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Analysis of Runx1 Using Induced Gene Ablation Reveals Its Essential Role in Pre-liver HSC Development and Limitations of an In Vivo Approach

Jordi Senserrich,1,3 Antoniana Batsivari,1 Stanislav Rybtsov,1 Sabrina Gordon-Keylock,1 Celine Souilhol,1,4 Frank Buchholz,2 David Hills,1 Suling Zhao,1 and Alexander Medvinsky1,*

1MRC Centre for Regenerative Medicine, University of Edinburgh, Edinburgh EH16 4UH, UK
2Max Planck Institute of Molecular Cell Biology and Genetics, Technische Universität Dresden, Dresden 01307, Germany
3Present address: Institut d’Investigació Biomèdica de Bellvitge (IDIBELL), Barcelona 08908, Spain
4Present address: Department of Infection, Immunity & Cardiovascular Disease, University of Sheffield, Sheffield S10 2RX, UK
*Correspondence: a.medvinsky@ed.ac.uk
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SUMMARY

Hematopoietic stem cells (HSCs) develop in the embryonic aorta-gonad-mesonephros (AGM) region and subsequently relocate to fetal liver. Runx1 transcription factor is essential for HSC development, but is largely dispensable for adult HSCs. Here, we studied tamoxifen-inducible Runx1 inactivation in vivo. Induction at pre-liver stages (up to embryonic day 10.5) reduced erythromyeloid progenitor numbers, but surprisingly did not block the appearance of Runx1-null HSCs in liver. By contrast, ex vivo analysis showed an absolute Runx1 dependency of HSC development in the AGM region. We found that, contrary to current beliefs, significant Cre-inducing tamoxifen activity persists in mouse blood for at least 72 hr after injection. This deferred recombination can hit healthy HSCs, which escaped early Runx1 ablation and resulted in appearance of Runx1-null HSCs in liver. Such extended recombination activity in vivo is a potential source of misinterpretation, particularly in analysis of dynamic developmental processes during embryogenesis.

INTRODUCTION

In the mouse, the first transient hematopoietic waves (primitive erythroid and erythromyeloid progenitors [EMPs]) emerge extra-embryonically in the early yolk (McGrath et al., 2015; Paliis et al., 1999). HSCs, which give rise to the adult hematopoietic system, appear only by mid-gestation intra-embryonically within the aorta-gonad-mesonephros (AGM) region (Ciau-Uitz et al., 2016; Medvinsky and Dzierzak, 1996; Medvinsky et al., 1993; Muller et al., 1994). HSCs emerge predominantly from the endothelial floor of the dorsal aorta (de Bruijn et al., 2002; North et al., 2002; Taoudi and Medvinsky, 2007) through a maturation process defined by induc­tive interactions within the AGM region (Fitch et al., 2012; Souilhol et al., 2016a) and signals from somites (Clements et al., 2011; Lee et al., 2014; Pouget et al., 2014). The origin of HSCs from aortic endothelium is supported by strong evidence in non-mammalian vertebrates and in humans (Bertrand et al., 2010; Ivanovs et al., 2014; Kissa and Herboldel, 2010).

Various signaling pathways are involved in early hematopoietic development (reviewed in Ciau-Uitz et al., 2016). HSC maturation in the mouse is a multistep process driven by SCF and IL3 (Robin et al., 2006; Rybtsov et al., 2011, 2014), accompanied by temporal changing signaling requirements for Notch, Shh, and Bmp (Gama-Norton et al., 2015; Lizama et al., 2015; Peeters et al., 2009; Richard et al., 2013; Souilhol et al., 2016a, 2016b). It is reasonable to assume that exact transcription factor machinery also attunes. Here we aimed to explore temporal requirements for Runx1, a transcription factor essential for HSC development, but which is far less significant in adult bone marrow HSCs (Cai et al., 2011; North et al., 1999; Okuda et al., 1996; Putz et al., 2006). EMPs and HSCs originate from different endothelial subsets through a Runx1-dependent process (Chen et al., 2011; Eliades et al., 2016; Lie et al., 2018). Conditional Runx1 ablation in vivo blocks the endothelial to EMP/HSC transition prior to liver colonization (Chen et al., 2009). More detailed analysis using a robust AGM explant system recapitulating HSC development, showed that, up to embryonic day 11.5 (E11.5) (immediately prior to fetal liver colonization), HSC development absolutely depends on Runx1, but EMPs become Runx1 independent at earlier stages (Tober et al., 2013).

