## **Characterization of hematopoietic progenitor cells that express the transcription factor SCL, using a** *lacZ* **''knock-in'' strategy**

ANDREW G. ELEFANTY\*, C. GLENN BEGLEY, DONALD METCALF, LOUISE BARNETT, FRANK KÖNTGEN, AND LORRAINE ROBB

The Walter and Eliza Hall Institute of Medical Research and the Cooperative Research Centre for Cellular Growth Factors, P.O. Royal Melbourne Hospital, Victoria 3050, Australia

*Contributed by Donald Metcalf, July 29, 1998*

**ABSTRACT Gene targeting experiments have demonstrated that the transcription factor SCL is essential for primitive and definitive hematopoiesis in the mouse. To study the functional properties of hematopoietic cells expressing** *SCL***, we have generated mutant mice (***SCL***lacZ**y**w) in which the** *Escherichia coli lacZ* **reporter gene has been ''knocked in'' to** the *SCL* locus, thereby linking  $\beta$ -galactosidase expression to **transcription from the** *SCL* **promoter. Bone marrow cells from heterozygous** *SCL***lacZ**y**<sup>w</sup> mice were sorted into fractions** expressing high, intermediate and low levels of  $\beta$ -galactosi**dase (designated lacZhigh, lacZint, and lacZneg). Cells that were lacZhigh or lacZint were enriched for day 12 spleen colonyforming units and myeloid and erythroid colony-forming cells (CFCs). These fractions included >99% of the erythroid and >90% of the myeloid CFCs. Culture of sorted bone marrow populations on stromal cells secreting interleukin-7 or in fetal thymic organ cultures showed that B and T lymphoid progenitors were also present in the lacZhigh and lacZint fractions. These data provide a functional correlation between** *SCL* **expression and colony-forming ability in immature hematopoietic cells. Our data also suggested that expression of** *SCL* was transient and confined to hematopoietic stem and/or **progenitor cells, because the differentiated progeny of most** lineages (except the erythroid) were  $\beta$ -galactosidase-negative.

Hematopoiesis in the developing mouse embryo is critically dependent on the expression of the basic helix–loop–helix gene *SCL*/*TAL1*, a gene initially identified as a partner in the t(1;14) translocation associated with human T cell leukemia (1). Indications that *SCL* might play a role in normal hematopoiesis came from Northern blot analysis of mRNA from hematopoietic cells that showed that *SCL* was selectively expressed in early myeloid, erythroid, megakaryocytic, and mast cell lineages (2–4). Reverse transcription–PCR analyses demonstrated *SCL* expression in CD34<sup>+</sup> bone marrow cells  $(5, 6)$ , which suggested that *SCL* might be expressed in hematopoietic progenitor cells.

The essential role played by *SCL* in hematopoietic development became apparent when it was shown that embryos in which the locus was ablated by homologous recombination failed to develop yolk sac hematopoiesis (7, 8). *SCL*-null embryonic stem (ES) cells did not generate hematopoietic colonies *in vitro* and did not contribute to hematopoiesis in chimeric mice, implying that *SCL* was also critical for definitive hematopoiesis (9, 10). Molecular analysis of differentiating *SCL*-null embryoid bodies revealed that they failed to express any hematopoietic-specific genes, although induction of genes coexpressed in endothelium was normal (11). These data supported a model in which *SCL* was absolutely required for

the commitment of a putative hemangioblast to the hematopoietic lineage but was dispensable for initial differentiation into endothelium.

However, these gene ablation studies could not verify by functional assays the expression of *SCL* in hematopoietic progenitor and stem cells suggested by mRNA and reverse transcription-PCR studies. To address this issue, we have generated mutant mice (*SCL*<sup>lacZ/w</sup>) in which the *Escherichia coli lacZ* reporter gene has been ''knocked in'' to the *SCL* locus. This paper focuses on an analysis of the functional properties of  $\beta$ -galactosidase-expressing cells in heterozygous *SCL*<sup>lacZ/w</sup> mice.

## **MATERIALS AND METHODS**

**Construction of the** *SCL-lacZ* **Targeting Vector.** The 5' arm of *SCL* homology, consisting of a 6-kb genomic fragment containing exon Ia–exon III, was cloned into the vector  $\beta$ -gal (12), which contained the *E. coli lacZ* gene coupled to the rabbit  $\beta$ -globin polyadenylation sequence. The 3' homology arm of the targeting vector, comprising the *PGK* promoterdriven neomycin resistance gene coupled to a 1.75-kb fragment from the 3' untranslated region of exon VI of *SCL*, was cloned downstream of the rabbit  $\beta$ -globin polyadenylation sequence.

**Isolation of Targeted ES Cell Clones and Production of Chimeric Mice.** The ES cell line W9.5 was maintained, electroporated, and selected with G418 (GIBCO) as described (7). Homologous recombinants were identified by Southern hybridization of DNA isolated from individual clones. Three targeted clones were injected into  $\left($  C57BL/ $/6 \times$  C57BL/ $/10$ )F<sub>2</sub> blastocysts from female mice 3.5 days post coitum. Chimeras were mated to C57BL/6 mice to produce heterozygotes, which were identified by Southern hybridization of tail DNA.

