
Endothelial Cell Gene Regulation

Takashi Minami and William C. Aird*

Endothelial cells (ECs) display phenotypic heterogeneity. Endothelial cell heterogeneity is mediated, at least in part, by site-specific and time-dependent differences in gene transcription. The goal of this review is to provide a conceptual framework for approaching EC gene regulation in the adult vasculature. We summarize data from cell culture studies that provide insight into the transcription factors involved in mediating gene expression in ECs. Next, we review the results of in vivo studies relating to gene regulation in the intact endothelium. Finally, we draw on both the in vitro and in vivo results to propose a model of gene regulation that emphasizes the importance of the extracellular environment in controlling site- and time-specific vascular gene expression. (Trends Cardiovasc Med 2005;15:174.e1–174.e24) © 2005, Elsevier Inc.

The endothelium lines the vasculature and is involved in multiple homeostatic functions including the control of vasomotor tone, the trafficking of cells and nutrients, the maintenance of blood fluidity, and the growth of new blood vessels (Cines et al. 1998). Importantly, these properties vary both in space and time, giving rise to the phenomenon termed endothelial cell (EC) heterogeneity (reviewed in Aird 2003a).

There are several reasons for studying transcriptional regulation in the endothelium. First, the phenotype of the endothelium is dictated in large part by space and time-specific differences in

gene expression. Therefore, the elucidation of mechanisms of transcriptional control should provide important insights into the molecular basis of vascular diversity. Second, transcriptional networks act as signal transducers in the endothelium, coupling input to output. Thus, transcription factors hold a key to understanding the link between microenvironment and cellular phenotype. Third, each transcription factor is coupled to multiple upstream signals and downstream target genes. Therefore, the characterization of these so-called hubs in the context of network topology will provide not only important mechanistic information, but also a powerful foundation for targeted therapy (Aird 2003b).

• Defining Endothelial Cells

An interesting question is how one defines an EC. From an anatomic standpoint, ECs are readily described by their location on the luminal side of the blood vessel wall. A developmental biologist might argue that ECs are defined by one or a small number of lineage switches that occur during embryogenesis. Ultrastructural properties that are classically associated with the endothelium, such as Weibel–Palade bodies and vesicular–

vacuolar organelles, are not expressed uniformly throughout the vascular tree. Other properties such as caveolae are not unique to the endothelial lineage. From the standpoint of molecular markers, few, if any, EC-specific transcripts or proteins are expressed in all ECs. Functionally, the endothelium displays remarkable division of labor. For example, most leukocyte trafficking takes place in post-capillary venules; endothelial-mediated vasorelaxation is a property of arterioles; barrier properties normally vary throughout the vasculature; and hemostatic balance is mediated by vascular bed-specific patterns of natural anticoagulants and procoagulants. Finally, in transgenic mouse assays, most EC-specific promoters contain information for expression in discrete subpopulations of ECs. To summarize, each definition—with the exception of anatomic location—falls short of fully capturing the endothelium.

• Phenotypic Heterogeneity of the Endothelium

When considering the remarkable degree of heterogeneity of the endothelium, two questions arise: (a) why are there so many differences between endothelial phenotypes, and (b) how are these differences generated and maintained? The first question requires an evolutionary explanation; the second calls for a proximate mechanism.

Several selective forces may explain the existence of endothelial heterogeneity. First, the endothelium must meet the diverse needs of the underlying tissue environment. For example, fenestrations within glomerular endothelium facilitate filtration function of the kidney; the tight junctions and enzymatic machinery of the blood–brain barrier protect this organ from fluctuations in blood composition; and the fenestrae and lack of organized basement membrane in hepatic sinusoids enable ready passage of substrates from nutrient-rich portal venous blood to underlying hepatocytes. Second, the endothelium must cope with different environments. For example, the endothelium of lung capillaries is exposed to high levels of oxygen, whereas the endothelium of the vasa recta in the inner medulla of the kidney is exposed to a profoundly hypoxic, hyperosmolar, and hyperkalemic tissue

Takashi Minami is at the Research Center for Advance Science and Technology, the University of Tokyo, Tokyo 153-8904, Japan. William C. Aird is at the Division of Molecular and Vascular Medicine, Beth Israel Deaconess Medical Center/Harvard Medical School, Boston, Mass.

* Address correspondence to: William C. Aird, MD, Molecular and Vascular Medicine, Beth Israel Deaconess Medical Center, RW-663, 330 Brookline Avenue, Boston, MA 02215, USA. Tel.: (+1) 617-667-1031; fax: (+1) 617-667-1035; e-mail: waird@bidmc.harvard.edu.

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microenvironment. Although little is known about the latter blood vessels, their endothelium must be uniquely adapted to withstand such extreme conditions. Finally, when outer epithelial layers are breached by pathogens, the endothelium plays a key role in orchestrating the host innate immune response. The greater the heterogeneity and adaptability the more poised the endothelium is to deal with the unpredictable properties of the outside world, particularly those arising from the host-pathogen arms race.

From a mechanistic standpoint, endothelial heterogeneity arises from cues within the extracellular environment. Each EC in the human body is analogous to a miniature adaptive input-output device (Figure 1). Extracellular input is coupled to output by a highly intricate array of nonlinear signaling pathways, which often begin at the cell surface and converge at the level of gene transcription.

Signal input varies from one site of the vascular tree to another and from

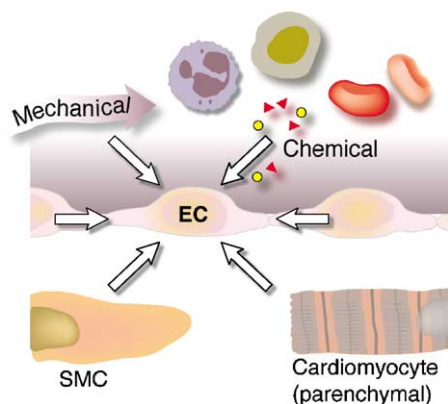


Figure 1. Endothelial cell as an input-output device. Each EC senses biochemical and biomechanical signals from the surrounding microenvironment. Signals may originate from blood vessel lumen, neighboring ECs, and/or abluminal surface. Shown (arrows) are (bio)mechanical input and (bio)chemical input. Chemical input may consist of paracrine signals derived from circulating blood cells, neighboring ECs, vascular smooth muscle cells (SMCs), and parenchymal cells (e.g., cardiomyocyte); or soluble signals that function over a distance (e.g., hormones, lipoproteins, pH, oxygen). For purposes of illustration, the arrows all point in one direction toward the EC. However, the dialogue between the EC and its environment is bidirectional. Not shown are the intracellular signal transduction networks or the cellular output/phenotype.

one moment to the next. For example, capillary ECs in the heart are exposed to unique regional biomechanical forces as well as cardiomyocyte-derived paracrine mediators, whereas the endothelium of the blood-brain barrier receives input from surrounding astroglial cells. As input varies in space and time, so does endothelial output or phenotype.

In addition to these reversible effects of the microenvironment, extracellular signals may also induce epigenetic modification of ECs. As a result, certain site-specific properties become irreversibly “locked in” and mitotically stable. These events are particularly important during embryogenesis, where they contribute to such fundamental processes as arterial-venous identity.

• Classification of Endothelial Cell Genes

Endothelial cell genes may be classified according to whether they are constitutively or inducibly expressed, whether they are specific or not to ECs, and whether they are expressed throughout the endothelium or in subsets of ECs (Figure 2).

A distinct advantage of studying genes which are specifically and constitutively expressed in ECs is that an understanding of their transcriptional control may provide important insights into the molecular basis of lineage determination. Moreover, the information derived from these studies may be useful for designing cell-type-specific targeting strategies for treatment of vascular diseases.

However, the intrinsic value of an endothelial gene, either as a functional entity or as a target of investigation, does not necessarily correlate with its degree of cell-type specificity. For example, E-selectin is expressed exclusively in ECs, whereas intercellular adhesion molecule (ICAM)-1 and vascular cell adhesion molecule (VCAM)-1 are also expressed in other cell types. There is no evidence that E-selectin is more important in mediating cell adhesion than its non-cell-type-specific counterparts. As another example, tissue factor is not normally expressed in the intact endothelium, but is expressed by monocytes, fibroblast, and many parenchymal cells.

	SPECIFICITY	INDUCIBILITY	LOCALITY
Gene A	EC	Inducible	Vasc. bed
Gene B	EC	Inducible	All-endo
Gene C	EC	Constitutive	Vasc. bed
Gene D	EC	Constitutive	All-endo
Gene E	Non-sp.	Inducible	Vasc. bed
Gene F	Non-sp.	Inducible	All-endo
Gene G	Non-sp.	Constitutive	Vasc. bed
Gene H	Non-sp.	Constitutive	All-endo

Figure 2. Schematic of classes of EC genes. Endothelial cell genes may be classified according to specificity, inducibility, and locality. Under the heading “specificity,” genes are either specific to ECs (EC), or expressed in other cell types as well (Non-sp., nonspecific). Under the heading “inducibility,” genes are either inducible (or repressible) by signals within the extracellular microenvironment, or they are constitutively expressed (constitutive). Locality refers to whether the gene is expressed in distinct subsets of ECs/vascular beds (Vasc. bed), or is pan-endothelial in its distribution (All-endo). Examples of class A genes include E-selectin, thrombomodulin, endothelial protein C receptor, eNOS, endocan, and vWF; class B genes unknown; class C genes include tissue factor pathway inhibitor, receptor tyrosine phosphatase μ , Ephrin B2, Ephrin B4; class D genes include PECAM-1 (CD31) and VE-cadherin; class E genes include VCAM-1, P-selectin, tissue factor, Egr-1; class F genes unknown; class G genes include P-glycoprotein, GLUT4; class H genes include β -actin and other “housekeeping” genes. The divisions between classes are not absolute—for example, there is increasing evidence that many of the constitutive genes are in fact modulated by the microenvironment. Moreover, there is a question as to whether there is any EC-specific gene that is expressed in every EC of the body. Finally, many genes in class A are expressed in a limited number of other cell types.

