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There was an error published in the supplementary material for *Development* **136**, 4043-4053.

In the legends for Figs S1, S2, S4, S5, S6 and S9, $Rac^{fl/fl}$ was incorrectly stated as Rac^{+}.

In the title of Fig. S5, Vegfr3 was incorrectly stated as VR3.

The supplementary figure legends have now been corrected.

We apologise to authors and readers for this mistake.

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Regulation of lymphatic-blood vessel separation by endothelial Rac1

Gabriela D'Amico[1,*,†], Dylan T. Jones[1], Emma Nye[2], Karen Sapienza[3], Antoine R. Ramjuan[1], Louise E. Reynolds[1], Stephen D. Robinson[1], Vassiliki Kostourou[1,8], Dolores Martinez[4], Deborah Aubyn[5], Richard Grose[6], Gareth J. Thomas[3], Bradley Spencer-Dene[2,9], Daniel Zicha[5], Derek Davies[4], Victor Tybulewicz[7] and Kairbaan M. Hodivala-Dilke[1,†]

Sprouting angiogenesis and lymphatic-blood vessel segregation both involve the migration of endothelial cells, but the precise migratory molecules that govern the decision of blood vascular endothelial cells to segregate into lymphatic vasculature are unknown. Here, we deleted endothelial *Rac1* in mice (*Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$) and revealed, unexpectedly, that whereas blood vessel morphology appeared normal, lymphatic-blood vessel separation was impaired, with corresponding edema, haemorrhage and embryonic lethality. Importantly, normal levels of Rac1 were essential for directed endothelial cell migratory responses to lymphatic-inductive signals. Our studies identify Rac1 as a crucial part of the migratory machinery required for endothelial cells to separate and form lymphatic vasculature.

KEY WORDS: *Rac1* conditional knockout, Lymphangiogenesis, Vegfr3 (Flt4), *Tie1-Cre*, Blood-filled lymphatics

INTRODUCTION

Sprouting angiogenesis in the developing mouse embryo involves endothelial cell activation and migration to form vascular tubes and occurs after embryonic day (E) 8.5, whereas early heart development and vasculogenesis occur before this stage (Risau, 1997; Risau and Flamme, 1995). By E11.5, endothelial progenitors, stimulated by vascular endothelial growth factor C (Vegf-C), migrate away from the cardinal vein and begin to form the lymphatic vascular system (Alitalo et al., 2005; Karkkainen et al., 2004; Oliver and Alitalo, 2005). Thus, endothelial cell migration is an essential process for both angiogenesis and lymphangiogenesis, but the endothelial migratory machinery that determines the precise coordination of these processes is unknown.

Rho GTPases play key roles in coordinating the cellular responses required for cell migration. In particular, Rac1 is considered essential for endothelial cell migration in vitro (Garrett et al., 2007; Nobes and Hall, 1999; Ridley et al., 2003; Soga et al., 2001; Zeng et al., 2002), and for lumen and tube formation in vitro (Bayless and Davis, 2002; Cascone et al., 2003; Connolly et al., 2002; Davis and Bayless, 2003; Koh et al., 2008). The constitutive ablation of *Rac1* results in embryonic lethality owing to defects during gastrulation (Sugihara et al., 1998). Nevertheless, the loxP-Cre-based conditional gene-targeting approach has been extensively applied to delete *Rac1* in a tissue- and cell-type-specific manner (Wang and Zheng, 2007). Both *Tie1-Cre* and *Tie2* (*Tek*)-*Cre* transgenic mice show Cre recombinase activity in the developing endothelial cells of embryos (Gustafsson et al., 2001; Iljin et al., 2002; Kisanuki et al., 2001; Schlaeger et al., 1997). Although early, tissue-specific deletion of *Rac1* in *Tie2-Cre* mice has revealed a role for this molecule in heart development and early vasculogenesis (Tan et al., 2008), because these embryos display an arrested phenotype at E8.5 and begin to die at E9.5 an examination of the role of Rac1 in developmental sprouting angiogenesis and lymphangiogenesis was not possible.

Here, we show by deleting *Rac1* in an alternative Cre-expressing model, *Tie1-Cre* mice, that embryo survival is increased, such that the role of Rac1 in both sprouting angiogenesis and lymphangiogenesis could be investigated. We demonstrate that when endothelial *Rac1* is deleted, blood vessels appear normal, but we reveal a previously unknown role for this Rho GTPase in regulating lymphatic-blood vessel separation during embryogenesis.

MATERIALS AND METHODS

Mice

Heterozygous (*Rac1*$^{fl/+}$) and homozygous (*Rac1*$^{fl/fl}$) floxed mice (Walmsley et al., 2003) were intercrossed with *Tie1-Cre* transgenic mice (Gustafsson et al., 2001) (provided by Prof. R. Fässler, Max-Planck Institute of Biochemistry, Germany) to generate *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ mice with conditional deletion of *Rac1* in endothelial cells. *Tie1-Cre*$^+$;*Rac1*$^{fl/+}$ and *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ were used as controls and no differences were observed between them (data not shown). The developmental stage of mouse embryos was determined by considering 10.00 h on the day of the vaginal plug as E0.5. For *Rac1* PCR genotyping, the following primers were used: forward primer 1, 5′-ATTTTGTGCCAAGGACAGTGACAAGCT-3′; forward primer 2, 5′-GAAGGAGAAGAAGCTGACTCCCATC-3′; and reverse primer 3, 5′-CAGCCACAGGCAATGACAGATGTTC-3′. Products are 300 bp (endogenous *Rac1* locus), 328 bp (floxed *Rac1* locus: flox allele) and 175 bp (Cre-excised *Rac1* locus: null allele). PCR analysis for *Tie1-Cre* transgenesis was performed in parallel. All procedures on mice were in accordance with United Kingdom Home Office regulations.

Antibodies and immunohistochemical analysis

Antibodies used were: rabbit anti-mouse Lyve1 (gift from Prof. K. Alitalo, Biomedicum Helsinki, Finland), Syrian Hamster anti-mouse podoplanin (Acris), rabbit anti-mouse Prox1 (Abcam), rat anti-mouse endomucin (gift

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from Prof. D. Vestweber, Max Planck Institute of Molecular Biomedicine, Germany), rabbit anti-laminin (Sigma), Cy3-conjugated mouse anti-α-smooth muscle actin (α-SMA; Acta2 – Mouse Genome Informatics; Sigma), rat anti-mouse Ki67 (Dako) and mouse anti-Rac1 (clone 23A8; Upstate Biotechnology). For Rac1 immunostaining, embryos were snap-frozen and 5 μm sections were processed as described (Benitah et al., 2005). For all other immunostaining, embryos were paraffin-embedded and 5 μm sections were treated with sodium citrate buffer (pH 6.0) or trypsin retrieval solutions. Fluorescent or 3,3-diaminobenzidene (DAB, Sigma)-chromogenic detections were carried out using fluorochrome-conjugated (Molecular Probes) or biotin-conjugated (Vector Laboratories) secondary antibodies, respectively. For DAB detection, the ABC Vectastain Elite Peroxidase-based Kit was also used (Vector Laboratories), and sections were counterstained with hematoxylin, cleared and mounted in Permount (Sigma). Fluorescently-stained sections were incubated with DAPI (Invitrogen) and mounted with Gelvatol (Calbiochem) containing anti-fade DABCO (Sigma). Immunostaining was examined either using a confocal laser-scanning microscope (Zeiss) with accompanying LMS 510 software, or a bright-field microscope (BX41, Olympus) with an Olympus camera (DP70) and DP version 1.2.1.108 software. Images were processed with Adobe Photoshop CS2.

