Dynamic regulation of PU.1 expression in multipotent hematopoietic progenitors

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PU.1 is an Ets family transcription factor that is essential for fetal liver hematopoiesis. We have generated a PU.1 reporter strain that allowed us to examine the expression of PU.1 in all hematopoietic cell lineages and their early progenitors. Within the bone marrow progenitor compartment, PU.1 is highly expressed in the hematopoietic stem cell, the common lymphoid progenitor, and a proportion of common myeloid progenitors (CMPs). Based on Flt3 and PU.1 expression, the CMP could be divided into three subpopulations, Flt3hi PU.1hi, Flt3lo PU.1hi, and Flt3lo PU.1lo. Colony-forming assays and in vivo lineage reconstitution demonstrated that the Flt3hi PU.1hi and Flt3lo PU.1hi CMPs were efficient precursors for granulocyte/macrophage progenitors (GMPs), whereas the Flt3lo PU.1lo CMPs were highly enriched for committed megakaryocyte/erythrocyte progenitors (MEPs). CMPs have been shown to rapidly differentiate into GMPs and MEPs in vitro. Interestingly, short-term culture revealed that the Flt3lo PU.1hi and Flt3lo PU.1hi CMPs rapidly became CD16/32hi (reminiscent of GMPs) in culture, whereas the Flt3lo PU.1lo CMPs were the immediate precursors of the MEP. Thus, down-regulation of PU.1 expression in the CMP is the first molecularly identified event associated with the restriction of differentiation to erythroid and megakaryocyte lineages.

Hematopoiesis is a continuous stepwise and controlled process in which the multipotent hematopoietic stem cell (HSC) undergoes differentiation to produce all the mature blood lineages. It has been postulated that the HSC differentiates to either a clonogenic common lymphoid progenitor (CLP) that produces lymphocytes and DCs (1) or a common myeloid progenitor (CMP) capable of giving rise to the erythroid/myeloid lineages. The CMP can further differentiate into either one of two more restricted progenitors, the granulocyte/macrophage progenitor (GMP) or the megakaryocyte/erythrocyte progenitor (MEP; reference 2).

The expression of a number of transcription factors is thought to orchestrate hematopoietic differentiation (for review see references 3 and 4). One of these key regulators is PU.1, a hematopoietic–specific Ets family member that is essential for fetal lymphoid and myeloid development (5–8). PU.1−/− mice die in late gestation and are devoid of fetal liver B lymphocytes, granulocytes, and macrophages. In adult hematopoiesis, recent data has suggested that PU.1 is an important tumor suppressor in murine and possibly human acute myeloid leukemia (AML; references 9–11). PU.1 regulates numerous genes within the myeloid and lymphoid lineages, including the receptors for a number of cytokines, M-CSFR, G-CSFR, GM-CSFRα (12), and IL-7Rα (13), highlighting the pivotal role this transcription factor plays in the early stages of several lineages.

It has been proposed that graded levels of PU.1 expression by hematopoietic progenitors are determinative of their lineage commitment as high PU.1 directs macrophage differentiation and lower levels are sufficient for fetal B cell development (14, 15), whereas in a more recent study, intermediate levels of PU.1 were required for granulocytes (16). However, the relevance of these results to endogenous PU.1 levels has not been demonstrated as these studies relied on overexpression systems. Further support for the concentration dependence model comes from the finding that PU.1 is haploinsufficient when the mutation is compounded with the loss of G-CSF (16). Moreover, mice with a hypomorphic PU.1 allele that express only 20% of wild-type protein develop AML at a high frequency, a malignancy thought to derive from primitive hematopoietic cells (9).
These studies predict that the levels of PU.1 will be differentially regulated within the distinct BM multipotent progenitors; however, in no case has the level of PU.1 expression in myeloid and lymphoid lineage precursor populations been clearly shown. In this study, we have generated a PU.1<sup>gfp</sup> reporter allele that enabled us to accurately determine the level and pattern of PU.1 expression at the single cell level. Using these mice, we have examined the rare BM hematopoietic progenitor populations and found that PU.1 is expressed by all HSC, CLP, GMP, Flt3<sup>+</sup> CMP, and by a proportion of Flt3<sup>−</sup> CMP. In contrast to expectations, the PU.1 levels in HSC and CLP were equivalent to those observed in the committed myeloid progenitors. The different levels of PU.1 expression within the Flt3<sup>−</sup> CMP population represented two functionally distinct precursor populations as assessed by in vitro colony-forming assays and in vivo lineage reconstitution. Therefore, the down-regulation of PU.1 in Flt3<sup>−</sup> CMP demonstrates the heterogeneity in this population and represents an early event in the restriction of the CMP to erythroid and megakaryocyte (Meg) differentiation.

