HES1 opposes a PTEN-dependent check on survival, differentiation and proliferation of TCRβ-selected mouse thymocytes

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ABSTRACT

The developmental progression of immature thymocytes requires cooperative input from several pathways, with Notch signals playing an indispensable role at the T cell receptor (TCR)-β selection checkpoint. Notch signals affect the activation of the PI3K/Akt pathway, which is required for pT\(\alpha\)/TCR\(\beta\) (preTCR)-induced survival, differentiation and proliferation of developing αβ-lineage thymocytes. However, the molecular players responsible for the interaction between the Notch and PI3K pathways at this critical developmental stage are unknown. Here, we show that Notch induction of \textit{Hes1} is necessary to repress the PI3K/Akt pathway inhibitor, PTEN, which in turn facilitates preTCR-induced differentiation. In support of this mechanism, deletion or down-regulation of \textit{Pten} overcomes the Notch signaling requirement for survival and differentiation during β-selection. Additionally, \textit{c-Myc} is a critical target of Notch at this stage, as c-Myc expression overcomes the Notch signaling requirement for proliferation during β-selection. Collectively, our results point to HES1, via repression of PTEN, and c-Myc as critical mediators of Notch function at the β-selection checkpoint.
INTRODUCTION

In the thymus, incoming lymphocyte progenitors encounter an inductive environment known to support intrathymic T cell development, which includes the Notch ligand Delta-like 4 (Dll4)\(^1,2\), the cytokine interleukin-7 (IL-7)\(^3,4\) and the chemokine CXCL12\(^5,6\). However, how signals derived from these factors are integrated by a developing thymocyte to realize the T cell differentiation program remains to be elucidated.

T cell development is a highly ordered process typically characterized by the surface expression of CD4 and CD8, with the earliest T cell subset contained among CD4-CD8- double-negative (DN), cells\(^7\), which can be further defined based on the expression of CD44, CD117, and CD25. The most primitive CD44\(^+\)CD117\(^+\)CD25\(^-\) DN1 cell subset contains multipotent progenitors\(^8,9\) and expression of CD25 marks entry into the T-lineage specified DN2 stage\(^7\). Here, expression of recombination-activating gene-1 (Rag1) and Rag2 induces TCR\(\beta\), TCR\(\gamma\), and TCR\(\delta\) gene loci to rearrange V(D)J gene segments, which continues into the subsequent CD44\(^-\)CD117\(^-\)CD25\(^+\) DN3 stage, wherein thymocytes irreversibly commit to the T-lineage and are subjected to their first developmental checkpoint, \(\beta\)-selection\(^7,10\). DN3 cells expressing a productively rearranged TCR\(\beta\) chain with its partner pT\(\alpha\) and CD3 form the pre-TCR complex that mediates passage across \(\beta\)-selection, resulting in rescue from apoptosis, cellular proliferation, TCR\(\beta\) gene allelic exclusion, and differentiation of DN3 cells to the subsequent CD4\(^+\)CD8\(^+\), double positive (DP), stage\(^10,11\).

Intrathymic Notch signaling is initiated when the Notch receptor (Notch1) engages its ligand (Dll4), which leads to the transcriptional activation of Notch target genes\(^12,13\). Notch signals induce adoption of the T cell fate in progenitors that enter the thymus\(^14\), and are essential for the survival, proliferation, and differentiation of DN thymocytes along the \(\alpha\beta\)-lineage, to the DP stage\(^7,14\). Previously, our findings revealed that Notch receptor-ligand interactions are crucial for maintaining cell size, glucose metabolism, and survival of DN3 cells prior to the initiation of \(\beta\)-selection\(^15\). This was due to Notch signals supporting the activation of the phosphatidylinositol-3-kinase (PI3K) pathway, leading to Akt/PKB phosphorylation. In support of this notion, pre-T cells deficient in phosphoinositide-dependent kinase 1 (PDK1), an enzyme which phosphorylates and activates AGC serine kinases, including Akt\(^16\), were found to be unresponsive to trophic effects of Notch signaling. Despite these studies establishing the critical role for Notch in activating PI3K signaling in developing T cells, the identity of relevant targets...
downstream of Notch responsible for bridging the two pathways remained unclear. Additionally, other signaling pathways mediated by IL-7R and CXCR4, known to promote PI3K/Akt activation were shown to act along with the pre-TCR during β-selection\textsuperscript{5,6,17}.

Recent studies examining the role of Notch in T-ALL have implicated HES1 and c-Myc as critical targets of Notch signaling in leukemic cells\textsuperscript{18,19}. Furthermore, PTEN (Phosphatase and Tensin homolog), an inhibitor of the PI3K pathway, was found to be an indirect target of activated Notch1 in T-ALL cells, via an HES1-mediated repression of the \textit{Pten} promoter\textsuperscript{20}. Together, these results suggested a potential mechanism for developing thymocytes by which Notch signaling supported the activation of the PI3K pathway, involving HES1 and PTEN as likely candidate genes.