Whole-mounts and vessel quantitation

E10.5 whole embryos, and yolk sacs and tissues from E12.5 embryos, were fixed in 4% paraformaldehyde (PFA), blocked in 0.3% Triton X-100 in PBS containing 10% normal goat serum, and incubated with rat monoclonal anti-mouse Pecam1 (clone MEC 13.3, Pharmingen) or rat anti-mouse endomucin antibodies. After incubation with Alexa Fluor 488-conjugated anti-rat antibodies (Molecular Probes), samples were analysed using a fluorescence stereomicroscope (M2 Bio Quad, Carl Zeiss) equipped with a colour digital camera (AxioCam HRc, Carl Zeiss) and multi-channel software (AxioVision4 P4, Carl Zeiss). Images were processed with Adobe Photoshop CS2. Whole-mount Pecam1 staining of E12.5 hindbrains was performed as described (Ruhrberg et al., 2002). For each genotype, the number of sprouting microvessels on the pial side and the number of vessel branch-points on the subventricular side were determined in six randomly chosen 0.25 mm^2 fields.

X-Gal staining in transgenic embryos

Tie1-Cre$^+$;*Rac1*$^{fl/+}$ mice were intercrossed with ROSA26R reporter mice (Soriano, 1999) (The Jackson Laboratory, ME, USA) and E9.5 and E10.5 embryos were used for whole-mount X-Gal staining to test for Cre activity (Gustafsson et al., 2001).

Three-dimensional (3D) embryonic vasculature reconstructions

Approximately 100 serial 5 μm transverse sections through comparable levels of the jugular region of E12.5 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, cranial to caudal orientated, were stained for Lyve1. Photographs were taken at 20× magnification using a Nikon E1000 with a DXM 1200 camera and associated Eclipse software (Nikon). Images were loaded and aligned using Autoaligner and Imaris software (Bitplane AG, Zurich, Switzerland). Left lymphatic sac and cardinal vein perimeters were outlined to create the solid contour surface of these vessels. Snapshots at various *x*, *y* and *z* positions of 3D rotational views were taken to illustrate the juxtapositional distance between the jugular lymph sac and the cardinal vein.

India ink visualisation of blood vessels

India ink (2-4 μl) was injected into the left ventricle, embryos fixed in 4% PFA, dehydrated for 30 minutes each in ascending concentrations of ethanol and cleared in 100% methyl salicilate (Sigma), and then photographs taken.

Isolation of embryonic endothelial cells

E12.5 embryos were dissected and livers and spleens removed to exclude hematopoietic cells. Embryos were digested in 2.4 U/ml Dispase/0.1% collagenase 1 (both Gibco) to produce single-cell suspensions. Cells were pelleted by low-speed centrifugation, resuspended in MLEC medium (Reynolds and Hodivala-Dilke, 2006) and plated onto tissue culture plates coated with 0.1% gelatin containing 10 μg/ml fibronectin (Sigma) and 10 μg/ml Vitrogen (Cohesion). At ~80% confluency, macrophages were removed from the culture by immunosorting using rat anti-mouse CD16/CD32 (Fcgr3/Fcgr2b) Fcγ receptor antibodies with a subsequent sort to positively select for endothelial cells using rat anti-mouse Icam2 antibodies (Reynolds and Hodivala-Dilke, 2006). Endothelial cell purity was 98% as assessed by Pecam1 expression. For some of our *Rac1* siRNA and Rac1 activity assays we isolated primary mouse lung endothelial cells (MLECs) from *Vegfr3*$^{+/-}$ and wild-type 4- to 6-week-old mice as reported (Reynolds and Hodivala-Dilke, 2006). *Vegfr3*$^{+/-}$ mice (Dumont et al., 1998) were provided by Dr T. Tammela and Prof. K. Alitalo (Biomedicum Helsinki, Finland).

Lymphatic microvascular endothelial cell culture

Dermal-derived normal neonatal human primary lymphatic microvascular endothelial cells (HMVEC-dLy-Neo; Lonza) were maintained in EGM 2-MV medium supplemented with appropriate BulletKit (Lonza) and used prior to passage 5.

Rac1 siRNA

siGENOME ON-TARGETplus SMARTpool reagents (Dharmacon) were used. MLECs and HMVEC-dLy-Neo cells were transfected with anti-mouse and anti-human *Rac1* siRNA, respectively, using Oligofectamine (Invitrogen). The final concentration of oligonucleotides in the transfection mixture was 100 nM and gene expression was examined 48 hours post-transfection by RT-PCR and/or western blot. In all transfections, scrambled siRNA (Dharmacon)-transfected cell samples were used as controls.

Western blot analyses

Cells were grown to ~80% confluency and lysed with RIPA buffer (50 mM Tris-HCl pH 7.4, 1% NP40, 0.25% sodium deoxycholate, 150 mM NaCl, 1 mM EDTA, 1 mM Na_3VO_4, 1 mM NaF, 1 mM PMSF) supplemented with a protease inhibitor cocktail (Calbiochem). Mouse antibodies against Rac1, Cdc42 (Chemicon), RhoA (Santa Cruz) and human VEGFR3 (clone 9D9F9, a gift from Prof. K. Alitalo, Biomedicum Helsinki, Finland) were used. A western blot for Vegfr3 identifies three bands (Bando et al., 2004). Membranes were stripped (Chemicon) and re-probed with mouse anti-Hsc70 (Hspa8) antibody (Santa Cruz). Densitometry was performed using a gel acquisition and analysis set-up (UV Products). Band densities were normalised to Hsc70.

Semi-quantitative RT-PCR

Rac1 isoform-specific primers and RT-PCR conditions were as described (Wells et al., 2004). As controls in *Rac2* and *Rac3* reactions, cDNA was synthesised from total RNA from spleen and brain tissues. RT-PCR of actin provided a loading control.

GTPase activity assays

A construct encoding glutathione S-transferase linked to amino acid residues 57 to 141 of the PAK-CRIB domain (gift from Drs J. Collard, King's College and V. Braga, Imperial College, London, UK) was used to pull down active Rac1 and Cdc42 (Nystrom et al., 2006) in MLECs transfected with scrambled or *Rac1* siRNA. For Rac1 activity in *Vegfr3*$^{+/-}$ endothelial cells, the cells were stimulated with 500 ng/ml Vegf-C156S for 30 minutes. RhoA activity was assessed using the G-LISA RhoA Activation Assay Biochem Kit (Cystoskeleton, CO, USA).

Separation of embryonic endothelial cell populations by FACS

E11.5 embryos were digested as above. Erythrocytes were excluded by treatment with Lymphoprep (Axis-Shield). Fcγ receptors were blocked with rat anti-mouse CD16/CD32 antibody. Cells were stained with the following antibodies at 1 μg/10^6 cells on ice for 30 minutes: mouse anti-mouse CD45 (clone 104), peridinin chlorophyll protein (PerCP) cyanine 5.5 (Cy5.5)-conjugated; rat anti-mouse CD31 (Pecam1) (clone MEC 13.3), fluorescein isothiocyanate (FITC)-conjugated; rat anti-mouse CD34 (clone RAM 34), R-phycoerythrin (R-PE)-conjugated (all from Pharmingen); biotinylated anti-mouse Lyve1 (eBioscience) and goat anti-mouse Vegfr3 (R&D Systems). Cells were incubated with allophycocyanin (APC)-conjugated streptavidin (Pharmingen) to visualise Lyve1-positive cells and with donkey anti-goat IgG F(ab′)2-APC-Cy7 (Santa Cruz) to visualise Vegfr3. Cell populations were analysed using an LSRII flow cytometer or with a FACSAria cell sorter (Becton Dickinson) and data analysed with FACS Diva software (BD Immunocytometry Systems). Several controls, including isotope antibodies, fluorescence-minus-one (Perfetto et al., 2004) and unstained samples were performed to determine appropriate gates, voltages and compensations.

Cytospin

$CD45^-$/$Pecam1^+$ FACS-sorted cells were cytospun, fixed in acetone, probed with rabbit anti-mouse Prox1, followed by anti-rabbit EnVision (Dako) and DAB staining. Cells were counterstained with Hematoxylin and Eosin.

