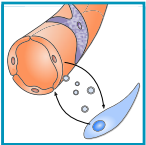


ENDOTHELIAL CELL METABOLISM

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Eelen G, de Zeeuw P, Treps L, Harjes U, Wong BW, Carmeliet P. Endothelial Cell Metabolism. *Physiol Rev* 98: 3–58, 2018. Published November 22, 2017; doi: 10.1152/physrev.00001.2017.—Endothelial cells (ECs) are more than inert blood vessel lining material. Instead, they are active players in the formation of new blood vessels (angiogenesis) both in health and (life-threatening) diseases. Recently, a new

concept arose by which EC metabolism drives angiogenesis in parallel to well-established angiogenic growth factors (e.g., vascular endothelial growth factor). 6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase-3-driven glycolysis generates energy to sustain competitive behavior of the ECs at the tip of a growing vessel sprout, whereas carnitine palmitoyltransferase 1 α -controlled fatty acid oxidation regulates nucleotide synthesis and proliferation of ECs in the stalk of the sprout. To maintain vascular homeostasis, ECs rely on an intricate metabolic wiring characterized by intracellular compartmentalization, use metabolites for epigenetic regulation of EC subtype differentiation, crosstalk through metabolite release with other cell types, and exhibit EC subtype-specific metabolic traits. Importantly, maladaptation of EC metabolism contributes to vascular disorders, through EC dysfunction or excess angiogenesis, and presents new opportunities for anti-angiogenic strategies. Here we provide a comprehensive overview of established as well as newly uncovered aspects of EC metabolism.

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I. INTRODUCTION

Even though cellular metabolism has been studied for over a century, endothelial cell (EC) metabolism has been receiving growing attention only during the last few years. Blood vessel forming ECs display a remarkable behavioral plasticity; while quiescent for years, ECs can switch almost instantaneously to an activated, highly proliferative, and migratory state in response to growth factor stimuli, primarily through vascular endothelial growth factor (VEGF) signaling (436). It has long been overlooked if this angiogenic switch (angiogenesis is the broad term for the formation of new blood vessels) is reflected by a metabolic switch and if so whether the altered metabolism is a key driver or merely a subsequent bystander adaptation. Recent papers on glycolysis and fatty acid oxidation (FAO) in ECs reveal that metabolism drives vessel sprouting in parallel to well-established

growth factor-based (genetic) signaling (114, 481). These seminal findings have paved the way towards a more in-depth understanding of EC metabolism, which gains further importance in light of limited overall successes of growth factor-centric therapies in treating pathological angiogenesis (38, 151, 583). Indeed, the endothelium, either by dysfunctionality or by excessive vessel sprouting, can be at the origin of devastatingly lethal disorders (145). Proof-of-principle studies demonstrate how targeting EC metabolism can be exploited as an alternative for growth factor-based approaches, with an advantageous reduction in resistance and escape mechanisms [as they occur for example in tumor vasculature upon anti-VEGF treatment (70); see sect. VIII]. This review aims to provide emerging insights in various aspects of EC metabolism both in health and disease and discusses our current knowledge on intricate topics such as heterogeneity and compartmentalization of EC metabolism and metabolic crosstalk between ECs and other cell types. Thorough understanding of metabolic programming of ECs in quiescent versus angiogenic state and in normal developmental and physiological angiogenesis versus dysfunctional and pathological angiogenesis promises to offer novel opportunities for future EC metabolism-centric therapeutics.

II. ANGIOGENESIS: GENERAL PRINCIPLES AND CONCEPTS

The vasculature is a truly remarkable organ. It is one of the first functional organs to form during embryogenesis and matures into a closed cardiovascular system to conduct

blood flow through an intricate network of large- to medium-size vessels extending into micrometer-size capillaries, adding up to an astonishing 90,000 km in total length in adults (436, 588). Apart from some exceptions (e.g., cartilage and cornea are avascular), all tissues rely on blood vessels for a continuous supply of nutrients and oxygen, and on lymphatic vessels to drain and filter interstitial fluids. In addition, blood vessels take part in controlling systemic pH and temperature homeostasis and in mediating immune responses (reviewed in Ref. 588).

During early embryo development, a primitive vascular plexus is formed in a process termed vasculogenesis. In brief, mesodermal angioblasts (EC progenitors) aggregate to form primitive vessel-like endothelial tubes lacking mural cell coverage (167, 424) (FIGURE 1). The hemangioblast, a precursor shared by ECs and hematopoietic cells, has also been proposed as another source to form endothelium during development (reviewed in Ref. 565). Subsequent extensive remodeling and growth of the primary plexus occurs through different mechanisms of vessel formation such as vessel splitting (intussusception) and vessel sprouting (generally known as angiogenesis). Vessel splitting or intussusceptive growth expands the capillary bed literally by “splitting” a capillary into two adjacent vessels. The opposite walls of the capillary project into the capillary lumen and have their ECs contact each other to locally form an endothelial bilayer, which is then holed by reorganization of intracellular junctions. Pericytes and myofibroblasts cover the resulting hollow transcapillary pillar, which increases in circumference to split the capillary in two parallel vessels (341) (FIGURE 1).

Sprouting angiogenesis, whereby new capillaries sprout from a preexisting vessel, is the more frequently studied and better-understood form of vessel formation, and typically entails a series of highly orchestrated processes driven by identified pro-angiogenic stimuli. Driving this phenomenon is the surrounding tissue’s need for oxygen and nutrients, which incites production of VEGF, fibroblast growth factors (FGFs), and other pro-angiogenic stimuli by nonvascular cells (70). Upon reaching the existing vessel, VEGF binds to its receptor VEGF receptor 2 (VEGFR2 also known as Flk1 or KDR) on ECs and, locally, the preexisting vessel “relaxes” to allow a new vessel sprout to arise: endothelial cell-cell contacts untighten, pericytes detach, and the basement membrane is broken down. The formation of the new sprout has been studied recently intensely in the context of retinal angiogenesis and occurs in a highly coordinated manner (reviewed in Ref. 436) whereby one EC, the one that was exposed to the highest VEGF level, is selected to become the “tip cell” and to migrate and guide the new sprout towards the very source of the growth factor (567). While migrating, the sprout needs to elongate by multiplying the number of “stalk cells” following immediately behind the tip cell (FIGURE 2A).

Even though originating from the same preexisting vessel, tip and stalk cells in the nascent vessel differ both functionally and morphologically. Tip cells have numerous filopodia and protrusions corresponding to their highly motile behavior, whereas stalk cells have relatively few filopodia (192). Tip versus stalk specification is highly dynamic and as such allows selection of the fittest EC for the tip position to lead the sprout at every given moment. ECs compete for

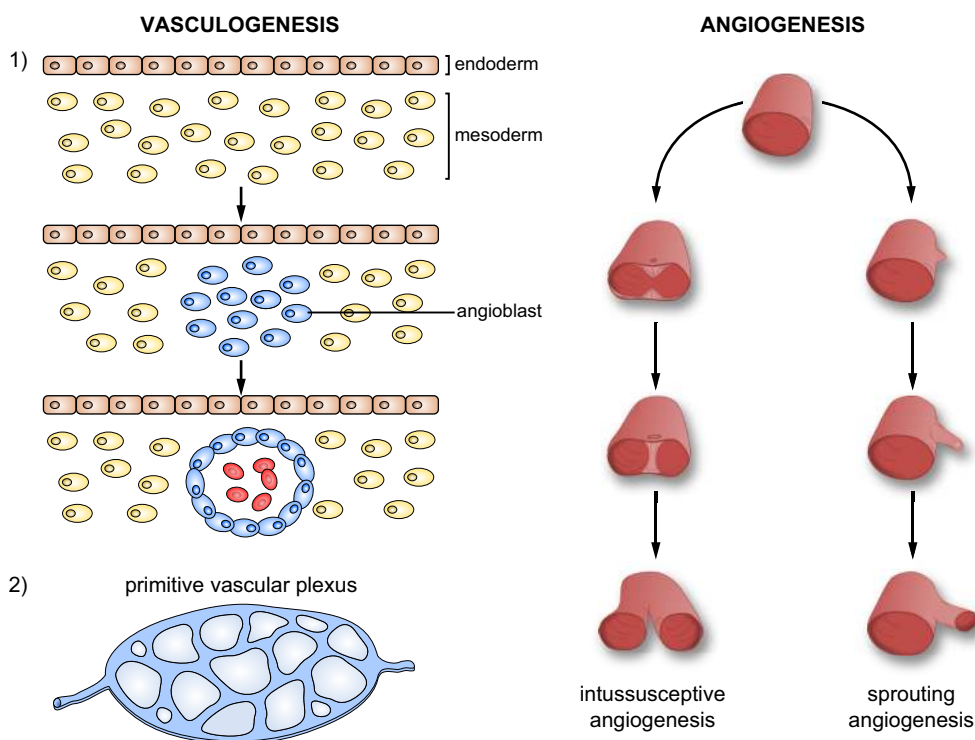


FIGURE 1. General concepts in angiogenesis: formation of a vascular plexus. During vasculogenesis, mesodermal EC progenitors (angioblasts) cluster to form vessel-like endothelial tubes [1] which eventually form a primitive vascular plexus [2]. This primitive plexus subsequently undergoes substantial remodeling by vessel intussusception whereby a preexisting capillary splits in two adjacent vessels or by sprouting angiogenesis whereby a new capillary sprouts of a preexisting vessel.

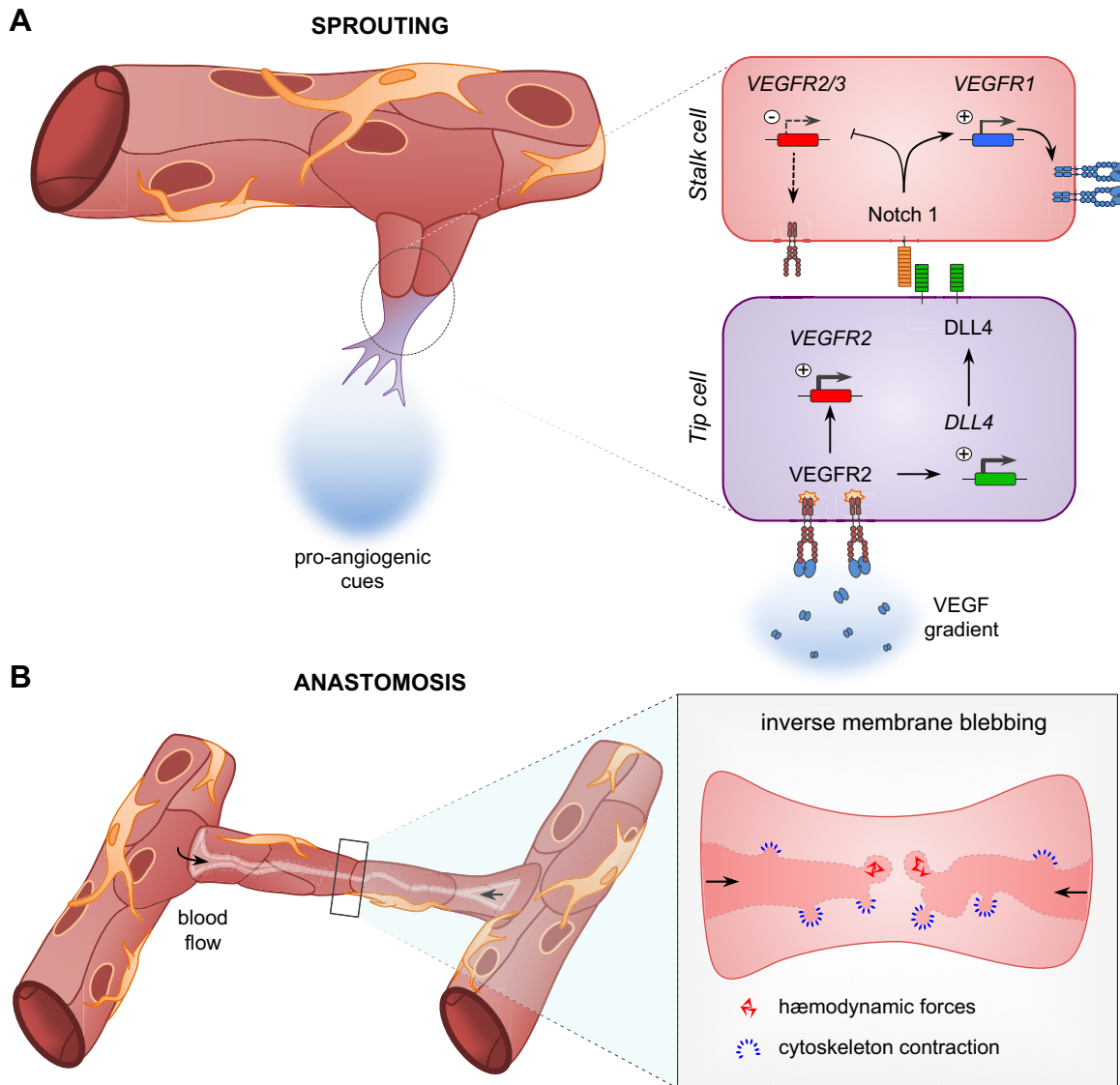


FIGURE 2. General concepts in angiogenesis: tip versus stalk specification and anastomosis. *A*: in sprouting angiogenesis, a pro-angiogenic growth factor gradient induces tip and stalk cell formation in a preexisting vessel to form a new sprout. In the tip cell, VEGF binds and activates its receptor VEGFR2, which induces DLL4 expression. In the neighboring ECs, DLL4 binds Notch receptors, which drive expression of the “decoy” VEGF receptor 1 (VEGFR1) while reducing VEGFR2 expression. Ultimately, this increases the VEGFR1/VEGFR2 ratio and lowers EC responsiveness to VEGF, causing the EC to adopt a stalk cell phenotype. Other genetic signals are involved in tip/stalk specification but are not included in the figure for reasons of clarity. *B*: newly formed sprouts from neighboring vessels meet and fuse through a process termed anastomosis. To allow blood flow, a fully functional, interconnected lumen needs to form in the new sprout; the hemodynamic force of the blood flow itself can cause lumen expansion by causing inverse blebbing of the ECs’ apical membrane. VEGF, vascular endothelial growth factor; VEGFR, vascular endothelial growth factor receptor; DLL4, Delta like 4.

the tip cell position in a process termed “tip cell overtaking” and “EC shuffling” (17, 255). Intriguingly, the tip cell itself maintains neighboring ECs in a stalk cell phenotype by expressing the Notch ligand Delta-like 4 (DLL4). In adjacent ECs, DLL4 binds Notch receptors, causing the Notch intracellular domain (NICD) to be released and to drive expression of the high-affinity/low-activity “decoy” VEGF receptor 1 (VEGFR1 also known as Flt1) (179) while reducing VEGFR2 expression. The increased VEGFR1/VEGFR2 ratio lowers EC responsiveness to VEGF and imposes a stalk cell phenotype (432) (FIGURE 2A). Continuous “cell shuf-

fling” at the utmost leading end of the sprout allows the EC with the lowest VEGFR1/VEGFR2 ratio (this is the fittest EC in terms of VEGF sensing) to obtain the tip position (17, 255). The shuffling causes continuous changes in cellular neighboring interactions, disrupting the DLL4-Notch lateral-inhibition feedback mechanism. However, in the new sprout, DLL4 levels fluctuate dynamically in individual cells, leading to a salt-and-pepper organization along the sprout of DLL4^{high} and DLL4^{low} ECs. This pattern guarantees that for every given tip-stalk configuration, the correct between-neighbors DLL4-Notch signaling can take place to support

the differential behavior between two neighboring ECs (255, 549). Based on findings that tip cell overtaking rates were not altered upon VEGF addition or Dll4-Notch signaling inhibition (17), a recent computational modeling study proposes that tip cell overtaking is a side effect arising from normal stochastic motion of ECs during sprout formation. The VEGF-Dll4-Notch signaling then ensures that the EC that has randomly acquired the tip position indeed adopts tip cell behavior, rather than dictating which EC takes the tip position (43).

