

How Much TCR Does a T Cell Need?

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Summary

Kinetic features of TCR:MHC/peptide interactions dictate their outcome in vitro, some important parameters of which include the number of molecules engaged and the duration of engagement. We explored the in vivo significance of these findings in transgenic mice expressing TCRs in a quantitatively and temporally controlled manner. As anticipated, reduced TCR levels resulted in attenuated reactivity, but response thresholds were substantially lower than expected—at as low as 1/20th the normal TCR numbers and with no indication of phenotypic skewing at suboptimal levels. We also studied survival of T lymphocytes stripped of their TCRs. Unlike B cells, T cells lacking antigen receptors did not die precipitously; instead, populations decayed gradually, just as previously reported in the absence of MHC molecules.

Introduction

The interaction between TCRs expressed by T cells and MHC/peptide complexes displayed on various cell types is the crux of T lymphocyte differentiation and acquisition of effector functions. Appropriate gauging of the quantity and quality of TCR:MHC/peptide engagements conditions the choices T cells make throughout their life cycle.

In the thymus, the newly assembled TCR of immature thymocytes interacts with MHC/self-peptide complexes on stromal epithelial cells. If strong, this engagement results in clonal deletion of thymocytes by apoptosis. If within an “acceptable” range of avidity, the outcome is positive selection and differentiation into mature, exportable T cells. If engagement is weak or absent, immature thymocytes quickly die of neglect. The affinity/avidity criteria that define acceptable are still unclear, as are the factors that condition commitment to the CD4⁺ versus CD8⁺ lineage.

In peripheral lymphoid organs, continued interaction

with MHC/self-peptide complexes is required for maintenance of the naive T cell pool. It has been shown, employing a variety of experimental systems, that T cells deprived of peripheral MHC/peptide engagements have a reduced life span (Rooke et al., 1997; Takeda et al., 1996; Kirberg et al., 1997; Brocker, 1997; Witherden et al., 2000; Tanchot et al., 1997; Nestic and Vukmanovic, 1998); engagement of the restricting element that promoted positive selection in the thymus appears to be necessary (Kirberg et al., 1997; Tanchot et al., 1997; Boursalian and Bottomly, 1999; Viret et al., 1999). Yet, a wide range of half-lives in the absence of MHC/peptide interactions has been reported with the different systems, and it is also not clear whether CD4⁺ and CD8⁺ T cell populations show the same decay kinetics. Very recently, a few reports even questioned the link between MHC/peptide engagement and T cell survival (Dorfman et al., 2000; Clarke and Rudensky, 2000). TCR:MHC peptide interactions also drive the homeostatic expansion that takes place in response to lymphopenic environments (Ernst et al., 1999, and references therein). Although proliferation in this context appears to be a response to environmental cues signaling that the T cell compartment is not full, TCRs vary in their ability to promote homeostatic proliferation, suggesting that the affinity/avidity constants of MHC/self-peptide recognition may come into play (Ernst et al., 1999; Goldrath and Bevan, 1999; Rocha and von Boehmer, 1991; Clarke and Rudensky, 2000; Kieper and Jameson, 1999; Oehen and Brduscha-Riem, 1999; Ferreira et al., 1999; Surh and Sprent, 2000; Correia-Neves et al., 2001).

Finally, active proliferation and terminal differentiation into effector cells are provoked by antigens presented as short peptide fragments encased within MHC molecules displayed on antigen-presenting cells (APCs). The signal induced by these strong agonist ligands is somehow read as being different from the “tickling” by MHC/self-peptide complexes that promotes the positive selection and survival of T cells, and the resulting proliferative response can be explosive. Again, the strength of the signal imparted through the TCR impinges on the differentiative choice. Cytokine and costimulatory influences on responding T cells certainly play a key role in coaxing them toward a Type 1 (Th1, Tc1) versus Type 2 (Th2, Tc2) phenotype, but there is also evidence that the strength/quality of the TCR signal can exert an important influence (Hosken et al., 1995; Constant et al., 1995; Tao et al., 1997; Rogers and Croft, 1999; Pfeiffer et al., 1995).

Thus, in these many instances, the TCR appears to act as a sensitive rheostat, translating the affinity/avidity of engagement into signals that somehow specify differential cell activity and/or fate. The agonist/antagonist nature of MHC/peptide complexes has generally correlated with differences in the off rate of the complexes they form with TCRs in vitro (Alam et al., 1996; Sykulev et al., 1994; Matsui et al., 1994; Lyons et al., 1996), differences that result in variable duration of productive interactions. The duration of TCR engagement does seem to have an important effect on its outcome, be it in the context of lineage commitment in association with

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positive selection or of effector phenotype choices during the activation of peripheral T cells (Yasutomo et al., 2000; Iezzi et al., 1998; Valitutti et al., 1995a). The number of TCR molecules engaged may be another key parameter of the interaction, having been directly correlated with the outcome (Valitutti et al., 1995b; Matsui et al., 1994; Lanzavecchia et al., 1999). It has been proposed that distinct thresholds, tunable by the concomitant influence of costimulatory molecules, are required for different phenotypic responses (Valitutti et al., 1996; Itoh and Germain, 1997). As a large number of productive interactions (5,000–20,000) seems to be needed, serial engagement of the limited number of MHC molecules loaded by the cognate peptide on each APC (in the hundreds at best) has been hypothesized.

The above conclusions frequently derived from *in vitro* experiments that entailed selecting cells with diverse TCR levels as the result of a prior exposure to antigen. It seems important to readdress some of the key questions *in vivo*, in an experimental system where TCR levels can be varied without intentional prior triggering. Thus, exploiting a tetracycline (tet)-based control system (Furth et al., 1994; Kistner et al., 1996), we generated transgenic mice expressing TCRs in a quantitatively and temporally regulated fashion and studied T cell responses to antigen challenges. We also used these animals to reinvestigate survival issues, in a system where CD4⁺ and CD8⁺ T cells can be studied in parallel and in the absence of external perturbations.

Results

Tet-Responsive TCR Transgenic Mice

To determine the influence of TCR levels on T cell responsiveness, we generated transgenic mice in which the expression of a transgene-encoded TCR of defined specificity could be modulated after a normal T cell compartment had been established. We chose the OT-1 receptor—specific for the OVA257-264 peptide, K^b-restricted (Kelly et al., 1993), composed of a V α 2/V β 5 chain combination, and the focus of numerous studies. Mice expressing the OT-1 α chain under tet control were generated using the binary transgenic strategy developed by Bujard and collaborators (Kistner et al., 1996; Furth et al., 1994). The first transgene encodes a tet-sensitive activator, the second a reporter whose expression is controlled by the transactivator. The combination of transgenes employed in the present study is illustrated in Figure 1A. First, the *lck* proximal promoter was used to drive T cell-specific expression of the TetR-VP16 transactivator (tTA). This *lck* promoter-driven vector is active in T-lineage cells, although expression in mature cells varies between different founder lines (Chaffin et al., 1990; Sohn et al., 1998). Second, the cDNA encoding the OT-1 α chain was placed under the control of a minimal promoter augmented with seven TetO sequences. Expression of tTA in T cells should turn on transcription of the TCR α chain, and this transactivation should be sensitive to tet, which inhibits tTA binding to the TetO motif. To complete the OT-1 TCR, we also employed a third transgene encoding the OT-1 TCR β chain and expressed constitutively in all T cells (Correia-Neves et al., 1999).

