

Dlk1 is a negative regulator of emerging hematopoietic stem and progenitor cells

Bahar Mirshekar-Syahkal,¹ Esther Haak,² Gillian M. Kimber,¹ Kevin van Leusden,² Kirsty Harvey,² John O'Rourke,³ Jorge Laborda,⁴ Steven R. Bauer,⁵ Marella F. T. R. de Bruijn,³ Anne C. Ferguson-Smith,⁶ Elaine Dzierzak,² and Katrin Ottersbach¹

¹Department of Haematology, Cambridge Institute for Medical Research, Wellcome Trust & MRC Stem Cell Institute, University of Cambridge, Cambridge, UK; ²Erasmus Stem Cell Institute, Department of Cell Biology, Erasmus Medical Center, Rotterdam, The Netherlands; ³MRC Molecular Haematology Unit, Weatherall Institute for Molecular Medicine, University of Oxford, Oxford, UK; ⁴Department of Inorganic and Organic Chemistry and Biochemistry, Medical School, Regional Center for Biomedical Research, University of Castilla-La Mancha, Albacete, Spain; ⁵Cellular and Tissue Therapies Branch, Division of Cellular and Gene Therapies, Center for Biologics Evaluation and Research, Food and Drug Administration, Bethesda, Maryland, USA, and ⁶Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK

©2013 Ferrata Storti Foundation. This is an open-access paper. doi:10.3324/haematol.2012.070789

Online Supplementary Design and Methods

Mice and embryo generation

The following mouse strains were used for this study: wild-type C57BL/6, *Gata3* knockout,¹ *Runx1* knockout,² *Runx1-LacZ* knockin,³ *Dlk1* transgenic⁴ and *Dlk1* knockout.⁵

Gene expression analysis

For the detection of the different *Dlk1* isoforms by conventional reverse transcriptase polymerase chain reaction (RT-PCR), the following primers were used; forward: GCTG-GATTCGTCGACAAGAC, reverse: CGCACTTGTTGA-GAAAGACG. For the quantification of *Dlk1* transcript levels by real-time RT-PCR analysis, the following primers were used; *Dlk1* forward: GCTGGATTTCGTCGACAAGAC, reverse: ATCCTTGACAGATGCACTGC; *Actb* forward: TCCTGGCCT-CACTGTCCA, reverse: GTCCGCCTAGAAGCACTTGC.

Immunohistochemistry and in situ hybridization

Tissue sections were stained with antibodies specific for CD34 (1:50, BD Biosciences, Oxford, UK), Dlk1 (1:500, Millipore, Watford, UK), smooth muscle actin, alpha (1:200, Sigma Aldrich, Gillingham, UK), Runx1 (a kind gift from Thomas Jessell, Columbia University, New York, USA),⁶ CD31 (1:30-1:100, BD Biosciences, Oxford, UK), tyrosine hydroxylase (1:500, Millipore, Watford, UK) and Ki67 (1:500, Abcam, Cambridge, UK) as described previously.⁷ For the detection of apoptotic cells by the TUNEL assay, an ApopTag Red In Situ Apoptosis Detection Kit was used following the manufacturer's instructions (Millipore, Watford, UK). Images were taken using a Zeiss LSM510 META Confocal Microscope or a Radiance 2000 Confocal Scanning System (Bio-Rad, Hemel Hempstead, UK) and analyzed with Zeiss LSM image software (Carl Zeiss Ltd., Weylyn, UK) or Laser Sharp 2000 software (Carl Zeiss Ltd., Weylyn, UK). For the detection of *Dlk1* transcripts, a riboprobe

was prepared by RT-PCR from embryonic day (E) 11 aorta-gonad-mesonephros (AGM) cDNA using the following primers; forward: GTGACCCCCAGTATGGATTTC, reverse: GCTTGCACAGACACTCGAAG. *In situ* hybridization experiments were performed as described previously⁸ and pictures were taken on a Zeiss AxioSkop2 Wide-Field Microscope and analyzed with Zeiss AxioVision software (Carl Zeiss Ltd., Weylyn, UK).