Migration assays

siRNA-treated HMVEC-dLy-Neo cells were plated at 375 cells/cm^2 on pre-coated tissue culture plastic and incubated for 18-36 hours in complete growth media. Before time-lapse microscopy, cells were serum-starved and stimulated, or not, with Vegf-C156S (500 ng/ml). Phase-contrast micrographs of live cells were taken using a 768×576 pixel 8-bit CCD camera and 10× Plan/Neofluar objective (Zeiss). Data sets were collected using kinetic imaging motion analysis software. Images were collected every 5 minutes for 8 hours. Tracking of at least 25 cells/sample was performed using MetaMorph software. Analyses of cell speed and persistence were carried out using Mathematica workbooks. Scratch assays were performed as described (Reynolds et al., 2004).

Analysis of statistical significance

Data sets were analysed using Student's *t*-test. $P<0.05$ was considered statistically significant. Results shown are the mean ± s.e.m. from at least three independent experiments.

RESULTS

Rac1 deletion in endothelial cells

To test whether Rac1 deficiency in endothelial cells affects developmental angiogenesis and lymphangiogenesis, *Rac1*-floxed mice (*Rac1*$^{fl/fl}$) were bred with mice expressing Cre recombinase under control of the *Tie1* promoter (*Tie1-Cre*) (Gustafsson et al., 2001). To confirm the onset of active Cre expression, *Tie1-Cre*$^+$;*Rac1*$^{fl/+}$ mice were intercrossed with the reporter strain Rosa26R (R26R) (Soriano, 1999) and tissues examined for Cre activity by X-Gal staining of whole embryos. It has been reported that *Tie1*-driven Cre activity is detectable in the developing heart tube, dorsal aorta and head mesenchyme as early as E8.5 (Gustafsson et al., 2001). Here we showed that, by E9.5, *R26R*$^+$;*Tie1-Cre*$^+$;*Rac1*$^{fl/+}$ double-transgenic embryos displayed clear Cre activity in the vast majority of primitive blood vessels, and by E10.5 in virtually all blood vessels (see Fig. S1A in the supplementary material). Moreover, by double immunostaining for Rac1 and endomucin [a blood vascular endothelial cell marker (Morgan et al., 1999)], we showed that Rac1 was not detectable in endomucin-positive blood vessels, despite its presence in surrounding cells, of E10.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. By contrast, Rac1 was expressed in both endomucin-positive blood vessels and surrounding cells of E10.5 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ control embryos (see Fig. S1B in the supplementary material).

Tie1-Cre-mediated recombination of the *Rac1*-floxed gene was demonstrated by examining the presence of *Rac1* flox (328 bp) and null (175 bp) alleles by PCR analysis of various embryonic tissues. Yolk sacs and aortae (tissues with a high proportion of endothelial cells) from *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos showed extensive loss of the *Rac1*-floxed allele to produce the *Rac1*-null allele, as compared with tail tissue (which has a lower proportion of endothelial cells). By contrast, no detectable recombination was observed in tissues from *Rac1*$^{fl/fl}$ embryos that do not carry the *Tie1-Cre* transgene (see Fig. S1C in the supplementary material) or those that were *Tie1-Cre*$^+$;*Rac1*$^{+/+}$ (data not shown). Furthermore, western blot analysis from cell populations enriched with endothelial cells isolated from *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos showed that Rac1 was barely detectable when compared with lysates from *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ controls (see Fig. S1D in the supplementary material). Together, these data indicate that in our model, embryonic Rac1 expression is depleted significantly, not only in endothelial cell cultures isolated from *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, but importantly and significantly, also in the vasculature of *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos in vivo.

Tie1-Cre$^+$;*Rac1*$^{fl/fl}$ mice die in utero

Genotyping of the progeny of *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/+}$ transgenic mice revealed that *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ mice did not survive to birth (see Fig. S1E in the supplementary material). To determine the onset of lethality, embryos were analysed at various gestational stages from E9.5 onwards. Up to, and including, E12.5, all *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos were viable and morphologically indistinguishable from *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ controls at the gross level. By contrast, after E13.5, *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryo survival was compromised, with only 64% of mutant mice surviving at E13.5 and 50% at E15.5. By E17.5, no mutant embryos were found alive.

Blood vessel morphology appears normal in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos

To determine the cause of death in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, we examined their vasculature at E10.5, when *Rac1* was clearly deleted from blood vessels (see Fig. S1B-D in the supplementary material). Whole-mount staining for endomucin revealed that the vascular pattern in E10.5 mutants was normal (Fig. 1). Since Rac1 has been postulated to be required for endothelial cell migration, at least in vitro, we hypothesised that Rac1 is likely to play a role in blood vessel formation. Surprisingly, the endocardium, perineural plexus and intersomitic vessels were all present and well developed in E10.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos (Fig. 1A). Furthermore, high-magnification examination revealed that blood vessel branching and sprouting patterns in the perineural plexus (Fig. 1B) and intersomitic vasculature (Fig. 1C) were normal in the mutant embryos.

Further analysis revealed that at E12.5, the normal appearance of *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos (Fig. 2A) correlated with normal vasculature both in the forelimbs and intestine (Fig. 2B). Yolk sac vasculature was also analysed by whole-mount staining for endomucin, which revealed that this vascular network was also normal in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos (Fig. 2C). Indeed, no change in the dilation of vessels or in their structure was apparent (Fig. 2A-C). Moreover, India ink injections into the left ventricle, in combination with anatomical, Hematoxylin and Eosin (H&E) and immunohistochemical analyses of E12.5 embryos did not reveal any obvious haemorrhage or edema and the vasculature of the *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos appeared normal (see Fig. S2A in the supplementary material). Overall, these results indicate that deletion of *Rac1* in the endothelium of *Tie1-Cre* mice does not inhibit the development of normal blood vasculature.

We next quantitated the degree of angiogenesis in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. During development, the cerebral cortex is vascularised by sprouting angiogenesis and produces a vascular plexus that contains a highly reproducible number of vessels and branch-points in mouse embryos (Ruhrberg et al., 2002). Examining the vasculature in the hindbrains of E12.5 embryos by immunostaining for Pecam1 [a pan-endothelial cell marker (Vecchi et al., 1994)] revealed that the number and patterning of sprouting vessels on the pial side were similar in *Tie1-*

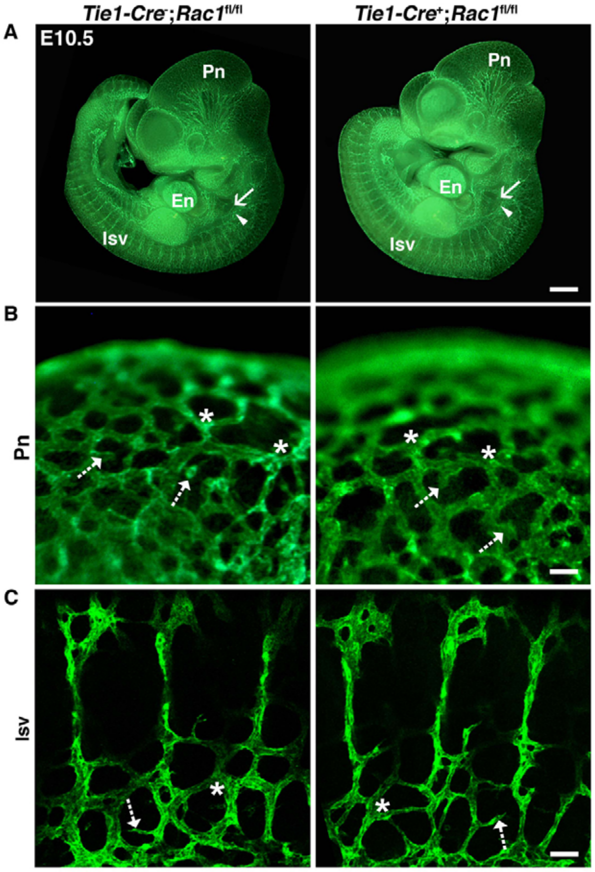

Fig. 1. Normal blood vessel morphology in E10.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ mouse embryos. (**A**) Whole-mount endomucin staining indicates similar vascular patterns in E10.5 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. Major vessels including dorsal aorta (arrowhead) and cardinal vein (arrow), perineural vascular plexus (Pn), endocardium (En) and intersomitic vessels (Isv) are present and well developed in the mutants. (**B**,**C**) High-magnification views of endomucin-stained (B) perineural vascular plexus and (C) intersomitic vessels reveal comparable patterns of vessel sprouting (dashed arrows) and branching (asterisks). Scale bars: 400 μm in A; 50 μm in B,C.