Expression of Dll4 itself is under transcriptional control of the Tel-CtBP repressor complex, which is disassembled from the Dll4 promoter by a VEGF stimulus to allow a transient rise in Dll4 levels (467). The Wnt- β -catenin signaling pathway, another important player in angiogenesis (reviewed in Ref. 456), can also affect Dll4 transcription (94). Next to Dll4, Jagged1 is another Notch ligand involved in tip versus stalk specification; in vitro data show how Jagged1 opposes Dll4 by acting as a negative regulator of Notch activity and promotes EC proliferation and sprouting (37). In addition, the PTEN (phosphatase and tensin homolog) tumor suppressor is crucial to establish the Notch-mediated stalk cell proliferation arrest and to procure normal vessel density and patterning in vivo (490). The VEGF-Dll4-Notch signaling cascade is a major control mechanism of tip-stalk specification, but other signaling axes codetermine this complex mechanism in vessel sprouting and patterning (reviewed in Refs. 149, 279, 436, 445).

The more mature, cobblestone-like “phalanx cells” (360) connect the growing sprout with the preexisting vessel and start forming a lumen to allow blood flow. To form a closed system, neighboring sprouts meet and their tip cells fuse (anastomosis); macrophages, through pro-angiogenic factors they secrete, act as linkers between two anastomosing tip cells (161). A key event after anastomosis is the development of an interconnected lumen to allow functional

blood flow. A number of different mechanisms have been suggested to drive lumen formation and extension (reviewed in Ref. 41). Recent findings show that the hemodynamic force of the blood flow itself can drive lumen formation in the newly forming sprout, by a mechanism termed “inverse blebbing”; blood flow pressure stimulates the apical membrane of ECs to form bleblike deformations causing local contraction of actomyosin, allowing lumen expansion (190) (FIGURE 2B). A fully functional vessel is finally established and stabilized by the recruitment of platelet-derived growth factor (PDGF) receptor β (PDGFR β) expressing perivascular cells through excretion of PDGF-B by the ECs (180).

III. ENDOTHELIAL CELL METABOLISM DRIVING ANGIOGENESIS

The following paragraphs aim to provide a comprehensive overview of normal (i.e., under nondiseased circumstances) EC metabolism confined to glucose, amino acids (AAs), and fatty acids (FAs), the three major substrates for energy and biomass production in ECs, as they have been most extensively studied (for schematic overview, see FIGURE 3). Even though they have greatly enhanced our insights into EC metabolism, most of the data discussed originate from ECs (often derived from specific vascular beds; see sect. VI for more details on EC heterogeneity) cultured in vitro in two-dimensional monolayers, which do not fully match the plethora of in vivo three-dimensional environmental cues and which have been shown to lead to differences in cellular metabolism in other cell types (112). Additionally, the traditional culture media in which ECs are grown fail to mimic the in vivo metabolite composition and might substantially rewire the EC’s metabolism (67). Still, phenotyping of mice lacking the metabolic target specifically in ECs, employed only since very recently, supports the basic relevance of the in vitro findings. Future in vivo EC metabolic studies (see

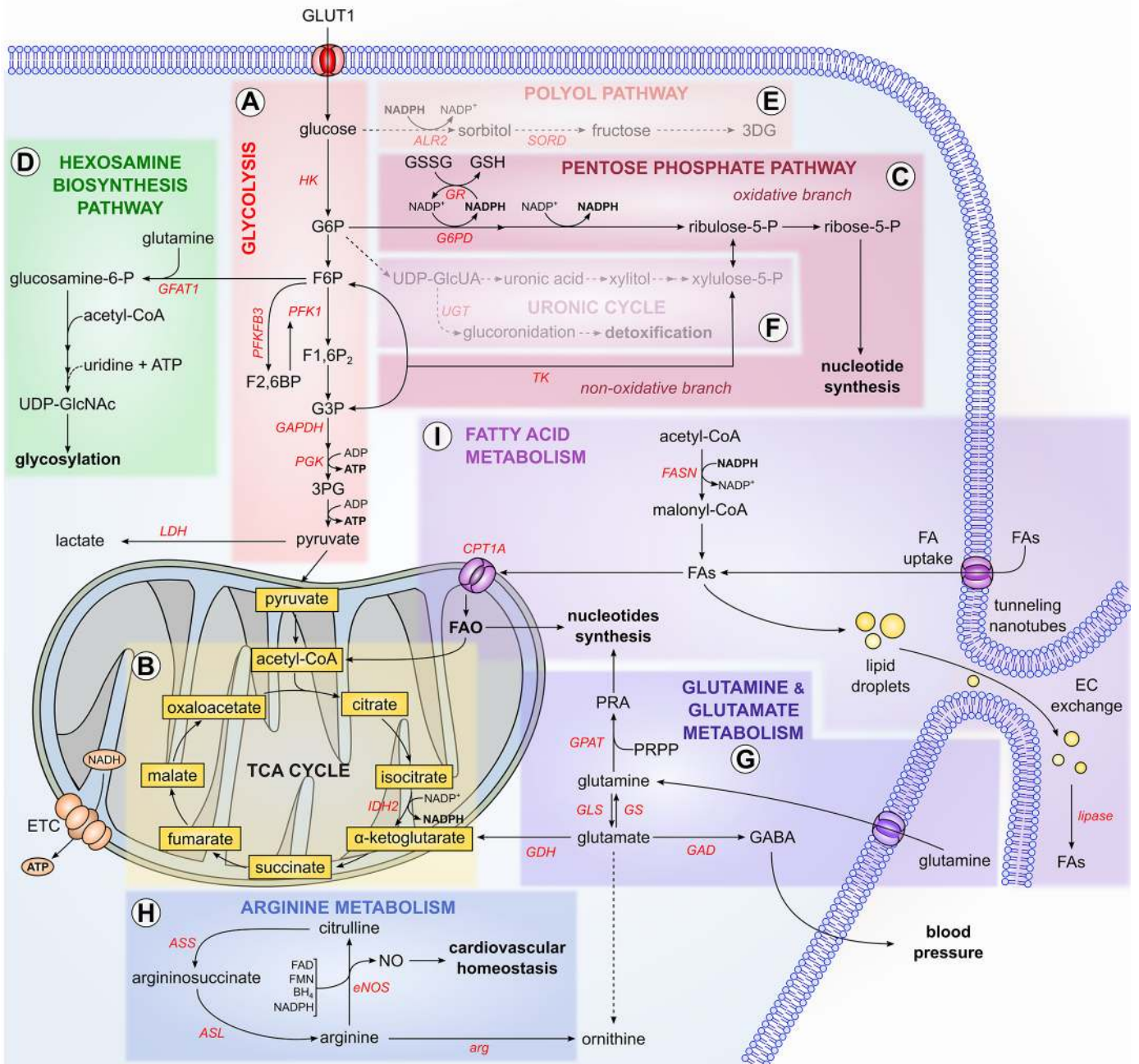
FIGURE 3. General overview of metabolic pathways in healthy ECs. Schematic representation of metabolic pathways in normal ECs (A, glycolysis; B, TCA cycle; C, pentose phosphate pathway; D, hexosamine biosynthesis pathway; E, polyol pathway; F, uronic cycle; G, glutamine and glutamate metabolism; H, arginine metabolism; I, fatty acid metabolism); to prevent overcrowding of the figure, not all individual steps in each pathway are shown. For the same reason, one-carbon metabolism, the mevalonate pathway, and cysteine-to-H₂S metabolism are omitted from this figure and described in detail in FIGURES 10 AND 11. Pathways with minimal activity in healthy ECs have lower opacity in the figure. 3DG, 3-deoxyglucosone; 3PG, 3-phosphoglycerate; α -KG, α -ketoglutarate; ALR2, aldose reductase 2; ARG, arginase; ASL, argininosuccinate lyase; ASS, argininosuccinate synthase; BH₄, tetrahydrobiopterin; CoA, coenzyme A; CPT1a, carnitine palmitoyltransferase 1a; DHAP, dihydroxyacetone phosphate; eNOS, endothelial nitric oxide synthase; ETC, electron transport chain; F1,6P₂, fructose-1,6-bisphosphate; F2,6BP, fructose-2,6-bisphosphate; F6P, fructose-6-phosphate; FA, fatty acid; FAD, flavin adenine dinucleotide; FAO, fatty acid oxidation; FASN, fatty acid synthase; FMN, flavin mononucleotide; G3P, glyceraldehyde-3-phosphate; G6P, glucose-6-phosphate; glucosamine-6-P, glucosamine-6-phosphate; G6PD, glucose-6-phosphate dehydrogenase; GABA, γ -aminobutyric acid; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GAD, glutamic acid decarboxylase; GDH, glutamate dehydrogenase; GFAT1, glutamine fructose-6-phosphate amidotransferase; GLS, glutaminase; GPAT, glutamine phosphoribosylpyrophosphate amidotransferase; GR, glutathione reductase; GlucN6P, glucosamine-6-phosphate; GLUT1, glucose transporter 1; GS, glutamine synthetase; GSH, reduced glutathione; GSSG, oxidized glutathione; HK, hexokinase; IDH2, isocitrate dehydrogenase 2; LDH, lactate dehydrogenase; NADPH, nicotinamide adenine dinucleotide phosphate; NO, nitric oxide; OAA, oxaloacetate; PGK, phosphoglycerate kinase; PFK1, phosphofructokinase-1; PFKFB3, 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3; PRA, 5-phosphoribosyl-1-amine; PRPP, 5-phosphoribosyl-1-pyrophosphate; ribose-5-P, ribose-5-phosphate; ribulose-5-P, ribulose-5-phosphate; ROS, reactive oxygen species; SORD, sorbitol dehydrogenase; TCA, tricarboxylic acid; THF, tetrahydrofolate; TK, transketolase; UDP-GlcNAc, uridine diphosphate N-acetylglucosamine; UDP-GlcUA, UDP-glucuronic acid; xylulose-5-P, xylulose-5-phosphate.

sect. XI) will further reinforce, complement, or adjust these data.

A. Glucose Metabolism: All About Glycolysis?

ECs prefer not to maximize energy (ATP) production by shunting all glucose they take up into oxidative phosphorylation (OXPHOS) but rely on glycolysis instead (FIGURE 3A) (114, 291). Indeed, in rat coronary microvascular ECs, ~98% of glucose is being metabolized to lactate while only a mere 0.04% was oxidized in the tricarboxylic acid (TCA) cycle (FIGURE 3B) (291). Similarly, in human umbilical vein

ECs (HUVECs), glycolytic flux (~1.5 μmol glucose·h⁻¹·mg protein⁻¹) was estimated to be >200-fold higher than glucose oxidation fluxes (114). This is in line with the relatively small mitochondrial volume in ECs (209) but seemingly contradicts the assumption that ECs could directly use the high oxygen levels in blood (e.g., arterial ECs are exposed to a partial oxygen pressure of ~100 mmHg; Ref. 148). Selecting glycolysis over oxidative phosphorylation lowers the net ATP yield per mole glucose (approximately 20-fold lower), but might offer ECs a number of payoffs. First, high glycolysis rates sustain lactate production, which functions as a pro-angiogenic signaling molecule (243, 471, 506, 557). Second, reactive oxygen species (ROS, typically gen-



erated by oxidative phosphorylation in ECs) are kept at a minimum, whereas amounts of oxygen available for transfer to surrounding cells and tissues are maximally preserved since they are not consumed by oxidative phosphorylation. Third, reliance on glycolysis preconditions ECs for sprouting into an avascular, hypoxic environment where interstitial glucose levels are not rate-limiting but oxygen levels are (58, 188). In addition, when external glucose is nonlimiting, high glycolysis rates can be even quicker in producing ATP than oxidative phosphorylation. As such, a direct comparison between pulmonary microvascular ECs (PMVECs; highly glycolytic, rapid growth) and pulmonary arterial ECs (PAECs, more oxidative, slower growth) revealed two-fold higher total cellular ATP content in PMVECs versus PAECs in spite of twofold higher oxygen consumption rates in the latter (423). Finally, high glycolysis rates sustain macromolecule synthesis by feeding glucose carbons into glycolytic side branches (see below in this section).

VEGF stimulation causes ECs to elevate their glycolytic flux and to increase expression levels of the glucose transporter 1 [GLUT1/SLC2A1; by activating phosphoinositide 3-kinase (PI3K)-Akt signaling (627)] and of glycolytic enzymes, such as lactate dehydrogenase-A (LDH-A) and the bifunctional 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase-3 (PFKFB3) (114, 423, 430). Whereas glycolytic cell types often express the monocarboxylate transporter 4 (MCT4) for adequate efflux of glycolysis-derived lactate (429), it remains to be substantiated if VEGF induces MCT4 expression/activity in ECs. Besides the glycolytic up-regulation in response to VEGF, the effects of other key angiogenic growth factors promoting EC growth, such as for example angiopoietin-1, on glycolytic metabolism are not well documented at present and warrant future research. Conversely, Dll4 reduces PFKFB3 protein levels and lowers glycolytic flux in HUVECs (114). PFKFB3 is a glycolysis regulator and uses its kinase activity (which is increased 700-fold over its phosphatase activity) to generate fructose-2,6-bisphosphate (F2,6BP), which allosterically activates the rate-limiting glycolytic enzyme phosphofructokinase-1 (PFK1). Even though genetic silencing or chemical inhibition of PFKFB3 only partially (by 40%) reduces glycolytic flux, probably inherent to its function as a regulator of glycolysis rather than a truly rate-limiting enzyme, it suffices to substantially impair *in vitro* EC sprouting as well as *in vivo* vessel branching and outgrowth (114, 483, 608). Additional compelling evidence for a prominent role of PFKFB3 in vessel sprouting derives from loss of tip cell behavior in PFKFB3-silenced HUVECs, even when genetically primed to acquire tip cell position by simultaneous Notch knock-down (114). Conversely, PFKFB3 overexpression overrules the pro-stalk signal from simultaneous NICD overexpression (114). Importantly, similar findings were obtained when mosaically overexpressing PFKFB3 and/or NICD selectively in ECs in zebrafish embryos, i.e., NICD transgene expressing ECs were usually observed at

the stalk position, while ECs expressing both the NICD and PFKFB3 transgene moved to the tip position (114). Furthermore, computational modeling, confirmed by experimentation, on tip-stalk behavior in EC sprouting, predicted that glycolytic ATP is indeed a driver for EC rearrangements in the sprout by enhancing filopodia formation and by decreasing intercellular adhesion (102). Furthermore, the computational approach accurately predicted that distorted EC rearrangements in the sprout caused by elevated VEGF stimulation (as in pathological angiogenesis; see sect. VIII) can be normalized by PFKFB3 inhibition (102). Not only the growing sprout but the fully lumenized, more mature, and quiescent endothelium too relies on tight PFKFB3 regulation. Indeed, the laminar shear stress, exerted on the quiescent endothelium by blood flow, induces the flow-responsive transcription factor Krüppel-like factor 2 (KLF2) to repress PFKFB3 expression through binding to a KLF2-binding site in the PFKFB3 promoter (126). The resulting reduced glycolysis rate, together with lower glucose uptake but also reduced mitochondrial content, ensures a metabolically quiescent state in the mature endothelium.

