Hemogenic endothelium specification and hematopoietic stem cell maintenance employ distinct Scl isoforms

Fenghua Zhen1*, Yahui Lan1*, Bo Yan1, Wenging Zhang2‡ and Zilong Wen1‡

SUMMARY
Recent studies have shown that nascent hematopoietic stem cells (HSCs) derive directly from the ventral aortic endothelium (VAE) via endothelial to hematopoietic transition (EHT). However, whether EHT initiates from a random or predetermined subpopulation of VAE, as well as the molecular mechanism underlying this process, remain unclear. We previously reported that different zebrafish stem cell leukemia (scl) isoforms are differentially required for HSC formation in the ventral wall of the dorsal aorta. However, the exact stage at which these isoforms impact HSC development was not defined. Here, using in vivo time-lapse imaging of scl isoform-specific reporter transgenic zebrafish lines, we show that prior to EHT scl-β is selectively expressed in hemogenic endothelial cells, a unique subset of VAE cells possessing hemogenic potential, whereas scl-α is expressed later in nascent HSCs as they egress from VAE cells. In accordance with their expression, loss-of-function studies coupled with in vivo imaging analysis reveal that scl-β acts earlier to specify hemogenic endothelium, which is later transformed by runx1 into HSCs. Our results also reveal a previously unexpected role of scl-α in maintaining newly born HSCs in the aorta-gonads-mesonephros. Thus, our data suggest that a defined hemogenic endothelial population preset by scl-β supports the deterministic emergence of HSCs, and unravel the cellular mechanisms by which scl isoforms regulate HSC development.

KEY WORDS: Zebrafish, Scl, Tal1, Hemogenic endothelium, Hematopoietic stem cells

INTRODUCTION
The formation of multipotent hematopoietic stem cells (HSCs) during development is crucial for the establishment of the blood system (Orkin and Zon, 2008). Understanding the developmental pathway through which HSCs arise and the associated molecular mechanisms would therefore provide new insights into stem cell biology and HSC-based regenerative therapies. Recent studies on cultured mouse mesoderm cells or isolated hemangioblasts have shown that the first pool of HSCs is directly initiated from endothelial cells through a specialized intermediate, termed the hemogenic endothelium, without apparent cell division (Eilken et al., 2009; Lancrin et al., 2009). These observations are supported by in vivo time-lapse confocal imaging that has captured the emergence of HSCs from the ventral aortic endothelial (VAE) cells through an endothelial to hematopoietic transition (EHT) in mouse aorta explants and in intact zebrafish embryos (Bertrand et al., 2010; Boisset et al., 2010; Kissa and Herbomel, 2010; Lam et al., 2010). Yet, whether EHT initiates stochastically from the uniform endothelial cells or deterministically from a specialized hemogenic endothelial population is not known. After EHT, the nascent HSCs either form intra-arterial clusters (mouse) or remain in the subaortic mesenchymal region (zebrafish) before they are released into the circulation to colonize downstream hematopoietic organs (Kissa et al., 2008; Bertrand et al., 2010; Kissa and Herbomel, 2010; Lam et al., 2010). The molecular control over the post-EHT development of HSCs in the aorta-gonads-mesonephros (AGM) remains largely unexplored, with only one study showing the extrinsic regulation of AGM HSC proliferation by II-3 (Robin et al., 2006).

The basic helix-loop-helix transcription factor stem cell leukemia (SCL, also known as TAL1) is a crucial regulator of both primitive and definitive hematopoiesis in teleosts and mammals (Robb et al., 1995; Shivdasani et al., 1995; Porcher et al., 1996; Robb et al., 1996; Dooley et al., 2005; Patterson et al., 2005). The expression of SCL is highly enriched in hematopoietic and endothelial cells, as well as in the central nervous system (Green et al., 1991; Green et al., 1992; Hwang et al., 1993; Kallianpur et al., 1994; Gering et al., 1998; Zhang and Rodaway, 2007). Loss-of-function of SCL impairs yolk sac hematopoiesis (Robb et al., 1995; Shivdasani et al., 1995), HSC formation and subsequent hematopoietic lineage differentiation (Porcher et al., 1996; Robb et al., 1996), as well as the vascular remodeling of the yolk sac endothelium (Visvader et al., 1998). In zebrafish, scl has been shown to play a similar role in regulating primitive hematopoiesis, HSC development and dorsal aorta formation (Dooley et al., 2005; Patterson et al., 2005). Recent studies have identified multiple scl isoforms: the full-length scl-α isoform and the N-terminal-truncated scl-β isoform. It was found that scl-β is essential whereas scl-α is dispensable for HSC generation in the ventral wall of the dorsal aorta (VDA) (Qian et al., 2007; Ren et al., 2010), which is the zebrafish equivalent of the AGM (the term AGM will be used hereafter) (Burns et al., 2005; Gering and Patient, 2005; Murayama et al., 2010). Despite the demonstration of a differential requirement for scl isoforms in definitive hematopoiesis, the developmental step at which scl-β acts to influence HSC formation remains to be elucidated. Whether scl-α has any essential role beyond the stage of AGM HSC generation is also unclear.