Transgenic mice carrying each construct were generated by independent microinjection. After analyzing the specificity and levels of transgene expression in offspring from various *lck*-tTA founders (data not shown), we selected one line, LTH1, whose properties are detailed in Figure 1. According to Northern blot analysis (Figure 1B), the LTH transgene was active only in lymphoid organs (with the exception of a weak signal in the ovaries). Transcripts were localized more precisely in the thymus and lymph nodes by *in situ* hybridization with a tTA-specific probe (Figure 1C). As might be expected, the thymic cortex labeled more intensely than the medulla, attributable to a lower density of T cells in the medulla compared with the cortex (a pattern characteristic of other probes corresponding to TCR components, such as CD3 [data not shown]). tTA mRNA could be detected only in the T cell areas of the lymph nodes, being largely excluded from the B cell follicles. A more quantitative assessment of tTA transcription in thymocytes was performed by RT-PCR analysis of sorted subpopulations (Figures 1D and 1E). tTA was transcribed in roughly equivalent amounts in CD4⁻CD8⁻ double-negative (DN), CD4⁺CD8⁺ double-positive (DP), and mature CD4⁺CD8⁻ and CD4⁻CD8⁺ single-positive (SP) cells. Among DNs, transcripts were detected in all four subpopulations delineated by the CD25 and CD44 differentiation markers, implying that the LTH-1 transgene was active quite early in T cell differentiation, consistent with a recent analysis of *lck* proximal promoter activity (Buckland et al., 2000).

The LTH1 transgene (hereafter abbreviated as L) was then bred into the TetO-TCR α -OT1 transgenic mice (referred to as TAO, for Tet-controlled Alpha OT-1 TCR) to yield animals with regulatable TCR expression (L/TAO double-transgenic mice). We also introduced into these crosses the TCR α knockout mutation (Philpott et al., 1992; hereafter abbreviated as C α ^o), which eliminates endogenously encoded TCR α chain expression and thereby T cell maturation beyond the DP stage; thus, positive selection and the appearance of fully mature T cells in L/TAO/C α ^o animals must reflect transgene-encoded TCR α expression. Lymph node T cells from such mice were examined by flow cytometry (Figure 2A). As expected, the reporter transgene alone could not complement the TCR α deficiency: mature T lymphocytes were not found in significant numbers in TAO/C α ^o mice. Therefore, this tet-regulatable system is not “leaky.” Addition of the LTH-1 transactivator transgene led to full restoration of peripheral CD4⁺ and CD8⁺ T cell populations in L/TAO/C α ^o mice. Expression of the transgene-encoded TCR was demonstrated by staining with an anti-V α 2 reagent: all T cells stained positively, most of them at levels comparable with those of wild-type mice (68% of WT levels on average). The relatively low proportion of CD8⁺ T cells in L/TAO/C α ^o mice was expected because the OT-1 TCR α chain has been associated with preferential selection into the CD4⁺ lineage (M. Correia-Neves, personal communication). The OT-1 TCR β chain transgene was then introduced to allow assembly of the complete OT-1 receptor in V β 5/L/TAO/C α ^o mice (third dot plot), yielding a dominant population of CD8⁺ T cells, as anticipated for a K^b-restricted TCR. Again, all T cells expressed V α 2. The lymphocytes whose maturation was induced by transgene expression

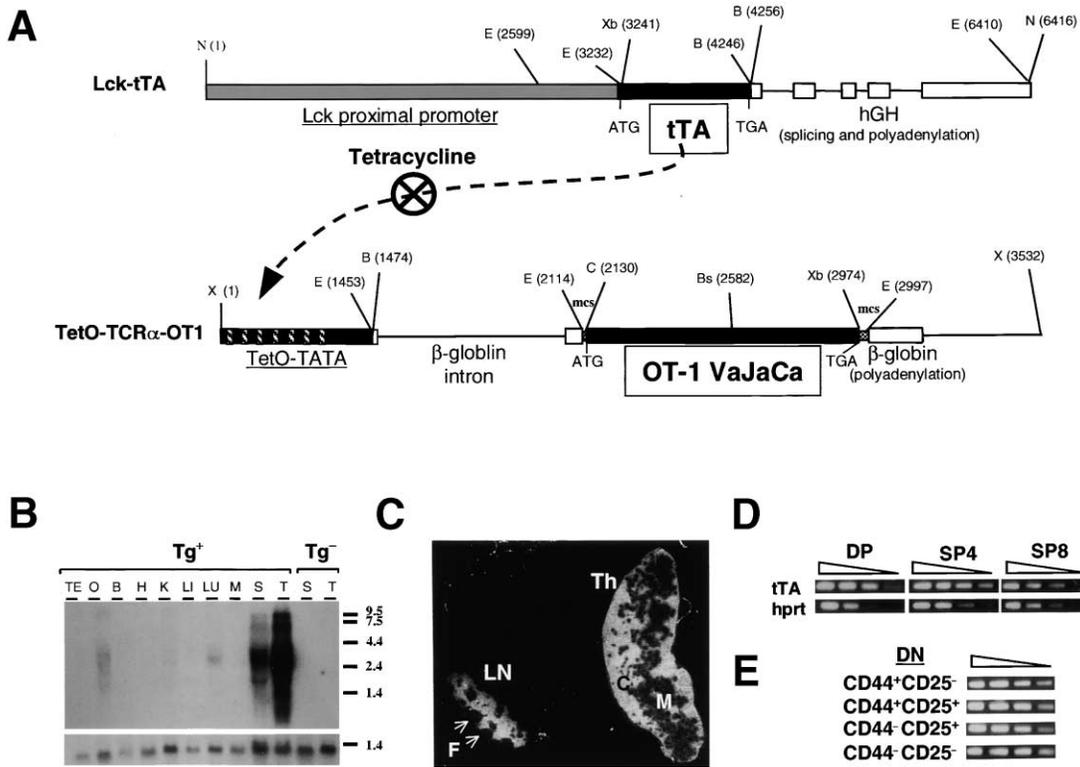


Figure 1. Constructs and Transactivator Expression

(A) Constructs. Top: the *lck*-tTA transactivator transgene: the microinjected fragment contains the *lck* proximal promoter (Chaffin et al., 1990) (gray bar), the tTA transactivator (solid bar), and several exons of the human growth hormone gene (white bars). Bottom: the TetO-TCR α -OT1 reporter transgene: the fragment contains the TCR α cDNA from the OT-1 hybridoma (K b -restricted, OVA specific) (solid bar), a minimal cytomegalovirus promoter (gray bar) linked to seven TetO sequences (hatched bars), and the rabbit β -globin intron/exon and polyadenylation sequences (white bar). B, BamHI; Bs, Bst1107i; C, ClaI; E, EcoRI; N, NotI; X, XhoI; Xb, XbaI; hGH, human growth hormone; mcs, multiple cloning site; and polyA, polyadenylation site. The numbers in parentheses indicate the positions of restriction enzyme sites.