Endothelial expression of tissue factor has been reported in certain pathologic conditions, including tumors (Contrino et al. 1996), atherosclerosis (Crawley et al. 2000), sickle cell anemia (Solovey et al. 2004), sepsis (Drake et al. 1993), and cardiac allograft rejection (Nagayasu et al. 2000). It is possible that under these conditions endothelial tissue factor plays an important pathogenic role and that an understanding of its transcriptional regulation would provide new insights into mechanisms of disease.

In summary, the site- and time-specific phenotype of an EC is dictated by its full complement of transcripts and proteins, and not simply by its

Table 1. Examples of agonist-mediated induction/repression of transcription factors and downstream target genes in EC^a

Agonist	Transcription factor	Target genes/cell function ^b	
<i>Oxygenation</i>			
Hypoxia	AP-1	HO-1 eNOS	
	Egr-1	–	
	Elk-1	–	
	HIF	CRLR Endoglin MDR-1 SDF-1	
	HIF+GATA-2+AP-1	ET-1	
	NERF-2	TIE-2	
	Smad2/3	TGF-β	
	Sp1	MDR-1	
	<i>Hemodynamic forces</i>		
	Laminar shear stress	GATA-6	Inhibits u-PA
KLF2		–	
Negative binding protein		Inhibits Tie-1	
c-Myc		MMP-9	
NF-κB		ICAM-1 eNOS	
Inhibits NF-κB		Inhibits PDGF-B	
GR		–	
Sp1		Flk-1	
Inhibits Sp1		Inhibits P2X4	
SREBP		–	
AP-1		eNOS	
Nrf2		NQO1, HO-1	
CRE binding protein		COX-2	
Cyclical strain		AP-1	ET-1
Stretch		NF-κB	IL-6
<i>Chemokines and cytokines</i>			
IFN-α	STAT-4	MCP-1, SOCS3	
IFN-γ	STAT-1	CD40 TAP-1, IRF1, Class 1 MHC	
IL-1	AP-1, Sp1 NF-κB, C/EBP	ICAM-1 iNOS	

Table 1. continued

Agonist	Transcription factor	Target genes/cell function ^b
<i>Chemokines and cytokines</i>		
IL-4	STAT-1	MCP-1
	AP-2, NF-1, Sp1, STAT-6, but not NF-κB or AP-1	–
IL-6	STAT-3	–
IL-10	STAT-3	eNOS
IL-18	NF-κB	IL-1, TNF-α
LIX	NF-κB	IL-1, TNF-α
PAF	STAT-3	–
TNF-α	ATF3 CREB E2F1 inhibition Id1, Id3	Cell death – Inhibits E2F1 E-selectin, not ICAM-1
	IRF-1 NF-κB	VCAM-1 E-selectin, TF
		Fractalkine IL-8 MadCAM MCP-1, IL-8, ICAM-1, VCAM-1, E-selectin
	NUR77 Sp1 Sp1, Sp3 inhibition	PAI-1 Fractalkine Inhibits eNOS
TNF-α+IFN-γ	STAT-1, IRF	CD40
HMGB1	NF-κB, Sp1	–
<i>Growth factors, hormones, glucose</i>		
AGE	NF-κB, AP-1	VEGF
Ang-1	Forkhead	–
Dihydrotestosterone	Androgen receptor/ NF-κB	VCAM-1
ET-1	Ets-1	–
FGF-2	Tcf-4 STAT-3 Egr-1	Cyclin D1 –
Glucose	AP-1 Egr-1 NF-κB	Fibronectin IL-8 Flt-1, PAI-1 VCAM-1 eNOS inhibits cell migration
	Fibronectin	
GM-CSF	NF-κB	–

Table 1. continued

Agonist	Transcription factor	Target genes/cell function ^b
<i>Growth factors, hormones, glucose</i>		
HGF	Forkhead Ets-1 Egr-1	– MMP-1, HGF, c-met ACE
IGF-1	RUNX2	Tube formation
Insulin	AP-1 Egr-1	eNOS Flt-1, PAI-1
Leptin	AP-1 STAT-3	ET-1 VEGF
Placental growth factor	AP-1	–
Prolactin (16-kD N-terminal fragment)	NF-κB	Caspases 3, 8, 9; E-selectin
Relaxin	NF-κB	ET _B
VEGF	Ets-1	Neuropilin, angiopoietin-2, cell proliferation
		Angiopoietin-2 DSCR-1 Proliferation DAF DSCR-1 COX-2 p27 ^{kip1} MnSOD MnSOD TF VEGF
	NF-AT	
	GATA	
	Forkhead	
	NF-κB	
	STAT-3 Egr-1 Id1, Id3	
		TF, Flt-1, u-PA ICAM-1, but not E-selectin; EC proliferation
	SREBP1/2	–
	Sp1 Vezf1	KDR VEGF-mediated proliferation, migration, and tube formation
Thymosin β4	AP-1	PAI-1
<i>Lipoproteins and related mediators</i>		
Cholesterol	AP-1	ICAM-1
Diabetic LDL	STAT-5B	p21 and G1 fraction
Native LDL	LXR	ABCA1
oxHDL	NF-κB	–
oxLDL	ATF3	Cell death

Table 1. continued

Agonist	Transcription factor	Target genes/cell function ^b
<i>Lipoproteins and related mediators</i>		
VLDL, oxVLDL	CREB, NF-κB	–
LPL+VLDL	PPARα	Ac-CoA-oxidase
LPA, S-1-P	NF-κB	ICAM-1
Fatty acids	Sp1	Heparanase
Oleic acid	NF-κB	ET-1
5(S)-HETE	STAT-3	–
Oxidized phospholipids (OxPAPC)	STAT-3	IL-8
		TF
	NFAT, Egr-1	–
	CREB	HO-1
	Egr-1	–
Epoxyeicosatrienoic acids (EET)	CRE	t-PA
Linoleic acid	NF-κB, AP-1	–
ω-3 fatty acids	PPAR-α	–
<i>Matrix and related factors</i>		
Fibronectin	NF-κB	E-selectin, VCAM-1, ET-1, CYR-61
Three-dimensional collagen type-1	GATA-2	MMP-2
Type 1 collagen	Ets-1	MMP-1
TGF-β	Smad2	eNOS
	Smad1/2/5, Id	Cell migration
	CREB	RANKL
	Smad3/4, AP-1	ET-1
	Smad6	Inhibits TM
<i>Serine proteases</i>		
Thrombin	AP-1	Prepro-ET
	dbpB	PDGF-B
	Egr-1	–
	NF-κB	ICAM-1
	NF-κB, GATA-2	VCAM-1
	NF-AT	DSCR-1
	Sp1	KDR
	SRF	Egr-1
<i>Cell-cell interactions</i>		
Platelet-EC	NF-κB	MCP-1, VCAM-1
Neutrophil-EC	Ets-1	Tube formation

Table 1. continued

Agonist	Transcription factor	Target genes/cell function ^b
Neutrophil-derived proteases	NF-κB (cleaves and inhibits)	
<i>Vasomotor tone</i>		
NO	Inhibits NF-κB	Inhibits ET-1
	Nrf2	HO-1
Ang II	AP-1	ET-1
	NF-κB	VCAM-1, ICAM-1
ANP	AP-1	HO-1
<i>Pathogens</i>		
<i>Orientia tsutsugamushi</i>	AP-1, NF-κB	MCP-1
<i>Chlamydia pneumoniae</i> PMP	NF-κB	IL-6, MCP-1
<i>Chlamydia pneumoniae</i> infection	NF-κB	ICAM-1
Shiga toxin	NF-κB	MCP-1, IL-8
African swine fever virus (infection)	Decreases p65 NF-κB	Inhibits IL-8, E-selectin, but increases TF
<i>Bartonella henselae</i> (infection)	NF-κB	ICAM-1, E-selectin
<i>Bartonella bacilliformis</i> infection	AP-1	–
EBV infection or LMP-1 overexpression	NF-κB	–
HIV protein Tat	NF-κB	E-selectin
HIV pcTat	NF-κB	Monocyte adhesion
HIV Tat1-72	NF-κB, AP-1	–
HHV-8 (retroviral infection of ORF74)	NF-κB	–
<i>Drugs/toxins</i>		
Arsenite	NF-κB, AP-1	–
Bleomycin	Egr-1	ACE
	NF-κB	E-selectin
	NF-κB, Nrf-1/2	γ-Glutamyl-cysteine synthetase
Cocaine	NF-κB, AP-1	–
Doxorubicin	p53, not NF-κB	CD95
	NF-κB	Cell apoptosis

Table 1. continued

Agonist	Transcription factor	Target genes/cell function ^b
HMG-Co reductase	Inhibits NF-κB, AP-1, HIF-1α	–
Isoproterenol	NF-κB	IL-18
<i>Drugs/toxins</i>		
Methamphetamine	NF-κB, AP-1	TNF-α
<i>Disease-related mediators</i>		
Human lymphoma-derived soluble factors	NF-κB	Leukocyte adhesion
Amyloid-β peptide	AP-1	Bim
Anti-phospholipid antibodies	NF-κB	–
Homocysteine	NF-κB	Fas
MetHb	NF-κB	E-selectin, IL-6, IL-8

See online supplement for references, endothelial cell types used, and full list of abbreviations.

