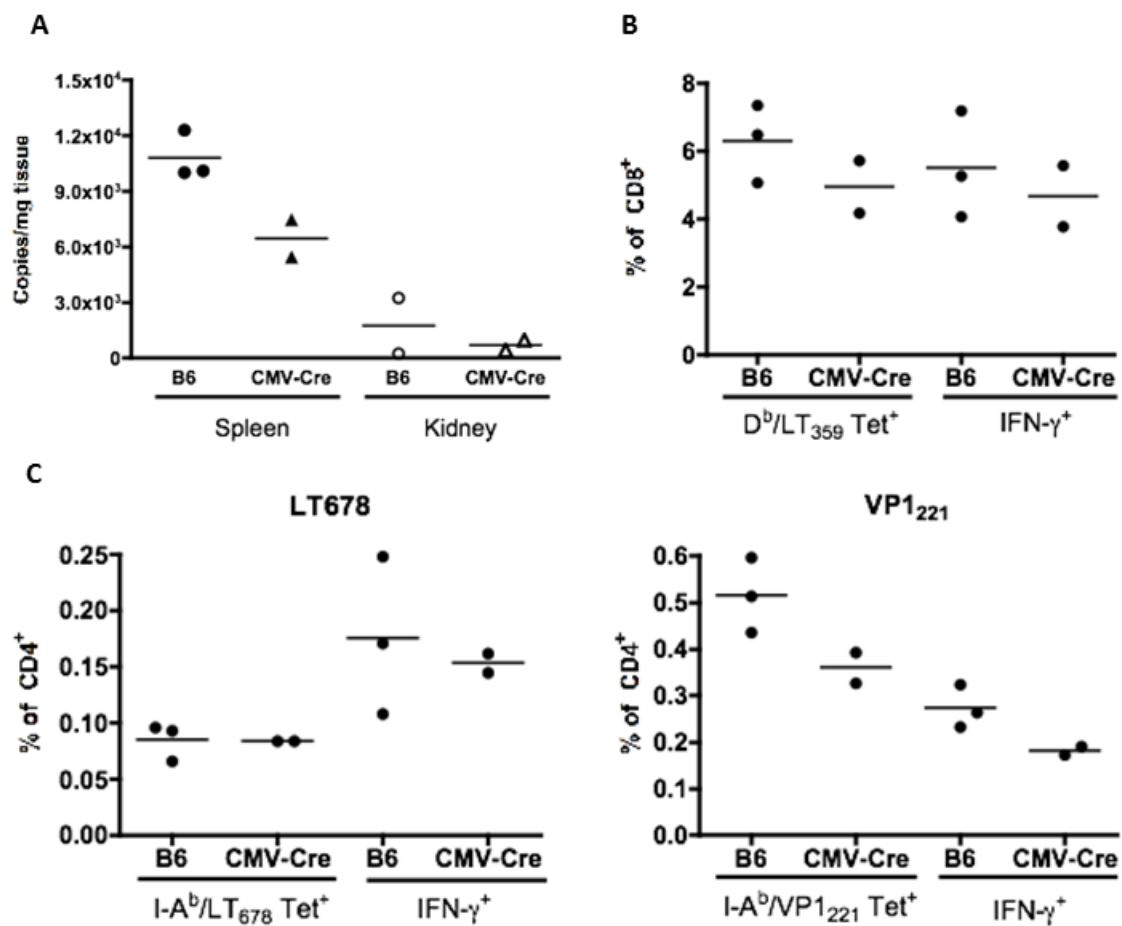
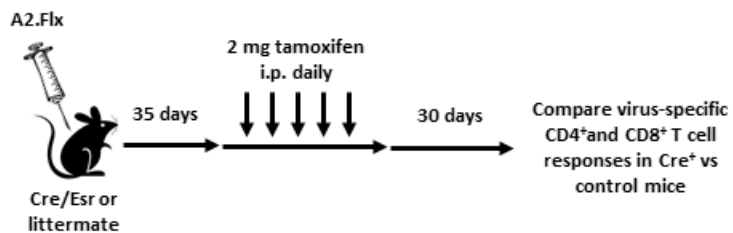
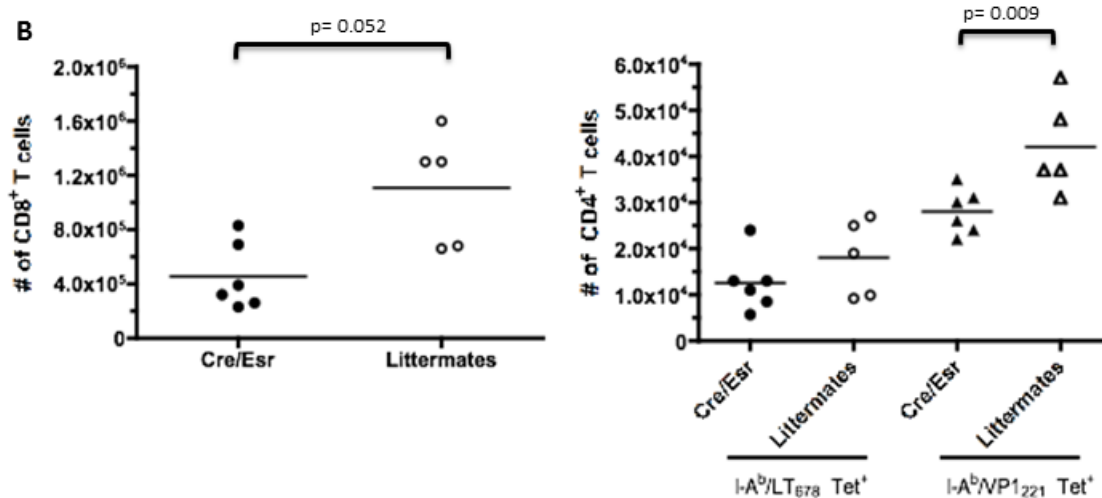