Here we followed the consequences of induced Runx1 ablation in the AGM region on HSC development in the fetal liver. We used a tamoxifen (4-OHT)-inducible Cre-ERT2 system to delete Runx1 and assessed the presence of EMPs and definitive HSCs in the E13.5 fetal liver. We observed a significant reduction of EMP numbers, but, contrary to our expectations and in apparent discrepancy with a previous report (Tober et al., 2013), we detected significant numbers of Runx1-null HSCs in the liver, implying that HSC development in the AGM region does not require Runx1. We then performed in vivo injections of 4-OHT, but in this case isolated E11.5 AGM regions and after culture transplanted them into irradiated recipients. We found no Runx1-null HSCs in repopulated irradiated recipients, which is in conflict with results of in vivo analysis.
Rosa26Cre$^{ERT2}$::sGFP::Runx1$^{fl/fl}$

B

<table>
<thead>
<tr>
<th></th>
<th>ipE8.5 -&gt; E13.5</th>
<th>ipE10.5 -&gt; E13.5</th>
<th>ipE9.5 -&gt; E13.5</th>
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<tbody>
<tr>
<td>EMPs/ee</td>
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<tr>
<td>Tam</td>
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</tr>
<tr>
<td>Runx1$^{wt/fl}$</td>
<td></td>
<td></td>
<td>Runx1$^{fl/fl}$</td>
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<td></td>
<td>%Δ/Δ</td>
<td>%fl/Δ</td>
<td>%fl/fl</td>
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<tr>
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<th>Runx1$^{fl/fl}$</th>
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<td>ipE9.5</td>
<td>Δ fl</td>
<td>Δ fl</td>
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<tr>
<td>ipE10.5</td>
<td>Δ fl</td>
<td>Δ fl</td>
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(legend on next page)
In search of an explanation, we tested how long 4-OHT or/and its active derivatives (cumulatively termed here 4-OHT/Der) remain in the circulation of adult mouse and found that, at least 3 days after injection, concentration of 4-OHT/Der in the peripheral blood of the animal remains sufficient to cause significant (up to 20%) Cre-mediated recombination in cells. Therefore, those HSCs, which have not recombined during the AGM stage could proceed with development, but could be hit by recombination later when Runx1 is no longer essential. This would inevitably lead to emergence of functionally active Runx1-null HSCs in the fetal liver. Such a problem does not exist when the AGM region is removed from the mouse and explanted in fresh culture medium free of 4-OHT/Der.

Thus, despite the advantages of in vivo analysis in principle, poor control over in utero development may bring about a significant uncertainty and cause misinterpretation of results. By contrast, the functionally validated and robustly controlled ex vivo system provides strong evidence for the essential role of Runx1 in HSC development, in keeping with previously published results.

RESULTS

4-OHT-Induced Runx1 Ablation at E8.5–E9.5, but Not Thereafter, Reduces EMP Formation

Here, we studied effects of in vivo-induced stage-specific Runx1 ablation on the appearance of EMPs in fetal liver. To this end, pregnant [Rosa26CreERT2::sGFP::Runx1wt/fl] females crossed with [Rosa26CreERT2::sGFP::Runx1fl/fl] males were treated with a single dose of 4-OHT between 8.5 and 10.5 days of gestation at a concentration of 2 mg/mouse. E13.5 livers containing both homozygous Runx1wt/wt and heterozygous Runx1wt/fl (control) embryos were harvested, and cell suspensions prepared from individual livers were analyzed in methylcellulose colony-forming unit (CFU) assays (Figure 1A). In homozygous Runx1fl/fl embryos ([Rosa26CreERT2::sGFP::Runx1fl/fl]), 4-OHT injections at E8.5 or E9.5 led to a significant reduction of fetal liver EMPs by ~50% compared with Runx1wt/wt heterozygous [Rosa26CreERT2::sGFP::Runx1wt/fl] controls (Figure 1B, blue and red bars). However, 4-OHT injection at later stage (E10.5) had no effect on EMPs in fetal livers (Figure 1B, green bars), indicating the essential role of Runx1 in EMP development at early stages but not after E10.5. This result is in agreement with temporal Runx1 dependency in embryonic EMPs reported previously (Tober et al., 2013).