^a Data are not all-inclusive, but rather are representative of published studies over the past 4 years. Studies of lymphatic EC are not included. The results (as shown in the table and, in most cases, in the original papers) do not discriminate between primary and secondary effects of transcription factors. For example, many of the transcription factors listed under hypoxia may lie downstream of HIF-1α. The reader should refer to the original paper for passage number, agonist dose(s), treatment time(s), and the rigor of assays establishing connection between transcription factor and target gene (e.g., promoter analysis, chemical inhibitor, antisense oligonucleotides, siRNA).

^b Induction of gene expression unless otherwise stated.

repertoire of lineage-specific genes. Indeed, a full understanding of the mechanisms by which differential gene expression determines phenotypic heterogeneity requires a consideration of both cell-type-specific and non-specific gene classes.

• Endothelial Cell Gene Regulation In Vitro

To date, studies of constitutively expressed, cell-type-specific genes (Figure 2,

classes C and D) have provided relatively few insights into the biology of adult endothelium. As a general rule, lineage-specific gene expression in adult ECs is mediated by combinatorial interactions between non-cell-type-specific transcription factors, including Sp1, GATA proteins (GATA-2, GATA-3, and GATA-6), and the Ets family of transcription factors (Ets-1, Ets-2, ELF-1, NERF2, and Fli-1). A possible exception is the transcription factor, *Vezf1*, which is restricted in its expression to ECs (Xiong et al. 1999), and has been shown to mediate expression of endothelin-1 (Ait-sebaomo et al. 2001). In contrast to other lineages, such as erythroid cells, hepatocytes, and skeletal myocytes, the endothelium does not seem to possess a cell-type-specific master switch that mediates differentiation and/or expression of multiple differentiation markers. However, it is formally possible that such factor(s) exists but awaits discovery. Perhaps lineage-specific transcription factors operate transiently during endothelial differentiation and/or angiogenesis, but are no longer necessary for

regulating target gene expression in mature endothelium of preexisting blood vessels. Alternatively, ECs possess yet-to-be-identified cell-type-specific co-activators that account for lineage-restricted gene expression.

Compared with the paucity of data relating to cell-type-specific gene regulation, there is a wealth of knowledge regarding modulatable gene expression (Figure 2, classes A, B, E, and F). Many extracellular signals have been shown to alter gene transcription in cultured ECs (Table 1). Unfortunately, differences in study design (e.g., cell type, passage number, and assay) hinder comparisons of the published data (Figure 3). These differences notwithstanding, several themes emerge from the in vitro studies. First, the various agonists activate overlapping yet distinct patterns of transcription factors and downstream target genes. In other words, EC activation is not an all-or-none phenomenon. Second, input is typically transduced by non-cell-type-specific transcription factors. Finally, the collective data from cell culture studies point to the truly remarkable

capacity of ECs to recognize and respond to extracellular signals.

• Endothelial Cell Regulation In Vivo

Well before the routine isolation of ECs, electron microscopic studies demonstrated clear differences in phenotype between vascular beds, perhaps the most striking example being the tight barrier properties of the blood-brain barrier (Reese and Karnovsky 1967). If one believes that such phenotypes are controlled at the level of gene transcription, then these differences in ultrastructure provided an early hint for the existence of differential gene expression. These observations were supported by immunohistochemical and in situ hybridization studies in the 1980s and 1990s, demonstrating regional variation in gene and/or protein expression within different vascular beds (Kumar et al. 1987, Page et al. 1992, Turner et al. 1987). More recently, sophisticated proteomic approaches have revealed extensive heterogeneity of the endothelium in vivo (Arap et al. 2002, Oh et al. 2004).

The availability of cell culture techniques in the mid-1970s marked the beginning of a new era in endothelial biology, one that saw a striking increase in the number of publications in the field (Nachman and Jaffe 2004). Endothelial cell cultures offer a powerful tool for dissecting molecular mechanisms of transcriptional regulation. However, because ECs undergo phenotypic drift when removed from their native environment, these assays do not lend themselves to a molecular dissection of site-specific regulatory mechanisms.

Perhaps the first evidence for regional differences in mechanisms of transcriptional regulation was provided by early standard transgenic approaches in the late 1980s and 1990s. The first reports demonstrated that a small fragment of the von Willebrand factor (vWF) promoter, or the *Tie-2* gene, directed expression of a reporter gene to limited subpopulations of ECs in the intact animal (Aird et al. 1995, Schlaeger et al. 1995). In each case, the addition of further 5' and/or 3' DNA sequences resulted in more widespread expression in the endothelium (Aird et al. 1997, Schlaeger et al. 1997). Many

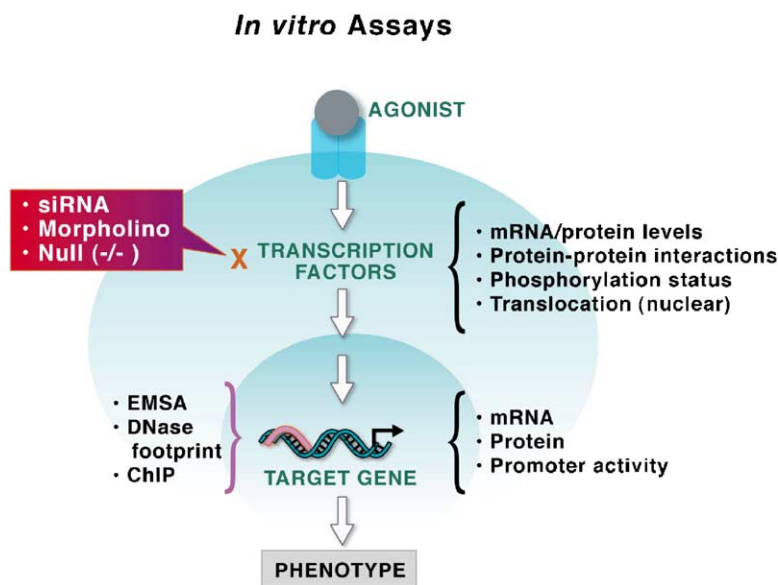


Figure 3. *In vitro* assays for studying EC gene regulation. Shown is an agonist binding to receptor in the surface of EC. Activation of receptor leads to changes in transcription factor(s) and downstream target genes. Assays at the level of transcription factor include mRNA or protein levels, interactions with other transcription factors and/or co-activators, phosphorylation or dephosphorylation, and/or nuclear exclusion/translocation. Binding of transcription factor to DNA may be assayed by electrophoretic mobility shift assay (EMSA), DNase footprint, or chromatin immunoprecipitation (ChIP). Target gene readouts include mRNA and protein levels as well as promoter-reporter gene activity, and cellular function. The above assays may be carried out in wild-type ECs, in cells null for one or another transcription factors, or in cells that have been transfected with siRNA or morpholino antisense oligonucleotides.