B. Glycolytic Side Branches: Pentose Phosphate Pathway and Hexosamine Synthesis

Glucose-6-phosphate (G6P), the first glycolytic intermediate after glucose, can shunt into the pentose-phosphate pathway (PPP) (FIGURE 3C) to be oxidized, albeit for pentose production for anabolic nucleotide and nucleic acid synthesis rather than for catabolic purposes (461). G6P dehydrogenase (G6PD) is the rate-limiting enzyme of the irreversible oxidative branch (oxPPP) that generates ribulose-5-phosphate, whereas transketolase (TK) rate-limits the reversible non-oxidative branch (non-oxPPP) in which ribose-5-phosphate (a substrate for nucleotide synthesis) is generated and, when the reaction occurs in the reverse direction, the glycolytic intermediates fructose-6-phosphate (F6P) and glyceraldehyde-3-phosphate (G3P) are produced. Inhibiting either of both enzymes lowers EC viability and migration (563, 638). The oxPPP produces NADPH, a crucial cofactor for (endothelial) nitric oxide synthase [(e)NOS]-driven nitric oxide (NO) synthesis (see below in this section). Additionally, NADPH is required for lipid and nucleotide synthesis, and used by glutathione reductase to convert oxidized glutathione disulfide (GSSG) to reduced glutathione (GSH), thereby controlling intracellular redox homeostasis (reviewed in Refs. 84, 425, 489).

Bovine aortic ECs overexpressing G6PD have higher NADPH levels, retain GSH levels, and as a result better withstand oxidative insult. Additionally, these cells display increased eNOS activity (313). The resulting increase in NO availability might partially underlie the enhanced angiogenic behavior in G6PD-overexpressing ECs upon VEGF treatment. Conversely, G6PD-silencing reduces migration, prolifera-

tion, and tube formation in response to VEGF (312). Additionally, VEGFR2, Akt, and eNOS (tyrosine) phosphorylation are induced upon G6PD overexpression by mechanisms requiring further elucidation, while being reduced by G6PD silencing, possibly further contributing to the above findings (312). Reciprocally, VEGF induces G6PD tyrosine phosphorylation and plasma membrane localization/activity in an Src tyrosine kinase-dependent manner (411). Of note, aortic rings from G6PD-deficient “Pretsch” mice, having only ~15% residual G6PD activity in homozygotes (437) and ~32% remaining NADPH levels (as measured in the kidneys) (609), show reduced vessel outgrowth in comparison with control animals (312).

One step further down the glycolytic pathway, fructose-6-phosphate (F6P) can be shunted into the hexosamine biosynthesis pathway (HBP) (FIGURE 3D). The HBP is often considered a “nutrient sensing pathway” given the requirement of glucose, glutamine, acetyl-CoA, uridine, and ATP to form the end product UDP-*N*-acetylglucosamine [UDP-GlcNAc; at ± 40 nmol/g tissue, the second most abundant nucleotide form in the organism after ATP (± 100 nmol/g tissue) (117)] of which the GlcNAc group is used in *O*- and *N*-linked protein glycosylation (26). Glutamine:fructose-6-phosphate aminotransferase 1 (GFAT1) is the first and rate-limiting enzyme in the pathway and condenses glutamine and F6P into glucosamine-6-P. GFAT1 was shown to be under transcriptional control of the spliced X-box binding protein 1 (XBP1s) and as such links the HBP with endoplasmic reticulum (ER) stress and the unfolded protein response (UPR) (576). Activating transcription factor 4 (ATF4), another UPR effector, induces GFAT1 expression upon glucose shortage and amino acid deprivation (76). By virtue of its nutrient sensing role, the HBP could be of vital importance in ECs when sprouting into avascular, nutrient-scarce surroundings. Nevertheless, the precise metabolic role of the HBP in ECs, beyond glycosylating and thereby sustaining proper functioning of key angiogenic regulators like VEGFR2 and Notch (37, 551), remains unknown and is likely highly contextual. For instance, supplying HUVECs and EA.hy926 ECs with glucosamine increases protein *O*-GlcNAc-ation and reduces EC migration and vascular tube formation, while reducing glycosylation by overexpressing *O*-GlcNAcase has opposite effects (335). If and how exactly these findings relate to the effect of glucosamine on the PPP flux and subsequently on eNOS activity (see below in this section) or other angiogenic factors, or to the role of glycosylation as a modifier of the “histone code,” thereby translating nutrient status into chromatin dynamics (117) (see sect. IX), remains to be determined.

2-Deoxy-*D*-glucose (2-DG) is best known as a glycolytic inhibitor: hexokinase phosphorylates 2-DG, which then competitively inhibits phosphoglucose isomerase, the next enzyme in the glycolytic pathway. Additionally, as a mannose-mimetic, 2-DG also reduces *N*-glycosylation by com-

peting with mannose to build dolichol-pyrophosphate-linked oligosaccharides, precursors for *N*-glycosylation (reviewed in Ref. 299). Low-dose 2-DG treatment disturbs endothelial *N*-glycosylation and reduces EC proliferation, migration, and in vitro capillary formation through VEGFR2 hypoglycosylation and ER stress resulting in reduced ERK and Akt levels (287, 369). EC-specific deletion of Nogo-B-interacting protein (NgBr), involved in the synthesis of dolichol (the anchor for oligosaccharides for protein glycosylation), causes embryonic vascular development defects with an underlying reduction in glycosylation of VEGFR2, CD31, and VE-cadherin (421), thus highlighting the importance of dolichol synthesis for angiogenesis.

C. Other Glucose Metabolism Pathways

Under physiological conditions, ~3% of glucose is diverted into the polyol pathway (FIGURE 3E), a two-step pathway in which cytosolic aldose reductase (ALR2) reduces glucose to sorbitol (at the expense of NADPH and ultimately GSH redox cycling) and sorbitol dehydrogenase (SORD) subsequently converts sorbitol to fructose (331, 347). Fructose, also a common source of sugar in natural foods, is a precursor of the noxious and highly reactive dicarbonyl compound 3-deoxyglucosone (3-DG) (260), which contributes to the nonenzymatic production of highly toxic advanced glycation end products (AGEs; see sect. VII) (577). Whether fructose can be metabolized to intermediates entering glycolysis, as occurs in hepatocytes (281), is unknown. Interestingly, an in vitro study indicated ALR2-related enzyme expression in rat retinal capillary ECs; however, sorbitol levels were barely detectable under basal conditions (618). These results are in line with the low baseline activity of the endogenous polyol pathway in ECs. Yet, in diabetic and atherogenic conditions, the deregulation of the polyol pathway accounts for disease progression, as discussed in section VII.

The uronic/glucuronate pathway (FIGURE 3F) is another alternative glucose metabolism pathway, accountable for ~5% of the total glucose catabolized per day in humans (68). Instead of generating ATP, it uses G6P to produce UDP-glucose (used in glycogen synthesis or galactose metabolism), which is subsequently oxidized to UDP-glucuronic acid (UDP-GlcUA) (3, 68). Through a stepwise process, UDP-GlcUA is converted to uronic acid, xylitol, and xylulose-5-phosphate to finally generate ribulose-5-phosphate, the end product of the oxPPP (see above in this section) (3). Moreover, the xylulose-5-phosphate can be converted back to F6P by TK and as such connects to the HBP or to glycolysis. Alternatively, UDP-GlcUA is used in glucuronidation, a detoxification pathway involving the UDP-glucuronyltransferase (UGT)-mediated covalent binding of glucuronic acid to drugs, xenobiotics, and endogenous compounds including bilirubin, bile acids, fatty acids (FAs) and steroid hormones (468). UGT isoforms are expressed in human

brain microvascular ECs, thereby contributing to the protection of the brain to toxic substances (408). Interestingly, UGT expression was also increased in a primary culture of epileptic brain ECs, suggesting the induction of a protective program upon pathological drivers (193).

D. Oxidative Metabolism: Too Few Mitochondria?

The dogmatic view on the mitochondrion as the cell's "powerhouse" does not fully reconcile with the EC's glycolytic nature. ECs rely only minimally on mitochondrial OXPHOS for ATP generation (114). Concurrently, endothelial mitochondrial volume is only 2–6% of the total cellular volume, whereas 28 and 32% have been reported for hepatocytes and cardiomyocytes, respectively (reviewed in Ref. 529). Still, mitochondria in ECs are not dysfunctional and remain fully coupled to ATP synthesis, implying normal flow through the electron transport chain (ETC) (129, 288). As such, and notwithstanding a low respiratory capacity, ECs triple their oxygen consumption upon switching from quiescence to proliferation during angiogenesis, although it remains to be determined for which purposes exactly this increase in respiration is used. This allows the mitochondrial uncoupling benzoquinone embelin to establish an anti-angiogenic effect in tumor xenografts and wound healing in vivo (101). Furthermore, ECs display the Crabtree effect, whereby lower glucose levels (~1 mM) cause mitochondrial respiration to increase, with opposite effects (growth inhibition and reduced respiration) in high glucose (e.g., 25 mM) (288, 291).

Beyond an obvious function in cellular metabolism, mitochondria in ECs are increasingly being recognized for their role in signaling events. Whereas the focus has mainly been on mitochondrial ROS as a signaling element, other mitochondrial factors may play a role, although this requires further study. For instance, coupling factor 6 (CF6) is a component of mitochondrial ATP synthase but is also present on the EC surface and released into the circulation. Even though this event is not merely a consequence of cellular damage (suggestive instead of an active transport system, Ref. 405), plasma CF6 levels might be indicative of EC dysfunction (see sect. VII) and inflammation (404, 406). The role of other mitochondria-derived signaling factors in ECs has been reviewed in References 265, 584.

Compared with ECs in other vascular beds, the mitochondrial volume in cerebrovascular ECs (CECs) at the blood-brain barrier (BBB) is almost double (401). The BBB is a highly dynamic yet selective interface between the blood and the central nervous system and rigorously safeguards neuronal environment homeostasis by controlling influx and efflux of substances to and from the brain. CECs turn to aerobic respiration to meet the energetic demands for sustaining multiple transport systems; additionally, it has been

hypothesized that oxidative stress from exposure to xenobiotic substances might be counteracted by the reducing equivalents generated through oxidative metabolism (104). Strikingly, shear stress-mediated induction of an endothelial BBB phenotype in vitro causes human brain microvascular ECs to have higher expression levels of TCA cycle enzymes, whereas glycolytic genes are downregulated, a finding that requires further study in light of the above (negligible) role of mitochondria in ECs (104). In vivo as well as in vitro, mitochondrial crisis in CECs severely compromises BBB function (127). Finally, heightened expression of miR-34a in CECs inhibits mitochondrial OXPHOS causing BBB breakdown probably through lowering of mitochondrial cytochrome C expression (59).

E. Amino Acid Metabolism

Amino acids (AAs) are traditionally classified as nonessential (NEAA) or essential (EAA), based on the organism's own ability of de novo synthesizing the AA or the need for dietary uptake, respectively. NEAAs can become conditionally essential under specific developmental or pathophysiological conditions; furthermore, whether an AA is essential or not differs between species. Apart from constituting building blocks for proteins, AAs can enter the TCA cycle as keto acids after transaminase-mediated removal of the amino group.

1. Glutamine and glutamate

Glutamine (single letter code: Q) and its deamidated derivative glutamate (single letter code: E) are both NEAAs, although glutamine becomes conditionally essential during severe trauma, and during chemo- or radiotherapy when excessive consumption outruns its synthesis (531). While glutamine is the most abundant extracellular AA (with physiological levels around 0.65 mM of the total ~2.5 mM free AA concentration in plasma), glutamate is the most abundant intracellular AA (at reported concentrations ranging from 2 to 20 mM) (390). Both glutamine and glutamate are readily being oxidized by microvascular ECs (up to 68 nM·h⁻¹·mg protein⁻¹ under glucose deprivation) and, together with alanine, rank in the class of high oxidation rate AAs (>35 nM·h⁻¹·mg protein⁻¹) (291). In HUVECs, ~30% of the TCA carbons is glutamine-derived, a share comparable to glycolysis- and FA-derived carbon (481). Radioactive flux measurements from the early 1990s have even suggested that glutamine oxidation, together with palmitate oxidation, would be the main energy source in liver ECs (507), although it is unclear whether this finding is restricted to liver ECs, given that other studies documented opposite findings, at least in relation to the role of palmitate as energy source (see below in this section). Glutamate enters the TCA cycle via a single enzymatic conversion [to α -ketoglutarate; catalyzed by glutamate dehydrogenase (GDH)], whereas glutamine needs one additional prior en-

zymatic conversion into glutamate [catalyzed by glutaminases (GLS)] (FIGURE 3G). Alanine requires three enzymatic conversions (to pyruvate by alanine aminotransferase, pyruvate to acetyl-CoA by pyruvate dehydrogenase and finally to citrate by citrate synthase-mediated condensation of acetyl-CoA and oxaloacetate) before entering the TCA cycle. In addition, in ECs the above enzymes are highly active; GLS activity for example is 20-fold higher in bovine pulmonary ECs than in cell types with established high glutaminolysis rates such as lymphocytes (308), although this finding requires additional confirmation in other EC subtypes and using different techniques. GLS inhibition causes HUVECs to adopt a senescence-like phenotype (550), further underscoring the role of EC glutamine metabolism. Most recently, endothelial glutamine metabolism was shown to be crucial for vessel sprouting in angiogenesis both in vitro and in vivo (using EC-specific knockout mice for the rate limiting enzyme GLS). Blocking endothelial glutamine metabolism perturbs tip/stalk dynamics and lowers EC proliferation. Mechanistically, glutamine in ECs contributes to TCA cycle anaplerosis and drives asparagine synthesis through asparagine synthetase (ASNS) activity, which by itself proves indispensable for vessel sprouting (242).

Mammalian cells generally express two different GLS isozymes, kidney-type GLS1 and liver-type GLS2, possibly serving two distinct functions. While glutamine carbons are driven into the TCA cycle by GLS1, GLS2 shunts glutamine carbon and nitrogen into glutathione for redox homeostasis. In cancer cells at least, this duality in function is reflected by a difference in transcriptional regulation: c-MYC controls GLS1 expression, whereas GLS2 expression is p53 driven (184, 241, 590). Whether a similar functional difference between GLS1 and GLS2 exists in ECs is not known at present, but, strikingly, in the mouse retinal microvasculature, tip cells display increased GLS2 expression in comparison with stalk cells (513).

Glutamine supplies the EC's central metabolism with carbon but also with nitrogen. Glutamine's γ -nitrogen is crucial for nucleotide synthesis and is incorporated into both the purine and the pyrimidine ring structure. In the purine nucleobases adenine and guanine, the nitrogens on position 3 and 9 are donated by glutamine, and guanine's amino group is additionally derived from glutamine. Glutamine phosphoribosylpyrophosphate amidotransferase catalyzes the rate-limiting step in purine synthesis by transferring NH_3 released from glutamine onto 5-phosphoribosyl-1-pyrophosphate (PRPP) to form 5-phosphoribosyl-1-amine (PRA); the amino group introduced (on position 9) will form the *N*-glycosidic bond of the nucleotide. 5'-Phosphoribosylformylglycinamide synthetase uses glutamine to introduce the nitrogen at position 3. In de novo pyrimidine synthesis, cytosolic carbamoyl phosphate synthetase II introduces glutamine's amide nitrogen at position 3 of the

uracil, cytosine, and thymine nucleobases (reviewed in Ref. 95). Interestingly, a recent elaborate labeling study in non-small cell lung cancer cell lines revealed that glutamine, exhibiting the highest consumption rates together with glucose, primarily contributes to protein production, whereas the majority of cellular carbon mass originates from AAs other than glutamine that display significantly lower consumption rates (239). These data imply that high consumption rates of a given substrate do not necessarily correlate with their use for cell carbon mass production; whether this holds true specifically for ECs too remains to be determined.