Transfection of aorta-gonad-mesonephros stromal cell lines

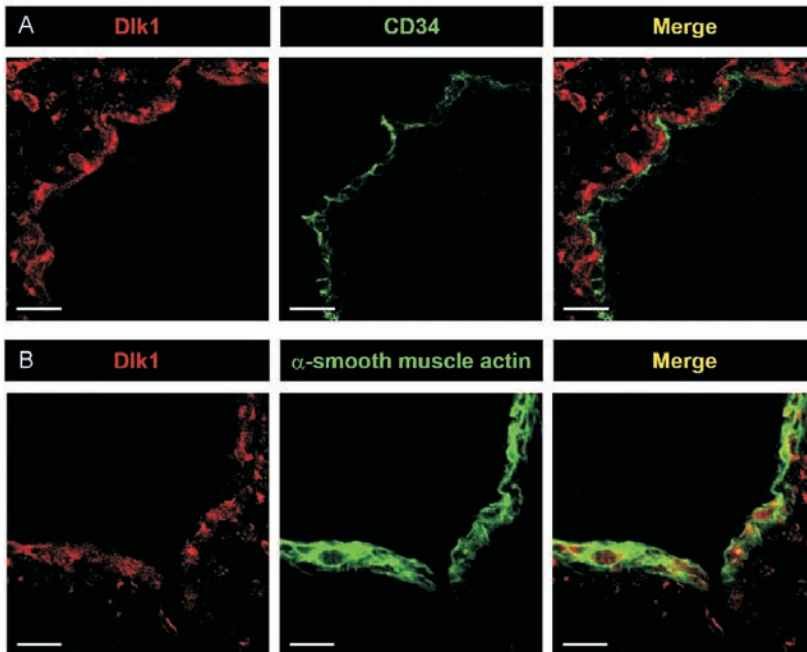
To obtain Dlk1 overexpression, KH9 stromal cells were stably transfected with either linearized empty pEGFP-N1 vector or with a linearized pEGFP-N1 vector containing full-length *Dlk1* (Open Biosystems, Rockford, USA). For the knockdown of *Dlk1*, UG26-1B6 cells were stably transfected with linearized pSUPER.retro.neo+GFP vector (Oligoengine, Seattle, USA) containing the siRNA sequence GCTGGATTTCGTCGACAAGA, which targets *Dlk1* at nucleotides 743-761 (NM_010052). Empty pSUPER.retro.neo+GFP vector was used as a control.

Co-culture experiments

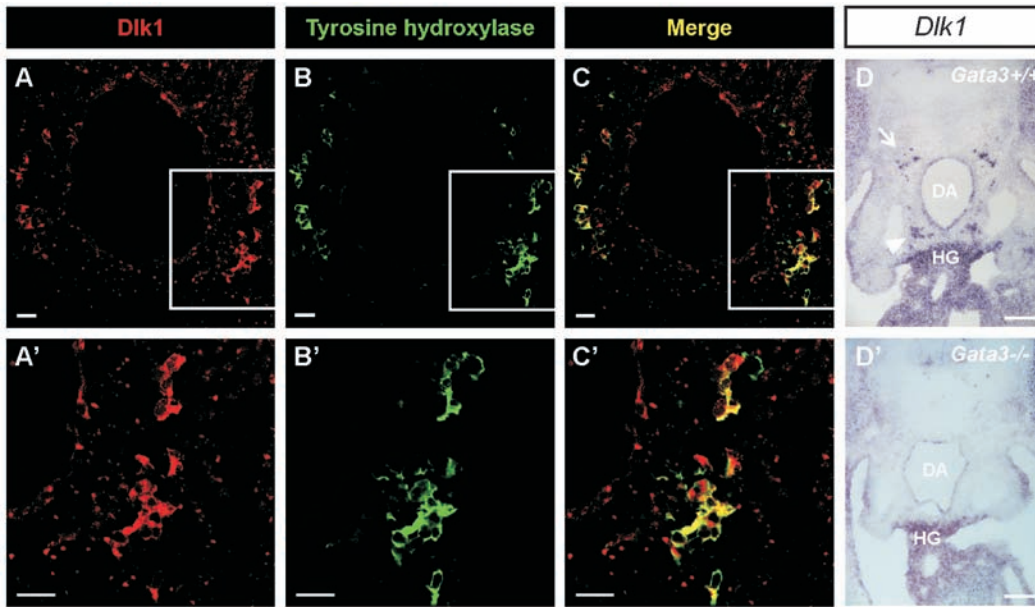
All stromal cell lines were maintained at 33°C in expansion medium containing 50% Myelocult M5300 (Stem Cell Technologies, Grenoble, France), 35% α -MEM (Invitrogen, Paisley, UK), 15% fetal calf serum (Sigma Aldrich, Gillingham, UK), 0.5% penicillin-streptomycin (Sigma Aldrich, Gillingham, UK) and 10 μ M β -mercaptoethanol. Bone marrow hematopoietic stem cell-enriched cell populations were obtained by either isolating low-density cells using the discontinuous Ficoll gradient method by E. Schneider *et al.*,⁹ followed by sorting for cells with the phenotype CD31^{med} Ly-6C⁺ ckit^{high},¹⁰ or by isolating cells with the Lin⁻ Sca1⁺ ckit⁺ (LSK) phenotype. These were seeded on irradiated stromal cell lines in Myelocult M5300/1% penicillin-streptomycin/10⁻⁶ M hydrocortisone or expansion medium.

