Knockdown of *Pu.1* by small interfering RNA in CD34+ embryoid body cells derived from mouse ES cells turns cell fate determination to pro-B cells

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The factors that regulate murine ES cell-derived hematopoietic progenitor cell (HPC) commitment to the B lymphocyte lineage remain unclear. *Pu.1* plays an essential role in the development of all lymphoid lineages; however, it also regulates commitment to other blood cell lineages. In this study, we found evidence for early B cell lineage commitment as determined by coexpression of CD19 and CD45R (B220) when *Pu.1* expression was knocked down in HPC by specific small interfering RNA (siRNA); moreover, the expression of early B cell factor (Ebf) and paired box protein 5 (Pax-S) transcription factors was induced when cells were treated by *Pu.1* siRNA, but not by control siRNA. We also found that siRNA-mediated knockdown of *Pu.1* expression was more efficient in generating progenitor B cells (pro-B cells) compared with the more common *in vitro* method of B lymphoid development by means of coculture of CD34+ embryoid body (EB) cells with OP9 stromal cells. To investigate whether this phenomenon also exists in HPC from other sources, we then knocked down *Pu.1* gene expression in CD34+ murine bone marrow cells and found a similar effect of increased production of CD19+CD43+CD45R+ progenitor B cells upon the siRNA-mediated decrease in *Pu.1* expression. We conclude that, in early B cell development from ES cell-derived HPC, constitutive *Pu.1* expression inhibits the earliest B cell development through repressing early B cell factor and paired box protein 5 expression, although lower levels of *Pu.1* expression in HPC play a key role in promoting B cell fate determination.

RNA interference | differentiation | paired box protein-5 | early B cell factor | IL-7

M urine ES cell (mES) differentiation is a robust system to study the regulation of hematopoietic cell development (1, 2). Differentiated mES cells express similar cell surface antigens and molecular expression patterns at the appropriate stages of progenitor cell development as observed in developing murine embryos *in vivo*. Mature blood cells, such as red blood cells, platelets, neutrophils, eosinophils, mast cells, and dendritic and natural killer cells have been generated from mES cells (3–6). B lymphocyte progenitors have also been generated from ES cell differentiation, through coculture with OP9 stromal cells (7). OP9 cells are a bone marrow stromal cell line that secretes both defined and undefined factors promoting hematopoietic progenitor cell (HPC) commitment to the B cell lineage. However, OP9 cell support for B cell development is not specific because numerous hematopoietic elements emerge from cocultured mES and OP9 cells. Thus, the disadvantage of using OP9 cells is that they introduce greater complexity in understanding the signals involved in hematopoietic progenitor–stromal cell interactions. Therefore, establishment of a nonstromal cell culture system for B cell development from mES cells would provide more precise and direct knowledge of B cell development.

B lymphocyte development from HPC is a multistep process that involves the ordered expression of intracellular and cell surface marker proteins, and stepwise rearrangement of gene segments in the *Igh* and *L* chain gene loci (8). Progenitor B (pro-B) cells express both CD19 and CD45R on their surface, and pro-B cells differentiate into precursor B (pre-B) cells when they complete VH to DH-JH recombination and begin to express cytoplasmic IgH protein (8). Previous *in vitro* studies demonstrate that B cell development from HPC proceeds in several steps requiring specific cofactors: (i) OP9 stromal cell interactions with HPC (no IL-7), (ii) a combination of OP9 stromal cells and IL-7 exposure, and (iii) IL-7 treatment alone. Our theory proposes that IL-7 is only a support factor in early B cell ontogeny and plays no role in B cell fate determination from HPC.

Transcription factors that play an important role in B cell development included *Pu.1*, Ikaros, E2A, early B cell factor (Ebf), and paired box protein-5 (Pax-5) (9). However, which transcription factors determine the commitment decision in HPC between lymphoid and myeloid fates is not well documented. Dekoter and Singh (10) have established a system for efficient retroviral transduction of murine fetal liver hematopoietic progenitors from *Pu.1* heterozygous (*Pu.1+/-*) and homozygous mutant (*Pu.1-/-*) mice, and find that different levels of *Pu.1* expression in murine fetal liver HPC could affect cell fate determination between the macrophage and B cell lineages; i.e., *Pu.1* protein at a low concentration induced a B cell fate, whereas a high concentration promoted macrophage differentiation and blocked B cell development. *Pu.1* also inhibits erythroid progenitor development by blocking binding of Gata-1 to DNA in mice (11).