The GFAT-mediated rate-limiting step in the HBP (FIGURE 3D) condenses F6P and glutamine's amino group into glucosamine-6-phosphate (GlcN6P) (505). In rat coronary microvascular ECs, increasing doses of glutamine have been reported to increase GFAT activity and GlcN6P levels. Increasing glucose levels (as precursor for F6P) similarly resulted in higher GlcN6P production, which was completely abrogated upon full glutamine deprivation. In ECs, the amount of glutamine used in the HBP has been estimated to account for only 0.3% of total glutamine metabolized (596). Of note, this value might be context-dependent given that GFAT activity can be >10-fold higher in cultured than in freshly isolated ECs (possibly reminiscent of a differentiation effect on GFAT) (596).

Both human umbilical venous and aortic ECs express glutamic acid decarboxylase (GAD) to produce γ -aminobutyric acid (GABA) from glutamate (487) (FIGURE 3G). Strikingly, GAD inhibition reduces cellular ATP levels, and GABA itself increases pyruvate oxidation and fatty acid oxidation. The mechanism behind the increased oxidative fluxes is not known yet. However, GABA dose-dependently increases palmitate uptake by mitochondria, thereby enhancing fatty acid oxidation (487). Even though the exact role of EC-produced GABA is not clear, it protects the endothelium from ROS and has anti-inflammatory effects on ECs. Possibly even more important, GABA reduces blood pressure, most likely in an autonomic ganglia-dependent way (487).

2. Arginine and urea cycle intermediates

Even though the liver is the main site for arginine metabolism and is generally believed to be the only tissue to express a complete urea cycle, arginine and urea cycle intermediates play important roles in ECs as well (FIGURE 3H). Much like glutamine, arginine is a conditionally EAA with plasma concentrations ranging from 0.095 to 0.250 mM (530) and intracellular levels varying between 0.1 and 0.8 mM in cultured ECs and 2 and 4 mM in freshly isolated ECs (reviewed in Ref. 346). In ECs, arginine is mainly competed for as a substrate by either arginase or by (e)NOS. Hydrolysis of arginine by arginases yields urea and ornithine, which can subsequently be used for polyamine, glutamate, or proline synthesis. Mammalian arginase comes in two different iso-

forms (coded for by two genes located on different chromosomes) displaying tissue-specific expression and distinct subcellular localization (258). Arginase I (arg I) is cytoplasmic and abundantly expressed by hepatocytes where it catalyzes the final step of the urea cycle. In contrast, arginase II (arg II) is a mitochondrial protein expressed in a wider variety of cell types. Both arg I- and arg II-derived ornithine can be used in polyamine synthesis, whereas additionally, arg II-derived ornithine can be used for glutamate and proline synthesis in a urea cycle-independent manner. HUVECs express both arg I and II, but specific isoform expression in ECs differs between species (detection of arg I and II isoforms in ECs from human, rat, mouse, pig, and cow origin has been reviewed in Ref. 379) and the specific role of either isoform in EC subtypes requires further study.

On the other hand, NOS converts arginine to citrulline, thereby producing NO and as such directly competing with arginases for arginine availability. In addition to this obvious substrate competition, *N*^ω-hydroxy-L-arginine (L-NOHA), an intermediate in the NOS reaction, potently inhibits arginase activity (51, 108). In mammals, three different NOS isozymes exist, sharing 50–60% protein homology: neuronal (nNOS/NOS1), inducible (iNOS/NOS2), and endothelial (eNOS). nNOS is constitutively expressed in neurons, whereas eNOS is predominantly expressed in ECs. Under basal conditions, iNOS is normally not expressed, yet different stimuli including immunologic and inflammatory cues can induce iNOS expression in various cell types (174, 450). iNOS further differs from the other NOS isoforms in calmodulin binding (required for NOS activity): nNOS and eNOS require increased levels of Ca²⁺ for calmodulin binding, whereas high-affinity iNOS-calmodulin binding occurs independently of Ca²⁺ (174). nNOS and iNOS are predominantly cytosolic, whereas eNOS can be both cytosolic or localized in membrane caveolae (22). nNOS, iNOS, and eNOS all require NADPH, tetrahydrobiopterin (BH₄), flavin mononucleotide (FMN), and flavin adenine dinucleotide (FAD) as cofactors for their activity (174). nNOS-derived NO is involved in synaptic plasticity as well as the control of blood pressure and can act as a neurotransmitter, whereas iNOS-derived NO controls various inflammation-linked symptoms and is causal in blood pressure falls upon septic shock (174).

eNOS-derived NO is widely known for its role as an important vasorelaxant and for sustaining cardiovascular homeostasis and vasoprotection (175). However, under certain (pathological) conditions (see sects. VII and VIII), NOS activity goes awry and the enzyme loses its ability to convert arginine into citrulline. In this “uncoupled” state, an electron from NADPH is being donated to molecular oxygen to produce superoxide (O₂⁻) instead of NO (599), which impacts cardiovascular function. As such, eNOS uncoupling is a source of oxidative stress as it produces O₂⁻, which yields peroxynitrite (ONOO⁻) upon reaction with residual NO or

can induce oxidation of the eNOS cofactor BH₄ into the biologically inactive dihydrobiopterin (BH₂). Both actions ultimately reduce overall NO bioavailability. Although fascinating and intensely studied, the mechanism of action of (e)NOS and its regulation (e.g., through posttranslational modifications) are beyond the scope of this review and have been excellently reviewed elsewhere (25, 332, 443, 464). From an EC metabolism point of view, it should be noted that in ECs, fatty acid synthase (FAS)-mediated de novo lipid synthesis is required to sustain eNOS palmitoylation (palmitate is a lipid product), membrane association, and activity (579). Furthermore, glutamine and glucosamine (derived from glutamine through GFAT activity, see above in this section) inhibit endothelial NO production by lowering PPP activity-coupled NADPH production, required for eNOS activity (595). The highly increased GFAT expression in cultured ECs warrants thoughtful interpretation of these findings. Both cationic (ornithine, lysine, homoarginine) and neutral AAs (glutamine, leucine, serine) in the extracellular environment were found to lower endothelial NO production in the EA.hy926 EC line by reducing intracellular arginine levels (through a combination of reduced arginine uptake and increased arginine efflux) (267). Finally, NO itself might have a crucial role in keeping EC mitochondrial respiration at a low rate by inhibiting cytochrome *c* oxidase (56, 86).

Through an abbreviated urea cycle, arginine can be resynthesized from citrulline by the consecutive action of the urea cycle enzymes argininosuccinate synthase (ASS) and argininosuccinate lyase (ASL) with argininosuccinate as an intermediate metabolite. In ECs, this citrulline to arginine flux has been estimated to vary between 0.7 and 1.9 nmol arginine produced·10⁶ cells⁻¹·h⁻¹ (reviewed in Ref. 346) and serves to maintain arginine levels in spite of continuous NO release (372). The relevance of this recycling mechanism is underscored by reduced endothelial NO production and significantly elevated blood pressure in ASL-deficient mice and humans (156).

3. Branched-chain amino acids

With a characteristic branch in their aliphatic side chains, branched chain amino acids (BCAAs) make up a distinct class of AAs. Of the proteinogenic BCAAs, leucine and valine in particular play an unexpected role in EC metabolism. Leucine induces GFAT activity [possibly by increasing mammalian target of rapamycin (mTOR)-mediated GFAT protein synthesis (reviewed in Ref. 625)] to produce more glucosamine, which, as mentioned above, lowers NO production from arginine (595, 625). In several cell types, leucine was found to allosterically activate GDH, thereby enhancing glutamine catabolism (reviewed in Refs. 319, 621); whether the same occurs in ECs remains undetermined. Valine, or more in particular its catabolic intermediate 3-hydroxyisobutyrate (3-HIB), is crucial for transendothelial FA transport. Indeed, muscle-secreted 3-HIB promotes

transendothelial FA transport, thereby increasing FA uptake and accumulation in muscle with insulin resistance as a final outcome (257). Whether 3-HIB also affects FA oxidation within ECs remains unknown. Finally, deletion of the large neutral amino acid transporter 1 (LAT1/SLC7A5) from ECs at the BBB perturbs the normal AA profile in the brain, lowering leucine and isoleucine levels in particular, thereby causing aberrant cap-dependent mRNA translation and leading to autism spectrum disorder-related neurobehavioral alterations (533). The above-mentioned role for leucine as a GDH activator seems less involved in this phenomenon as brain glutamate levels were only minimally affected.

F. Fatty Acid Metabolism

In general, FAs enter the cell by passive diffusion (flip-flop; referring to the complete reorientation of the FA carboxyl head group when moving from the outer to the inner plasma membrane leaflet) or by fatty acid translocase (FAT)/CD36-mediated transfer (facilitated diffusion) (221, 352) (FIGURE 3A). Very-long-chain FAs are preferentially being transported by fatty acid transport protein (FATP) 1 or other FATPs. For an in-depth overview of cellular FA uptake mechanisms and related controversies, the following review is suggested (201). Their low aqueous solubility (estimated 1–10 nM; Ref. 566) causes FAs to be mostly protein (or membrane) bound. Therefore, in the cytoplasm, FAs are either free or rely on binding to FA binding proteins (FABPs) for transportation to their destination. Expression of FAT/CD36, FATP3 and 4, and FABP3, 4, and 5 has been demonstrated in ECs (reviewed in Ref. 221).

bFGF and VEGF-VEGFR2 signaling induces FABP4 expression in ECs, the latter in a Dll4-Notch signaling dependent manner (152, 153, 220). Loss of FABP4 expression impairs EC proliferation and migration and increases apoptosis susceptibility. Angiogenic sprouting is hampered in ex vivo aortic rings from FABP4^{-/-} mice (152, 153). Furthermore, FABP4 silencing causes ECs to heighten their fatty acid oxidation (FAO) rate, presumably to remove unbound FAs (which lost their FABP4 “chaperone”) (219, 602). In such conditions, increased FAO leads to ROS production, presumably by enhancing mitochondrial respiration (219). Whereas FABP4 is predominantly expressed in microvascular endothelium, FABP5 expression is seen in both micro- and macrovascular ECs, but seems not to be induced by VEGF-A or bFGF. Like FABP4, FABP5 silencing reduces EC proliferation and chemotactic migration but, unlike FABP4 silencing, confers resistance to apoptotic cell death (630), suggesting contextual roles for these FA binding chaperones. In FA consuming tissues (e.g., muscle and heart), FABP4 and FABP5 in capillary ECs transport FAs across the endothelium and towards the tissue (252). In vitro, FATP3 and FATP4 expression in ECs is induced by muscle-released VEGF-B, suggesting a VEGF-B-mediated

transendothelial transport of FAs into muscle tissues. Notwithstanding a reduced FA uptake and accumulation in heart and muscle in VEGF-B^{-/-} mice (215, 216), the possible implications for insulin resistance (and its possible treatment by targeting the VEGF-B axis) remain debated (276). Of note, to ensure their own uptake of FAs, muscle and fat cells release lipoprotein lipase (LPL), which hydrolyzes triglyceride-rich lipoproteins, in the capillary lumen. Capillary ECs aid in the transendothelial FA transport by facilitating transport of LPL from these parenchymal cells to the capillary lumen (113).

Once FAs are taken up, they can either be fueled into catabolic processes or esterified and stored. Lipid droplets (LDs) are specialized intracellular organelles, in which excess lipids are stored. They contain triglycerides and sterol esters, thereby providing a reservoir for energy fuel and membrane synthesis (538). The abundance of intracellular LDs increases in response to increasing amounts of extracellular FAs, indicating that exogenous FAs, when in excess, are incorporated into LDs (340) that can potentially be accessed via lipolytic enzymes in times of nutrient scarcity. ECs contain LDs (21, 219, 340) and express hormone-sensitive lipase, a key enzyme required for the lipolytic breakdown of triglycerides from LDs (219). Furthermore, non-adjacent ECs can be connected by thin membrane bridges, which form tunneling nanotubes (TNT). TNTs permit intercellular exchange of signals or various components such as ions, proteins, and organelles (FIGURE 3A). Interestingly, LDs have been shown to be a cargo of TNTs, and the extent of LD transport via TNT was increased in response to VEGF (21). Although the functional significance is yet to be validated, this observation provides evidence for a potential nutrient exchange between ECs under a pro-angiogenic cue.

With accessible FA sources in their immediate vicinity (i.e., in the blood) and equipped with various FA uptake mechanisms, it remains enigmatic why ECs express the key enzymes for de novo FA synthesis. Indeed, ECs express acetyl-CoA carboxylase and FA synthase (FASN) required for conversion of acetyl-CoA into malonyl-CoA and production of long-chain FAs (e.g., palmitate) from acetyl- and malonyl-CoA, respectively (reviewed in Ref. 221). Whether endothelial FA synthesis is used to generate lipids for membrane or signaling is not known, but endothelial FA synthesis might serve additional purposes. Indeed, FASN silencing reduces posttranslational palmitoylation and subsequent membrane localization of eNOS (see above in this section). As a result, EC sprouting (in aortic rings) is compromised while EC permeability is increased (579). Given the number of possible palmitoylation targets in ECs (580), it is tempting to speculate that FASN silencing affects additional EC functions.

Endothelial FAO plays a rather unexpected role in vessel sprouting. EC-specific deletion of carnitine palmitoyltrans-

ferase 1a (CPT1a), which imports FAs into mitochondria and thereby rate-limits FAO flux, decreases EC proliferation (not migration) and causes sprouting defects both in vitro and in vivo (481). Even though ECs have been shown to increase their FAO flux to cope with nutrient scarcity (e.g., glucose deprivation) in an AMP-activated protein kinase (AMPK)-dependent way (107), the observed sprouting defect is unlikely to be caused by energy distress given the minimal contribution (~5%) of FAO to total cellular ATP production in ECs (114, 481). By virtue of its indirect contribution to cellular NADPH production (reviewed in Ref. 220), endothelial FAO could also sustain redox homeostasis; however, CPT1a-silenced ECs do not display significant levels of redox imbalance nor oxidative stress (483). Strikingly, and contrasting cancer cell types that mainly rely on glucose and glutamine as carbon sources for TCA cycle intermediates (555), stable isotope tracing in ECs revealed that the TCA cycle intermediate citrate incorporated comparable amounts of carbons from palmitate as from glucose and glutamine (481). FAO in ECs regulates biomass synthesis and more in particular deoxyribonucleotide (dNTP) production required for DNA synthesis during EC proliferation (FIGURE 3A). Notably, this process does not rely on net replenishment (anaplerosis), but palmitate contributes to sustaining TCA cycling for biomass synthesis in conjunction with (an)other anaplerotic substrate(s) (480). Hence, endothelial CPT1a silencing depletes dNTP levels without affecting RNA levels, even though [¹⁴C]palmitate labeling showed incorporation of palmitate carbons into ribonucleotides for RNA synthesis; most probably, RNA salvage pathways sustain RNA homeostasis upon CPT1a silencing. Protein synthesis is not affected by blocking FAO either, likely again because of compensatory mechanisms. Remarkably, however, the dNTP synthesis defect was not compensated by glucose or glutamine metabolism, possibly implying specific usage of carbons from different nutrients for particular cellular processes in ECs. Also, ECs turn out to be rather unique in the use of the above metabolic pathway; out of an array of different (normal and malignant) cell types assayed, only fibroblasts show a similar use of FAO for DNA synthesis (481). One could wonder why other (especially rapidly proliferating) cells do not use this pathway given that 1 molecule palmitate can contribute 16 carbons, whereas glucose and glutamine only have a 6- and 5-carbon backbone to contribute, respectively. Perhaps, ECs sprouting into the avascular tissue rely on internal lipid sources when other nutrients become more scarce.