RESULTS
Generation and validation of PU.1<sup>gfp</sup> reporter mice
To produce a reporter of PU.1 expression, an internal ribosome entry site (IRES)-GFP cassette was inserted by homologous recombination in embryonic stem (ES) cells into the 3′ untranslated region of mouse PU.1 (Fig. 1 A). The detailed strategy and confirmation of appropriate gene targeting will be reported elsewhere (unpublished data). The targeted allele resulted in the transcription of a bicistronic mRNA that produced wild-type PU.1 protein and GFP. The targeting strategy predicted that the IRES-GFP cassette would not affect the up-

![Figure 1. Generation and validation of a PU.1<sup>gfp</sup> reporter strain.](image)

(A) The targeted PU.1<sup>gfp</sup> locus is shown with the exons indicated as boxes and the introns as black lines. Coding regions are in gray and nontranslated regions are white. Arrows indicate direction of translation from initial methionine. pA, polyadenylation signal sequence; circles, frt sites; triangles, loxP sites; stop, stop codon; splice acc., splice acceptor. The targeted allele translates full-length PU.1 and GFP from the same mRNA transcript. (B) GFP expression in PU.1<sup>gfp/−</sup> BM. Cells were stained for CD19 (B cells) and Mac-1 (myeloid cells). (C) GFP expression in B cells and macrophage/ granulocytes of adult spleen of +/+; PU.1<sup>gfp/−</sup>; and PU.1<sup>gfp/gfp</sup> mice. (D) Quantitation of mean fluorescence of B cells (CD19<sup>+</sup> B220<sup>+</sup>), granulocytes (Mac-1<sup>+</sup> Gr-1<sup>+</sup>), and immature myeloid cells (Mac-1<sup>+</sup> Gr-1<sup>−</sup> intermediate [Gr.1<sup><sup>−</sup></sup>]) from BM and spleen. n = 4–10 mice per group. Relative mean fluorescence was determined relative to identically gated C57BL/6 cells and is shown in arbitrary units. (E) Western blotting for PU.1 in BM Mac-1<sup>+</sup>/Gr.1<sup>+</sup> myeloid cells (BMM), CD19<sup>+</sup> B220<sup>+</sup> spleen B cells, and CD4<sup>+</sup> T lymphocytes. β actin was a loading control. (F) Determination of PU.1 and GFP stability in splenocytes. Cells were cultured for up to 12 h in the protein synthesis inhibitor cycloheximide, and equivalent cell numbers were assayed for PU.1, GFP, and β actin levels by Western blotting. The calculated half-life of the proteins is indicated (left).
stream \textit{PU.1} mRNA transcript. To confirm this, homozygous \textit{PU.1^{	ext{gfp/gfp}}} mice were generated. In contrast to the embryonic or postnatal lethality of \textit{PU.1^{-/-}} pups (5, 6), \textit{PU.1^{	ext{gfp/gfp}}} mice were indistinguishable in survival, hematopoietic cellularity, and lineage composition from C57BL/6 controls (unpublished data). As predicted, \textit{PU.1} protein level in B lymphocytes and myeloid cells was not affected by the host genotype (Fig. 1 E).

\textbf{\textit{PU.1^{	ext{gfp}}}} expression by mature hematopoietic lineage cells

\textit{PU.1} expression by mature myeloid and lymphoid lineage cells has been previously examined at mRNA and/or protein levels (14, 17). However, the results obtained from these studies could not distinguish whether all, or only a proportion, of cells within a given population express \textit{PU.1}. The \textit{PU.1^{	ext{gfp}}} reporter mice provided an excellent tool to clarify this issue. We examined the GFP fluorescence of different hematopoietic cell populations from BM and spleen as defined by flow cytometry. The levels of \textit{PU.1} expression were quantified as the mean fluorescence of GFP expression by these cells. \textit{PU.1} is expressed at significantly higher levels in macrophages as compared with B cells (14). Analysis of the lymphoid organs of adult \textit{PU.1^{	ext{gfp/+}}} mice confirmed these lineage-specific expression levels with approximately eightfold higher GFP observed in all Mac-1^{+} myeloid cells compared with CD19^{+} B cells (Fig. 1, B and C). The Mac-1^{+} fraction contains immature granulocytes/monocytes (Gr-1^{int}) and mature granulocytes (Gr-1^{hi}), all of which displayed similar GFP fluorescence, indicating relatively uniform \textit{PU.1} transcription throughout granulocytic/monocytic differentiation (Fig. 1, C and D). A similar uniformity was observed for B lineage cells (Fig. 1, C and D). Analysis of B cell and macrophage/granulocyte populations revealed an exquisite gene dosage sensitivity of the reporter allele, with \textit{PU.1^{	ext{gfp/gfp}}} cells containing almost exactly twice the GFP fluorescence of heterozygous cells (Fig. 1, C and D). Moreover, determination of the half-life of the proteins revealed relatively similar turnover rates (5.5 h for \textit{PU.1} and 7.5 h for GFP), indicating that GFP loss is also an accurate reporter for \textit{PU.1} down-regulation (Fig. 1 F). The lineage-specific and gene dosage-sensitive levels of GFP in the \textit{PU.1^{	ext{gfp}}} mice validate the allele as an accurate reporter of endogenous transcription and enabled full characterization of \textit{PU.1} expression in a number of cell types that have not been fully characterized, including DCs, NK cells, and erythrocyte lineages.