In this study, we generated scl-α and -β isoform-specific reporter transgenic zebrafish lines in which the dynamic expression of these two isoforms could be followed individually in vivo. Through time-
lapse imaging with these transgenics, we showed that prior to EHT, 
$scl-\beta$ is predominantly expressed in a subset of VAE cells. These 
$scl-\beta^+$, but not $scl-\beta^-$, VAE cells were traced to transform into HSCs 
in the AGM, suggesting that $scl-\beta$ expression marks hemogenic 
endothelial cells. By contrast, the expression of $scl-\alpha$ was not 
detectable in VAE cells but initiated later, in budding HSCs, and 
gradually accumulated in these cells thereafter. Loss-of-function 
detection in VAE cells but initiated later, in budding HSCs, and 
gradually accumulated in these cells thereafter. Loss-of-function 
studies combined with high-resolution

Taken together, our results suggest a defined hemogenic 
endothelial subpopulation preset by $scl-\beta$ in the aortic endothelium 
that governs the deterministic emergence of EHT, and unravel the

**Materials and Methods**

**Zebrafish husbandry**

Zebrafish were mated and embryos were raised and staged according 
to standard protocols (Kimmel et al., 1995). Zebrafish strains AB, 
$Tg(scl-\beta:d2eGFP; scl-\alpha:DsRed)$, $Tg(scl-\beta:d2eGFP)$, $Tg(scl-\alpha:DsRed)$, 
$Tg(kdrl:eGFP)$ (Jin et al., 2005), $Tg(kdrl:Ras-mCherry^{\beta966}$ (Lee et al., 
2009), $Tg(cmyb:eGFP)$ (North et al., 2007), $Tg(CD41:eGFP)$ (Lin et al., 
2005) and runx1^{H446} (Jin et al., 2009; Sood et al., 2010) were used in this 
study.

**Generation of PAC targeting constructs**

The $scl$ PAC clone (BUSM-129I22) was purchased from the Chris T. 
Amenyi lab via ZFIN (www.zfin.org) and transformed by 
electroporation into $E.\ coli$ strain DH10B. The transformants were selected by 
kanamycin resistance and introduced into electroporation-competent cells. 
To construct the PAC used to generate $Tg(scl-\beta:d2eGFP; scl-\alpha:DsRed)$ 
(Fig. 1B), we first generated the DsRed expression cassette. The DsRed 
coding sequences and SV40 poly(A) signal (Clontech, pDsRed-Express-1) 
and a chloramphenicol selection cassette (CSC) flanked by two FRT sites 
(Gene Bridges, FRT-h2-erm-FRT) were PCR amplified and sequentially 
ligated into the pGEM-Teasy vector. To generate the exon 1 recombination 
construct, two DNA fragments of identical sequence to (AL592495) 37932- 
39209 and 39209-40520 were amplified by PCR, and an enzyme bridge 
($EcoRI$-$EcoRV$-$EcoRI$-$EcoRV$) was used to generate the 
PAC used to generate $scl$ PAC. The modified 
PAC used to generate $scl$ PAC was purchased from the Chris T. 
Amenyi lab via ZFIN (www.zfin.org) and transformed by 
electroporation into $E.\ coli$ strain DH10B. The transformants were selected by 
kanamycin resistance and introduced into electroporation-competent cells. 
To construct the PAC used to generate $Tg(scl-\beta:d2eGFP; scl-\alpha:DsRed)$ 
(Fig. 1B), we first generated the DsRed expression cassette. The DsRed 
coding sequences and SV40 poly(A) signal (Clontech, pDsRed-Express-1) 
and a chloramphenicol selection cassette (CSC) flanked by two FRT sites 
(Gene Bridges, FRT-h2-erm-FRT) were PCR amplified and sequentially 
ligated into the pGEM-Teasy vector. To generate the exon 1 recombination 
construct, two DNA fragments of identical sequence to (AL592495) 37932- 
39209 and 39209-40520 were amplified by PCR, and an enzyme bridge 
($EcoRI$-$EcoRV$-$HindIII$-$SalI$-$XhoI$) between these two fragments was

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**Fig. 1. Generation of $scl$ transgenic lines and expression of d2eGFP and DsRed coincides with that of the endogenous $scl-\beta$ and $scl-\alpha$ isoforms.**

