The ability of antigen receptors to engage self-ligands with varying affinity is crucial for lymphocyte development. To further explore this concept, we generated transgenic mice expressing GFP from the immediate early gene Nr4a1 (Nur77) locus. GFP was up-regulated in lymphocytes by antigen receptor stimulation but not by inflammatory stimuli. In T cells, GFP was induced during positive selection, required major histocompatibility complex for maintenance, and directly correlated with the strength of T cell receptor (TCR) stimulus. Thus, our results define a novel tool for studying antigen receptor activation in vivo. Using this model, we show that regulatory T cells (Treg cells) and invariant NKT cells (iNKT cells) perceived stronger TCR signals than conventional T cells during development. However, although Treg cells continued to perceive strong TCR signals in the periphery, iNKT cells did not. Finally, we show that Treg cell progenitors compete for recognition of rare stimulatory TCR self-ligands.

T cells encounter several checkpoints as they develop, and their fate often relies on the strength of signal perceived by the antigen receptor. For example, CD4+CD8+ double-positive (DP) thymocytes with low affinity for self-peptide MHC (pMHC) ligands undergo positive selection, whereas those with high affinity undergo negative selection (Starr et al., 2003). Multiple studies suggest that DP thymocytes are exquisitely sensitive and exhibit a broader range of recognition of pMHC than mature T cells (Davey et al., 1998; Lucas et al., 1999). Nonetheless, mature T cells continue to perceive low-affinity self-pMHC ligands in the periphery, and these interactions are essential for survival and effector function (Kirberg et al., 1997; Stefaňová et al., 2002; Lo et al., 2009). Thus, the ability of the TCR to distinguish pMHC ligands of different affinity is a fundamental principal of immunological tolerance and homeostasis.

Although the affinity model explains the lineage commitment of a majority of T cell progenitors, some T cell subsets seem to have survived strong TCR signals during development as displayed by their activated phenotype (Baldwin et al., 2004; Kronenberg and Rudensky, 2005; Kronenberg and Gapin, 2007). CD4+Foxp3+ regulatory T cells (Treg cells), invariant NKT cells (iNKT cells), and CD8αα+ intraepithelial lymphocytes (IELs) are hypothesized to be positively selected via strong TCR signals in the thymus (Leishman et al., 2002; Godfrey et al., 2004; Zhou et al., 2004). In the case of Treg cells, Jordan et al. (2001) first demonstrated that expression of a neo-self-antigen in the thymus of mice with TCRs specific for that antigen promoted the development of Treg cells. Yet use of a TCR with an intrinsically lower affinity for the same neo-self-antigen failed to select Treg cells, suggesting a role for strong TCR signals. Moreover, T cells transduced with TCRs cloned from Treg cells underwent homeostatic expansion in lymphopenic recipients to a greater extent than cells transduced with receptors cloned from conventional T cell (Tconv cell) CD4 T cells, which is consistent with the idea that Treg cells recognize self-pMHC more avidly (Hsieh et al., 2006). Studies of the TCR repertoire from Treg and
T_{h cohort} CD4 T cells illustrated that they are equally diverse but different from each other (Hsieh and Rudensky, 2005). However, these TCR repertoires were not entirely unique; thus, others have suggested that T_{reg} cells are not shaped by agonistic interaction with self but rather by some stochastic event (Pacholczyk et al., 2006, 2007). In addition, when T_{reg} TCR transgenics were created, no overt thymic clonal deletion was observed (Bautista et al., 2009; Leung et al., 2009), nor was self-reactivity evident. Thus, it remains unclear precisely what type of TCR signals are involved in T_{reg} cell development in the thymus.

iNKT cells are CD1d-restricted αβ T cells that recognize lipid antigens. In the steady-state, they have a memory phenotype and have been proposed to develop after agonist or stimulatory interaction with a lipid self-ligand in the thymus, yet the precise ligand remains unidentified (Kronenberg and Gapin, 2007). Finally, CD8αα IELs have an activated phenotype and were increased in transgenic models in which the cognate stimulatory antigen was also present (Leishman et al., 2002). Thus, the term agonist selection has been applied to all three subsets, indicating encounter with a stimulatory (presumed high affinity) TCR ligand during development.

Short of cloning TCRs and identifying the selecting ligand in the thymus, it is difficult to know if a given T cell perceives a strong or weak TCR signal during development. Therefore, we sought to make a reporter mouse in which the level of a fluorescent protein reflects the strength of antigen receptor signal. We generated a transgenic mouse in which we inserted GFP into the Nr4a1 (Nur77) locus of a bacterial artificial chromosome (BAC). Nur77 is an immediate early gene up-regulated by TCR stimulation in thymocytes and T cells (Osborne et al., 1994). It is an orphan nuclear receptor whose function in T cells is not completely understood, although data suggest it may play a role in thymocyte apoptosis (Cainan et al., 1995; Cho et al., 2003). In a microarray screen, we showed that thymocytes undergoing both positive and negative selection induced Nr4a1 but to different expression levels (Baldwin and Hoggquist, 2007). Thymocytes undergoing positive selection showed a twofold increase in Nr4a1 expression, whereas those undergoing negative selection showed a 10-fold increase. Together, these observations suggested that a Nur77 reporter mouse might be a useful system for understanding the role of TCR signal strength during T cell development.