References

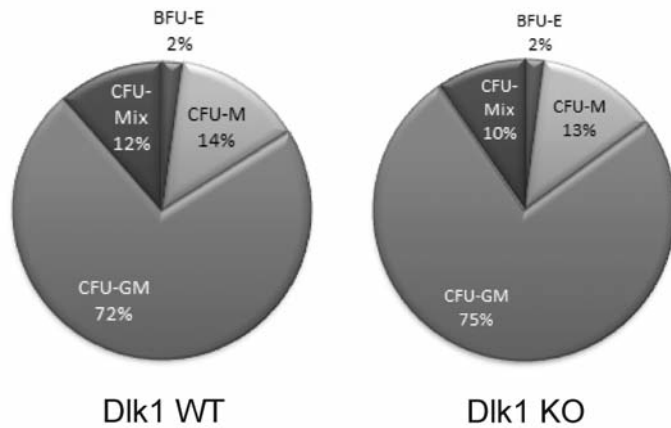
- Pandolfi PP, Roth ME, Karis A, Leonard MW, Dzierzak E, Grosveld FG, et al. Targeted disruption of the GATA3 gene causes severe abnormalities in the nervous system and in fetal liver haematopoiesis. *Nat Genet.* 1995;11(1):40-4.
- Wang Q, Stacy T, Binder M, Marin-Padilla M, Sharpe AH, Speck NA. Disruption of the Cbfa2 gene causes necrosis and hemorrhaging in the central nervous system and blocks definitive hematopoiesis. *Proc Natl Acad Sci USA.* 1996; 93(8):3444-9.
- North T, Gu TL, Stacy T, Wang Q, Howard L, Binder M, et al. Cbfa2 is required for the formation of intra-aortic hematopoietic clusters. *Development.* 1999;126(11):2563-75.
- da Rocha ST, Charalambous M, Lin SP, Gutteridge I, Ito Y, Gray D, et al. Gene dosage effects of the imprinted delta-like homologue 1 (*dlk1/pref1*) in development: implications for the evolution of imprinting. *PLoS Genet.* 2009;5(2):e1000392.
- Raghuveer R, Ruiz-Hidalgo M, Jia Y, Ettinger R, Rudikoff E, Riggins P, et al. Dlk1 influences differentiation and function of B lymphocytes. *Stem Cells Dev.* 2008;17(3):495-507.
- Kramer I, Sigrist M, de Nooij JC, Taniuchi I, Jessell TM, Arber S. A role for Runx transcription factor signaling in dorsal root ganglion sensory neuron diversification. *Neuron.* 2006;49(3):379-93.
- de Bruijn MF, Ma X, Robin C, Ottersbach K, Sanchez MJ, Dzierzak E. Hematopoietic stem cells localize to the endothelial cell layer in the mid-gestation mouse aorta. *Immunity.* 2002;16(5):673-83.
- Ostersbach K, Dzierzak E. The murine placenta contains hematopoietic stem cells within the vascular labyrinth region. *Dev Cell.* 2005;8(3): 377-87.
- Schneider E, Pollard H, Lepault F, Guy-Grand D, Minkowski M, Dy M. Histamine-producing cell-stimulating activity. Interleukin 3 and granulocyte-macrophage colony-stimulating factor induce de novo synthesis of histidine decarboxylase in hemopoietic progenitor cells. *J Immunol.* 1987;139(11):3710-7.
- Oostendorp RA, Harvey KN, Kusadasi N, de Bruijn MF, Saris C, Ploemacher RE, et al. Stromal cell lines from mouse aorta-gonads-mesonephros subregions are potent supporters of hematopoietic stem cell activity. *Blood.* 2002;99(4):1183-9.



Online Supplementary Figure S1. Expression analysis of Dlk1 in the mid-gestation embryo. (A,B) Immunohistochemical co-staining for Dlk1 (red, Cy3 in A and FITC in B) and (A) CD34 (green, FITC) or (B) smooth muscle actin, alpha (green, Cy3) on sections of E11.5 wild-type aortas. The scale bar is 20 μ m.



Online Supplementary Figure S2. *Dik1* is expressed in cells of the developing sympathetic nervous system. (A-C) Immunohistochemical co-staining of E11.5 embryo sections showing the dorsal aorta (ventral down) and *Dik1* in red (Cy3) and tyrosine hydroxylase in green (Alexa 488). Close-up of boxed region shown in A'-C'; the scale bar is 20 μm. *Dik1* expression analysis by *in situ* hybridization on *Gata3*^{+/+} (D) and *Gata3*^{-/-} (D') E11.5 embryo sections. *Dik1*-expressing sympathetic ganglia (arrow) and adrenal anlage (arrowhead) in wild-type embryos are indicated; the scale bar is 100 μm; DA, dorsal aorta; HG, hindgut.



Online Supplementary Figure S3. *Dik1* knockout AGMs have a similar ratio of definitive hematopoietic progenitors. E11.5 wild-type and *Dik1* knockout AGM cells were plated in methylcellulose assays. The total number of colonies was counted after 1 week and the colony types scored; n=3.