(A) The structure of the zebrafish $scl$ locus in the PAC clone BUSEM-129I22. The transcription start sites of $scl-\alpha$ and $scl-\beta$ are indicated (black arrows). The black box in exon 4 represents sequences encoding the basic helix-loop-helix (bHLH) domain. (B) The modified $scl$ PAC used to generate $Tg(scl-\beta:d2eGFP; scl-\alpha:DsRed)$. $Tg(scl-\beta:d2eGFP)$ and $Tg(scl-\alpha:DsRed)$. DsRed, an SV40 polyadenylation signal and a remaining FRT site were inserted behind exon 1 
(B,D). $d2eGFP$, a SV40 polyadenylation signal and a remaining FRT site 
were inserted in exon 4 (C). The transcription activity of $scl-\alpha$ was interrupted 
by an SV40 polyadenylation signal immediately after exon 1 (C), whereas $Scl-\beta$ expression was disrupted by the reversal of the protein coding 
sequences in exon 4 (D, blue arrow). (E-M) Expression of fluorescent reporter proteins in a 22 hpf $Tg(scl-\beta:d2eGFP; scl-\alpha:DsRed)$ embryo. $Scl-\beta:d2eGFP$ is largely expressed in the head vasculature (E, arrow), the developing common cardinal vein (CCV) (F-I, arrows) and posterior part of the posterior blood island (PBI) (E, asterisk). By contrast, $scl-\alpha:DsRed$ is restricted in the intermediate cell mass (ICM) (J-M, bracket). (F-I) Higher magnification of $d2eGFP$ and 
DsRed expression in the anterior lateral plate mesoderm region. D2eGFP is highly expressed in endothelial cells of the CCV across the yolk sac (arrows), 
whereas DsRed is almost undetected. (J-M) Higher magnification of $d2eGFP$ and DsRed expression in the ICM region. DsRed is largely expressed in 
erthrocytes of the ICM, whereas $d2eGFP$ is less expressed in ICM but dominant in neurons of the whole trunk segment of the spinal cord (arrowheads). 
The embryos are shown in lateral (E-J-M) or dorsal (F-I) views, with anterior to the left. ov, otic vesicle; sc, spinal cord. Scale bars: 50 μm.
introduced by stepwise PCR amplification. The fragment 37932-EcoRV-"EcoRV-HindIII-SalI-XhoI-40520 was then cloned into the pBluescript SK vector. We then inserted the DsRed expression cassette (DsRed-SV40-FRT-CSC-FRT) into the EcoRV/XhoI sites of the exon 1 recombination construct. The DNA fragment 37932-DsRed expression cassette-40520 was then digested and used for homologous recombination. Similarly, the fragment d2eGFP (Clontech, pd2eGFP)-SV40-FRT-CSC-FRT was generated and inserted into the NruI/Smal sites of the exon 4 recombination construct (pBluescript SK-45292-49127). The DNA fragment 45292-d2eGFP expression cassette-49127 was then digested and used for homologous recombination. To construct the scl PAC used to generate Tg(scl-β:scl-β:d2eGFP) (Fig. 1C), the fragment SV40-FRT-CSC-FRT was inserted into the exon 1 recombination construct. To construct the scl PAC used to generate Tg(scl-α:DsRed) (Fig. 1D), the DNA sequences 45346-46973, LoxP-CSC-LoxP, reversed DNA sequences of 46931-47476 and 47472-49003 were sequentially ligated into pBluescript SK to generate the exon 4 recombination construct. Finally, the DNA fragment 45346-CSC-(47476-46391)-49003 was digested and used for homologous recombination.

Homologous recombination and PAC injection
To introduce targetting recombination constructs into the designated site in the PAC, we performed a recombinase-mediated recombination modified from previous studies (Yang et al., 2006). The linearized targeting recombination constructs described above were transformed into E. coli DH10B cells containing both the original scl PAC and pGETrec (recombinase) plasmid by electroporation. The recombination was induced by adding l-arabinose during 1 hour of culture, then recombinants were selected by growth under both kanamycin and chloramphenicol selection conditions. After confirmation that the positive recombinants harbored the correct targeting constructs, the CSC fragment was removed by Flp-mediated excision. Prior to microinjection, the modified PAC was digested by I-SceI for 1 hour (Rembold et al., 2006). A final concentration of 50 ng/μl linearized PAC was injected into one-cell stage embryos, which were raised to adulthood to generate transgenics.

Morpholinos (MOs) and injection
scl MOs (Gene Tools) were used as previously described (Qian et al., 2007); 3 ng scl-α MO (5'-GGGGGACACCACTGACACACACTC-3') and 8 ng scl-β MO (5'-GGGGGACACCACTGACACACACTC-3') were injected (Burns et al., 2005). A mixture containing a final concentration of 0.6 mM runx1 MO3 (5'-TGTAAAACGACGGCCAGA-3') and 1 mM runx1 MO5 (5'-AATGTGTAAACTCACAGTGTAAAGC-3') was prepared prior to microinjection (Burns et al., 2005). MOs were injected into one-cell stage embryos and the injected embryos were raised to the required developmental stages.