IV. COMPARTMENTALIZATION OF ENDOTHELIAL CELL METABOLISM

From the unicellular to multicellular level, all organisms display a complex structural and functional organization. Organs, tissues, cell types, and subcellular organelles exemplify different layers of functional specification and compartmentalization. Interestingly, spatial organization also

occurs at the metabolite level, where metabolic pathways are organized in specific intracellular compartments.

A. Glycolytic Compartmentalization

When vessels start to sprout, quiescent ECs become highly motile and face increased energy demands to support the ATP-consuming process of actin remodeling by the contractile force generating actomyosin ATPase (105). In quiescent ECs, glycolytic enzymes are detectable primarily in the perinuclear cytosol (114). In contrast, when these ECs become motile and start to form lamellipodia and filopodia to migrate, they relocate their glycolytic machinery also to these projecting cell extensions (114). In agreement, biosensing techniques reveal high levels of ATP at membrane ruffles in lamellipodia of motile ECs, which disappear upon PFKFB3 silencing, thus indicating a glycolytic origin (114). Bulky mitochondria on the other hand are excluded from these thin and motile structures, most likely because of size incompatibility (reviewed in Refs. 114, 144). Poisoning mitochondrial respiration does not affect EC sprouting, underscoring that highly localized glycolytic but not mitochondrial ATP generation primarily drives EC motility (114).

Moreover, PFKFB3 coimmunoprecipitates with β -actin and is enriched in the filamentous (F-) actin fraction in migrating versus quiescent ECs (114). Given that it is a conserved mechanism, the ability to bind glycolytic enzymes to actin during migration provides organisms (cells) an evolutionary advantage (303). By connecting with the cytoskeleton, and particularly with F-actin, glycolytic enzymes cluster into “glycolytic hubs” (FIGURE 4A). Such multienzymatic complexes (also known as metabolons) offer several advantages: 1) increased catalytic efficiency by channeling intermediary metabolites from one enzyme to the next neighbor, 2) increased kinetic constant, 3) enhanced coordination of enzymatic actions in the same pathway, 4) retention of potentially toxic metabolic intermediates, 5) circumvention of enzymatic inhibition or degradation, and 6) prevention of ATP depletion from other cellular subcompartments (11, 71, 356). As such, in erythrocytes and skeletal muscle, the association with F-actin increases the flux through aldolase and promotes the tetrameric conformation of PFK (454, 569). Furthermore, increasing glycolysis-derived ATP production on the same spot of high demand prevents the cell from suffering global (possibly life-threatening) ATP depletion. Noteworthy, in mammary epithelial MCF10A cells, insulin disrupts the actin cytoskeleton and thereby releases aldolase from its F-actin-bound state. This PI3K signaling-driven mechanism procures sufficient levels of cytosolic aldolase and glycolytic activity to meet the cell’s demand for macromolecule synthesis during increased growth and possibly involves fueling the non-oxPPP for biomass synthesis (240). If and to which extent a similar mechanism is also present in ECs remains to be determined.

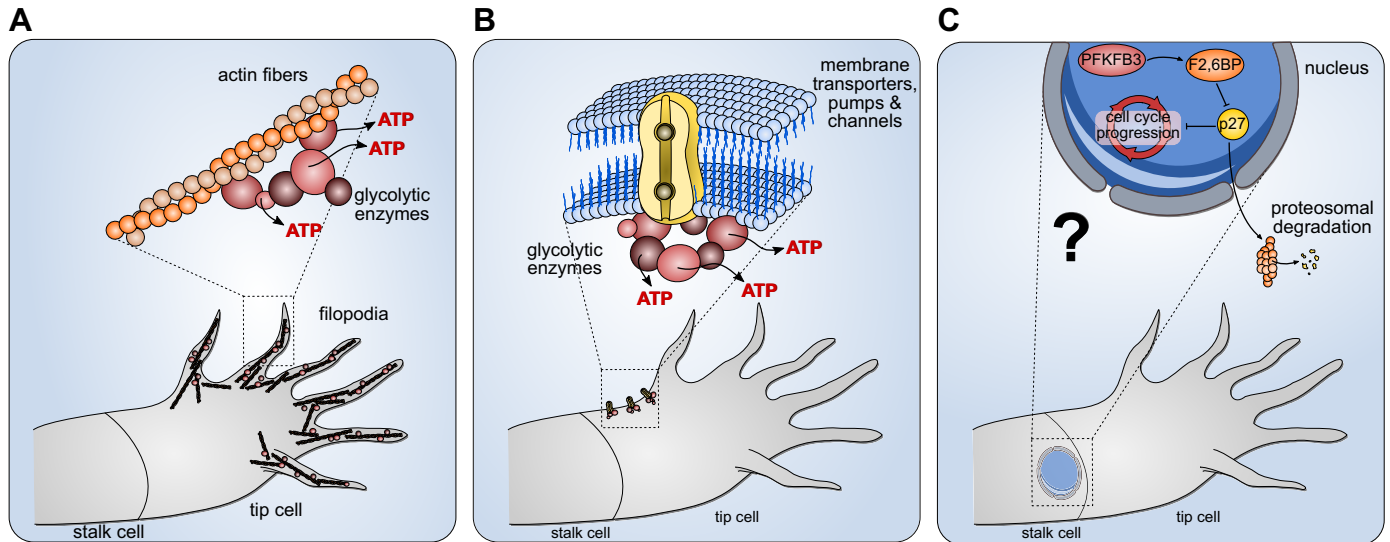


FIGURE 4. Glycolytic compartmentalization in ECs. Glycolytic enzymes and glycolytic activity in quiescent ECs are primarily located in perinuclear regions (not shown in figure) but additionally compartmentalize with highly specific cellular structures or components to locally generate ATP or to perform other functions. **A:** motile ECs colocalize glycolytic enzymes such as PFKFB3 with F-actin fibers in migratory structures like filopodia and lamellipodia. This allows rapid and on-the-spot generation of the energy required by these structures to drive cellular movement and bypasses the need for mitochondria that are too large to fit inside these specialized structures. **B:** membrane-located transporters, pumps, and channels require ATP to function. This ATP can be delivered in situ by colocalizing glycolytic enzymes. **C:** in other cell types, PFKFB3 is also present in the nucleus to locally produce F2,6BP which enhances phosphorylation and subsequent proteasomal degradation of the Cdk inhibitor p27^{Cip/Kip}; as a result, cellular proliferation is increased. Whether this also occurs in ECs remains unknown. PFKFB3, 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase-3; F2,6BP, fructose-2,6-bisphosphate; p27, cyclin-dependent kinase inhibitor 1B.

Compartmentalization of glycolytic enzymes is not a sole privilege of the actin cytoskeleton. Fast axonal transport of vesicles in neurons requires large amounts of ATP to fuel the molecular motors (dynein, kinesin) that drive vesicle movement (632). Intriguingly, this process too does not rely on mitochondrial respiration but requires the activity of the glycolytic enzyme GAPDH. In a huntingtin-dependent manner, GAPDH associates with the vesicles and provides on-board energy (ATP) for vesicle transport (632). Interestingly, in ECs, glycolytic ATP is required for VE-cadherin endocytosis and thus remodeling of cell-cell junctions (66). Whether a similar compartmentalization of glycolytic enzymes occurs on VE-cadherin containing endocytic vesicles in ECs remains to be determined. Glycolytic hubs also coexist with and directly supply ATP to membrane ion transporters and pumps (Ca^{2+} -ATPase and Na^{+} - K^{+} -ATPase), exchangers ($\text{Na}^{+}/\text{H}^{+}$), and channels (ATP-sensitive K^{+}) in vascular and other cell types (reviewed in Ref. 120) (FIGURE 4B). The above data suggest that mitochondrial oxidative phosphorylation is crucial to maintain long-term steady-state metabolism, whereas local, and short-term, high-energy demands are met by compartmentalized glycolysis (155, 500).

In addition to its lamellipodial compartmentalization, PFKFB3 has also been shown to localize in the nucleus. Two specific carboxy-terminal lysines (K472; K473) are involved in PFKFB3's nuclear localization. Even though this

nuclear PFKFB3 generates F2,6BP within the nucleus and activates PFK1, it does not lead to an increase in glycolytic flux (613, 614). Instead, F2,6BP enhances cyclin-dependent kinase (Cdk)-mediated phosphorylation of the Cdk inhibitor p27^{Cip/Kip} (a potent blocker of G₁-to-S cell cycle phase transition) leading to its proteasomal degradation; as a result, cellular proliferation is increased (613). F2,6BP within the nuclear compartment reflects the rate of glucose uptake and might thus translate glucose availability into cell proliferation. Whether nuclear F2,6BP is also important for the proliferation control of glycolysis-addicted ECs remains unknown (FIGURE 4C). One could hypothesize that, in line with the high expression of PFKFB3 in malignant cells (79), tumor-derived ECs (see sect. VIII) in particular may have high nuclear PFKFB3 expression to connect glycolytic flux to high cell proliferation rates.

B. The Arginine Paradox: A Matter of Compartmentalization?

As outlined above, eNOS-mediated production of NO makes arginine metabolism a highly studied topic, mostly because of its direct link with the pathophysiology of atherosclerosis (see sect. VII). Also, endothelial arginine metabolism features an intriguing yet controversial compartmentalization. In order of abundance, eNOS predominantly localizes to specific microdomains of the plasma

membrane (including caveolae and lipid rafts), the *cis*-Golgi and then the cytosol, nucleus, and mitochondria (77). The same ranking holds for the enzyme's activity with a 9- to 10-fold increased activity in caveolae over the EC plasma membrane, and a 7-fold increased activity in plasma membrane fraction over the cytosolic fraction (493). Further underscoring the location-activity relationship is the reduction in NO production in intact HEK 293 cells expressing a palmitoylation- and myristoylation-defective eNOS mutant (abolishing its sequential localization to Golgi and caveolae), while this mutant proved catalytically competent in cell-free assays (491). Intriguingly, in ECs, eNOS interacts at the plasma membrane with the arginine transporter CAT-1 (SLC7A1) and with ASS and ASL, both enzymes involved in recycling arginine from citrulline (reviewed in Ref. 77). This is suggestive of another endothelial metabolite channeling (*cfr* glycolysis), whereby substrate (arginine) delivery from extracellular sources (CAT-1), conversion of substrate to end product (NO by eNOS), and recycling of end product (NO) into substrate (arginine by ASS, ASL) are spatially clustered.

Arginases on the other hand compete with eNOS for arginine and are mainly localized in the cytosol (arg I) or mitochondria (arg II), distant from the major site of eNOS activity (258, 380). Despite evidence showing decreased NO production upon arginase overexpression and, conversely, induction of NO synthesis after arginase inhibition, this seemingly logical one to one equation gets troubled when one takes substrate concentrations and enzyme kinetics into account. ECs in culture have intracellular arginine levels ranging from 0.1 to 0.8 mM, which would amply suffice to guarantee near-maximal eNOS activity given eNOS' high arginine affinity ($K_m = 1\text{--}5\ \mu\text{M}$). Arginase has a rather low affinity for arginine ($K_m = 1\text{--}20\ \text{mM}$); simple comparison of the K_m values precludes efficient competition between both enzymes for the substrate they share. A possible explanation for the above competition has been proposed to relate to the higher catalysis rate (V_{\max}) of arginase than eNOS (475); similarly, in activated macrophages arginase has a higher V_{\max} than iNOS (378). The above numbers reveal another feature of endothelial arginine/eNOS metabolism, commonly known as the "arginine paradox": even though under physiological conditions, eNOS would be fully saturated with intracellular arginine levels, both in vitro and in vivo data show that increasing extracellular arginine further induces NO production.

C. Compartmentalization of Reducing Power

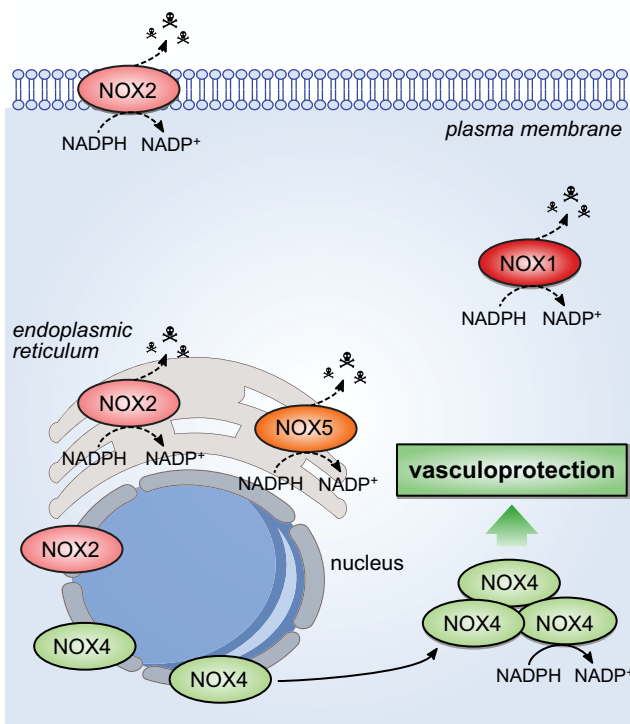
NADPH provides reducing power in different cellular compartments, yet the NADPH pool is rather limited, certainly in light of the high fluxes through pathways that use it [$\pm 25\%$ of all reactions listed in the KEGG database involve the use of NAD(P)H (403)]. Remarkably, none of the NAD(P)H forms is known to be transported across intracellu-

lar membranes, which suggests a highly optimized compartmental organization (392, 434). Two distinct subcellular pools of NADPH have been documented: cytosolic NADPH regenerated by the oxPPP and the mitochondrial fraction (434). While not fully established yet, NADPH compartmentalization is likely to occur in ECs too. A recently developed method with deuterium (^2H)-labeled metabolites to trace hydrogen in compartmentalized reactions that use NADPH as a cofactor, would allow more detailed analysis of the different NADPH pools in ECs (315).

Further evidence for NADPH compartmentalization in ECs derives from the finding that the endothelial NADPH oxidase (NOX) system is compartmentalized. NOXs use NADPH to produce ROS, and the human vasculature expresses isoforms NOX1, NOX2, NOX4 (predominant isoform in ECs), and NOX5, which are sources of ROS in the vessel wall (130, 367). NOX expression is induced by an armamentarium of signals including proinflammatory cytokines, growth factors (i.e., VEGF, thrombin), hypoxia, hyperglycemia (see sect. VII), elevated FFA levels, and atheroprone-perturbed shear stress (see sect. VII) (123, 204, 244, 248, 367, 492, 504). While NOX1, 2, and 5 increase oxidative stress and reduce NO bioavailability and promote EC dysfunction (see sect. VII), NOX4-produced H_2O_2 can have a vasoprotective role by maintaining endothelial function (see sect. VII and **FIGURE 5**) (300). It is not entirely uncommon for moderate endothelial ROS levels to have a beneficial rather than a detrimental effect in angiogenesis. The pro-angiogenic VEGF stimulus uses ROS as signaling molecules downstream of VEGFR2, a phenomenon involving PI3K and Rac1 activity as upstream regulators (89). ROS can also mediate angiogenesis by VEGF-independent mechanisms, for example, through the oxidation of lipids, thereby generating pro-angiogenic species (e.g., ω -carboxyethylpyrrole), or by activating ataxia-telangiectasia mutated kinase, which promotes pathological angiogenesis (275). Under physiological conditions, NOX2 is mainly expressed in the membranes of the nucleus and ER at relatively low levels, to contribute to intracellular redox signaling pathways (130). In contrast, under diseased conditions, NOX2 mainly associates in clusters at the plasma membrane, generating excess levels of (extracellular) superoxides (130) (**FIGURE 5**). In normoxic human pulmonary arterial ECs, NOX4 mainly resides in the nucleus; strikingly, hyperoxia-induced motility and tube formation in these cells depends on NOX4-generated ROS and is accompanied by increased levels of cytoplasmic NOX4 (427).