To confirm this conclusion, we tested the status of Runx1 loci in individual fetal liver EMPs using PCR. We picked only liver-derived methylcellulose colonies expressing GFP, indicative of prior activity of Cre-recombinase. Due to their clonal origin, PCR analysis of individual CFU colonies reveals the Runx1 status of individual EMPs. We found that a fraction of tested colonies (20%–36%) escaped any Runx1 recombination despite activation of GFP (Figures 1B right, 1C, and S1A; Table 1). The recombined fraction (64%–80%) contained those colonies that retained one intact Runx1 allele (Runx1fl/fl) or had both loci recombined (Runx1fl/fl). Of note, 4-OHT injection at E8.5, E9.5, and E10.5 resulted in progressive growth of the proportion of Runx1fl/fl EMPs in the FL (11%, 25%, and 47%, respectively) (Figures 1B right and 1C; Table 1). A particularly high fraction of Runx1fl/fl EMPs was observed after 4-OHT injection at E10.5, when no reduction of EMP numbers was observed. All together this implies progressive acquisition of Runx1 independence by EMPs during development, in line with a previous report (Tober et al., 2013).

Induced Runx1 Ablation from E9.5 onward Does Not Eliminate HSC Development in the Fetal Liver

We tested whether a single 4-OHT injection between E8.5 and E10.5 would block HSC development in vivo. After injection, embryos continued development in utero until E13.5. Cells from individual E13.5 fetal livers were then isolated and transplanted separately into irradiated recipients, as depicted in (Figure 2A). To our surprise, robust multilineage donor-derived long-term engraftment was observed in all 37 recipient animals, regardless of injection time (Figure 2B, left, and data not shown). Cre activity in these experiments was very efficient as seen by the presence of a large GFP+ cell fraction in most recipients (ranging from 85% to 97%, Figure S2).

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Figure 1. Tamoxifen (4-OHT)-Induced Runx1 Ablation at E8.5–E9.5, but Not Thereafter, Reduces EMP Formation

(A) Experimental design: studying the effect of conditional Runx1 deletion on EMPs. A single dose of 4-OHT was administered intraperitoneally (i.p.) to [Rosa26CreERT2::sGFP::Runx1fl/fl] pregnant females crossed with [Rosa26CreERT2::sGFP::Runx1wt/fl] males at E8.5–E10.5. E13.5 embryos were collected and EMPs from individual FLs quantified by clonogenic methylcellulose assays. A representative 4-OHT-induced E13.5 GFP+ embryo is shown.

(B) Left: numbers of E13.5 FL EMPs per embryo equivalent (e.e.). Time of i.p. injection indicated for, e.g., as IpE8.5. Mean values and standard errors are shown (three independent experiments, at least three embryos in each experiment). Unpaired Student t statistical tests were performed (**p = 0.001; ***p = 0.0002). Right: Runx1 recombination in [Rosa26CreERT2::sGFP::Runx1fl/fl] E13.5 FL erythromyeloid progenitors after 4-OHT injection at pre-liver stages, indicating the percentage of each genotype (at least two independent experiments; mean values and standard errors shown).

(C) Representative Runx1 genotyping PCR gels of EMP colonies, showing wt, fl, and Δ bands.
Since Cre-mediated GFP activation does not guarantee Runx1 recombination in the same cells, the recombination status of Runx1 was verified using PCR. To this end, individual donor-derived GFP+ colonies obtained from blood and bone marrow of long-term (16 weeks) reconstituted animals were analyzed by PCR (Figures 2B right, 2C, and S1B; Table 2). When 4-OHT was injected at E8.5, all but one GFP+ donor-derived methylcellulose colonies obtained cumulatively from 18 recipients contained at least one functional Runx1 allele, indicating that Runx1D/D HSCs did not develop. However, injection at E9.5 gave a significant proportion of donor-derived Runx1D/D colonies (17%) in 13 repopulated recipients. Injection at E10.5 resulted in further increase (33%) of Runx1D/D donor-derived colonies obtained from long-term transplanted animals (a total of six recipients were analyzed) (Figures 2B right and 2C; Table 2).