Table 2. Promoter analysis in transgenic mice

Gene	Assay	Promoter (species)	Reporter gene	Pattern of expression	Non-EC
Activin receptor-like kinase 1	Stable transgenics	Various promoter fragments (mouse)	<i>LacZ</i>	9.2-kb promoter directs arterial specific expression in adults	
CD34	Stable transgenics	160-kb (human)	Human CD34	ECs in many vascular beds in adult	Bone marrow
c-mpl	Stable transgenics	2-kb (mouse)	Human placental alkaline phosphatase	Some ECs in blood vessels of embryo (and yolk sac); none in adult	Megakaryocytes
eNOS	Stable transgenics	1.6-kb (human)	<i>LacZ</i>	Expression in ECs of brain, heart, skeletal muscle, and aorta. β -Galactosidase activity was consistently absent in vascular beds of the liver, kidney, and spleen	
	Stable transgenics	5.2-kb (mouse)	<i>LacZ</i>	ECs of large- and medium-sized blood vessels in several tissues	Brain
	<i>Hprt</i> locus targeting	1.6-kb (human)	<i>LacZ</i>	ECs in arteries > veins	Cardiomyocytes, VSMC
EPCR	Stable transgenics	-1080 to -1, -350 to -1 (mouse)	GFP	Expression in multiple tissues of adult, although cell type not defined	
Flt-1	<i>Hprt</i> locus targeting	1-kb (human)	<i>LacZ</i>	ECs in all vascular beds except for the liver	Cardiomyocytes
ICAM-2	Stable transgenics	0.33- and 3-kb (human)	CD59	Uniform EC expression in both lines	Granulocytes
KDR/Flk-1	Transient and stable transgenics	Various promoter fragments	<i>LacZ</i>	939-bp promoter+510-bp first intron fragment drives expression in most ECs, but expression lost with age	
	Transient transgenics	-640 to +299 and 510-bp intronic enhancer; with or without mutation of HoxB5 binding site (mouse)	<i>LacZ</i>	Wild-type promoter directs uniform expression in ECs of embryo; mutation abolishes expression	
	Stable transgenics	4.5-kb+510-bp intronic enhancer (mouse)	Luciferase	Most tissues; decreased expression with age	
Mef2c	Transient transgenics	Various fragments (mouse)	<i>LacZ</i>	4.66-kb directs uniform EC expression in embryos; patchy expression in adult; mutation of Ets sites disrupted expression	Some circulating blood cells
Notch4	Transient transgenics	Various promoter fragments (human)	<i>LacZ</i>	Different promoter fragments, different vascular beds	
PAI-1	Stable transgenics	2.9-kb (human)	eGFP	2.9-kb directs expression in "glomeruli" and "venous structures" of lung	Kidney tubular cells; lung epithelial cells; pyramidal cells of cerebellum
Pre- and pro-endothelin	Stable transgenics	5.9-kb (murine)	Luc	ECs of arteries and arterioles > veins, capillaries	VSCM, certain epithelial cells
PrP	Stable transgenics	6.9-kb (bovine)	GFP	ECs of mucosal capillaries and venules in lamina propria mucosa of intestinal villi; small vessels of intestinal submucosa; peri-tubular vessels in renal cortex	Purkinje cells, lymphocytes, keratinocytes
Scl/tal-1	Transient transgenics	Various promoter fragments (mouse)	<i>LacZ</i>	5.5-kb directs expression to embryonic endothelium	Blood cells
Tie-1	Standard transgenics	0.74-kb (mouse)	<i>LacZ</i>	ECs in arterial segments at vascular junctions	
	Standard transgenics	1.15-kb (mouse)	Cre		
	Transient transgenics	0.54-kb (mouse) (WT and oct mutant)	<i>LacZ</i>	Patchy EC expression in embryo; reduced expression and cell-type specificity with oct mutant	

Table 2. continued

Gene	Assay	Promoter (species)	Reporter gene	Pattern of expression	Non-EC
Tie-1	Standard transgenics	0.8-kb (mouse)	<i>LacZ</i>	Predominantly ECs of arterioles and capillaries in adult mice	
		1.1-kb (mouse)	eGFP	Throughout vasculature of embryo up to E11.5; later in embryogenesis A>V; very little expression in adult vascular beds	
Tie-2	Transient transgenics	Deletants and mutants of the 0.8-kb mouse promoter	<i>LacZ</i>	Ets mutations resulted in decreased EC expression in most organs	
	Standard transgenics	0.8-kb (mouse)	Growth hormone		
	Standard transgenics	1.2-kb promoter (mouse)	<i>LacZ</i>	Patchy EC expression in embryo, absent in adult	
	Standard and transient transgenics	2.1-kb promoter+10-kb intron 1; several mutations also tested (mouse)	<i>LacZ</i>	Uniform EC expression of full-length WT promoter in embryo and adult	
		2.1-kb promoter+1.7-kb intronic enhancer (mouse)	t-TA	In binary system (Tie-2-tTA+TRE-β-galactosidase), “near uniform” expression in endothelium	
	<i>Hprt</i> locus targeting	2.1-kb promoter+10-kb intron 1 (mouse)	Cre	Bred with CAG-CAT-Z transgenic mice; in contrast to standard transgenic mice, expression in mesenchymal cells of atrioventricular canal (only embryos analyzed)	
		0.72-kb fragment containing a 300-bp intronic enhancer coupled upstream to a 423-bp core promoter—with or without Ets mutations (mouse)	<i>LacZ</i>	Widespread EC expression in adult (lost with Ets mutation, except in brain)	
VE-cadherin	Standard transgenics	–2486 to +24 (mouse)	CAT	ECs of all vascular beds except brain capillaries in adult	
vWF	Standard transgenics	–487 to +246 (human)	<i>LacZ</i>	ECs in blood vessels in adult brain	
	Standard transgenics	–2186 to end of first intron (human)	<i>LacZ</i>	ECs in blood vessels in brain, microvessels of heart and skeletal muscle in adult	
	Standard transgenics	–2645 and the end of the first intron (mouse)	<i>LacZ</i>	ECs in blood vessels in brain, microvessels of heart and skeletal muscle in adult; megakaryocytes in one line	
		<i>Hprt</i> locus targeting	–2186 to end of first intron (human)	<i>LacZ</i>	ECs in blood vessels in brain, microvessels of heart and skeletal muscle in adult

See online supplement for references.

EC indicates endothelial cell; eNOS, endothelial nitric oxide synthase; EPCR, endothelial protein C receptor; GFP, green fluorescent protein; ICAM, intercellular adhesion molecule; PAI-1, plasminogen activator inhibitor-1; PrP, prion protein; VSMC, vascular smooth muscle cells; vWF, von Willebrand factor.

other EC promoters were subsequently tested in standard transgenic mice (Table 2). Interestingly, the majority of these DNA sequences were found to direct vascular bed- or cell subtype-specific expression.

In standard transgenic mice, multiple copies of the promoter-reporter gene

cassette are randomly integrated into the mouse genome (Figure 4). Random integration of variable transgene copies may give rise to significant line-to-line variation in expression. One approach to overcome these variables is to employ a “plug-in-socket” strategy in which a single copy of the transgene is inserted

into a defined locus of the genome. For example, a number of EC-specific promoters (linked to the *LacZ* reporter gene) have been targeted to the *Hprt* locus of mice, using homologous recombination. Under these more stringent conditions, different EC promoters continue to direct expression to specific

In vivo Promoter Assays

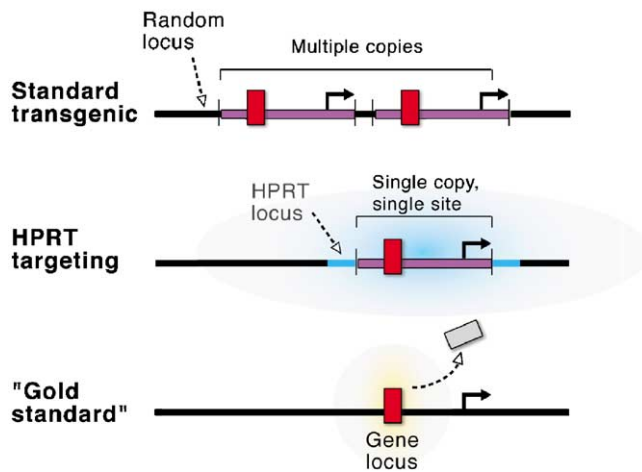


Figure 4. *In vivo* assays for studying promoter function. Three different approaches are shown. Standard transgenesis involves the injection of linearized DNA (containing promoter coupled to reporter gene cDNA) into fertilized oocytes. The procedure typically results in random integration of multiple transgene copies. In *HPRT* targeting, a single copy of the transgenic cassette is introduced into a defined (albeit heterologous) locus of the mouse genome through homologous recombination. In the last approach (“gold standard”), homologous recombination is employed to replace the endogenous wild-type allele with one containing a mutation of a single *cis*-regulatory element.

vascular beds (Evans et al. 2000, Guillot et al. 2000, Minami et al. 2002, 2003).

Thus, these various DNA promoter fragments represent molecular markers or probes for vascular bed-specific transcriptional activity. An important question is whether these differences reflect intrinsic (fixed) properties of the EC or whether they reflect differences within the cell's microenvironment. To cite a specific example, a fragment of the vWF promoter is expressed in blood vessels of the brain and the microvascular endothelium of the heart and skeletal muscle, but not in other organs (Aird et al. 1997). Do ECs in the brain, heart, and skeletal muscle possess cell-type-specific transcriptional networks that are unique to these cells? Or do these cells only appear different because they are following instructions that are unique to the tissue microenvironment? When noncardiac ECs of the mice were exposed to heart-derived signals, they expressed the transgene (Aird et al. 1997). In another study, the human Flt-1 and vWF promoters were targeted to the *Hprt* locus (Minami et al. 2002). The Flt-1 transgene was active in the endothelium of tumor xenografts, whereas the VWF promoter was not (Minami et al. 2002). Under in vitro conditions, conditioned medium

from tumor cells resulted in a significant upregulation of Flt-1 mRNA and promoter activity, but no change in vWF levels (Minami et al. 2002). Taken together, these findings suggest that vascular bed specificity is programmed by the tissue microenvironment (at least in the case of vWF and Flt-1) and is not a fixed property of the EC.

One limitation that is common to standard transgenic and *Hprt*-targeting approaches is that exogenous DNA is introduced into a foreign genomic locus. Although the data from these studies provide powerful proof of principle for vascular bed-specific gene regulation, ultimate proof for the involvement of one or another *cis*-regulatory element (or DNA promoter fragment) in mediating vascular bed- or cell-subtype-specific regulation of a given gene will require selective deletion or mutation of that element from the endogenous locus (Figure 4). Such an approach has been carried out with other lineage-specific genes, but to our knowledge has yet to be applied in the endothelial field.