(B-E) tTA transgene expression in LTH1 mice. (B) Northern blot analysis of tissue RNA, hybridized with probes specific for tTA (upper panel) and a riboprotein as control (lower panel). Organs were testes (TE), ovary (O), brain (B), heart (H), kidney (K), liver (LI), lung (LU), skeletal muscle (M), spleen (S), and thymus (T). (C) In situ mRNA expression in mesenteric lymph nodes (LN) and thymus (Th). Sections were hybridized with a tTA anti-sense probe. F, B follicles; M, medulla; and C, cortex. (D) Semiquantitative RT-PCR analysis of tTA mRNA expression in CD4 $^+$ CD8 $^+$ (DP), CD4 $^+$ CD8 $^-$ (SP4), and CD4 $^-$ CD8 $^-$ (SP8) thymocytes. (E) CD4 $^-$ CD8 $^-$ thymocyte subpopulations. Hprt mRNA levels are shown to control for amounts. RT-PCR was performed on serial dilutions (1/10) of cDNA from the different sorted populations with primers specific for the tTA or hGH sequences.

had the phenotypic characteristics of naive T cells—CD25 $^-$ CD69 $^-$ CD44 $^-$ CD62L hi and little cycling (data not shown).

Thus, the combination of transgenes seemed to function as had been hoped for: expression of the OT-1 TCR was transactivator dependent, at levels sufficient for selection and maintenance of a normal complement of T cells. L/TAO/C α^0 mice also showed normal thymocyte subsets, including ample populations of mature CD3 hi cells absent from C α^0 littermates (Figure 2B), with the TCR density expected of thymic subsets. In V β 5/L/TAO/C α^0 mice, the anti-CD4/CD8 staining pattern on gated TCR hi cells (Figure 2C) revealed the existence of a large population of transitional CD4 $^+$ 8 0 cells as is typical for the OT-1 TCR (Hogquist et al., 1994).

It was also important to assess the efficiency of L/TAO expression in a situation where the transgene-encoded product competes with the products of endogenous TCR α loci. The histograms in Figure 2D illustrate that approximately 15%–25% of CD4 $^+$ and CD8 $^+$ T cells ex-

pressed the transgene-encoded TCR α chain, more than double the background of endogenous V α 2 expression. As expected, the presence of a transgene-encoded V β 5 chain boosted selection into the CD8 $^+$ compartment.

We then asked whether TCR levels were responsive to treatment of the mice with tet. The effect was quite graphic, as illustrated in Figure 3A. While sizeable numbers of thymocytes were positively selected into the SP compartments of the untreated V β 5/L/TAO/C α^0 mouse (upper right), a 3 week course of tet treatment completely eliminated SP cells in its littermate (lower right). The absence of mature thymocytes correlated with the shutdown of TCR expression in DP thymocytes (data not shown). It did not represent a toxic effect of the drug itself, since the same treatment had no effect in a wild-type control.

To measure the rate of extinction of TCR expression in peripheral T lymphocytes, L/TAO mice were treated with a high dose (1 mg/ml) of tet, and blood samples were collected at different times and stained with an

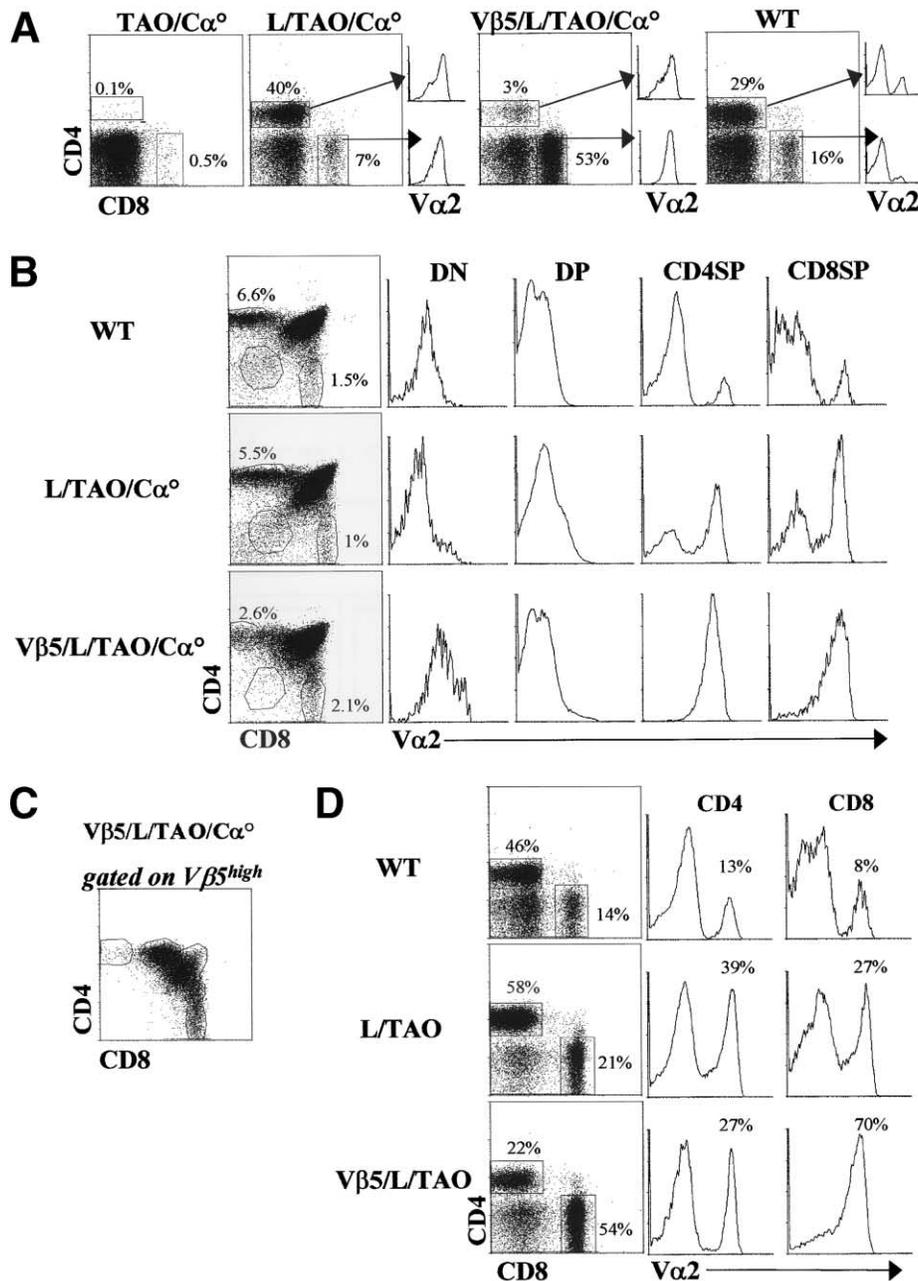


Figure 2. T Cell Compartments

(A) CD4/CD8 profiles of lymph node cells from wild-type, TAO/Cα°, L/TAO/Cα°, and Vβ5/L/TAO/Cα° mice. Juxtaposed small histograms display the expression of the Vα2 chain encoded by the TetO-OT1α transgene in CD4⁺ and CD8⁺ T cells.