The role of \textit{PU.1} in DC development is not clear. \textit{PU.1} has been reported to be required for the differentiation of all DCs (18) or more specifically, for myeloid-derived DCs (19), with no data available for plasmacytoid DCs (pDCs). We examined the \textit{PU.1^{	ext{gfp}}} expression by freshly isolated thymic and splenic CD11c^{+} CD45RA^{+} conventional DCs (cDCs) and the type I IFN–producing CD11c^{int} CD45RA^{+} pDCs. As shown in Fig. 2, A and B, all of the cDCs from the thymus and spleen expressed levels of GFP comparable to B cells (Fig. 2, A and B). As both CMPs and CLPs can produce all DC types in vivo, these data indicate that \textit{PU.1} expression in cDCs is unrelated to their developmental origin (20).

\begin{figure}[h]
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\caption{\textbf{\textit{PU.1^{	ext{gfp}}}} expression in DCs and NK cells. (A) The thymic and (B) splenic cDCs and pDCs were prepared from the \textit{PU.1^{	ext{gfp/gfp}}} mice. The GFP fluorescent intensities of cDCs and pDCs were analyzed on gated cDC (CD11c^{hi}CD45RA^{-}) and pDC (CD11c^{int}CD45RA^{-}) populations and presented as histograms. (C) \textit{PU.1} expression by cDCs and pDCs were quantified as the mean fluorescence of GFP. (D) \textit{PU.1^{	ext{gfp}}} expression in mature NK cells isolated from BM (CD122^{+} DX5^{+} NK1.1^{+}). NK cells were also generated from BM cultures in the presence of IL-15 for 7 d and assessed for GFP. The solid lines represent the \textit{PU.1^{	ext{gfp}}} levels and the dotted lines represent the background from wild-type mice.}
\end{figure}
It was also reported by an earlier study that NK cells express *PU.1* mRNA (21). However, we have not observed any GFP fluorescence in mature NK cells either freshly isolated from mouse BM (CD122⁺ DX5⁺ NK1.1⁺) or obtained in culture with IL-15 (Fig. 2 D). *PU.1* might be expressed in pro–NK cells (CD122⁺ DX5⁺ NK1.1⁺) and down-regulated upon maturation; however, a definitive analysis has not been possible as we have not been able to exclude *PU.1-*expressing myeloid cells from this population (unpublished data).

*PU.1* was originally isolated from a virally induced erythroleukemia (22) and is expressed in developing erythroid progenitors from fetal liver (7, 23). In contrast, adult BM erythrocytes, neither mature (Ter-119⁺ CD71⁻) nor immature (Ter-119⁺ CD71⁺), showed expression of GFP, indicating that *PU.1* is silenced at an early stage of erythropoiesis (unpublished data).

In summary, the *PU.1* allele described here has allowed the rapid and quantitative determination of *PU.1* expression levels in a variety of hematopoietic lineages and revealed a complex and dynamic expression pattern throughout adult hematopoiesis.

**PU.1** expression during thymocyte development

Analysis of the *PU.1* expression during T lineage cell development revealed that the majority of thymocytes, including CD4⁺⁺⁺, CD4⁺⁺⁻, and CD4⁺⁻⁺ were GFP⁺ (Fig. 3 A). In contrast, a small fraction of the CD4⁺⁻⁺ thymocytes was GFP⁺⁺, suggesting that the T cell precursors express *PU.1*. The earliest intrathymic precursor population (CD4⁺⁺⁺) displayed intermediate levels of GFP, whereas the majority of the CD3⁻⁺⁻⁺ CD25⁺ CD117⁺ (triple negative [TN]1) pro–T cells expressed GFP at a slightly lower level than that of the CD4⁺⁺⁺ precursors (Fig. 3, B–D). GFP expression was maintained in the CD25⁺ CD117⁺ (TN2) precursors before being markedly down-regulated at the CD25⁺ CD117⁺ (TN3) stage, coinciding with the onset of TCR gene rearrangement (Fig. 3, C and D). These results were consistent with a previous study in which the *PU.1* mRNA expression by these T cell precursor populations was examined (24). This loss of *PU.1* was permanent as mature peripheral T cells were GFP⁻ (Fig. 1 E).

**PU.1** expression by BM hematopoietic progenitor populations

The graded levels of *PU.1* reported here and observed by others, has led to a model whereby distinct *PU.1* levels arise in multipotent progenitors and are deterministic of lineage choice (25). Some of these studies have shown that *PU.1* mRNA was expressed at different levels by different hematopoietic progenitor populations (2, 26). These data are problematic because of technical limitations of amplifying *PU.1* from these rare populations. These assays did not indicate if the protein levels were of functional significance, and finally, they are not able to distinguish whether all of the cells or only a subset of the cells within a given population expressed *PU.1*. The *PU.1* reporter mice enabled us to examine the *PU.1* expression by different rare hematopoietic progenitors at the single cell level.