We have used small interfering RNA (siRNA) to knock down *Pu.1* expression in CD34+ cells derived from mES cells, and found that *Pu.1* is a repressor of Ebf and Pax-5 expression in HPC, and that reduction of *Pu.1* expression by siRNA in HPC is sufficient for B cell development. We propose that modulating *Pu.1* expression is a powerful method to differentiate B cells from mES cells *in vitro* and that this system should permit a more detailed analysis of the transcriptional regulation of the emergence of this lineage from HPC.

Materials and Methods

**Cells and Reagents.** The D3 ES cells were purchased from American Type Culture Collection. The cytokines murine leukemia inhibitory factor (mLIF), murine (m) IL-3, mL-7, murine granulocyte-macrophage-colony stimulating factor (mGM-CSF), murine stem cell factor (mSCF), and methylcellulose-based ES cell differentiation medium and collagenase were purchased from StemCell Technologies (Vancouver). Rabbit anti-mouse *Pu.1* antibody, goat

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anti-human EBF, and anti-actin antibodies were purchased from Santa Cruz Biotechnology. Rabbit anti-human Pax-5 antibody was purchased from Zymed Laboratories. Oligofectamine was purchased from Invitrogen.

**In Vitro Differentiation of ES Cells.** ES cell differentiation into embryoid bodies (EBs) was carried out as described in our previous report (12). Briefly, ES cell culture was established on 90-mm dishes at 11% methylcellulose, and distributed to four 35-mm bacterial-grade dishes at 37°C. The average number of each colony was harvested for CD19 and CD45R expression analysis by flow cytometry. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The cells were stained with FITC-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies. The CD19, phycoerythrin (PE)-labeled anti-mouse CD43 and allophycocyanin (APC)-labeled anti-mouse CD45R antibodies.

**Generation of Mature Mitogen-Response Ig-Secreting B Lymphocytes.** The individual CFU-pre-B colonies were picked and transferred to six-well plates with mIL-7 and mIL-10 for another 3 weeks and analyzed for CD21 expression by FACS. To demonstrate further the functional capabilities, the in vitro-generated B cells were then cultured with LPS for 3 days (3). CD80, a costimulatory molecule that is normally up-regulated on mature B cells after activation (3), was analyzed by flow cytometry following the LPS exposure. Culture supernatants in LPS-treated cultures were collected for ELISA analysis of IgM (Fig. 1).

**Western Blot Analysis.** Protein was isolated from cultured cells after 72 h of siRNA treatment. *Pu.1* Western blot analysis was performed as described (12). For Ebf and Pax-5 Western blot analysis, 50 µg of protein was separated by SDS/PAGE by using a 10% (wt/vol) polyacrylamide resolving gel and transferred electrophoretically to a nitrocellulose membrane. The blots were blocked with 5% TBS/T buffer for 1 h. Immunoblotting was performed overnight at 4°C by using the Ebf primary antibody (Santa Cruz Biotechnology) at a 1:700 dilution, Pax-5 antibody at 1:500 dilutions, or actin antibody at 1:1,000 dilutions, and the peroxidase-conjugated sec-
ondary antibodies (Amersham Pharmacia). All immunoblots were visualized by ECL reagent according to the manufacturer’s instructions (Amersham Pharmacia Biotech).

**VDJ Recombination Assay.** CD19+/CD43+/CD45R+ cells were sorted from total cells treated with Pu.1 siRNA for 3 days. The genomic DNA was isolated, and VH7183-DJH4 (VDJ) recombination detection was performed as described (14). The VH7183-specific primer was 5'-TGG TGG AGT CTA GGG AGG GCT TA-3' and the 3' JH4 primer was 5'-GGC TCC CTC AGG GAC AAA TAT CCA. The expected size for the VDJH4 product was 0.4 kb.