Whole-mount in situ hybridization (WISH) and antibody staining
Single (Qian et al., 2007) and double (Jin et al., 2007) WISH were performed as previously described. The protocol for single immunohistochemical staining (Qian et al., 2007) and double was also used to detect d2eGFP and Scl-β simultaneously. Goat anti-GFP (Abcam, Ab6658; 1:400) and rabbit Ab-Scl-α [made by ourselves (Qian et al., 2007); 1:50] were used as primary antibodies; anti-goat Alexa Fluor 488 (Invitrogen, A11055; 1:400) and anti-rabbit Alexa Fluor 555 (Invitrogen, A11023; 1:400) were used as secondary antibodies.

Time-lapse confocal microscopy
For time-lapse confocal micrography, embryos were first anaesthetized in 0.02% tricaine in embryo water, then mounted in 0.5% low-melting agarose on a 35-mm plastic Petri dish (Iwaki), and covered with embryo water containing 0.02% tricaine. Embryos were examined using a Zeiss LSM 510 confocal microscope or an Olympus Fluoview 1000 confocal microscope equipped with an environmental chamber to maintain temperature (28°C) and humidity. Confocal z-stacks of 3 μm steps were taken every 8-10 minutes, and 25-30 stacks were typically imaged for each embryo.

Processing of time-lapse confocal images
Raw data of time-lapse confocal imaging were analyzed using either LSM Image Browser (Zeiss) or FV10-ASW 2.0 Viewer (Olympus) software. Confocal planes at each time point were individually analyzed to select the most representative images and to perform the projection. The images after projection were exported and saved through time, then imported to generate a sequence file in SPOT Advanced software (SPOT Imaging Solutions). After annotation, the sequence file was exported as a .mov movie in QuickTime (Apple) format.

RESULTS
Generation of scl-α and scl-β isoform-specific reporter transgenic zebrafish lines
To visualize the dynamic expression of individual scl isoforms and provide clues as to the possible roles of these isoforms in the development of AGM HSCs, we created three stable scl transgenic zebrafish lines: a dual scl isoform reporter line Tg(scl-β:scl-β:d2eGFP; scl-α:DsRed) (Fig. 1B), an scl-β reporter line Tg(scl-β:scl-β:d2eGFP) (Fig. 1C), and an scl-α reporter line Tg(scl-α:DsRed) (Fig. 1D). To generate these lines, a P1 artificial chromosome (PAC) clone containing the zebrafish scl genomic locus was modified to express GFP and/or DsRed corresponding to the expression of scl-β and/or scl-α (Fig. 1A-D). A destabilized eGFP form (d2eGFP) with a shorter half-life of only 2 hours was used to minimize the carryover of fluorescent protein from the GFP-expressing ancestor cells to their non-GFP-expressing progeny, while a fast-folding version of DsRed (DsRed-Express) was implemented to minimize the signal retardation during dual-color imaging studies (Bevis and Glick, 2002).

We then examined the expression patterns of d2eGFP and DsRed in Tg(scl-β:scl-β:d2eGFP; scl-α:DsRed) embryos (Fig. 1E-M), focusing on 22 hours postfertilization (hpf), when the spatial expression patterns of the endogenous isoforms clearly differ (Qian et al., 2007). At 22 hpf, scl-β:scl-β:d2eGFP was predominantly expressed in the head vasculature (Fig. 1E, arrow), in endothelial cells of the developing common cardinal vein (a characteristic scl-β-expressing population that shows no expression of scl-α (Qian et al., 2007)] (Fig. 1E-I), and in the caudal part of the posterior blood island (Fig. 1E, asterisk). By contrast, the expression of scl-α:DsRed was restricted in the intermediate cell mass region (Fig. 1E,J-M). These results show that the expression of both transgenes coincides with that of the endogenous scl-β and scl-α isoforms as previously reported (Qian et al., 2007).

In addition, 5′-rapid amplification of cDNA ends (RACE) experiments confirmed that the d2eGFP and DsRed transcripts were initiated from the designated transcription start sites of the scl-β and scl-α isoforms, respectively (supplementary material Fig. S1A) (Qian et al., 2007). Consequently, a fusion protein between d2eGFP and the N-terminal 75 amino acids of Scl-β was produced, leading to the nuclear location of d2eGFP (supplementary material Fig. S1B). Moreover, double-staining experiments confirmed that d2eGFP and DsRed colocalize with the endogenous expression of Scl-β and scl-α, respectively (supplementary material Fig. S1C).

Taken together, these data indicate that the fluorescent reporter expression in the isoform-specific transgenic zebrafish lines faithfully mimics the endogenous expression of scl-α and scl-β.