Taken alone, these results suggest that Runx1 is not required for HSC development from as early as E9.5, which contradicts the previous report showing Runx1 dependency of HSC development up to E11.5 (Tober et al., 2013). We investigated reasons for this discrepancy as described below.

Active Concentrations of 4-OHT or/and Its Derivatives Persist in the Mouse for No Less than 72 hr

We reasoned that if, after 4-OHT injection, recombination does not occur in all cells at once and 4-OHT activity continues further, HSCs (known to become Runx1 independent when fully mature) may undergo late Runx1 ablation without adverse consequences. Upon transplantation, such Runx1-null HSCs could be generating Runx1<sup>D/D</sup> progeny detectable in the methylcellulose assay.

To investigate this possibility, we tested how long 4-OHT/Der persists in the mouse and causes recombination. To this end, wild-type C57BL/6 adult females were intraperitoneally injected with 4-OHT, and serum obtained at different time points after injection was added to cultures of primary AGM cells isolated from E10.5 and E11.5 [RosaCreERT2::sGFP] embryos (Gilchrist et al., 2003) (Figure 3A). We observed maximum recombination efficiency (100% GFP activation) using serum obtained 5 hr after 4-OHT administration. Nevertheless, serum collected after 48 and 72 hr could also cause 20%–40% recombination (Figure 3B). Specifically, 72 hr serum caused 52% ± 8.7% recombination in CD45+ cells, 16% ± 7.6% in VE-Cad+ cells, and 26% ± 13.2% in stromal cells (CD45-/VE-Cad–) (data not shown). (Note that recombination in non-hematopoietic cells is underestimated due to known mosaicism of GFP expression in non-hematopoietic cells in these mice [Gilchrist et al., 2003]).

These experiments show that, after injection of 4-OHT, cells in the mouse containing loxP sites can recombine over a period of at least 3 days. Thus, those cells in the embryo which have not undergone rapid Cre-mediated recombination of the Runx1<sup>lox</sup> allele continue to be exposed to 4-OHT/Der and can recombine, even 3 days after 4-OHT injection.

The extended circulation of 4-OHT/Der in vivo creates uncertainty as to when exactly during development Runx1 becomes dispensable for HSC development. The next set of experiments was designed to control and reduce the duration of HSC exposure to 4-OHT/Der to obtain more interpretable results.

Runx1 Deletion at E9.5 Abrogates HSC Activity in the E11.5 AGM Region

To avoid prolonged exposure to 4-OHT/Der, we switched from the entirely in vivo design to experiments incorporating a highly controllable in vitro HSC maturation system (Rybtsov et al., 2011, 2014; Taoudi et al., 2008). As in previous setups, embryos for these experiments contained either

<table>
<thead>
<tr>
<th>Experiment</th>
<th>Embryo Genotype</th>
<th>CFU-Cs in E13.5 FL</th>
<th>Total Colonies Analyzed</th>
</tr>
</thead>
<tbody>
<tr>
<td>iE8.5 -&gt; E13.5 FL</td>
<td>R26CreERT2::Runx1&lt;sup&gt;wt/Δ&lt;/sup&gt;</td>
<td>9/9 (11%–42%)</td>
<td>111</td>
</tr>
<tr>
<td></td>
<td>R26CreERT2::Runx1&lt;sup&gt;Δ/Δ&lt;/sup&gt;</td>
<td>12/13 (17%–86%)</td>
<td>159</td>
</tr>
<tr>
<td>iE9.5 -&gt; E13.5 FL</td>
<td>R26CreERT2::Runx1&lt;sup&gt;Δ/Δ&lt;/sup&gt;</td>
<td>7/7 (8%–58%)</td>
<td>85</td>
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<tr>
<td></td>
<td>R26CreERT2::Runx1&lt;sup&gt;Δ/Δ&lt;/sup&gt;</td>
<td>13/13 (14%–80%)</td>
<td>134</td>
</tr>
<tr>
<td>iE10.5 -&gt; E13.5 FL</td>
<td>R26CreERT2::Runx1&lt;sup&gt;Δ/Δ&lt;/sup&gt;</td>
<td>5/6 (33%–100%)</td>
<td>36</td>
</tr>
<tr>
<td></td>
<td>R26CreERT2::Runx1&lt;sup&gt;Δ/Δ&lt;/sup&gt;</td>
<td>10/12 (20%–80%)</td>
<td>60</td>
</tr>
</tbody>
</table>

Recombination range refers to proportion of recombined colonies.