Mouse BM hematopoietic progenitor populations were isolated as described previously (20). The enriched BM HSCs were defined as Lin⁻ c-kit⁺ Sca-1⁺ cells and were uniformly *PU.1*⁺⁺⁺ high (*PU.1*⁺⁺⁺; Fig. 4 A), suggesting a role of *PU.1* in the earliest stage of hematopoiesis. Interestingly, although the mature B lymphoid cells were low for *PU.1*⁺⁺⁺, almost all of the CLPs were *PU.1*⁺⁺⁺ (Fig. 4, A and C). The *PU.1* decrease appeared to correlate with B lineage commit-
ment as pre-pro–B cells (defined as CD19+ B220+ CD43+ c–kit+) had already decreased the PU.1gfp expression to a level comparable with mature B cells (Fig. 4, B and C).

We previously reported that the CMP population could be divided into two fractions based on the surface Flt3 expression (20). As shown in Fig. 4 A, all of the Flt3+ CMPs were PU.1hi, but the Flt3– CMPs could be further divided into two fractions based on differing GFP expression. Approximately 30–40% of Flt3– CMPs expressed high levels of PU.1gfp compared with the Flt3+ CMPs, whereas the remaining Flt3– CMPs (60–70%) were PU.1lo (Fig. 4, A and C). The correlation between PU.1 and GFP expression was further confirmed using RT-PCR (Fig. 5 C). Therefore, the CMP, originally described as a homogeneous clonogenic population, contains at least three subsets, i.e., Flt3+ PU.1hi, Flt3– PU.1hi, and Flt3– PU.1lo. Of the more downstream committed progenitors, the GMP contained the strongest PU.1gfp fluorescence of any population, whereas the committed MEP expressed the lowest (Fig. 4, A and C).

Down-regulation of PU.1 expression is associated with the restriction of CMPs to erythroid and Meg differentiation

The majority of CMPs (>90%) had the morphology of large undifferentiated blast cells (Fig. 5 A, a and b) and exhibited mitotic figures. GMPs were generally similar in size but frequently contained small numbers of large granules in the cytoplasm resembling those of promyelocytes (Fig. 5 A, c and d). In contrast, MEPs often had dark cytoplasm and some of these cells resembled early erythroblasts (Fig. 5 A, e and f). The fractionated CMP populations had a generally similar morphology to one another except that some CMP Flt3– PU.1hi cells had some cytoplasmic granules and some CMP Flt3– PU.1hi cells had dark cytoplasm (Fig. 5 B).

Table I. Colony-forming potential of the CMP subpopulations

| CMP Fractions | Stimulus | Blast | G  | GM | M  | Megb | E  |
|---------------|----------|-------|----|----|----|------|----|
| Flt3+ SCF 3.0 ± 1.6 | 7.5 ± 1.9 | 1.2 ± 0.6 | 1.2 ± 0.8 | 0  | 0  |
| Flt3+ IL-3 4.7 ± 0.9 | 6.0 ± 1.4 | 9.0 ± 2.9 | 24.3 ± 8.3 | 0  | 0  |
| PU.1hi SCF + IL-3 + EPO 6.0 ± 2.8 | 11.0 ± 1.6 | 13.3 ± 4.2 | 16.3 ± 6.2 | 0  | 0  |
| PU.1hi SCF 2.6 ± 1.2 | 30.3 ± 11.3 | 0.3 ± 0.5 | 0.3 ± 0.5 | 0  | 0  |
| Flt3– IL-3 3.3 ± 1.2 | 29.7 ± 6.1 | 11.7 ± 4.1 | 18.0 ± 4.9 | 2.3 ± 0.6 | 0  |
| PU.1hi SCF + IL-3 + EPO 4.3 ± 1.9 | 29.0 ± 10.0 | 13.0 ± 2.2 | 14.0 ± 3.3 | 5.7 ± 3.7 | 0.3 ± 0.6 |
| PU.1hi SCF 0.3 ± 0.5 | 0.4 ± 0.4 | 0  | 0.4 ± 0.1 | 0  | 0  |
| Flt3– IL-3 1.3 ± 0.8 | 0.3 ± 0.4 | 0.2 ± 0.2 | 0.2 ± 0.2 | 3.7 ± 0.8 | 0  |
| PU.1hi 1.3 ± 0.9 | 1.5 ± 0.7 | 0.3 ± 0.5 | 1.0 ± 1.4 | 30.9 ± 3.5 | 4.0 ± 3.0 |

100 purified cells of each fraction were cultured for 7 d in 0.3% agar with the growth factors indicated.

The numbers of colonies are the mean number of colonies ± SD from three separate experiments.

15–27% of these Meg colonies also contained erythroid cells.