scl-β+ endothelial cells give rise to scl-β+/scl-α+ HSCs in the AGM
We then characterized the dynamic expression of the isoform-specific reporters by high-resolution in vivo time-lapse imaging during definitive hematopoiesis, specifically around the time that HSCs are born in the AGM region. Recent studies have delineated the emergence of HSC from the aortic lumen by means of EHT, in which VAE cells bend and round up to become HSCs (Bertrand et
al., 2010; Kissa and Herbomel, 2010; Lam et al., 2010). Prior to EHT, which normally occurs between 32 and 60 hpf (Kissa and Herbomel, 2010), scl-β:dsRed, but not scl-α:DsRed, expression was clearly detected in a thin layer of cells lining the prospective AGM at ~25-26 hpf (Fig. 2A-C). These scl-β:dsGFP+/scl-α:DsRed cells co-expressed an endothelial-specific transgene, kdrl:Ras-mcherry (Lee et al., 2009), indicating their endothelial identity (Fig. 2D-F). When the embryos developed to the stage of EHT, scl-α:DsRed began to be weakly expressed in the AGM and this expression was strictly restricted to scl-β:dsGFP+ cells, defining the transition of scl-β:dsGFP+ cells to scl-β:dsGFP+/scl-α:DsRed+ cells. Along with the subsequent intensification of DsRed signals, these scl-β:dsGFP+/scl-α:DsRed+ cells were seen to bend ventrally to become round cells, just as budding HSCs normally do (supplementary material Fig. S2). Consequently, by 36 hpf, the round scl-β:dsGFP+/scl-α:DsRed+ cells were readily observable in the AGM (Fig. 2G-I). These cells displayed behavior characteristic of HSCs (Bertrand et al., 2010; Kissa and Herbomel, 2010; Lam et al., 2010): they normally remained in the subaortic space for 4-5 hours, during which time some underwent cell division, and subsequently entered the blood circulation through the axial vein (supplementary material Movie 1). Finally, these cells were observed to populate downstream hematopoietic tissues: the caudal hematopoietic tissue (CHT) (Murayama et al., 2006; Jin et al., 2007), thymus and kidney (supplementary material Fig. S3). To confirm the identity of these scl-β:dsGFP+/scl-α:DsRed+ cells, we examined the expression of HSC-specific markers. They co-expressed two HSC-specific transgenes, emyb:eGFP and CD41:eGFP, in the AGM (Fig. 2J-O), confirming that they are indeed HSCs.

Collectively, these data suggest that the differential expression of scl isoforms identifies two sequential cell populations in the AGM, with the earlier scl-β:dsGFP+ cells being hemogenic endothelium and later transiting to scl-β:dsGFP+/scl-α:DsRed+ HSCs.

Expression of scl-β marks hemogenic endothelium

To further explore the relationship between the expression of scl-β and the hemogenic potential of VAE cells (which is defined here by the ability of these cells to become HSCs via EHT), we crossed the Tg(scl-β:dsGFP) line with the Tg(kdrl:Ras-mcherry) line, which has been used to score all possible EHT events during HSC formation in the AGM (Lam et al., 2010). Time-lapse confocal imaging on Tg(scl-β:dsGFP; kdrl:Ras-mcherry) embryos revealed that about half of kdrl:Ras-mcherry+ VAE cells were also scl-β:dsGFP+ prior to EHT (25-28 hpf). These scl-β:dsGFP+/kdrl:Ras-mcherry+ cells were of the typical elongated endothelial cell shape and were morphologically indistinguishable from the remaining kdrl:Ras-mcherry+/scl-β:dsGFP+ population. During the observation period (from 28 to 54 hpf), the vast majority (~80%) of these scl-β:dsGFP+/kdrl:Ras-mcherry+ cells underwent EHT to form HSCs (Fig. 3B-K; supplementary material Table S1, Movie 2). More importantly, of 46 EHT events observed in six embryos (supplementary material Table S1), all instances of EHT were initiated from scl-β:dsGFP+ endothelial cells, and none of the scl-β:dsGFP+ endothelial cells were observed to undergo EHT. These results suggest that early scl-β expression in the AGM uniquely and exclusively marks the hemogenic endothelium capable of producing HSCs via EHT.

scl-β is required for the specification of hemogenic endothelium

In light of our previous studies showing the requirement of scl-β for AGM HSC formation (Qian et al., 2007) and the above results illustrating the specific expression of scl-β in hemogenic VAE cells, we speculate that scl-β might regulate HSC formation by specifying hemogenic endothelium. To examine this possibility, we employed in vivo time-lapse imaging to track the transformation of endothelial cells into HSCs in embryos in which scl-β expression was inhibited by an scl-β-specific morpholino (MO) (Qian et al., 2007). Because the scl-β MO interfered with the translation of dsGFP through recognizing the scl 5'UTR sequence in the dsGFP transcript (supplementary material Fig. S1A), we could not evaluate the effect of MO knockdown in Tg(scl-β:dsGFP) embryos; instead, Tg(scl-α:DsRed; kdrl:eGFP) embryos were used.