Table 1. Runx1 Status of E13.5 Fetal Liver GFP+ Erythromyeloid Progenitors (CFU-Cs) Derived from Individual Embryos after 4-OHT Injection at Pre-liver Stages
Figure 2. Induced Runx1 Ablation from E9.5 onward Does not Eliminate HSC Development in the Fetal Liver

(A) Experimental design analogous to that described in Figure 1A, with cell suspensions from individual E13.5 FL embryos transplanted into irradiated adult mice.

(B) Left: donor-derived contribution in recipient mice blood 16 weeks after transplantation is shown. Each point represents an individual recipient mouse, representing data from at least two independent experiments. Numbers of analyzed mice for Runx1wt/fl 4-OH-T series (legend continued on next page).

(C) Runx1 genotypes for donor cells in blood.
both or one conditional Runx1 allele (Runx1fl/fl and Runx1wt/fl, respectively). 4-OHT was administered in vivo at E9.5 as described previously; but, instead of allowing the embryos develop in utero until E13.5, E11.5 AGM regions were dissected and individually explanted (Medvinsky and Dzierzak, 1996). Placement of the AGM region in fresh culture medium ends the exposure of developing HSCs to 4-OHT/Der. After 4 days in culture, AGM cells were transplanted into irradiated recipients (Figure 4A). Twelve recipients transplanted with control [Rosa26CreERT2::sGFP::Runx1wt/fl] AGM cells showed high-level, long-term multilineage donor-derived engraftment. Fourteen of 16 recipients transplanted with [Rosa26CreERT2::sGFP::Runx1fl/fl] AGM cells were also repopulated at high level (only one showed low-level donor-derived chimerism and one lacked engraftment) (Figure 4B). We observed highly efficient GFP recombination in [Rosa26CreERT2::sGFP::Runx1wt/fl] and [Rosa26CreERT2::sGFP::Runx1fl/fl] repopulated cells (98% and 89%, respectively) (Figure S3). However, analysis of methylcellulose colonies obtained from these 14 long-term repopulated mice showed that, by contrast to liver, [Rosa26CreERT2::sGFP::Runx1fl/fl] AGM region transplants contained no Runx1D/D HSCs (repopulated mice gave no Runx1D/D myeloid colonies) (Figure 4C; Table 3), indicating an absolute requirement of Runx1 for HSC development prior to liver colonization. Of note, variance in efficiency of recombination suggests a considerable difference in accessibility of loxP sites for Cre-mediated recombination between GFP and Runx1 loci.

### DISCUSSION

During maturation, pre-HSCs undergo massive expansion in the AGM region, sequentially upregulating hematopoietic CD41, CD43, and CD45, and some other markers (Boisset et al., 2015; Ferkowicz et al., 2003; Rybtsov et al., 2011, 2014, 2016; Taoudi et al., 2008; Tober et al., 2018; Zhou et al., 2016). This stepwise developmental process is driven by dynamic gene actions. Temporal requirements for genes driving HSC development can vary, and accurate staging of gene involvement is essential for understanding this process. For example, acquisition of adult phenotype is accompanied by gradual loss of Notch, Shh, and Bmp dependency by HSCs in the AGM region (Gama-Norton et al., 2015; Lizama et al., 2015; Peeters et al., 2009; Richard et al., 2013; Souilhol et al., 2016a, 2016b).

