Diabetes Causes Bone Marrow Endothelial Barrier Dysfunction by Activation of the RhoA–Rho-Associated Kinase Signaling Pathway

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Objective—Diabetes mellitus causes bone marrow (BM) microangiopathy. This study aimed to investigate the mechanisms responsible for BM endothelial dysfunction in diabetes mellitus.

Methods and Results—The analysis of differentially expressed transcripts in BM endothelial cells (BMECs) from type-1 diabetic and nondiabetic mice showed an effect of diabetes mellitus on signaling pathways controlling cell death, migration, and cytoskeletal rearrangement. Type-1 diabetic-BMECs displayed high reactive oxygen species levels, increased expression and activity of RhoA and its associated protein kinases Rho-associated kinase 1/Rho-associated kinase 2, and reduced Akt phosphorylation/activity. Likewise, diabetes mellitus impaired Akt-related BMEC functions, such as migration, network formation, and angiocrine factor-releasing activity, and increased vascular permeability. Moreover, high glucose disrupted BMEC contacts through Src tyrosine kinase phosphorylation of vascular endothelial cadherin. These alterations were prevented by constitutively active Akt (myristoylated Akt), Rho-associated kinase inhibitor Y-27632, and Src inhibitors. Insulin replacement restored BMEC abundance, as assessed by flow cytometry analysis of the endothelial marker MECA32, and endothelial barrier function in BM of type-1 diabetic mice.

Conclusion—Redox-dependent activation of RhoA/Rho-associated kinase and Src/vascular endothelial cadherin signaling pathways, together with Akt inactivation, contribute to endothelial dysfunction in diabetic BM. Metabolic control is crucial for maintenance of EC homeostasis and endothelial barrier function in BM of diabetic mice. (Arterioscler Thromb Vasc Biol. 2013;33:00-00.)

Key Words: bone marrow • diabetic microangiopathy • endothelial dysfunction • oxidative stress • RhoA

A typical form of microangiopathy, consisting of microvascular rarefaction and endothelial barrier dysfunction, contributes to the pathogenesis of retinopathy, nephropathy, neuropathy, cardiomyopathy, and foot ulcers in patients with diabetes mellitus. Our group was the first to describe a new form of microangiopathy in the bone marrow (BM) of diabetic animal models. Microvascular disease threatens stem cell viability through reduced nutrition and perfusion, and increased oxidative stress. In addition, the marrow vascular niche acts as a controller of stem cell mobilization and a source of trophic factors instrumental to proper hematopoiesis. An impoverished vascular niche might fail to accomplish these crucial functions with detrimental consequences for stem cell homeostasis and cardiovascular repair.

Glycemic control is crucial for prevention of cardiovascular events, and especially effective in reducing the risk of microvascular complications. However, it remains unknown whether improved control of hyperglycemia by insulin replacement prevents BM microangiopathy. Furthermore, the mechanisms underpinning BM endothelial dysfunction remain poorly understood.

The present study investigates the signaling pathways implicated in diabetes mellitus–induced BM microangiopathy. Results newly show that diabetes mellitus causes redox-dependent activation of small guanosine triphosphatases (GTPases), phosphorylation of vascular endothelial cadherin (VE-cadherin), and reorganization of cytoskeletal proteins leading to increased permeability to macromolecules and passive efflux of BM mononuclear cells (BM-MNCs). Furthermore, the diabetic endothelium exhibits reduced Akt activity and impairment of Akt-related functions, including migration, network formation, and angiocrine factor–releasing activity. Importantly, endothelial barrier dysfunction is rescued by the metabolic control of diabetes mellitus.

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Materials and Methods

Animal Procedures

Experiments were performed in accordance with the Guide for the Care and Use of Laboratory Animals (the Institute of Laboratory Animal Resources, 1996) and with approval of the British Home Office. Type-1 diabetes mellitus (T1D) was induced in male CD1 mice (Charles River, Margate, Kent, UK) by streptozotocin. Age-matched male CD1 mice injected with the streptozotocin vehicle served as controls. Diabetes mellitus was monitored by measurements of glycemia at fast and glycosuria.

Insulin Implants

Four weeks after induction of diabetes mellitus, mice were randomized to receive continuous insulin supplementation, through subcutaneous implants (LinBit, LinShin, Toronto, Canada), at the rate of 0.1 unit/implant per day or vehicle. The number of insulin implants was titrated according to the mouse body weight, according to manufacturer’s instructions. Glycaemia was monitored every 4 weeks, whereas glycosuria was assessed at 2 weeks after diabetes mellitus induction and reassessed at the end of the study (Figure I in the online-only Data Supplement).

Cell Cultures

Human BM endothelial cells (hBMECs) were kindly provided by Prof van der Schout (Sanquin University, Amsterdam, The Netherlands) and cultured as described previously. In selected experiments, cells were cultured in normal glucose (5 mM L-D-glucose) or high glucose (HG; 15 mM L and 25 mM L-D-glucose) for 96 hours before use in expression and functional studies. Equivalent concentrations of L-glucose were used as osmotic control.

BMECs were also isolated from T1D mice (14–18 weeks after diabetes mellitus induction) and age-matched nondiabetic controls, as described previously. Purity was assessed by flow cytometry detection of the endothelial marker MECA32, which was consistently expressed by >90% of the isolated cells.

Infection of BMECs

BMECs were infected separately with 2 different adenoviruses: an adenovirus carrying constitutively active myristoylated Akt and an adenovirus carrying the dominant negative form of RhoA. AdNull (empty vector Ad66) was used as control. BMECs were grown in complete medium in 10-cm petri dishes until 60% to 70% confluent, and then infected overnight with adenoviral vectors at 200 multiplicity of infection for both adenoviruses. The medium was then changed and then infected overnight with adenoviral vectors at 200 multiplicity of infection for both adenoviruses. The medium was then changed and cells were used for experiments after 2 days.

Illumina Gene Array

An Illumina bead-array interrogating 24,600 murine transcripts was performed on T1D and control BMECs (4 biological replicates each). Microarray expression data are available at the NCBI Gene Expression Omnibus (GEO) (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE14035.

Differentially expressed genes were associated with biofunction networks and canonical pathway using Ingenuity Pathway Analysis software core analysis (Ingenuity Systems, Redwood City, CA, www.ingenuity.com). Transcripts with expression changes at false discovery rate (q-value) <0.05, induced or repressed >1.25-fold, were associated with biological functions in Ingenuity Knowledge database, and the association was tested for statistical significance as described below.

Flow Cytometry Staining of BMECs

Freshly harvested BM cells were washed with ice-cold Hank balanced salt solution containing 0.5% bovine serum albumin and 0.02% sodium azide. To recognize ECs, BM cells were stained with anti-MECA-32 biotin-conjugated antibody (BD Biosciences, Oxford, UK), followed by streptavidin–allophycocyanin–conjugated secondary antibody.