In scl-β-deficient embryos, we observed the fragmentation of a subset of kdrl:eGFP+ VAE cells taking place before the onset of EHT (32 hpf) (Fig. 4B-D'; supplementary material Movie 3).
TUNEL staining indicated that the fragmented \textit{kdrl:eGFP} VAE cells were undergoing apoptosis (supplementary material Fig. S4I-N). These events occurred in single endothelial cells throughout the entire dorsal aorta, and were detected as early as 25 hpf (data not shown) and continued until 31 hpf (supplementary material Movie 3). Consistent with the fragmentation occurring before EHT, these apoptotic \textit{kdrl:eGFP} cells were of the elongated endothelial cell shape, and none showed any morphological sign of EHT (Fig. 4B-D; supplementary material Movie 3). As a result, the \textit{CD41:eGFP} HSCs were almost undetectable in \textit{scl-β} morphants (Fig. 4E,F). The loss of the HSC phenotype could be partially rescued by introducing a PAC expressing \textit{scl-β}, demonstrating the specificity of \textit{scl-β} MO targeting (supplementary material Fig. S4E-H). This endothelial cell apoptosis phenotype was not associated with any gross impairment in vascular differentiation, as shown by the normal expression of \textit{kdrl:eGFP} (Fig. 4A), the vessel-specific marker \textit{fltl} (Brown et al., 2000), and the artery-specific marker \textit{dll4} (Leslie et al., 2007), as well as the normal growth of intersegmental vessels in \textit{scl-β}-deficient embryos (supplementary material Fig. S4A-D; data not shown). Rather, it reflected the selective loss of hemogenic endothelial cells in \textit{scl-β}-deficient embryos (Fig. 4E,F; supplementary material Movie 3). Altogether, our data suggest that \textit{scl-β} deficiency inhibits HSC formation in the AGM by depleting the hemogenic endothelium.

\textit{scl-α} is required for the maintenance of HSCs in the AGM

Given that the expression of \textit{scl-α}:\textit{DsRed} colocalized with the HSC-associated markers \textit{cmyb:eGFP} and \textit{CD41:eGFP} in the AGM (Fig. 2J-O), we further correlated the \textit{scl-α}:\textit{DsRed} expression with EHT progression by time-lapse imaging of \textit{Tg(scl-α:DsRed; kdrl:eGFP)} embryos. As EHT proceeded, \textit{scl-α}:\textit{DsRed} expression increased and became abundant in the mature HSCs in the AGM. Such correlated expression of \textit{scl-α}:\textit{DsRed} with EHT was observed in all 34 EHT events scored in four embryos (Fig. 5A-D'; supplementary material Table S2). Thus, these results suggest that the expression of \textit{scl-α} in the AGM is intimately associated with the emergence of HSCs from VAE.

We next examined the role of \textit{scl-α} in HSC development. As previously reported (Qian et al., 2007), the expression of \textit{cmyb} in the AGM of \textit{scl-α} morphants was indistinguishable from that of controls at 26 hpf (Fig. 6A,D). However, whereas \textit{cmyb} expression persisted until 2 dpf in control embryos, it decreased rapidly in \textit{scl-α} morphants, being approximately half of that in control embryos at 40 hpf (Fig. 6B,E). Similar results were obtained through scoring \textit{CD41:eGFP} cells in the AGM of \textit{Tg(CD41:eGFP)} \textit{scl-α} morphants (Fig. 6G,H). Consistent with the reduction of HSCs in the AGM, the expression of \textit{cmyb} in the CHT was greatly reduced by 3 dpf in \textit{scl-α} morphants (Fig. 6C,F). This phenotype could be
that prior to EHT (24-30 hpf), the endothelial cell apoptosis seen in \( \text{scl-} \beta \text{-morphants (Fig. 4A-D); supplementary material Movie 3) was not observed in runx1 morphants.} \)

Consistently, the hemogenic endothelial cell population marked by \( \text{scl-} \beta \) was not affected in runx1 morphants (Fig. 7A,B). At the time of active ongoing EHT in controls (30-40 hpf), in runx1 morphants some of the \( \text{kdr}l: \text{eGFP}\) endothelial cells did initiate EHT by bending ventrally but then burst into fragments as they rounded up. In accordance with some initiation of EHT in runx1 morphants, \( \text{scl-} \alpha: \text{DsRed} \) expression was observed in the apoptotic \( \text{kdr}l: \text{eGFP}\) endothelial cells (Fig. 7C-E; supplementary material Movie 5).

Overall, these results suggest that runx1 specifically regulates EHT without influencing the formation of hemogenic endothelium. Based on the timing at which the apoptosis phenotype occurred in the three morphants, and the cellular phenotypes elicited by knocking down \( \text{scl-} \beta \), \( \text{scl-} \alpha \) and runx1, we concluded that \( \text{scl-} \beta \), \( \text{runx1} \) and \( \text{scl-} \alpha \) act at distinct, but sequential, steps during AGM HSC development: \( \text{scl-} \beta \) first confers hemogenic potential to a selective subset of VAE cells, runx1 then transforms hemogenic endothelial cells into HSCs, and \( \text{scl-} \alpha \) finally maintains newly born AGM HSCs (Fig. 7F).