(B) Thymocyte differentiation in L/TAO/Cα° and Vβ5/L/TAO/Cα° mice: CD4/CD8 profiles are in the left-most panels; Vα2 expression for the different gated populations are to the right of them.

(C) CD4/CD8 profiles on gated Vβ5-high cells from a Vβ5/L/TAO/Cα° thymus.

(D) Expression of the inducible OT-1 TCRα chain in lymph node T cells of Cα-wild-type mice: CD4/CD8 profiles of lymph node cells from wild-type, L/TAO, and Vβ5/L/TAO mice (left panel); Vα2 expression on gated CD4⁺ or CD8⁺ cells in the middle and left histograms. The percentage of CD4⁺ and CD8⁺ cells in each dot plot is shown and the percentage of Vα2⁺ T cells is indicated on the histograms for Cα-wild-type mice. All stainings were performed on mice that were not tet treated.

anti-Vα2 mAb. A significant decrease in TCR levels was observed already after 4 days of tet treatment, and expression reached baseline values by day 14 (Figure 3B). As expected, cells expressing endogenous Vα2 showed no such drop. The same kinetics were observed for

CD4⁺ and CD8⁺ T cells. Quantitative flow cytometry with calibrated beads as standards (Davis et al., 1998) (Figure 3C) showed about 40,000 molecules on wild-type CD4⁺ cells, in good agreement with previous reports (Blichfeldt et al., 1996; Schodin et al., 1996; Valitutti et al.,

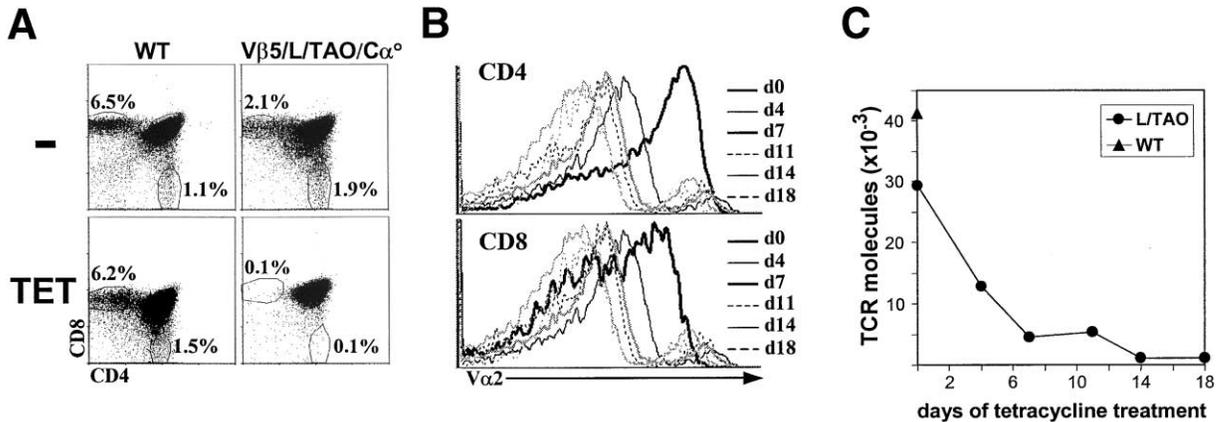


Figure 3. Tet-Controllable TCR Expression

(A) Lack of mature thymocytes in Vβ5/LTAO/Cα° mice after tet treatment. Wild-type (left panels) or Vβ5/LTAO/Cα° animals (right panels) were treated (lower panels) with 1 mg/ml of tet for a 3 week period or not (top panels) and their thymi were stained for CD4 and CD8. (B) Disappearance of TCR expression following tet treatment. Overlay histograms for Vα2 expression in LTAO mice are shown for CD4⁺ or CD8⁺ PBL of a single mouse sampled at day 0, 4, 7, 11, 14, and 18 after initiation of tet administration (1 mg/ml in drinking water). (C) Quantitation of the number of TCR molecules expressed by CD4⁺ T cells during the course of tet treatment (from [B]).

1995b); 30,000 molecules/cell were found on CD4⁺ cells from untreated L/TAO mice. Within 2 weeks after initiation of tet treatment, L/TAO cells were essentially denuded of TCRs. A careful analysis of TCR levels over long periods of tet treatment revealed that while the bulk of molecules had disappeared by 14 days, a very low residual expression (equivalent to 200-300 molecules/cell) persisted beyond that time and was stable for months. This low-level persistence, also observed when the cells were stained with anti-CD3 or anti-TCRβ reagents, was distinguishable from the background seen with irrelevant antibody staining and was absent from nontransgenic mice. It is not clear what biochemical form or functional relevance these long-lived TCR molecules might have, although they are clearly incapable of signaling in response to antigenic stimulation (see below) or to promote positive selection in the thymus (Figure 3A).

Graded doses of tet were then used to quantitatively regulate TCR expression levels in Vβ5/LTAO/Cα° mice. The protocol, chosen for its reliability, was to leave the animals with no tet (permitting full TCR expression) for their first 3 weeks of life and then to switch them to 0, 5, 10, or 400 μg/ml of tet for 2 weeks or more. TCR expression was maintained stably at intermediate levels in animals treated with these low tet doses and levels correlated with tet concentration (Figure 4). TCR levels could thus be "adjusted" to 20- to 40-fold below normal (using cells expressing endogenous Vα2 as an internal standard).

TCR Density and T Cell Responsiveness

The possibility of regulating TCR levels, both quantitatively and temporally, in these transgenic mice permitted us to analyze the influence of TCR density on T cell responses *in vivo*. To quantitate TCR levels in individual experimental mice, a single inguinal lymph node was surgically removed from Vβ5/LTAO animals fed different tet doses. Two days after the biopsy, the animals

were challenged by intravenous injection of the antigenic peptide SIINFEKL. Two doses were used: 0.1 μg, which is near saturating for the induction of a proliferative response in mice expressing the normal complement of OT-1 TCRs; and 20 μg, a 100-fold excess. This

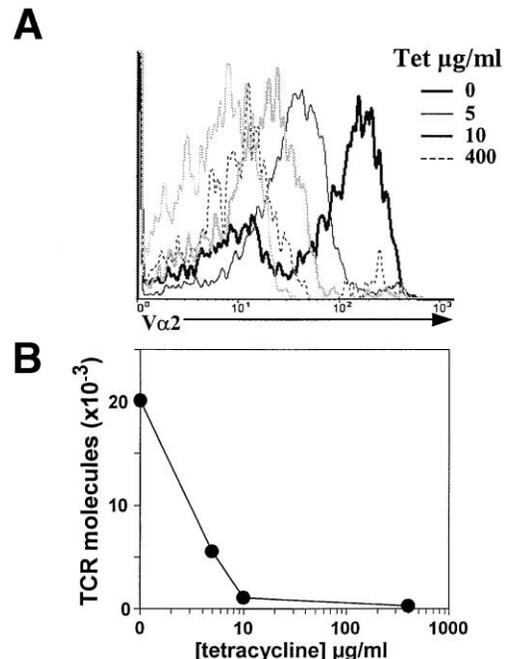


Figure 4. Tet Dose-Dependent Expression of the TCR in Vβ5/LTAO Mice

(A) The overlay histogram represents the expression of the transgene-encoded α chain by lymph node CD8⁺ T cells from Vβ5/LTAO mice treated for 2 weeks with different tet doses (0, 5, 10, and 400 μg/ml) in a representative experiment. (B) Quantitation of the number of TCR molecules using standardization microbeads containing a known number of fluorescent molecules.

