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Development of Thymically-Derived Natural Regulatory T Cells

Matthew L. Bettini and Dario A.A. Vignali

Department of Immunology, St. Jude Children's Research Hospital, Memphis, TN 38105, USA

Abstract

Natural regulatory T cells (nT_{regs}) are defined by their inherent ability to establish and maintain peripheral self-tolerance. In recent years, the development of nT_{regs} has come under close examination with the advent of FOXP3-GFP reporter mice that pinpointed the initiation of FOXP3 expression within the thymus. The mechanism and pathway of nT_{reg} development has only recently been studied in detail and to a large degree still remains unclear. In this review, we will discuss our current understanding of nT_{reg} lineage choice and development from a cellular and intracellular standpoint.

Keywords

Regulatory T cell; FOXP3; TCR; co-stimulation; cytokines; thymus; peripheral tolerance

Introduction

For several decades, the idea of a cell population that has an inherent ability to suppress a variety of immunological relevant cells has been hotly debated. However, in the last 20 years, it has now been firmly established that T_{regs} are a vital player in establishing peripheral self-tolerance. Sakaguchi and colleagues elegantly demonstrated that the depletion of a CD5⁺ splenocyte subpopulation could elicit multiorgan autoimmunity¹. CD5⁺ T cells were further distinguished by the presence of CD4⁺, CD45 RB^{low} and finally CD25⁺, the high-affinity subunit of the IL-2 receptor.^{2,3,4} It was also determined that neonatal thymectomy three days after birth blocked the emergence of peripheral CD4⁺CD25⁺ cells, confirming the thymic origin of T_{regs}.³

In 2003, Forkhead Box P3 protein (FOXP3) was identified as a unique marker for T_{regs} which was predominantly expressed within CD25⁺CD4⁺ T cells.^{5,6} FOXP3 is a transcription factor required for the development and function of CD4⁺CD25⁺ T_{regs}.⁷ It was later established that T_{regs} are not only required in protection from multiorgan autoimmunity, but also play an important role in specific autoimmune conditions including inflammatory bowel disease (IBD) and type 1 diabetes.^{8,9}

FOXP3 has been the focus of considerable interest since its discovery in humans in 1982¹⁰ and in mice in 1949,^{11,12} before it was linked to T_{regs}. It was determined that a mutation found within FOXP3 in humans led to immunodysregulation, polyendocrinopathy, enteropathy, X-linked (IPEX) syndrome. As the name describes, IPEX syndrome is an X-linked recessive disorder caused by mutations in the Forkhead Box P3 (FOXP3) gene located at Xq11.23-Xq13.3 of the X chromosome.^{10,13} Immunopathology associated with the IPEX syndrome becomes apparent around the first month after birth and includes

eczema or psoriasiform lesions, watery diarrhea, type 1 diabetes mellitus, excessive cytokine production and chronic inflammation leading to death.¹⁴ To date, there are over 20 known FOXP3 mutations resulting in the manifestation of IPEX syndrome. The majority of the mutations are missense mutations found in the DNA-binding domain of FOXP3. Various mutations within FOXP3 can lead to multiple dysregulations including a loss in transcriptional repression, mRNA stability of FOXP3, DNA binding, and FOXP3 dimerization.¹⁵

Mice that carry the lethal *scurfy* mutation also have defective FOXP3 and are characterized as runted with thickening and scaling of the ears and scaling of eyelids, feet, and tails.^{11,16} High quantities of lymphocyte infiltrates are present in the skin and liver, and these mice are anemic with splenomegaly, hepatomegaly and lymphadenopathy.^{12,17} All male mice with the *scurfy* mutation die between three and four weeks of age. Interestingly, heterozygous females remain healthy and are only carriers of the lethal FOXP3 mutation and lymphoproliferative disorder. It was established that the symptoms of the *scurfy* mouse were T cell mediated and the *scurfy*-like phenotype could be replicated in T cell-deficient animals by transfer of T cells from *scurfy* mice.¹⁶ Together these studies first established FOXP3⁺ T cells as the primary cell type that prevents severe autoimmunity. However, it was only recently established that FOXP3 is the master regulator of T_{reg} function and development. While significant advances have been made, much remains to be defined regarding T_{reg} develop in both the thymus and the periphery. The remainder of this review will focus on recent advances in understanding lineage choice of natural Tregs (nT_{regs}) within the thymus.