**DISCUSSION**

The promise of HSC-based therapy has brought about a long-standing interest in how HSCs normally arise during embryogenesis. Over recent years, joint experimental efforts in multiple species have provided compelling evidence for the emergence of HSCs from the AGM region. A recent breakthrough came with studies showing that HSCs directly transit from a subset of aortic endothelial cells, namely the hemogenic endothelium (Bertrand et al., 2010; Boisset et al., 2010; Kiss and Herbomel, 2010; Lam et al., 2010). Although a number of transcription factors have been implicated in the development of AGM HSCs, primarily by mouse gene-targeting studies, few have been characterized in terms of mapping their function to defined stages of HSC development. In the current study, using high-resolution *in vivo* time-lapse imaging to make observations that might otherwise not be possible by conventional methods, we documented distinct cellular and developmental defects leading to the same loss of AGM HSCs in \( \text{scl-} \beta \)-, \( \text{scl-} \alpha \)- or runx1-deficient embryos. Inferred from these phenotypes and their consistent occurrence, we defined three distinct but sequential steps in the development of AGM HSCs, each of which is uniquely regulated by one of these three factors: hemogenic endothelium is first specified by \( \text{scl-} \beta \), the emergence of HSCs from hemogenic endothelium is then controlled by \( \text{runx1} \), and finally nascent HSCs are sustained by \( \text{scl-} \alpha \). Thus, for the first time, the exact developmental stage at which \( \text{scl} \) or \( \text{scl-isoforms act to regulate AGM HSCs is defined. Along with previous results showing that cMyc is indispensable for the egression of HSCs from the AGM (Zhang et al., 2011), we propose a transcription factor relay that coordinates the orderly progression of AGM HSC development from hemogenic endothelium to regulated HSC exit (Fig. 7F). In mammalian systems, the N-terminal-truncated SCL isoform corresponding to zebrafish Scl-\( \beta \) was reported to be expressed in certain human T-cell leukemia cell lines (Bernard et al., 1992; Pulford et al., 1995). However, the expression and specific function of full-length and truncated mammalian SCL isoforms in the context of hemogenic endothelium formation and HSC development have not been explored. Considering the high similarity between zebrafish and mammalian hematopoiesis in terms of molecular regulation, our research provides a framework to untangle isoform-specific roles of mammalian SCL isoforms in HSC formation.

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**Table 1**

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<td><img src="image1.png" alt="Image A" /></td>
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<td><img src="image4.png" alt="Image B" /></td>
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<td><img src="image7.png" alt="Image C" /></td>
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**Fig. 5. Expression of scl-\( \alpha \):DsRed correlates with EHT.** (A-D) Time-lapse confocal imaging of a live Tg(scl-\( \alpha \):DsRed; kdr:eGFP) zebrafish embryo from 34 to 37 hpf. Selected planes are presented to show EHT of an scl-\( \alpha \):DsRed\( ^{\dagger} \)/kdrl:eGFP\( ^{\dagger} \) cell (blue arrows). An scl-\( \alpha \):DsRed\( ^{\dagger} \)/kdrl:eGFP\( ^{\dagger} \) cell in the AGM before recording (A-A, blue arrowheads) enters circulation shortly after (B-B, dashed circles and arrows). White arrow (D') indicates the direction of blood flow in the dorsal aorta. Scale bar: 20 \( \mu \)m.

**Fig. 6.** (A-D) Time-lapse confocal imaging of a live Tg(scl-\( \alpha \):DsRed; kdrl:eGFP) zebrafish embryo from 34 to 37 hpf. Selected planes are presented to show EHT of an scl-\( \alpha \):DsRed\( ^{\dagger} \)/kdrl:eGFP\( ^{\dagger} \) cell (blue arrows). An scl-\( \alpha \):DsRed\( ^{\dagger} \)/kdrl:eGFP\( ^{\dagger} \) cell in the AGM before recording (A-A, blue arrowheads) enters circulation shortly after (B-B, dashed circles and arrows). White arrow (D') indicates the direction of blood flow in the dorsal aorta. Scale bar: 20 \( \mu \)m.

**Fig. 7.** (A-D) Time-lapse confocal imaging of a live Tg(scl-\( \alpha \):DsRed; kdrl:eGFP) zebrafish embryo from 34 to 37 hpf. Selected planes are presented to show EHT of an scl-\( \alpha \):DsRed\( ^{\dagger} \)/kdrl:eGFP\( ^{\dagger} \) cell (blue arrows). An scl-\( \alpha \):DsRed\( ^{\dagger} \)/kdrl:eGFP\( ^{\dagger} \) cell in the AGM before recording (A-A, blue arrowheads) enters circulation shortly after (B-B, dashed circles and arrows). White arrow (D') indicates the direction of blood flow in the dorsal aorta. Scale bar: 20 \( \mu \)m.