Figure 3

A



B



C

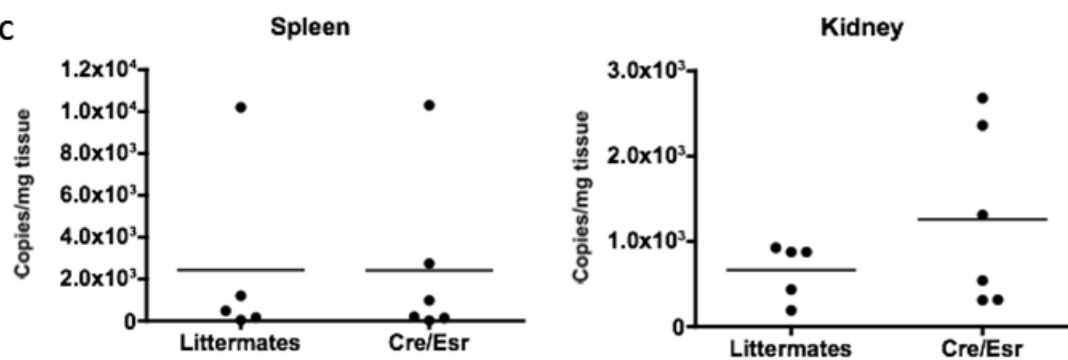


Figure 4