T cell development

In order to discuss how T_{regs} develop in the thymus, it is critical to understand the basis of T cell development as a whole. In 1961 Jacques Miller first characterized the thymus as the place for lymphocyte development.^{18,19} Following this landmark discovery, Miller went on to describe the role of the thymus and its direct relationship with immunological tolerance.²⁰ The more comprehensive terms of “central tolerance” and “peripheral tolerance” took into account the deletion of autoreactive T cells in the thymus before they reach the periphery (central tolerance) and the control or suppression of autoreactive T cells that escape deletion and circulate in the periphery (peripheral tolerance).^{21,22} Both central and peripheral tolerance are crucial in preventing the onset autoimmunity. T_{regs} are generally regarded as the key mediator of peripheral tolerance, where they are able to suppress self-reactive T cells and efficiently prevent autoimmunity.²³ As nT_{regs} originate in the thymus, it is thought they initially undergo the same selective pressure and developmental checkpoints as conventional ($\alpha\beta$) T cells (T_{conv}).

Two vital checkpoints that occur very close together, if not simultaneously, during thymocyte development are positive selection and negative selection. At this point in development, randomly rearranged TCRs act in concert with CD4 and CD8 co-receptors to interact preferentially with either MHC class I or MHC class II.^{24,25} The ligation of TCR with cognate peptide-MHC allows for a cacophony of signaling events and the development of immature thymocytes into either CD8⁺ or CD4⁺ single positive (SP) T cells, respectively. This engagement of TCR/co-receptor with MHC is vital in generating a T cell population that can distinguish self from non-self. Understanding the detailed mechanism of positive selection has garnered considerable attention over the last two decades. From these studies it was discovered that over 97% of all thymocytes that become DP cells will die by their failure to recognize, at any level, the presence of MHC and therefore will not receive survival signals through the TCR²⁶. These cells are said to die by neglect. The remaining thymocytes are thought to survive initially by the recognition of low-affinity peptides as described in the “kinetic signaling” model.²⁷ In this model it is proposed that signal intensity

allows for positive selection and then signal duration allows for CD4/CD8 lineage commitment. Recently, a variation of the kinetic signaling model has been proposed in which serial low affinity triggering by peptide-MHC complexes can promiscuously ligate enough TCRs to generate a persistent signal.²⁸ In opposition to this model, it has been shown that MHC class I-restricted thymocytes lacking CD8 can be driven to choose the CD8 lineage by interacting with high-avidity ligands.²⁹ Furthermore, CD4⁺CD8^{10/-} thymocytes are not always observed within TCR transgenic mice as seen in some mice that express MHC class I specific TCRs.³⁰ Both of these rare observations may only present themselves in default pathways to allow survival of thymocytes when selective pressures are applied. Regardless of the detailed events in positive selection, less than 1% of all thymocytes will recognize self-peptide at high enough affinity/avidity to receive survival signals but also low enough to avoid the activation threshold for apoptosis.^{31,32}

The recognition of self-peptide with high affinity/avidity by the TCR will direct the thymocyte towards controlled apoptosis and deletion.²¹ This process is also known as negative selection. An alternative to negative selection and deletion is the ability of these cells to undergo TCR editing and subsequently lose their autoreactive TCR and become anergic.³³ Recently, a fourth pathway has been described detailing the development of T cells selected against high affinity peptides that normally induce negative selection, sometimes referred to as agonist selection.³⁴ These cell types include NKT cells, CD8_{αα} intestinal intraepithelial lymphocytes (IEL), and possibly CD4⁺CD25⁺ regulatory T cells and $\gamma\delta$ T cells. It is still unclear how the intracellular signaling and genetic signatures differ between those cells selected on high affinity peptides versus low affinity peptides during positive selection. A more detailed review of the signaling environment believed to mediate nT_{reg} development will be discussed in a later section.