**FACS Sorting of CD34+ Murine Bone Marrow Cells.** Bone marrow was collected from adult mice, and the CD34+ cell population was isolated by FACS sorting. Sorted cells were then transfected with Pu.1 siRNA or control siRNA, then placed in culture with mSCF. After 72 h, cells were collected for phenotype assay by using B lymphocyte lineage markers (CD19+/CD43+/CD45R+).

**Results**

**Knockdown of Pu.1 Gene Expression in CD34+ EB Cells Induces the Production of CD19+ Cells.** Differentiated ES cells regularly form EBs under specific differentiation conditions. Culture of sorted CD34+ EB cells with mGM-CSF and mIL-3 led to proliferation and differentiation of myeloid cells and inhibition of early B cell development (15). In this study, CD34+ EB cells maintained in culture in the presence of mSCF alone gave rise to a detectable level of CD19 expression in hematopoietic cells when Pu.1 expression was knocked down by Pu.1 siRNA treatment (Fig. 2A and B). Further experiments demonstrated that CD19 expression was detectable in cells derived from CD34+ EB cells cultured with mGM-CSF and mIL-3 when cells were treated with Pu.1 siRNA, but not with control siRNA (Fig. 2B). These CD19+ cells also coexpressed CD45R and CD43 on their surface (Fig. 2B), but not slgM (data not shown). Furthermore, siRNA-mediated reduction in Pu.1 expression was associated with a more robust differentiation of CD34+ HPC to the B lymphocyte lineage than CD34+ HPC cocultured with OP9 cells (Fig. 2 C and D). The CD19+ cells did not coexpress progenitor T cell markers, such as CD25 and CD44 (data not shown), indicating that the siRNA effect was restricted to B lymphoid development. In the CD19+/CD43+/CD45R+ cells, VDJ recombination was detected by PCR (Fig. 2E).

**The Kinetics of Pro-B (CD19+/CD43+/CD45R+) Cell Development in Pu.1 siRNA-Treated CD34+ EB Cells and a Comparison of the Potential for Pro-B Cell Development of These Cells from Different EB Ages.** After Pu.1 siRNA treatment, we found that pro-B cell formation was very low (<5%) on day 1; on day 2, ~20% of cells are pro-B cells; on day 3, the percentage of pro-B cells has been increased to 70%; and it continues to increase slightly till day 5 (Fig. 3A). Our study also reveals that CD34+ EB cells from different age EBs have similar potential for Pro-B cell development under the condition of Pu.1 treatment (Fig. 3B).

The CD19+/CD43+/CD45R+ Cell Population Could Develop into CFU-Pre-B Colonies in Vitro in the Presence of mIL-7 and mIL-10. To examine whether the CD19+/CD43+/CD45R+ cells formed in Pu.1 siRNA-treated CD34+ EB cocultures could form pre-B colonies, we isolated this population by FACS sorting and performed colony-forming assays. CFU-pre-B colonies could form with mIL-7 and mIL-10 stimulation in the culture for 7 days (Fig. 4). Without mIL-7 in the culture, there was no colony formation. Moreover, mIL-10 could increase the frequency of CFU-pre-B colonies primed by mIL-7 compared with mIL-7 administration alone (P < 0.05). In contrast, the CD19-/CD43+/CD45R- cell population had minimal potential to develop to pre-B colonies in the same culture conditions (Fig. 4).
detected by Western blot analysis (Fig. 5).

To determine whether murine Ebf and Pax-5 genes are involved in the increased emergence of CD19⁺ cells from CD34⁺ HPC, whole cell protein was isolated from the cultured cells for Western blot assay. Neither siRNA untreated cells nor cells treated with control siRNA (Lamin A siRNA) expressed Ebf or Pax-5 protein; however, cells treated with Pu.1 siRNA expressed both Ebf and Pax-5 proteins as detected by Western blot analysis (Fig. 5).