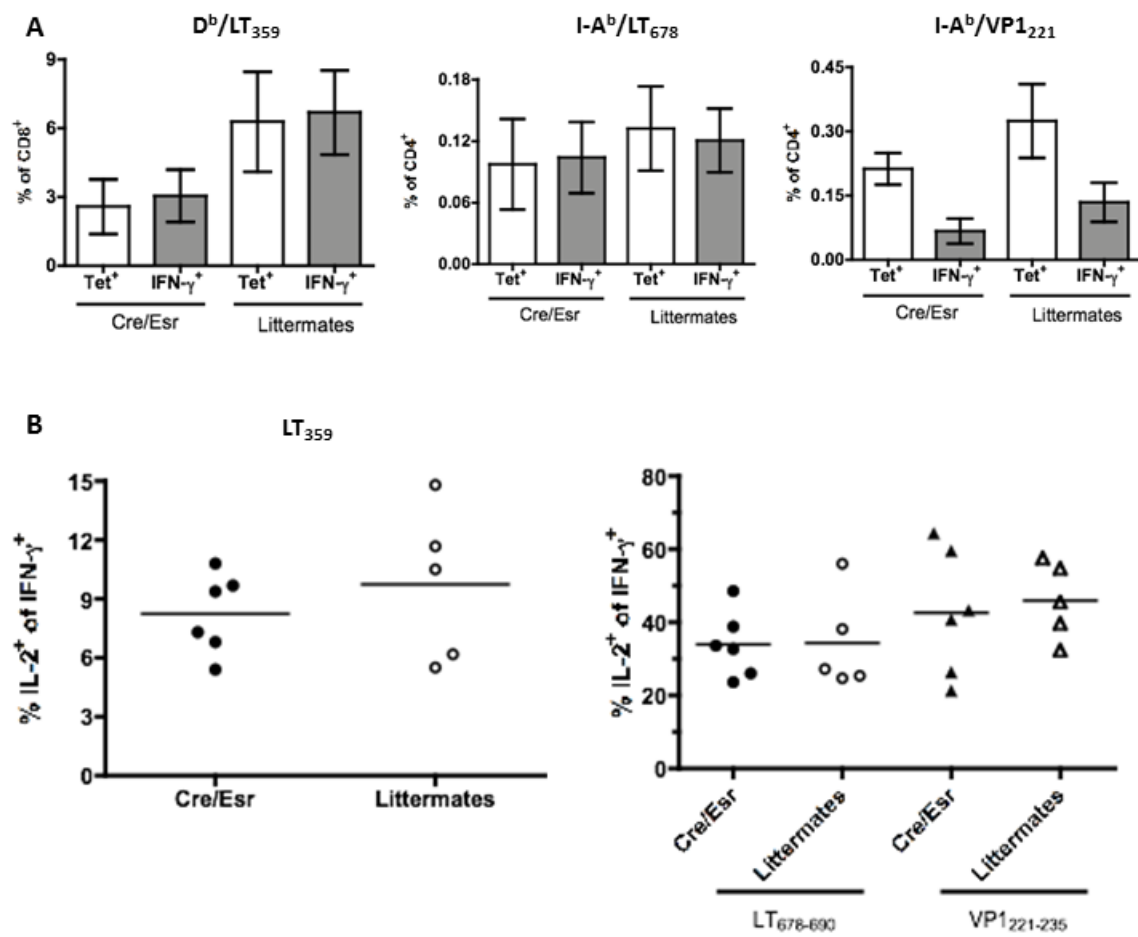
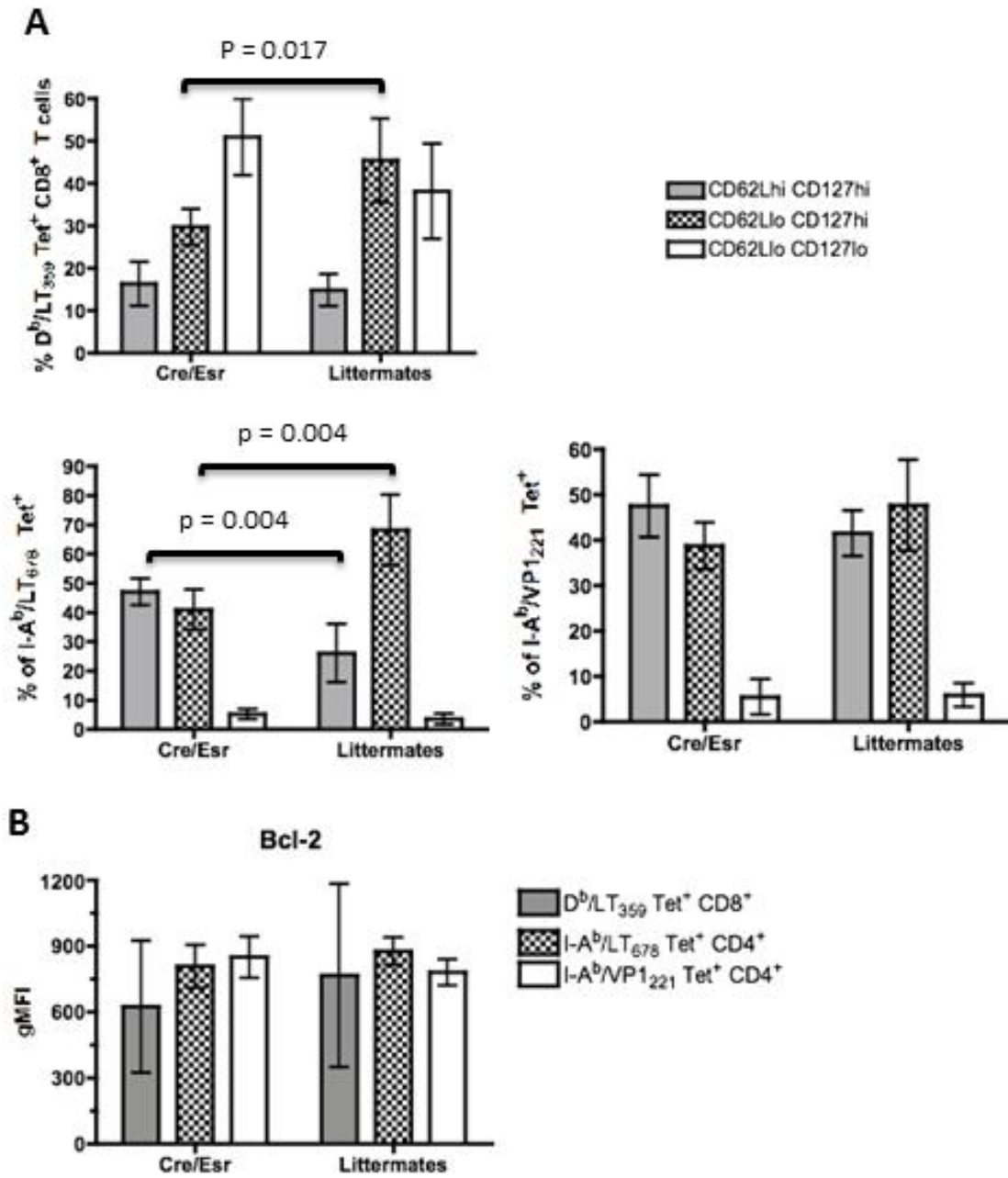


