Inhibitors of DNA Binding Proteins Restrict T Cell Potential by Repressing Notch1 Expression in Flt3-Negative Common Lymphoid Progenitors

Ana Pereira de Sousa, Claire Berthault, Alessandra Granato, Sheila Dias, Cyrille Ramond, Barbara L. Kee, Ana Cumano and Paulo Vieira

*J Immunol* 2012; 189:3822-3830; Prepublished online 12 September 2012; doi: 10.4049/jimmunol.1103723
http://www.jimmunol.org/content/189/8/3822

**Supplementary Material**
http://www.jimmunol.org/content/suppl/2012/09/12/jimmunol.1103723.DC1

**References**
This article cites 60 articles, 37 of which you can access for free at:
http://www.jimmunol.org/content/189/8/3822.full#ref-list-1

**Why *The JI*?** Submit online.
- **Rapid Reviews!** 30 days* from submission to initial decision
- **No Triage!** Every submission reviewed by practicing scientists
- **Fast Publication!** 4 weeks from acceptance to publication

---

**Subscription**
Information about subscribing to *The Journal of Immunology* is online at:
http://jimmunol.org/subscription

**Permissions**
Submit copyright permission requests at:
http://www.aai.org/About/Publications/JI/copyright.html

**Email Alerts**
Receive free email-alerts when new articles cite this article. Sign up at:
http://jimmunol.org/alerts
Inhibitors of DNA Binding Proteins Restrict T Cell Potential by Repressing Notch1 Expression in Flt3-Negative Common Lymphoid Progenitors

Ana Pereira de Sousa,*,† Claire Berthault,*,‡† Alessandra Granato,*,†,† Sheila Dias,§,2 Cyrille Ramond,*,†,‡ Barbara L. Kee,§,‖,‡ Ana Cumano,*,† and Paulo Vieira*,†

Lineage commitment is regulated during hematopoiesis, with stepwise loss of differentiation potential ultimately resulting in lineage commitment. In this study we describe a novel population of B/NK bipotent precursors among common lymphoid progenitors in the fetal liver and the bone marrow. The absence of T cell precursor potential, both in vivo and in vitro, is due to low Notch1 expression and secondary to inhibition of E2A activity by members of the inhibitor of DNA binding (Id) protein family. Our results demonstrate a new, Id protein-dependent, molecular mechanism of Notch1 repression, operative in both fetal and adult common lymphoid progenitors, where T cell potential is selectively inhibited without affecting either the B or NK programs. This study identifies Id proteins as negative regulators of T cell specification, before B and NK commitment, and provides important insights into the transcriptional networks orchestrating hematopoiesis. The Journal of Immunology, 2012, 189: 3822–3830.

The hematopoietic system continuously generates mature blood cells belonging to multiple lineages. The integrity of this process depends on self-renewing multipotential hematopoietic stem cells (HSCs) that are able to sustain blood cell production throughout life. HSCs are found among a population of hematopoietic precursors coexpressing high levels of Sca-1 and c-Kit, but lacking lineage-associated markers (LSK) (1–3). Among LSK cells, expression of Flt3 (also known as Flk2) identifies multipotent progenitors (MPPs) that have lost self-renewing capacity (4). Those MPPs with the highest expression of Flt3, called lymphoid-primed multipotent progenitors (LMPPs), have little ability to generate megakaryocytes or erythrocytes, both in vivo and in vitro, but are efficient myeloid and lymphoid progenitors (5). LMPPs further differentiate to express the α-chain of the IL-7 receptor, becoming common lymphoid progenitors (CLPs) that have minimal myeloid potential but are able to give rise to T, B, and NK cells (6). It was recently shown that expression of Flt3 can be used to separate the originally defined CLP population into two major subsets: the Flt3-expressing CLPs (CLP<sub>Flt<sup>+</sup>3</sub>), which have a robust T, B, and NK cell differentiation potential, and the Flt3-negative fraction (CLP<sub>Flt<sup>-</sup>3</sub>), which is thought to include only progenitors restricted to the B lymphocyte lineage (7).