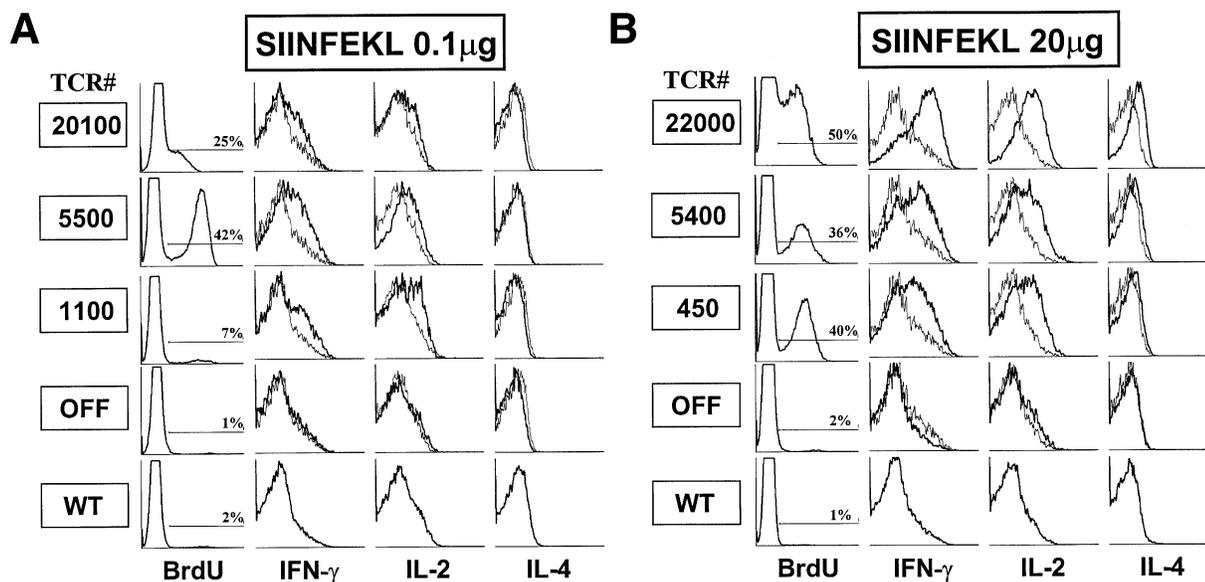


Figure 5. T Cell Responses in Vβ5/L/TAO Mice Expressing Various TCR Levels

Vβ5/L/TAO animals treated with different doses of tet for 16 days were immunized with 0.1 μg (A) or 20 μg (B) SIINFEKL peptide intravenously, and T cell responses were analyzed 48 hr later. The histograms, from left to right, show BrdU incorporation, IFN-γ, IL-2, and IL-4 production by CD8⁺ mesenteric lymph node T cells from control nontransgenic (thin line), and Vβ5/L/TAO (thick line) mice. TCR densities are indicated at the left (determined as above). The tet doses were 0, 5, 10, and 400 μg/ml (from top to bottom). The fifth line of histograms shows results for an immunized nontransgenic control mouse (WT).

response is dependent on both TCR transgenes (there is no response in mice or cells expressing the Vβ5 transgene together with endogenous Vα chains [data not shown]). The antigen induces a downmodulation of the transgene-encoded TCR (4-fold at the lowest dose, complete at the highest). To test for proliferation, we injected the animals with bromodeoxyuridine (BrdU) 34 and 42 hr after immunization and sacrificed them at 48 hr. Spleen and lymph node T cells were stained for BrdU incorporation. As illustrated in Figure 5A, the lowest doses of immunizing peptide elicited significant proliferation only in mice exhibiting the two highest TCR densities. Perhaps surprisingly, mice with as few as 500–1000 TCR molecules per CD8⁺ T cell responded, although substantially only at the high immunogen dose. In no case did we see any proliferation, beyond that observed with unimmunized or nontransgenic mice, in animals treated with the maximum tet dose, indicating that the residual TCR molecules displayed by these cells did not suffice to induce a response to even a high density of agonist ligand.

Cytokine production was also examined by intracytoplasmic staining of the same cells 48 hr after immunization. Substantial IL-2 and γ-IFN induction was seen only at the high dose of immunizing peptide. The proportion of positive cells and cytokine levels decreased with diminishing TCR density, but cytokines were still clearly detectable in cells displaying <1000 surface TCR molecules. Importantly, the decreased γ-IFN expression in mice showing a low TCR density did not correlate with an induction of IL-4, absent in all mice examined except for untreated animals receiving the highest peptide dose.

These points are highlighted in the compiled indices

of Figure 6. At the high antigen dose, the cycling of T cells with even very low TCR density resulted in a marked expansion of the CD8⁺ compartment. At the low antigen dose, there was more of a correlation between the degree of proliferation and TCR levels. In addition, cytokine responses seemed to correlate more with antigen dose than with TCR numbers. This was particularly clear for IL-2.

In short, not only was the threshold of TCR density for responsiveness to antigen surprisingly low, but the intensity of the response seemed more cued on the density of antigen ligands than on the number of TCRs available to engage them.

Turnover of CD4⁺ and CD8⁺ T Cells in the Absence of TCR Expression

Given the profound and fairly rapid shutdown of TCR expression that can be induced in L/TAO mice and the loss of thymocyte positive selection and peripheral T cell responsiveness that ensues, it seemed worthwhile to exploit this system to investigate the *in vivo* fate of mature T cells denuded of TCRs subsequent to undergoing a normal selection process. As discussed above, a number of investigators have claimed that persistent engagement of TCRs by MHC/self-peptide complexes is necessary for the long-term survival of naive peripheral T cells, although population decay kinetics have varied for CD4⁺ and CD8⁺ cells, and of late there has been some debate on the whole issue. Furthermore, a recent study (Lam et al., 1997) reported that B cells show a strikingly rapid demise after elimination of their surface Igs via inducible gene targeting, as if the very presence of an assembled antigen receptor is required for B cell survival. We wondered whether a parallel shutdown of