Figure 5



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Chapter 4: Discussion

CD4⁺ T cells are an integral component of the immunosurveillance against viral infection. Much of the literature demonstrates a critical impact of CD4⁺ T cell “help” on the generation of optimal antibody responses and optimal virus-specific CD8⁺ T cell responses in models of both acutely resolved and persistent infections (1-4). Effector CD4⁺ T cells express a wide array of cytokines and surface molecules that have been the focus of studies into the molecular mechanisms of CD4⁺ T cell help. However, CD4⁺ T cells differentiate into subsets of T helper (T_H) cells that express different sets of effector molecules and perform different functions. T_H differentiation is mercurial, and changes in the surrounding conditions could alter the particular properties of an effector CD4⁺ T cell (5). This issue could be particularly problematic during persistent viral infections, where the environment is dynamic. Thus, there is a need to study virus-specific CD4⁺ T cell responses as they develop over the course of persistent infection.

Studies of acutely resolved infections showed that virus-specific CD4⁺ T cells could develop into functional and heterogeneous memory T cells that are maintained by antigen-independent self-renewal (6). However, during chronic high load viral infections such as with HIV/SIV (7) and chronically infecting strains of LCMV (e.g., clone 13 (8)), virus-specific CD4⁺ T cells become functionally exhausted and increase expression of inhibitory receptors (9-11). Although more recent studies with LCMV chronic infection models suggest that virus-specific CD4⁺ T cells are not actually exhausted but driven into an altered differentiation state by the high antigen load (12), less is known regarding how CD4⁺ T cells cope with low-level persistent infections. We and others working with low-level persistent viruses such as mouse polyomavirus, mouse and human cytomegalovirus (CMV) (13, 14), and mouse γ -herpesvirus 68 (MHV68) (15, 16) have begun to address this knowledge gap. In addition, we could not find studies addressing the issue of CD4⁺ memory T cell development during persistent infection (i.e., “chronic memory CD4⁺ T cells”). This is in marked contrast to chronic memory CD8⁺ T cells for which studies

using multiple persistent viral infection models show that maintenance requires antigen for self-renewal and/or de novo priming of virus-specific CD8⁺ T cells (17-21).

Mouse polyomavirus (MPyV) has proven to be a valuable model for studying T cell responses in the setting of low-level persistent infection. Taking advantage of its rather small size genome, which encodes only 6 genes, Kemball et al. identified several CD8⁺ T cell epitopes in nonstructural T antigen proteins in B6 (H-2^b) mice by screens of overlapping peptides covering the viral proteins (17). Studies of immunodominant D^b-restricted LT₃₅₉-specific CD8⁺ T cell populations showed that MPyV-specific CD8⁺ T cells remain polyfunctional despite persistent infection (17, 22). More importantly, maintenance of MPyV-specific chronic memory CD8⁺ T cell populations was found to require continual recruitment of new naïve antigen-specific CD8⁺ T cells during persistent infection (17, 20). This process depends on CD4⁺ T cell help (23). However, a detailed analysis of the functional profile and fate of MPyV-specific CD4⁺ T cells had to wait until we identified I-A^b-restricted epitopes. The identification of two CD4⁺ T cell epitopes and our ability to track the responding populations over the course of infection through newly developed peptide:major histocompatibility complex (pMHC) II tetramers and intracellular cytokine assays mark major steps forward. These tools enabled us to determine if MPyV-specific CD4⁺ T cells become dysfunctional over time and whether chronic memory CD4⁺ T cell populations decline or are maintained.