In mammals, HSCs reside and differentiate in two major primary lymphoid organs: the fetal liver (FL), responsible for most of the hematopoiesis occurring in embryonic life, and the bone marrow (BM), where blood-borne cells are produced postnatally. Whereas our understanding of hematopoiesis has relied to a large extent in the identification and purification of the various progenitor populations from adult BM, the fetal counterparts of hematopoietic precursors are much less well studied. The observation that the FL counterpart of the adult CLPs can give rise to macrophages and lymphoid tissue inducer (LTi) cells (8) led to the proposition that fetal and adult hematopoiesis follow different rules (9).

Differentiation and commitment of multipotent progenitors depend on the activation of signaling pathways and on the expression of transcription factors that induce lineage-specific genes and repress alternative cell fates. Some of these pathways and factors regulate cell fate by inducing specific genetic programs that ultimately result in lineage commitment. For example, signaling by Notch1 regulates T cell differentiation. Inactivation of Notch1 results in a block of T cell development and a striking accumulation of B cells in the thymus, at least some of which arise from T cell progenitors (10–15). Proper T cell differentiation requires tight control of Notch1 expression and activity, both inside and outside the thymus, but the regulatory mechanisms controlling its expression in lymphoid progenitors are still not fully understood. Early B cell factor (Ebf)1, in contrast, plays a crucial role in the development and specification of B lineage cells. Mice deficient in this transcription factor do not express many B cell-associated genes, such as CD79a, CD79b, IgH1, and V-pre-B, and the cells do not...
undergo H chain recombination (16, 17). Ebf1-deficient cells also do not express paired box protein 5 (Pax5), an essential factor in B cell commitment owing to its capacity to directly repress B lineage-inappropriate genes (17, 18).

E proteins are transcription factors containing a basic DNA-binding region juxtaposed to a helix-loop-helix domain that mediates protein dimerization. They bind with high affinity to E box sites that are present in the promoter and enhancer regions of multiple T and B cell-specific genes (19). One member of this family, E2A, exists in two alternative splice forms, designated E12 and E47, and is essential for the establishment of the B and T cell programs by regulating the expression of several lymphoid genes, including Ebf1 and Notch1. E2A cooperates with IL-7R signaling to induce Ebf1 expression at the CLP stage and, together with Ebf1, regulates Pax5 expression (17, 20–22). Additionally, E2A induces the expression of Notch1 and of several components of the Notch1 signaling pathway, thus promoting T lineage differentiation (23–27). The inhibitors of DNA binding (Id) proteins act as dominant negative regulators of E2A function, because Id proteins associate with members of the E protein family and prevent their binding to target sites in the genome (19). Four members, Id1–Id4, have been identified in mammals, but only Id2 and Id3 are highly expressed in lymphoid cells. These Id molecules are essential for NK development and appear to play an important role in the transcriptional regulation of the NK versus T cell fate (28–30).

In this study we identified a population of lymphoid-restricted progenitors in the FL that are able to generate T, B, and NK cells, but are devoid of myeloid differentiation potential, both in vitro and in vivo. Phenotypically and functionally FL CLPs resemble the BM CLPs, and in both hematopoietic organs the loss of Flt3 expression in CLPs is associated with the specific loss of T lineage potential, revealing a novel intermediate stage in lymphoid differentiation that displays B and NK cell, but not T cell, potential. We further demonstrate that the mechanism underlying this lineage restriction is a stage-specific upregulation of Id2/3 proteins that reduces E protein activity and consequently Notch1 expression. Importantly, the elevated expression of Id proteins in CLPId2/3− cells does not prevent B lineage differentiation under the appropriate conditions. Thus, this work uncovers a novel role for Id proteins in the regulation of E2A activity at the CLP stage.

Materials and Methods

Mice

CS7BL/6 control mice (Ly5.1 and Ly5.2) were purchased from Charles River Laboratories. Rag2−/− (31), IL-7R−/− (32), Flt3 ligand−/− (33), and Rorc(γt)−/−GFP mice (34) were mated with specific pathogen-free conditions at the Pasteur Institute. All animal experiments were done in accordance with the guidelines of the Pasteur Institute, which were approved by the French Ministry of Agriculture. Id2−/− (35), Id3−/− (36), and E47−/− (37) mice were housed at the University of Chicago Animal Resources Center, and experiments were performed in accordance with the guidelines of National Institutes of Health with protocols approved by the Institutional Animal Care and Use Committees of the University of Chicago and the Pasteur Institute.