Detection of Oxidative Stress Markers

BMECs were seeded on 6-well plates, cultured until reaching confluence, and then assessed for reactive oxygen species (ROS) levels by flow cytometry detection of MitoSox red (Invitrogen, Carlsbad, CA), a mitochondria-specific hydroethidine-derivative fluorescent dye, or DCF (Molecular Probes, Paisley, UK), a marker of total oxidative stress. Four separate experiments in triplicates were analyzed and averaged.

In addition, BMECs were seeded in 8-chamber slide wells and stained for 45 minutes with MitoTracker Red Cm-H2-ROS (500 nM/L) at 37°C. Cells were fixed with paraformaldehyde, and pictures were taken with identical settings for all conditions.

In Vitro Permeability Assay

BMECs and BMECs were seeded onto transwell inserts (pore size: 0.3 μm) coated with 0.5 μg/mL fibronectin, and grown until they reached confluence. Then, the media was replaced in the lower chamber and fresh media containing 70 kDa FITC-labeled dextran was added to the upper chamber. The increase in fluorescence in the lower chamber was evaluated at different time points over 16 hours, with identical exposure settings using FLUOstar Optima fluorometer (Berthold Technologies Wildbad, Germany). Three independent experiments in triplicate were analyzed and averaged.

In Vivo Permeability Assay

Mice were intracardially injected with a 500 μL bolus of 70 kDa FITC-labeled dextran (200 μM), followed after 3, 5, or 7 minutes by an equal bolus of 70 kDa TRITC-labeled dextran (n=3 mice each time point). Animals were euthanized 30 seconds after the last injection. FITC and TRITC fluorescence was measured using a FLUOstar Optima fluorometer, with identical exposure settings for all conditions in plasma and in bone flask.

Data were plotted as mg FITC (I F) in BM interstitium per mg BM tissue (W) against time. Three independent experiments were carried out for each time point and condition.

Transendothelial Migration of BM-MNCs

Transendothelial migration of BM-MNCs was assessed using transwell cell culture inserts equipped with 3-μm pore size filters (BD Biosciences) using stromal cell-derived factor-1 as the chemotactant. BM-MNCs from T1D and control mice were labeled with CM-Dil (Life Technologies, NY) and then added to the top compartment (3×10⁴ cells per well in 300 μL). After 16 hours incubation at 37°C, nonmigrated cells on the upper side of the membrane were removed by scraping. All inserts were fixed for 10 minutes in methanol and mounted on slides counterstained with DAPI. Three separate experiments in triplicate were analyzed and averaged.

BMEC Migration

Migration of cultured BMECs was studied, as described previously. Briefly, BMECs were seeded on the upper part of 24-transwell plate filters coated with fibronectin. The lower wells contained basal medium supplemented with vascular endothelial growth factor A (100 ng/mL, R&D, Abingdon, UK). After 8 hours incubation, BMECs migrated to the lower part of the filter membrane were counted. Five random fields per each filter were evaluated at ×200 magnification using a fluorescent microscope (Olympus). Four separate experiments in triplicate were performed.

Matrigel Assay

BMECs (3×10⁴ in a total volume of 100 μL DMEM) were added on top of 100 μL gelled, growth-enriched Matrigel (BD Biosciences, Oxford, UK) in each well of 8-well chamber slides. After 8 hours at 37°C, gels were gelled with sterile PBS and fixed with 2% paraformaldehyde, and then mounted with glycerol. Three samples per group were analyzed in triplicate to compute the cumulative tube length of the endothelial network.
Immunohistochemistry and Immunocytochemistry
Paraffin-embedded sections (5 µm thick) of BM from T1D and control mice (n=6 per group) were used for in situ identification of vascular structures (Alexa Fluor 568-conjugated isoclinet B4 [Invitrogen]) expressing phosphorylated VE-cadherin (VE-cad pY731 or pY658 rabbit polyclonal antibodies [Invitrogen]). A goat antirabbit Alexa488 was used as secondary antibody (Invitrogen). All samples were counterstained with DAPI. Microphotographs were taken with a Leica SP5 confocal imaging system (Leica, Milton Keynes, UK) at ×400 magnification.
To study cytoskeletal rearrangements, BMECs were stained with rhodamine phallodin (Sigma). Five images per field were captured at ×200 magnification using a fluorescent microscope (Olympus, Southend on Sea, UK).

Quantitative PCR
Total RNA was isolated from murine BMECs (RNasy, Qiagen, Manchester, UK), and RNA quality confirmed using the RNA Nano LabChip in a bioanalyzer (Agilent, Stockport, UK). RNA was reverse transcribed (SensiScript reverse transcriptase, Qiagen, Crawley, UK) and quantitative PCR was performed in a LightCycler480 (Roche). Primers for PCR amplification for housekeeping gene, 18S rRNA, used were: forward, GATGCCTGATTGTGGCC; reverse, GTGTTGCTGTTGATATCATGG. The ΔCt obtained was used to find the gene relative expression according to the formula: relative expression=2−ΔΔCt, where ΔΔCt is equal to ΔCt of a given gene in experimental group subtracted by the ΔCt of the same gene in control group. The analyses were performed on at least 4 samples per time and repeated 3 times. Primers used are detailed in Table I in the online-only Data Supplement.

Assay for Akt Activity
Protein preparations (25 μg) from BMECs of T1D and control mice were assessed for Akt activity using the Kinase Activity Assay Kit, according to the manufacturer's instructions (Enzo Life Sciences, Exeter, UK). Three independent experiments in triplicate were performed.

Assay for Rho Activity
GTP-bound active Rho was assessed by pulldown assays, according to the manufacturer's instructions (Millipore, Billerica, MA).

Western Blot
The analysis of protein expression was performed on lysates from confluent hBMECs and BMECs using phosphospecific antibodies against antiphospho Ser 1177 eNOS (Cell signaling technologies), NADPH oxidase isoform 2 (BD Biosciences, Oxford, UK), VE-cadherin-Y731, VE-cadherin-Y658, and Pyk2-Y402 (Cell Signaling Technologies, MA), antibodies raised against respective total proteins and a monoclonal antibody for recognition of tubulin. Blots were analyzed with an enhanced chemiluminescence detection system (Amersham Biosciences, Buckinghamshire, UK).

Immunoprecipitation
Membrane samples were obtained, as described previously,13 in lysis buffer, 20 mmol/L Tris-HCl, 150 mmol/L NaCl, 1 mmol/L EDTA, 1 mmol/L EGTA, 1% Triton-X, 2.5 mmol/L sodium pyrophosphate, 1 mmol/L β-glycerophosphate, 1 mmol/L Na 3VO 4, 1 μg/mL leupeptin. Cav1 was immunoprecipitated using anti-Caveolin-1 (Cav-1) antibody (Abcam) and protein A (Santa Cruz). After washing of the immune complexes in wash buffer, 20 mmol/L Tris-HCl, 137 mmol/L NaCl, 1% Triton-X, 2 mmol/L EDTA, the complexes were run on a SDS-PAGE gel and blotted for total eNOS (Cell Signaling Technologies). Samples incubated with nonimmune rabbit IgG, instead of anti–Cav-1 antibody, were used as controls.