Tracking both the large T antigen (LT)- and major capsid protein VP1- specific CD4⁺ T cells from acute to persistent phases of MPyV infection unveiled unexpected heterogeneity in function and phenotype (Chapter 2). Much of this diversity may well have remained hidden without access to pMHC II tetramers for both epitopes. In particular, we were struck by the diminished functionality displayed by VP1-specific CD4⁺ T cells starting early in acute infection and sustained through the persistent phase, which was not seen with LT-specific CD4⁺ T cells. This was not expected since MHC class Ia-restricted MPyV-specific CD8⁺ T cells were fully

functional. The difference in function between the two epitope-specific CD4⁺ T cell populations extended to the pattern of effector cytokine polyfunction (IFN- γ , TNF- α , IL-2). Heterogeneity in effector cytokine polyfunctionality amongst epitope-specific CD4⁺ T cells to low-level persistent infection was also recently observed by Arens et al in MCMV infection (13). However, unlike us, they did not utilize pMHC II tetramers, and it remains unclear whether MCMV-specific CD4⁺ T cells too can lose function. pMHC II tetramers also allowed us to detect the heterogeneity in CD127 and PD-1 expression within the VP1-specific but not LT-specific CD4⁺ T cell population. Thus, reliance only upon cytokine assays may not provide a full picture of what is going on with CD4⁺ T cells in a low-level persistent infection.

The phenotypic and functional heterogeneity between both MPyV-specific CD4⁺ T cell populations could be the result of differences during priming in the strength and duration of antigenic signaling, which are critical determinants that drive differentiation of CD4⁺ T cells (24). The pattern of viral protein expression could impact access to the MHC class II presentation pathway and subsequent antigen availability. MPyV capsid proteins like VP1 are expressed in productively infected cells, whereas nonstructural proteins like LT are produced in all infected cells regardless of virion production. As LT is produced in the cytoplasm of infected cells, it is likely inefficiently shunted into the MHC class II presentation pathway unless taken up by phagocytic APCs from the debris of lysed cells. VP1 could be acquired via the same route, but as MPyV virions bind to sialylated glycoproteins and glycolipids expressed on the surface of cells (25), receptor mediated endocytosis could provide an additional source of VP1 for processing by the MHC class II pathway. As a result, the chances for antigen encounter by VP1-specific CD4⁺ T cells would be much greater than for LT-specific CD4⁺ T cells. Alternatively, VP1-specific CD4⁺ T cells may express higher avidity TCRs. Others have shown a direct correlation between mean fluorescence intensity (MFI) of tetramer binding and TCR affinity for pMHC (26, 27). The higher I-A^b/VP1₂₂₁ tetramer gMFI compared to that of I-A^b/LT₆₇₈ (data not shown) would seem to

support this. Additional evidence for high avidity TCR comes from the narrow TCR V β repertoire for VP1-specific CD4⁺ T cells. The work of Baumgartner and colleagues has shown that the efficiency of T cell activation by antigen impacts clonotypic diversity (28). Less stable pMHC II complexes and lower antigen doses focus antigen-specific CD4⁺ T cell responses toward a less diverse TCR repertoire composed of higher affinity clonotypes. Since dendritic cells (DCs) can be infected by MPyV (29) and production of viral capsid protein presages cell death, only high affinity VP1-specific CD4⁺ T cell clones would be expected to be primed if antigenic signal were to suddenly dissipate. Overall, VP1-specific CD4⁺ T cells appear to be more strongly stimulated with a visible proportion of cells being CD127^{lo} and PD-1^{hi}. In future, it may be of interest to generate antigen-specific T cell clones to test the impact of antigen dose on activation and differentiation. Recently a novel 2D assay that measures TCR-pMHC binding affinity by T cell:pMHC-coated red blood cell contact was used to compare affinities of viral antigen-specific and autoantigen-specific CD4⁺ T cells (30). This could be used to test the TCR affinity of sorted VP1- versus LT-specific CD4⁺ T cells.