Whether metabolite channeling is broadly conserved and generally applies to metabolic pathways is currently unknown, but is definitely important to better apprehend the fine-tuned regulations of metabolic fluxes in ECs. However, setting up the required and relevant in vitro models to study this aspect of EC metabolism is a highly challenging endeavor (138).

PHYSIOLOGICAL CONDITIONS



PATHOLOGICAL CONDITIONS

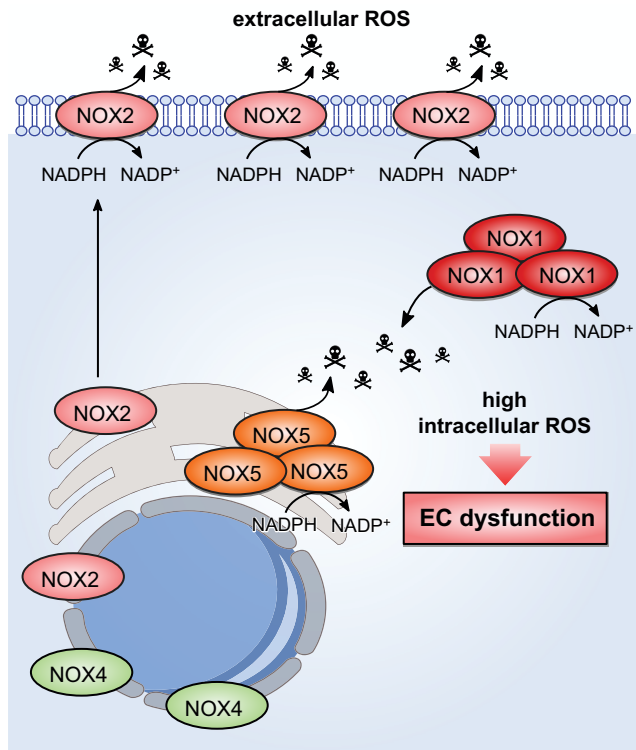


FIGURE 5. Compartmentalization of NOX activity in ECs. Schematic and simplified overview of the role and subcellular localization of different NADPH oxidases (NOX) in ECs under normal conditions (*left panel*) and pathological conditions (*right panel*). Note that, in contrast to other NOXs, NOX4 activity can have vasculo-protective actions. More details on the role of NOXs in ECs are discussed in the main text. NADPH, nicotinamide adenine dinucleotide phosphate; NOX, NADPH oxidase; ROS, reactive oxygen species, represented in the figure by skull and crossbones.

V. CHANGES IN METABOLISM DURING ENDOTHELIAL CELL DIFFERENTIATION

During vertebrate development, after fertilization, the vascular system is one of the first organ systems to form, ensuring rapid delivery of nutrients and oxygen to tissues in the growing embryo. In contrast to angiogenesis, which involves the formation of new blood vessels from preexisting ones as a result of the balance of pro- and anti-angiogenic signals, vasculogenesis occurs from the de novo formation of a primary capillary plexus from mesodermal cell precursors (see sect. II).

Changes in cellular metabolism of stem cells have been described to be modulated in a number of ways: 1) extrinsic signals such as growth factors and cytokines or intrinsic signals such as transcription factors and signaling pathways can direct changes in cell cycle and differentiation, leading to changes in metabolic demand (i.e., for biosynthesis of building blocks) and metabolic flux (i.e., signal-mediated activation of metabolic pathways); 2) differentiation leads to parallel changes in metabolic enzyme expression/activity, leading to metabolic rewiring reflected by altered metabolic demands of differentiated cells; and 3) changes in metabolic flux lead to alterations in the activation of signaling path-

ways, epigenetic modifications, and the availability of metabolites as substrates or “signals” (5).

Embryonic and induced pluripotent stem cells have been reported to have higher rates of glycolysis compared with more differentiated cells such as cardiomyocytes and fibroblasts. It is believed that stem cells are preferentially glycolytic due to an immature mitochondrial network, with few mitochondria and reduced oxidative capacity (157, 438).

ECs and the vascular system develop from the mesoderm. Soon after gastrulation, signals from the visceral endoderm pattern the underlying mesoderm to form the mammalian extraembryonic yolk sac (35, 564). As described above, VEGFR2 is a key signaling receptor in ECs (402), and VEGFR2-positive mesodermal progenitor cells can serve as vascular progenitors (617). Metabolic traits of progenitors during differentiation need further characterization, but seem to be dynamic. VEGFR2-positive mesodermal progenitor cells have lower oxygen consumption rates than their VEGFR2-negative counterparts, and temporarily undergo suppression of (glucose) metabolism during mesoderm differentiation (647). Of note, a more oxidative-prone metabolism has been described to sustain embryonic stem cell differentiation (619). It is not clear if and to what extent

this also occurs during differentiation towards ECs which, as mentioned above, are highly glycolytic and rely on PFKFB3-driven glycolysis for generation of ATP (114). This would mean that in the further differentiation from the mesoderm lineage to ECs, the cellular metabolism switches back from oxidative to glycolysis. Furthermore, the exact transcriptional regulators that control this effect during differentiation remain to be determined. However, key regulators of endothelial function might be prime candidates such as the VEGF-VEGFR2 signaling axis (114, 128) in proliferating ECs and the Dll4-Notch (268) and FoxO1-MYC (586) signaling pathways in quiescent ECs.

Human and mouse embryonic stem cells can be differentiated to ECs *in vitro* (199, 314). Furthermore, arterial versus venous EC differentiation is possible (509), as well as differentiation to lymphatic ECs (323) (see sect. VI). These *in vitro* models would be useful to determine the exact molecular controls for the changes in EC metabolism during their differentiation.

VI. ENDOTHELIAL CELL HETEROGENEITY, REFLECTED BY DIFFERENCES IN METABOLISM?

ECs are found throughout all tissues of the body and are comprised of three main systems: arterial (delivering oxygen-rich blood and nutrients to tissue), venous (removing deoxygenated blood and waste products from tissues), and lymphatic (involved in the regulation of interstitial fluid balance, serving as a route for immune cell extravasation and regulation of intestinal lipid uptake via the lacteals) (2). The further differentiation into specialized arterial, venous, and lymphatic subtypes is driven by a combination of environmental, mechanical, and transcriptional factors (348).

EC metabolism is emerging as a determining factor in these processes too.

Arteriovenous differentiation is controlled in part by Notch signaling (540), which has also been reported to modulate EC metabolism (268). While a molecular signature of key transcription factors involved in arterial specification (Prdm16, ROX2, NKX2.3, EMX2, MSX1, Sox17, Hey2, Aff3) was recently reported, transcriptomic data suggest increased expression of the glucose transporters GLUT1/GLUT3 in human umbilical arterial ECs (15). However, these arterial ECs have been reported to have a similar glycolytic flux as their venous EC (114, 591) counterparts and, conversely, PAECs have even been shown to have lower glucose consumption rates than PMVECs (see sect. III) (423). These seemingly contradictory findings might further exemplify the metabolic heterogeneity of ECs residing in different tissues. FAO flux may be higher in arterial than in venous ECs (481) but exactly which signals regulate increased FAO flux in arterial ECs remains unknown. Possible candidates involve other key factors and phenomena regulating arterial EC phenotypes such as flow/shear-stress as well as vasoactive and growth factor/signaling interactions with smooth muscle cells (SMCs) (i.e., PDGF-B/D, PDGFR β , Ang1/Tie2, S1P, transforming growth factor- β , Notch, Eph/ephrin, connexin) (324). In other cell types, loss of Prdm16 results in mitochondrial fragmentation and decreased oxidative phosphorylation (88, 124, 334), but the exact link between Prdm16 and cellular metabolism in ECs remains largely unstudied.

As mentioned above, specification into tip or stalk cells also entails differences in EC metabolism (FIGURE 6A). Lowering glycolytic flux through PFKFB3 silencing compromises both tip cell competitiveness and stalk cell proliferation

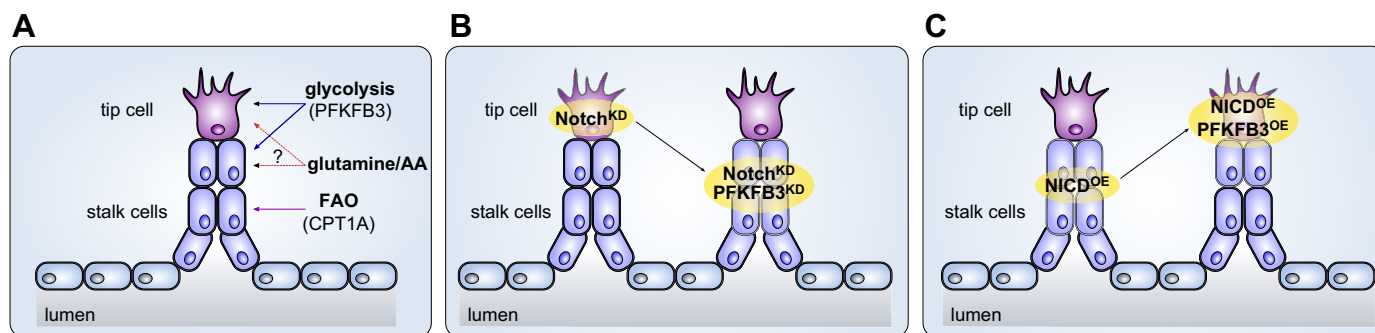


FIGURE 6. Metabolic heterogeneity in tip versus stalk cells. *A*: endothelial tip and stalk cells display differences in metabolic wiring. PFKFB3-driven glycolysis sustains both tip cell competitiveness and stalk cell proliferation, whereas CPT1a-mediated FAO is crucial for stalk cell proliferation but not for tip cell behavior. If and how other metabolic substrates like glutamine (or AAs by extension) drive either tip or stalk cell behavior, or both, requires further study. *B*: EC metabolism can override genetic tip versus stalk cues. ECs that have been genetically instructed to adopt tip cell behavior by silencing of Notch revert to a stalk cell phenotype upon simultaneous silencing of PFKFB3. *C*: conversely, overexpression of PFKFB3 provokes tip cell behavior, even in ECs that receive a strong genetic pro-stalk cue from NICD overexpression. PFKFB3, 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase-3; AA, amino acids; FAO, fatty acid oxidation; CPT1a, carnitine palmitoyl-transferase 1a; KD, knock-down; OE, overexpression; NICD, Notch intracellular domain.

(114). Remarkably, the defect in tip cell behavior is maintained under a strong pro-tip cell cue created by simultaneous Notch knock-down (FIGURE 6B). Conversely, ECs that were instructed to assume stalk cell behavior by overexpression of NICD regained tip cell behavior upon overexpression of PFKFB3, even in vivo (114) (FIGURE 6C). Inhibition of endothelial FAO (see sect. III) selectively affects stalk cell proliferation without impeding tip cell behavior (481). These data imply the existence of a tip versus stalk metabolic signature acting in parallel or even overriding genetic instructions. Whether and how metabolic pathways, other than glycolysis and FAO, complete this metabolic signature needs further research (FIGURE 6A). Nearly nothing is known about how amino acid metabolism, glutamine metabolism in particular, differs between tip and stalk cells. In T-ALL cells, Notch signaling supports growth by promoting glutamine metabolism and injection of glutamine-derived carbons into the TCA cycle (227). Whether Notch, as a pro-stalk cue, has similar effects on glutamine metabolism in ECs is not fully understood. In case tip and stalk ECs feature different glutamine metabolism-related traits, it will be of key importance to determine if glutamine metabolism and genetic signals co-define the tip-stalk identity (as is the case for PFKFB3).

Lymphatic EC (LEC) differentiation in vertebrates occurs primarily from venous ECs (VECs) (12), although some lymphatic beds develop from non-venous EC origins (278, 351, 391, 511), and is mainly driven by VEGF-C/VEGFR3 signaling and the transcription factors Sox18 (177) and prospero homeobox protein 1 (Prox1) (238, 431, 585, 624). Lymphatic biology is less well studied than blood vascular biology and only most recently was the first characterization of LEC metabolism performed (591). LECs have higher FAO flux compared with venous or other vascular ECs, and the VEGF-C/VEGFR3 signaling axis is important in the activation of FAO (591). Furthermore, Prox1, a transcription factor which is essential for LEC differentiation and maintenance of LEC identity (431), binds the CPT1a (rate-controlling in FAO, see sect. III) promoter. The resulting upregulation in FAO is required for Prox1-mediated VEC-to-LEC differentiation through the regulation of lymphatic gene expression, particularly VEGFR3 (591). Strikingly, this Prox1-mediated increase in FAO affects LEC differentiation and function, not via the regulation of energy or redox homeostasis, but rather through the production of acetyl-CoA, which fuels epigenetic modifications (histone acetylation) preferentially at lymphatic genes over blood vascular genes (591). This specificity stems from the interaction of the histone acetyltransferase p300 with Prox1, which specifically binds promoters of genes involved in lymphangiogenesis. These novel findings extend the dogmatic view that only transcription and growth factors regulate VEC-to-LEC differentiation, and now show that Prox1 not only functions as a transcription factor solely driving pure lymphangiogenic genes, but is

also driving FAO and acetyl-CoA production to sustain histone acetylation of its target genes (591) (FIGURE 7). Since histone acetylation makes the promoter region of these target genes more accessible to transcription factors, Prox1 enhances its own transcriptional effect to induce LEC differentiation by “hijacking” FAO metabolism through this epigenetic mechanism.

Even though the role of epigenetics in EC differentiation was previously recognized [for example, histone demethylation at the VEGFR2 and VE-cadherin promoter in the differentiation of embryonic stem cells to ECs (597)], the involvement of specific metabolic pathways herein remains unclear. As such, the above findings provide evidence for FAO-mediated regulation of histone acetylation in cellular differentiation, whereas glucose metabolism and other pathways have been previously shown to impact histone acetylation in other cell types (306, 362, 382, 582). Although LECs have lower levels of glycolytic flux compared with VECs or other blood vascular EC types (591), the role of glycolysis and other metabolic pathways in LEC activation and function remains to be explored.

Of note, LECs also utilize FAO to regulate nucleotide synthesis for proliferation (591), akin to blood vascular ECs (see sect. III). Also, the effect of FAO to upregulate VEGFR3 in LECs renders these cells more responsive to the promigratory effect of VEGF-C (342), the ligand activating VEGFR3, possibly explaining why silencing of CPT1a impairs LEC migration. These combined effects may explain why selective loss of CPT1a in LECs causes lymphatic defects during embryonic development and why pharmacological blockade of CPT1 by etomoxir treatment inhibits pathological injury-induced lymphangiogenesis (591). The therapeutic implications of these seminal findings are discussed in more detail further below.

Investigation of the metabolic characteristics of other organ-specific vascular beds is still in its infancy, although one would expect a degree of vascular specialization in accordance with the differences in local microenvironments of such specialized tissues as the heart, brain, liver, kidneys, etc. Indeed, transplantation of “generic” ECs into various tissues results not only in engraftment, but these ECs also acquire some features of organotypic ECs (393), raising the question whether organ-specific features may also alter the metabolic properties of these specialized ECs. For example, it was recently demonstrated that Meox2/Tcf15 heterodimers program heart capillary endothelium for cardiac FA uptake (93), which is important in regulating the transport of FFAs and very-low-density lipoprotein (VLDL) across the endothelium to provide FAs for cardiac energy metabolism. Future efforts directed towards the characterization and understanding of the metabolic characteristics of organotypic EC types could pave the way for tailored therapeutics in specific vascular beds.