Cell purification

FL cells were obtained from embryos at day 15.5 gestation (with the day of appearance of vaginal plug being taken as day 0.5). Spleens were isolated from adult mice (>8 wk old). Single-cell suspensions were obtained by disruption of FL or spleen with a nylon mesh in culture medium that was HBSS with 1% FCS. BM cells were recovered by flushing the femurs with 2 ml HBSS using a 27.5-gauge needle.

Flow cytometry and sorting

For the purification of fetal-derived lymphoid progenitor cells, freshly isolated day 15.5 FL cells were incubated with biotinylated Abs to CD3, CD11c, NK1.1, Gr-1, and Ter119. For isolation of adult (>8 wk old)-derived lymphoid progenitor cells, freshly isolated BM cells were incubated with biotinylated Abs to CD3, CD4, CD8, B220, CD11c, NK1.1, CD11b, Gr-1, and Ter119. In both cases lineage (Lin)+ cells were removed with a MACS cell separation system (Miltenyi Biotec) according to the manufacturer’s recommendations. After depletion, Lin− cells were stained with anti–Sca-1-FITC, anti–Flt3-PE, anti–IL-7R-PE-Cy7, anti–c-Kit-allophycocyanin-C7, anti–Ly6D-allophycocyanin, and biotinylated anti–CD90.5 Ab. For the detection of biotinylated Abs, streptavidin-allophycocyanin-Cy7 and streptavidin-Pacific Blue were used. Abs were purchased from either BD Biosciences or eBioscience. Dead cells were excluded with propidium iodide. Stained cells were analyzed on a FACS1 (Becton Dickinson) with FlowJo software (Tree Star) or sorted with a MoFlo (Beckman Coulter) or a FACS (Becton Dickinson). Intracellular staining was performed as previously done (25) with purified H47 mAb (BD Biosciences), and background staining was assessed with an isotype control of irrelevant specificity (BD Biosciences). CLPs (Lin− IL-7R−c-Kit−Sca-1−Flt3− and Ly6D−) were first sorted in the FL on day 15.5 after conception, and then fixed and stained. E47 and isotype control staining were revealed with an allophycocyanin-coupled anti-mouse IgG1 Ab (BD Biosciences).

Limiting dilution assays

For analysis of lymphoid/myeloid potential, single cell-sorted progenitors were cocultured with OP-9 (B/NK and myeloid cell potential) or OP9-DL4 (T cell potential) on 96-well plates in Opti-MEM with 10% FCS, penicillin (50 U/ml), streptomycin (50 μg/ml), and 2-ME (50 μM). The culture medium was supplemented with saturating amounts of c-Kit ligand, Flt3 ligand, and IL-7 (38). For clonal analysis of NK/B cell potential, purified human IL-2 (provided by J.P. Di Santo, Institut Pasteur, Paris, France) was added to the cultures. After 11–13 d, cells were harvested, stained for CD19, CD3, CD4, CD8, NK1.1, and CD11b, and analyzed by FACSCalibur. The growth of B cell colonies was scored by staining with CD19 and IgM on days 7–8.

In vivo reconstitutions

BM or FL HSCs, CLPId2−/−, and CLPId2−/− were purified by cell sorting and injected i.v. into irradiated (600 rads) Rag2−/− mice. Four to 5 wk later, recipients were analyzed for the presence of donor type cells in the BM and spleen by flow cytometry.

Quantitative RT-PCR analysis

RNA was extracted using an RNeasy Micro kit (Qiagen) according to the manufacturer’s instructions. Total cDNA was prepared using random primers and SuperScript II reverse transcriptase (Invitrogen) according to the manufacturer’s instructions. Quantitative PCR reactions were performed in triplicate with TaqMan Universal Master mix (Applied Biosystems), and detection was done using an ABI Prism 7000 sequence detection system (Applied Biosystems) and normalized to the amount of hypoxanthine phosphoribosyltransferase (HPRT). For quantification of expression, the following TaqMan gene expression assays were used (all from Applied Biosystems): HPRT (Mm 00440608_m1), EBF1 (Mm 01288946_m1), Pax5 (Mm 00435501_m1), Notch1 (Mm 00435245_m1), Id2 (Mm 00711781_m1), and Id3 (Mm 00492575_m1). Reactions were incubated at 95°C for 10 min and then run thought 45 cycles of 95°C for 15s and 60°C for 1 min.