Despite differences, both LT- and VP1-specific CD4⁺ T cell populations appear to be maintained by the same mechanism. Both underwent minimal contraction and were stably maintained through the persistent phase of infection, which contrasts with some reports that pathogen-specific CD4⁺ memory T cells emerging after resolution of an acute infection steadily decline over time (31-33). This would seem to reinforce assertions by some that memory CD4⁺ T cells are dependent on some antigen for optimal survival (34). However, we found that MPyV-specific CD4⁺ T cells in persistently infected mice minimally proliferate and are highly apoptotic. This largely rules out antigen-driven proliferation, which is exhibited by LCMV chronic memory CD8⁺ T cells (18), as the mechanism of maintenance of MPyV-specific chronic memory CD4⁺ T cell populations. Instead, the striking similarity to the lack of proliferation and poor survival of MPyV-specific CD8⁺ T cells (20) led us to investigate the possibility that naive virus-specific

CD4⁺ T cells are still being primed during persistent infection. The partial bone marrow (BM) chimera protocol used to demonstrate de novo CD8⁺ T cell priming (17, 20) proved highly useful as it allowed us to demonstrate de novo priming of both MPyV antigen-specific CD4⁺ T cells using our pMHC II tetramers. The finding that naive CD4⁺ T cells specific for both LT and VP1 are de novo recruited in persistently infected mice affirms our long-held contention that MPyV productively replicates continually at low levels. It is interesting that both virus-specific CD4⁺ and CD8⁺ T cell populations are actively maintained by de novo recruited antigen-specific cells. This reflects on the close cooperation between these two critical cell types. CD4⁺ T cells may be needed to license APCs to drive de novo priming of naïve virus-specific CD8⁺ T cells as a result of reduced inflammation during persistent infection. Although we are not the first to clearly demonstrate de novo priming of CD4⁺ T cells specific for persisting viruses, the study showing de novo generation of CD4⁺ T cells against persistent viral infections in baboons merely placed this in the context of immune reconstitution (35). We, however, are showing it as a mechanism to maintain CD4⁺ T cell immunosurveillance. As both virus-specific CD8⁺ T cell and anti-MPyV antibody responses are drastically diminished in persistently infected mice lacking CD4⁺ T cells (23), we feel that continual de novo recruitment of new MPyV-specific CD4⁺ T cells is critical for maintaining support for B cells and CD8⁺ T cells to keep persistent virus in check. Since CD4⁺ T cells are critical for control of other persistent infections as well, others are starting to look at the possibility of continued recruitment of virus-specific CD4⁺ T cells in their systems. Most recently, Freeman et al demonstrated that adoptively transferred TCR transgenic (Tg) CD4⁺ T cells specific for an epitope in MHV68 were activated during both acute and latent phases of infection (15).

Continual de novo generation of MPyV-specific CD4⁺ T cells throughout the course of persistent infection has potential implications regarding CD4⁺ T cell heterogeneity in vivo. The literature is replete with studies demonstrating that differentiation of CD4⁺ T cells into distinct T_H subsets is regulated by the antigenic, inflammatory, and costimulatory environment during

priming of naïve CD4⁺ T cells (36, 37). There is increasing evidence, however, that CD4⁺ T cells may be far more plastic than originally thought. For instance, Hegazy et al. recently showed that they could convert in vitro generated LCMV-specific memory T_{H2} cells into dual personality T_{H1+2} cells, which simultaneously expressed characteristics of both T_{H1} and T_{H2} cells, when rechallenged in vivo with LCMV (38). As persistent infection is a state of continuous rechallenge, shifts in the overall cytokine and antigen environment could reprogram chronic memory antigen-specific CD4⁺ T cells. This has been shown to occur during chronic LCMV infection where virus-specific CD4⁺ T cells lose IL-2 production but ramp up production of IL-21 and are redirected from a T_{H1} into a T follicular helper (T_{FH}) cell program (8, 12, 39). Although we did not observe a loss in IL-2 production, we too see increased IL-21 production by both VP1- and LT-specific CD4⁺ T cells during persistent MPyV infection (Chapter 2, Figure 3). We would argue, however, that this is unlikely to be because of just reprogramming of antigen-experienced virus-specific CD4⁺ T cells but could reflect differential programming of de novo recruited cells primed under conditions different from those primed earlier in acute or persistent infection.