Other approaches for studying EC gene regulation in vivo are less direct and provide only circumstantial data. For example, the immunolocalization

of transcription factors—with or without putative target genes—in the endothelium in health or disease may yield insight into vascular-bed-specific regulatory programs (Table 3). Alternatively, the forced overexpression and/or inhibition/knockout of a transcription factor in vivo may provide clues about downstream target genes and cellular function.

• Bridging In Vitro and In Vivo Assays

There are advantages and disadvantages associated with in vitro and in vivo approaches for studying EC gene regulation. The major advantage of EC cultures is that they enable high throughput, detailed, and tightly controlled analyses. The chief disadvantage is that the cultured EC has been uncoupled from its native microenvironment and is therefore a “shadow of its former self.” In vivo approaches have the distinct advantage that they enable investigators to study ECs in the context of their native microenvironment. Disadvantages include the difficulty in controlling experimental conditions, the costs and time associated with carrying out such studies, and the enormous complexity of in vivo biology.

An important challenge then is to improve the validity of in vitro assays, to simplify the nature of the in vivo analyses, and to use one approach to inform the other. There are several ways to improve the biological meaningfulness of in vitro assays. First, to facilitate comparisons across studies, it would be helpful to qualify results according to the origin (species and vascular bed) and passage number of the cells. Second, it would be of interest to systematically compare transcriptional profiles in cultured (multi-passaged) ECs from different vascular beds. This approach, which has been carried out for some subtypes of cells (Chi et al. 2003, Lacorre et al. 2004), will capture those differences in gene expression that are intrinsic to the cells—that is, the site-specific properties that are epigenetically fixed and mitotically heritable. Finally, an important priority is to learn how to recapitulate the microenvironment in vitro. The many reports that describe the

Table 3. Examples of in situ localization of transcription factors in endothelium

<i>Transcription factor</i>	<i>Tissue</i>	<i>Pattern of expression</i>	<i>Assay</i>
ATF-3	Human iliac artery	ECs in atherosclerotic lesions	IH
c-Jun, NF-κB	Dog heart	Nuclear localization in venular endothelium in heart following brief ischemia	IH
Egr-1	Human carotid artery	Expression in ECs overlying atherosclerotic lesion	IH
Egr-1	Mouse organs	Vascular-bed-specific expression; site-specific induction with systemic administration of VEGF, EGF	IF
ERβ1, ERβcx/β2	Human endometrial tissue	Human endometrial ECs	IH
Ets-1	Human synovium	Synovial ECs in patients with RA	IH, ISH
HIF-1α, HIF-2α	Rat kidney	Various patterns of upregulation in ECs of renal cortex and medulla in response to ischemia, carbon monoxide, and cobaltous chloride	IH
HIF-1α and 1β	Human lung	Plexiform lesions in PH-PPH	IH, ISH
HoxD10, HoxD3	Human breast	HoxD10 in microvascular EC normal tissue, HoxD3 in neovessels of cancerous tissue	ISH
Id1 and Id3	Human synovium	RA synovial EC	IH
KLF2	Human thoracic aorta	Microheterogeneity in ECs	ISH
NF-AT	Human heart	Human pulmonary valve ECs	IH
NF-κB	Rat heart	ECs in infarcted heart	p65 IH
NF-κB	Rat aorta	ECs in aortas from rats with hyper-homocysteinemia	IF
NF-κB	Mouse aorta	Microheterogeneity in ECs; site-specific increases in endotoxemic and atherosclerosis models	IF
Nur77	Human coronary artery	ECs in atherosclerotic plaque	IH
Smad6/7	Human coronary artery	Smad 6 increased, Smad7 decreased in EC of atherosclerotic vessels	IH
SREBP-1	Pig aorta	Decreased in abdominal aorta of hypercholesterolemic pigs	mRNA in whole tissue (aortic rings)
SREBP	Rabbit skin	ECs in rabbit skin partial-thickness wound-healing model (neovessels)	IF
STAT-5	Human carotid artery	ECs in atherosclerotic lesions	IF

See online supplement for references.

ATF indicates activating transcription factor; EC, endothelial cell; EGF, epidermal growth factor; ER, estrogen receptor; HIF, hypoxia inducible factor; HOX, homeobox; Id, inhibitor of DNA binding; IF, immunofluorescence; IH, immunohistochemistry; ISH, in situ hybridization; KLF, Kruppel-like factor; NF-AT, nuclear factor of activated T cell; RA, rheumatoid arthritis; SREBP, sterol regulatory element binding protein; STAT, signal transducer and activator of transcription; VEGF, vascular endothelial growth factor.

effect of one or another agonist on gene regulation in ECs represent an important starting point. Goals for the future

include studying the effects of multiple mediators added at different concentrations and in different time

sequences. Moreover, the continued development of co-culture systems (and neutralizing antibodies to soluble mediators) should provide new insights into environmentally regulated gene expression.

From the standpoint of in vivo assays, important goals are to elucidate the distribution of transcription factors in the endothelium and to develop a catalogue of vascular bed-specific EC promoters that direct expression of a gene-of-interest to one or another vascular bed. One of the best ways to understand a biological system is to place it under stress and observe its response. For example, the use of mouse or rat models of sepsis has yielded fascinating results that point to the highly complex and vascular bed-specific response capacity of the endothelium. Increasingly, the study of EC properties in disease states (e.g., cancer, pulmonary hypertension, and rheumatoid arthritis) is providing clues to basic mechanisms of gene regulation. Endothelial-cell-specific knockout of transcription factors promises to improve our understanding of transcriptional networks in this cell type. Finally, future improvements in the resolution of laser capture microdissection will provide an invaluable platform for mapping the transcriptome in intact endothelium.

• Revisiting the Definition of an Endothelial Cell

The endothelium consists of a giant mosaic of phenotypes. Indeed, it seems likely that at any given point in time, there do not exist two phenotypically identical ECs in the human body. Thus, with the exception of its anatomic location, there are few unifying features of the endothelium.

Perhaps an EC is defined less by any panel of cell-type-specific mRNA or protein markers, and more by its *behavioral repertoire* (Figure 5). With each EC representing an input-output device, the endothelium is analogous to a bio-sensor or barcode reader, constantly taking inventory of its immediate microenvironment. The EC transcriptional machinery serves to integrate and transduce these extracellular signals, generating an output that is appropriate for that time and place (see

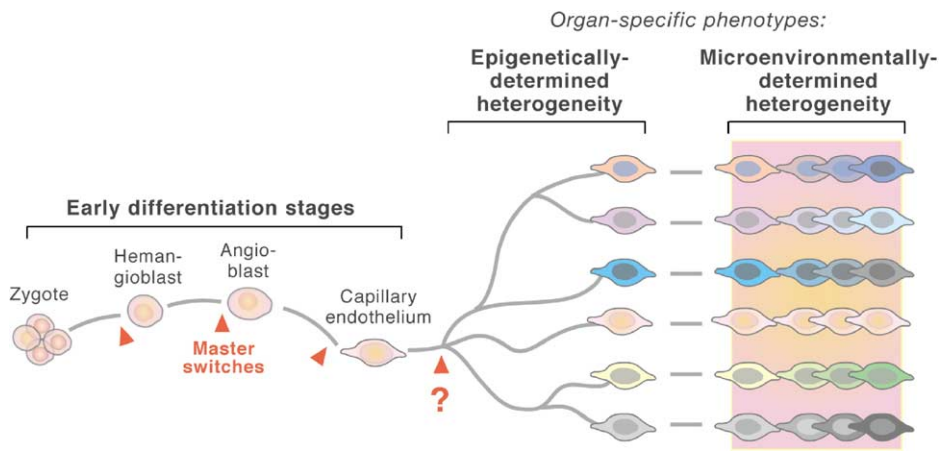


Figure 5. The behavioral repertoire of the endothelium. Endothelial-cell phenotypes arise from two mechanisms. First, epigenetic modification of DNA leads to mitotically heritable changes (these are shown as “master switches”, or triangles). Data support the role for such switches in mediating early lineage determination and perhaps arterial/venous identity (the latter is not shown). The extent to which epigenetic events normally dictate organ or site-specific phenotypes of microvascular endothelium is not clear (shown as question mark, and labeled as “epigenetically determined heterogeneity”). In contrast, there is increasing evidence that many site-specific properties of capillary endothelium are reversibly governed by signals residing in the microenvironment (“microenvironmentally determined heterogeneity”). Each color shade represents a distinct cellular phenotype (e.g., transcriptome, proteome, and/or function).

model, Figure 6). Like all cells of the human body, ECs follow local rules to generate complex global behavior. The uniqueness of the endothelium lies not so much in its constituent parts (e.g., cells), but rather in its emergent properties of plasticity, adaptability, and heterogeneity.