Retroviral transduction

CLPs were sorted in culture medium with IL-7 and spinoculated for 2 h at 2500 rpm in the presence of 5 μg/ml polybrene with MigR1, MigR1-ICN1, or MigR1-E47 retroviral supernatants and infected as described (39). In the case of MigR1-ICN1 infection, cells were cultured with OP9-DL4 stroma in the presence of c-Kit ligand, Flt3 ligand, and IL-7. At day 11, cells were harvested and stained for CD4, CD8, and CD3. For MigR1-E47 transduction, cells were cultured for 36 h in medium with c-Kit ligand, Flt3 ligand, and IL-7. Subsequently, GFP+ cells were sorted and the expression of Notch1 was measured by RT-PCR. We estimated the efficiency of GFP+ cell expression by analyzing GFP expression in GFP+ cells 6 h postinfection. GFP expression was detected by flow cytometry in 25, 20, and 10% of the cells transduced with MigR1, MigR1-ICN1, and MigR1-E47, respectively.

The Journal of Immunology 3823

Downloaded from http://www.jimmunol.org/ by guest on June 4, 2022
Results
Identification of a Lin<sup>−</sup>Sca-1<sup>−</sup>c-Kit<sup>−</sup>IL-7Rα<sup>−</sup> population in the FL

We analyzed lymphocyte progenitor populations in the FL at day 15.5 after conception. By flow cytometry we found a Lin<sup>−</sup>Sca-1<sup>low</sup>c-Kit<sup>low</sup>IL-7Rα<sup>−</sup> population that phenotypically resembles bone marrow CLPs. Within this population, expression of Flt3 at the cell surface distinguished two subsets: CLP<sup>Flt3<sup>+</sup></sup> (75–85%) and CLP<sup>Flt3<sup>−</sup></sup> (15–25%) (Fig. 1A). Within the Lin<sup>−</sup>Sca-1<sup>low</sup>c-Kit<sup>low</sup>IL-7Rα<sup>−</sup> population, high levels of expression of Flt3 identified the LMPP population (5). The same fractions are also found in similar proportions in the BM (data not shown). Further characterization of these precursor populations revealed that fetal CLP<sup>Flt3<sup>+</sup></sup> expressed higher amounts of CD34 than did their BM counterparts, and they also expressed low amounts of CD4 and CD11b. Additionally, fetal CLPs, both Flt3<sup>+</sup> and Flt3<sup>−</sup>, expressed low levels of B220 (Supplemental Fig. 1B). In contrast, adult CLPs expressed low to undetectable levels of these surface markers (Fig. 1B, Supplemental Fig. 1B).

Expression of IL7Rα by FL CLPs and lack of T cell potential in CLP<sup>Flt3<sup>−</sup></sup>

To evaluate the differentiation capacity of these two subsets of fetal progenitors, we performed in vitro assays at the single cell level. Individual cells were cultured with OP-9 or OP9-DL4 stroma under conditions that efficiently support lymphoid and myeloid lineage development (38). FL-derived progenitors had a higher cloning efficiency and generated larger clones compared with those from the adult (data not shown). No FL IL-7Rα<sup>−</sup> precursors were able to produce myeloid colonies, and CLP<sup>Flt3<sup>−</sup></sup> cells efficiently generated all lymphoid subsets in this in vitro assay (Fig. 2A). Addition of M-CSF to the OP9 cultures did not result in the appearance of myeloid cells from fetal CLPs (data not shown). Strikingly, although 78% of individual CLP<sup>Flt3<sup>−</sup></sup> cells efficiently generated simultaneously B and NK cell progeny, they differentiated into T cells at a very low frequency (Fig. 2A), similar to what was seen with BM CLP<sup>Flt3<sup>−</sup></sup> (Supplemental Fig. 1D).