**Murine Ebf and Pax-5 Expression Is Induced in CD34⁺ EB Cell Differentiation When Pu.1 Expression Is Knocked Down by siRNA.** To determine whether murine Ebf and Pax-5 genes are involved in the increased emergence of CD19⁺ cells from CD34⁺ HPC, whole cell protein was isolated from the cultured cells for Western blot assay. Neither siRNA untreated cells nor cells treated with control siRNA (Lamin A siRNA) expressed Ebf or Pax-5 protein; however, cells treated with Pu.1 siRNA expressed both Ebf and Pax-5 proteins as detected by Western blot analysis (Fig. 5).

**CFU-Pre-B Cells Develop to Mature B Cells.** To test whether B precursor cells generated from EB cells are able to develop into mature B cells, single CFU-pre-B colonies were picked and transferred to a six-well plate. After 3 weeks of culture with mIL-7 and mIL-10, the pre-B cells differentiated to mature B cells that coexpress IgM and CD19 (Fig. 6A and B). These functional B cells also exhibit phenotypic changes, such as up-regulation of CD21 expression, a marker of mature B cells that was highly expressed (Fig. 6B). We then further examined these cells' response to LPS stimulation. CD80 expression was noticeably up-regulated, and secretion of IgM also increased >5-fold (Fig. 6C and D) when the B cells were cultured with LPS (P < 0.01). Thus, the B lymphoid cells generated from the CD34⁺ EB cells can fully differentiate into mature B cells in the absence of any supportive stromal elements.

**mIL-7 Receptor (mIL-7R) Expression Was Induced When Pu.1 Gene Was Knocked Down by siRNA.** In this study, we found that neither CD34⁺ HPC in mouse bone marrow or CD34⁺ EB cells express the mIL-7R (data not shown). Furthermore, mIL-7R was not expressed in CD34⁺ EB cells after 3 days of culture in which the cells were maintained in the presence of SCF alone. However, mIL-7R expression was induced when Pu.1 gene expression was knocked down by siRNA treatment of the CD34⁺ EB cells. Further experiments revealed that mIL-7R was also induced in the progenitor cell differentiation culture of CD34⁺ EB cells driven by mGM-CSF and mIL-3 when Pu.1 expression was knocked down (Fig. 7).

**Knockdown of Pu.1-Enhanced Pro-B Cell Development Mediated by Cytokines mIL-7, mIL-11, and Murine Flt3-Ligand (mFL).** Early B cell development from HPC can be induced in vitro by several cytokines without stromal cell support. Combinations of mIL-7, mIL-11, and mFL have been reported to induce early B cell development from HPC isolated from mouse fetal liver after 5–10 days (16). We added these cytokines to cultured CD34⁺ cells derived from mES cells. We found that, after 72 h, <5% of cells coexpressed both CD19,
CD34+ cells were treated with Pu.1 siRNA (Fig. 2). Further examination with PCR revealed that these CD19+CD43+CD45R+ cells exhibited VDJ rearrangement, which is a critical marker of pro-B cells. These cells were negative for progenitor T cell markers, such as CD25 and CD44 (data not shown), suggesting that the siRNA effect was specific to B lymphoid development.

Discussion

HPC target gene expression can be efficiently modulated by siRNA treatment in vitro (for a review, see ref. 17). In this article, we described our observation that B cell development was induced when Pu.1 gene expression was knocked down by siRNA treatment in CD34+ EB cells derived from mES cells. Pu.1 levels played a key role in cell fate determination from HPC to pro-B cell differentiation. Up to 90% of cells expressed CD19, CD43, and CD45R when CD34+ cells were treated with control siRNA, but not control siRNA. Representative data from one of three individual experiments are shown.