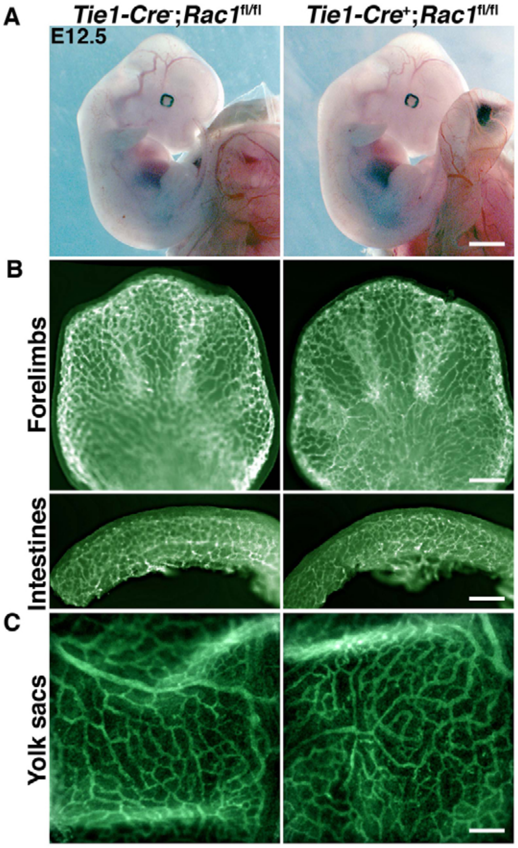

Fig. 2. Embryonic and extra-embryonic blood vessels are normal in E12.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. (**A**) Macroscopic examination of E12.5 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ mouse embryos does not reveal any obvious morphological differences. (**B**) Whole-mount Pecam1 staining of E12.5 control and mutant forelimbs and intestines reveals comparable microvascular networks. (**C**) Whole-mount endomucin staining reveals comparable yolk sac vascular networks in both genotypes. Scale bars: 2.5 mm in A; 250 μm in B,C.

Cre$^+$;*Rac1*$^{fl/fl}$ and controls (Fig. 3A). In addition, the number of branch-points per unit area on the subventricular side of the hindbrains was also comparable between the genotypes (Fig. 3B). These data corroborated our previous results and showed that the degree of angiogenesis in E12.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos is normal.

Other Rho GTPases do not compensate for the loss of Rac1 in endothelial cells

It is conceivable that the absence of an angiogenic phenotype in the *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ mice is due to compensation by other Rho-related GTPases. To test this, levels of Rac2, Rac3, Cdc42 and RhoA were analysed in wild-type and Rac1-depleted microvascular endothelial cells. RT-PCR analysis of Rac1-depleted endothelial cells showed significantly reduced *Rac1* mRNA levels ($P<0.01$; see Fig. S3A in the supplementary material). Similar analysis showed that *Rac2* and *Rac3* mRNAs were not detectable in isolated lung endothelial cells, although positive expression was found by RT-PCR analysis of mRNA extracted from control tissues such as spleen and brain, respectively (see Fig. S3A in the supplementary material). Using western blot analysis and GST-PAK pull-downs, both Rac1 total protein ($P<0.001$; see Fig. S3B in the supplementary material) and active Rac1 levels ($P<0.01$, see Fig. S3C in the supplementary material) were reduced significantly in Rac1-depleted endothelial cells. By contrast, transfection of endothelial cells using a scrambled siRNA (Con siRNA) had no effect on Rac1 expression or activity (see Fig. S3A-C in the supplementary material). In addition, Cdc42 and RhoA total protein and active levels were not affected by Rac1 depletion (see Fig. S3C in the supplementary material). These results indicate that other members of the Rho family of small GTPases, at least those tested, do not compensate for the loss of Rac1 in endothelial cells in vitro.

Lymphatic vessels of E13.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos are filled with blood

Until E12.5, *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos appeared morphologically normal. By E13.5, however, embryo survival was reduced to 64%. From E13.5 onwards, 39% of *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos could be identified by a combination of phenotypes including the appearance of edema, blood-filled lymphatics, blood vessel tortuosity,

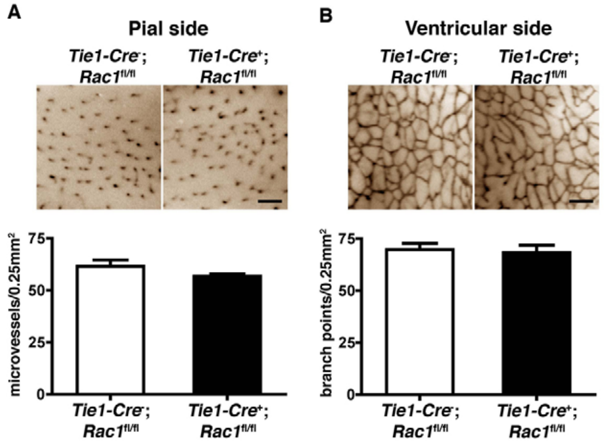

Fig. 3. Sprouting angiogenesis does not rely on endothelial Rac1 expression in vivo. (**A**,**B**) The perineural vascular network was visualised at E12.5 by whole-mount Pecam1 staining on mouse hindbrains. Quantitation of (A) the number of sprouting vessels on the pial side and (B) the microvessel branch-points on the subventricular side in random areas of 0.25 mm^2 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ hindbrains shows no significant differences. *n*=8 embryos per genotype. Scale bars: 100 μm.

haemorrhage and involuting limbs (Fig. 4A). Analysis of H&E-stained sections of these embryos confirmed edema in the dorsal skin and haemorrhage in the mesenchyme of the developing forelimbs (Fig. 4B). In addition, the blood vessels in these involuting forelimbs, detected by immunostaining for laminin, appeared collapsed (Fig. 4B). Additional examination of aortae by double immunostaining for laminin and α-smooth muscle actin [a mural cell marker (Gerhardt and Betsholtz, 2003)] revealed that these blood vessels also appeared collapsed in the *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos and were of significantly smaller diameter than those of controls ($P<0.001$; Fig. 4C). These defects in blood vessel morphology might reflect either a secondary response to the haemorrhage in these mice, as they were not observed in non-haemorrhagic mutant mice, or the onset of increased fragility. Together, these results raised the question as to why *Rac1* deletion in endothelial cells might cause this phenotype at this stage of development, especially considering that angiogenesis is normal in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos.