Different antigen and inflammation conditions can also influence the development of memory T cells into either central memory T (T_{CM}) cells or effector memory T (T_{EM}) cells. So-called “latecomer” T cells primed after acute infection or immunization receive lower antigenic and inflammatory cues and develop into CD62L^{hi} T_{CM} cells, which are considered intermediately differentiated (40-43). Repetitive and/or overly robust antigen stimulation, on the other hand, pushes T cells into more terminally differentiated CD62L^{lo} effector T (T_{Eff})/T_{EM} cells as seen in chronic LCMV(44). We thus expected to find that de novo primed MPyV-specific CD4⁺ T cells would also be CD62L^{hi}. However, we were unable to satisfactorily phenotype the donor-derived I-A^b tetramer⁺ CD4⁺ T cells in our chimeras due to mouse-to-mouse variability and low frequencies. De novo primed MPyV-specific CD8⁺ T cells, on the other hand, have been shown to have a CD62L^{hi} CD27^{hi} T_{CM} cell phenotype as compared to the predominant CD62L^{lo} T_{Eff}/T_{EM}

cell phenotype of the bulk population (17, 20). Furthermore, the frequency of T_{CM} phenotype virus-specific CD8⁺ T cells in normal infected mice gradually increases over time. This suggested that de novo recruited virus-specific CD8⁺ T cells are actively contributing to the overall heterogeneity of the virus-specific T cell pool (20). Indirect evidence that de novo primed virus-specific CD4⁺ T cells also contribute to chronic memory T cell heterogeneity can be seen in the biphasic staining for PD-1 and CD127 on VP1-specific CD4⁺ T cells during persistent infection at d60 p.i. (Chapter 2, Figure 5). It is possible that the CD127^{hi} and PD-1^{lo} VP1-specific CD4⁺ T cells represent recently recruited cells while CD127^{lo} and PD-1^{hi} cells are older, more stimulated cells. Besides the low detectability of donor-derived CD4⁺ T cell priming, another key issue of the BM chimera approach is the length of time (about 90 days for the CD4⁺ T cell experiments) between bone marrow transfer and analysis of virus-specific T cells. This was given to allow for engraftment and thymic selection to take place. As a result, the donor population itself is an amalgam of cells primed at different times and enduring varying degrees of persistent stimulation. A legitimate question is how we would know that the changes in phenotype over time are due to newly emerging virus-specific T cells rather than cells primed earlier that retained plasticity and were reprogrammed.

To control the timing of priming, we need a TCR Tg cell adoptive transfer system. This approach is being used to compare acute versus persistent phase infection primed CD8⁺ TCR Tg cells specific for an epitope in SV40 LT antigen, which was engineered into MPyV by site-directed mutagenesis of the homologous immunodominant D^b-restricted LT epitope. Like the de novo primed CD8⁺ T cells, TCR-I Tg cells primed during the persistent phase of MPyV.LT206 infection adopt more T_{CM}-like properties including higher CD127 expression, increased cytokine production per cell (e.g., IL-2), improved survival, and superior recall capacity over acute primed cells (JJ Wilson, manuscript submitted). Hoping to make similar comparisons with antigen-specific CD4⁺ T cells, we created two new MPyVs carrying the epitopes recognized by OT-II and

SMARTA TCR Tg CD4⁺ T cells. In several experiments, we found that although the OT-II and SMARTA TCR Tg cells are primed during acute infection with MPyV.OVA-II and MPyV.GP66, respectively, only 1 out of every 3 recipient mice still retains detectable cells past d30 p.i. In contrast, after transfer into mice persistently infected with MPyV.GP66 (d35 p.i.), we have been able to detect priming of about 40-50% of adoptively transferred SMARTA cells at 60d post-transfer. These cells are mainly CD62L^{lo} and CD127^{hi} (unpublished data). The CD62L^{lo} phenotype may be a result of continued stimulation after initial priming. Nonetheless, the results confirm the CD8⁺ TCR Tg data that acute primed T cells may not survive as well as those primed during the persistent phase of infection. Future studies using the SMARTA TCR Tg system in conjunction with MPyV.GP66 could be done to address the requirements for persistent phase priming as well as the mechanisms of CD4⁺ T cell help during persistent infection. A major issue with the recombinant MPyVs, however, is that the epitopes are expressed in frame with T antigens. The TCR Tg cells would probably give us insights into regulation and function of the LT-specific CD4⁺ T cells, but these potential findings may not necessarily apply to capsid-specific CD4⁺ T cells. Ideally, it would be useful to have both VP1-specific and LT-specific CD4⁺ TCR Tg cells so that we would not have to modify MPyV and risk attenuating the virus.