TCR signaling in thymocyte development

The $\alpha\beta$ TCR is composed of two polypeptides that contain variable regions specifically designed to ligate peptide-bound MHC. In the thymus, the $\alpha\beta$ TCR is expressed on thymocytes entering the DP stage of development. The TCR itself is unable to transmit any intracellular signals from external stimulation due to short cytoplasmic tails, however, it does associate with the CD3 complex ($\epsilon\gamma, \delta\epsilon$ and $\zeta\zeta$ chains) that mediate signal transduction.³⁵ Each of the four ($\epsilon, \gamma, \delta, \zeta$) chains in the TCR-CD3 complex contain immunotyrosine activation motifs (ITAMs) that can be phosphorylated by protein tyrosine kinases to recruit downstream signaling molecules. It was not known if the 10 CD3 associated ITAMs were functionally redundant, and because of the high number of ITAMs found in the ζ subunit (6 ITAMs), it was presumed that the CD3 ζ chains held the most control over the TCR signaling threshold.³⁶ To address this question, a scalable model of TCR signaling was proposed and tested, confirming that the CD3 ζ chain is indeed critical for the signaling events needed in the establishment of central tolerance.³⁷ In this model, lowering the number of functional ITAMs within the TCR:CD3 complex translates into lower TCR signal strength and loss in negative selection of autoreactive cells. The reduction in the number of ITAMs led to a breakdown in central tolerance and widespread autoimmunity. However, at this time it is not clear what impact, if any, individual ITAMs have on the signaling requirements for T_{reg} development. When CD3 $\epsilon\zeta^{-/-}$ bone marrow was transduced with either 10 functional ITAMs or 4 functional ITAMs and used to reconstitute *Rag1*-deficient mice, there did not appear to be any difference in the proportion of FOXP3⁺ T_{regs} or their ability to suppress *in vitro*.³⁷ Further characterization of the role of individual ITAMs is needed to address if any particular ITAM or combination of ITAMs are necessary in the development of FOXP3⁺ T_{regs}.

From these studies, it appears that the relatively high number of ITAMs found within the CD3 complex is needed to ensure a critical threshold of signaling possibly through the recruitment and activation of certain downstream signaling molecules such as the tandem Src homology 2 (SH2) domain-containing ζ -chain-associated protein of 70 kDa (ZAP-70).³⁸ It has been shown that recruitment and activation of the ZAP-70 substrate, linker of activated T cells (LAT), is essential in the development of FOXP3⁺ T cells in the thymus and the periphery.³⁹ In this study a key tyrosine residue was mutated (Y136F), inhibiting the binding of phospholipase C γ 1 (PLC γ 1) to activated LAT, causing a complete block in T_{reg} development. However, it appears there is also a partial block in thymocyte development in Y136F mice and this may lead, indirectly, to the loss of FOXP3 expression and impairment of T_{reg} development.

The CD3-associated ITAMs may also have distinct signaling responsibilities following TCR ligation. The TCR must translate extracellular stimuli into an intracellular response of a particular fate and by using finely tuned signals emanating from the TCR/CD3 complex, T cells can decide whether to proliferate, die or simply survive. The 21 kDa form of the CD3 ζ -chain is in a constitutively phosphorylated state, possibly acting as a hair trigger for TCR signaling events including differentiation and survival.^{40,41} The other CD3-associated ITAMs, ϵ , γ and δ , are thought to be more difficult to phosphorylate⁴² and may have specific roles in mediating activation of downstream effector molecules. For example, it has been shown that the CD3 δ chain is necessary for ERK signaling and lipid raft recruitment while the CD3 γ chain is necessary for ERK signaling leading to positive selection of thymocytes. Collectively, these data indicate the need for a threshold of signaling within developing thymocytes and potentially mediating signals necessary for development of T_{regs}. Clearly, the CD3-associated ITAMs have differential roles in TCR signaling and T cell development, and in combination, the ten ITAMs allow for a determined strength of signal or threshold to initiate pre-TCR signaling, central tolerance, homeostatic expansion, and maintenance of T cells.

Co-stimulatory molecules and T_{reg} development

As previously mentioned, nT_{reg} development is thought to take place solely in the thymus, however, it is currently unknown what signaling pathway(s) allow(s) for positive selection and survival of T_{regs} and their escape from deletion. It is widely known that FOXP3 expression does not commence until day 3 in neonates and it has been postulated that the lack of an organized thymic architecture may lead to the inability of developing thymocytes to receive the proper co-stimulatory signals for FOXP3 expression.⁴³ Many co-stimulatory signals have been implicated in the development and lineage commitment of nT_{regs} including: CD28 ligation by CD80/CD86, IL2R, thymic stromal-derived lymphopoietin receptor (TSLPR), CD154, glucocorticoid-induced tumour necrosis factor receptor (GITR), and STAT5 signaling.^{44–48} For instance, nT_{regs} are somewhat resistant to apoptotic signals, and this is in part due to the expression of GITR.⁴⁹ GITR may not be the only molecule responsible for the resistance of apoptosis in T_{regs} as anti- and pro-apoptotic molecules Bim and Bcl2 also appear to have a hand in T_{reg} development.⁵⁰ For example, it was reported that *Bim*^{-/-} mice have an increase in total T_{regs} while there is an increase in the frequency of FOXP3⁺ T_{regs} in Bcl2 transgenic mice.