• Unanswered Questions

Previous studies of EC gene regulation have provided important insights into vascular biology. However, many questions still remain. For example, how do non-cell-type-specific transcription fac-

tors cooperate to promote EC-restricted expression? Are there as of yet undiscovered “master switches,” which, like MyoD in skeletal muscle or PU.1 in the myeloid lineage, govern lineage determination and/or expression of cell-type-specific genes in the adult endothelium? If and when bone-marrow-derived ECs repopulate the intact vasculature, to what extent do these cells acquire the phenotype of the resident ECs? Is disease and/or aging associated with increased epigenetic changes within the endothelium?¹ Do the promoter regions of EC genes contain functionally relevant polymorphisms? The answer to

these, and many other interesting questions related to EC gene regulation, requires further study.

• Acknowledgments

This work was supported in part by the National Institute of Health Grants HL076540 and HL36028. Artwork was done by Steven Moskowitz.

• Appendix A. Abbreviations for Table 2

Agonist abbreviations: ABCA1, ATP-binding cassette transporter-1; AGE, advanced glycation end products; Ang-1, angiopoietin-1; Ang II, angiotensin II, ANP, atrial natriuretic peptide; CRP, C reactive protein; EBV, Epstein-Barr virus; EPCR, endothelial protein C receptor; ET, endothelin; FGF, fibroblast growth factor; GM-CSF, granulocyte monocyte-colony stimulating factor; Hb, hemoglobin; HGF, hepatocyte growth factor; HHV, human herpesvirus; HIV, human immunodeficiency virus; HMGB1, High mobility group box 1; HMG-Co, hydroxymethylglutaryl-coen-

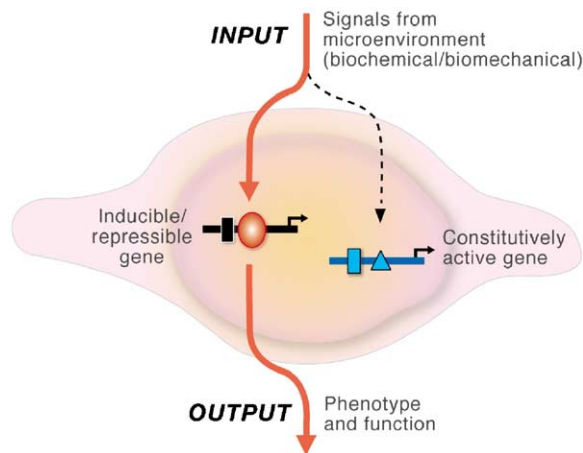


Figure 6. Model of endothelial gene regulation. Consistent with the analogy of the EC as an input–output device, many genes are modulated by signaling pathways, which begin in the extracellular milieu and end at distinct regions (or modules) of the gene promoter. Inducible/repressible and constitutively expressed genes are normally regulated by non-cell-type-specific transcription factors. The dotted line indicates that many, if not all, of so-called constitutive genes are coupled (at least to some extent) to the extracellular environment. The black and blue lines represent promoters of modulatable and constitutively expressed genes, respectively. The arrows represent transcriptional start sites, and the shapes denote *cis*-regulatory elements.

¹ Preliminary studies point to the importance of aging and disease in mediating epigenetic changes in endothelium. For example, in co-culture studies, cardiac myocytes induce the expression of PDGF-B in passaged cardiac microvascular ECs isolated from 3-month-old mice, but not 18-month-old C57BL/6 mice (Edelberg et al. 2002). Endothelial cells cultured (passage 3–6) from the aorta of diabetic mice (db/db) display increased monocyte adhesion, compared with ECs cultured from wild-type C57BL/6 mice (Hatley et al. 2003).

zyme A; IGF, insulin like growth factor; IFN, interferon; IL, interleukin; LDL, low density lipoprotein; LIX, lipopolysaccharide-induced CXC chemokine; LMP, latent membrane protein; LPL, lipoprotein lipase; NO, nitric oxide; PAF, platelet activating factor; PMP, polymorphic membrane protein; TGF, transforming growth factor; TNF, tumor necrosis factor; t-PA, tissue type plasminogen activator; VEGF, vascular endothelial growth factor; VLDL, very low density lipoprotein.

Transcription factor abbreviations: AP-1, activating protein-1; ATF, Activating transcription factor; CREB, cyclic AMP response element binding protein; dbpb, DNA-binding protein B; Egr-1, early growth response-1; GR, glucocorticoids receptor; HIF, hypoxia inducible factor; Id, inhibitor of DNA binding; IRF, interferon regulatory factor; KLF, Kruppel-like factor; LXR, liver X receptor; NF-AT, nuclear factor of activated T cell; NF-1, nuclear factor-1; PPAR, peroxisome proliferator-activated

receptor; RUNX, Runt-related gene; SREBP, sterol regulatory element binding protein; STAT, signal transducer and activator of transcription; Tcf, T-cell-specific factor.

Target gene abbreviations: ACE, angiotensin converting enzyme; COX, cyclo-oxygenase; CRLR, calcitonin receptor-like receptor; DAF, decay accelerating factor; DSCR, Down syndrome critical region; eNOS, endothelial nitric oxide synthase; ET, endothelin; HO-1, hemeoxygenase-1; ICAM, intercellular adhesion molecule; iNOS, inducible nitric oxide synthase; IRF1, interferon regulatory factor-1; MCP, monocyte chemoattractant protein; MDR, multiple drug resistance; MMP, matrix metalloproteinase; MnSOD, manganese superoxide dismutase; NQO1, NAD(P)H:quinone oxidoreductase-1; PAI, plasminogen activator inhibitor; PDGF, platelet-derived growth factor; RANKL, receptor activator of nuclear factor kappa B ligand; SDF, stromal cell-derived factor-1; SOCS3, suppressor of cytokine signaling

3; TAP-1, transporter associated with antigen processing-1; TF, tissue factor; u-PA, urokinase type plasminogen activator; VCAM, vascular cellular adhesion molecule.

Cell abbreviations: bAdEC, bovine adrenal cortex capillary EC; BLEC, bovine lung microvascular EC; BPAEC, bovine pulmonary artery EC; BREC, bovine retinal microvascular EC; CDEC, mouse cardiac-derived EC; GenC, mouse glomerular EC; HAEC, human aortic EC; HBME-1, human bone marrow EC; HBMVEC, human brain microvascular EC; HCMEC, human cardiac microvascular EC; HMEC-1, human microvascular EC line; HMVEC, human microvascular EC; HPMEC, human pulmonary microvascular EC; HPVEC, human pulmonary valve EC; HSVEC, human saphenous vein EC; MaoEC, murine aortic EC; MBEC, murine cerebral EC; PAEC, porcine aortic EC; PRET, porcine retinal EC; RCEC, rat cardiac EC; RPAEC, rat pulmonary aortic EC; RPVEC, rat pulmonary microvascular EC.

• Appendix B. References for Tables

Table 1. Examples of agonist-mediated induction/repression of transcription factors and downstream target genes in EC †

Agonist	Transcription factor	Target genes/cell function	Cell type(s)	Ref
Oxygenation				
Hypoxia	AP-1	HO-1	RPAEC	1
	AP-1	eNOS	PAEC	2
	Egr-1	—	BAEC	3
	Elk-1	—	BAEC	3
	HIF	CRLR	HMEC	4
	HIF	Endoglin	HMEC-1	5
	HIF	MDR-1	BAEC	6
	HIF	SDF-1	HUVEC	7
	HIF+GATA-2+AP-1	ET-1	HUVEC	8
	NERF-2	TIE-2	HUVEC	9
Smad2/3	TGF-β	HUVEC	10,11	
Sp1	MDR-1	BAEC	6	
Hemodynamic forces				
Laminar Shear Stress	GATA-6	Inhibits u-PA	HCAEC	12
	KLF2	—	HUVEC	13
	Negative SSRE binding protein	Inhibits Tie-1	BAEC	14
	c-Myc	MMP-9	Murine lymphoid EC line	15
	NF-κB	ICAM-1	BAEC	16
	NF-κB	eNOS	BAEC	17
	Inhibits NF-κB	Inhibits PDGF-B	BAEC	18
	GR	—	BAEC	19