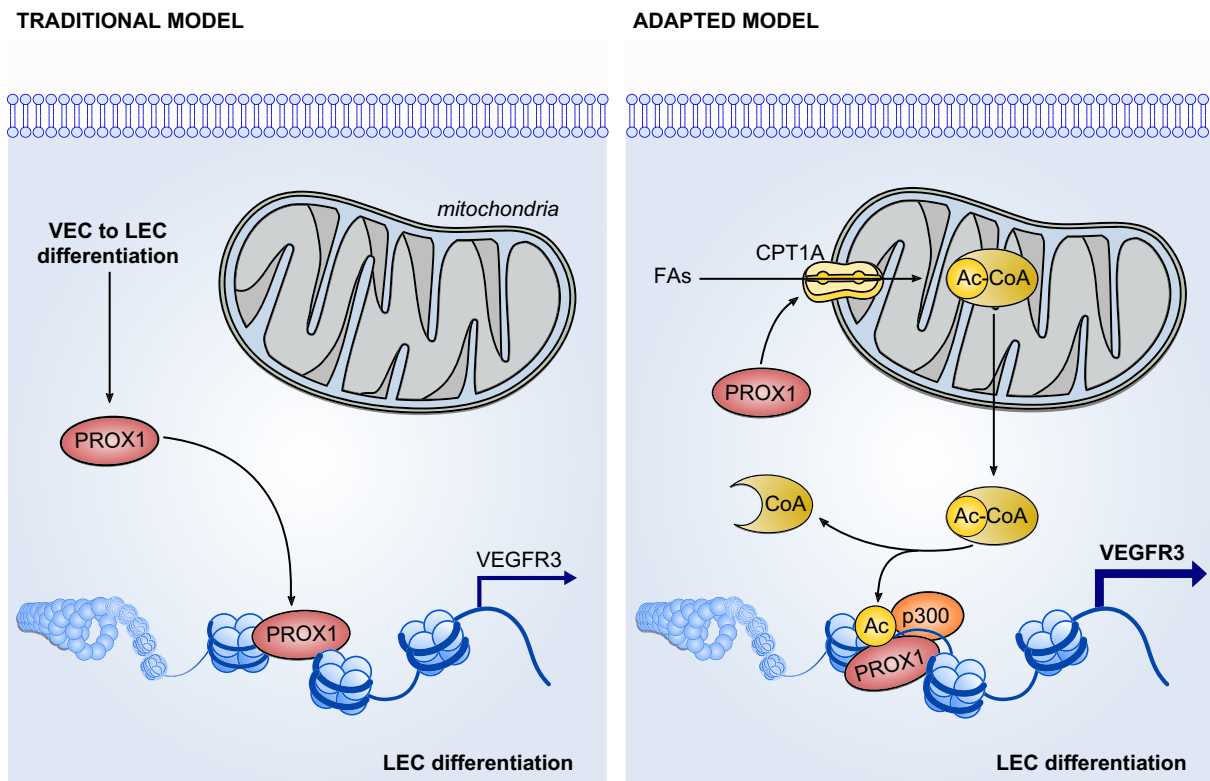


FIGURE 7. Novel role for fatty acid oxidation in differentiation of lymphatic ECs. The dogmatic view on lymphangiogenesis states that at the onset of VEC to LEC differentiation, the transcription factor Prox1 induces the expression of typical lymphangiogenic genes such as VEGFR3. In light of recent findings, this traditional model has been adapted and refined. The binding of Prox1 in the promoter region of lymphangiogenic genes involves an interaction between Prox1 and the histone acetyltransferase p300 to acetylate histones and remodel chromatin. The required acetyl groups are supplied by acetyl-CoA which derives from CPT1a-mediated fatty acid oxidation. Prox1 directly induces the expression of CPT1a to enhance fatty acid oxidation flux. As such, the transcription factor Prox1 teams up with central metabolism to drive lymphatic differentiation. VEC, venous endothelial cell; LEC, lymphatic endothelial cell; Prox1, prospero homeobox protein 1; VEGFR3, vascular endothelial growth factor receptor 3; FAs, fatty acids; CPT1a, carnitine palmitoyltransferase 1a; Ac, acetylated; Ac-CoA, acetyl coenzyme A.

VII. ENDOTHELIAL CELL METABOLISM IN VASCULAR DISORDERS: ENDOTHELIAL CELL DYSFUNCTION

In healthy individuals, the endothelium maintains vascular tone, structure, and homeostasis. In contrast, EC dysfunction results in the development of several pathologies, including diabetes and atherosclerosis (a frequent complication of diabetes). Metabolic aberrations in ECs can mediate vascular complications associated with the pathogenesis of the above-mentioned disorders.

A. Diabetes and the Endothelium

Diabetes has a high and incessantly increasing prevalence of 8.8% globally (in adults, in 2015) (250a). Diabetes is hallmarked by hyperglycemia [excessive levels of blood glucose, attributable to a deficiency of (type 1) or resistance to (type 2) insulin], which contributes to EC dysfunction. The EC dysfunction arises early and plays a key role in the

pathogenesis of diabetes-associated micro- and macrovasculopathies. Moreover, it causes the acceleration of atherosclerosis (33, 61, 479, 603) (see below in this section). While diabetic EC dysfunction tilts the physiological balance towards vasoconstrictive, proinflammatory, and prothrombotic effects, the resulting vascular disease phenotype can be paradoxically tainted by either excessive or impaired angiogenesis (282, 285, 350, 604). Excessive angiogenesis contributes to diabetic retinopathy, early stage nephropathy, and atherosclerotic plaque destabilization. Insufficient angiogenesis, on the other hand, plays a role in macrovascular disorders (coronary artery disease, peripheral vascular disease, and ischemic stroke), impaired wound healing and skin ulcers (diabetic foot ulcers), embryonic vasculopathies, and transplant rejection in diabetic subjects. Lastly, peripheral neuropathy is a microvasculopathy linked to reduced nutritive blood flow (secondary to diabetes) to the sensory nerve fibers (512).

The integrity of the endothelium is also highly dependent on endothelial repair and regeneration, which are partly co-

determined by migration and proliferation of surrounding mature vessel wall-resident ECs. Circulating bone marrow-derived endothelial progenitor cells (EPCs) may also contribute to endothelial regeneration and mitigate EC dysfunction (20, 142, 233, 453). Diabetic patients present with reduced numbers of circulating EPCs, which are linked to reduced endothelial regeneration and to the severity of peripheral vascular disease and as such may serve as a biomarker of vasculopathy in diabetic patients (146, 158, 202, 247, 330, 466, 536). Rather than hyperglycemia, (pre-diabetic) insulin resistance (see below in this section) is suggested to be the culprit in adversely affecting EPC-mediated repair (103, 385, 447).

The time and severity of exposure to hyperglycemia highly influences the progression of diabetes-associated vasculopathies (10, 263). In early intervention studies, reduction of hyperglycemia decreases the development and progression of micro- and macrovascular complications (388a, 514, 549a, 593). However, the efficacy of glycemic control in patients with long-standing hyperglycemia is less pronounced for macrovascular complications, and very stringent glycemic control (via insulin treatment) can even aggravate cardiovascular disease (1, 4, 136, 183). This indicates that in long-term diabetic patients, besides an aberrant metabolic memory (see sect. IX), additional factors such as insulin resistance and dyslipidemia may also play a dominant role in the development of diabetic vasculopathies. Here below, we focus on the effects of hyperglycemia and

insulin resistance on EC metabolism and how this leads to EC dysfunction (FIGURE 8). Many of the reports discussed below are observations from in vitro experiments; while these have shed light on underlying mechanisms, in vivo verification is necessary in the prospect of clinical translation.

B. Hyperglycemia

1. Hyperglycemia and cytosolic/mitochondrial ROS

Hyperglycemia-induced increases in endothelial cytosolic ROS levels mainly derive from NADPH oxidases (NOXs; see sect. IV) via the protein kinase C (PKC)-dependent pathway (130, 213), from endothelial xanthine oxidase (27, 118, 359, 465) and from eNOS uncoupling (see sect. IV). Both veins and arteries of diabetic coronary artery bypass patients show increased levels and activity of NOX protein subunits (p22phox, p67phox, p47phox), which are normalized by PKC inhibition (213). Endothelial xanthine oxidase, one of the two isoforms of xanthine oxidoreductase (a key enzyme in purine metabolism) is another enzymatic source of ROS linked to diabetic vascular disease, causing vascular inflammation and atherogenesis (27, 118, 359, 465). A recent metabolomics study confirmed that hyperglycemia-induced elevated levels of xanthine oxidase and perturbed purine metabolism promote diabetic nephropathy in streptozotocin (STZ)-treated diabetic rats (326).

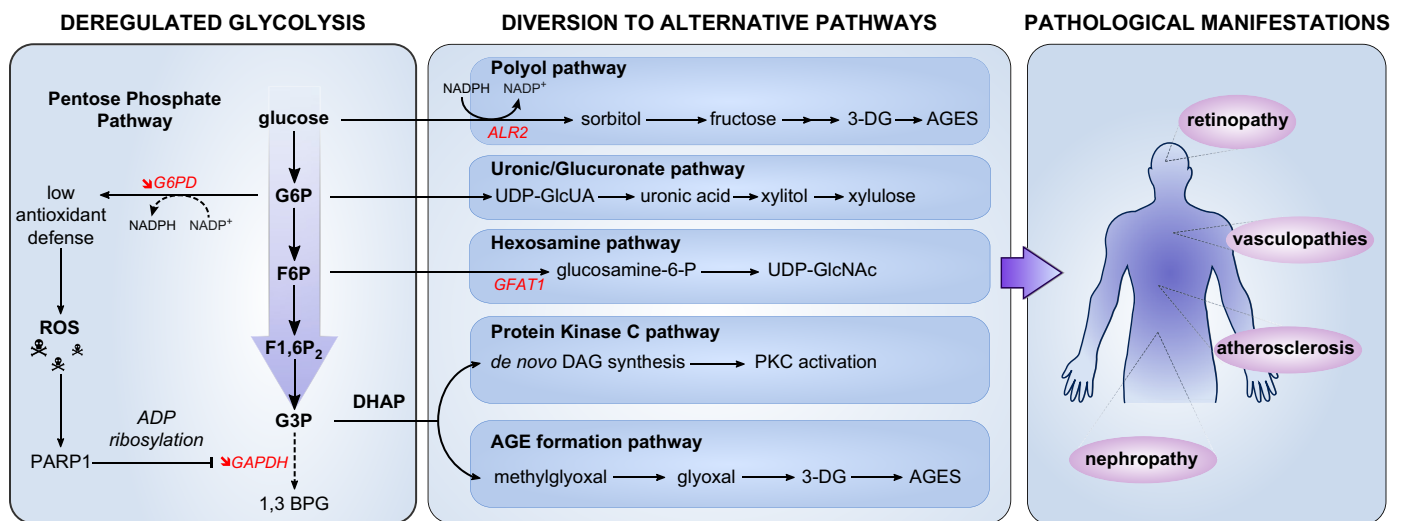


FIGURE 8. Pathological glycolytic side branches in hyperglycemic dysfunctional ECs. In diabetic ECs, hyperglycemia-induced ROS accumulation (for example caused by impairment of G6PD-mediated PPP flux) causes glycolysis to stall at GAPDH. Upstream glycolytic intermediates pile up and are diverted into pathological glycolytic side branches giving rise to further increases in ROS levels and the formation of noxious AGEs all contributing to the different vascular disease manifestations. 1,3BPG, 1,3-bisphosphoglycerate; 3-DG, 3-deoxyglucosone; ALR2, aldose reductase 2; AGES, advanced glycation end products; DAG, diacylglycerol; DHAP, dihydroxyacetone phosphate; F1,6P₂, fructose-1,6-bisphosphate; F6P, fructose-6-phosphate; G3P, glyceraldehyde-3-phosphate; G6P, glucose-6-phosphate; G6PD, glucose-6-phosphate dehydrogenase; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GFAT1, glutamine fructose-6-phosphate amidotransferase; glucosamine-6-P, glucosamine-6-phosphate; NADPH, nicotinamide adenine dinucleotide phosphate; PARP1, poly-ADP-ribose polymerase 1; PKC, protein kinase C; UDP-GlcUA, UDP-glucuronic acid; UDP-GlcNAc, uridine diphosphate *N*-acetylglucosamine.

Likewise, eNOS uncoupling was shown to contribute to EC dysfunction in diabetic mouse models (63, 476, 523), and to mediate peripheral neuropathy in Zucker diabetic rats (496). The increase in eNOS uncoupling-derived oxidative stress in diabetic vessels was alleviated by BH₄ supplementation (213). Mechanisms contributing to eNOS uncoupling-derived oxidative stress in diabetes include interrupted metabolism of arginine and cofactors BH₄ and NADPH, resulting in their decreased availability, endothelial insulin resistance (203, 217, 251, 446, 498), aberrant O-glycosylation (24, 134, 165), increased levels of advanced glycation end products (AGEs) (515, 516), and hyperglycemia-induced restriction of PPP flux (310, 638) (see below in this section; **FIGURE 8**).

High intracellular glucose levels in ECs also cause mitochondriopathy featuring dysfunctional mitochondrial biogenesis and autophagy (causing damaged mitochondria to pile up), impaired mitochondrial function, and increased mitochondrial fission (reviewed in Refs. 420, 469, 495). In general, increased fission is associated with mitochondrial ROS production, while reducing mitochondrial DNA content and the activity of metabolic processes, including the ETC and ATP synthesis. The hyperglycemia-induced mitochondrial fission is driven by rho-associated protein kinase (ROCK)-1-mediated dynamin-related protein-1 (Drp1) recruitment to the mitochondria, previously established as a key event in fission (572). Since healthy mitochondria in ECs are presumably important for Ca²⁺ homeostasis, to generate physiological ROS levels, and to initiate apoptosis (with energy production relying primarily on glycolysis), dysfunctional mitochondria may promote EC dysfunction or apoptosis through Ca²⁺ overload or by exacerbating oxidative stress (529).

In health, damaging insults, such as oxidative stress, are often counterbalanced by protective (antioxidant) mechanisms to maintain vascular homeostasis; these are especially important for quiescent ECs that are continuously exposed to a high oxygen environment in the peripheral blood. The metabolic regulators peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC1 α), AMP-activated protein kinase (AMPK), and NF-E2-related factor-2 (Nrf2) are candidates to counter hyperglycemia-induced ROS. For instance, NO mediates ROS protection via up-regulation of PGC1 α (50, 325), and PGC1 α regulates mitochondrial antioxidant defenses in ECs (552). However, the effects of high glucose on these molecular orchestrators are complex and contextual, since high glucose induces endothelial PGC1 α expression, blunting activation of eNOS, and impairing EC migration and vasculogenesis; moreover, the antioxidant N-acetylcysteine (NAC) blocks the induction of PGC1 α (478).

Pharmaceutical activation of AMPK in ECs can alleviate oxidative stress in hyperglycemic ECs. For instance, rosigli-

tazone (PPAR γ agonist that activates AMPK) reduces NOX activity in hyperglycemic ECs (72). Activation of AMPK by metformin or 5-aminoimidazole-4-carboxamide-riboside (AICAR) also alleviates oxidative stress by inducing mRNA expression of manganese superoxide dismutase (MnSOD; with mitochondrial antioxidant function) (574) and inducing mitochondrial biogenesis via PGC1 α (294), although it remains unclear how the latter process alleviates oxidative stress (possibly via replacing damaged ROS-producing mitochondria with new healthy ones). This overall beneficial effect has been confirmed in vivo: EC-specific AMPK activation prevented diabetes-induced EC dysfunction (317).