Blast, blast cell colony; G, granulocytic colony; GM, granulocyte-macrophage colony; M, macrophage colony; Meg, megakaryocytic colony; E, erythroid colony.
To examine the correlation of different levels of Flt3/PU.1 and cell differentiation potential, in vitro colony-forming assays were performed (Table I). In the presence of stem cell factor (SCF), which stimulates the formation of blast and granulocytic colonies, the Flt3⁺ PU.1hi and Flt3⁻ PU.1hi CMPs formed small numbers of blast colonies and a significant number of granulocytic colonies. In contrast, few Flt3⁻ PU.1lo CMPs exhibited blast or granulocytic colony-forming potential. Similarly, in the presence of IL-3, which stimulates the colony formation of all cell types, both Flt3⁺ PU.1hi and Flt3⁻ PU.1hi CMPs formed significant numbers of granulocytic, granulocyte-macrophage, and macrophage colonies, whereas the Flt3⁻ PU.1hi CMPs lacked this potential. Interestingly, the Flt3⁻ PU.1hi CMPs expressed slightly higher levels of GFP and were more efficient in generating granulocytic colonies than the Flt3⁺ PU.1hi CMPs (Table I).

Most importantly, when a combination of SCF, IL-3, and erythropoietin, the most potent stimulus for Meg colony formation, was used, the Flt3⁺ PU.1hi and Flt3⁻ PU.1hi CMPs virtually lacked clonogenic Meg progenitors, whereas, strikingly, >30% of the Flt3⁻ PU.1lo CMP cells formed Meg colonies, from 15–27% of which also contained erythroid
cells. In addition, cells of this type formed small numbers of pure erythroid colonies (Table I). Thus, the Flt3− PU.1hi CMPs showed the lowest capacity to form myeloid lineage colonies, but the highest capacity for megakaryo-erythroid poiesis. These results demonstrate that the down-regulation of PU.1 expression is closely associated with loss of myeloid lineage potential and restriction to Meg and erythroid (MegE) differentiation.

In support of these clonogenic assays, sorted Flt3hi PU.1lo and Flt3− PU.1hi CMPs and GMPs expressed the mRNA for m-csf and g-csf, whereas the Flt3− PU.1hi CMPs lacked these transcripts and in contrast expressed low levels of the MegE regulator gata-1 (Fig. 5 C). This gene expression profile suggests that the Flt3− PU.1hi CMP exhibits the initial activation of the MegE differentiation pathway.

We have also performed in vivo cell transfer and lineage reconstitution assays with these sorted populations. Purified progenitor populations from PU.1gfp/gfp mice (Ly5.2+) were intravenously injected together with 5 × 10⁴ recipient-type BM cells into lethally irradiated Ly5.1+ recipient mice. The potential of these cells to generate myeloid cells and DCs was analyzed at 10 and 14 d after transfer. Both the Flt3+ PU.1lo and Flt3− PU.1hi CMPs were able to efficiently produce the Mac-1+ Gr-1+ myeloid cells and CD11c+ DCs in vivo, with the Flt3− PU.1hi CMPs being slightly more efficient in generating these cells (Table II). In contrast, the Flt3− PU.1lo CMPs gave rise to only a small number of myeloid cells and very few DCs. These results were consistent with that of colony-forming assays and again demonstrated that the Flt3− PU.1lo CMPs had the lowest potential to generate myeloid lineage cells. The CMP has previously been shown to rapidly differentiate into GMPs and MEPs upon in vitro culture (2). In an attempt to reveal the developmental relationship amongst the three CMP populations, an identical short-term culture system was used. Purified Flt3+ PU.1lo, Flt3− PU.1hi, or Flt3− PU.1lo CMPs were cultured on S17 stromal cells in the presence of SCF (Fig. 6). After 40 h, the cultured cells were analyzed for CD16/32, Flt3, and c-kit expression. The majority of the Flt3+ PU.1lo cells had developed into CD16/32hi Flt3− PU.1hi, a phenotype of GMP (Fig. 6 B). Similarly, the Flt3− PU.1hi cells also developed into CD16/32hi Flt3− PU.1lo GMP (Fig. 6 C). In contrast, most of the Flt3− PU.1lo cells developed into CD16/32−/hi Flt3− PU.1hi, a phenotype of MEP (Fig. 6 D). Therefore, based on the levels of Flt3 and PU.1, the originally defined “CMP” population contains three separate populations that did not display any precursor-product relationship. Moreover, the combination of three approaches to determine the developmental potential of these newly identified CMP fractions demonstrated that PU.1 down-regulation is a very early event in the divergence of the myeloid and MegE lineages.

**DISCUSSION**

One model of hematopoietic lineage commitment proposes that the relative levels of key transcription factors, including PU.1, influence cell fate decisions (4, 27). The multiple lineages and developmental stages of hematopoietic cells and the rarity of the multipotent progenitors have made testing this model using endogenous expression levels in primary cells problematic. Therefore, most studies have focused on model cell lines and/or overexpression systems. To study the function of PU.1 in adult hematopoietic cell development, we generated a PU.1flox reporter allele that has allowed us to determine accurately the levels of PU.1 expression in all hematopoietic cell types and their early progenitors.