In this study, we report that GFP is up-regulated by antigen receptor stimulation in Nur77GFP mice, but unlike CD69, another common marker of T cell activation, it is not induced by inflammatory stimuli. Furthermore, the level of GFP expressed during acute activation reflects the strength of TCR stimulation, and the low basal level of GFP expressed in mature naive T cells is dependent on continued interaction with MHC. We applied this novel tool to study the TCR signal strength perceived by different T cell subsets during development.

RESULTS

A Nur77GFP transgenic mouse reports antigen receptor activation in lymphocytes

To create a fluorescent reporter that would be activated by antigen receptor signaling in lymphocytes, we inserted a GFP-Cre fusion protein at the start codon of the Nr4a1 (Nur77) gene in a BAC (Fig. 1 A). The Cre recombinase gene was included for fate mapping experiments that are not reported in this study. One B6 × SJL F1 and two C57BL/6J founders were generated. Each founder expressed a slightly different overall level of GFP, but the pattern of expression was identical, and endogenous Nur77 expression was consistent with GFP expression (Fig. S1 A). All three showed normal lymphoid and myeloid development (unpublished data). A subset of myeloid lineage cells in the spleen expressed high levels of GFP in the steady-state (Fig. 1 B), whereas mature T and B lymphocytes expressed low levels of GFP (Fig. 1 C).

To determine whether TCR stimulation induced GFP expression, we injected Nur77GFP mice with 50 µg anti-CD3 i.v. and 12 h later harvested lymphocytes. We observed robust induction of GFP (Fig. 1 D, left) and CD69 on T cells (not depicted) after α-CD3 stimulation. We also stimulated bulk splenocytes with 10 µg α-IgM in vitro for 3 h. Again, robust

Figure 1. A Nur77GFP BAC transgenic mouse expresses GFP upon TCR activation. (A) A GFP-Cre fusion protein was inserted at the start site of the Nr4a1 (Nur77) gene of a BAC construct and used to generate B6 or B6SJLF1 transgenic lines. (B) GFP was highly expressed in a subset of myeloid cells of the spleen but not lymph node. (C) T and B lymphocytes expressed a low level of GFP. Three founder lines showed similar cell-specific patterns of GFP expression, but higher levels were observed in the B6-820 line (n = 5 mice). (D) GFP was up-regulated in T cells 12 h after anti-CD3 injection in vivo or in B cells after 3 h of anti-IgM treatment in vitro (n = 4 mice and three experiments).
GFP expression was observed in B cells (Fig. 1 D, right) but not T cells. Thus, we conclude that GFP expression can be induced after lymphocyte antigen receptor activation both in vitro and in vivo.

Initial microarray experiments showed differential expression of Nr4a1 in thymocytes undergoing positive versus negative selection. In light of this, we asked whether the level of GFP induced in T cells would correlate with the strength of TCR signal perceived. We used K\textsuperscript{b}/OVA-specific OT-I TCR transgenic mice, for which many variant peptide ligands have been characterized (Hogquist et al., 1994; Daniels et al., 2006). DP thymocytes from OT-I/Nur77\textsuperscript{GFP} mice lacking the transporter associated with antigen process 2 gene (Tap\textsuperscript{a}) were stimulated with APCs pulsed with OVA peptide (OVAp) variants in vitro. In Fig. 2 A, these are listed according to stimulatory strength, with the cognate OVAp on the left and the weakest variant (E1) on the right. The level of GFP induced by each directly correlated with its stimulatory activity (Fig. 2 A). Interestingly, even the low-affinity variant E1 and the self-peptide β-CAT induced GFP above the background level (control peptide p815; Fig. 2 A, inset). Neither of these weak peptides stimulates OT-I T cells to proliferate, but they support positive selection of OT-I in organ cultures (Hogquist et al., 1994; Santori et al., 2002) and in vivo (Stefanski et al., 2001).

GFP up-regulation was transient after TCR stimulation with maximum expression observed between 12 and 24 h (Fig. 2 B). The up-regulation of endogenous Nur77 protein was also determined in parallel, and endogenous levels also correlated with strength of stimulus (Fig. S1 B), although peak induction of endogenous Nur77 occurred earlier than GFP, presumably reflecting the time required for maturation of a fully fluorescent GFP and the greater stability of GFP (Fig. S1 C).

Analogous experiments were performed in vivo using OT-I/Nur77\textsuperscript{GFP} cells transferred into mice and infected with strains of Listeria monocytogenes expressing variants of the OVAp. As seen with peptides in vitro, the level of GFP in OT-I T cells in vivo reflected the stimulatory strength of the variant peptide ligand, even in the context of an infection (Fig. S2). Thus, the Nur77\textsuperscript{GFP} mouse has the potential to be a sensitive reporter of TCR signal strength both in vitro and in vivo.