In vertebrates, the lymphatic vasculature develops after the blood vasculature has formed. Edema is a read-out of the malfunction of the blood vessels or lymphatic vasculature, but because we did not detect any changes in the blood vasculature until E12.5, we focused our attention on the lymphatics. As originally proposed by Sabin, a subpopulation of endothelial cells migrates centrifugally from the cardinal veins to form lymph sacs and finally develops into the lymphatic network (Sabin, 1902; Sabin, 1904). In adult mice, lymphatic and blood vessels do not communicate, except at the point where the thoracic duct empties into the subclavian vein, and aberrant, persistent connections between the two systems lead to blood-congested lymphatic vessels (Abtahian et al., 2003). Immunohistochemical examination of sections at comparable levels of the thoracic region from E13.5 embryos for the expression of Lyve1 and podoplanin [lymphatic endothelial cell markers (Kaipainen et al., 1995; Prevo et al., 2001)] and endomucin (a blood vascular, but not lymphatic, endothelial cell marker), showed the presence of red blood cells not only in blood vessels, but also in the lymphatic vasculature of *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. Importantly, this was not evident in any of the control embryos examined (Fig. 4D). In contrast to control *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ embryos, blood-congested lymphatic vessels were apparent in E13.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos (see Fig. S4A-C in the supplementary material). Furthermore, we found blood-filled lymphatic vessels not only in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos that displayed haemorrhage, but also in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos that did not (Fig. 4D). These data indicated that the appearance of blood-filled lymphatic vasculature in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos was unlikely to be due to the bleeding observed in these animals at this developmental stage. However, it is interesting to speculate that this phenotype might reflect the presence of abnormal, persistent, direct veno-lymphatic communications between blood vessels and lymphatic vasculature. It is conceivable that the haemorrhage observed might be caused by a combination of increased blood vessel fragility and the rupture of blood-congested lymphatic vessels. Although no blood vessel defects were evident at E12.5 (see Fig. 3 and Fig. S2 in the supplementary material), some loss of blood vessel integrity was observed at E13.5 (see Fig. 4B,C). Moreover, the rupture of blood-congested lymphatic vessels and subsequent haemorrhage into the surrounding mesenchyme was detected in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos (see Fig. S4D in the supplementary material).

Given that we observed blood in lymphatic vessels in E13.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, even in the absence of any overt bleeding, this suggested that somehow blood was entering the lymphatics directly from the blood vasculature and that this might be due to a defect in the separation of blood vessels and lymphatic vessels. Indeed, the separation of the jugular lymph sac from the parental cardinal vein in mice is normally considered to be complete by E12.5 (Oliver, 2004; Oliver and Alitalo, 2005), so blood should not be detectable in the lymphatics at E12.5. To investigate the possibility that endothelial *Rac1* deletion affects lymphatic-blood vessel separation, we analysed *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos at E12.5. Similar to observations made at E13.5, in E12.5 embryos red blood cells were evident in both endomucin-positive cardinal veins and Lyve1- and podoplanin-positive jugular lymph sacs of *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, but never in controls (Fig. 5A). Furthermore, the distance between the cardinal veins and the laterally located jugular lymph sacs was reduced significantly in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos compared with controls at similar thoracic levels ($P<0.0001$; Fig. 5A). It is important to note that although a common reason for the appearance of blood in the lymphatics is overt haemorrhage into tissue stroma, our results are distinct from this: in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, the presence of blood in the lymphatics is not due to prior bleeding, and blood-filled lymphatic vessels appear before haemorrhage in these mice.

In addition, by performing unilateral three-dimensional reconstructions of the jugular lymphatic sac and cardinal vein using over one hundred 5 μm serial sections from E12.5 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, we demonstrated that endothelial *Rac1* deletion substantially reduced the distance between these two vessels (Fig. 5B). These results suggested that expression of Rac1 in endothelial cells is crucial for proper lymphatic-blood vessel separation during embryonic development.

Endothelial Rac1 deficiency impairs the transition from blood endothelial cell to lymphatic endothelial cell

We then sought to determine the mechanism underlying the poor separation between the lymphatic and blood vasculature in the *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. A pre-requisite for lymphatic vessel

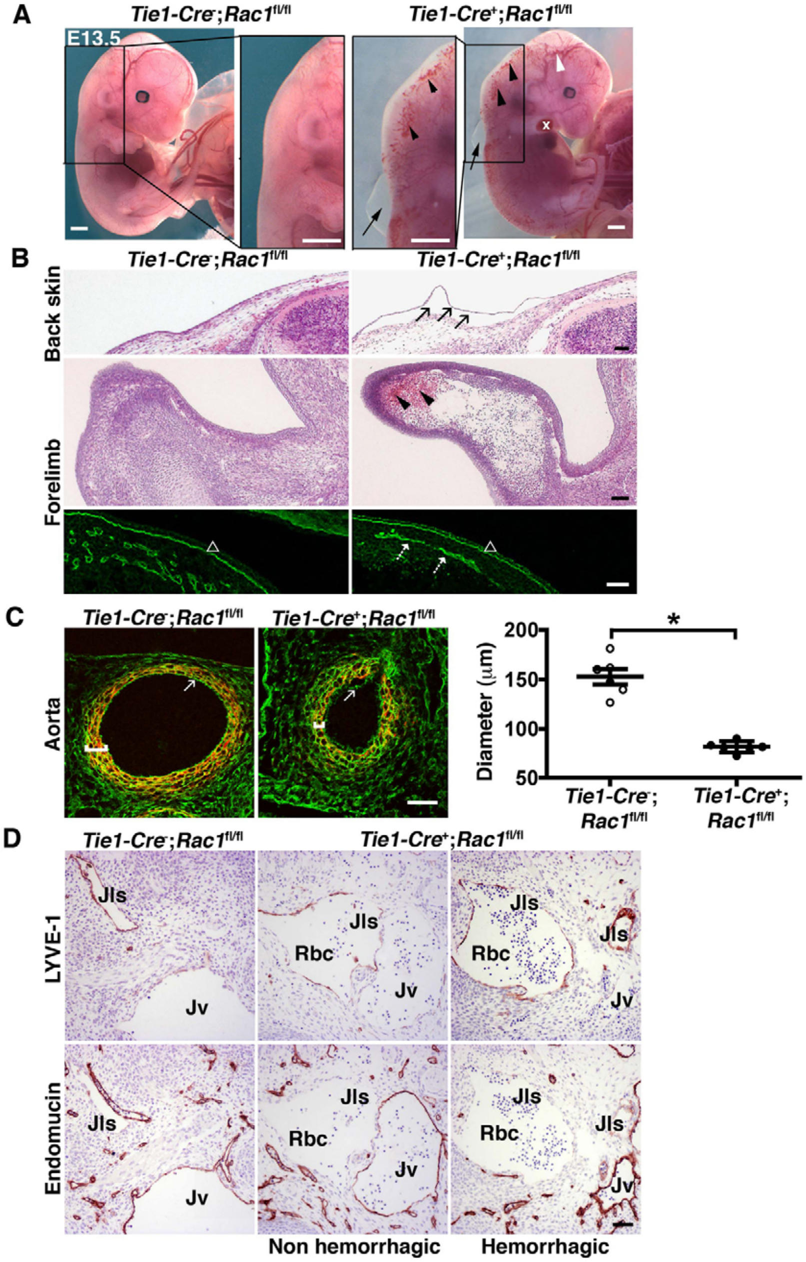

Fig. 4. E13.5 *Tie1-Cre*$^+$*;Rac1*$^{fl/fl}$ embryos display gross morphological abnormalities and blood-filled lymphatic vessels. (**A**) Macroscopic examination shows that 39% of E13.5 *Tie1-Cre*$^+$*;Rac1*$^{fl/fl}$ mouse embryos display edema (arrow), tortuous blood vessels (white arrowhead), blood-filled lymphatics (black arrowheads) and haemorrhagic involuting forelimbs (white ↔). Insets show high-magnification views of edema and blood-congested lymphatics. (**B**) Transverse sections of H&E-stained back skin and forelimb and laminin-stained forelimbs. Arrows, epidermal blisters; arrowheads, haemorrhage; white dashed arrowheads, capillary collapse; open arrowhead, epidermal basement membrane. (**C**) Merged images of transverse sections double immunostained for laminin (green) and α-smooth muscle actin (α-SMA; red); endothelium (arrow) and mural cell coverage (bracket). Graph shows that aortic diameters are significantly smaller in mutant embryos. $^*P<0.001$, $n=6$ embryos per genotype. (**D**) Serial transverse sections through the thoracic region of *Tie1-Cre*$^-$*;Rac1*$^{fl/fl}$ embryos and of *Tie1-Cre*$^+$*;Rac1*$^{fl/fl}$ embryos without and with haemorrhage. Lyve1 identifies the endothelium in jugular lymph sacs (Jls) and endomucin identifies the endothelium in jugular vein (Jv) in both genotypes. Red blood cells (Rbc) are present in lymphatic vessels of mutants but not controls. Scale bars: 1 mm in A; 50 μm in B-D.