Table 1 continued

Agonist	Transcription factor	Target genes/cell function	Cell type(s)	Ref
Hemodynamic forces				
Laminar Shear Stress	Sp1	Flk-1	HUVEC	20,21
	Inhibits Sp1	Inhibits P2X4	HUVEC, BAEC	22
	SREBP	—	BAEC	23,24
	AP-1	eNOS	Lamb fetal vs. pulmonary artery EC	25
	Nrf2	NQO1, HO-1	HAEC, HMEC	26
	CRE binding protein	COX-2	BAEC	27
Cyclical strain	AP-1	ET-1	HUVEC	28
Stretch	NF-κB	IL-6	HUVEC	29
Chemokines, and Cytokines				
IFN-α	STAT-4	MCP-1, SOCS3	HUVEC	30
IFN-γ	STAT-1	CD40	HUVEC	31
	STAT-1	TAP-1, IRF1, Class 1 MHC	HUVEC	32
IL-1	AP-1, Sp1	ICAM-1	mAoEC	33
	NF-κB, C/EBP	iNOS	rPVEC	34
IL-4	STAT-1	MCP-1	HUVEC	35
	AP-2, NF-1, Sp1, STAT-6, but not NF-κB or AP-1	—	HUVEC	36
IL-6	STAT-3	—	BAEC	37
IL-10	STAT-3	eNOS	HUVEC	38
IL-18	NF-κB	IL-1, TNF-α	HCMEC	39
LIX	NF-κB	IL-1, TNF-α	rCEC	40
PAF	STAT-3	—	HUVEC	41,42
TNF-α	ATF3	Cell death	HUVEC	43
	CREB	—	HUVEC	44
	E2F1 inhibition	Inhibits E2F1	BAEC	45
	Id1, Id3	E-selectin, not ICAM-1	HUVEC	46
	IRF-1	VCAM-1	HAEC	47
	NF-κB	E-selectin, TF	HDMEC vs. HUVEC	48
	NF-κB	Fractalkine	HUVEC	49
	NF-κB	IL-8	HAEC	50
	NF-κB	MadCAM	SVEC	51
	NF-κB	MCP-1, IL-8, ICAM-1, VCAM-1, E-selectin	HUVEC	52
	NF-κB	TF	HUVEC	53
	NUR77	PAI-1	HUVEC	54
	Sp1	Fractalkine	HUVEC	49
	Sp1, Sp3 inhibition	Inhibits eNOS	BAEC	55
TNF-α + IFN-γ	STAT-1, IRF	CD40	HUVEC	31
HMGB1	NF-κB, Sp1	—	HMEC-1	56
Growth factors, hormones, glucose				
AGE	NF-κB, AP-1	VEGF	HDMEC	57
Ang-1	Forkhead	—	HUVEC, BLMEC	58
Dihydrotestosterone	Androgen receptor/NF-κB	VCAM-1	HUVEC, BAEC	59
ET-1	Ets-1	—	BAEC	60
FGF-2	Tcf-4	Cyclin D1	HUVEC	61
	STAT-3	—	HUVEC	42
	Egr-1	—	BAEC	62
Glucose	AP-1	Fibronectin	HUVEC, HMEC	63
	AP-1	IL-8	HAEC, PAEC	64
	Egr-1	Flt-1, PAI-1	GEnC	65
	NF-κB	VCAM-1	HAEC	66
	NF-κB	eNOS, inhibits cell migration	HAEC	67
	NF-κB	Fibronectin	HUVEC, HMEC	63

Table 1 continued

Agonist	Transcription factor	Target genes/cell function	Cell type(s)	Ref
GM-CSF	NF-κB	—	HUVEC	68
HGF	Forkhead	—	HCAEC	69
	Ets-1	MMP-1, HGF, c-met	HAEC	70
	Egr-1	ACE	BPAEC	71
IGF-1	RUNX2	Tube formation	HBME-1	72,73
Insulin	AP-1	eNOS	PAEC	74
	Egr-1	Flt-1, PAI-1	GEnC	65
Leptin	AP-1	ET-1	HUVEC, BAEC	75
	STAT-3	VEGF	PRET	76
Placental growth factor	AP-1	—	HUVEC, HPAEC	77
Prolactin (16-kDa N' terminal fragment)	NF-κB	Caspases 3, 8, 9; E-selectin	bAdEC	78
Relaxin	NF-κB	ET _B	HUVEC, BAEC	79
VEGF	Ets-1	Neuropilin, Angiopoietin-2, cell proliferation	BREC	80
	Ets-1	Angiopoietin-2	HUVEC	81
	NF-AT	DSCR-1	HUVEC	82
	NF-AT	Proliferation	HPVEC	83
	NF-AT	DAF	HUVEC	84
	GATA	DSCR-1	HUVEC	82
	GATA	COX-2	HMEC-1	85
	Forkhead	p27 ^{kip1}	HCAEC	86
	Forkhead	MnSOD	HCAEC	69
	NF-κB	MnSOD	HCAEC	69
	NF-κB	TF	HUVEC	87
	STAT-3	VEGF	BREC, BAEC, HDMEC	88
	Egr-1	TF, Flt-1, u-PA		89
	Id1, Id3	ICAM-1, but not E-selectin; EC proliferation	HUVEC	46
	SREBP1/2	—	HPMEC	90
	Sp1	KDR	BAEC	91
	Vezf1	VEGF-mediated proliferation, migration and tube formation	MSS31 mouse EC line	92
Thymosin β4	AP-1	PAI-1	EA.hy 926	93
Lipoproteins and related mediators				
Cholesterol	AP-1	ICAM-1	HUVEC	94
Diabetic LDL	STAT-5B	p21 and G1 fraction	HUVEC	95
Native LDL	LXR	ABCA1	HUVEC, HCAEC	96
oxHDL	NF-κB	—	HUVEC	97
oxLDL	ATF3	Cell death	HUVEC	43
VLDL, oxVLDL	CREB, NF-κB	—	Eahy926, HUVEC	98
LPL+VLDL	PPAR _α	Ac-CoA-oxidase	BAEC	99
LPA, S-1-P	NF-κB	ICAM-1	HUVEC	100
Fatty acids	Sp1	Heparanase	HMVEC, BAEC	101
Oleic acid	NF-κB	ET-1	HAEC	102
5(S)-HETE	STAT-3	—	HMVEC	103
Oxidized phospholipids (OxPAPC)	STAT-3	IL-8	HAEC	104
	NFAT, Egr-1	TF	HUVEC	53
	CREB	HO-1	HUVEC	105
Epoxyeicosatrienoic acids (EET)	Egr-1	—	HUVEC	106
	CRE	t-PA	HSVEC	107
Linoleic acid	NF-κB, AP-1	—	HUVEC	108
Omega-3 fatty acids	PPAR-α	—	HUVEC, BAEC	109
Matrix and related factors				

Table 1 continued

Agonist	Transcription factor	Target genes/cell function	Cell type(s)	Ref
Fibronectin	NF-κB	E-selectin, VCAM-1, ET-1, CYR-61	HUVEC	110
3-dimensional collagen type-1	GATA-2	MMP-2	Rat skeletal muscle EC	111
Type 1 collagen	Ets-1	MMP-1	BAEC	60
TGF-β	Smad2	eNOS	BAEC, HUVEC, BAEC	112
	Smad1/2/5, Id	Cell migration	BAEC, mouse embryonic EC	113
	CREB	RANKL	Bone marrow-derived EC line	114
	Smad3/4, AP-1	ET-1	HUVEC, BAEC	115
	Smad6	Inhibits TM	HUVEC	116
Serine proteases				
Thrombin	AP-1	Prepro-ET	PAEC	117
	dbpB	PDGF-B	HUVEC, BAEC	118
	dbpB	EPCR	BAEC	119
	Egr-1	—	HPAEC	120
	NF-κB	ICAM-1	HUVEC	121
	NF-κB, GATA-2	VCAM-1	HUVEC	122
	NF-AT	DSCR-1	HUVEC	82
	Sp1	KDR	BAEC	91
	SRF	Egr-1	HPAEC	120
Cell-cell interactions				
Platelet-EC	NF-κB	MCP-1, VCAM-1		123
Neutrophil-EC	Ets-1	Tube formation	BAEC	124
Neutrophil-derived proteases	NF-κB (cleaves and inhibits)		HUVEC	125
Vasomotor tone				
NO	Inhibits NF-κB	Inhibits ET-1	PAEC	126
	Nrf2	HO-1	BAEC	127
Ang II	AP-1	ET-1	HUVEC	128
	NF-κB	VCAM-1, ICAM-1	HUVEC, BAEC	129
ANP	AP-1	HO-1	HUVEC	130
Pathogens				
Orienta tsutsugamushi	AP-1, NF-κB	MCP-1	HUVEC	131
Chlamydia pneumoniae PMP	NF-κB	IL-6, MCP-1		
	HUVEC	132		
Chlamydia pneumoniae infection	NF-κB	ICAM-1	HAEC	133
Shiga toxin	NF-κB	MCP-1, IL-8	HUVEC/GEC	134
African swine fever virus (infection)	Decreases p65 NF-κB	Inhibits IL-8, E-selectin, but increases TF	PAEC, bushpig EC	135
Bartonella henselae (infection)	NF-κB	ICAM-1, E-selectin	HUVEC	136
Bartonella bacilliformis infection	AP-1	—	HUVEC	137
EBV infection or LMP-1 over-expression	NF-κB	—	HUVEC	138
HIV protein Tat	NF-κB	E-selectin	HUVEC	139
HIV pcTat	NF-κB	Monocyte adhesion	HUVEC	140
HIV Tat1-72	NF-κB, AP-1	—	Porcine brain MEC	141
HHV-8 (retroviral infection of ORF74)	NF-κB	—	HDMEC	142
Drugs/toxins				
Arsenite	NF-κB, AP-1	—	PAEC	143
Bleomycin	Egr-1	ACE	BPAEC	144
	NF-κB	E-selectin	HUVEC	145