**Fluorescence-Activated Cell Sorter** b**-Galactosidase (FACS-Gal) Analysis.** The FACS-Gal assay was performed basically as described (13). Bone marrow cells harvested from *SCL*<sup>lacZ/w</sup> or *SCL*<sup>wt/wt</sup> mice were washed in Hepes and potassium phosphate-buffered balanced salt solution supplemented with 5% fetal calf serum. The erythrocytes were lysed by incubation in 156 mM ammonium chloride, pH 7.3, at 37°C for 3 min. Nucleated cells were pelleted and resuspended in 150  $\mu$ l of balanced salt solution/ $5\%$  fetal calf serum and warmed to 37°C. Hypotonic loading was accomplished by diluting the cells 1:1 with warmed 2 mM fluorescein di- $\beta$ -D-galactopyranoside (FDG; Sigma) and incubating at 37°C for 2 min. Three milliliters of cold balanced salt solution/5% fetal calf serum was added to stop loading and intracellular hydrolysis of FDG to fluorescein catalyzed by  $\beta$ -galactosidase was allowed to

The publication costs of this article were defrayed in part by page charge payment. This article must therefore be hereby marked ''*advertisement*'' in accordance with 18 U.S.C. §1734 solely to indicate this fact.

<sup>© 1998</sup> by The National Academy of Sciences 0027-8424/98/9511897-6\$2.00/0 PNAS is available online at www.pnas.org.

Abbreviations: CFU, colony-forming unit; CFU-E, erythroid CFU; BFU-E, erythroid burst-forming unit; SCF, stem cell factor; FACS, fluorescence-activated cell sorter; IL, interleukin; Epo, erythropoietin; ES, embryonic stem; CFC, colony-forming cell; CFU-S, spleen CFU.

 $*$ To whom reprint requests should be addressed. e-mail: elefanty@ wehi.edu.au.

proceed on ice for 3 h. Propidium iodide was added to a final concentration of 1  $\mu$ g/ml before analysis. Cells were analyzed and sorted on a FACStar Plus (Becton Dickinson).

**Clonogenic Assays for Hematopoietic Progenitors.** Fractionated and unfractionated bone marrow cells from *SCL*<sup>lacZ/w</sup> or *SCL*<sup>w/w</sup> mice were cultured in 0.3% agar for myeloid colony formation or in 0.9% methylcellulose for erythroid colony formation as described (14). Day 7 myeloid colonies were stimulated with 1,000 units/ml interleukin (IL)-3 or 100 ng/ml stem cell factor (SCF); day 7 erythroid burst-forming units  $(BFU-E)$ , with the combination of 1,000 units/ml IL-3 and 4 units/ml human erythropoietin (Epo); and day 2 erythroid colony-forming units (CFU-E), with 4 units/ml Epo. Differential colony counts were determined from agar cultures that had been fixed, dried, and stained with hematoxylin and luxol fast blue, and tested for acetylcholinesterase activity as described (14).

**Limiting Dilution Analysis of Pre-B Cells.** Between 10 and 3,000 fractionated and unfractionated bone marrow cells were deposited into individual wells of 96-well plates seeded with irradiated (30 Gy) IL-7-expressing NIH 3T3 cells (a gift from A Rolink, Basel Institute for Immunology). Wells were scored for growth after 7 days and cells pooled from multiple wells were stained with May–Grünwald–Giemsa and analyzed by flow cytometry by using directly conjugated antibodies to Mac-1 and B220 antigens as described (15).

**Fetal Thymic Organ Culture.** Embryonic day (E)15.5 thymic lobes from  $129/Sv$  mice were depleted of endogenous lymphoid precursors by organ culture in medium containing 1.35 mM deoxyguanosine (Sigma) for 5–7 days as described (16). Individual lobes were then reconstituted by cocultivation for 24 h in hanging drops (17) with fractionated and unfractionated bone marrow cells from syngeneic *SCL*<sup>lacZ/w</sup> mice, followed by an additional 3-week period of organ culture. Cell suspensions of reconstituted thymic lobes were stained with May–Grünwald–Giemsa and analyzed by flow cytometry using directly conjugated antibodies to Thy-1, CD4, CD8, TCR $\beta$ , TCR $\gamma$ , Mac-1, and B220 antigens as described (15).

**Day 12 CFU-S Assay.** Fractionated and unfractionated bone marrow cells from *SCL*<sup>lacZ/w</sup> mice were injected into the retro-orbital venous plexus of irradiated C57BL/6 recipients (two doses of 5.5 Gy separated by 3 h). Spleens were harvested after 12 days, weighed, and fixed in a 100:5:12 (vol/vol) ratio of  $70\%$  ethanol/glacial acetic acid/10% neutral buffered formalin. The macroscopic colonies were counted.