formation and separation is the transition of a subset of committed venous endothelial cells to differentiate into lymphatic endothelial cells (Alitalo et al., 2005; Oliver, 2004). This occurs at ~E11.5 and involves a stage in which some cells transiently express both endothelial and lymphatic vessel markers. Previous work has shown that Spred1/2 doubly deficient mice have lymphatic defects, which correlates with increased numbers of Lyve1/CD34 double-positive cells (Taniguchi et al., 2007). To examine whether Rac1 expression in endothelial cell populations [CD45$^-$ (Ptprc)/Pecam1$^+$] from E11.5 embryos affected the proportion of cells expressing either blood endothelial cell (BEC) markers (Lyve1$^-$/CD34$^+$), lymphatic endothelial cell (LEC) markers (Lyve1$^+$/CD34$^-$) or both [Lyve1/CD34 double-positive], we carried out FACS analysis of CD45$^-$/Pecam1$^+$ endothelial cells for Lyve1 and CD34. The proportion of cells that were CD45$^-$/Pecam1$^+$ was similar in both genotypes (see Fig. S5A in the supplementary material). In *Tie1-Cre*$^+$*;Rac1*$^{fl/fl}$ embryos, although the percentage of LECs and BECs appeared normal, a significantly increased Lyve1/CD34 double-positive cell population, which was likely to represent a transition state of LECs from BECs, was found in mutant embryos when compared with controls ($P<0.03$; see Fig. S5B in the supplementary material).

Vegf receptor 3 (Vegfr3; Flt4) identifies blood vasculature during early embryonic development, but at ~E11.5-12.5 its expression becomes restricted to the lymphatic vasculature (Kaipainen et al., 1995). We performed similar assays replacing analysis of Lyve1 with that of Vegfr3 and showed that loss of Rac1 in endothelial cells leads to an increase in Vegfr3/CD34 double-positive cells ($P<0.05$; see Fig. S5C in the supplementary material). This could reflect either a delay in maturation of BECs or a delay of committed differentiating LECs in downregulating BEC markers. Since we did not observe any change in blood vascular morphology or function, our data suggest that Rac1 might be responsible for regulating, at least temporarily, the degree of transition of BECs to LECs.

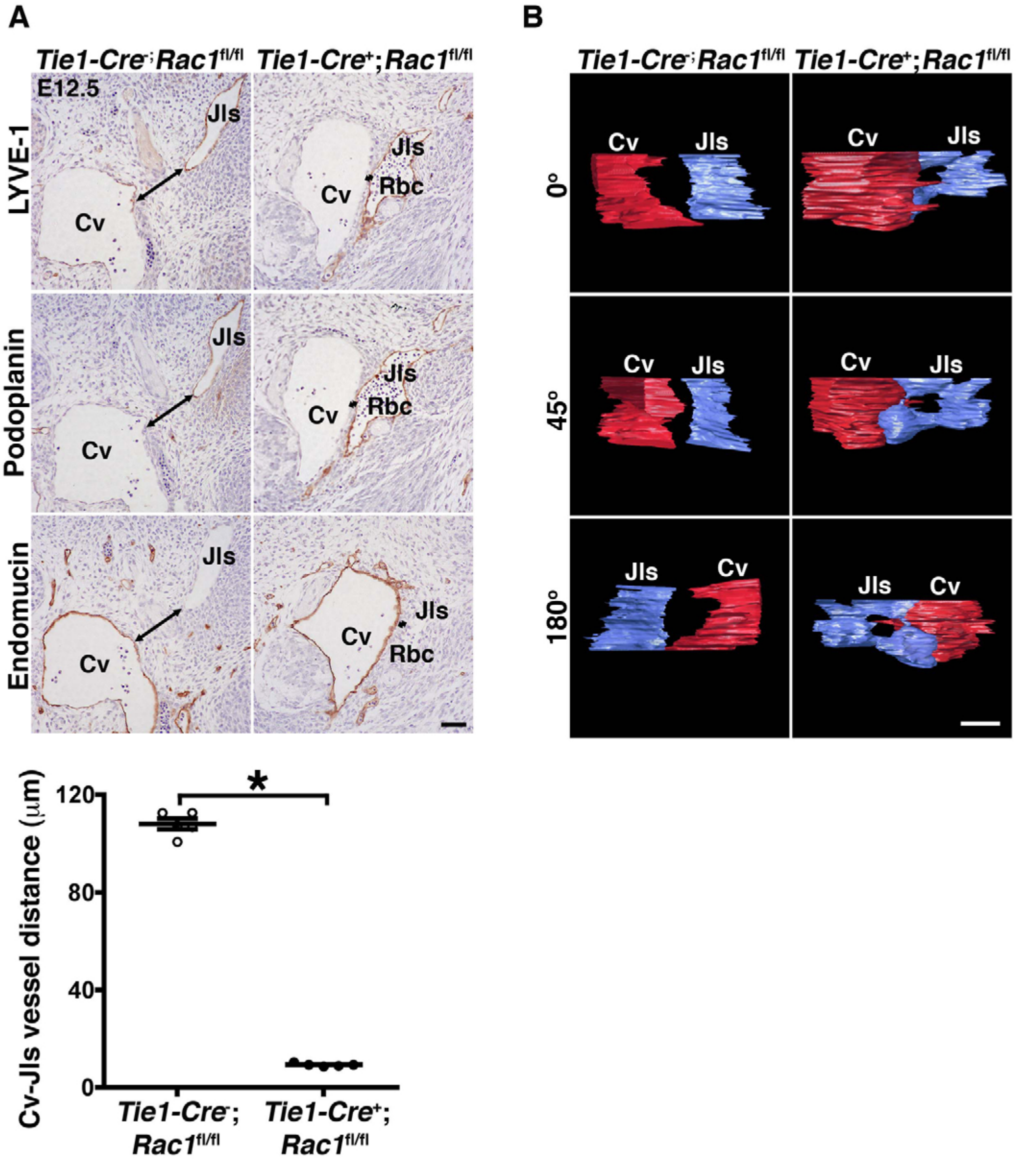

Fig. 5. Abnormal lymphatic-blood vessel segregation in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. (**A**) Serial transverse sections through the jugular region of E12.5 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ mouse embryos. Lyve1 and podoplanin staining identify jugular lymph sacs (Jls) in both genotypes. Red blood cells (Rbc) are present in the lymphatic vasculature of mutants but not controls. Juxtaposition (double arrowheads) of jugular lymph sacs to the cardinal vein (Cv) is closer in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos than in controls. Endomucin staining of blood vascular endothelium, including that of the cardinal vein, showed no apparent differences between genotypes. Graph of shortest vein-lymphatic vessel distances at comparable levels through the jugular region of E12.5 mutants and controls, showing that the juxtaposition is closer in mutants. *$P<0.0001$, $n=5$ embryos per genotype. (**B**) Unilateral 3D reconstruction of the cardinal vein (red) and lymphatic sac (blue) from E12.5 *Tie1-Cre*$^-$;*Rac1*$^{fl/fl}$ and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. Snapshots from movies of reconstructions were taken at 0° (top), 45° (middle) and 180° (bottom) of rotational views on the *y*-axis to illustrate the juxtaposition distance between these two vessels in each genotype. Scale bars: 50 μm in A; 250 μm in B.