Data Analysis and Statistical Procedures
Values are presented as mean±SEM. If data failed to pass normality and equal variance tests, a nonparametric analysis was applied and results were expressed as median with 5 to 95 percentile distribution. Multiple groups were compared by parametric 2-way ANOVA, followed by Bonferroni post t test, 1-way ANOVA, followed by Bonferroni Multiple Comparison test, or nonparametric ANOVA on ranks, followed by Tukey pairwise comparison or Dunn test for multiple comparisons against a single control group. Comparison of 2 groups was performed by paired or unpaired Student t test. In gene array studies, the right-tailed Fisher exact test was used to evaluate the probability that the association of differentially expressed genes and biological functions or canonical pathways is because of chance. The significance of the association between the data set and a given canonical pathway was also measured as the ratio of the number of differentially expressed genes in a pathway and the total number of genes in the same pathway. A P value <0.05 was considered significant.

Results
To determine the mechanisms underlying BM endotheliopathy, we performed an Illumina gene array on primary BMECs isolated from T1D (18 weeks from diabetes mellitus induction) and age-matched nondiabetic mice. Of 792 transcripts with expression changes at false discovery rate (q value) <0.05, 448 were induced or repressed ≥1.25-fold. Table II in the online-only Data Supplement shows the list of differentially expressed genes within canonical pathways. Among top-ranked functions, Ingenuity Pathway Analysis showed a highly significant effect of diabetes mellitus on signaling pathways associated with cellular death, assembly, organization, trafficking, and inflammation (Figure 1A).
Functional enrichment analysis identified small GTPases (RhoA and CDC42), actin cytoskeleton dynamics, integrin, leukocyte extravasation/vascular permeability signaling, and other pathways most enriched with differentially expressed genes (Figure 1B). Moreover, within the actin cytoskeleton and leukocyte extravasation/vascular permeability signaling pathways, we found that 14 of 209 and 12 of 183 genes, respectively, were modulated by diabetes mellitus (Figure II in the online-only Data Supplement). Actin-related protein 2/3 (nucleation site for actin filaments polymerization), membrane-organizing extension spike protein (moesin, a cross-linker between the endothelial plasma membrane and actin-based cytoskeleton), and the Rho-associated kinase-2 (ROCK2, an activator of moesin through phosphorylation on Thr558) were all upregulated in diabetic BMECs.
Taken together, these gene array data indicate transcriptional alterations compatible with loosened adhesive intercellular contacts and increased endothelial permeability.11

Altered RhoA/ROCK and Akt Activity in Diabetic BM Endothelium
RhoA and ROCK regulate a wide range of cellular functions, including cytoskeletal rearrangement, migration, and proliferation. Using a RhoA–GTP-bound pulldown assay, we found that diabetes mellitus increases Rho activity in BMECs (Figure 2A). It is known that oxidative stress is a potent inducer of RhoA.14–16 Here, we confirm our previous finding of increased oxidative stress at the mitochondrial level in T1D-BMECs (Figure IIIA in the online-only Data Supplement).2 Moreover, we found polyADP-ribose polymerase 1 to be upregulated and transcription factor nuclear factor (erythroid-derived 2)-like 2 (Nfr2) downregulated in T1D-BMECs (Figure IIIB in the online-only Data Supplement). It is known
that oxidative stress induces DNA strain breaks, which in turn activate polyADP-ribose polymerase, whereas Nfr2 exerts antioxidant activity to protect vascular cells from HG-induced damage. In contrast, the expression of NADPH oxidase isoform 2, another important source of ROS, was similar in BMECs from healthy and diabetic mice (Figure IIIC in the online-only Data Supplement). Thus, oxidative stress in BM endothelium is attributable to increased ROS production in mitochondria and reduced antioxidant defense. In accordance, we found that preconditioning T1D-BMECs with the ROS scavenger, N-acetyl-cysteine (NAC), inhibits RhoA activation (Figure 2A). Furthermore, RhoA upregulation was accompanied by increased ROCK1 and ROCK2 mRNA levels, which was again prevented by NAC (Figure 2B). The influence of activated RhoA on Akt is controversial, with reports indicating that RhoA/ROCK causes induction...
or suppression of Akt activity in ECs. We found that Akt
activity is remarkably depressed in diabetic BM endothelium.
Notably, this deficit was partially reverted by NAC, the ROCK
inhibitor Y27632, or by transfecting cells with adenovirus car­
rying the dominant negative form of RhoA (Figure 2C), thus
suggesting that small GTPase activation by oxidative stress is
responsible for Akt inhibition.

Akt activation in ECs reportedly induces the release of angio­
crine factors that support BM stem cell expansion. Several
of these angiocrine substances, such as fibroblast growth fac­
tor 2, Jag1, and Jag2, were downregulated in diabetic BMECs,
but restored after antioxidant treatment (Figure 2D and 2E).
The ROCK inhibitor Y27632 and RhoA knockdown recov­
ered fibroblast growth factor 2, but not Jag1 and Jag2 mRNA
expression (Figure 2D).

**Rescue of Endothelial Dysfunction by ROCK Inhibition or Akt Activation**

We next investigated whether an altered RhoA–Akt axis has
specific consequences for the BMEC function-type. Akt is
a potent inducer of eNOS activity, which synthesizes nitric
oxide, a key molecule in EC function. In total membrane frac­
tions from T1D BMECs, we observed a decrease in eNOS phospho­
ylation as well as a reduction in Cav-1 expression. Cav-1 negatively regulates eNOS by directly interacting with it. Immunoprecipitation of Cav-1 confirmed that Cav-1 and eNOS interact both in Ctrl and T1D BMECs (Figure 3A and 3B). Taken together, these data suggest a reduced NO avail­
ability in diabetic cells.

We next investigated the effect of Akt activation (by transfection of BMECs with a constitutively active form),
of RhoA knocking down (by a transfection with a dominant negative form), and of pharmacological ROCK inhibition
with the compound Y27632. Successful transduction of cells
by adenovirus carrying constitutively active myristoylated
Akt and adenovirus carrying the dominant negative form
of RhoA was documented by Western blot for Akt and Rho
activity assay (Figure I IID and IIIE in the online-only Data
Supplement).