**GFP expression is induced by positive selection and maintained by tonic MHC signals**

Because Nr4a1 message was up-regulated during positive selection (Baldwin and Hogquist, 2007) and GFP could be induced by low-affinity TCR ligands (Fig. 2 A), we sought to determine whether GFP was up-regulated by positive selection in vivo. In the thymus of Nur77\textsuperscript{GFP} mice, only a fraction of cells expressed GFP (Fig. 3 A). Further analysis revealed that the GFP\textsuperscript{+} population was enriched for DP dull, CD4, and CD8 single-positive (SP) cells (Fig. 3 A, right). Among DP thymocytes, the GFP\textsuperscript{+} cells were high for CD69 and the TCR–β chain (Fig. 3 B, dot plot), suggesting that induction of GFP occurred at the time of positive selection (Fig. 3 B, histogram). Furthermore, we observed very low expression of GFP in DP thymocytes from OT-I Tap\textsuperscript{a} (nonselecting) mice compared with OT-I (selecting) control mice (Fig. 3 C), demonstrating that positive selection induced GFP in vivo. Consistent with the induction of GFP expression during positive selection, the majority of GFP bright cells were located in the medulla with only a few GFP–positive thymocytes found in the cortex (Fig. 3 D).

Like mature SP thymocytes, naive T cells in the periphery expressed GFP, although at slightly lower levels (Fig. 4 A, right), suggesting a decay of GFP with maturation. In fact, there was a modest stepwise decrease in GFP expression during development with semimature SP thymocytes expressing the highest level of GFP, followed by mature SP, then recent thymic emigrants (RTEs; HSA\textsuperscript{hi}Qa2\textsuperscript{lo}), and finally naive non-RTE T cells (Fig. S3). Nonetheless, naive non-RTE T cells expressed a level of GFP in the steady-state that was significantly above background and did not vary with age. Interestingly, this basal level of GFP was higher in CD4 than CD8 T cells, which is consistent with some models that have proposed that the CD4 coreceptor delivers a stronger signal than the CD8 coreceptor (Veillette et al., 1988; Legname et al., 2000). Memory phenotype CD4 and CD8 T cells did not express significantly different levels of GFP when compared with their...
Thymocytes undergoing negative selection express high levels of GFP

If GFP levels reflect the strength of the TCR signal perceived, one would predict higher GFP expression in thymocytes undergoing negative selection compared with positive selection. To test this, we used the OT-I/rat insulin promoter (RIP)–membrane OVA (mOVA) system, in which negative selection occurs via clonal deletion in CD8 SP thymocytes (Kurts et al., 1997). However, cells undergoing clonal deletion are rapidly cleared by thymic macrophages (Surh and Sprent, 1994). Thus, we created OT-I/Bimo/Nur77GFP transgenic mice, in which deficiency of the proapoptotic molecule Bim prevented apoptosis. Accordingly, bone marrow chimeras were created using OT-I/Nur77GFP or OT-I/Bim+/Nur77GFP mice as donors and B6 or RIP-mOVA mice as recipients (Fig. 5). As expected, we observed efficient positive selection of OT-I in B6 recipients and efficient deletion in RIP-mOVA recipients (Fig. 5 A, left). Moreover, OT-I/Bimo cells underwent efficient positive selection in B6 recipients, but Bim deficiency completely rescued OT-I cells from deletion in RIP-mOVA recipients (Fig. 5 A, right; and Fig. S5). Interestingly, GFP expression was substantially higher in OT-I/Bimo thymocytes rescued from deletion in RIP-mOVA recipients compared with cells undergoing positive selection in B6 recipients (Fig. 5 B). Therefore, we conclude that GFP levels were induced to higher levels by negative selection signals as compared with positive selection stimuli.

Induction of GFP is TCR specific

Many immunological studies use the expression of CD69 as a read-out for TCR activation. One caveat to this is that CD69 expression can be induced by inflammatory stimuli such as type I interferons (Sun et al., 1998; Shiow et al., 2006), thereby limiting its use as a marker of TCR stimulation in infection or inflammatory settings. We sought to determine whether inflammatory stimuli would also induce GFP expression in Nur77GFP mice. Neither polyinosinic:polycytidylic acid (pI:pC; Fig. 6 A) nor LPS (Fig. 6 B) induced GFP expression, although both induced CD69 up-regulation. To confirm this observation in the context of an infection, we transferred OT-I/Nur77GFP T cells into congenic WT or MHC II–deficient hosts and analyzed them after 6 or 9 d. The GFP level in naive phenotype, non-RTE CD4 T cells was maintained after adoptive transfer into WT recipients (Fig. 4 B, red line). In contrast, GFP was lost from CD4 T cells in MHC II–deficient recipients. These data suggest that TCR signals maintain GFP expression in peripheral T cells.
CD4+ T cells (Fig. 7 and Fig. S6). These data together suggest that Treg cells perceive stronger TCR signals than Tconv cells during development and that this perception continues in the periphery. Interestingly, the GFP histograms for Treg and Tconv cells are not completely distinct, but overlap. This is consistent with TCR repertoire studies (Hsieh et al., 2006; Pacholczyk et al., 2006), which showed that some clones are unique to Treg cells, some are unique to Tconv cells, and some are shared. STAT5 signaling does not increase GFP levels in Treg or Tconv cells