## **RESULTS**

**Generation of** *SCL***lacZ**y**<sup>w</sup> Mutant Mice.** The *E. coli lacZ* reporter gene was inserted by homologous recombination into the 5' untranslated region of the mouse *SCL* gene, placing it under the control of *SCL* regulatory elements. The targeting event simultaneously deleted all *SCL* coding sequences, thereby also creating an *SCL*-null allele (Fig. 1*A*). This strategy ensured that *SCL* regulatory regions upstream of exon III and downstream of exon VI were left intact (18). Correctly targeted ES cell clones were identified by Southern hybridization of DNA using the 3' flanking probe A. The structure of the targeted allele was verified by using a 5' flanking probe and single integration of the targeting vector was confirmed with a *neo* probe (data not shown).

Three targeted ES cell clones were used to generate independent lines of mice. These were genotyped by Southern hybridization of tail DNA (Fig. 1*B*) or using a PCR-based strategy, as described previously (7). As expected, mice heterozygous for the *SCL-lacZ* allele (denoted *SCL*lacZ/w) appeared normal but homozygous *SCL*<sup>lacZ/lacZ</sup> embryos died by E9.5 with absent yolk sac hematopoiesis, a phenocopy of the  $SCL^{-/-}$  embryos previously described (7, 8).

Histochemical staining of  $SCL^{\text{lacZ/w}}$  embryos for  $\beta$ -galactosidase activity revealed *lacZ* expression in the fetal liver, circulating blood cells, endothelium, and the developing brain, consistent with the sites of *SCL* mRNA and protein expression detected in previous studies (refs. 4 and 19 and data not shown). The same pattern was observed in all three targeted lines. This indicated that the expression pattern of the *SCL*targeted *lacZ* gene reliably reflected endogenous *SCL* gene expression.

**Characterization of** b**-Galactosidase-Expressing Cells in the Bone Marrow of Adult** *SCL*<sup>lacZ/w</sup> **Mice.**  $\beta$ -Galactosidaseexpressing hematopoietic cells in *SCL*<sup>lacZ/w</sup> mice were identified by using the FACS-Gal technique (13). This highly sensitive method permitted the recovery of viable populations of cells for morphological and functional evaluation. Because FACS-Gal fluorescence is proportional to the number of  $\beta$ -galactosidase molecules per cell (13), the level of fluorescence reflected *SCL* gene expression.

Bone marrow cells from adult *SCL*<sup>lacZ/w</sup> mice were separated into those expressing low (lacZ<sup>neg</sup>; 93.3  $\pm$  1.3%, mean  $\pm$ SD derived from 13 experiments), intermediate (lacZ<sup>int</sup>; 5.2  $\pm$ 0.8%), and high (lacZ<sup>high</sup>;  $1.5 \pm 0.6\%$ ) levels of  $\beta$ -galactosidase activity (Fig. 2*A*). A small subset of wild-type  $(SCL^{w/w})$  bone marrow cells  $(1.5 \pm 0.4\%)$  expressed intermediate levels of



FIG. 1. *SCL-lacZ* gene targeting strategy. (*A*) The *SCL-lacZ* targeting vector is shown above the map of the *SCL* genomic locus. Regions of homology where recombination occurred are indicated as crosses and the correctly targeted locus is depicted below. Exons are shown as numbered, solid boxes. The positions of the *E. coli lacZ* gene (lacZ), the polyadenylation signal (pA), and the *PGKneo* cassette (neo) are indicated. Abbreviations: B, *Bam*HI; R, *Eco*RI; S, *Sac*I; X, *Xba*I. (*B*) Southern hybridization of *Bam*HI-digested DNA from wild-type (wyw) and heterozygous  $(lacZ/w)$  mice hybridized with probe A, indicating germ-line (5 kb) and targeted (3 kb) alleles.



FIG. 2. Expression of  $\beta$ -galactosidase in *SCL*<sup>lacZ/w</sup> bone marrow cells. (*A*) Representative FACS profiles of forward scatter plotted against  $\beta$ -galactosidase activity (measured as fluorescence) for FACS-Gal-labeled bone marrow cells from *SCL*<sup>lacZ/w</sup> and *SCL*<sup>w/w</sup> mice. Gating windows and the percentage of cells in each window are shown for lac $Z<sup>neg</sup>$ , lac $Z<sup>int</sup>$ , and lac $Z<sup>high</sup>$  fractions. (*B*) May-Grünwald-Giemsa stained cytocentrifuge preparations of unsorted and sorted bone marrow fractions from  $\hat{S}CL^{\text{lacZ/w}}$  mice.