Runx1 is a key transcription factor involved in EMP and HSC development (Cai et al., 2000; Chen et al., 2009; North et al., 2002; Okuda et al., 1996). However, exact action points of Runx1 during this multistep process require clarification. Initial hematopoietic specification associated with upregulation of CD41 does not require Runx1 (Liakhovitskai et al., 2014). Runx1 sensitivity of the embryonic endothelium is limited to the period around E7.5–E8.5 (Tanaka et al., 2012; Yzaguirre et al., 2018). Induced stage-specific inactivation using explant cultures followed by long-term transplantations showed that, up to E11.5, Runx1 is absolutely required for HSC development but becomes dispensable after that (Tober et al., 2013). Here we

### Table 2. Runx1 Status of E13.5 Fetal Liver HSCs Assessed by PCR Analysis of Donor-Derived GFP+ Erythromyeloid Progenitors from Long-Term Engrafted Recipients

<table>
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<tr>
<th>Experiment</th>
<th>Embryo Genotype</th>
<th>Embryos with Runx1 Recombined Alleles/Total Embryos (Recombination Range)</th>
<th>Total Colonies Analyzed</th>
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<td>iE8.5 -&gt; E13.5 FL</td>
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<td>33</td>
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<td>R26CreERT2::Runx1fl/fl</td>
<td>8/11 (33%–100%)</td>
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<td>iE9.5 -&gt; E13.5 FL</td>
<td>R26CreERT2::Runx1wt/fl</td>
<td>5/5 (6%–55%)</td>
<td>63</td>
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<td>R26CreERT2::Runx1fl/fl</td>
<td>8/8 (18%–80%)</td>
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<td>iE10.5 -&gt; E13.5 FL</td>
<td>R26CreERT2::Runx1wt/fl</td>
<td>2/3 (71%–100%)</td>
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<td>R26CreERT2::Runx1fl/fl</td>
<td>3/3 (31%–54%)</td>
<td>52</td>
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Recombination range refers to proportion of recombined colonies.

(ipE8.5, ipE9.5, and ipE10.5) were 6, 10, and 10, respectively; for Runx1fl/fl + 4-OH-T series (ipE8.5, ipE9.5, and ipE10.5) were 18, 13, and 6, respectively. Right: Runx1 status of [Rosa26CreERT2::sGFP::Runx1fl/fl] E13.5 FL HSCs, assessed by analysis of donor-derived erythromyeloid progenitors from long-term (16 weeks) engrafted recipients. Percentages of each genotype (at least two independent experiments; mean values and standard errors) are shown.

(C) Representative Runx1 genotyping PCR gels of HSC-derived progenitors, indicating wt, fl, and Δ bands, are shown.
explored whether the conclusions of this study can be corroborated by in vivo tracking.

To this end, we injected pregnant females with 4-OHT during active EMP/HSC formation. Instead of analysis of E11.5 AGM explants (Tober et al., 2013), we followed HSC development in utero up to E13.5 in the fetal liver. Injections at E8.5/E9.5, but not at E10.5, reduced EMP numbers in the E13.5 liver, indicating that by this stage EMPs become Runx1 independent, which was corroborated by increased emergence of Runx1/D, in agreement with previously reported results (Tober et al., 2013).

We then focused on the HSC development. After a single 4-OHT injection at E8.5, E9.5, or E10.5, the embryos were allowed to develop in utero up to E13.5, after which fetal liver cells were transplanted into irradiated recipients. Unexpectedly, all long-term repopulated animals (transplanted with E9.5 cells onward) contained Runx1-null HSCs, in apparent contradiction with previous data obtained in AGM cultures (Tober et al., 2013).

We then reasoned that in vivo results might depend on the persistence of 4-OHT/ Der activity in the mouse. Indeed, 4-OHT injections at E8.5/E9.5 yielded non-recombined (Runx1/D) and partly recombined (Runx1/D) HSCs. If 4-OHT/Der persisted in the mouse beyond E11.5 stage (when HSCs become Runx1 independent), delayed recombination could transform non-recombined (Runx1/D) and partly recombined (Runx1/D) HSCs into Runx1/D HSCs without adverse effect. Indeed, we found that substantial 4-OHT/Der activity, capable of inducing CRE-ERT2, persists in the mouse for at least 3 days, introducing major uncertainty as to when exactly recombination took place and making in vivo experiments poorly interpretable. Crucially, under highly controlled experimental conditions, where after a single 4-OHT injection at E9.5, E11.5 AGM regions