Another co-stimulatory pathway necessary for nT_{reg} development is mediated by the interaction of CD28 with CD80/CD86. In mice that lack either CD80/CD86 or CD28, there is a marked reduction of FOXP3⁺ T_{regs}.⁵¹ It was later shown that CD28 has cell intrinsic and extrinsic roles in T_{reg} development.⁵² Extrinsicly, without CD28 expression there is a reduction in global IL-2 production leading to insufficient IL-2R signaling and reduction in FOXP3 expression. Intrinsicly, CD28 costimulation is required for T_{reg} precursors as

shown in an experiment where $Cd28^{-/-}$ HSC's have reduced numbers of FOXP3⁺ T_{regs} in the presence of exogenous IL-2.⁵²

It is well known that nT_{regs} constitutively express the high-affinity IL-2R chain CD25, however they are unable to secrete IL-2 themselves.⁵³ IL-2 appears to have a significant role in development and maintenance of T_{regs} as is evident from IL-2Rβ-deficient mice that have a loss of functional T_{regs}.⁴⁶ In addition, when there is a lack of IL-2 or the IL-2R, there is a 50% reduction in thymic T_{regs}. The incomplete block in T_{reg} development indicates IL-2 signaling through STAT5 is only a part of several signals needed for optimal T_{reg} development.^{47,54} Based upon these observations, a two-step model of nT_{reg} development has been postulated.^{55,56} In this model, recognition of high affinity self-peptide by developing thymocytes upregulates CD25 allowing for the rescue of these cells by IL-2- and STAT5-mediated signaling within the medulla and their progression into the T_{reg} lineage.

In addition to IL-2R signaling, ligation of TGFβR also appears to be involved in development and maintenance of nT_{regs}. Initially, the role of TGFβ was unclear as mice deficient in TGFβ or TGFβ receptor II had normal numbers of T_{regs} in adult thymi.⁵⁷ However, after close examination of mice with T cell restricted deletion of TGFβ receptor I, it was found that numbers of CD4⁺CD25⁺FOXP3⁺ thymocytes were greatly reduced in young mice, between days 3 and 5 of age.⁵⁸ It appears the reduction in CD4⁺CD25⁺FOXP3⁺ thymocytes is only temporary, and the numbers of thymic FOXP3⁺ T_{regs} rapidly recover due to increased production of IL-2. Also important to note is that CD4⁺CD25⁺FOXP3⁺ thymocytes were completely lost when mice lacking both TGFβRI and IL-2 were generated. From this work it is apparent that TGFβ is an important upstream mediator of FOXP3 expression although other signals, including TCR signaling, are necessary.

Spatial and temporal development of nT_{regs}

Visualizing and pinpointing the initial expression of FOXP3 within the thymus was greatly facilitated by the generation of FOXP3-GFP reporter mice, which have broadened our understanding of nT_{reg} development.⁷ Using these mice it was clearly established that FOXP3 expression is predominantly seen at the CD4 SP stage of development. However, a small percentage of GFP⁺ cells were also seen in the DP and CD8 SP populations, and, interestingly, at the immature DN stage of thymocyte development. In support of this notion, studies have identified a FOXP3⁺CD4⁻CD8⁻ (DN) population within the human thymus that was αβTCR and pTCRα negative.⁵⁹ These FOXP3 expressing cells were also negative for γδTCR, monocyte, B cell or NK cell markers. Interestingly the FOXP3⁺ DN cells were only found in the cortex region of the thymus.