**Scl-\( \beta \), Runx1 and Scl-\( \alpha \) constitute a molecular hierarchy regulating sequential steps of AGM HSC development**

Previous studies have shown that EHT events are impaired in runx1-deficient embryos (Kissa and Herbomel, 2010), suggesting that runx1 is essential for EHT. However, whether Runx1 has a contributing pre-EHT role in AGM HSC development is not known. To address this, we examined the impact of runx1 deficiency on HSC development in detail. By time-lapse imaging Tg(scl-\( \alpha \):DsRed; kdrl:eGFP) embryos injected with runx1 MO, we found

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Our data show that prior to the onset of EHT and blood flow, scl-β is expressed in a selective subset of VAE cells destined to become HSCs and is functionally required for the formation of these cells. Remarkably, only the scl-β+ VAE subset, and not the remaining scl-β− cells, gives rise to HSCs via EHT. This suggests that hemogenic potential is not widely distributed across the entire VAE but is restricted to a defined subpopulation, and is thus in support of the emergence of HSCs from VAE as a deterministic rather than stochastic event. To our knowledge, scl-β is the first molecular determinant for hemogenic endothelial cells, a crucial intermediate.
in the development of AGM HSCs, providing a genetic handle for further study of this important, yet less well understood, cell population. An intriguing observation is that, although the vast majority (80%) of the scl-β-eGFP VAE cells give rise to HSCs via EHT, ~20% of them gradually lose scl-β expression (data not shown), at least during the imaging period (from 28 to 54 hpf), and presumably remain as aortic endothelial cells thereafter. This implies that a larger endothelial cell population (scl-β) might initially acquire hemogenic potential to support HSC generation and that they might also lose their hemogenic potential when not needed. In light of the rapid development of early zebrafish embryos, this redundancy and plasticity of endothelial to hematopoietic conversion might ensure that a sufficient number of HSCs is produced within a short permissive time window without compromising vascular integrity.

We show that runx1 is dispensable for hemogenic endothelium formation but becomes essential upon the transformation of endothelial cells into HSCs. Together with a previous study reporting that deletion of runx1 immediately after the completion of EHT has no effect on HSCs (Chen et al., 2009), we suggest that, during the emergence of HSCs, runx1 is only required at the stage of EHT, and not before or thereafter. It is currently unknown whether scl-β is also required for the activation of the EHT program besides acting in the formation of hemogenic endothelium. It is plausible that scl-β might prime hemogenic endothelium for EHT by activating the expression of runx1. Prior work in mouse has suggested that SCL directly regulates Runx1 promoter activity during yolk sac and fetal liver hematopoiesis, unconventionally through GATA2 binding sites rather than SCL binding sites (Porcher et al., 1999; Landry et al., 2008). Further studies have shown that GATA/ETS/SCL motifs in a +23 enhancer element control RUNX1-mediated HSC emergence (Nottingham et al., 2007; Ng et al., 2010). In zebrafish, however, cis-regulatory elements that govern runx1 expression in HSCs remain poorly defined, although two large genomic fragments encompassing runx1 distal and proximal promoters have been shown to label distinct definitive hematopoietic progenitors (Lam et al., 2009). The mouse Runx1 +23 enhancer can direct reporter expression in HSCs in zebrafish embryos (our unpublished data), making it likely that an analogous scl-runx1 regulatory mechanism might operate in zebrafish.

Finally, our study has uncovered a previously unidentified role of scl-α in maintaining HSCs in the AGM. This role of scl-α is supported by the findings that the depletion of HSC-associated markers in AGM, CHT and pronephros follows a normal EHT, and the normal initial expression of these markers in the AGM in scl-α morphants. However, in contrast to the severe loss of HSCs in CHT and pronephros, T-cell development is marginally affected, as rag1 expression in the thymus is either unaffected or only slightly reduced in scl-α morphants as compared with controls (Qian et al., 2007) (supplementary material Fig. S6). Accordingly, we observed that a few scl-α-DsRed+/kdrl:eGFP+ HSCs were released into the circulation after 60 hpf in scl-α morphants (data not shown). Unlike gene knockout, MO-mediated knockdown tends to be incomplete. As such, a possible explanation for the spared T-cell development could be the insensitivity of this lineage to the incomplete suppression of scl-α, for example through the compensatory proliferation or differentiation of residual hematopoietic progenitors in the thymus of scl-α morphants. Alternatively, this might be attributed to the scl-α-independent emergence of the first T-cells in developing embryos. It is plausible that the first T-cells are produced from 32 to 40 hpf, when HSC markers are normally expressed in the AGM of scl-α morphants. Clarification of this issue would benefit from the creation of a zebrafish line stably deleted for the scl-α isoform.

Collectively, our findings demonstrate the importance of the orderly action of the transcription factors scl-β, runx1 and scl-α in the progressive development of HSCs from the AGM in vertebrates. These results have direct implications for the quest to derive blood cells from endothelial cells or induced pluripotent stem cells (Szabo et al., 2010).

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Competing interests statement
The authors declare no competing financial interests.

Author contributions
F.Z., Y.L. and B.Y. designed the research, performed experiments and analyzed data. W.Z. and Z.W. designed the research and analyzed data.

Supplementary material
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References