Although continual de novo recruitment of virus-specific T cells may be a way to maintain a functional anti-viral T cell pool during persistent infection, thymic involution associated with aging would be expected to diminish the available pool of naïve antigen-specific T cell precursors (45). Thus, a key question is whether MPyV-specific T cells are capable of developing into antigen-independent memory T cells. Preliminary experiments using the A2.Flx/tamoxifen-inducible Cre system (Chapter 3) showed an impact on MPyV-specific T cell survival when Cre was induced during persistent infection that was epitope-dependent. The significant decline in both the LT-specific CD8⁺ and the VP1-specific CD4⁺ T cells but not the LT-specific CD4⁺ T cells in Cre⁺ mice may be related to the strength and duration of their stimulation by

antigen. Stronger repetitive antigen stimulation may have led to terminal differentiation, while weaker and/or less stimulation led to an intermediate state that permitted some plasticity when antigen conditions changed. This hypothesis could be tested by adoptive transfer of virus-specific TCR Tg cells at various time points prior to Cre induction and observe their fate as viral replication/antigen diminishes.

As costimulatory molecules play a key role in T cell priming (46), it would be interesting to determine the costimulatory requirements for de novo MPyV-specific CD4⁺ T cell priming. The CD40:CD154 (CD40L) interaction has been shown to be critical for priming of CD4⁺ T cells during the primary response as well as programming of effector function in memory cells in a peptide immunization model (47). CD27, which is highly expressed by both MPyV-specific CD4⁺ T cell populations during persistent infection (Chapter 2, Figure 5), is also reported to play a role in CD4⁺ T cell activation (48-50). In addition, we found high expression of inducible costimulator (ICOS) on both LT- and VP1-specific CD4⁺ T cells during persistent MPyV infection (unpublished data). ICOS expression is upregulated following activation on CD4⁺ T cells and is a critical regulator of CD4⁺ T cell proliferation, survival, effector function, and memory development (51). In particular, ICOS is critical for the development of the T_{FH} subset that is directly involved in helping B cells (36). The effect of blocking any of these pathways on MPyV-specific CD4⁺ T cells should be investigated.

As previously mentioned, there was enhanced peptide-stimulated production of the cytokine IL-21, a member of the IL-2 family, by both LT- and VP1-specific CD4⁺ T cells during persistent infection. Activated CD4⁺ T cells are the predominant source of IL-21, which is a pleiotropic cytokine with effects on various immune cells including CD8⁺ T cells and B cells. IL-21 appears to enhance the generation of memory CD8⁺ T cells and inhibits T cell senescence (52). Recently, three groups showed that IL-21 is critical for maintenance of functional virus-specific CD8⁺ T cells in persistent high load infection by chronically infecting strains of LCMV (39, 53,

54). The importance of IL-21 to CD8⁺ T cells during low-level persistent infections is thus far unclear, but a recent paper studying memory inflation of MCMV-specific CD8⁺ T cells reported IL-21 not to be critical for that process (55). IL-21 is highly expressed by T_{FH} cells, the CD4⁺ T cell subset responsible for B cell help, and has critical roles in driving plasma cell differentiation and class switching depending on the additional signals (1). Intriguingly, some VP1-specific CD4⁺ T cells during persistent MPyV infection might be T_{FH} cells, which express high levels of ICOS and PD-1 in addition to IL-21 (1). It remains to be seen what exactly IL-21 is doing during persistent MPyV infection, but given the multiple cells affected, we should proceed with caution.

Prior to work covered in this dissertation, we knew very little about how virus-specific CD4⁺ T cells cope with low-level persistent infections. Although we have found that the impact of persistent MPyV infection on the differentiation and function of virus-specific CD4⁺ T cells to be more complex than previously thought, our work has furthered understanding of how highly critical virus-specific CD4⁺ T cell populations can be sustained in the face of continuous bombardment by antigen. Despite differences between low-level persistent viruses, there may also be commonalities in the way CD4⁺ T cells respond to them. Clearly, further studies are needed to better understand the mechanisms that drive and control CD4⁺ T cell responses to persistent viral infection. Findings regarding MPyV-specific CD4⁺ T cells could have applicability for CD4⁺ T cell responses to infection by human polyomaviruses (HuPyV), which though normally clinically silent, can cause severe disease in the immunosuppressed. Like MPyV, CD4⁺ T cell responses to BK virus (BKV), which is associated with kidney transplant rejection, have been identified directed toward LT and VP1 (56). Recent work has also identified CD4⁺ T cells responding to the newly discovered HuPyV Merkel cell polyomavirus (57), a potential cause of aggressive Merkel cell carcinoma. Our host immune defenses must be kept on constant alert for not only incoming viral threats but also those that have managed to evade them and establish a niche within us. Continual support by CD4⁺ T cells other immune cells is essential to maximizing

the effectiveness of immunosurveillance against the ever-present threats posed by even normally clinically silent pathogens.

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