Because GFP levels reflected TCR signal strength in Nur77GFP mice, we sought to use these mice to test whether Treg cells perceive stronger TCR signals compared with Tconv cells during development. Thymic Foxp3+ Treg cells expressed approximately twofold higher mean fluorescence intensity (MFI) for GFP than conventional CD4SP (Fig. 7). A higher level of GFP in Treg cells might arise if they were developmentally younger than Tconv cells because we observed a slight decrease in GFP as cells matured in the thymus (Fig. S3). This is unlikely because a previous study showed that thymic Treg cells are, on average, developmentally more mature than conventional CD4SP (McCaughtry et al., 2007). Furthermore, thymic Treg cell progenitors (defined as CD4SP, CD25+, CD122hi, Foxp3−; Burchill et al., 2008) had an even higher GFP expression level (Fig. 7). Finally, a twofold higher GFP level was also observed in peripheral Treg cells compared with Tconv cells express higher levels of GFP than Tconv cells

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STAT5 signaling does not increase GFP levels in Treg or Tconv cells

Although it is proposed that avid interactions with self-ligands are required for Treg cell development, γc cytokines (IL-2 and to a lesser extent IL-15 and IL-7) are also known to be crucial (Burchill et al., 2007; Vang et al., 2008). To address the potential contribution of cytokine signaling to GFP expression, we isolated thymocytes and lymphocytes from Nur77GFP mice and cultured them for 3–12 h with 25 ng/ml IL-2 and observed no increase in GFP expression (unpublished data). A previous study showed that constitutive expression of STAT5 (Stat5b−CA) increased the frequency and number of Foxp3+ Treg cells (Burchill et al., 2003). Therefore, we generated Nur77GFP/Stat5b−CA mice.

Figure 5. Thymocytes undergoing negative selection express higher levels of GFP compared with those undergoing positive selection. OT-I/Nur77GFP mice or OT-I/Bim−/Nur77GFP mice were generated and used as bone marrow donors. 5–10 × 10⁶ bone marrow cells were injected into lethally irradiated B6 or RIP-mOVA recipients. (A) Expression of CD4 and CD8 on thymocytes from the indicated chimeric mice. (B) GFP expression on Vα2+ CD8SP from the indicated chimeric mice. Representative data are from five experiments with more than five mice.

Figure 6. Induction of GFP is TCR specific. (A and B) Nur77GFP mice were injected i.v. with pI:pC (A) or LPS (B). After 6 h, cells were analyzed for GFP (left) and CD69 (right) expression. (C) 5 × 10⁶ OT-I/Nur77GFP lymph node cells were adoptively transferred into B6 recipients and infected with L. monocytogenes expressing the OVAa (LM-OVA) or not (LM). GFP expression on Vα2+:CD8+ transferred cells was evaluated after 12 h. Histograms show representative data from three independent experiments with at least three mice.

B6 recipient mice and infected them with L. monocytogenes that did or did not express OVA. Only when the pathogen expressed the OVA antigen was GFP up-regulation observed in OT-1 T cells (Fig. 6 C). Together, these results suggest that GFP expression is driven by antigen receptor signaling in T cells in Nur77GFP mice and not by other homeostatic or inflammatory signals.

Treg cells express higher levels of GFP than Tconv cells

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Thymocytes and lymphocytes were harvested and analyzed for Foxp3 expression and total GFP. As previously described (Burchill et al., 2003), we observed an increase in Treg cells in Nur77GFP/Stat5b-CA mice in both the thymus and the periphery when compared with WT littermate controls (Fig. 8 A). However, the total MFI of GFP in Treg cells from Nur77GFP/Stat5b-CA thymocytes did not increase but rather decreased in both the thymus (42 ± 2% decrease) and the periphery (32 ± 8% decrease; Fig. 8 B), whereas GFP expression in conventional CD4 thymocytes and lymphocytes did not change (Fig. 8 C). These data suggest that γc cytokine signaling via Stat5 does not account for the increased expression of GFP observed in the CD4+Foxp3+ population. Rather, the decrease in the total GFP MFI in the Treg cell population of Stat5-CA mice likely reflects the recruitment of low-affinity TCR, clones normally found in the naive repertoire into the Treg cell population as previously suggested (Burchill et al., 2008).