Table 1 continued

Agonist	Transcription factor	Target genes/cell function	Cell type(s)	Ref
	NF- κ B, Nrf-1/2	γ -glutamylcysteine synthetase	BPAEC, rat pulmonary microvascular EC	146
Cocaine	NF- κ B, AP-1	—	HBMVEC	147
Doxorubicin	p53, not NF- κ B	CD95	HUVEC	148
	NF- κ B	Cell apoptosis	BAEC	149
HMG-Co reductase inhibitors	Inhibits NF- κ B, AP-1, HIF-1 α	—	Ea.hy926, HAEC	150
Isoproterenol	NF- κ B	IL-18	CDEC	151
Methamphetamine	NF- κ B, AP-1	TNF- α	hBMVEC	152
Disease-related mediators				
Human lymphoma-derived soluble factors	NF- κ B	Leukocyte adhesion	HUVEC	153
Amyloid-beta peptide	AP-1	Bim	mBEC	154
Anti-phospholipid antibodies	NF- κ B	—	HUVEC, HMEC-1	155
Homocysteine	NF- κ B	Fas	HUVEC	156
	NF- κ B	—	HUVEC, HAEC	157
MetHb	NF- κ B	E-selectin, IL-6, IL-8	HUVEC	158

Table 2. Promoter Analysis in transgenic mice

Gene	Assay	Promoter	Reporter gene	Pattern of expression	Non-EC	Ref
Activin Receptor-like Kinase 1	Stable transgenics	Various promoter fragments (mouse)	LacZ	9.2-kb promoter directs arterial specific expression in adults		159
CD34	Stable transgenics	160-kb (human)	Human CD34	EC in many vascular beds in adult	Bone marrow	160
c-mpl	Stable transgenics	2-kb (mouse)	Human placental alkaline phosphatase	Some EC in blood vessels of embryo (and yolk sac); none in adult	Megakaryocytes	161
eNOS	Stable transgenics	1.6-kb bp (human)	LacZ	Expression in EC of brain, heart, skeletal muscle, and aorta. β -galactosidase activity was consistently absent in vascular beds of the liver, kidney, and spleen		162
	Stable transgenics	5.2-kb (mouse)	LacZ	EC of large and medium sized blood vessels in several tissues	Brain	163
	Hprt locus targeting	1.6-kb (human)	LacZ	EC in arteries > veins	Cardiomyocytes, VSMC	164
EPCR	Stable transgenics	-1080 to -1, -350 to -1 (mouse)	GFP	Expression in multiple tissues of adult, though cell type not defined		119
Flt-1	Hprt locus targeting	1-kb (human)	LacZ	EC in all vascular beds except for the liver	Cardiomyocytes	165
ICAM-2	Stable transgenics	0.33-kb and 3-kb (human)	CD59	Uniform EC expression in both lines	Granulocytes	166
KDR/Flk-1	Transient and stable transgenics	Various promoter fragments	LacZ	939-bp promoter + 510-bp first intron fragment drives expression in most EC, but expression lost with age		167
	Transient transgenics	-640 - + 299 and 510-bp intronic enhancer; with or without mutation of HoxB5 binding site (mouse)	LacZ	Wild type promoter directs uniform expression in EC of embryo; mutation abolishes expression		168

Table 2 continued

Gene	Assay	Promoter	Reporter gene	Pattern of expression	Non-EC	Ref
Mef2c	Stable transgenics	4.5 Kb + 510-bp intronic enhancer (mouse)	Luciferase	Most tissues; Decreased expression with age		169
	Transient transgenics	Various fragments (mouse)	LacZ	4.66-kb directs uniform EC expression in embryos; patchy expression in adult; mutation of Ets sites disrupted expression	Some circulating blood cells	170
Notch4	Transient transgenics	Various promoter fragments (human)	LacZ	Different promoter fragments, different vascular beds		171
PAI-1	Stable transgenics	2.9-kb (human)	eGFP	2.9-kb directs expression in “glomeruli” and “venous structures” of lung	Kidney tubular cells; lung epithelial cells; pyramidal cells of cerebellum	172
Pre-pro-endothelin	Stable transgenics	5.9-kb (murine)	Luc	EC of arteries and arterioles > veins, capillaries	VSCM, certain epithelial cells	173
PrP	Stable transgenics	6.9-kb (bovine)	GFP	EC of mucosal capillaries and venules in lamina propria mucosa of intestinal villi; small vessels of intestinal submucosa; peritubular vessels in renal cortex	Purkinje cells, lymphocytes, keratinocytes	174
SCL/TAL-1	Transient transgenics	Various promoter fragments (mouse)	LacZ	5.5-kb directs expression to embryonic endothelium	Blood cells	175
TIE-1	Standard transgenics	0.74-kb (mouse)	LacZ	EC in arterial segments at vascular junctions		176
	Standard transgenics	1.15-kb (mouse)	Cre			177
	Transient transgenics	0.54-kb (mouse) (WT and oct mutant)	LacZ	Patchy EC expression in embryo; reduced expression and cell type specificity with Oct mutant		178
	Standard transgenics	0.8-kb (mouse)	LacZ	Predominantly EC of arterioles and capillaries in adult mice		179
TIE-2		1.1 kb (mouse)	eGFP	Throughout vasculature of embryo up to E11.5; later in embryogenesis A>V; very little expression in adult vascular beds		180
	Transient transgenics	Deletants and mutants of the 0.8 kb mouse promoter	LacZ	Ets mutations resulted in decreased EC expression in most organs		181
	Standard transgenics	0.8 kb (mouse)	Growth hormone			181
	Standard transgenics	1.2 kb promoter (mouse)	LacZ	Patchy EC expression in embryo, absent in adult		182
	Standard and transient transgenics	2.1 kb promoter + 10 kb intron 1; several mutations also tested (mouse)	LacZ	Uniform EC expression of full length WT promoter in embryo and adult		183
		2.1 kb promoter + 1.7 kb intronic enhancer (mouse)	t-TA	In binary system (Tie-2-tTA + TRE-βGal), “near uniform” expression in endothelium		184
		2.1 kb promoter + 10 kb intron 1 (mouse)	Cre	Bred with CAG-CAT-Z transgenic mice; In contrast to standard transgenic mice, expression in mesenchymal cells of atrioventricular canal (only embryos analyzed)		185
	Hprt locus targeting	0.72-kb fragment containing a 300-bp intronic enhancer coupled upstream to a 423-bp core promoter – with or without Ets mutations (mouse)	LacZ	Widespread EC expression in adult (lost with Ets mutation, except in brain)		186

Table 2 continued

Gene	Assay	Promoter	Reporter gene	Pattern of expression	Non-EC	Ref
VE-cadherin	Standard transgenics	-2486 to +24 (mouse)	CAT	EC of all vascular beds except brain capillaries in adult		187
vWF	Standard transgenics	-487-+246 (human)	LacZ	EC in blood vessels in adult brain		188
	Standard transgenics	-2186 – to end of first intron (human)	LacZ	EC in blood vessels in brain, microvessels of heart and skeletal muscle in adult		189
	Standard transgenics	-2645 and the end of the first intron (mouse)	LacZ	EC in blood vessels in brain, microvessels of heart and skeletal muscle in adult; megakaryocytes in one line		190
	Hprt locus targeting	-2186 – to end of first intron (human)	LacZ	EC in blood vessels in brain, microvessels of heart and skeletal muscle in adult		165

Table 3. Examples of in situ localization of transcription factors in endothelium

Transcription factor	Tissue	Pattern of Expression	Assay	Ref
ATF-3	Human iliac artery	EC of atherosclerotic lesions	IH	43
c-Jun, NF- κ B	Dog heart	Nuclear localization in venular endothelium in heart following brief ischemia	IH	191
Egr-1	Human carotid artery	Expression in EC overlying atherosclerotic lesion	IH	192
Egr-1	Mouse organs	Vascular bed specific expression; site-specific induction with systemic administration of VEGF, EGF	IF	193
ER β 1, ER β cx/ β 2	Human endometrial tissue	Human endometrial EC	IH	194
Ets-1	Human synovium	Synovial EC in patients with RA	IH, ISH	195
HIF-1 α , HIF-2 α	Rat kidney	Various patterns of upregulation EC of renal cortex and medulla in response to ischemia, carbon monoxide, and cobaltous chloride	IH	196
HIF-1 α and 1 β	Human lung	Plexiform lesions in PH-PPH	IH, ISH	197
HoxD10, HoxD3	Human breast	HoxD10 in microvascular EC normal tissue, HoxD3 in neovessels of cancerous tissue	ISH	198
Id1 and Id3	Human synovium	RA synovial EC	IH	199
KLF2	Human thoracic aorta	Microheterogeneity in EC	ISH	200
NF-AT	Human heart	Human pulmonary valve EC	IH	83
NF- κ B	Rat heart	EC in infarcted heart	p65 IH	201
NF- κ B	Rat aorta	EC in aortas from rats with hyper- homocysteinemia	IF	157
NF- κ B	Mouse aorta	Microheterogeneity in EC; site-specific increases in endotoxemic and atherosclerosis models	IF	202
Nur77	Human coronary artery	EC in atherosclerotic plaque	IH	54
Smad6/7	Human coronary artery	Smad 6 increased, Smad7 decreased in EC of atherosclerotic vessels	IH	116
SREBP-1	Pig aorta	Decreased in abdominal aorta of hypercholesterolemic pigs	mRNA in whole tissue (aortic rings)	203
SREBP	Rabbit skin	EC in rabbit skin partial-thickness wound-healing model (neovessels)	IF	90
STAT-5	Human carotid artery	EC of atherosclerotic lesions	IF	95

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