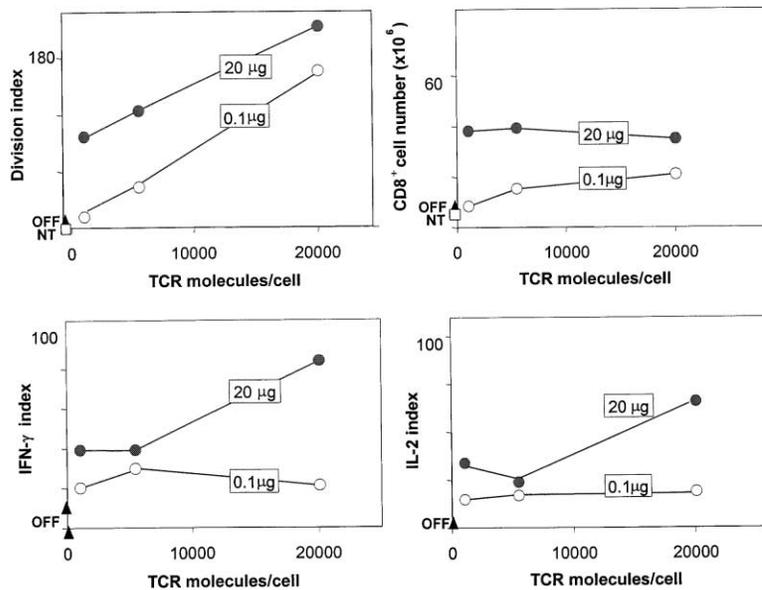


Figure 6. TCR Density and T Cell Responsiveness

CD8⁺ T cell division factor (upper left), CD8⁺ T cell number (upper right), IFN- γ production index (bottom left), and IL-2 production index (bottom right) following intravenous immunization with SIINFEKL peptide are plotted as a function of the number of TCR molecules on the surface of T cells. The division factor was determined using the percentage of BrdU⁺ cells and correcting for cells that had divided more than once (see Experimental Procedures); CD8⁺ T cell numbers were quantitated for mesenteric lymph nodes; cytokine production indices were calculated from the percentage of cytokine-positive cells and their level of expression (see Experimental Procedures). The number of surface molecules/cell was determined as in Figure 4. The control values obtained with totally shutoff expression ("off") or in nontransgenic mice (NT) are shown.

TCR expression on T cells (though by another genetic trick) would rapidly precipitate their death.

These experiments were performed on L/TAO or V β 5/L/TAO mice harboring a wild-type endogenous TCR α locus, thereby allowing for sizeable populations of mature T cells that do or do not express the inducible TCR α transgene (Figure 2D). The behavior of transgene-positive cells "in a crowd" of cells expressing other clonotypes should more closely mimic the normal situation and avoid complications due to the "homeostatic" proliferation in a lymphopenic setting. T cells that have lost TCR expression can easily be monitored by staining with anti-CD3 and anti-CD4 or -CD8 mAbs, registering as CD3-negative, CD4-, or CD8-positive cells (Figure 7A). Both L/TAO and V β 5/L/TAO animals were used because CD4⁺ and CD8⁺ T cells predominate in the former and latter, respectively (Figure 2). The animals were allowed to generate normal lymphocyte compartments until 6 weeks of age, when TCR expression was shut off. T cell numbers and phenotypes were then followed over time in individual mice by sequential surgical removal of single lymph nodes (inguinal and axillary nodes, which we find to have essentially identical cell numbers in individual control mice over time), followed by cytofluorimetry. Since tet administration also halts thymic positive selection (Figure 3), these experiments tracked the survival of peripheral T cells without the complicating influences of thymocyte export.

A reproducible decline in both the CD4⁺ and CD8⁺ populations of individual mice was observed (Figure 7B). This was not due just to the tet treatment, because no loss of T cells was observed in control animals that drank the same antibiotic-laced water (open triangles). The decay was also not due to toxicity of the residual, unpaired TCR β chain, as there are numerous examples of fully viable cells expressing unpaired TCR β chains (Mertsching et al., 1997; Saint-Ruf et al., 1994). The data were replotted after normalization on the starting T cell number for each mouse and exponential curve fitting, taking day 8 as the starting point to account for the time

needed to substantially shut down surface TCR levels, visible as a lag in the upper right panel, for example. Calculated half-lives were 26.8 and 19.0 days for CD4⁺ and CD8⁺ populations, respectively (bottom panels). These values are quite consistent with those obtained by most investigators for T cells placed in an MHC-deficient environment. Thus, the life expectancy of T cells without TCRs is remarkably similar to that in the absence of MHC/self-peptide ligands.

Discussion

The combination of transgenes engineered for these studies performed as we had hoped. The OT-1 TCR α chain was expressed at near-normal levels in the absence of tet and effectively promoted the selection and maintenance of CD4⁺ and CD8⁺ T cells. The partitioning of T cells into thymic and peripheral subsets mimicked the peculiarities of the original OT-1 TCR transgenic line (Hogquist et al., 1994). Upon high-dose tet treatment, TCR expression was extinguished over a matter of days; it could also be maintained at intermediate levels with limited tet doses. While it has not been possible to reproduce in mice the 1000-fold dynamic range of reporter gene expression reported for tissue culture transfectants, the 20-fold range in TCR display does allow very useful analyses. This system offers the possibility of modulating or eliminating TCR:MHC/peptide contacts in a noninvasive manner, in an otherwise normal environment, in particular without the perturbations implicit in cell labeling and transfer protocols.

Number of TCRs Needed for T Cell Responsiveness

Very few surface TCR molecules (1000 or less) were needed for T cells to respond to immunization *in vivo*, and the density/response relationship was surprisingly nonexponential. This was true when suboptimal tet treatments resulted in a low level of TCR expression (Figures 4 and 5) and also when mice were immunized 8 days after tet administration, when incomplete shutoff