Treg cells compete for strong TCR ligands in the thymus

Previous studies with Treg TCR transgenic mice showed that development of the Foxp3+ Treg cell lineage is impaired at high precursory frequency, suggesting that Treg cell progenitors compete for a limited factor during development (Bautista et al., 2009; Leung et al., 2009). This factor might be a cytokine, given the profound requirement for γc cytokine signaling during Treg cell development (Burchill et al., 2007). Alternatively, Treg cell progenitors might compete for recognition of rare high-affinity self-ligands during development. In the Nur77GFP mouse, the level of GFP reflects TCR signal strength; thus, we postulated that if Treg cell development were limited by competition for high-affinity ligands, GFP would be increased at low precursor frequency of a TCR specific for high-affinity ligands. Alternatively, if Treg cell development were limited by non-TCR factors, GFP would not increase with less competition for the selecting ligand. To test this, using a mixed bone marrow chimera strategy, we generated animals with varying frequencies of Nur77GFP/G113 TCR transgenic precursors. G113 was cloned from a naturally occurring Treg cell, although its TCR specificity is unknown (Hsieh et al., 2006). Similar to what was previously reported (Bautista et al., 2009), we observed that monoclonal G113 mice have an almost undetectable frequency of CD25+ Treg cells in the thymus (Fig. 9 A) or periphery (not depicted). Interestingly, the level of GFP was not higher on intact G113 CD4SP compared with the polyclonal CD4SP population (Fig. 9 A, top row). This suggests that Treg cell-encoded TCRs do not have an intrinsically higher affinity for ubiquitous self-antigens and that both Treg and conventional CD4 precursors are positively selected through similar (low) affinity interactions in the cortex. In contrast to monoclonal G113 mice, when chimerism was <1%, the frequency of CD4+Foxp3+ cells dramatically increased, as previously reported (Bautista et al., 2009). Surprisingly, the level of GFP increased on all G113 precursors (Fig. 9 A) when they were at low precursor frequency, with an inverse relationship between percent chimerism and the GFP MFI (Fig. 9 B). This was true for both CD25+ and CD25− G113 CD4SP thymocytes. GFP did not increase on non-Treg cell (OT-II) precursors in analogous control chimeras (Fig. 9 B). These data demonstrate that thymic Treg cell precursors compete for interactions that lead to strong TCR stimulations and imply that the high-affinity self-antigens that support Treg cell development are rare.

NKT cells express high levels of GFP during thymic selection

iNKT cells have been described as autoreactive by design with a preponderance of indirect data suggesting
that precursors interact with a stimulatory self-lipid ligand, which remains incompletely identified (Bendelac et al., 2001; Gapin, 2010). Surprisingly then, both thymic and splenic iNKT cells expressed very low levels of GFP in Nur77GFP mice (Fig. 10 A). To confirm that iNKT cells could in fact up-regulate GFP after TCR stimulation, we injected mice i.p. with 5 µg α-galactosylceramide (α-GalCer). There was robust induction of GFP in splenic CD1d tetramer–positive cells (Fig. 10 B). The lack of GFP in thymic iNKT cells was seemingly contradictory to data implicating agonistic TCR stimulation in thymic selection of iNKT cells. However, it is well known that iNKT cells undergo cell division after selection (Benlagha et al., 2002) and that mature iNKT cells can be retained in the thymus for extremely long periods of time (Berzins et al., 2006). Thus, to inquire more specifically about the intensity of TCR stimulation during iNKT cell selection, we sought to evaluate the earliest iNKT cell precursors, previously named stage 0 precursors, which can be identified as binding CD1d/α-GalCer tetramer, and are HSA hi, CD44 lo, NK1.1– (Benlagha et al., 2005). Because such cells are rare in the thymus, we performed CD1d/α-GalCer tetramer–based magnetic enrichment. As expected, the majority of thymic iNKT cells were stage 3 mature cells (CD44 hi, NK1.1+), with a smaller subset of stage 2 and 1 cells (NK1.1–; Fig. 10 C). CD44− iNKT cells were further defined as stage 1 (HSA lo) or stage 0 (HSA hi). Interestingly, stage 0 iNKT cell progenitors expressed a higher level of GFP than age-matched conventional CD4 SP T cells. However, unlike Tconv and Treg CD4 T cells, most iNKT cells lost GFP expression after maturation in the thymus and persisted like this in the periphery (Fig. 10 A).

**DISCUSSION**

In this study, we introduced a unique BAC transgenic mouse useful for studying T cell activation in vivo. We showed that antigen receptor signaling was a major inducer of GFP in lymphocytes in Nur77GFP mice. GFP was not induced by...
TLR (toll-like receptor) ligands or other inflammatory stimuli, did not require co-stimulation, and was dependent on MHC for induction and maintenance in T cells. This finding is surprising in light of evidence that mechanical force, hormones, growth factors, and cytokines could induce Nur77 expression at the transcriptional level in nonlymphoid tissues (Pei et al., 2005; Pols et al., 2007). The only other stimulus reported to induce Nur77 in T cells is the thymotoxic plastic stabilizer DBTC (di-n-butylin dichloride; Gemnari et al., 2002), whose biochemical effect is not understood.