Although in vitro clonal assays efficiently reproduce the extension of lineage potential at the single cell level (38), they may not always reproduce the physiologic conditions cells encounter in vivo. Therefore, we determined the ability of fetal CLP<sup>Flt3<sup>+</sup></sup> and CLP<sup>Flt3<sup>−</sup></sup> cells to reconstitute sublethally irradiated (600 rads) alymphoid recipients. Four weeks after transfer into Rag<sup>γc</sup>−/−, both FL-derived CLP<sup>Flt3<sup>+</sup></sup> and CLP<sup>Flt3<sup>−</sup></sup> generated lymphoid cells, but no myeloid cells, in the spleen of recipient mice and, in keeping with their progeny in vitro, CLP<sup>Flt3<sup>−</sup></sup> cells were completely devoid of T cell potential in vivo, but readily gave rise to B and NK cells (Fig. 2B). It is noteworthy that a few (<1%) donor-derived CD11b<sup>+</sup>Gr-1<sup>−</sup> cells could be detected in the recipients’ BM, from either CLP<sup>Flt3<sup>+</sup></sup> or CLP<sup>Flt3<sup>−</sup></sup> input populations, but all these cells coexpressed CD11c and PDCA-1 (data not shown), markers characteristic of plasmacytoid dendritic cells, suggesting...
that both FL CLP subsets differentiated into plasmacytoid dendritic cells, as is known for BM CLPs (40).

BM-derived CLP Flt3<sup>−</sup> cells were also devoid of T cell potential in vivo, as already observed (7), but they generated B cells and NK cells in recipient mice (data not shown). Analysis of their differentiation potential in vitro revealed that ∼15% of BM-derived CLPFlt3<sup>−</sup> cells could be identified as bipotent B/NK precursors, unable to give rise to T cells when cultured with OP9-DL4 stromal cells (Supplemental Fig. 1D).

Taken together, these results indicate that expression of IL-7Rα marks lymphoid commitment, with loss of myeloid potential, during either BM or FL hematopoiesis. Furthermore, the absence of Flt3 expression identifies a B/NK cell-restricted progenitor that lacked T cell potential.

**Loss of T cell potential in CLPFlt3** is due to low Notch1 expression

To understand the molecular mechanisms involved in the loss of T cell potential observed in CLPFlt3<sup>−</sup>, we studied the expression pattern of Notch1, which is known to regulate T lymphocyte differentiation. We found that, coincident with their loss of T cell potential, CLPFlt3<sup>−</sup> showed lower expression of Notch1 compared with CLPFlt3<sup>+</sup>, which readily generated T cells (Fig. 3A). Similar results were observed in BM-derived CLPs (Supplemental Fig. 1C).

We transduced CLPFlt3<sup>−</sup> with a GFP-expressing retroviral vector encoding ICN1, a constitutively active form of Notch1, and plated them on stromal cells in the presence of c-Kit ligand, Flt3 ligand, and IL-7. After 11–13 d culture, T cell development was assessed in the GFP<sup>+</sup> progeny by analyzing the expression of CD4 and CD8. Retroviral expression of ICN1 in CLPFlt3<sup>−</sup> led to the acquisition of T cell potential by 27% of the cells in the culture (Fig. 3B, Supplemental Fig. 2A), indicating the acquisition of T cell potential. These data indicated that T cell potential in CLPFlt3<sup>−</sup> can be rescued by supplementing the cells with a Notch1-derived signal.

Notch1 expression in CLPs is regulated by E2A

In pluripotent hematopoietic progenitors Notch1 expression is known to be regulated by members of the E family of proteins (23, 25, 26). We observed that this is also true in CLPs because Notch1 expression was much reduced in CLPFlt3<sup>−</sup> of E2A-deficient mice (Fig. 4A). In the FL of E2A<sup>−/−</sup> embryos there is a less marked reduction in the number of CLPs (Supplemental Fig. 2B) than what is observed in the BM of adult mice (25). The phenotypic profiles of FL CLPs of E2A<sup>+/+</sup>, E2A<sup>+/−</sup>, and E2A<sup>−/−</sup> day 15 embryos is shown in Supplemental Fig. 2C. Transduction of CLPFlt3<sup>−</sup> with a retroviral vector encoding E47 induced a 4-fold upregulation in Notch1 transcription in these cells (Fig. 4B). CLPFlt3<sup>−</sup> cells downregulate significantly their expression of Notch1.
during the 24 h in culture with the empty virus, but also in these cells, expression of E47 induced a 2-fold upregulation of mRNA for Notch1 (Fig. 4B).