In a network formation assay on matrigel, T1D-BMECs
showed reduced tube-formation capacity, which was restored
by constitutively active Akt, adenovirus carrying the dominant

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**Figure 3.** Rho-associated kinase (ROCK) inhibition or Akt activation rescues endothelial dysfunction. A, eNOS activity (ii) along with Caveolin-1 (Cav-1) (iii) expression were measured by WB (i) in membrane fractions. B, Diabetes mellitus impairs eNOS activation and interaction with Cav-1, as demonstrated by Western blot for eNOS in Cav-1 immunoprecipitates (IP Cav-1). Nonimmunogenic IgG was used as control. C, Representative microphotographs (scale bars 100 μm; i) and bar graph (ii) showing network-forming activity of control and diabetic bone marrow endothelial cells (BMECs). The deficit of network formation in diabetic BMECs was rescued by ROCK inhibition with Y27632 or transfection with constitutively active Akt or adenovirus carrying the dominant negative form of RhoA. Images were captured 16 hours after BMEC seeding. D, Bar graph showing percentage of migrated BMECs after stimulation with vascular endothelial growth factor A or vehicle (BSA). Diabetic BMECs showed impaired migratory capacity toward vascular endothelial growth factor A that was rescued, in part, by constitutively active Akt, but not by ROCK inhibition or adenovirus carrying the dominant negative form of RhoA infection. Data are expressed as mean±SEM. *P<0.05; **P<0.01; ***P<0.001; ***P<0.001 vs Ctrl; #P<0.05; ##P<0.01 vs type-1 diabetic (T1D); ǂǂP<0.01; and ǂǂǂP<0.001 vs BSA. Each experiment was performed in triplicate.
negative form of RhoA, or ROCK inhibition (Figure 3C). In addition, T1D-BMECs displayed a reduced migratory response to vascular endothelial growth factor A, with this defect being partially recovered by Akt activation, but not by RhoA/ROCK inhibition (Figure 3D). ROS are known to induce the rearrangement of F-actin stress fibers and cell contraction via RhoA–ROCK activation and phosphorylation of moesin, resulting in increased endothelial permeability. We asked whether this mechanism is activated in T1D-BMECs. Accordingly, we found that diabetes mellitus triggers the formation of F-actin stress fibers in BMECs, which is reduced by ROCK inhibition and to a lesser extent by Akt activation (Figure 4A). Furthermore, moesin mRNA (Figure 4B) and protein phosphorylation levels (Figure 4C) were increased in T1D-BMECs, with the latter effect being blunted by NAC and ROCK inhibitor Y27632.

We next asked whether ROS- and ROCK-dependent activation of BMEC cytoskeleton translates into increased endothelial permeability and barrier dysfunction. Size-selective assessment of paracellular permeability was performed using fluorescently labeled dextran. Figure 4D shows that the T1D-BMEC monolayer is more permeable to dextran compared with BMECs from healthy mice. This increased permeability was prevented by NAC, myristoylated Akt, and RhoA/ROCK inhibition. The presence of endothelial barrier dysfunction was further assessed using a transendothelial migration assay on BM-MNCs. Results confirm our previous findings indicating that spontaneous transendothelial migration of BM-MNCs is increased in the presence of diabetic BMECs compared with control BMECs, whereas directed migration toward stromal cell-derived factor-1 is abolished. Moreover, we newly show that endothelial barrier function is rescued, in part, by ROS scavenging and RhoA/ROCK inhibition (Figure 4E). In contrast, Akt activation did not reduce the increased basal migration of BM-MNCs, but restored responsiveness to stromal cell-derived factor-1.

**Figure 4.** Rho-associated kinase (ROCK) inhibition and Akt activation rescues diabetes mellitus–induced endothelial barrier dysfunction in bone marrow endothelial cells (BMECs). **A**, Microphotographs (scale bars 100 µm) showing BMECs stained for F-actin with rhodamine–associated phalloidin. Diabetes mellitus induces actin fiber activation, which is blunted by ROCK inhibitor Y27632, adenovirus carrying constitutively active myristoylated Akt or adenovirus carrying the dominant negative form of RhoA. **B** and **C**, Representative blots and graphs showing the effect of diabetes mellitus on mRNA expression (B) and the phosphorylation state of moesin (C) in BMECs. Upregulation of moesin is blunted by N-acetyl-cysteine (NAC) and ROCK inhibition. **D**, Bar graph showing the effect of diabetes mellitus on endothelial permeability using FITC-labeled 70-kDa dextran. The increase in endothelial permeability is blunted by NAC, ROCK inhibition, constitutively active Akt or the dominant negative form of RhoA. **E**, Bar graph showing BM-MNC transendothelial migration after exposure to stromal cell–derived factor-1 (directed migration) or PBS (vehicle, spontaneous migration). Spontaneous transmigration was enhanced and directed migration suppressed by diabetes mellitus. These alterations were prevented by treating BMECs with NAC and ROCK inhibitors. Constitutively-active Akt improves directed migration without reducing the exaggerated spontaneous migration of bone marrow mononuclear cells (BM-MNCs). Data are means±SEM. *P<0.05; **P<0.01; ***P<0.001 vs Ctrl; #P<0.05; and ##P<0.01 vs type-1 diabetic (T1D). Each experiment was performed in triplicate.
Altogether, these data indicate that the Rho/ROCK–Akt axis plays a crucial role in the functional alterations of diabetic BMECs.

**HG Increases BMEC Permeability Through VE-Cadherin Phosphorylation**

We next investigated the direct effect of HG on BMEC permeability. To this end, we established an in vitro model consisting of hBMECs cultured in normal (5 mmol/L, normal glucose) or high (15 and 25 mmol/L, HG) D-glucose for 96 hours. ROS levels were augmented by progressive increases of glucose concentration, as assessed by flow cytometry detection of MitoSox and DCF-2A. The ROS production was brought back to control levels totally by catalase treatment, and partially reduced by superoxide inhibitor and antioxidant diethyldithiocarbamate (Figure IV in the online-only Data Supplement). HG alters hBMEC permeability in a dose-dependent manner, as assessed in an in vitro assay using 70 kDa dextran (Figure IVB in the online-only Data Supplement). The increase in permeability was completely reversed by treating hBMECs with NAC or catalase; however, neither the hydroxyl scavenger MCI-186 nor diethyldithiocarbamate modified the effect of HG on permeability. The inhibition of detoxifying chain at superoxide level suggests that this ROS, and the ones generated as peroxynitrite, can trigger molecular changes leading to increased permeability.

ROS reportedly modifies the activity of several tyrosine kinases. Among them, Src increases vascular permeability through phosphorylation of VE-cadherin, a key component of EC adherens junctions. We found that HG increases the phosphorylation of VE-cadherin at Y731 and Y658, which are binding sites for β-catenin and p120, respectively. Moreover, VE-cadherin phosphorylation was prevented by both NAC treatment and Src inhibition, suggesting a pivotal role of Src kinase in adherens junction disassembly through a redox-sensitive mechanism (Figure VA and VB in the online-only Data Supplement). Of note, the HG-induced increase in permeability was reverted by Src inhibitor SU6656 (Figure IVB in the online-only Data Supplement). Another redox-sensitive kinase controlling adherens junctions is represented by the proline-rich kinase 2 (Pyk2), which has the same targets as Src. In accordance, the active phosphorylated form of Pyk2 was increased in hBMECs under HG. This effect was totally prevented by NAC (Figure VC in the online-only Data Supplement).