Here, we investigate the role of HES1, PTEN and c-Myc downstream of Notch signaling in DN3 thymocytes. Using the OP9-DL1 T-cell differentiation system\textsuperscript{21,22}, we show that loss of Notch-ligand interactions in DN3 cells led to the down-regulation of \textit{Hes1} with a concomitant rise in \textit{Pten} mRNA expression. DN3 cells with reduced HES1 function exhibited a phenotype similar to loss of Notch signaling, including elevated levels of PTEN expression even in the presence of Notch signaling, supporting the previous report identifying HES1 as a transcriptional repressor of the \textit{Pten} promoter\textsuperscript{20}. This was accompanied with impaired proliferation and differentiation along the αβ-cell lineage to the DP stage. Thus, HES1 plays an important role in mediating PI3K regulation and trophic effects by Notch at the β-selection checkpoint. In support of this connection, restoration of PI3K signaling in pre-T cells, through the loss or down-regulation of PTEN, was sufficient to mediate β-selection in the absence of Notch signaling. However, without Notch signals, ectopic expression of c-Myc was critical to also ensure cellular proliferation. Taken together, these findings suggest that Notch signals at β-selection serve to promote PI3K-mediated survival and differentiation through HES1 repression of PTEN, as well as induce c-Myc expression to drive proliferation of thymocytes as they reach the CD4\textsuperscript{*} CD8\textsuperscript{*} stage of T cell development, at which point Notch signaling ceases, which serves to avoid an otherwise inevitable path to leukemic transformation.
METHODS

Mice
Rag2-deficient mice were bred and maintained in the animal facility of Sunnybrook Research Institute in specific pathogen-free conditions. Pten<sup>fl/fl</sup> Lck-cre mice<sup>23</sup> were obtained from the University Health Network (Toronto, Canada). Rag2<sup>-/-</sup> Pten<sup>fl/fl</sup>Lck-cre+ mice were generated by crossing Rag2<sup>-/-</sup> mice with Pten<sup>fl/fl</sup>Lck-cre+ mice. C57Bl/6 and CD1 timed-pregnant mice were obtained from Charles River Laboratories (Montreal, Canada). All animal procedures were approved by the Sunnybrook Health Science Centre Animal Care Committee.

Generation of HES1 and PTEN shRNA constructs and viral-producing cells
shRNA sequences were ordered from Sigma-Aldrich, or obtained from the RNAi consortium and oligonucleotides were ordered from Invitrogen. shRNA sequences were subsequently digested with XhoI and EcoRI and ligated with the Rapid DNA Ligation Kit (Roche) into the LMP vector digested with the same enzymes. Bacterial clones were screened for insert by PCR. GP+E.86 cells transfected for each of these shRNA constructs were generated.

OP9 co-culture and retroviral transduction
HES1 and dominant-negative HES1 constructs were kindly provided by Dr. R. Kageyama (Kyoto University, Japan) and Dr. A. Strom (Karolinska Institute, Sweden). Retroviral constructs were generated by subcloning cDNAs into MigR1, and stable retroviral-producing GP+E.86 packaging lines were generated for each construct. OP9-DL1, OP9-DL4 and OP9-Ctrl cells were produced and maintained as previously described<sup>24</sup>, and cultures were supplemented with 1 ng/ml mouse IL-7 and 5 ng/ml human recombinant Flt-3L (Peprotech). Fetal liver was obtained from timed-pregnant Rag2<sup>-/-</sup> or CD1 female mice on d 14 of gestation, and bone marrow was harvested from 6-8 week old Rag2<sup>-/-</sup> Pten<sup>fl/fl</sup>Lck-cre+ or Rag2<sup>-/-</sup> Pten<sup>fl/+</sup>Lck-cre+ mice. Single-cell suspensions were generated by disruption through a 40-mm nylon mesh screen using a syringe plunger. Bone marrow cell suspensions were purified for Lin<sup>-</sup> CD117<sup>+</sup> Sca1<sup>+</sup> HPCs by cell sorting before culture with OP9-DL1 cells. For retroviral transduction of HPCs, CD24<sup>lo/-</sup> CD1 fetal liver cells were enriched for HPCs by complement-mediated lysis with CD24 antibody, and transduced by overnight culture with stable retrovirus-producing GP+E.86 packaging cells. Transduced (GFP<sup>+</sup> or GFP<sup>+</sup>YFP<sup>+</sup>) or non-transduced Lin<sup>-</sup> CD117<sup>+</sup> Sca1<sup>+</sup> HPCs were purified by cell sorting cultures as previously described<sup>25</sup> and returned to culture with OP9-DL4 cells for T-lineage differentiation. For retroviral transduction of DN3 cells, d 7 HPC OP9-
DL1 co-cultures were passaged onto an overnight culture with stable retrovirus-producing GP+E.86 packaging cells. Transduced (GFP+ or GFP*YFP*) or non-transduced CD44-CD25+ DN3 cells were purified by cell sorting from day 8 cultures as previously described25.

**Flow cytometry and cell sorting**

All single-cell suspensions were stained with commercially available antibodies (BD Pharmigen and e-biosciences) and analyzed with a BD-LSRII flow cytometer, using Flowjo software (Treestar, Inc.). Dead cells were excluded from the analyses using DAPI gating.

**Quantitative Real-Time PCR**

Thymocyte populations were purified by flow cytometry or selection using magnetic anti-CD45 beads (Miltenyi Biotech). Total RNA was extracted using TRIZol (Invitrogen) and converted to cDNA using Quantitect Reverse Transcription Kit (Qiagen). Expression of the indicated genes was measured by quantitative real-time PCR using SYBR GreenER (Invitrogen). Primer sequences will be supplied upon request. β-actin was used to normalize cycle thresholds.

**Immunoblots**

Whole cells lysates were prepared by resuspending cell pellets in RIPA lysis buffer with protease inhibitors. Protein concentrations were determined by Bradford Assay. Equal amounts of protein from each sample were loaded and resolved using 10% SDS-PAGE, and transferred onto polyvinylidifluoride membranes (Amersham Biosciences). PTEN (Cell Signaling Technology), phospho-GSK3β (Ser9) (Cell Signaling Technology) and GAPDH (Millipore) specific antibodies were used to probe the immunoblots.

**PTEN-luciferase reporter assays**

293T cells were transfected with a PTEN-luciferase reporter construct (pGL3 PTEN HindIII-NotI)20 along with plasmids encoding HES1 (pcDNA3-HES1, generously provided by Dr. A. Strom) and/or dnHES1 (pcDNA3-dnHES1, generously provided by Dr. A. Strom) and/or shHES1. PTEN reporter activity was normalized to pRL-CMV Renilla-luciferase expression plasmid. PTEN reporter activity and Renilla luciferase levels (normalization control) were measured 48 h after transfection with the Dual-Luciferase Reporter Assay kit (Promega).
RESULTS

Loss of Notch signaling in DN3 cells leads to cellular atrophy, but not decreased levels of CD127 and CXCR4 expression.