The analysis of GFP expression by mature hematopoietic cells of adult PU.1flox mice confirmed the previous findings that monocytes/granulocytes expressed significantly higher levels of PU.1 (approximately eightfold) as compared with B cells (14, 17). The strikingly uniform expression of PU.1 in both lineages, the relatively similar protein stability between GFP and PU.1, and the exquisite sensitivity of the fluorescence (heterozygous cells contained exactly 50% GFP levels of homozygous cells) demonstrated that the reporter would enable the quantitative analysis of the mean GFP fluorescence in defined cell populations. A broader analysis revealed that PU.1 is silenced at an earlier stage in erythrocytes, NK cells, and T cells. Within the DC lineages, PU.1 showed specific expression levels, with the cDCs populations having uniformly high levels of PU.1 comparable to that of myeloid cells, whereas the pDCs expressed moderate levels of PU.1 similar to that of B cells. cDC ontogeny is complex with at least three distinct subsets, CD8+, CD4+, and double negative, which are derived from both lymphoid and myeloid progenitors (for review see reference 28). However, GFP expression was uniform within all cDCs, suggesting that PU.1 levels are not related to the phenotype or origins of the lineage. The similar levels of GFP in pDCs compared with B

**Table II. Generation of myeloid cells and DCs in vivo by CMP subpopulations**

| CMP subpopulations | Injected (×10⁴) | Mac-1⁺ Gr-1⁺ cells in BM⁺ | Mac-1⁺ Gr-1⁺ cells per spleen | CD11c⁺ DCs per spleen |
|--------------------|----------------|--------------------------|-----------------------------|---------------------|
| Flt3⁺ PU.1hi       | 3.1–16.0       | 52.0–78.1                | 26.5–59.2                   |
| Flt3− PU.1hi       | 7.9–8.5        | 34.4–52.9                | 3.1–8.5                     |
| Flt3− PU.1lo       | 0.4–0.6        | 2.9–15.9                 | 0.1–0.5                     |

Purified BM progenitor populations from PU.1flox mice (Ly5.2+) were intravenously injected into lethally irradiated Ly5.1 recipient mice. For myeloid cell generation, the recipient mice were analyzed 10 d after injection. For DC generation, recipient mice were analyzed 14 d after injection. The values in this table are the ranges of donor-derived cell numbers obtained from two experiments. Each experiment included two to three recipients for each precursor population.

*aDonor-derived cells in the BM of two femur and two tibia collected from each mouse.*
cells may reflect the shared genetic program between these cell types, regardless of lymphoid or myeloid origin, resulting in D-JH recombinations at the IgH locus (29) and the expression of common transcriptional regulators, including Spi-B (30, 31).

The analysis of expression of PU.1 in multipotent BM progenitors has to date been restricted to RT-PCR (2, 26, 32). These approaches have suggested that PU.1 is expressed in all progenitor fractions but are problematic due to the difficulties inherent in controlling for sorting purity, generating cDNA from these rare cells, and the interpretation of the data due to the reported promiscuous low level transcriptional priming of noncommitted progenitor cells (32). For example, the original description of PU.1 expression in defined erythroid-myeloid progenitors suggested equally low expression in all populations (2), whereas a subsequent study has suggested that PU.1 mRNA levels are higher in GMPs than MEPs (26). The heterogeneity of the CMP reported here makes such a population level analysis uninformative.

In contrast, the PU.1<sup>10<sup>th</sup> reporter mice enabled us to quantify the levels of PU.1 expression at a single cell level. Overexpression studies have shown that the lineage fate of PU.1<sup>−/−</sup> fetal liver progenitors can be directed by the ectopically expressed PU.1(14–16). These experiments have led to the prediction that PU.1 will be lowly expressed in most primitive progenitors, up-regulated in the CMP, and remain low in the CLP (15). Our results suggest an alternate model as we found that PU.1 was already expressed at high levels in the HSC. Moreover, we found that the CLP and CMP were comparably GFP fluorescent, suggesting that the PU.1 level was not the determining factor of lympho-myeloid lineage commitment. In contrast, the high level PU.1 expression in this early progenitor stage and undetectable CLPs and CMPs in the BM of mice with induced deletion of PU.1 (unpublished data) support a requirement for PU.1 in the transition of HSCs to the CLP or CMP stages of adult hematopoiesis.

Within the lymphoid lineages, the earliest progenitor, the CLP, expressed high levels of PU.1, which was down-regulated during the transition from CLPs to committed T or B cells. All B cells expressed low levels of PU.1, whereas PU.1 is silenced at the TN3 stage of T lymphopoiesis, a finding consistent with previous RT-PCR studies (24). This down-regulation is required for progression in the T cell lineage because enforced constitutive expression of PU.1 during T cell development results in growth inhibition and an arrest at the pro-T cell (TN2) stage (24). These findings suggest that the high PU.1 expression in the CLP is repressed upon B/T cell commitment to the characteristic low B cell expression state and completely repressed to allow T cell development.

In contrast to the uniform expression of PU.1<sup>10<sup>th</sup></sup> in the HSC and CLP, we found clear evidence of heterogeneity in the CMP. The CMPs were originally reported as clonogenic myeloid precursors (2). However, recent studies of ours (20) and others (33) demonstrated that the CMP could be divided into two fractions based on the Flt3 expression. The Flt3<sup>+</sup> CMPs were shown to be more efficient progenitors for myeloid cells and DC populations than the Flt3<sup>−</sup> CMPs (20, 33). The Flt3<sup>+</sup> CMPs also contain precursors of B cells (20).