Determining where within the thymus FOXP3 is first expressed has been hotly debated, as both the thymic medulla and cortex may be responsible for nT_{reg} development.^{60–63} For example, one recent study implicated expression of the autoimmune regulator gene (*Aire*) within medullary thymic epithelial cells (mTECs) as a critical cell type in nT_{reg} development.⁶⁴ In this study, medullary regions of MHC class II negative mTECs had significantly less FOXP3⁺ T_{regs} compared to MHC class II positive regions. Furthermore, using GFP as a marker for FOXP3 expression, it was determined that the overwhelming majority of GFP⁺ cells are found within the medulla of the thymus.⁷ In addition, it has been shown that thymic stromal-derived lymphopoietin (TSLP) produced in the medullary region of the human thymus is critical for T_{reg} development⁴⁴ giving credence to the notion that nT_{reg} development is medullary. It is important to note that thymic dendritic cells (tDCs) also make TSLP and these cells may infrequently be found in the thymic cortex.⁶⁵ Another study examined the role of MHC class II expressed in the cortex in nT_{reg} development and

demonstrated that mice expressing MHC-II only in the cortex were able to give rise to nT_{regs}, suggesting that nT_{regs} receive TCR signals early in development and require a combination of other co-stimulatory signals to mature into functionally suppressive nT_{regs}.^{61,63,66} To address the ability of the cortex to support T_{reg} development, a study was performed where thymic migration from the cortex to the medulla was blocked by administering pertussis toxin and therefore inhibiting G protein-coupled receptor signaling. In these treated mice there was an accumulation of CD4^{SP} FOXP3⁺ thymocytes within the cortex indicating the thymic cortex is sufficient to initiate FOXP3 expression.⁶³ It was also determined that about 25% of total FOXP3⁺ T_{regs} found within the thymus are CD4⁺CD8⁺ double positive thymocytes. Finally, in the case of CCR7 deficient mice, which have impaired thymocyte trafficking from the cortex to the medulla, there is an accumulation of SP cells, as well as, an increase in FOXP3⁺ T_{regs} in the cortex.^{63,67} Clearly nT_{regs} are capable of developing within the cortical region of the thymus, but require other co-stimulatory signals for lineage commitment and survival.

Within the cortex, DP thymocytes interact primarily with low affinity self-antigens expressed on cTEC's while other cells including fibroblasts and tDCs may be presenting higher affinity peptides.⁶⁸ One could theorize that DP thymocytes actively engage high affinity self-peptide/MHC, possibly by the association with an infrequent tDC population or other APCs in the cortex, which initiates expression of FOXP3.

It is thought that a major contributor of negative selection and T cell tolerance is mediated by expression of the autoimmune regulator gene (*Aire*).⁶⁹ *Aire* is expressed in thymic medullary epithelial cells (mTEC) and this allows for expression of many, but not all peripheral-tissue antigens that would otherwise be absent during negative selection. It is possible that interactions with AIRE-expressing mTECs could also initiate FOXP3 expression within CD4 SP immature thymocytes.⁶⁴ However, AIRE expressing mTECs undergo rapid turnover, allowing for cross-presentation of antigens by traveling tDCs.⁷⁰ The infrequent tDCs may then present AIRE antigens in the cortex allowing for nT_{reg} development at the DP stage. Taken together, these data indicate that initiation of FOXP3 expression within DP and SP thymocyte populations may be due to a combination, and possibly an accumulation, of signals mediated by the TCR, cytokine receptors and co-stimulatory molecules. From these observations a variation of the two-step model has been proposed⁷¹ where nT_{reg} development begins with a population of pre-T_{regs} generated by unknown mechanisms. After successful rearrangement of the TCR, pre-T_{regs} will recognize a diverse repertoire of self and foreign antigens but only progress to mature nT_{regs} by the accumulation of TCR-dependent and independent signals including a pathway that allows for survival under negative selection conditions.⁴⁵ In this model, TCR dependent and independent signals have variable levels of importance within any give developing nT_{reg}.

MicroRNA's and phosphatases

One area that needs closer inspection is the role of microRNAs (miRNAs) and phosphatases, as mediators of gene regulation and ultimately TCR signal strength during T_{reg} development^{72,73} and how they might affect FOXP3 expression. Recent studies have shown that the miRNA, miR-181a, represses multiple tyrosine phosphatases within mature T cells leading to dysregulated TCR signaling.⁷² These studies also found differential levels of miR-181a expression within the various stages of thymocyte development, coinciding with TCR signaling checkpoints and sensitivity to cell fates. One phosphatase found to be sensitive to miR181a, DUSP6, has also been described to have a role in regulating TCR-mediated ERK activation, and subsequently, the signaling threshold required for thymocyte positive selection.⁷⁴ Other miRNAs have been implicated in T_{reg} fitness and homeostasis.^{73,75} For instance, it has been suggested that miR-155 is necessary for the regulation of T_{reg}

homeostasis by targeting SOCS1, which allows T_{regs} to become sensitive to IL-2.⁷³ Dicer, a protein involved in miRNA processing, was shown to be critically important in FOXP3⁺ T_{reg} development as well as their peripheral maintenance.^{75,76} It is likely that other regulators of activation will be uncovered and it will be of great interest to determine if any contribute to the regulation of FOXP3 expression.