 $\beta$ -galactosidase activity, but very few cells (0.1  $\pm$  0.1%) were lacZhigh. Undifferentiated blast cells were more frequent in the lacZ<sup>int</sup> (22 ± 3%) and lacZ<sup>high</sup> populations (32 ± 5%) than in the lacZ<sup>neg</sup> fraction (3  $\pm$  1%) and nucleated erythroblasts were also increased in the lac $Z^{\text{high}}$  fraction (Fig. 2*B* and data not shown). This latter fraction was depleted of mature granulocytic and monocytic cells. These data were consistent with previous observations linking *SCL* expression to the erythroid lineage and to immature hematopoietic cells.

**Myeloid and Erythroid Progenitor Cells Are Enriched in the** b**-Galactosidase-Positive Fraction from** *SCL***lacZ**y**<sup>w</sup> Bone** Marrow. Fractionated bone marrow cells from *SCL*<sup>lacZ/w</sup> and control *SCL*<sup>wt/wt</sup> mice were cultured in agar. As shown in Fig.  $3A$ , there was a  $>100$ -fold enrichment of myeloid progenitor cells in the lacZ<sup>int</sup> and lacZ<sup>high</sup> fractions compared with lacZ<sup>neg</sup> bone marrow cells from *SCL*<sup>lacZ/w</sup> mice. In contrast, there was little difference in the frequency of progenitor cells in the lacZ<sup>int</sup> vs. lacZ<sup>neg</sup> fractions of wild-type bone marrow cells. Microscopy of stained agar cultures revealed granulocyte, macrophage, eosinophil, and megakaryocyte colonies in the cultures derived from lacZ<sup>int</sup> and lacZhigh *SCL*lacZ/w bone marrow cells in the same proportions as were observed in cultures of unfractionated bone marrow cells (data not shown). There was an increased frequency of blast cell colonies in the lacZhigh fraction (33  $\pm$  6%) compared with unfractionated



FIG. 3. Enrichment for myeloid and erythroid CFCs in the lacZpositive bone marrow fractions of *SCL*<sup>lacZ/w</sup> mice. (*A*) Frequency of day 7 myeloid CFC in agar cultures of unsorted and sorted bone marrow fractions from *SCL*<sup>lacZ/w</sup> and *SCL*<sup>w/w</sup> mice cultured in IL-3 or SCF. Values represent the mean  $\pm$  SD from five experiments for *SCL*<sup>lacZ/w</sup> and the mean from two experiments for *SCL*<sup>w/w</sup> bone marrow cells. The percentage of bone marrow cells that were sorted into each fraction is indicated. (*B*) Frequency of day 2 CFU-E, day 7 BFU-E, and myeloid (GM) CFC in methylcellulose cultures of unsorted and sorted bone marrow fractions from  $SCL^{\text{lacZ/w}}$  mice cultured in Epo (for day 2 CFU-E) or IL-3/Epo (for day 7 BFU-E and GM CFC). Values represent the mean  $\pm$  SD from three experiments. The percentage of bone marrow cells that were sorted into each fraction is indicated.

bone marrow cells (21  $\pm$  8%) in cultures stimulated with SCF. Mast cell progenitors, detected by culturing bone marrow cells in the presence of IL-3, were also enriched in the  $\beta$ -galactosidase-positive fractions (data not shown).

The frequency of erythroid precursors in bone marrow populations from *SCL*<sup>lacZ/w</sup> mice was determined by culturing cells in methylcellulose. The enrichment for CFU-E and BFU-E in the  $lacZ<sup>int</sup>$  and  $lacZ<sup>high</sup>$  bone marrow cells was even greater than for the myeloid colony-forming cells (CFCs), with the CFU-E being particularly numerous in the lac $Z^{\text{high}}$  fraction (Fig. 3*B*). The degree of myeloid CFC enrichment observed in the  $\beta$ -galactosidase-positive populations was similar to that seen in the agar cultures, indicating that the greater enrichment for erythroid progenitors in the  $\beta$ -galactosidase-positive fractions was not simply due to the different culture methods.

When the absolute number of clonogenic cells in each fraction was calculated,  $>90\%$  of the myeloid progenitor cells in *SCL*<sup>lacZ/w</sup> bone marrow agar cultures were lacZ<sup>int</sup> or lac-Zhigh. Conversely, only 5% of the clonogenic cells in *SCL*<sup>w/w</sup>





\*Bone marrow cells from mice of the indicated genotype were cultured in duplicate in agar or methylcellulose in the presence of growth factors for 2 or 7 days and the colonies counted. The number of experiments is shown in parentheses.

 $^{\dagger}$ IL-3 was used at 1,000 units/ml, SCF at 100 ng/ml, and Epo at 4 units/ml.

 $\text{FThe number of CFCs in cultures of } 2.5 \times 10^4$  bone marrow cells (unsorted) compared with the calculated recovery of CFCs from the sorted fractions. This figure was calculated for each experiment by summing (progenitor frequency  $\times$  % of cells) for each fraction and then determining the mean for each group of experiments. Values given represent the mean  $\pm$  SD. The mean progenitor frequency and the mean % cells in each fraction are shown in Fig. 3.

§The distribution of CFCs in the sorted bone marrow fractions given as a percentage.