As cytokine and chemokine-driven responses in developing T cells are often regulated at the level of receptor expression\(^ {17,26}\), we sought to address whether Notch signals target the PI3K pathway directly, or indirectly by affecting the expression of these receptor-mediated pathways. In particular, we compared the expression levels of CD127 (IL7R\(\alpha\)) and CXCR4 in Rag2\(^ {−}\) DN3 cells cultured in the presence or absence of Notch signaling. To this end, hematopoietic progenitor cells (HPCs) from Rag2\(^ {−}\) fetal livers (E14) were cultured for 8 days on OP9-DL1 cells to allow for T cell lineage commitment and differentiation to the DN3 stage\(^ {25}\). Co-cultures were subsequently sorted for DN3 cells, returned to OP9-DL1 or OP9-Ctrl cells, and analyzed 2 days later (Fig. 1A). As IL-7 is supplemented at 1 ng/ml, and SDF-1\(\alpha\) is endogenously expressed in OP9 cells\(^ {6}\), IL-7 and SDF-1 (CXCL12) levels are equivalent in OP9-DL1/Ctrl co-cultures. Importantly, Rag2\(^ {−}\) cells were used to circumvent the confounding effects of pre-TCR signaling on survival, proliferation, and differentiation. As expected, Rag2\(^ {−}\) DN3 cells remained CD44\(^ {−}\) CD25\(^ {+}\) on both OP9-DL1 and OP9-Ctrl cells, albeit CD25 expression appeared to be reduced in the absence of Notch signals, consistent with the report of Notch signaling targeting CD25 expression\(^ {27}\). Additionally, Rag2\(^ {−}\) DN3 cells experienced accelerated cell death and atrophy in the absence of Notch ligand, demonstrated by decreased cell numbers (data not shown) and cell size (FSC), respectively (Fig. 1A), consistent with our previous findings\(^ {15}\). This was accompanied by a slight decrease in surface expression of CD127 and CXCR4. However, these changes in surface expression were likely due to the observed cellular atrophy.

Transcriptional changes in DN3 cells upon loss of Notch signaling.

As loss of PI3K signaling in Rag2\(^ {−}\) DN3 cells cultured in the absence of Notch signals was not likely due to alterations in CD127 and CXCR4 expression, we sought to identify relevant downstream Notch targets responsible for Notch interaction with PI3K at the \(\beta\)-selection checkpoint. To this end, we identified and measured by QRT-PCR the changes in transcript levels that occur upon Notch signaling withdrawal, using mRNA from Rag2\(^ {−}\) DN3 cells cultured for 24 and 48 hours on OP9-DL1 or OP9-Ctrl cells. As expected, loss of Notch signaling in Rag2\(^ {−}\) DN3 cells was accompanied by decreased transcript levels for known Notch target genes Deltex1, c-Myc and Hes1 (Fig. 1B). Recently, HES1 was found to bind and repress the promoter of Pten, an inhibitor of the PI3K pathway\(^ {20}\). A gene expression reporter assay
confirmed that HES1 expression decreased Pten promoter activity (Suppl. Fig. 1). Furthermore, Notch signaling withdrawal in Rag2⁻/⁻ DN3 cells resulted in decreased Hes1 mRNA, coupled with increased Pten transcripts (Fig. 1B), making HES1 and PTEN likely candidates for bridging upstream Notch signals to downstream effects on the PI3K pathway. In support of this, analyses of ex vivo thymocytes revealed that, upon loss of Notch signaling associated with traversing β-selection⁷, similar changes in transcript levels are observed. Specifically, upon the down-regulation of Notch signaling from the DN4 to the DP stage of development, transcript levels of Notch target genes Deltx1, c-Myc and Hes1 are decreased, concomitantly with an increased Pten transcripts (Fig. 1C). Considering these data together, particularly the inverse relationship between HES1 and PTEN levels observed with loss of Notch signaling, we sought to determine whether HES1 played a critical role in the Notch-mediated activation of the PI3K pathway in DN3 cells at the β-selection checkpoint.

Transcriptional changes, decreased cellularity and DP development following inhibition of HES1 function.

HES1 is critically required for proliferation in early T cell progenitors²⁸-³⁰. Here, we retrovirally co-transduced DN3 cells to express two key Notch target genes, Hes1 and c-Myc, and assessed whether these cells could traverse the β-selection checkpoint in the absence of Notch signaling (OP9-Ctrl cultures). Flow cytometric analysis revealed that HES1 and c-Myc over-expression in DN3 cells did not overcome the need for Notch-mediated signals at this checkpoint, as seen by the failure to give rise to DP cells (Suppl. Fig. 2). Interestingly, HES1/c-Myc-transduced DN3 cells were smaller in size, as compared to c-Myc only (MigR1/c-Myc) transduced cells, but expressed higher levels of CD71, an indicator of increased PI3K/Akt pathway activity¹⁶.