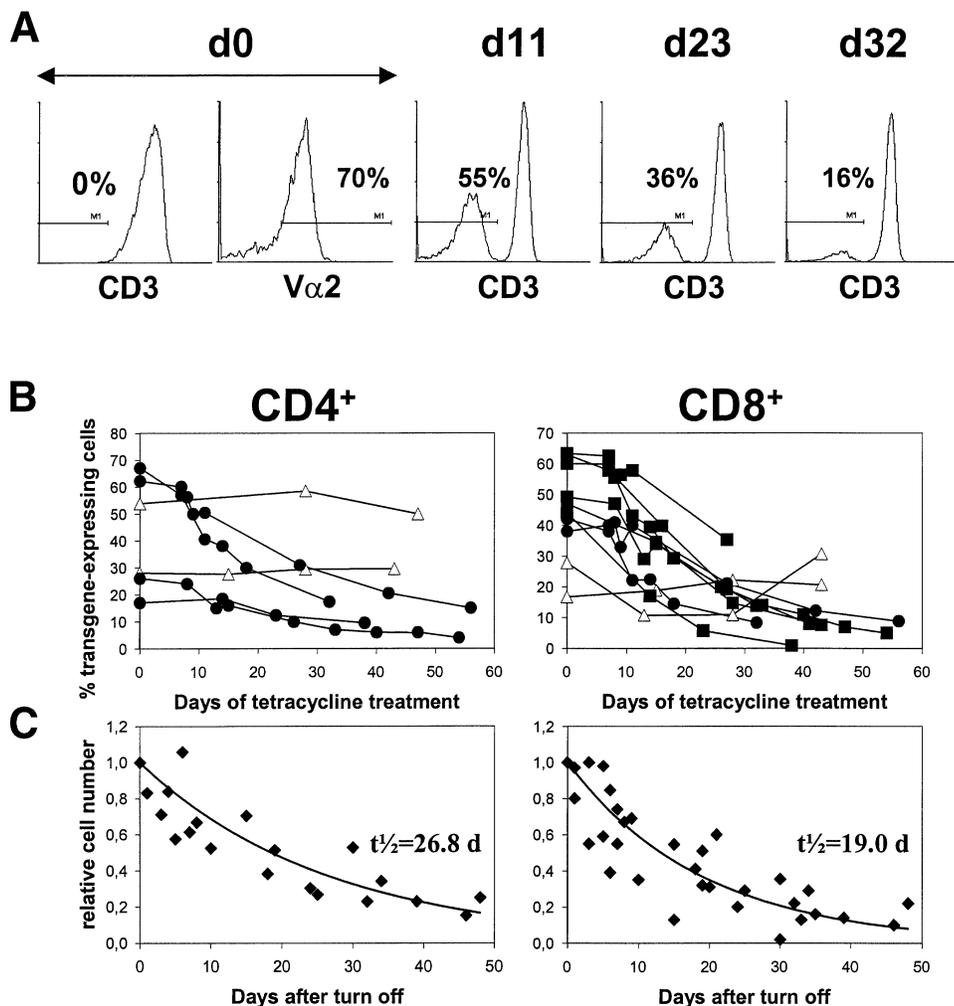


Figure 7. Decay of CD4⁺ and CD8⁺ T Cells Stripped of TCR Molecules

(A) Representative profiles of gated CD8-positive cells of a single V β 5/L/TAO mouse, from individual lymph nodes surgically removed at different times of high-dose tet treatment.

(B) The proportion of transgene-expressing CD4⁺ or CD8⁺ T cells from tet-treated L/TAO (black circles), V β 5/L/TAO (black squares), or control (open triangles) mice was determined as in (A); transgene-expressing T cells were identified as CD3⁻ cells after the shutoff.

(C) Regression analysis of the data from (B), normalized on the pretreatment value for each mouse. To account for the 7–10 day delay before the surface TCR is effectively cleared, the regression assumes that the decline initiates on day 8. The half-life of the T cell population is indicated.

still left a thousand or so molecules at the cell surface (data not shown). One might argue that a minor fraction of the cells was still displaying intermediate to high TCR levels in treated mice and accounted for the responses observed. However, this is very unlikely. For example, in the mouse with a mean level of 450 molecules per CD8⁺ cell, the 40% of cells that incorporate BrdU or produce γ -IFN 48 hr after immunization cannot have been generated from the gaussian trail (<5%) of cells that express more than 5000 molecules in this mouse (particularly as only 50% of cells respond even at full TCR levels). These results are consistent with those from studies that employed laser-mediated micromanipulation in vitro to show that the engagement of 200–400 TCR molecules by anti-CD3 was sufficient to induce a robust Ca flux (Wei et al., 1999). Schodin et al. (1996) had also shown that a lower number of active TCR was

sufficient for target killing by a CTL clone in vitro. There is also an interesting parallel with patients carrying mutations in the CD3 ϵ gene, some of which have T lymphocytes with low TCR levels but comparatively robust T cell function (Soudais et al., 1993). On the other hand, they contrast with reports that T cell reactivity showed a marked dependence on TCR density, in particular one describing up to a 10⁴-fold drop in antigen sensitivity when the number of TCR molecules/cell was lowered from 25,000 to 8,000, reflected in a highly exponential density/response profile (Viola and Lanzavecchia, 1996; Blichfeldt et al., 1996). In most of these experiments, however, cells of varying TCR densities were obtained by 3 day preculture with antigen to induce TCR downmodulation; this manipulation may have conferred a refractory state on the T cells. Another explanation for the differences may be a strong influence of costimulatory

and adhesion molecules active in the natural *in vivo* setting, amplifying the response and lowering the numbers of TCRs that need to be engaged. Indeed, the clones used by Viola and Lanzavecchia were CD28 negative, and costimulatory molecules tuned the T cells to lower thresholds for activation in these assays. Finally, it is also conceivable that T cells “adapt” to progressively lower TCR levels by an increased sensitivity of downstream signal transduction pathways, an adaptation perhaps not possible in the time frame of the *in vitro* experiments.

T cells face a daunting challenge in maintaining specificity: the TCR recognizes its MHC/peptide ligand with very low affinity, there is often only a limited number of the specific ligand molecules available on APCs *in vivo*, and TCR:MHC/peptide engagement must persist over tens of hours. How can TCR:MHC/peptide interactions with half-lives on the order of 10 s account for such prolonged cellular interactions? Some element of TCR and MHC/peptide clustering has been invoked (reviewed in Germain, 1997; Dustin and Chan, 2000). Two different lines of reasoning have been advanced. First, TCRs and MHC molecules may have a natural propensity to dimerize, there being some structural data in support of this notion (Brown et al., 1993; Fernandez-Miguel et al., 1999; Reich et al., 1997); productive TCR triggering would entail crosslinking via multimerization of the TCR and MHC molecules into stable two-dimensional “pseudo-crystals” (reviewed in Germain, 1997). Here, the TCR:MHC/peptide complexes would drive the clustering, possibly through preformed TCR dimers or multimers, as recently suggested for antigen receptors on B cells (Schemel and Reth, 2000). The second proposal is the “immunological synapse” concept: shortly after initial TCR:MHC/peptide contact, a major rearrangement of the cytoskeleton draws TCR molecules into the center of a “bull’s eye” formation. The cytoskeletal reorganization induced by the very first contacts would be the driving force that clusters TCR molecules, whether or not they have already been engaged (reviewed in Dustin and Chan, 2000). Our results are clearly more consistent with the latter proposal: a model invoking a higher order assembly driven by the crosslinking of TCR molecules themselves would be more highly dependent on TCR density; on the contrary, cytoskeletal herding of TCR molecules into the synapse could be far less dependent, drawing on whatever molecules the cell displays.

A few years ago, the serial engagement model was advanced to explain the seeming paradox of thousands of TCR molecules being engaged by only a few hundred MHC/peptide ligands (Valitutti et al., 1995b; Viola and Lanzavecchia, 1996). The key assumption underlying this model, that each molecule downmodulated from the cell surface upon activation, was one that had been productively engaged and resultingly internalized. This plausible interpretation was supported by a close correlation between the degree of downmodulation and the extent of cell activation. Recent results make one question this interpretation, however, as TCR downmodulation is now shown to result from an absence of reexpression instead of an induced internalization, with no evidence that individual TCR molecules that fail to be reexpressed are those that have been engaged (Liu et

al., 2000). If anything, the opposite is true (Niedergang et al., 1997). Our results render serial engagement unnecessary, as it is not 10,000 to 20,000 TCR molecules that must be engaged to elicit activation, but only several hundred. Thus, these results are compatible with models in which TCR:MHC/peptide complexes form on a one to one basis and persist monogamously for a long time thereafter, as in an immunological synapse.