In addition, we found that the proapoptotic and proinflammatory redox-sensitive kinases p38 and JNK are activated in both HG-treated hBMECs and T1D-BMECs. This effect was reversed by NAC and catalase. Finally, the MAPK kinase kinase, MEK1, which control angiogenesis and proliferation in ECs, was found increased in hBMECs treated with HG, but not in diabetic cells (Figure VI in the online-only Data Supplement).

**Redox-Dependent Activation of VE-Cadherin in BMEC Leads to Endothelial Barrier Dysfunction in T1D Mice**

We next asked whether phosphorylation events associated with VE-cadherin activation occur in BMECs from diabetic mice. As for HG-treated hBMECs, phosphorylation of VE-cadherin and Pyk2 was increased in diabetic murine BMECs, but reduced by NAC (Figure 5A–5C). Fluorescence microscopy demonstrated in situ phosphorylation of VE-cadherin in BM vascular cells of T1D mice (Figure 5D and Figure VII in the online-only Data Supplement).

Finally, we assessed the abundance of BMECs by flow cytometry of MECA32-positive cells and BM endothelial barrier function in vivo using a double tracer technique. We found that MECA-32-positive ECs are reduced in BM of T1D mice (Figure 6A and 6B). Moreover, vascular permeability is increased by diabetes mellitus (Figure 6C and 6D), which was confirmed at different times from diabetes mellitus induction (Figure VIII A and VIIIB in the online-only Data Supplement). To verify whether the observed changes can be contrasted by metabolic control, we treated diabetic animals with insulin implants. Of note, insulin replacement resulted in maintenance of BMECs abundance and normalization of vascular permeability (Figure 6A–6D). Furthermore, in vitro insulin treatment of BMECs was capable of reducing VE-cadherin phosphorylation at site Y731. Conversely, p-Pyk2 seemed not to be affected by insulin (Figure VIIIA and VIIIB in the online-only Data Supplement).

**Discussion**

This study provides new mechanistic insights into BM endothelial dysfunction induced by diabetes mellitus. BMECs from T1D mice showed a spectrum of functional alterations, including defects in angiogenic activity, migration, network formation, and permeability. Endothelial dysfunction can be traced back to mitochondrial oxidative stress triggered by high levels of glucose and alteration of the RhoA/ROCK/Akt signaling pathway. Moreover, BMEC availability and endothelial barrier dysfunction were confirmed in vivo and corrected by insulin.

RhoA controls several cellular functions, including migration, angiogenesis, and apoptosis. In ECs, this Ras-like protein is committed to the formation of stress fibers through its effector ROCK. In recent years, RhoA has gained attention in the field of diabetes mellitus, being acknowledged as a primary target for oxidative stress or advanced glycation end products, and as an initiator of a series of transcriptional and posttranscriptional events leading to endothelial dysfunction. Here, we newly demonstrate that diabetes mellitus increases RhoA expression and activity, as well as the mRNA levels of ROCK isoforms in diabetic BMECs. ROCK1 activation is involved in permeability changes under inflammatory conditions, whereas ROCK2 contributes to the increase in adhesion molecules via nuclear factor-κB p65. Activation of moesin by ROCK-mediated phosphorylation induces rearrangement of the actin cytoskeleton and cell contraction instrumental to endothelial permeability. Importantly, we found that moesin is transcriptionally upregulated and phosphorylated in BMECs of T1D mice, leading to the activation of stress fibers and increased permeability to MNCs and macromolecules. These effects were prevented by the ROS scavenger and ROCK inhibitor, thus delineating a causal association between oxidative stress, RhoA/ROCK activation, stress fiber contraction, and endothelial barrier dysfunction.
Diabetic endotheliopathy is characterized by an alteration in the phosphorylation state and activity of several kinases. We have previously reported that diabetic BMECs have higher phosphorylation levels of VE-cadherin (at tyrosine 731, the β-catenin–binding site) and Pyk2 (at tyrosine 402, which is the autophosphorylation site for Pyk2) compared with control BMECs.2 Here, we newly report that HG-induced oxidative stress causes phosphorylation of VE-cadherin via the redox-sensitive kinases Src and Pyk2, thereby favoring the disassembly of adherens junctions and BM-MNC extravasation.

Furthermore, we found that both diabetes mellitus and HG trigger the phosphorylation of apoptosis-related kinases, such as p38 and JNK, in human and murine cells. The redox-sensitive MAPK kinase kinase, MEK1, which in turn activates...
ERK1/2 exerts a modulatory control of angiogenesis.\textsuperscript{31} We found that in vitro exposure of hBMECs to HG increases the phosphorylation of MEK1, however, MEK1 levels were similar in BMECs from diabetic or nondiabetic mice. Thus, this specific pathway seems to be particularly sensitive to acute increases in glucose levels. We also observed a differential effect of various antioxidants on vascular permeability. The alteration of endothelial barrier function diabetes mellitus is more likely to depend on the formation of peroxynitrite, which is an activator of the RhoA/ROCK pathway, whereas redox-sensitive kinases are triggered by an increase in hydrogen peroxide production.

Another hallmark of BM endotheliopathy consists of Akt inactivation. NAC, RhoA dominant negative transfection, and ROCK inhibitor Y27632 were able to rescue Akt activity, suggesting an intertwined relationship between redox-dependent activation of RhoA–ROCK and Akt suppression. In fact, either inhibiting ROCK or enhancing Akt activity rescued diabetes mellitus–induced dysfunctions, including migratory and angiogenic defects, and increased permeability. Akt seems to be crucial for BMECs to manifest a migratory phenotype, as Akt inactivation in diabetes mellitus reduces their migratory and network-forming capacity, whereas Akt reactivation rescues both defects. In accordance with this hypothesis, we observed an impairment in eNOS activity. Therefore, the picture that emerges from a joint analysis of molecular and functional readouts is that of a contracted and leaky BM endothelium, incapable of responding to migratory signals as a consequence of dysfunctional Akt. In addition, it has been recently shown that Akt is essential for BMECs to convey self-renewal and differentiation signals to long-term hematopoietic stem cells through the release of angiocrine factors.\textsuperscript{3,4} We newly report the decreased expression of some Akt-dependent factors in diabetic BMECs, that is, the Notch ligands Jag1 and Jag2 and the angiogenic factor fibroblast growth factor 2. Further studies are warranted to investigate whether a depressed angiocrine signaling may contribute to BM stem cell depletion in diabetes mellitus.