We observed that lymphocytes in the steady-state expressed a low level of GFP that was nonetheless consistently above the nontransgenic background. Polyclonal T and B lymphocytes expressed similar levels of GFP, and both responded to antigen receptor activation with rapid induction of GFP. Moreover, the thymic and peripheral expression pattern of GFP was consistent with antigen receptor regulation of signaling and TCR “tuning” and suggests this reporter mouse may be useful for imaging selection events in the thymus. Consistent with the idea that Nur77 expression is tightly regulated by the TCR, we found that adoptive transfer of CD4 T cells into an MHC II–deficient environment resulted in a loss of GFP expression that was otherwise maintained in the presence of MHC. This suggests that the tonic TCR signals perceived by T cells sustain the elevated GFP expression in the steady-state. Whether GFP expression in B cells requires tonic BCR signals is unknown. Naive CD4 T cells expressed higher basal levels of GFP compared with naive CD8 T cells. These data may suggest that CD4 T cells as a population express TCRs that perceive stronger self-pMHC signals through the TCR/coreceptor than CD8 T cells, but more experiments are required to address this hypothesis.

Using the Nur77GFP mouse as a reporter of TCR signal strength, we tested the idea that CD4+Foxp3+ Treg cells perceive a stronger signal during thymic development than Tconv CD4 T cells. We showed that polyclonal Treg cells expressed a higher level of GFP, implying they perceived stronger TCR stimulation upon selection and continued to do so in the periphery. These data are consistent with previous work with TCR transgenic mice in which coexpression of a neo-self-antigen and specific TCRs skewed the T cell repertoire to a higher frequency of CD4+Foxp3+ T cells (Jordan et al., 2001; Kawahata et al., 2002). It is also consistent with the fact that mutations in LAT (linker of activated T cells) led to Tconv cell development but not CD4+Foxp3+ cell development (Koonpaew et al., 2006). Interestingly, we noted that there was distinct overlap in the GFP levels between Treg and non-Treg cells. This pattern is conceptually reminiscent of the repertoire analysis of Treg and non-Treg cells, which showed distinct receptor specificities that were found predominantly in one population or the other and some receptor specificities that were shared (Hsieh et al., 2006; Pacholczyk et al., 2006).

Stat5 signaling is known to be required for CD4+Foxp3+ Treg cell development (Burchill et al., 2007). In light of this, it was possible that increased cytokine sensitivity and signaling in Treg cells accounts for the increased GFP expression. However, the failure of IL–2 to increase GFP expression in vitro or Stat5b-CA to increase GFP in vivo suggested otherwise. In fact, Treg cells from Stat5b-CA mice showed an overall decrease in GFP MFI. This is consistent with the TCR repertoire analysis performed by Burchill et al. (2008) in the Stat5b–CA mice, in which they observed that overexpression of Stat5 diverted TCR clones from the naive population into the Treg cell repertoire. Because naive T cells expressed lower GFP when compared with Treg cells, this resulted in a decrease in the total GFP MFI of the Treg cell population in Stat5b–CA mice.

Using a Treg TCR transgenic model (G113) at low precursor frequency, we were able to provide evidence that Treg cells compete for strong TCR ligands during development. We observed that when there was high competition, as seen in the 100% G113 chimeras, there was no increase in the overall level of GFP on Tconv cells, suggesting that the G113 TCR does not have an intrinsically higher affinity for ubiquitous (presumably positive selecting) self-antigens. However, the level of GFP in G113 cells was higher when the progenitor was present at low precursor frequencies. This finding implies that G113 precursors compete for rare higher affinity ligands, either because the proteins they are derived from are low abundance or because the APCs that process and present such ligands are not numerous. The Nur77GFP mouse may provide a useful tool to distinguish between these possibilities in the future. Interestingly, even at very low precursor frequencies, where all G113+ thymocytes were GFP+, not all were converted to the Treg cell lineage. This may suggest that there are other factors that also limit Treg cell development. Alternatively, it may reflect the delay between time of TCR stimulation and CD25 up-regulation and Foxp3 induction or clonal deletion of some of this population. A delay is consistent with work suggesting that Foxp3 is not required for the initial lineage decision in the thymus, but is downstream of a TCR signal and thus a delay in lineage differentiation (Gavin et al., 2007; Lin et al., 2007).

Finally, we show that iNKT cells also perceive a stronger TCR stimulus than Tconv cells upon selection in the thymus. However, unlike Treg cells, iNKT cells do not continue to perceive this stimulus as they mature and emigrate to the periphery. Interestingly, the level of GFP on iNKT cells in the spleen and liver was so low that it suggests they receive very weak if any TCR stimulation in the steady-state. Given this, it is unclear why iNKT cells express intermediate levels of the T cell activation marker CD69, although it is well established that other stimuli can induce CD69 (Shiow et al., 2006). However, our findings are consistent with a published report that iNKT cells can persist long term in the absence of CD1d (McNab et al., 2005).