Rac1 regulates budding of Prox1-expressing endothelial cells from the cardinal vein

Lymphatic vessel development involves the migration of differentiating LECs from the cardinal vein into the mesenchyme in a process known as budding. This process can be morphologically identified at E11.5 when Prox1-expressing LEC progenitors migrate away from the cardinal vein and begin to organise into primitive lymph sacs (Wigle and Oliver, 1999; Oliver and Alitalo, 2005). We hypothesised that the abnormal lymphatic-blood vessel separation found in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos might reflect abnormal cell migration during budding, and examined the expression patterns of Prox1-positive cells in E11.5 *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ and control embryos. In both genotypes, Prox1-positive staining was restricted to a subpopulation of endothelial cells located on one side of, and budding off, the cardinal vein. However, analysis of Prox1-stained sections revealed that the percentage of Prox1-positive endothelial cells within the wall of the cardinal vein was reduced significantly in mutant embryos ($P<0.0001$; Fig. 6A-C). Furthermore, the distribution patterns of budding Prox1-positive cells were altered in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. Whereas in control embryos Prox1-positive cells appeared to follow a narrow path of migration, the distribution pattern of the majority of Prox1-positive cells in the *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos appeared to be wider and more random (Fig. 6A,B). Analysis of these areas showed that the average maximum width to maximum length ratio was elevated significantly in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos when compared with controls ($P<0.005$; Fig. 6B). In addition, the number of Prox1-positive cells in these areas was reduced significantly in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos ($P<0.01$; Fig. 6A-C). Ki67/Prox1 double immunostaining of this region showed that this reduction in Prox1-positive cells did not correlate with a decrease in the percentage of Ki67-positive proliferating cells (see Fig. S6A,B in the supplementary material). Moreover, quantitation of the numbers of Prox1-positive cells in cytospins of CD45$^-$/Pecam1$^+$ FACS-sorted cells from E11.5 embryos showed no significant difference between genotypes (see Fig. S6C in the supplementary material). This indicated that the total number of Prox1-positive cells in the CD45$^-$/Pecam1$^+$ population was not affected by *Rac1* deletion. Taken together, these data

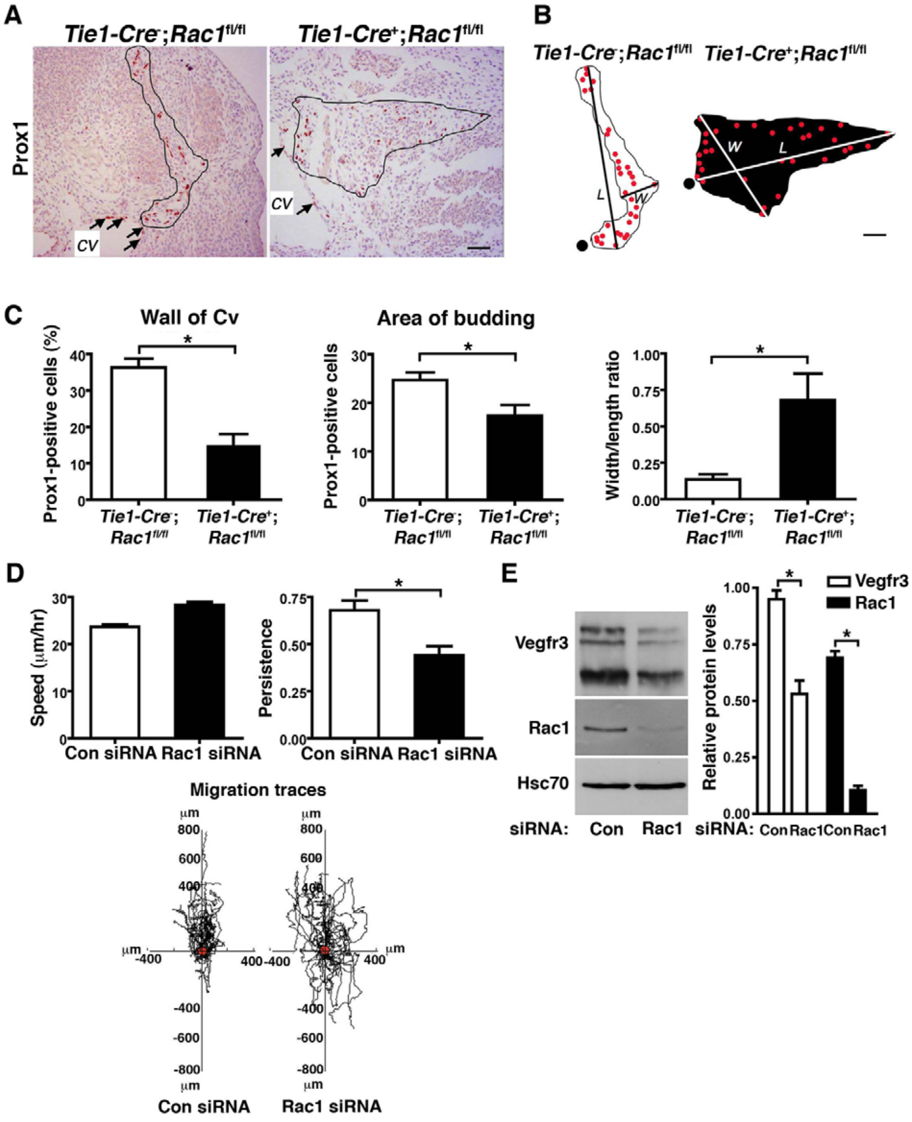

Fig. 6. Endothelial Rac1 regulates the distribution patterns of budding Prox1-positive cells, Vegf-C156S-mediated motility and Vegfr3 expression. (**A**) Transverse sections at comparable levels of E11.5 control and *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ mouse embryos immunostained for Prox1. Prox1 expression was observed in a subset of cardinal vein (Cv) endothelial cells (arrows) and in cells budding off into the mesenchyme (enclosed by black outline). (**B**) Schematic of the patterning of budding Prox1-positive cells in vivo. Black dot represents the closest point of cardinal vein to the area of budding Prox1-positive cells. W, maximum width; L, maximum length. Graph shows mean ± s.e.m. of width:length ratios. *$P<0.005$. Scale bars: 50 μm. (**C**) Percentage of Prox1-positive endothelial cells in the cardinal vein wall and number of Prox1-positive cells in the area of budding were significantly reduced in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos (mean ± s.e.m.). *$P<0.01$. n=9 embryos per genotype. (**D**) Vegf-C156S-mediated migratory responses of scrambled (Con) or *Rac1* siRNA-transfected lymphatic endothelial cells (LECs). Rac1 depletion in LECs modestly increased Vegf-C156S-stimulated cell speed and dramatically decreased persistence (*$P<0.001$). Bar charts represent mean ± s.e.m. n=175-200 cells per condition. Representative migration traces for Con and *Rac1* siRNA-transfected LECs are given. (**E**) Con and *Rac1* siRNA-transfected LEC extracts immunoblotted for Vegfr3 and Rac1 show that Rac1 depletion reduces Vegfr3 expression. Hsc70, loading control. Densitometry results (means ± s.e.m.) of relative protein levels. *$P<0.01$, n=3.

suggest that endothelial Rac1 deficiency not only appears to alter the degree of transition of BECs to LECs, but also that it is sufficient to impair the pattern of cell migration during lymphatic budding.

Aberrant motility of Rac1-depleted LECs is associated with reduced Vegfr3 protein levels

The migration of Prox1-expressing endothelial cells from the cardinal vein to newly forming lymph sacs is regulated by a concentration gradient of Vegf-C within the surrounding mesenchyme (Karkkainen et al., 2004). Given that the distribution patterns of Prox1-positive cells were altered in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos, we tested whether *Rac1* depletion in LECs would affect Vegf-C-mediated migration in vitro. Although Vegf-C is a ligand for both Vegfr3 and Vegfr2 (Kdr), its mutant form Vegf-C156S binds to Vegfr3 only (Joukov et al., 1998). Despite the fact that Rac1-depleted LECs did not show a change in the rate of Vegf-C156S-mediated migration compared with control cells, by calculating the ratio of linear distance between start and end migration points to actual distance travelled per cell (persistence), Rac1-depleted LECs were found to exhibit a significantly lower persistence than controls ($P<0.001$; Fig. 6D). These data indicate that Rac1-depleted LECs have a more random path of Vegf-C156S-stimulated migration than control cells ($P<0.001$; Fig. 6D). As predicted, knockdown of Rac1, using *Rac1*-specific siRNA, in endothelial cells inhibited Vegf-A164-mediated two-dimensional migration (see Fig. S7 in the supplementary material). Given this change in Vegf-C156S-mediated migration, we next tested the effect of Rac1 depletion on Vegfr3 expression. Western blot analysis showed that Vegfr3 levels were reduced significantly in Rac1-depleted cells compared with controls ($P<0.01$; Fig. 6E). By contrast, Vegf-C156S-stimulated *Vegfr3*$^{+/-}$ endothelial cells showed no change in Rac1 activity, suggesting that although Rac1 can regulate Vegfr3 expression, a substantial loss of Vegfr3 is not sufficient to affect active levels of Rac1 (see Fig. S8 in the supplementary material). It is likely that as LECs were not removed from these preparations, they persist in the endothelial cell cultures. These data suggest that regulation of Vegfr3 expression is a possible mechanism by which the Rac1 Rho GTPase regulates LEC migration and lymphatic-blood vessel separation in vivo.