Regulatory T cell repertoire

In the last few years there has been a heated debate about whether TCRs expressed by T_{regs} have a higher propensity to recognize self-antigen or have a restricted repertoire in comparison to T_{conv} cells.^{62,77,78} In support of higher self-reactivity of n T_{reg} TCRs, it was shown that there is an enhancement in n T_{reg} development when agonist self-peptide is presented in the thymus.⁶⁰ However it was subsequently determined, following analysis of individual TCRs expressed by T_{regs} and T_{conv} cells, that neither preferentially recognizes self-antigen as their cognate antigen.⁷⁹ Moreover, isolated T_{regs} have been shown to be reactive to not only self-peptide, but also antigens derived from bacteria, viruses and parasites, neo-antigens and allo-antigens (Reviewed in ref. ⁷⁹). However, it is possible that these analyses did not take into account the differences in TCR repertoire expressed by natural versus induced T_{regs} . In a recent study that was performed in mice with a fixed TCR β and freely rearranged TCR α , there appeared to be no difference in T_{reg} TCR repertoire compared to T_{conv} TCR repertoire.⁷⁸ Moreover, the reported $\alpha\beta$ TCR diversity of T_{regs} in mouse and human appears to be comparable in terms of TCR variable region usage ($V\beta$ or $V\alpha$) between T_{conv} and T_{regs} .^{80,81} In addition, when TCR transgenic mice were engineered from an isolated and cloned T_{reg} TCR, these mice did not generate any T_{regs} or mature T cells in the periphery.⁸² Taken together, the current data suggest a diverse TCR repertoire that may rival that of conventional $\alpha\beta$ T cells. However, the analysis of a greater pool of isolated naive T_{reg} and naive T_{conv} TCRs will ultimately reveal if there is any skewing of the T_{reg} repertoire towards self or non-self. Currently, no reliable method has been described to isolate and sequence large number of TCRs from individual naive T_{regs} and T_{conv} cells (ie. from the current approaches which sequence several hundred TCR to approaches that can sequence several million). Most methods employ the use of single cell sorting or by isolating T_{regs} and T_{conv} cells from antigen-primed environments. To fully appreciate the complete T_{reg} repertoire, innovative approaches need to be developed to distinguish n T_{reg} from iT $_{\text{regs}}$ in order to determine TCR diversity between these two T_{reg} populations.

n T_{regs} versus iT $_{\text{regs}}$

Although n T_{regs} are perhaps more abundant within a quiescent immune system, iT $_{\text{regs}}$ may play an important role in maintaining proper immune function and regulation.⁸³ While n T_{regs} need costimulation via CD28, iT $_{\text{regs}}$ do not need any costimulation.⁸⁴ This is not surprising considering the inflammatory environment and milieu of cytokines that are present at the presumed site of iT $_{\text{reg}}$ development. Currently there are two types of iT $_{\text{regs}}$; type 1 regulatory T cells (Tr1) and T helper-3 T cells (Th3). Tr1 cells are induced by IL-10 and suppress via the same cytokine along with the production of TGF β ⁸⁵, but they lack FOXP3 expression.⁸⁶ In certain cases, Tr1 cells can secrete additional cytokines such as IL-5 and IFN γ . In contrast, Th3 cells are induced by TGF β and express FOXP3 as well as TGF β after conversion into the T_{reg} phenotype.⁸⁷ Th3 cells are predominately found within the intestinal tissue and mice lacking Th3 cells at this tissue site will develop spontaneous autoimmunity (Reviewed in ⁸⁸). Both types of iT $_{\text{regs}}$ can control the development of autoimmunity and promote transplantation tolerance.^{89,90} The distinction between n T_{regs} and iT $_{\text{regs}}$ may be in their cognate antigen. Whereas n T_{regs} are selected on endogenous self-peptide and may be responsible for controlling autoreactive T cells before tolerance is

broken, iT_{regs} are more likely to be found at sites of inflammation where it makes sense to convert activated T cells into suppressor cells.^{84,91} Interestingly, many iT_{regs} are found at mucosal sites and gut-associated lymphoid organs, where there is a tendency for a steady state of activation and exposure to foreign antigen.