Many cell types in the body express CD1d (Bendelac et al., 1997). The glycosphingolipid iGb3 was identified as a potential self-lipid ligand for NKT cells, although it is not clear that it is the sole endogenous antigen that stimulates iNKT cells (Zhou et al., 2004; Gapin, 2010). There is emerging evidence that stimulatory lipids are continually catabolized...
in lysosomes, and it was recently shown that when the catabolic enzyme α-galactosidase is absent, CD1d^+ cells are able to activate iNKT cells (Bendelac et al., 1995; Zhou et al., 2004; Darmoise et al., 2010). Importantly, TLR signaling seems to inhibit α-galactosidase activity, thereby allowing for iNKT cell activation in the context of infection (Darmoise et al., 2010). The Nur77^GFP mice may therefore be useful in determining what types of infections and stimuli activate APCs to display self-lipids that then stimulate iNKT cells.

Historically, CD69 has been used to study T cell activation. However, CD69 expression is up-regulated by inflammatory stimuli (Shiow et al., 2006), whereas GFP in Nur77^GFP mice was not. Therefore, this difference may make the Nur77^GFP tool useful for determining whether certain populations of T cells, such as CD8αα IELs that express high levels of CD69, are being activated through their antigen receptor or whether the environmental stimuli cause the activated phenotype.

In light of the tight regulation of GFP expression by TCR ligation and the differential expression of GFP based on TCR signal strength, we propose that the Nur77^GFP mouse may be a novel model for studying TCR signal strength in vivo. In addition, because inflammatory stimuli that induce CD69 expression fail to up-regulate GFP expression, we expect that these mice will be a useful tool for tracking activated T cells in several different experimental contexts such as acute and chronic infection, cancer, and transplantation.

MATERIALS AND METHODS

Mice. A Nur77^GFP targeting construct was created by insertion of a GFP-Cre fusion protein cDNA into the start site of the Nrdh1 gene on a 167-kb BAC vector. An ~135-kb fragment from this vector was purified via BuWI restriction sites and microinjected into C57BL/6j (B6) embryos at the Mouse Genetics Laboratory at the University of Minnesota. Alternatively, a 167-kb linearized DNA fragment was injected into B6 × SJL F1 embryos at the Transgenic and Chimeric Mouse Core Facility at the University of Pennsylvania.

B6 and B6.SJL (CD45.1 congenic B6) mice were obtained from the National Cancer Institute. MHC I-α^-deficient mice were obtained from Taconic. CD28-deficient mice were obtained from The Jackson Laboratory. G113 TCR transgenic mice were provided by C.-S. Hsieh (Washington University in St. Louis, St. Louis, MO), and Stat5b-CA mice were provided by M. Farrar (University of Minnesota, Minneapolis, MN). All animal experimentation was approved by and performed according to guidelines from the Institutional Animal Care and Use Committee at the University of Minnesota.

Flow cytometry. Cell surface staining was performed with antibodies from eBioscience, BD, or BioLegend. For intracellular Foxp3, cells were stained with the Foxp3 Staining Buffer set (eBioscience). For endogenous Nur77 detection, cells were fixed with fresh 4% PFA, vortexed well, and permeabilized with 0.1% Triton X-100. Antibody was used at 1.5 µg for staining. Biotinylated CD1d/α-GalCer monomers were obtained from the tetramer facility at the National Institutes of Health. Isolation of CD1d/α-GalCer binding cells via tetramer enrichment was performed as previously described (Matsuda et al., 2000). Samples were analyzed on an LSR II (BD). Data were processed with FlowJo software (Tree Star).

Bone marrow chimeras. Bone marrow was depleted of T cells with anti-Thy1.2 antibody and complement. Bone marrow was injected into lethally irradiated (1,000 rad) recipient mice. Chimeras were euthanized and analyzed at 8–12 wk after transplant.

Immunofluorescence. Tissue was harvested and immediately placed in 4% PFA in PBS overnight. Tissue was washed three times with PBS before being placed in 15% sucrose in PBS overnight. Tissue was then embedded in OCT compound and frozen with 2-methylbutane with dry ice and stored at −80°C for long-term use. After cutting tissue sections, slides were dried for 30 min and then submerged in 0.1% Triton X-100 in PBS at room temperature for 5 min. Blocking was performed with 3% BSA in PBS before general antibody staining or endogenous GFP detection.

Tetramer-based enrichment of thymic iNKT cells. Enrichment of CD1d^+ cells was performed using an adult thymus as previously described (Matsuda et al., 2000). After tetramer enrichment, cell surface stains were performed, and a dump strategy (including B220, CD11c, Gr1, and CD25) was used to eliminate nonspecific events. The smallest gate (stage 0) included a mean of 115 events.

In vivo and in vitro stimulation. For stimulation with α-CD3, 50 µg α-CD3 was injected i.v., mice were euthanized, and tissues were harvested and analyzed 12 h later. Stimulation of NKT cells was performed by i.v. injection of 5 µg α-GalCer 4–6 h before harvesting the spleen and liver. 50 µg LPS and 100 µg pi:pC were administered i.v., and tissues were harvested 6 h or 12 h later, respectively. For stimulation with α-IgM, 10^6 bulk splenocytes were cultured with 10 µg soluble α-IgM for 3 h at 37°C and then stained for FACS analysis. Plate-bound stimulation was performed by precoating 48-well plates with 10 µg α-CD3 or 10 µg α-CD2/CD3 and 50 µg α-CD28/O/N at 4°C and then culturing thymocytes and lymphocytes at 10^6 cells/well for 3 h at 37°C. OT-I Tap^+ stimulation was performed by peptide pulsed APCs with saturating concentrations of peptides and then adding thymocytes at a 1:4 ratio. Cells were incubated for 3 h at 37°C before FACS analysis.