The increased production of ROS plays a pivotal role in the pathogenesis of diabetes mellitus and the resulting complications. Along with several other tissues (kidney, eye, and nervous system), we have shown that oxidative stress plays a pivotal role in diabetic microangiopathy observed in BM. Thus, our results reinforce the concept that antioxidant administration can be helpful in managing diabetic complications. Indeed, several other investigations have been carried out to evaluate the ability of antioxidants to manage diabetic complications. For instance, NAC, vitamin C, vitamin E, and α-lipoic acid showed positive results in reducing diabetic complications.\textsuperscript{42–45} However, these previous clinical trials yielded promising yet inconsistent results because of the lack of data regarding optimal antioxidant concentration required to manage diabetic complications, with the lowest side effects possible.\textsuperscript{46} For this reason, it is important to understand the molecular mechanisms triggered by oxidative stress in different tissues so that a systemic antioxidant approach can be combined with a more tailored one; for example, ROCK inhibitors have already given promising results in in vitro study tissues other than BM.\textsuperscript{14,47,48}

In summary, the present study highlights a molecular network responsible for endothelial barrier dysfunction in BM and identifies candidate mechanistic targets for rectification of the dysfunctional phenotype (Figure IX in the online-only Data Supplement). Importantly, insulin replacement exerts significant protection of BM vasculature. The notion that insulin is a potent inducer of Akt,\textsuperscript{49} and an inhibitor of RhoA in vascular cells,\textsuperscript{50} confirms the validity of the proposed molecular network.

BM-specific microangiopathy might have relevant clinical consequences. First, microvascular rarefaction endangers BM stem cell viability through reduction of perfusion and suspension of paracrine trophic signaling. Second, plasma extravasation is particularly harmful for a tissue like the marrow that is contained in nonexpandable bone. Third, barrier dysfunction might impinge on the release of stem cells, as illustrated by experiments showing exaggerated spontaneous transendothelial migration and reduced directed migration toward chemottractants. These considerations call for urgent investigation into the status of BM in patients with complicated diabetes mellitus. Here, we show that hBMECs develop typical molecular and functional alterations when exposed to HG. We have also gathered new evidence that microvascular rarefaction occurs together with hematopoietic tissue remodeling and stem cell depletion in BM of diabetic patients (Madeddu, unpublished results 2012). Hence, preserving the fitness of BM microvasculature represents a novel therapeutic target in the management of patients with diabetes mellitus.

Sources of Funding
This study was supported with funds from a British Heart Foundation project grant entitled “Bone marrow dysfunction alter vascular homeostasis in diabetes” to Paolo Madeddu.

Disclosures
None.

References


Diabetes Causes Bone Marrow Endothelial Barrier Dysfunction by Activation of the RhoA–Rho-Associated Kinase Signaling Pathway
Giuseppe Mangialardi, Rajesh Katare, Atsuhiko Oikawa, Marco Meloni, Carlotta Reni, Costanza Emanueli and Paolo Madeddu

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Supplemental material

Cell cultures
Human BM endothelial cells (hBMECs) were kindly provided by Prof. van der Schout (Sanquin University, Amsterdam, The Netherlands) and cultured, as described previously, in Medium 199 (Gibco BRL), supplemented with 10% (v/v) heat-inactivated human serum (Invitrogen), 10% (v/v) heat-inactivated FCS, 1 ng/mL Basic Fibroblast Growth Factor (bFGF, Boehringer Mannheim, Mannheim, Germany), 5 U/mL heparin (Leo Pharmaceutical Products, Weesp, The Netherlands), 300 μg/mL glutamine (Sigma), 100 U/mL penicillin, 100 μg/mL streptomycin. In selected experiments, cells were cultured in normal glucose (NG) (5 mM D-glucose) or high glucose (HG) (15 mM and 25 mM D-glucose) for 96 hour.

BMECs were also isolated from 14 to 18 weeks T1D mice and age-matched non-diabetic controls as described previously. Briefly, freshly harvested BM cells were immunomagnetically depleted of CD11b-expressing cells to eliminate myeloid/monocyte fraction and cultured on 0.1% gelatin in DMEM containing supplemented with 20% FBS and tetrapeptide Ac-Ser-Asp-Lys-Pro (AcSDKP) to avoid stem cells and fibroblasts contamination. Cells were grown until confluence and then used for experiments. Purity was assessed by flow cytometry detection of the endothelial marker MECA32, which was consistently expressed by > 90% of the isolated cells.

Western Blot
Confluent hBMECs and BMECs were washed twice with ice-cold Ca\(^{2+}\)- and Mg\(^{2+}\)-containing PBS, and lysed in lysis buffer (25 mM Tris, 150 mM NaCl, 10 mM MgCl\(_2\), 2 mM EDTA, 0.02% (w/v) SDS, 0.2% (w/v) deoxycholate, 1% Nonidet P-40, 0.5 mM orthovanadate with the addition of fresh protease-inhibitor-mixture tablets (Roche Applied Science, Burgess Hill, UK). After 30 min on ice, cell lysates were collected and the supernatant was separated from the insoluble fraction by centrifugation (14,000 g, 10 min at 4°C). Supernatants were diluted with boiling 2x SDS-sample buffer containing 4% 2-mercaptoethanol (Bio-Rad, Hemel Hempstead, UK). The samples were analyzed by SDS-PAGE. Proteins were transferred to 0.45-μm nitrocellulose and the blots were blocked with 5% BSA in Tris-buffered saline with Tween-20 (TBS-T) for 1 h and subsequently incubated at RT with phospho-specific antibodies against Nox2 (BD Biosciences, Oxford, UK), VE-cadherin-Y731, VE-cadherin-Y658 and Pyk2-Y402 and with a monoclonal antibody against Tubulin, followed by incubation with goat-α-rabbit-IgG-horseradish peroxidase or a goat-antimouse-IgG-horseradish peroxidase for 1 h at RT. Between the various incubation steps, the blots were washed 5 times with TBS-T and finally developed with an enhanced chemiluminescence detection system (Amersham Biosciences, Buckinghamshire, UK).

Immunohistochemistry
Paraffin embedded BM sections (5 μm-thick) were kept at 60°C overnight and then deparaffinized in xylene and rehydrated through passages in alcohol (100% to 70%) and distilled water. Heat-induced antigen retrieval was carried out in 10 mM citrate buffer (pH6) for 15 min in a microwave oven. Sections were cooled down and then washed in distillate water/PBS. Samples were incubated with blocking solution of 10% goat serum in PBS Triton X 0.1%. Samples were incubated overnight with Alexa Fluor 568-conjugated isolectin B4 and then with VE-cad pY731 or pY658 rabbit polyclonal antibody for 2 h at RT. A goat anti-rabbit Alex488 was used as secondary antibody for 1 h at RT. All samples were counterstained with DAPI and then mounted in Fluoromont-G mounting media. Microphotographs were taken with Leica SP5 confocal imaging system (Leica, Milton Keynes, UK), at 400x magnification.
Rhodamine staining
BMECs were seeded in 8-well chamber slides to reach semi-confluence. Cells were fixed
with 2% paraformaldehyde for 15min at RT. After incubation in rhodamine phalloidin
staining solution (200µM) for 20min at 4°C, cells were washed twice with PBS and then
mounted with Fluoromont G mounting media. Representative microphotographs for each
condition were taken on a fluorescent microscope (Olympus, Southend on Sea, UK) at
200x magnification.