In this study, we showed that the different levels of PU.1 expression further subdivided the Flt3<sup>−</sup> CMP into two populations, namely the Flt3<sup>−</sup> PU.1<sup>hi</sup> and the Flt3<sup>−</sup> PU.1<sup>lo</sup> CMPs. These populations were morphologically very similar but in vitro colony formation and the in vivo precursor transfer assays demonstrated the differences in progenitor potentials of these three CMP populations, with the Flt3<sup>+</sup> PU.1<sup>10<sup>th</sup></sup> cells as the most efficient progenitors for myeloid cells and DCs, the Flt3<sup>−</sup> PU.1<sup>hi</sup> cells as efficient progenitors for myeloid cells but not for DCs, and the Flt3<sup>−</sup> PU.1<sup>lo</sup> cells as containing progenitors mainly for MegE. CMPs have been demonstrated to be direct precursors of the GMP and MEP populations (2). Here we have shown that the Flt3<sup>+</sup> PU.1<sup>10<sup>th</sup></sup> and Flt3<sup>−</sup> PU.1<sup>hi</sup> CMPs directly differentiated into GMP-like cells, whereas the Flt3<sup>−</sup> PU.1<sup>lo</sup> cells differentiated to MEPs.

The lack of true bipotent cells in these fractions in this assay suggests that the true CMP is either a relatively small proportion of the defined gate or confined to an as yet unidentified earlier stage. In summary, we have demonstrated that the CMP contains at least three phenotypically, functionally, and developmentally distinct cell subsets.

The fact that the Flt3<sup>−</sup> PU.1<sup>10<sup>th</sup></sup> cells were highly enriched for clonogenic MegE progenitors together with the very low levels of PU.1 expression by the MEP and the induction of the MegE regulator gata-1 by these cells suggests that down-regulation of PU.1 is one of the first events associated with the restriction to MegE differentiation. Although it is at present not definitively known whether this down-regulation is essential for erythroid commitment, studies using viral integration or transgenic overexpression demonstrate that PU.1 is incompatible with normal erythropoiesis as ectopic PU.1 blocks early erythroid differentiation, resulting in erythroleukemia (22, 34). In contrast, forced gata-1 expression in vivo reprograms CLP and GMP to the MegE lineages (26). It has been proposed that the interactions of these proteins are direct and result in functional antagonism of either partner (35–38). These results emphasize the importance of considering the functionality of PU.1 as well as its expression level. PU.1 can be serine phosphorylated and interacts with a variety of other transcription factors (8). Although the PU.1<sup>10<sup>th</sup></sup> model does not allow us to discern such posttranslational influences, the transcriptional down-regulation or PU.1 in the Flt3<sup>−</sup> PU.1<sup>10<sup>th</sup></sup> CMP and MegE lineages allows us to propose that the primary determinant of PU.1 versus GATA-1 stoichiometry and lineage determination occurs via transcriptional regulation as few or no progenitors coexpress high levels of both transcripts.

The genetic elements underlying this dynamic expression pattern of PU.1 have not been determined. Deletion of a distal enhancer ∼14-kb upstream of the start of transcription was recently shown to reduce expression to 20% that of wild-type cells (9). However, that study did not ascertain if the re-
duction in PU.1 was uniform or lineage/differentiation-stage specific. Interestingly, these mice developed AML with a high frequency, indicating that the regulation of PU.1 expression is an essential process in controlling hematopoietic malignancies. PU.1 has also been proposed to autoregulate its own transcription with PU.1 \textasciitilde\textasciitilde\textasciitilde fetal liver cells lacking the truncated PU.1 mRNA (5, 39). Therefore, antagonizing PU.1 function would break this autoregulatory loop and provide a simple method to reduce expression. The PU.1\textsuperscript{+} mice will provide an excellent tool to address this question.

This study has revealed a complex and dynamic expression pattern of PU.1 throughout adult hematopoiesis. We propose that PU.1 transcription is controlled at multiple points in hematopoiesis. PU.1 is induced in the most primitive HSC and maintained at this high level in lymphoid and myeloid progenitors. In contrast, PU.1 down-regulation is postmitotic HSC and maintained at this high level in lymphoid and myeloid progenitors. In contrast, PU.1 down-regulation is an early event in the loss of myeloid differentiation capacity associated with commitment to megakaryo-erythropoiesis. Upon unilineage commitment, PU.1 expression is further modified to result in the characteristic high levels in macrophages, low levels in B cells, and transcriptional silencing in a number of other cell types.