<sup>¶</sup>NA, not applicable, since all lacZ-positive *SCL<sup>w/w</sup>* bone marrow cells were lacZ<sup>int</sup>.

bone marrow were in the lacZ<sup>int</sup> fraction (Table 1). Comparing the number of myeloid progenitor cells observed in unsorted bone marrow and the yield calculated by summing the sorted fractions indicated that there was no significant progenitor cell loss during the sorting procedure (Table 1). Similarly, when the distribution of progenitor cells in methylcellulose cultures was compared,  $>99\%$  of the CFU-E and BFU-E and 90% of the myeloid CFCs were  $\beta$ -galactosidase-positive. The level of  $\beta$ -galactosidase activity in the CFU-E was the highest, because 84% were lacZhigh, followed by the BFU-E (49% lacZhigh) and myeloid CFCs (30% lacZhigh). The calculated recovery of CFU-E after sorting was only 37% of the input number (compare ''sorted'' with ''unsorted'' columns in Table 1), whereas the calculated recovery of day 7 CFCs was in excess of 100%. This suggested that day 2 CFU-E may have been sensitive to the sorting procedure and that fractionation actually removed cells inhibitory for day 7 CFCs.

Summing the numbers of IL-3/Epo-responsive myeloid and erythroid colonies in methylcellulose cultures gave an estimated frequency of clonogenic precursors of 4.6% for lacZint cells and  $26\%$  for lacZhigh cells.

Day 12 CFC-S Are Enriched in  $\beta$ -Galactosidase-Positive **Cells from** *SCL***lacZ**y**<sup>w</sup> Bone Marrow.** The genetic background of the *SCL*<sup>lacZ/w</sup> mice precluded experiments to examine long-term repopulating stem cells. However, we found that a more mature multipotential precursor cell, the day 12 CFU-S, displayed a degree of enrichment in the lacZ<sup>int</sup> and lacZ<sup>high</sup> fractions similar to the day 7 myeloid colony forming cells, being 50- to 100-fold more frequent than in the  $lacZ<sup>neg</sup>$ population (Table 2). As was the case with the myeloid CFCs, most of the day 12 CFU-S resided in the lacZ<sup>int</sup> fraction.

Table 2. Frequency of day 12 CFU-S in *SCL*<sup>lacZ/w</sup> bone marrow

Bone marrow*	Cells injected	Spleen <sup>†</sup>	Spleen weight, mg	
fraction	per recipient	colonies		
Uninjected (4)		$0.3 \pm 0.5$	$20 \pm 1$	
Unsorted $(4)$	$5 \times 10^4$	$+2$ 10	$94 \pm 33$	
$lacZ^{neg}$ (5)	$5 \times 10^4$	$+2$	$28 \pm 17$	
$lacZint$ (5)	$6 \times 10^3$	$+43$ 50	$62 \pm 35$	
$lacZhigh$ (5)	$6 \times 10^3$	$+27$ 103	$151 \pm 37$	

\*Bone marrow cells from *SCL*lacZy<sup>w</sup> mice were injected into irradiated recipients. The number of recipients for each fraction is given in parentheses.

†Spleens were harvested after 12 days and macroscopic colonies counted. Values represent the mean  $\pm$  SD colony numbers calculated per  $5 \times 10^4$  cells injected.

**B** and T Lymphoid Progenitors Are Present in the β-Galac**tosidase-Positive Fractions of** *SCL***lacZ**y**<sup>w</sup> Bone Marrow.** FACS-Gal staining of thymocytes or splenocytes from *SCL*<sup>lacZ/w</sup> and *SCL*<sup>w/w</sup> mice did not reveal any *SCL*<sup>lacZ/w</sup> lymphoid populations with increased  $\beta$ -galactosidase activity (data not shown), consistent with the absence of *SCL* expression in these cell types (3, 5). However, this analysis did not address whether more primitive lymphoid precursors expressed *SCL*.

Bone marrow fractions were cultured in limiting dilution on stromal layers of IL-7-expressing NIH 3T3 cells to detect the growth of pre-B cells  $(20, 21)$ . In each of three experiments, clonogenic cells were present in the  $\beta$ -galactosidase-positive as well as -negative fractions at a frequency of  $\approx$ 1:100 (data not shown). However, the populations of hematopoietic cells that were evident by 7 days of culture were heterogeneous, especially in wells into which lacZ<sup>int</sup> or lacZ<sup>high</sup> cells had been sorted.

Examination of cytocentrifuge preparations of cells grown from unsorted bone marrow or lacZneg seeded wells revealed a predominance of lymphocytes, but there were also some macrophages (data not shown). Approximately one-third of the cells in lac $\bar{Z}^{\text{int}}$  and lac $Z^{\text{high}}$  wells were lymphocytes and the remaining cells were macrophages or immature myeloid cells. Flow cytometry of the harvested cells labeled with antibodies recognizing the B cell antigen, B220, and the myeloid antigen, Mac-1 confirmed these lineage assignments (Fig. 4). It is likely that the enrichment for myeloid precursors in the  $\beta$ -galactosidase-positive fractions contributed to the dominance of macrophages in cultures initiated with lacZ-positive cells.