To more clearly evaluate the role of HES1 in early T cell development, we expressed a dominant-negative version of HES1 (dnHES1)³¹ in DN3 cells. Importantly, a gene expression reporter assay confirmed that dnHES1 expression functionally repressed HES1 activity (Suppl. Fig. 1A). HES1 has been proposed to influence proliferation through inhibition of cyclin-dependent kinase inhibitors³²,³³. In agreement with this notion, expression of dnHES1 in Rag2⁻/⁻ DN3 cells cultured on OP9-DL1 cells increased Cdkn1a, Cdkn1b, and Cdkn1c transcript levels (Fig. 2A). GSK-3β is an important downstream target of PI3K/Akt signaling³⁴, and its phosphorylation at Ser9 is mediated by Akt. In support of our hypothesis that decreased HES1 function decreases PI3K/Akt pathway activity, dnHES1-expressing cells show increased PTEN mRNA and protein levels (Fig. 2A-C), corresponding to a decrease in phosphorylated GSK3β
protein levels (Fig. 2B). Together, these results further confirm HES1’s role as a repressor of PTEN expression in DN3 cells, and further support a mechanism by which Notch signaling influences PI3K pathway activation in thymocytes undergoing β-selection.

We addressed the role of HES1 during T-lineage differentiation by retrovirally transducing fetal liver-derived HPCs to express dnHES1 and/or GFP (MigR1), and using flow cytometry to assess their ability to respond to Notch signals, in co-culture with OP9-DL4 cells24. Figure 2D-F shows that dnHES1-transduced HPCs displayed a reduced efficiency in T cell differentiation that is particularly noticeable by day 10 of culture, when over 6-times more control (MigR1)-transduced HPCs differentiated to the DP stage than dnHES1-transduced cells (Fig. 2F). To circumvent the possibility of non-specific interference by dnHES1 on other bHLH or HES-family transcription factors, shRNA targeting Hes1 was used35. A gene expression reporter assay confirmed that shHES1 expression functionally repressed HES1 activity (Suppl. Fig. 1B). Consistent with results from dnHES1-transduced cells, shHES1-transduced DN3 cells showed increased PTEN protein levels (Fig. 2C), and shHES1-transduced HPCs showed reduced efficiency in differentiation along the T cell lineage (Suppl. Fig. 3A-C). Together, these findings are consistent with previous reports showing that Hes1-deficiency in hematopoietic precursors arrests T cell development28,29.

Inhibition of HES1 function allows for non-T lineage differentiation in the presence of Notch signals.

The apparent delay and impairment of T cell development in dnHES1-transduced HPCs is evident before and during β-selection. Previous studies using human hematopoietic cells showed that while over-expression of HES1 could induce a partial block on B cell development, but could not impose T cell differentiation36. Here, we find that loss of HES1 function with dnHES1-expression did not promote B cell development of HPCs in OP9-DL1 cultures, but instead increased myeloid-lineage (CD11b+) cell potential (Suppl. Fig. 4), based on absolute numbers (data not shown) and percentages. While HES1 does not appear to play a critical role in Notch-mediated T vs B lineage bifurcation, it is involved downstream of Notch signaling in the divergence away from myeloid lineage outcomes.

HES1 function is required for efficient β-selection.

To examine the specific role of HES1 in T cell differentiation at the β-selection checkpoint separately of its role in early proliferation and differentiation, HES1 function was manipulated at
the later DN3 stage of development. To this end, DN3 cells were isolated and transduced to express dnHES1 and/or GFP (MigR1), and cultured on OP9-DL4 cells. Expression of dnHES1 resulted in a marked reduction in the number of cells reaching the DP stage of differentiation (Fig. 3A,B). Additionally, DN3 cells transduced to express an shRNA targeting Hes1 when cultured on OP9-DL4 cells showed a similar decrease in their ability to develop to the DP stage, as compared to GFP (MigR1)-only transduced DN3 cells (Fig. 3C,D). Furthermore, to more precisely examine the effect of interfering with HES1 function at the β-selection checkpoint, Rag2−/− DN3 cells were co-transduced to express dnHES1 and/or a rearranged TCRβ chain, and preTCR-induced differentiation was analyzed. As expected, in the absence of a TCRβ chain, after 6 days of culture with OP9-DL4 cells, MigR1/MIY- and dnHES1/MIY-transduced Rag2−/− DN3 cells remained at the DN stage, while MigR1/TCRβ-expressing cells underwent differentiation from the DN to DP stage (Suppl. Fig. 5A). In contrast, dnHES1/TCRβ-expressing Rag2−/− DN3 cells showed a marked decrease in differentiation to the DP stage and failed to expand, while MigR1/TCRβ-transduced cells proliferated extensively in response to preTCR-derived signals (Suppl. Fig. 5B). Additionally, dnHES1/TCRβ-expressing Rag2−/− DN3 cells showed lower levels of CD71 surface expression, but differences in cell size were not observed (Suppl. Fig 5C). In keeping with the results from HPCs or DN3 cells transduced to express dnHES1, Rag2−/− DN3 cells co-transduced with dnHES1 and TCRβ developed beyond the DN3 stage but exhibited defects in differentiation and decreased cell numbers compared to controls, suggesting that the Notch-dependent differentiation and survival of DN3 cells at the β-selection checkpoint is at least partially mediated by HES1 and likely due to its ability to repress the PI3K inhibitor, PTEN.

PTEN enforces the Notch-dependent survival and differentiation of DN3 cells across the β-selection checkpoint.

PTEN dephosphorylates phosphatidylinositol-3,4,5-triphosphate (PIP3), thus opposing the activity of PI3K. Deletion of PTEN in pre-T cells was found to substitute for IL-7 and pre-TCR signals, both of which lead to downstream activation of the PI3K pathway, and mediate survival and differentiation to the DP stage37. As Notch signals also provide trophic effects at the β-selection checkpoint via PI3K pathway activation, and considering previous findings showing that HES1 represses PTEN expression, we sought to define the relationship between PTEN and Notch in early thymocytes. To this end, we made use of Ptenflox/flox (Lck-cre+) mice, in which deletion of Pten in Ptenflox/flox;Lck-cre+ T cells begins at the DN3 stage and is
complete by the DP stage (Fig. 4A). To test whether the absence of PTEN allows DN3 cells to survive and differentiate across the β-selection checkpoint without Notch signals, bone marrow-derived HPCs from of Pten\textsuperscript{ff:Lck-cre} and Pten\textsuperscript{+/+;Lck-cre} mice were cultured with OP9-DL1 cells for 14 days. From these cultures, DN3a (prior to β-selection)\textsuperscript{38} cells were sort-purified, placed back in culture in the presence or absence of Notch-ligand interactions, and analyzed 5 days later (Figure 4B, and Suppl. Fig. 6). Consistent with our hypothesis, DN3a cells from Pten\textsuperscript{ff:Lck-cre} mice were able to differentiate into DP cells, while Pten\textsuperscript{+/+;Lck-cre} DN3a cells failed to survive and differentiate in the absence of Notch signals (Fig. 4B,C).