Knockdown of Pu.1 expression results in mIL-7R expression on CD34+ EB cells (Fig. 2). Further examination with PCR revealed that these CD19+CD43+CD45R+ cells exhibited VDJ rearrangement, which is a critical marker of pro-B cells. These cells were negative for progenitor T cell markers, such as CD25 and CD44 (data not shown), suggesting that the siRNA effect was specific to B lymphoid development.
It is generally agreed that acquisition of cell surface expression of CD19, CD43, and CD45R defines commitment to the B cell lineage (8). To exclude the possibility that isolated CD19 cells were follicular dendritic cells (FDC) (which also express this marker), flow cytometry was performed to examine CD35 expression, which is a specific marker on FDC. CD35 was not expressed on these CD19-expressing cells (data not shown). Thus, these CD19+ cells are B precursors.

mIL-7R expression in CD34 cells is one of the earliest detectable events in B lymphoid development from hematopoietic precursors. In our study, mIL-7R expression could be detected when CD34 cells were also induced to express CD19 after Pu.1 siRNA treatment (Fig. 7). Blocking of mIL-7R expression induced by Pu.1 siRNA treatment by anti-mIL-7R antibody could inhibit the CD19 expression in CD34+-derived progeny (data not shown). Thus, CD19 expression seems to be triggered by endogenous mIL-7/mIL-7R interactions as B lymphoid precursors differentiate from CD34+ HPC. Because the reduction of Pu.1 in CD34+ cells promotes mIL-7R expression in this study, we speculate that constitutive Pu.1 expression in the CD34+ HPC may prevent mIL-7R expression and thus block B cell development. This finding is consistent with other observations in which mIL-7R-mediated signaling is necessary for the development of the earliest B cells (18).

These CD19+ cell populations generated from the CD34+ HPC matured in the presence of LPS and secreted IgM, indicative of B cell maturation. Therefore, our data demonstrate that differentiation of mES cell-derived CD34+ HPC to an early B lymphoid progenitor stage is highly influenced by the level of Pu.1 expression (Figs. 8 and 9). In separate experiments, we also found the same phenomenon using adult murine bone marrow hematopoietic cells. Knockdown of Pu.1 expression in bone marrow CD34+ cells also causes cell commitment to pro-B cells as judged by coexpression of CD19, CD43, and CD45R in cells cultured with either mSCF alone or mGM-CSF plus mIL-3 (data not shown). These data support an interpretation that a low level of Pu.1 expression is a critical factor in the transition of a HPC to a pro-B cell.

Transcription factors play a key role in control of the commitment of progenitors along different lineages. DeKoter and Singh (9) described that low concentrations of Pu.1 protein induced a B cell fate, whereas a high concentration promoted macrophage differentiation and blocked B cell development in fetal liver HPC. Recently, they further reported (19) that transduction of exogenous Ebf into Pu.1+ murine fetal liver progenitors restored early B cell development. The transcription factors Ebf and Pax-5 are essential regulators in early B cell development (20). Ebf can restrict lymphopoiesis to the B cell lineage by blocking development of other lymphoid-derived cell pathways (21). Ebf is an upstream regulator of Pax-5 gene transcription in B cells (22). Pax-5 acts as a traffic signal in the commitment of progenitors. When it is on, hematopoiesis will proceed to the B-lineage; when it is off, the cell commitment is routed to the myeloid and T-lymphoid lineages (22).

We propose that induction of both Ebf and Pax-5 gene expression in CD34+ cells treated with Pu.1 siRNA leads to B cell differentiation. Conversely, constitutive Pu.1 expression leads to the suppression of Ebf and Pax-5 expression, thus preventing HPC commitment to the B cell lineage.

Stromal cells OP9 are frequently required to study B cell ontogeny from lineage uncommitted hematopoietic stem cells or from ES-derived EB cells (23, 24). The disadvantage of this strategy is that the signals required inducing B cell lineage commitment from the stem cells or ES-derived EB cells are unknown. In the present work, we have determined that decreasing the level of Pu.1 expression in combination with mGM-CSF, mIL-3, or mSCF stimulation is sufficient to induce B cell lineage commitment from EB-derived CD34+ cells. Knockdown of Pu.1 is more efficient in inducing B cell lineage commitment than the OP9 coculture system. We propose that this method of siRNA-mediated regulation of transcription factor expression will further promote discovery of the molecular signals regulating B cell lineage development in ES-derived cells and may be applicable to human ES cells, where B cells have been recently reported to emerge from CD34+ hEB cells in OP9 coculture (25).

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