Rho activity assay
Guanosine triphosphate (GTP)-bound active Rho was assessed by pulldown assays,
following the manufacturer’s instructions (Millipore, Billerica, Ma, USA). Briefly, BMECs
were cultured until 70-80% confluent. The medium was changed to DMEM without serum,
and after an overnight incubation, cell lysates were harvested. Precipitated GTP-bound
Rho was run on a 10% SDS-PAGE and subjected to immunoblotting, using anti-Rho
monoclonal antibodies. After washing and applying anti-mouse HRP-conjugated antibody,
enhanced chemiluminescence reagent (Amersham Biosciences, Bath, UK) was used for
visualization.

Trans-endothelial migration
Trans-endothelial migration (TEM) of BM mononuclear cells (BM-MNCs) was assessed
using transwell cell culture inserts equipped with 3µm pore size filters (BD Biosciences)
using SDF-1 as chemoattractant. Inserts were pre-coated with 0.5 µg/mL fibronectin in
0.1% gelatin. BMECs were seeded on coated transwell filters (8x10^4/well) and cultured for
24h before the experiment was performed. SDF-1 (100ng/mL) or vehicle was added to the
lower compartment of the transwell system, in DMEM containing 0.1% BSA. Freshly
isolated BM-MNCs from T1D and control mice were labeled with CM-DiL (Life
Technologies, NY, US) following the manufacturer’s instructions, resuspended at 1x10^6
cell/mL and then added to the top compartment (3x10^5 cells per well in 300μL). After 16h
incubation at 37°C, non-migrated cells on the upper side of the membrane were removed
by scraping; all inserts were fixed for 10min in methanol, and mounted on slides
counterstained with DAPI. The number of fluorescent BM-MNCs transmigrated to the
lower side of the membrane was quantified in duplicates. Five random view-fields at x200
magnification were captured and the number of CM-DiL-positive BM-MNCs was
determined. Three separate experiments in triplicate were analyzed and averaged.

In vitro permeability assay
HBMECs and BMECs were seeded onto transwell inserts (0.3 µm, pore size) coated with
0.5 µg/mL fibronectin and grown until they reached confluence. Cells were preconditioned
with Src inhibitors, PP2 (10 µM, Sigma, Saint Louise, MO, USA) and SU6656 (2.5 µM,
Calbiochem, Darmstadt, Germany) for 30min. Then media were replaced in the lower
chamber and fresh media containing 70 kDa FITC-labelled dextran were added in the
upper chamber. The increase in fluorescence in the lower chamber was evaluated at
different time points over 16h with identical exposure settings using FLUOstar Optima
fluorimeter (Berthold Technologies Wildbad, Germany). The intensity of fluorescence was
plotted versus time by linear regression in order to obtain the endothelial permeability
slope, P_{se}. The P_{se} value was divided by the area of the porous membrane and the result
was the permeability coefficient (P_{e}, cm/s). Results were expressed as fold change of
relative control. Three independent experiments in triplicate were analyzed and averaged.
**In vivo permeability assay**

Mice were intra-cardially injected with a 500µl bolus of 70 kDa FITC-labeled dextran followed, after 3, 5 or 7 min by an equal amount of 70 kDa TRITC-labeled dextran (n=3 each time point). Animals were sacrificed 30sec from last injection. Peripheral blood and bones (femura and tibiae) were collected. Peripheral blood was spun down at 1.3x10^4 rpm for 15min in order to obtain plasma. BM was flushed out from bones with sterile saline solution with equal volume for all samples and weighed. Bones were weighted before and after drying. FITC and TRITC fluorescence was measured at FLUOstar Optima fluorimeter with identical exposure settings for all conditions in plasma and flush.

Data were plotted as mg FITC (I_F) in BM interstitium per mg tissue (W) against time. W is given by:

\[ W = (F - P) + (B + D) \]

Where F is the weight of flush, P the weight of saline solution, B the weight of wet bones and D the weight of dry bones.

I_F is given by:

\[ I_F = V.(F_F - F_T.(P_F/P_T)) \]

where V is the volume of flushing, F_F is the concentration of FITC-dextran in the flush-out, F_T is the concentration of TRITC-dextran in the flush-out., P_F and P_T are the concentrations of FITC and TRITC dextran in plasma, respectively. Three independent experiments were carried out for each time point and condition.
Supplemental Figure I: Experimental plan for insulin treatment of T1D mice. Four weeks after induction of diabetes, mice received subcutaneous implants for continuous insulin supplementation at the rate of 0.1 unit/implant/d or vehicle. Glycemia was monitored every 4 weeks, while glycosuria was assessed at 2 weeks after diabetes induction and reassessed at the end of the study (A). Glycemia values at different time points in control group (white bars), T1D group (black bars), and T1D group receiving insulin supplementation (grey bars) (B). Data are expressed as mean ± SEM. *** P<0.001 vs. ctrl, ### P <0.001 vs. T1D.

Supplemental Figure II: IPA analysis highlights the remarkable effect of diabetes on key components of the signaling network controlling vascular permeability and leukocyte extravasation. Molecules are represented as nodes, and the biological relationship between two nodes is represented by an edge line. All edges are supported by at least 1 reference from the literature, a textbook, or canonical information stored in Ingenuity Pathways Knowledge database. The color indicates up (red) or down (green) regulation. Nodes are displayed using various shapes that represent the functional class of the gene product.

Supplemental Figure III: (A) Microphotograph (i) (scale bars 100 um) and bar graphs (ii) showing BMECs stained with MitoTracker © Red CM-H2ROS, a marker of mitochondrial ROS. (B) DNA damage repair enzyme PARP-1 is upregulated whereas antioxidant transcription factor NRF2 is downregulated in T1D-BMECs. Expression was assessed by qPCR. (C) WB analysis of Nox2 expression in BMECs. Data (mean±SEM) indicate fold changes vs. control non-diabetic BMECs. Each experiment was performed in triplicate. (D) Transfection of T1D-BMECs with Ad.myrAkt was verified by western blot of active Akt. Data (mean±SEM) indicate fold changes relative to control. (E) Rho pulldown assay after transfection of T1D-BMECs with an adenovirus carrying RhoA N19 dominant negative. *P<0.05 and **P<0.01 vs. Ctrl, ###P<0.01 vs. T1D.

Supplemental Figure IV: HBMECs were cultured under increasing glucose concentrations from 5mM (white bars) to 15mM (grey bars), and 25mM (black bars). (A) Representative FACS images (i) and bar graph (ii) showing ROS levels in hBMECs assessed using flow cytometry detection of mitochondrial superoxide by MitoSox and intracellular peroxide and superoxide free radicals by DCF-2DA. The latter was measured after treatment with catalase (cat.) (100 U/ml), edavarone (MC-86)(100 μL), and diethyldithiocarbamate (DDC)(100 μM). (B) In vitro permeability of hBMECs exposed to increasing concentrations of glucose in the presence of antioxidants DDC (100 μM), catalase (100 U/ml), MCI-186 (10 μM), and NAC or Src inhibitors (PP2, SU6656) or vehicle. Data (mean±SEM) indicate fold changes relative to normal glucose (NG). *P<0.05, **P<0.01 and ***P<0.001 vs. NG; #P< 0.05 vs. HG15; §P <0.05, §§§P<0.001 vs. HG25. Each experiment was performed in quadruplicate.