**MATERIALS AND METHODS**

**Generation of PU.1\textsuperscript{+} mice.** The pKw11 vector consists of a splice acceptor, stop codons in all reading frames, an IRES, followed by PE-avidin. The HSC was identified as Lin\textsuperscript{−}c-kithi. The CLP was identified as Lin\textsuperscript{−}c-kithi, Flt3\textsuperscript{−}, CD122 (Tm-RII/III (CD16/32)), CD45RA (14.8), and Flt3\textsuperscript{−}. The donor-derived B and T cells were defined as CD19\textsuperscript{+} and Ly5.2\textsuperscript{+} respectively. For DC production, the recipient mice were analyzed 14 d after precursor transfer. The splenic DCs were prepared and stained as described elsewhere (45), and the donor-derived DCs were identified as Ly5.2\textsuperscript{+} DCs. The purity of sorted cells was determined by reanalyzing a small sample of the collected cells and was usually \textasciitilde99%. Fractionated BM progenitors were cytospun on slides and stained with May-Grünsfeld-Giensa solution.

**Pu.1\textsuperscript{+} expression.** The Pu.1\textsuperscript{+} expression by different hematopoietic cell populations was examined by flow cytometric analysis. The level of Pu.1\textsuperscript{+} was determined by the relative mean fluorescence, i.e., the mean fluorescence of equivalent cell populations was examined by flow cytometric analysis. As the fluorescence intensity of equivalent cell populations was examined by flow cytometric analysis.

**Determination of Pu.1\textsuperscript{+} expression.** The Pu.1\textsuperscript{+} expression by different hematopoietic cell populations was examined by flow cytometric analysis. The level of Pu.1\textsuperscript{+} was determined by the relative mean fluorescence, i.e., the mean fluorescence of equivalent cell populations was the same as those defined previously (for details see Fig. S1, available at http://www.jem.org/cgi/content/full/jem.20041535/DC1). The Pu.1\textsuperscript{+} was identified as Lin\textsuperscript{−}Sca-1\textsuperscript{−}IL-7Ra\textsuperscript{−}c-kithi. The CLP was identified as Lin\textsuperscript{−}Sca-1\textsuperscript{−}IL-7Ra\textsuperscript{−}c-kithi. The CMPs can be further divided into three populations based on CD34 and Flt3 expression. PU.1\textsuperscript{+} and PU.1\textsuperscript{−} cells were used for second-stage staining. The previously described CMP population was defined as Lin\textsuperscript{−}Sca-1\textsuperscript{−}IL-7Ra\textsuperscript{−}c-kithi. The CD16/32\textsuperscript{+} cells. The CMPs can be further divided into three populations based on Flt3 and PU.1\textsuperscript{+} expression, namely Flt3\textsuperscript{−} PU.1\textsuperscript{−}, Flt3\textsuperscript{−} PU.1\textsuperscript{−}, and Flt3\textsuperscript{−} PU.1\textsuperscript{+}. Because of limitations in the available fluorescent channels, our gating for the CMP populations differed from that previously published in that it did not include CD34 (2). We believe that the parameters used in this study identify the same CMP population as those defined previously (for details see Fig. S1, available at http://www.jem.org/cgi/content/full/jem.20041535/DC1).

**In vitro hematopoietic cell lineage reconstitution.** The CMP populations were purified from the BM of PU.1\textsuperscript{+} (C57BL/6 Ly5.2) mice and then intravenously injected together with 5 \texttimes\texttimes 10\textsuperscript{5} recipient-type BM cells into lethally irradiated (550 rads, twice) C57BL/6 Ly5.1 recipient mice. 10 d after injection, the donor-derived cells in the recipient thymus, spleen, and BM were analyzed by flow cytometry. Donor-derived myeloid cells were identified as Ly5.2\textsuperscript{−} Mac-1\textsuperscript{−} or Gr-1\textsuperscript{−}. The donor-derived B and T cells were identified as Ly5.2\textsuperscript{−} CD19\textsuperscript{+} B220\textsuperscript{+} and Ly5.2\textsuperscript{−} CD4\textsuperscript{+} or CD8\textsuperscript{+}, respectively. For DC production, the recipient mice were analyzed 14 d after precursor transfer. The splenic DCS were prepared and stained as described elsewhere (45), and the donor-derived DCS were identified as Ly5.2\textsuperscript{−} CD11c\textsuperscript{+}.
cytokines were used at the following concentrations: 10 ng/ml IL-3, 100 ng/ml SCF, and 2 IU/ml erythropoietin. Differential colony counts were performed on fixed preparations stained for acetylcholinesterase, Luxol fast blue, and hematoxylin.

**RT-PCR analysis.** Semiquantitative RT-PCR was performed as described previously (47). cDNA concentrations were normalized to hprt by dilution analysis. PU.1 primers were as follows: PU1 number 1: GTTTTCCCTCACGGCCCTCCAT; PU1 number 2: CTGCCCTCTACCCCTTCTCTCAC. All other primer sets have been described (48).

**cDNA.** Amplification products all spanned introns and were visualized on 2% agarose gels.

**Online Supplemental Material.** Fig. S1 shows the parameters used for RT-PCR analysis. Amplification products all spanned introns and were visualized on 2% agarose gels.

Amplification products all spanned introns and were visualized on 2% agarose gels.

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