Summary

Over the last 10 years there have been many advances in understanding the role of FOXP3 in T_{reg} function and development.⁹² It has been shown that both nT_{regs} and iT_{regs} are vital in controlling and mediating suppression in autoimmune and inflammatory disease models, such as IBD, T1D and EAE.⁸⁹ It is becoming increasingly clear that nT_{regs} are a distinct lineage pathway determined at the DP stage of thymocyte development due in part to co-stimulatory signals initiating FOXP3 expression. Prevailing evidence suggests that nT_{regs} development may shadow the process used by $\alpha\beta$ T cells^{63,71,79}, where early TCR signals in concert with co-stimulatory signals at the DP stage of development dictate a divergence from T_{conv} development and induce FOXP3 expression and T_{reg} development. The advent of reporter mice highlighted FOXP3 expression at early time points within the thymus, and revealed the location nT_{reg} development. FOXP3 expression in both the cortex and medulla suggests that selection of T_{regs} may begin in the cortex. Engagement of rare tDC or other APCs found in the cortex may provide the early TCR signal for T_{reg} lineage development. Understanding the relationship between APCs and T_{reg} progenitors at this initial engagement is key to understanding the earliest signals involved in T_{reg} differentiation.

There are many questions regarding T_{reg} lineage development that remain unanswered. (1) What co-stimulatory and or cytokine signals are responsible for T_{reg} lineage commitment beyond what is already known? (2) What are the upstream regulators of FOXP3 and the dominant signaling pathways that determine T_{reg} lineage fate? (3) Is there a unique APC that mediates T_{reg} development? (4) Is the nT_{reg} TCR repertoire more restricted compared to T_{conv} cells and how do nT_{reg} and iT_{reg} repertoires compare? (5) Just as there are induced T_{regs} in the periphery, is it possible that CD4 SP FOXP3⁻ cells in the medulla can become induced FOXP3⁺ T_{regs} ? More, specifically, are there iT_{regs} in the CD4 SP stage of thymocyte development? The recent explosion of genome and transcriptome sequencing technologies, and other advances, will undoubtedly lead to a more complete understanding of nT_{reg} and iT_{reg} development and homeostasis and help address these questions.

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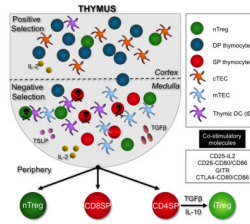


Figure 1.

As double positive (DP) thymocytes navigate the cortex of the thymus, they will encounter cortical thymic epithelial cells (cTECs) and rare thymic dendritic cells (tDCs). Only a few DPs will encounter cognate peptide/MHC and with co-stimulation by CD28 or other unknown mechanisms, upregulate FOXP3 and progress to the medulla. Most DPs, however, will undergo positive selection and progress to the medulla as FOXP3⁻ cells. Within the medulla, lingering DPs and the more abundant single positive (SP) CD4 and CD8 thymocytes will encounter AIRE⁺ medullary thymic epithelial cells (mTECs) and tDCs. mTECs and tDCs present higher affinity peptides that allow for deletion of potentially autoreactive thymocytes. They also provide the co-stimulation necessary for the initiation of FOXP3 expression. tDCs and perhaps other antigen presenting cells (APCs) provide a source for the IL-2, TSLP and TGFβ molecules necessary but not required for nT_{reg} development.

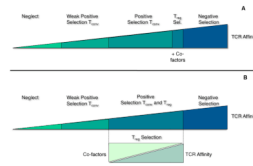


Figure 2.

Schematic diagram of nT_{reg} development as it relates to T cell receptor (TCR) affinity and co-factors. The current model (A) of nT_{reg} development indicates selection is mediated by high TCR affinity interactions with cognate peptide/MHC (pMHC) plus additional co-factors such as CD28-CD80/CD86 and IL-2 found in the medulla. A more recent model proposes nT_{reg} development can occur in both the medulla and cortex based upon a balance between TCR/pMHC and multiple co-factors. In this model (B), nT_{regs} that have high affinity for pMHC will need less co-factors such as the cytokines, TGF β and IL-2 or co-stimulatory molecules, GITR and CD28.