DN3a cells cultured on OP9-Ctrl cells simultaneously experience the absence of two critical signals: Notch and pre-TCR. To circumvent this issue, and to more precisely time the induction of a concomitant gain of pre-TCR signals and a reduction of PTEN expression, we employed Rag2\textsuperscript{−/−} DN3 cells co-transduced to express TCRβ and PTEN-shRNAs, respectively. This approach not only coordinates the timing of pre-TCR expression, but ensures that any death of DN3 cells is not due to a lack of pre-TCR signals\textsuperscript{25}. Two PTEN-shRNA lentiviral constructs (LMP-HP_522, LMP-HP_524) were tested in Rag2\textsuperscript{−/−} DN3 cells, with HP_522 and and HP_524 shRNA constructs knocking down Pten mRNA by 50% and 75%, respectively (Fig. 5A). A similar decrease was seen in PTEN protein expression (Fig. 5B). While PTEN-shRNA transduced TCRβ\textsuperscript{+} Rag2\textsuperscript{−/−} DN3 cells bypassed the requirement for Notch signals at the β-selection checkpoint, as measured by the presence of DP cells on OP9-Ctrl cells (Fig. 5C,D), control firefly luciferase-shRNA (LMPff)-transduced TCRβ-expressing cells failed to traverse the β-selection checkpoint in the absence of Notch signals. The survival and differentiation of PTEN-shRNA-transduced TCRβ\textsuperscript{+} Rag2\textsuperscript{−/−} DN3 cells was PTEN-dose dependent, as greater knockdown of PTEN with HP_524 shRNA led to greater differentiation capacity in the absence of Notch signals. Similar to what was seen with Pten\textsuperscript{ff:Lck-cre} cells, PTEN-knockdown in TCRβ\textsuperscript{+} Rag2\textsuperscript{−/−} DN3 cells cultured without Notch signals had dramatically reduced proliferative potential compared to those receiving Notch signals.

**c-Myc induction is required for Notch-mediated cellular proliferation.**

While conditional Pten-deleted DN3a cells survive and differentiate to DP cells in the absence of Notch signaling, they fail to undergo cellular proliferation. This may be due to the loss of additional Notch-mediated proliferation mechanisms that cannot be compensated by the absence of PTEN. To address this, we generated Rag2\textsuperscript{−/−} Pten\textsuperscript{ff:Lck-cre} mice, which allowed for a
more precise definition of the interactions between pre-TCR, Notch, and PTEN at the β-selection checkpoint, as the timing of pre-TCR expression, loss of PTEN, and Notch availability can be manipulated by TCRβ-transduction, Lck-mediated Pten deletion and Delta-like availability in OP9 cell cultures. In vitro-derived DN3 cells from Rag2−/− Ptenff/Lck-cre+ and Rag2−/− Pten+/+Lck-cre+ mice were transduced to express TCRβ and YFP (MIY) and cultured in the absence or presence of Notch signals (Figure 6). As seen before, proliferation of TCRβ-transduced Rag2−/− Ptenff/Lck-cre+ DN3 cells receiving Notch signals was dramatically higher than that of the other groups (Fig. 6C). Also in agreement with the previous experiments, TCRβ-transduced Rag2−/− Pten+/+Lck-cre+ DN3 cells could not survive or differentiate in the absence of Notch signals, while Pten-deleted cells overcame this block (Fig. 6), albeit with much reduced cellularity compared to cells receiving Notch signals.

Considering c-Myc transcript levels are reduced in the absence of Notch signals (Fig. 1B), we examined whether restoring c-Myc expression in DN3 cells could allow for cellular proliferation in the absence of Notch signals. To this end, we co-transduced Pten+/+Lck-cre+ or Ptenff/Lck-cre+ Rag2−/− DN3 cells to express c-Myc and TCRβ. In the absence of Notch signaling, only TCRβ/c-Myc-expressing Ptenff/Lck-cre+, but not Pten+/+Lck-cre+, DN3 cells traversed the β-selection checkpoint and differentiated into DP cells (Fig 6A, B). Furthermore, Rag2−/− Ptenff/Lck-cre+ DN3 cells proliferated appreciably, generating DP cells at percentages comparable to TCRβ+ Rag2−/− Pten+/+Lck-cre+ cells cultured on OP9-DL1 (Fig. 6). In the presence of Notch signaling, TCRβ/c-Myc co-transduced DN3 cells from mice of both genotypes differentiated across β-selection and proliferated extensively.

Together, these results indicate that loss of PTEN partly substitutes for the required Notch receptor-ligand interactions, with an added requirement for ectopic c-Myc expression to restore the Notch-induced proliferative burst associated with cells traversing the β-selection checkpoint.
DISCUSSION

In this study, we addressed the mechanism by which Notch signals mediate trophic effects at the β-selection checkpoint. Our lab recently showed that Notch-ligand interactions were crucial for maintaining PI3K/Akt pathway activity, leading to survival and glucose metabolism in DN3 cells. Despite these studies demonstrating a relationship between Notch signaling and the PI3K pathway, the precise mechanism for this interaction was unknown. Here, we find HES1, PTEN, and c-Myc as key molecular players downstream of Notch for the regulation of survival, differentiation and proliferation at the β-selection checkpoint (Suppl. Fig. 7).