We also assessed the ability of the different bone marrow fractions to reconstitute T lymphopoiesis in deoxyguanosinetreated fetal thymic lobes. As detailed in Table 3, visible enlargement of thymic lobes after a 3-week culture period correlated with colonization of the thymic rudiment. Both the frequency of thymic lobe enlargement and the cellular recovery were greater in lobes reconstituted with  $\beta$ -galactosidasepositive than  $\beta$ -galactosidase-negative cells, indicating that T lymphoid precursors were enriched in  $lacZ<sup>int</sup>$  and  $lacZ<sup>high</sup>$  bone marrow fractions of *SCL*<sup>lacZ/w</sup> mice. Examination of cytocentrifuge preparations of cells recovered from the reconstituted lobes revealed an identical lymphoid morphology in all cases (data not shown). Over 95% of cells stained brightly for Thy-1, confirming the T cell lineage of the recovered cells. Most cells  $(65-90\%)$  were immature CD4<sup>-8-</sup> thymocytes and only 15– 25% expressed T cell receptors on their surface (Fig. 5). The same immunophenotype was observed regardless of the bone marrow fraction used to reconstitute the thymic lobes. This suggested that thymic precursors with similar kinetics of



FIG. 4. B lymphoid progenitor cells are found in lacZ-positive and -negative bone marrow fractions of *SCL*<sup>lacZ/w</sup> mice. Flow cytometric profiles of cells harvested from IL-7/NIH 3T3 cultures seeded with unsorted or sorted bone marrow fractions and labeled with directly conjugated antibodies against the B lymphoid antigen, B220, and the myeloid antigen, Mac-1.

differentiation were responsible for reconstituting the thymic lobes in all cases.

## **DISCUSSION**

To investigate the functional attributes of *SCL*-expressing hematopoietic cells, we have used homologous recombination to ''knock-in'' the *E. coli lacZ* gene into the murine *SCL* locus, thereby linking the production of  $\beta$ -galactosidase to transcription from the *SCL* promoter. The expression pattern of the *SCL*-targeted *lacZ* gene mirrored known sites of *SCL* gene expression, indicating that  $\beta$ -galactosidase activity in *SCL*<sup>lacZ/w</sup> animals represented a valid facsimile of endogenous *SCL* expression. We employed the FACS-Gal technique to identify and recover viable hematopoietic cells with different levels of  $\beta$ -galactosidase activity from *SCL*<sup>lacZ/w</sup> mice.

A major finding from these experiments was that myeloid and erythroid progenitor cells were enriched in the lacZpositive bone marrow fractions from *SCL*<sup>lacZ/w</sup> mice. Interestingly, there was a correlation between the level of  $\beta$ -galactosidase activity and the type of colony observed (see Fig. 3*B* and Table 1). The highest lacZ expression levels correlated with enrichment for day 2 CFU-E, which were 20-fold more abundant in lacZhigh than in lacZint populations. Although >99% of day 7 BFU-E were  $\beta$ -galactosidase-positive, their frequency was only 3-fold greater in lac $Z<sup>high</sup>$  than in lac $Z<sup>int</sup>$  cells. As a group, day 7 myeloid progenitors expressed lower levels of  $\beta$ -galactosidase. In fact,  $\approx 60\%$  of these cells were lacZ<sup>int</sup> and  $10\%$  were lac $Z<sup>neg</sup>$ . However, examination of fixed, stained agar cultures of the myeloid colonies revealed that blast cell colonies were more frequent in the lacZhigh fraction. Similarly, day 12 CFU-S, the most primitive multipotential precursor assayed in our experiments, were also enriched in the  $lacZ<sup>high</sup>$  populations (Table 2).

From these data, we can propose a model in which *SCL* is expressed in multipotential and myeloid progenitor cells but is rapidly extinguished once cells begin to differentiate and lose proliferative potential. The pattern differed in the erythroid lineage, where levels of *SCL* rose during initial differentiation from multipotential progenitor to day 2 CFU-E. As judged by the distribution of nucleated erythroblasts between the  $\beta$ -galactosidase-positive and -negative populations, it is likely that only a subset of these cells continued to express *SCL*. This model is consistent with the results of *in situ* hybridization that demonstrated *SCL* transcripts in a subset of CD34<sup>+</sup> cells and immature erythroblasts (5) and analyses that revealed more abundant *SCL* expression early in erythroid colony development (6, 22, 23). *SCL* transcripts were detected at lower levels in early progeny of myeloid precursors and were lost as cells differentiated (23). We have demonstrated that there are clonogenic lymphoid as well as myeloid progenitors that express *SCL*. Although the majority of lymphoid precursors that grow on stromal cell layers in the presence of IL-7 are  $B220<sup>+</sup>$  Kit<sup>+</sup> pre-B-I cells (24), more primitive progenitors have also been identified, including a common lymphoid progenitor with T, B, and natural killer cell reconstituting capacity (25). Thus, the presence of B lymphoid progenitors in the  $\beta$ -galactosidase-negative and -positive bone marrow fractions from the *SCL*<sup>lacZ/w</sup> mice may indicate that the expression of *SCL* varies within the hierarchy of B lymphoid progenitor cells.