Supplemental Figure V: HBMECs were cultured under increasing glucose concentrations from 5mM (white bars) to 15mM (grey bars), and 25mM (black bars). Western blot was performed for VEcadherin p731 (A), and VEcadherin pY658 (B), and pPyk2 (C). Data are expresses as mean ± SEM. ¶P<0.05, **P<0.01, ***P<0.001 vs. vehicle of the same group, *P< 0.05 and ***P<0.001 vs. 5 mM; §P< 0.05 vs. 15 mM. Each experiment was performed in triplicate.
**Supplemental Figure VI:** (A) Expression of phosphorylated form of redox sensitive kinase p38, JNK, and mapk kinase kinase MEK1 was assessed by western blot. (B) p-p38 (i) and p-JNK (ii) were increased in T1D-BMECs (upper panels) and HBMEC treated with HG (lower panels). Antioxidants NAC (250 μM) and catalase (100 U/ml) reverted the effect of HG and diabetes. p-MEK1 (iii) was also increased in HBMEC exposed to HG but not in T1D-BMECs. **P< 0.01 vs. ctrl; #P<0.05 vs. T1D; §P<0.05 vs. NG; ¥P<0.05 vs. HG25.

**Supplemental Figure VII:** Representative confocal single channel and merged microphotographs (scale bars, 80 µm) of BM sections stained with isolectin B4 (Red) and VEcadherin pY658 or VEcadherin pY731 (green) counterstained with DAPI to identify nuclei (blue). Diabetes increases VEcadherin phosphorylation in BMECs.

**Supplemental Figure VIII:** Bar graph showing the plateau concentration of FITC-labeled dextran in BM from femura (A) and tibiae (B) of T1D mice at 14 (white bars) and 18 weeks (black bars) from diabetes induction as compared with age-matched non-diabetic mice. Effect of insulin (100 nM) treatment in BMECs on VE-cadherin pY731 (C), VE-cadherin pY658 (D), and pPyk2 (E). Data are expressed as mean ± SEM. **P<0.01 vs. ctrl, #<0.05 vs. T1D. Each experiment was performed from triplicate to quadruplicate.

**Supplemental Figure IX:** Proposed mechanistic network responsible for endothelial dysfunction in diabetic bone marrow and therapeutic targets (green).
Table I: List of qPCR primers

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Table II: Summary of microarray analysis comparing the expressional profile of BMECs from T1D and non-diabetic mice. List of single genes modulated in the enriched canonical pathways according to the IPA analysis.

### a. Cdc42 signaling

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<th>Symbol</th>
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<th>FDR (q-value)</th>
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<td>other</td>
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<td>ARPC1A</td>
<td>actin related protein 2/3 complex, subunit 1A, 41kDa</td>
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<td>Integrin, alpha 6</td>
<td>-1,289</td>
<td>0,019</td>
<td>Plasma Membrane</td>
<td>other</td>
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<tr>
<td>ITGA2B</td>
<td>integrin, alpha 2 (platelet glycoprotein lib of lib/IIia complex, antigen CD41)</td>
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<td>0,003</td>
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<td>0,008</td>
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<td>kinase</td>
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<tr>
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<td>0,033</td>
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### c. Integrin signaling

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<tr>
<th>Symbol</th>
<th>Synonyms</th>
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<th>FDR (q-value)</th>
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<th>Type(s)</th>
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<td>phosphatase and tensin homolog</td>
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**b. RhoA signaling**

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<tr>
<td>ARPC2</td>
<td>actin related protein 2/3 complex, subunit 2, 34kDa</td>
<td>1,492</td>
<td>0.013</td>
<td>Cytoplasm</td>
<td>other</td>
</tr>
<tr>
<td>ARPC1A</td>
<td>actin related protein 2/3 complex, subunit 1A, 41kDa</td>
<td>1,488</td>
<td>0.047</td>
<td>Cytoplasm</td>
<td>other</td>
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<td>MSN</td>
<td>moesin</td>
<td>1,93</td>
<td>0.001</td>
<td>Plasma Membrane</td>
<td>other</td>
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<tr>
<td>MYLK</td>
<td>myosin light chain kinase</td>
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<td>0.008</td>
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<td>PPP1R12A</td>
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<td>phosphatase</td>
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<tr>
<td>ROCK2</td>
<td>Rho-associated, coiled-coil containing protein kinase 2</td>
<td>1,584</td>
<td>0.015</td>
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<td>kinase</td>
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**c. Tight Junctions signaling**

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<th>Fold change</th>
<th>FDR (q-value)</th>
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<td>kinase</td>
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<tr>
<td>PTEN</td>
<td>phosphatase and tensin homolog</td>
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<td>0.008</td>
<td>Cytoplasm</td>
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</tr>
</tbody>
</table>
Supplemental Figure IV

A

1. **MitoSOX**
   - **Graph i:**
     - **Y-axis:** PE-A
     - **X-axis:** Log 10
     - **Legend:**
       - Unstained
       - 5 mM D-galactose
       - 15 mM D-galactose
       - 25 mM D-galactose
   - **Graph ii:**
     - **Y-axis:** Fold change relative to control
     - **X-axis:** NG, HG15, HG25
     - **Legend:**
       - NG
       - HG15
       - HG25
       - Statistic symbols: *
       - **Statistical Tests:**
         - **MitoSOX:**
           - HG15 vs. NG: ***
           - HG25 vs. NG: ***, #
         - HG15 vs. HG25: #

2. **DCF-2DA**
   - **Graph:**
     - **Y-axis:** FITC-dextran (Fold change of untreated cells)
     - **X-axis:** Vehicle, DDC, Catalase, Edaravone, NAC, PP2, SU6656
     - **Legend:**
       - Vehicle
       - DDC
       - Catalase
       - Edaravone
       - NAC
       - PP2
       - SU6656
     - **Statistic symbols:**
       - *
       - **
       - ***
       - **
       - **
       - ***

**Notes:**
- The graphs illustrate the effect of different concentrations of D-galactose on MitoSOX and DCF-2DA fluorescence.
- Statistical significance is indicated by asterisks and hash symbols.
- HG15 and HG25 represent experimental conditions.
- The FITC-dextran graph shows the fold change in comparison to untreated cells.
Supplemental Figure VIII

A. Femura

B. Tibiae

C. i

VEcad p-Y731
VEcad p-Y658
Total VEcad
Tubulin

ii

iii

Protein fold change relative to control

VEcad p-Y731
VEcad p-Y658

Tubulin

D. i

ii

P-Pyk2
Pyk2
Tubulin

Protein fold change relative to control

Ctrl T1D T1D + Insulin

Ctrl T1D T1D + Insulin