L. monocytogenes infection. 5 × 10^6 OT-I (CD45.2^+) hosts. 24 h after transfer, mice were infected i.v. with 5 × 10^6 CFU of L. monocytogenes or variants expressing either the OVA or one of the OVA altered peptide ligands (Zehn et al., 2009) provided by M. Bevan (University of Washington, Seattle, WA). Mice were euthanized, and spleens were harvested 24 h after infection. Tissue was incubated with 5% collagenase D in serum-free HBSS for 30 min with mild agitation before performing cell surface staining.

Statistical analysis. Prism software (GraphPad Software) was used for statistical analysis. Paired and unpaired, two-tailed Student’s tests were used for data analysis and generation of p-values.

Online supplemental material. Fig. S1 shows that GFP and endogenous Nur77 reflect strength of antigen receptor signal but that GFP decays more slowly. Fig. S2 shows that GFP expression correlates with TCR signal strength during infection in vivo. Fig. S3 shows that GFP expression changes with developmental age. Fig. S4 shows that GFP expression is independent of CD28. Fig. S5 shows that peripheral OT-I T cells that escaped deletion in RIP-mOVA recipients expressed a high level of GFP. Fig. S6 shows the normalized MFI of GFP in various lymphocyte subsets. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20110308/DC1.

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SUPPLEMENTAL MATERIAL

Moran et al., http://www.jem.org/cgi/content/full/jem.20110308/DC1

Figure S1. GFP and endogenous Nur77 reflect strength of antigen receptor signal, but GFP decays more slowly. (A) OT-I/Nur77GFP lymphocytes were either stimulated with 1 μM OVAp (black) or PBS (gray) for 3 h in vitro. Cells were fixed and permeabilized and stained for endogenous Nur77. GFP expression was also analyzed in parallel. (B) OT-I/Nur77GFP thymocytes were incubated with WT splenocytes pulsed with varying OVAp or altered OVAp variants for 4 h. Thymocytes were then fixed and permeabilized and stained for endogenous Nur77 expression. cntl, control. (C) OT-I/Nur77GFP lymphocytes were pulsed with OVAp, and the kinetics of endogenous Nur77 and GFP expression were assessed.

Figure S2. GFP expression correlates with TCR signal strength during infection in vivo. 5 × 10⁶ OT-I/Nur77GFP lymphocytes were adoptively transferred into congenically different B6 mice. 24 h after transfer, mice were infected with 5 × 10⁷ CFU LM-N4 (OVAp) or the indicated altered peptide ligand. 12 h after infection, lymph nodes and spleen were harvested, and tissue was digested in collagenase D for 30 min. Graph indicates the level of GFP on donor Vα2⁺ T cells. Error bars indicate standard deviation. LM, L. monocytogenes.
Figure S3. **GFP expression changes with developmental age.** Nur77\textsuperscript{GFP} thymi were harvested and stained, and FACS analysis was performed. The cell surface markers TCR-\(\beta\) and CD69 were used to distinguish preselection and postselection thymocytes. CD24 (HSA) and Qa2 were used to distinguish semimature (HSA\textsuperscript{hi}Qa2\textsuperscript{lo}) from mature (HSA\textsuperscript{lo}Qa2\textsuperscript{hi}) SP thymocytes as well as RTEs from non-RTEs. Histogram overlays of each developmental age are displayed. Data are representative of more than six mice. Mat, mature; Ntg, nontransgenic.

Figure S4. **GFP expression is independent of CD28.** CD28\textsuperscript{−/−}/Nur77\textsuperscript{GFP} mice were generated, thymi were harvested, cell surface was stained, and FACS analysis was performed. Histogram overlays represent the overall level of GFP on the indicated thymocyte population in the steady-state (\(n = 7\) mice). NTg, nontransgenic.
Figure S5. Peripheral OT-I T cells that escaped deletion in RIP-mOVA recipients express a high level of GFP. (A) OT-I[Nur77GFP or OT-I[Bim0/\nNur77GFP mice were generated, and bone marrow from mice was transplanted into either B6 or RIP-mOVA recipients. 8–12 wk after transplant, thymus
and lymph nodes were harvested, and FACS was analysis performed. Dot plots show CD4 and CD8 expression on lymph node cells. (B) Histogram overlays
show the level of GFP on V simulate+CD8 lymphocytes from the indicated chimeric mice (n = 5). NTg, nontransgenic.
Figure S6. Normalized MFI of naive lymphocytes. (A and B) MFIs were compiled for the cell subsets shown in the thymus (A) and periphery (B) and normalized to the CD4 value. Paired and unpaired two-tailed Student’s t tests were used to calculate p-values shown. Error bars indicate standard deviation.