T lymphoid precursor cells were selectively enriched in the  $\beta$ -galactosidase-positive vs.  $\beta$ -galactosidase-negative bone marrow fractions. It is likely that the lac $Z<sup>int</sup>$  and lac $Z<sup>high</sup>$  bone marrow cells that seeded the thymic rudiment were at least oligopotential lymphoid precursors if not multipotential lymphomyeloid stem cells, because the spectrum of bone marrowderived cells capable of reconstituting the thymus is restricted to primitive and more mature multilineage hematopoietic stem cells (26) and common lymphoid progenitors (25). Indeed, the

Table 3. T cell progenitors are enriched in lacZ-positive cells from *SCL*<sup>lacZ/w</sup> bone marrow

Bone marrow fraction*	Input cells per lobe <sup>†</sup>	Lobe enlargement#	Cells recovered <sup>§</sup>		Fold
			Per lobe	Per $5 \times 10^4$ cells	increase <sup>ll</sup>
No cells		0/5	$5.5 \times 10^{2}$		
Unsorted $(100\%$	$5 \times 10^4$	8/8	$1.6 \times 10^{4}$	$1.6 \times 10^{4}$	1.0
lacZ neg $(89\%)$	$5 \times 10^4$	1/8	$1.4 \times 10^3$	$1.4 \times 10^3$	0.1
lacZ int $(7.5\%)$	$2 \times 10^3$	6/7	$1.8 \times 10^{4}$	$4.5 \times 10^{5}$	27.5
lacZ high $(3.5\%)$	$1 \times 10^3$	6/8	$1.3 \times 10^{4}$	$6.3 \times 10^{5}$	38.5

\*Bone marrow cells from *SCL*<sup>lacZ/w</sup> mice were cocultivated with deoxyguanosine-treated thymic lobes for 24 h prior to organ culture. The percentage of bone marrow cells gated into each fraction is given in parentheses. Results are given for one representative experiment of two performed.

<sup>†</sup>The number of cells cocultivated with each thymic lobe.

‡Visible lobe enlargement was assessed after a 3-week culture period.

§Cellularity of pooled thymic lobes expressed per lobe or per  $\dot{5} \times 10^4$  input cells.

"Ratio of cells recovered compared to unsorted bone marrow per  $5 \times 10^4$  input cells.

Only stromal cells were recovered.



FIG. 5. T lymphoid cell surface markers expressed by the progeny of bone marrow cells reconstituting fetal thymic lobes in organ culture. Identical flow cytometric profiles were obtained regardless of whether  $\beta$ -galactosidase-positive or -negative bone marrow fractions were used to repopulate the thymic lobes.

earliest intrathymic precursors still retain the ability to differentiate along T, B, and natural killer cell lineages (26).

Fluorescence-activated cell sorting has permitted purification and characterization of hematopoietic stem and progenitor cells largely based on their expression of a diverse range of cell surface proteins including class I histocompatibility antigens, Thy-1, Ly-6AyE (Sca-1), c-*kit*, CD4, and CD34 (27). Unfortunately, with the exception of c-*kit*, very little is known about the role that any of these molecules plays in hematopoietic stem cell development. This study has succeeded in stratifying hematopoietic cells into functional groups based on their expression of the developmentally ''relevant'' transcription factor, *SCL*. The association of *SCL* expression with a broad range of lymphoid and myeloid hematopoietic progenitors, including the earliest precursors assayed, complements prior gene ablation studies and is consistent with the postulated role of *SCL* as a "master regulator" of hematopoiesis.

We thank Dr. Andreas Strasser for helpful discussions and the provision of monoclonal antibodies, Dr. A. Rolink for the IL-7 expressing NIH 3T3 cells, and Dr. Kathy Kelly for advice on fetal thymic organ cultures. Dr. Frank Battye assisted with cell sorting. Bette Papevangioulou, Koula Kosmopoulos, Ladina Di Rago, Sandra Mifsud, Angela D'Amico, Rachel Mansfield, Vicki Lapatis, Dora Kaminaris, and Jenny Parker provided expert technical assistance. We thank Jodie De Winter and the staff of the Walter and Eliza Hall Institute animal facility for their expertise and Drew Berry and Simon Olding for the production of figures. This work was supported by the Lions Special Fellowship of the AntiCancer Council of Victoria (A.G.E.), the Colin Syme Fellowship (L.R.), the National Health and Medical Research Council (Canberra), the AntiCancer Council of Victoria, the Australian Federal Government Cooperative Research Centres Program, the Rotary Bone Marrow Research Laboratories, and a grant from the National Institutes of Health (CA22556, to D.M.).