PI3K signaling and downstream Akt/PKB activation is essential for the survival and metabolism of proliferating pre-T cells. In the thymus, known upstream inducers of this pathway include IL-7R (CD127) and CXCR4. However, whether these signaling pathways or their molecular intermediates are the targets of Notch, and the means by which Notch regulates activation of the PI3K pathway remained unclear. Although cytokine and chemokine-based responsiveness of a developing T cells is often regulated at receptor expression levels, no changes in CD127 and CXCR4 expression were found with the loss of Notch signaling, suggesting that decreased PI3K signals are not due to receptor down-regulation. Additionally, we previously showed that IL-7R function, as measured by STAT5 phosphorylation, is retained following the loss of Notch signals. Recently, IGF1R expression was reported to be regulated by Notch signals in T-ALL, providing a potential link to PI3K pathway activation in leukemic cells. However, a gene expression microarray analysis from Rag2−/− DN3 cells cultured on OP9-DL1 or OP9-Ctrl cells failed to show changes in Igf1r expression upon loss of Notch signals (unpublished results). These results suggest that receptors that can activate PI3K are operationally available for DN3 cells, but that concomitant Notch signals are required to ensure that this signaling pathway becomes active and responsive to external cues.

The importance for Notch signaling at the DN3 stage and its ability to support PI3K activation is additionally critical when considering the dual signaling properties of CXCR4, namely its ability to promote either cell survival or apoptosis via PI3K/Akt or p38/MAPK, respectively. Under circumstances where Notch signaling is discontinued and CXCR4 continues to operate with a diminished capacity to induce PI3K signals, the observed loss of DN3 cells could be due to CXCR4-induced p38 signaling, which has been shown to disrupt early thymocyte...
differentiation. In this regard, we previously showed that inhibition of p38 signaling leads to increased survival and proliferation of β-selected DN3 cells cultured on OP9-DL1 cells.

A key question that arises is how a signaling pathway like Notch, which directly regulates gene transcription within the nucleus, can affect the activity of receptor proximal signals that engage the PI3K pathway. Here, we establish a mechanism of interaction between Notch and the PI3K pathway, whereby Notch-dependent transcriptional activation of HES1 mediates the down-regulation of PI3K pathway inhibitor, PTEN. This interplay explains how Notch is able to influence the signaling outcomes from cell surface receptors that employ the PI3K pathway (Suppl. Fig. 7). The functional interaction among these players was also observed in T-ALL, highlighting the need for tight regulation of these interactions during normal T cell development. This is achieved by the temporal regulation of Notch receptor expression after the β-selection checkpoint, as well as the auto-inhibitory loop of HES1, which limits the heightened level of PI3K responsiveness in DN cells.

Our findings point to HES1 as the key executor of Notch signals that ultimately affects PI3K activity. HES1 appears to not only repress the expression of various cyclin-dependent kinase inhibitors, but also represses Pten promoter activity, ensuring that β-selected cells can maximize their ability to proliferate and respond to the growth-promoting cues provided by the pre-TCR and the thymus microenvironment. Experimentally, interfering with HES1 function in DN3 cells increases PTEN expression, resulting in decreased ability to differentiate and progress across β-selection. However, a complete blockage in T cell development is not seen, and this is likely due to incomplete inhibition of HES1 function by dnHES1 or shHES1, or compensation by Hes1 related genes, e.g., Hey genes. However, HES5 and HES6 did not appear to play compensatory roles in dnHES1-expressing cells (data not shown). Although HES1 was previously observed to promote proliferation of thymocytes, HES1 over-expression, even with ectopic c-Myc expression, was unable to compensate for Notch signal withdrawal at the β-selection checkpoint. This is likely due to the strong transcriptional repressor activity of HES1, which becomes unchecked with a retroviral expression system. Nonetheless, HES1 over-expression in DN3 cells led to increased CD71 expression, an indicator of PI3K/Akt pathway activity in thymocytes, supporting the proposed regulatory gene network.
A recent report using $\textit{Hes1}^{\text{fl}}$ mice revealed a critical role for HES1 in early T-lineage commitment, proliferation, and differentiation, while it appeared to be dispensable through and beyond the $\beta$-selection checkpoint\textsuperscript{29}. Our findings that interfering with HES1 function affected early T cell development and expansion, and led to an increase in non-T lineage cells are consistent with that report. Similarly, the lower cell yields observed in the thymus of $\textit{Hes1}$-deleted mice are in agreement with the effects of decreased cellular proliferation in cells expressing dnHES1 or shHES1. However, our results point to a mechanistically important role for HES1 at the $\beta$-selection checkpoint, which was not seen in the $\textit{Hes1}^{\text{fl}}$ mice. Several potential explanations exist for the apparent discrepancies. Key differences exist between the approaches used, including the stage of T cell development at which HES1 function is manipulated, and the timing for when the developmental effects are interrogated. For example, we used of $\textit{Rag2}^{-/-}$ DN3 cells to more precisely pinpoint the developmental stage at which the requirement for HES1 function was examined, either before or after DN3 cells are induced to receive signals from the pre-TCR or Notch receptors. With this approach, we were able to discern a clear role for HES1 in $\beta$-selecting DN cells to down-regulate PTEN expression. However Wendorff et al.\textsuperscript{29} did not offer a potential mechanism of action for HES1 in T cell development, and did not see a role for HES1 in regulating PTEN expression. This last conclusion was based on an analysis of DP leukemic cells, and not normal DN cells, and as such, it is likely that DP cells, which typically do not express HES1, would not show a change in PTEN expression when the $\textit{Hes1}$ gene is deleted. Additionally, we found that $\textit{Pten}$ deletion efficiently restored DN3 survival and differentiation to the DP stage upon Notch signal withdrawal.