Figure 3. Active Concentrations of 4-OHT or/and Its Derivatives Remain in the Mouse for No Less than 72 hr
(A) Experimental schematics: wild-type C57BL/6 adult females were intraperitoneally injected with 4-OHT and serum obtained at different time points after injection. Then, it was added to cultures of primary E10.5 and E11.5 [RosaCreERT2::sGFP] AGM cells, and recombination was assessed by monitoring GFP expression by fluorescence-activated cell sorting after 24 hr.
(B) GFP recombination in AGM cells upon incubation with serum isolated at different time points (0, 5, 20, 48, and 72 hr) after 4-OH-tamoxifen intraperitoneal injection (at least two independent experiments; three mice/experiment; mean values and standard errors are shown).
were isolated and cultured in fresh medium free of 4-OHT/Der, subsequent transplantations showed complete ablation of Runx1-null HSCs. This result points to a critical role for Runx1 in HSC development in the AGM region before colonization of the fetal liver, in agreement with a previous report (Tober et al., 2013).

Interestingly, although we observed near 100% recombination of the GFP transgene, the efficiency of Runx1 recombination was significantly lower, emphasizing that accessibility of loxP sites in various genetic loci further confounds interpretation of in vivo results. Our recent study exploring the role of Notch in HSC development (Souilhol et al., 2016b) failed to obtain any useful data using in-utero-induced gene ablation due to the highly resistant nature of the floxed Rbpj allele (our unpublished data).

In summary, our current study shows a crucial role for Runx1 in HSC development in the AGM region prior to liver colonization, and emphasizes the value of in vitro models recapitulating developmental processes. Although studying biological processes in vivo is undeniably important, experiments involving induced gene modifications to analyze dynamic developmental processes in utero can incur major uncertainties. We believe that recapitulation of developmental processes in vitro using highly controlled conditions, supported by functional validation, will continue to play an important role in various areas of developmental biology.

**EXPERIMENTAL PROCEDURES**

**Mice**

All transgenic mice used to generate embryos and adult mice were on the C57BL/6 (CD45.2/2) background. Rosa26CreER<T2::Runx1<sup>fl/fl</sup> and Rosa26CreER<T2::sGFP::Runx1<sup>fl/fl</sup> mice were used to obtain Rosa26CreER<T2::sGFP::Runx1<sup>fl/fl</sup> conditional knockout and Rosa26CreER<T2::sGFP::Runx1<sup>fl/fl</sup> control embryos. The morning of discovery of the vaginal plug was designated as day 0.5. E11.5 embryos were harvested at E11.5. AGM regions were dissected and cultured as explants for 4 days, and cell suspensions from individual explants were transplanted into irradiated adult mice.

**E11.5 AGM Explant Culture**

AGM regions were dissected from E11.5 embryos and incubated for 2 hr at 37°C and 5% CO<sub>2</sub> in IMDM medium (Invitrogen).
supplemented with 20% fetal calf serum (FCS) (HyClone, Fisher Scientific), L-glutamine (L-Gln), and penicillin/streptomycin (P/S). AGM regions were transferred individually onto 0.8 μm mixed cellulose MF membranes (AAWP02500, Millipore) for 5–7 days (37°C, 5% CO2) and cultured at the liquid-gas interface with IMDM medium consisting of 20% FCS, L-Gln, P/S IMDM, and growth factors (interleukin-3, SCF, and FLT3L, 100 ng/mL each; all from PeproTech). After 4 days of culture, explants were dissociated by enzymatic digestion (collagenase/dispace in PBS containing CaCl2 and MgCl2). Methylcellulose CFU-C and long-term repopulation assays were subsequently performed.

Hematopoietic Clonogenic Progenitor (CFU-C) and Colony Genotyping

Cell suspensions from either fresh or cultured embryonic tissues were plated into semi-solid Methocult M3434 medium (StemCell Technologies). After 7–12 days of culture, CFU-C colonies were scored and recombination in the Runx1 locus analyzed by PCR. In brief, colonies were individually transferred into 50 μL of lysis buffer, incubated for 1 hr at 56°C followed by 5 min at 95°C. Runx1wt (251 bp), Runx1fl (325 bp), and Runx1Δ (382 bp) products were amplified by simultaneously using the primers 5'-TAGGGAGTGCTGCTTGCTCT-3' and 5'-GCCGGGTGCAA. ATTAAAGTC-3', and P7 (5'-CTCTGGGAAACCAGGGAGTG-3'), under the following PCR conditions: 94°C 5 min; [94°C 30 s; 60°C 30 s; 72°C 1 min] × 35 cycles; 72°C 10 min.