- 1. Robb, L. & Begley, C. G. (1997) *BioEssays* **19,** 607–613.
- 2. Visvader, J., Begley, C. G. & Adams, J. M. (1991) *Oncogene* **6,** 187–194.
- 3. Green, A. R., Salvaris, E. & Begley, C. G. (1991) *Oncogene* **6,** 475–479.
- 4. Green, A. R., Lints, T., Visvader, J., Harvey, R. & Begley, C. G. (1992) *Oncogene* **7,** 653–660.
- 5. Mouthon, M.-A., Bernard, O., Mitjavila, M.-T., Romeo, P.-H., Vainchenker, W. & Mathieu-Mahul, D. (1993) *Blood* **81,** 647– 655.
- 6. Cheng, T., Shen, H., Giokas, D., Gere, J., Tenen, D. G. & Scadden, D. T. (1996) *Proc. Natl. Acad. Sci. USA* **93,** 13158– 13163.
- 7. Robb, L., Lyons, I., Ruili, L., Hartley, L., Köntgen, F., Harvey, R. P., Metcalf, D. & Begley, C. G. (1995) *Proc. Natl. Acad. Sci. USA* **92,** 7075–7079.
- 8. Shivdasani, R. A., Mayer, E. L. & Orkin, S. H. (1995) *Nature (London)* **373,** 432–434.
- Robb, L., Elwood, N. J., Elefanty, A. G., Köntgen, F., Li, R., Barnett, L. D. & Begley, C. G. (1996) *EMBO J.* **15,** 4123–4129.
- 10. Porcher, C., Swat, W., Rockwell, K., Fujiwara, Y., Alt, F. W. & Orkin, S. H. (1996) *Cell* **86,** 47–57.
- 11. Elefanty, A. G., Robb, L., Birner, R. & Begley, C. G. (1997) *Blood* **90,** 1435–1447.
- 12. Ogilvy, S., Elefanty, A. G., Visvader, J., Bath, M. L., Harris, A. W. & Adams, J. M. (1998) *Blood* **91,** 419–430.
- 13. Fiering, S. N., Roederer, M., Nolan, G. P., Micklem, D. R., Parks, D. R. & Herzenberg, L. A. (1991) *Cytometry* **12,** 291–301.
- 14. Metcalf, D. (1984) *Clonal Culture of Hemopoietic Cells: Techniques and Applications* (Elsevier, Amsterdam).
- 15. Strasser, A., Harris, A. W. & Cory, S. (1991) *Cell* **67,** 889–899.
- 16. Jenkinson, E. J., Franchi, L. L., Kingston, R. & Owen, J. J. T. (1982) *Eur. J. Immunol.* **12,** 583–587.
- 17. Kingston, R., Jenkinson, E. J. & Owen, J. J. T. (1985) *Nature (London)* **317,** 811–813.
- 18. Göttgens, B., McLaughlin, F., Bockamp, E.-O., Fordham, J. L., Begley, C. G., Kosmopoulos, K., Elefanty, A. G. & Green, A. R. (1997) *Oncogene* **15,** 2419–2428.
- 19. Kallianpur, A. R., Jordan, J. E. & Brandt, S. J. (1994) *Blood* **83,** 1200–1208.
- 20. Sudo, T., Ito, M., Ogawa, Y., Iizuka, M., Kodama, H., Kunisada, T., Hayashi, S., Ogawa, M., Sakai, K. & Nishikawa, S. (1989) *J. Exp. Med.* **170,** 333–338.
- 21. Rolink, A., Kudo, A., Karasuyama, H., Kikuchi, Y. & Melchers, F. (1991) *EMBO J.* **10,** 327–336.
- 22. Miller, B. A., Floros, J., Cheung, J. Y., Wojchowski, D. M., Bell, L., Begley, C. G., Elwood, N. J., Kreider, J. & Christian, C. (1994) *Blood* **84,** 2971–2976.
- 23. Hoang, T., Paradis, E´., Brady, G., Billia, F., Nakahara, K., Iscove, N. N. & Kirsch, I. R. (1996) *Blood* **87,** 102–111.
- 24. Rolink, A., Haasner, D., Nishikawa, S.-I. & Melchers, F. (1993) *Blood* **81,** 2290–2300.
- 25. Kondo, M., Weissman, I. L. & Akashi, K. (1997) *Cell* **91,** 661–672.
- 26. Wu, L., Livak, F. & Petrie, H. T. (1998) in *Molecular Biology of B-Cell and T-Cell Development*, eds. Monroe, J. G. & Rothenberg, E. V. (Humana, Totowa, NJ), pp. 285–303.
- 27. Morrison, S. J., Uchida, N. & Weissman, I. L. (1995) *Annu. Rev. Cell. Dev. Biol.* **11,** 35–71.