Can T Cells Survive without TCRs?

Initially, yes. Our results on the decay of TCR-negative T cell populations differ significantly from those on Ig-negative B cells (Lam et al., 1997). The latter died precipitously, such that it was essentially impossible to visualize B cells devoid of surface Igs in cytometric profiles. In contrast, denuded CD4⁺ and CD8⁺ T cells were readily observed (Figures 3B and 7A). These divergent outcomes may well stem from differences in the physiology of B and T cells. On the other hand, it is conceivable that the downmodulation of MHC class I molecules induced on B cells when their Igs were lost (Lam et al., 1997) rendered them efficient NK cell targets soon after the gene excision event, accelerating their death.

The CD4⁺ and CD8⁺ T cell populations decayed progressively after extinction of TCR expression. This behavior is consistent with results from diverse experimental setups indicating that CD4⁺ T cells have only limited survival potential in the absence of MHC molecules, with a half-life very similar to that observed here (Takeda et al., 1996; Rooke et al., 1997; Witherden et al., 2000). It contrasts with the long-term persistence of naive CD4⁺ T cell pools in thymectomized mice. Recent experiments, however, did not detect any differences in population decay when CD4⁺ T cells were directly transferred into MHC-proficient and -deficient hosts, and invoked possible artifacts due to homeostatic proliferation to explain the discrepancy with prior results (Clarke and Rudensky, 2000; Dorfman et al., 2000). Our data serve to reaffirm the need for TCR:MHC/peptide engagement for the maintenance of naive T cell pools. Proliferation did not play a role in our experiments, as significant cycling was not observed, whether or not the cells had been exposed to tet (Figure 5). It is probably more than a coincidence that the two dissenting results came after simple transfer of CFSE-labeled cells, rather than the more elaborate experimental protocols that generated peripheral T cell populations via natural export of thymocytes (Takeda et al., 1996; Rooke et al., 1997; Witherden et al., 2000).

Comparison of the results from different experimental systems has given the impression that populations of CD8⁺ T cells decay more rapidly than CD4⁺ populations when deprived of their MHC/peptide ligands (discussed in Witherden et al., 2000). However, in all of these systems, only one or the other of the two compartments could be studied. The results reported here, exploiting an experimental setup that permits simultaneous analysis of the CD4⁺ and CD8⁺ populations, argue for decay kinetics of the same order, only slightly faster for CD8⁺ cells. This conclusion bolsters prior proposals (Murali-Krishna et al., 1999; Dorfman et al., 2000) that the near-instantaneous disappearance of CD8⁺ T cells described in certain cases (e.g., Tanchot et al., 1997) may have been complicated by rejection phenomena.

Our findings show that quantitative relationships between TCR density and T cell responsiveness that were clear in *in vitro* settings did not hold in an *in vivo* environment, likely due to the influence of elaborately structured microenvironments and the opportunity for the full panoply of costimulatory and adhesion molecules to impinge on the process. Likewise, a striking characteristic of B cells denuded of their antigen receptors was not a feature of TCR-less T cells. No doubt more examples of such divergences will arise in the future as regulatable, cell-type-specific transgenesis systems permit us to explore *in vivo* questions that before could only be addressed *in vitro*.

Experimental Procedures

Construction and Analysis of Transgenic Mice

Details of the constructs, mouse genotyping, and RNA analysis are presented as supplemental data (see <http://www.immunity.com/cgi/content/full/15/1/71/DC1>). Flow cytometry was performed as previously described (Rooke et al., 1997). The quantification of the number of TCR molecules on T cells was done by cytofluorometry, comparing T cells stained with a saturating concentration of anti-V α 2 mAb with standardization microbeads containing a known number of fluorescent molecules (QuantibritePE beads, Becton Dickinson). T cells were stained with saturating concentrations of anti-V α 2 mAb and their staining intensity (minus background autofluorescence) was compared to a standard curve of microbeads carrying known numbers of phycoerythrin molecules. The V β 5 transgenic and C α ^o lines have been described previously (Correia-Neves et al., 1999; Philpott et al., 1992). Tet treatment was performed by supplementing the drinking water with the indicated concentration of tet plus 2% sucrose. Bottles were changed twice a week during the course of the treatment.

In Vivo T Cell Responses

V β 5/LTAO mice treated for 2 weeks with 0, 5, 10, or 400 μ g/ml of tet in the drinking water (supplemented with 2% sucrose) were immunized intravenously with either 0.1 μ g or 20 μ g of SIINFEKL peptide diluted in sterile PBS, and T cell responses were analyzed 48 hr afterward. To measure T cell proliferation, mice were injected with 1 mg of BrdU *intra peritoneally* 36 and 42 hr after immunization, sacrificed 6 hr after the last injection and their lymph nodes removed. Cells were stained for BrdU incorporation as described (Giffillan et al., 1994). In brief, cells were stained with anti-CD4-PE and anti-CD8-tricolor and then fixed in 70% ethanol for 30 min. After washing, cells were permeabilized overnight in 1% paraformaldehyde, 0.1% Tween-20 in PBS, treated with Dnase, and stained with anti-BrdU-FITC (Becton Dickinson). At high proliferation rates, the intensity of BrdU staining decreases (Figure 5), likely through secondary divisions or stimulation of *de novo* pyrimidine synthesis. To correct for this effect, a "proliferation index" was calculated by multiplying the percent labeled cells by the shift in the mean fluorescence intensity (MFI) relative to the MFI of unstimulated cells. Cytokine production was analyzed by flow cytometry as described (Openshaw et al., 1995). Lymph node cells were stimulated for 4 hr *in vitro* with PMA (50 ng/ml, Sigma) and ionomycin (500 ng/ml, Sigma); brefeldin A (Sigma) was added to a final concentration of 10 μ g/ml during the last 2 hr of incubation. Cells were then fixed in 1% formaldehyde for 30 min and washed in PBS. The fixed cells were stained for intracellular cytokines in the presence of 0.5% saponin with anti-IL-2-FITC, anti-IL-4-FITC, and anti- γ IFN-FITC mAbs (Pharmingen), counterstained with anti-CD4-PE and anti-CD8-tricolor, and analyzed on a flow cytometer. A cytokine production index was determined by summing the fraction of positive cells with the shift in mean fluorescence intensity.

T Cell Survival Assays

To follow in individual mice the fate of T cells lacking TCR expression, we surgically removed lymph nodes at different time points, as described previously (Rooke et al., 1997). The right axillary lymph

node was taken before the beginning of tet treatment, and three other data points were collected at various times by removal of the left inguinal, and right and left axillary lymph nodes. The mesenteric lymph nodes were taken at the time of sacrifice. When more than six points are shown, the other data derive from blood sampling, taken in between the removal of lymph nodes. Cells were stained with anti-CD4-PE, anti-CD8-Tricolor, and anti-CD3 (KT3) followed by goat anti-rat-FITC.

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