Long-Term Hematopoietic Repopulation Assays

Cell suspensions from embryos at different stages were injected into irradiated adult recipients (CD45.1/2) either directly (E13.5 FL, 0.2 embryo equivalents per recipient mouse) or after explant culture (E11.5 AGM, 0.1 embryo equivalents per recipient mouse), along with 80,000 CD45.1/2 bone marrow carrier cells. Recipients were irradiated by split dose (472 + 472 rad with 3-hr interval) of γ irradiation. Donor-derived chimerism was monitored in blood at 6 and 16 weeks after transplantation using FACScalibur (BD). Peripheral blood was collected by bleeding the lateral tail vein into 500 μL 5 mM EDTA/PBS, and erythrocytes were depleted using PharM Lyse (BD). Cells were stained with anti-CD16/32 (Fc-block, cat. no. 16-0161-86), CD45.1-APC (clone A20, cat. no. 17-0453-82), and anti-CD45.2-PE (clone 104, cat. no. 12-0454-83) monoclonal antibodies (eBioscence). Appropriate isotype controls were used. Dead cells were excluded using 7AAD (eBioscence).

Mice demonstrating ≥5% donor-derived multilineage chimerism after 8 weeks were considered to be reconstituted.

Intraperitoneal Injections

Rosa26CreERT2::sGFP::Runx1wt/fl and Rosa26CreERT2::sGFP::Runx1fl/fl embryos were induced in vivo by intraperitoneal injection of 2 mg 4-OHT (Sigma) into Rosa26CreERT2::sGFP::Runx1wt/fl x Rosa26 CreERT2::sGFP::Runx1fl/fl pregnant females. 4-OHT was prepared in 100% ethanol, diluted 1:10 in corn oil. Embryos were allowed to develop in utero up to E11.5 or E13.5 before harvesting tissues for analysis by CFU-C, flow cytometry, and repopulation assays.

Testing Persistence of 4-OHT in Peripheral Blood of Adult Mice

C57BL/6 females were injected with 4-OHT as described above. Peripheral blood was collected by submandibular bleeding before 4-OHT injection (0 hr), 5, 20, 48, and 72 hr following injection. After centrifugation (400 x g/5 min), serum was collected and additionally centrifuged (400 x g/5 min) to remove remaining blood cells. Serum was frozen at −80°C and used at the same time in two independent sets of experiments. Total E10-11 AGM cells cultured for 24 hr in IMDM + 50% mouse serum were collected and analyzed by flow cytometry for GFP expression (dead cells were excluded by 7AAD). In some cases the cells were stained for CD45-PE (Pharmingen, cat. no. 553081) and VE-Cadherin-AlexaFluor-647 (eBioscence, cat. no. 51-1441-82; 138006).

SUPPLEMENTAL INFORMATION

Supplemental Information includes three figures and can be found with this article online at https://doi.org/10.1016/j.stemcr.2018.08.004.

AUTHOR CONTRIBUTIONS


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Table 3. Runx1 Genotype of E11.5 AGM Explant HSCs Assessed by PCR Analysis of Donor-Derived GFP+ Erythromyeloid Progenitors from Long-Term Engrafted Recipients

<table>
<thead>
<tr>
<th>Experiment</th>
<th>Embryo Genotype</th>
<th>Embryos with Runx1 Recombined Alleles/Total Embryos (Recombination Range)</th>
<th>Total Colonies Analyzed</th>
</tr>
</thead>
<tbody>
<tr>
<td>iE9.5 -&gt; E13.5 FL</td>
<td>R26CreERT2::Runx1wt/fl</td>
<td>4/6 (11%–43%)</td>
<td>71</td>
</tr>
<tr>
<td>R26CreERT2::Runx1fl/fl</td>
<td>10/12 (14%–64%)</td>
<td>127</td>
<td></td>
</tr>
</tbody>
</table>

Table 3. Runx1 Genotype of E11.5 AGM Explant HSCs Assessed by PCR Analysis of Donor-Derived GFP+ Erythromyeloid Progenitors from Long-Term Engrafted Recipients

Recombination range refers to proportion of recombined colonies. NA, not applicable.
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REFERENCES