DISCUSSION

Our data provide the first evidence that in vivo deletion of *Rac1* in *Tie1-Cre* mice is not sufficient to impair sprouting angiogenesis, but is required for the correct migration of committed LECs during lymphatic vessel segregation from blood vessels (see Fig. S9 in the supplementary material). Indeed, deletion of *Rac1* in *Tie1-Cre* mice gives rise to poor veno-lymphatic separation, resulting in leakage of blood into the lymphatic system. Although we cannot rule out the possibility that the haemorrhage observed at this stage could be due to a sudden increase in blood vessel fragility, our data on the normal appearance of functional blood vessels would not appear to support this. Despite the generally accepted involvement of Rac1 in the migration of cultured cells (Nobes and Hall, 1999; Ridley et al., 2003), our data indicate that its role during cell migration in the whole organism is not as clear. We show that *Rac1* deletion in LECs does not affect the Vegf-C-mediated migration rate, but does affect the persistence of migration. Others have reported that the role of Rho GTPases in the migration of cells in 3D, mimicking the in vivo scenario, versus 2D may not be the same (Sahai et al., 2007; Sahai and Marshall, 2003). Indeed, our data showing an apparent lack of effect of *Rac1* deletion on endothelial cell migration during angiogenesis in vivo is reminiscent of other studies that reported that *Rac1* deletion in macrophages does not inhibit migration (Wells et al., 2004).

Recently, it has been shown that *Rac1* deletion in *Tie2-Cre* mice results in gross defects in the development of major vessels by E8.5 and embryonic lethality soon after (Tan et al., 2008). By contrast, our studies show that *Rac1* deletion in *Tie1-Cre* mice is not sufficient to impair sprouting angiogenesis. How can we explain the discrepancies between the *Tie1-Cre*- and *Tie2-Cre*-driven *Rac1* deletion studies? One explanation is that Cre expression in *Tie1-Cre* mice is sometimes found to be rather patchy, giving rise to a chimeric loss of targeted genes (Enge et al., 2002). However, this appears not to be the case in the *Tie1-Cre*$^{+}$;*Rac1*$^{\mathrm{fl/fl}}$ embryos that we have analysed, as we see excellent Cre activity throughout the vasculature and concomitant deletion of *Rac1* expression in the endothelial cells of *Tie1-Cre*$^{+}$;*Rac1*$^{\mathrm{fl/fl}}$ embryos both in vivo and in vitro. Thus, we believe that insufficient deletion of *Rac1* is not the reason for the apparently normal sprouting angiogenesis in *Tie1-Cre*$^{+}$;*Rac1*$^{\mathrm{fl/fl}}$ embryos. Another possible explanation includes the involvement of hematopoietic cells in embryonic angiogenesis (Suda and Takakura, 2001). Indeed, the functional role of hematopoietic cells, including platelets, in lymphatic vascular development is a matter of some debate (Sebzda et al., 2006; Srinivasan et al., 2007; Taniguchi et al., 2007). For example, platelets have been implicated as important in the separation of lymphatics from blood vessels (Suzuki-Inoue et al., 2007; Uhrin, 2006), and as Tie1 is known to be expressed in platelets (Batard et al., 1996; Tsiamis et al., 2000), it is possible that Rac1 deficiency in this population might contribute to the poor lymphatic-blood vessel separation that we observed. However, as there is no evidence for *Tie1* promoter-driven Cre expression in platelets (Gustafsson et al., 2001) and thus no evidence for Rac1 deficiency in them, we cannot comment upon whether the loss of Rac1 in platelets is responsible for the defect we observed. Since in *Tie2-Cre* mice over 80% of hematopoietic cells display Cre activity (Constien et al., 2001; Griffin et al., 2008), as opposed to only 13% in *Tie1-Cre* mice (Gustafsson et al., 2001), we hypothesise that the resultant loss of Rac1 in the vast majority of *Tie2-Cre*-positive developing hematopoietic cells might well be the cause of the gross vascular defects in the *Tie2-Cre*$^{+}$;*Rac1*$^{\mathrm{fl/fl}}$ mice, something that the *Tie1-Cre*$^{+}$;*Rac1*$^{\mathrm{fl/fl}}$ embryos would be relatively protected from. Unfortunately, there is presently no way to test the functional consequence of the potential deficiency in Rac1 in the 13% of hematopoietic cells on lymphatic separation in E12.5 embryos in vivo. In addition, the lethality of *Tie2-Cre*$^{+}$;*Rac1*$^{\mathrm{fl/fl}}$ mice prior to lymphatic vessel development prevents an examination of the role of Rac1 in lymphatic development and thus makes the *Tie1-Cre* mice a more appropriate model for such studies.

Since *Tie1-Cre*$^{+}$;*Rac1*$^{\mathrm{fl/fl}}$ endothelial cells display clear Cre activity and show significant *Rac1* deletion both in vivo and in vitro, we have concentrated our investigations on the role of Rac1 in endothelial cells. Importantly, our data show abnormal migration specifically of LECs during the first stages of lymphatic budding, and demonstrate that different subpopulations of endothelial cells can have different dependencies on a single migratory molecule, such as Rac1, in vivo. This differential dependency is manifested in apparently normal vascular endothelial cell migration during sprouting angiogenesis, but abnormal migration during lymphatic vessel segregation. How this is regulated and what stimulates different subpopulations of cells to react differently to their neighbours in vivo will be subjects for future studies. Others have shown that mice carrying one hypomorphic *Vegfr3*$^{\mathrm{neo}}$ allele have normal blood vessel development but impaired lymphatic vessel development and Vegfr3 levels (Haiko et al., 2008). We show that loss of Vegfr3 does not affect Rac1 expression or activity and this might explain why *Vegfr3*$^{+/-}$ mice do not display a lymphatic separation defect (Dumont et al., 1998). By contrast, our study shows that the combination of Rac1 deficiency with a reduction in Vegfr3 expression, which is likely to be via signalling control of other molecules, may be sufficient to affect the persistence of Vegf-C-stimulated LEC migration, and therefore might be one mechanism by which this Rho GTPase regulates lymphatic-blood vessel separation.

Our data suggest that *Rac1* deletion in *Tie1-Cre* mice leads to malfunctioning lymphatics, which is likely to give rise to the edema in these mutant embryos. In addition, they suggest that abnormal veno-lymphatic separation might lead to blood-congested lymphatics. Clinically, it is common to see blood-filled lymphatics in lymphatic malformations, but how the blood gets there has never been demonstrated. Furthermore, the presence of excessive blood in the lymphatics could be one reason for the blood vessel collapse observed in *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos at E13.5, as it leads to lymphatic vessel rupture that would result in interstitial haemorrhage, loss of tissue integrity and, finally, to the death of *Tie1-Cre*$^+$;*Rac1*$^{fl/fl}$ embryos. Alternatively, we cannot exclude the hypothesis that the gross haemorrhage and loss of blood vessel function might be independent of the lymphatic defect and instead reflect an increase in blood vessel fragility in these mutant mice.

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Supplementary material

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/136/23/4043/DC1

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