While conditional loss of PTEN in DN3a cells allows for their survival and differentiation to the DP stage in the absence of Notch signals, their proliferative capacity is greatly diminished, indicating that other pathways downstream of Notch are responsible for this outcome. Several studies of T-ALL have implicated c-Myc as a direct downstream target of Notch signaling, and as a critical component in transformation and cell growth\textsuperscript{18,19}. In T cell development, c-Myc is reported as a mediator of proliferation, but not developmental progression\textsuperscript{45,46}. In agreement with these reports, we find that Notch-induced c-Myc expression at this stage of development is responsible for promoting cellular expansion, leading to a large DP cell pool, and proliferation within the DN cell subset. While we showed that loss of HES1 function leads to increased expression of cell cycle inhibitors, ectopic expression of c-Myc in the absence of Notch signals would likely counter the loss of HES1-mediated $\textit{Cdkn}$ gene repression\textsuperscript{47}, thus enabling cell cycle
progression and bypassing the need for Notch signaling to support the proliferative burst typically associated with pre-TCR signaling. Collectively, our findings show that more than one downstream effector is responsible for the trophic effects of Notch signaling at the β-selection checkpoint.

Notch signaling is required by pre-T cells to traverse the β-selection checkpoint. Here, we identify key signaling intermediates downstream of Notch that are responsible for T-lineage differentiation, proliferation, survival and cellular metabolism. HES1 and PTEN are largely responsible for coordinating differentiation, survival and metabolism of pre-T cells at the critical β-selection checkpoint by bridging Notch signals to the activation of the PI3K/Akt pathway, while Notch induction of c-Myc expression drives the proliferation of β-selected cells that reach the DP stage of T cell development, at which point Notch signaling ceases to avoid an otherwise inevitable path to leukemic transformation.
ACKNOWLEDGEMENTS

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AUTHOR CONTRIBUTIONS

GWW designed and performed experiments; GK performed flow cytometric cell sorting and data analysis; AAF and TWM provided critical reagents and experimental expertise and advice; and JCZP designed experiments and supervised the study. GWW and JCZP wrote the manuscript.

CONFLICT-OF-INTEREST DISCLOSURE

The authors have no conflict of interests to declare.
REFERENCES


FIGURE LEGENDS

Figure 1. Notch signaling in developing thymocytes inversely affects the expression of HES1 and PTEN. A) *Rag2*<sup>−/−</sup> E14 fetal liver (FL)-derived hematopoietic progenitor cells (HPCs) cultured with OP9-DL1 cells for 8 d are used to give rise to CD44<sup>+</sup> CD25<sup>+</sup> DN3 cells, which are then sorted and returned to either OP9-DL1 or OP9-Ctrl cells for 2 d prior to analysis. Flow cytometric analysis of CD44, CD25, CD127 and CXCR4 expression is shown for *Rag2*<sup>−/−</sup> DN3 cells cultured for 2 d in the absence (Ctrl) or presence (DL1) of Notch signaling. Overlay histograms showing cell size (FSC), and surface expression of CD127 and CXCR4 of DN3 cells, cultured as indicated, are shown on the right. Data are representative of at least three independent experiments. B) QRT-PCR analysis of mRNA expression, normalized to β-actin, of Notch downstream target genes (*Deltex1*, *Hes1* and *c-Myc*) and *Pten* is shown for *Rag2*<sup>−/−</sup> DN3 cells cultured for 1 or 2 d as indicated. Data are representative of at least three independent experiments, with standard deviation of the mean shown as error bars. C) QRT-PCR analysis of mRNA expression (as above) is shown for C57BL/6 *ex vivo*-isolated DN4 and DP thymocyte subsets. Data are representative of at least three independent experiments.

Figure 2. Expression of a dominant negative form of HES1 (dnHES1) leads to up-regulation of *Cdkn1* and *Pten* expression, and impaired T cell development. A) QRT-PCR analysis of mRNA expression of HES1 target genes (*Cdkn1a,b,c* and *Pten*) in *Rag2*<sup>−/−</sup> DN3 cells retrovirally-transduced to express dnHES1 and/or GFP (MigR1), and then cultured with OP9-DL1 cells for 2 d prior to analysis. QRT-PCR results are normalized to β-actin expression levels, and the data are representative of three independent experiments. B-C) Analysis of PTEN and phosphorylated GSK3β (Ser9) protein expression in B) BWZ.36 cells or C) DN3 cells retrovirally-transduced to express dnHES1, shHES1, and/or GFP (MigR1) is shown as immunoblots of whole cell lysates probed with antibodies specific for PTEN, GSK3β (Ser9), or GAPDH. Data are representative of three independent experiments. D-F) Developmental progression of FL-derived HPCs transduced to express dnHES1 and/or GFP (MigR1) and subsequently cultured for 10 d with OP9-DL4 cells. Flow cytometric analysis of D) CD44 and CD25; and, E) CD4 and CD8, surface expression is shown for GFP<sup>+</sup> gated cells on days 4, 7, and 10 of co-culture, as indicated; while, F) shows the corresponding cellularity of DP cells present in the cultures, as indicated. DP cellularity was obtained by multiplying the total cellularity by the percentage of DP cells present in the cultures of each independent experiment. Data are representative of three independent experiments.
Figure 3. Expression of a dominant negative form of HES1 (dnHES1) in DN3a cells impairs T cell differentiation across the β-selection checkpoint. A) Developmental progression of DN3a cells transduced to express dnHES1 and/or GFP (MigR1) and subsequently cultured with OP9-DL4 cells for 2-4 d. Flow cytometric analysis of CD4 and CD8 surface expression is shown for GFP+ gated cells on days 2, 3, and 4 of co-culture as indicated with the cellular fold expansion (total cellularity at each time point divided by the number of cells used at the start of the culture, input) observed in the cultures shown for the indicated times and conditions. C) Developmental progression of DN3a cells transduced to express shHES1 and/or GFP (MigR1) and subsequently cultured with OP9-DL4 cells for 1-3 d. Flow cytometric analysis of CD4 and CD8 surface expression is shown for GFP+ gated cells on days 1, 2 and 3 of co-culture as indicated with D) the total cellularity observed in the cultures shown for the indicated times and conditions. Data are representative of three independent experiments, with standard deviation of the mean shown as error bars.