These results indicate that E2A proteins are necessary for expression of Notch1 also at the CLP Flt3+ stage. Additionally, the results also demonstrated that increased activity of E2A is sufficient to upregulate Notch1 expression in CLPFlt3+ cells.

CLPFlt3− cells express elevated levels of Id2 and Id3

We then went on to study the expression in CLPs of Id2 and Id3, two well-known modulators of E protein activity in lymphoid precursors (41). For that purpose it was important to exclude LTi cells because of the high amounts of Id2 they express (35), although they represent only a small fraction of the cells in our CLP gate owing to the distinctly higher levels of IL-7Rα on their surface (see Supplemental Fig. 3C).

LTi cells are found in FL, but not in BM (42, 43), and they can be identified by the expression of retinoic acid orphan receptor (ROR)γt (42–44). We therefore isolated Rorc(γt)-GFPTG mice (34). Additionally, we purified CLPs that were Ly6D2 to restrict our analysis to precursors not yet engaged in the first steps of B lineage specification (45, 46) (Fig. 6A).
We found that FL CLP^{Flt3-} cells express Id2 and Id3 at higher levels than do CLP^{Flt3+} cells (Fig. 6B). Again, CLP^{Flt3-} showed lower expression of Notch1 compared with CLP^{Flt3+}. Furthermore, and consistent with lower E2A activity, CLP^{Flt3-} cells also expressed lower levels of Ebf1 and Pax5 than did CLP^{Flt3+} cells (Fig. 6B). No difference in the levels of mRNA for E2A could be detected in these two populations (Fig. 6B), but detection of the protein by intracellular staining (Fig. 6C) showed a small reduction of E2A in CLP^{Flt3-} (mean fluorescence intensity of 2959) compared with CLP^{Flt3+} (mean fluorescence intensity of 3797).

Similar results for the expression of Id2, Id3, Notch1, Ebf1, and Pax5 were obtained with CLPs isolated from the BM (Supplemental Fig. 1A, 1C), where no Ror^gt+ LTi cells can be found (42, 43).

Id proteins repress Notch1 expression in CLP^{Flt3-}

Because the E2A inhibitors Id2 and Id3 were upregulated in CLP^{Flt3-}, we analyzed Id-deficient embryos to assess the role of these factors in Notch1 downregulation. Analysis of mRNA expression revealed an increase of Notch1 expression in CLP^{Flt3-} of Id2^-/- mice, when compared with wild-type (Fig. 7A). It has been suggested that Id3 compensates for Id2 function, as Id2^-/- mice, although displaying a severe defect in NK development, have normal numbers of NK progenitor cells and increased expression of Id3 (47). We could not analyze Id2^-/- Id3^-/- mice because the double mutant is embryonic lethal (data not shown). However, by intercrossing Id2^+/^- and Id3^+/^- mice we obtained Id2^-/- Id3^-/- day 15 embryos and assessed the effect of the loss of these three Id alleles on the CLP compartment and on Notch1 expression. In the FL of Id2^-/- Id3^-/- animals CLPs display a normal phenotype...
Id PROTEINS SPECIFY BIPHOTON B/NK PRECURSORS

Discussion

Lymphoid commitment is thought to follow different pathways in the BM and FL microenvironments (9) because the fetal counterpart of BM CLPs was found to give rise also to macrophages in vitro (8). However, we now showed that expression of IL-7Rα in the FL marks a population of CLPs that lacks myeloid potential, similar to the BM. The E15.5 CLPs described in this study do not give rise to detectable myeloid progeny in vivo, similarly to the ones described by Mebius et al. (8) on embryonic day 14.5. It is probable that the small burst size of fetal CLPs would render their macrophage potential undetectable in our in vitro assay.

Adult CLPs are known to be heterogeneous with respect to expression of the receptor tyrosine kinase Flt3 (7, 45). Expression of this receptor identifies lymphoid progenitors with full T, B, and NK cell potential, whereas the population of CLPFlt3− had no T cell potential and was thought to contain only committed B cell progenitors that are unable to generate NK and DC cells after transfer into C57BL/6 recipient mice (7). We found, however, that >80% of FL CLPFlt3− cells generated both B and NK progeny in vitro. Furthermore, adoptive transfer of CLPFlt3− into Ragyc−/− recipients led to the development of B and NK cells, demonstrating that these cells were not irreversibly committed to the B cell lineage. NK cell progeny from CLPFlt3− may be competed away in sublethally irradiated C57BL/6 recipients, because such mice, contrary to the Ragyc−/− animals we used, can produce NK cells from endogenous precursors.