Figure 4. Conditional Pten deletion in DN3 cells allows for T cell differentiation across the β-selection checkpoint in the absence of Notch signals. A) Deletion of exons 4 and 5 of the Pten allele in Ptenfl/fl;Lck-cre+ mice is initiated at the DN3 stage of development and completed by the DP stage. DNA from whole thymus of Ptenfl/fl;Lck-cre+ or Ptenfl/+ mice, and from sorted DN2, DN3, DN4 and DP thymocyte subsets of Ptenfl/fl;Lck-cre+ mice was extracted and amplified by PCR. Agarose gels with the PCR products corresponding to the deleted and floxed alleles are shown, as indicated. Data are representative of at least three independent experiments. B) Developmental progression of culture-derived Ptenfl/fl;Lck-cre+ DN3 cells cultured for 6 d with OP9-Ctrl cells. Flow cytometric analysis of CD4 and CD8 cell surface expression is shown for CD45+ gated cells; while C) shows the corresponding fold expansion and DP cellularity, as indicated. Lin- c-Kit+ Sca-1+ cells sorted from BM of Ptenfl/fl;Lck-cre+ or Ptenfl/+;Lck-cre+ mice were cultured with OP9-DL1 cells for 14 d, sorted for DN3a cells, and returned to OP9-Ctrl cells for 6 d. Fold expansion was obtained from the total cellularity divided by the number of cells used at the start of the culture (input), and DP cellularity by multiplication of the total cellularity by the percentage of DP cells present in the cultures. Results are representative of three independent experiments.

Figure 5. Knockdown of Pten expression in Rag2−/− DN3 cells with TCRβ allows for T cell differentiation across the β-selection checkpoint in the absence of Notch signals. A) QRT-PCR
analysis (normalized to β-actin) of Pten mRNA expression in Rag2−/− DN3 cells transduced to express PTEN shRNA (LMP-HP_522 or LMP-HP_524) or firefly luciferase shRNA (LMPff). Data are representative of three independent experiments. B) Analysis of PTEN protein expression in NIH3T3 cells retrovirally-transduced to express the indicated shRNAs is shown as immunoblots of whole cell lysates probed with antibodies specific for PTEN or GAPDH. Data are representative of three independent experiments. C-D) Developmental progression of culture-derived Rag2−/− DN3a cells transduced to express shRNAs, as indicated, and subsequently cultured for 6 d with OP9-DL1 or OP9-Ctrl cells. C) Flow cytometric analysis of CD4 and CD8 surface expression is shown for GFP+ (shRNAs) and YFP+ (TCRβ or MIY) gated cells; while, D) shows the corresponding cellularity of DP cells present in the cultures, as indicated. DP cellularity was obtained by multiplying the total cellularity by the percentage of DP cells present in the cultures of each independent experiment. Data are representative of three independent experiments.

Figure 6. Conditional Pten deletion and ectopic expression of c-Myc allows for survival, differentiation and proliferation of DN3 cells across the β-selection checkpoint in the absence of Notch signals. Developmental progression of culture-derived Rag2−/− PTEN+/−;Lck-cre+ or Rag2−/− PTENf/f;Lck-cre+ DN3 cells retrovirally co-transduced to express TCRβ (GFP+) and MIY or c-Myc (YFP+) and cultured with OP9-Ctrl or OP9-DL1 cells for 6 d. A) Flow cytometric analysis of CD4 and CD8 cell surface expression is shown for GFP+, YFP+, CD45+ gated cells; while B-C) shows the corresponding DP cellularity and fold expansion, respectively, as indicated. Lin− c-Kit+ Sca-1+ cells sorted from BM of PTENf/f;Lck-cre+ or PTEN+/−;Lck-cre+ Rag2−/− mice were cultured with OP9-DL1 cells for 14 d, retrovirally-transduced, then sorted for YFP+ and GFP+ DN3 cells, and cultured as indicated. Fold expansion was obtained from the total cellularity divided by the number of cells used at the start of the culture (input), and DP cellularity by multiplication of the total cellularity by the percentage of DP cells present in the cultures. Results are representative of three independent experiments.
Wong_Figure 1

A.

- Reg2<sup>−/−</sup> FL HPC
- OP9-DL1
- OP9-DL1
- OP9-DL1
- OP9-DL1

CD44
CD25
CD127
CXCR4

FSC
CD127
CXCR4

B.

- Deltex1
- Hes1
- c-Myc
- Pten

Day1
Day2
Day1
Day2
Day1
Day2
Day1
Day2

C.

- Deltex1
- Hes1
- Myc
- Pten

DN4
DP
DN4
DP
DN4
DP
DN4
DP

Wong_Figure 3

A. 

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B. 

Fold Expansion / input

Day

MigR1  dnHES1

C. 

Day 1  Day 2  Day 3  

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D. 

Cellularity (x10^6)

Day

MigR1  shHES1
Wong_Figure 5

A. Relative to LMPff

B. PTEN and GAPDH Western Blot

C. Flow cytometry analysis of CD4 and CD8

D. Cellularity of DP (10^6)
HES1 opposes a PTEN-dependent check on survival, differentiation and proliferation of TCR β-selected mouse thymocytes

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