Our results support developmental models with a fundamental segregation between the lymphoid and myeloid lineages. The lymphoid branch is identified in early progenitors by the expression of the IL-7Rα already during fetal hematopoiesis. This is consistent with fate mapping studies in adult animals showing that, in contrast to lymphocytes, the vast majority of myeloid cells develop from IL-7Rα− progenitors (48).

Our work also revealed that lymphopoiesis proceeds along similar paths in fetal and adult environments. During lymphopoiesis, both fetal and adult CLPs can lose the potential to give rise to T cells before they lose NK potential. Although in the most common hierarchical models of hematopoiesis NK cells appear more closely related to the T cell lineage (49–54), our findings point to the existence of an intermediate stage of lymphocyte development unable to generate T cells, but with combined NK and B cell potential. This intermediate stage could be identified in both fetal and adult hematopoietic environments.

The loss of T cell potential in CLPFlt3− is due to downregulation of Notch1. Enforced expression of the E2A gene product E47 restored Notch1 expression in CLPFlt3−, as did impaired expression of the dominant-negative regulators of E2A activity Id2 and Id3. Taken together, these results indicate that Id proteins (specifically Id2 and Id3) inhibit Notch1 by counteracting E protein activity in CLPFlt3−. Because double Id2/Id3 knockout animals are not viable, we could only study T lineage potential in mutant CLPFlt3− cells still carrying one active allele. Notably, even in this case a sizable fraction of the cells had T lineage potential. The recovery of T cell potential in the Id mutant cells is only partial, perhaps because residual Id protein activity can still impair Notch1 expression in a fraction of the cells, although no reduction is observed at the population level.

Importantly, CLPFlt3− from either Id2−/−Id3−/− or Id2−/−Id3−/− embryos generated T cells, suggesting that these two proteins compensated for each other in their function. Accordingly, and similarly to what is seen in NK precursors (47), Id3 mRNA expression was higher in CLPs from Id2−/− mice (data not shown). In the thymus, Id proteins favor NK cell development while repressing T cell potential (28–30). We now show that Id-mediated inhibition of Notch1, and consequent suppression of T cell potential, occurs also extrathymically in the FL and BM. Our findings implicate Id proteins in lineage restriction through the inhibition of E2A activity, already at the CLP stage of development.
The B cell specification factor Ebf1 is also induced by E2A (17, 22), and consistent with reduced E2A activity in CLP<sup>Flt3</sup> cells, we observed lower expression of Ebf1 in those cells. Engagement of CLP<sup>Flt3</sup> into the B lineage requires sustained IL-7 signaling, which is necessary to maintain Ebf1 and Pax5 expression (39, 46, 55, 56). After development of pro-B cells, Id protein expression is inhibited by Ebf1 (21, 57) enabling full activity of E2A, whose continued expression is indispensable later in B cell development (19, 58). At the pro-B cell stage, however, Pax5 reaches its maximal continued expression is indispensable later in B cell development (19, 58). At the pro-B cell stage, however, Pax5 reaches its maximal expression (19, 58) and directly represses Notch1 (59).

CLP<sup>Flt3</sup> cells are distinct from the recently described NK-committed precursors (60), which have very low B cell potential and high levels of IL-7Rα on their surface. Because CLP<sup>Flt3</sup>-cells are B/NK bipotent, they are likely to be upstream of the pro-NK cells, giving rise to them under conditions where the IL-7 signal is not strong enough to drive B cell differentiation. In the absence of signals to positively regulate Ebf1 expression, and consequently B cell development, Id2/Id3 maintain low E protein activity, thus allowing B/NK bipotent progenitors to be driven into the NK pathway (47).

In conclusion, this study demonstrated that Id protein expression in CLPs regulates the functional activity of E2A, thus playing a central role in the gene regulatory network (19, 61) that controls specification to the T, NK, or B cell lineages.

Acknowledgments
We thank G. Eberl for the kind gift of Rorc-GFP<sup>tg</sup> mice.

Disclosures
The authors have no financial conflicts of interest.

References