Nrf2 is considered to play a prominent role in the maintenance of structural and functional integrity of mitochondria, and to be a principal regulator of cellular redox homeostasis (125). In ECs exposed to hyperglycemia, Nrf2 regulates the activity of antioxidant enzymes such as glyoxalase I (GLO1; key enzyme in detoxifying methylglyoxal, see below in this section) (611). There is even evidence of cross talk between Nrf2 and AMPK resulting in the prevention of cardiomyopathy in diabetic mouse models (373, 575, 639). Despite these promising findings, outcomes of clinical trials using antioxidant therapies have been rather disappointing (309).

2. Hyperglycemia and diversion of glycolytic intermediates into alternative metabolic pathways

In the nucleus, elevated levels of ROS and reactive nitrogen species contribute to the activation of the DNA repair mechanism enzyme poly(ADP-ribose) polymerase 1 (PARP1) upon hyperglycemia-induced DNA single-strand break formation, resulting in subsequent inhibition of GAPDH through PARP1-dependent ribosylation and intracellular NAD⁺ depletion (119, 133, 135). GAPDH is a key glycolytic enzyme whose activity is essential for maintaining glycolytic flux. As such, GAPDH inhibition stalls glycolysis, and accumulated upstream glycolytic intermediates subsequently divert into several alternative metabolic pathways (**FIGURE 8**) known to be altered in ECs by glucotoxicity: 1) the polyol pathway, 2) the glucuronate cycle, 3) the HBP, and 4) the glycation pathway. Competitive PARP1 antagonists, inhibiting PARP1 activity in aortic ECs, can abolish the hyperglycemia-induced activation of each of these pathways (133). Therefore, oxidative stress is often considered an initial event in EC dysfunction, which also fits with the notion of hyperglycemia-induced Nrf2-dependent transcription of antioxidant enzymes and its prevention of diabetes-associated vascular complications.

Excess glucose, not being metabolized because of stalled glycolysis, is diverted into the polyol pathway to produce sorbitol and fructose, which promotes nonenzymatic generation of noxious AGEs (195, 347, 479, 577). In HUVECs, high concentrations of fructose also provoke a prothrombotic phenotype (85). Overexpression of an ALR2 trans-

gene in ECs from diabetic mouse models promotes atherosclerosis, whereas its inhibition reduces ROS levels and EC proliferation (396, 527, 556, 612). In the *db/db* mouse model of diabetes, the early events in diabetic retinopathy were linked to increased ALR2 levels (82).

Theoretically, elevated G6P levels can feed into the glucuronate cycle, but comprehensive studies on the glucuronate cycle in diabetic ECs are lacking. However, increased glucose metabolism via glucuronate and L-xylulose has been reported in diabetic murine models and patients, resulting in diabetes-associated renal dysfunction (68, 547, 589). Inhibitors targeting the enzyme L-xylulose reductase, catalyzing a NADPH-linked reduction of L-xylulose into xylitol, have been proposed for the treatment of long-term complications in diabetes (68).

F6P overload causes increased flux into the HBP, where it is converted into GlcN6P and subsequently into UDP-GlcNAc by GFAT (see sect. III). Under physiological conditions, UDP-GlcNAc is crucial for reversible posttranslational protein O-glycosylation; however, under hyperglycemic conditions, aberrant protein glycosylation results in altered protein activity, EC dysfunction, and accelerated pathogenesis of diabetes-associated atherosclerosis (165, 343, 349, 501). Aberrant O-glycosylation deregulates endothelial insulin signaling by obstructing key phosphorylation sites on insulin receptor substrate (IRS)-1 and eNOS, thereby impairing eNOS activity and interfering with NO synthesis (24, 134, 165). Lastly, expression of O-GlcNAcase, which reverses protein O-glycosylation, is decreased in coronary ECs from diabetic mice (343).

In a similar fashion, other accumulated glycolytic intermediates, i.e., G3P and dihydroxyacetone phosphate (DHAP), are diverted towards the production of highly reactive dicarbonyl compounds such as methylglyoxal, glyoxal, and 3-DG in the glyoxalase system. These reactive aldehydes modify (through glycation) DNA and (cytosolic and mitochondrial) proteins, resulting in the nonenzymatic formation of toxic AGEs. Also, excess G3P and DHAP fuel de novo diacylglycerol (DAG) synthesis, which subsequently activates PKC, resulting in vascular abnormalities via increased levels of NOXs and eNOS uncoupling (111, 248, 250). DAG-dependent PKC activation occurs under conditions of excessive circulating levels of glucose and FFAs.

As end products of dysfunctional EC metabolism, elevated levels of AGEs promote oxidative stress in the endothelium via several detrimental mechanisms (see sect. III), further exacerbating diabetes-associated vasculopathies. First, they modify intracellular protein signaling after posttranslational modifications of lysine and arginine residues of proteins (459). Second, they render the endothelium dysfunctional by altering collagen-type proteins through protein

cross-linking, causing decreased vessel elasticity, cell adhesion, and matrix-matrix interaction (357). Additionally, AGEs can adversely affect other cell types, mediated at least in part through interaction of AGEs with their receptor (RAGE; present on several cell types) and subsequent PKC and nuclear factor-kappa B (NF κ B) activation (357, 626). While NF κ B promotes endothelin-1-mediated vasoconstriction and inflammation (441), elevated levels of PKC can disturb insulin signaling pathways and glucose metabolism in skeletal muscle cells (370) or result in the dephosphorylation of PDGFR β and subsequent apoptosis of perivascular mural pericytes (191). Notably, loss of pericyte coverage, resulting in leaky endothelium, is one of the earliest signs of diabetic retinopathy (494).

In ECs, methylglyoxal is considered to be the main reactive aldehyde formed under hyperglycemic conditions (52, 497). Elevated methylglyoxal levels in diabetic patients are linked to diabetes-associated vasculopathies (365, 387, 397, 488). In vitro, methylglyoxal triggers eNOS uncoupling; however, the exact mechanism remains poorly defined (515). It was recently suggested that methylglyoxal exposure may also lead to alterations in EC redox status, via the inhibition of NADPH-generating enzymes, thereby depleting GSH levels and intensifying overall oxidative stress (377). Rats overexpressing GLO1, a key enzyme detoxifying methylglyoxal (regulated by Nrf2; see above in this section), showed signs of reduced endothelial glycation and oxidative stress and alleviated EC dysfunction (262). Of note, normalization of glucose levels in diabetic patients did not entirely prevent elevation of methylglyoxal levels and subsequent diabetic vasculopathies, and progressive ROS production and AGE accumulation persisted after glucose normalization (73, 171), begging for a better understanding of EC metabolism perturbation in diabetes.

3. Hyperglycemia and restricted PPP flux

Hyperglycemia has also been reported to impair G6PD-mediated entry of glucose into the PPP (638), resulting in reduced availability of NADPH. As NADPH is a critical cofactor of eNOS, this ultimately results in increased oxidative stress and decreased NO bioavailability (310). Restoring the oxPPP flux, possibly through activation of G6PD, could promote NADPH and GSH redox cycling and is therefore an attractive target to reduce overall oxidative stress in the context of hyperglycemia. Noteworthy, under hyperglycemic conditions and subsequent stalled glycolysis, increasing the activity of the non-oxPPP enzyme TK with benfotiamine treatment diverts excess glycolytic triosephosphates (F6P and G3P) into the non-oxPPP, rather than into the alternative toxic metabolic pathways (discussed above). Benfotiamine treatment prevented diabetic nephropathy in STZ-treated rats (23, 218, 610).

C. Insulin Resistance

Since inhibition of hyperglycemia-induced oxidative stress, pharmacologically or via endogenous antioxidant mechanisms, prevents the hyperglycemia-associated activation of the above-mentioned pathways, oxidative stress is considered to be a key initial event in EC dysfunction. However, apart from hyperglycemia, insulin resistance has recently emerged as another major precursor of atherothrombotic events and poor cardiovascular outcome (34, 414). Insulin resistance is the prediabetic state of glucose intolerance (early stages of diabetes type 2) and is characterized by impaired insulin sensitivity and hyperinsulinemia (state of increased secretion and decreased clearance of insulin). Previously, insulin resistance was primarily linked to target tissues like liver, skeletal muscle, and adipose tissue, but emerging evidence indicates that insulin resistance also occurs in ECs (417).

While insulin signaling stimulates glucose uptake in target tissues mainly via intracellular trafficking of GLUT4, ECs display insulin-independent glucose uptake via GLUT1 (other GLUTs are less abundantly expressed in ECs) and intraendothelial glucose levels are therefore independent of insulin sensitivity (266). Furthermore, ECs do not downregulate GLUT1 expression in response to high extracellular glucose concentrations, causing glucose concentrations in ECs to reflect glucose levels in the blood, which can explain why ECs are particularly susceptible to hyperglycemia. Still, there exists extensive literature on EC dysfunction secondary to insulin resistance in vascular endothelium (132, 181, 223, 283, 292, 320, 452, 559). While hyperglycemia-induced oxidative stress is now generally accepted to trigger vascular complications in both diabetes type 1 and 2, endothelial insulin resistance may explain the incidence of EC dysfunction predating the onset of diabetes type 2 (in the absence of hyperglycemia). Yet, targets of insulin signaling in ECs and their metabolism remain incompletely understood.

Insulin signals via MAPK- and PI3K-dependent pathways with different downstream effector proteins in the endothelium versus other target tissues (168, 375). The insulin-induced MAPK signaling (the “mitogenic/pro-atherogenic arm of insulin signaling”), which stimulates inflammation, vasoconstriction, and apoptosis, is not affected when ECs become insulin resistant (261). As a counter balance, PI3K-Akt signaling (the “metabolic arm” of insulin signaling) activates eNOS, resulting in NO-dependent vasodilation (633). Obesity-associated endothelial insulin resistance impairs eNOS activation, resulting in oxidative stress and reduced vasodilation and capillary recruitment (132, 139, 181, 261, 292). The latter causes a progressive decline of peripheral insulin distribution and subsequent glucose disposal in the skeletal muscle (292). As such, insulin resistance creates an imbalance between the metabolic and mitogenic/pro-atherogenic arms of insulin signaling (376), re-

sulting in EC dysfunction with a subsequent net increase in vasoconstriction (hypertension and systemic insulin resistance) and a pro-inflammatory/thrombotic state (atherosclerosis) (16). Endothelial insulin resistance may therefore be causally linked to cardiovascular pathologies preceding and following the onset of diabetes type 2 that are additionally exacerbated by the compensatory hyperinsulinemia (447, 545).

Forkhead box O (FoxO) proteins regulate endothelial insulin resistance. Indeed, endothelial deletion of the three major FoxO isoforms (FoxO^{ECKO}) attenuates endothelial insulin resistance, increases NO bioavailability, and protects low-density lipoprotein receptor knockout (Ldlr^{-/-}) mice from atherosclerosis (546) (FIGURE 9). Downstream of the PI3K-Akt pathway, these FoxO proteins (encoded by FoxO1, FoxO3a, and FoxO4) inhibit insulin signaling and eNOS expression while enhancing iNOS expression upon oxidative stress, causing ONOO⁻ production and EC dysfunction (284, 389, 528, 542, 546, 628). For these reasons, endothelial FoxO inhibition has been postulated as a potential therapeutic target to tackle endothelial insulin resistance and cardiovascular disease in diabetes type 2 patients (270, 452). However, subsequent experiments with FoxO^{ECKO} mice demonstrated that, while increased levels of EC-derived NO have a favorable effect on EC dysfunction in Ldlr^{-/-} mice (with advanced insulin resistance), they also impair insulin-dependent suppression of glucose production in hepatocytes of healthy mice (with early stage insulin resistance) (545). This suggests that the therapeutic value of vascular insulin sensitization via FoxOs may depend on the degree of metabolic disease or may only be beneficial for atherosclerosis-prone vessels (270). Furthermore, another reason for caution is that FoxO1 couples EC metabolic activity with vascular expansion and acts as a gatekeeper of endothelial quiescence by reducing glycolysis and mitochondrial respiration (586). Hence, EC-specific FoxO1 deletion results in EC hyperplasia and vessel enlargement (586). The FoxO1-induced reduction of endothelial oxidative metabolism may be a protective mechanism against excessive mitochondria-derived ROS in ECs, and therefore its inhibition (expected to increase ROS levels) may not directly benefit diabetic type 2 patients after all.

While hyperglycemia has been clearly connected to increased oxidative stress in ECs, the link between endothelial insulin resistance and oxidative stress is less well established to date. One possible mechanism relates to the increased circulating FFA levels, linked to obesity-associated dyslipidemia and insulin resistance in type 2 diabetics. Indeed, elevated FFA levels increase oxidative stress in ECs via NOX activation and eNOS inactivation, concomitant with PKC activation and de novo DAG synthesis (248, 273). DAG and PKC levels are elevated in diabetic animal models and contribute to diabetes-related vasculopathies, as excess levels of DAG negatively affect blood flow and vasodila-

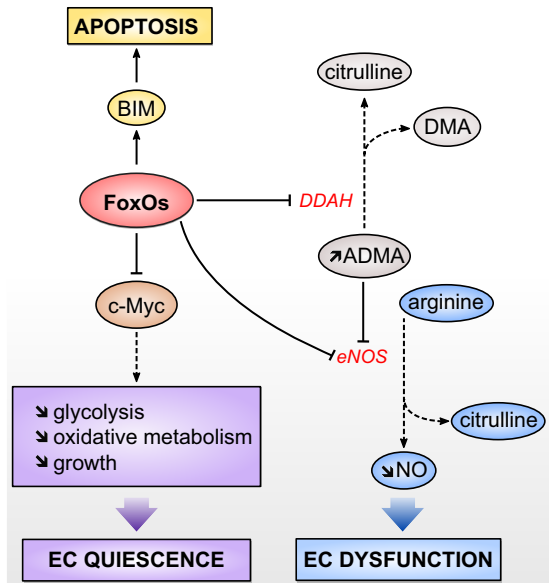


FIGURE 9. Different roles of FoxO transcription factors in ECs. Schematic representation of the dual role FoxO transcription factors can play in ECs, either as metabolic gatekeepers to sustain EC quiescence or, conversely, contributing to EC dysfunction. ADMA, asymmetrical dimethyl arginine; BIM, BCL2 like 11; DMA, dimethylamine; FoxO, forkhead box O; NO, nitric oxide.

tion, and increase fibrosis and vascular permeability (111, 248, 250). Another candidate possibly involved in endothelial insulin resistance-mediated oxidative stress and EC dysfunction is NOX2 (131, 181).

Systemic insulin induces endothelial FASN, required for eNOS palmitoylation and subsequent localization to caveolae where sources of arginine and BH₄ are optimal to produce NO (579). Diabetic animal models showed reduced endothelial FASN levels and decreased eNOS palmitoylation resulting in increased oxidative stress, inflammation, and impaired angiogenesis (579). Whether the diabetic vascular dysfunction can be rescued via FASN signaling remains unstudied. Nonetheless, insulin also regulates palmitoylation of proteins in ECs required for insulin-induced angiogenesis and EC migration (580). Proteomics could therefore be useful to identify novel insulin-dependent palmitoylation targets, possibly dysregulated by insulin resistance in diabetes, related to endothelial function and angiogenesis.

Lastly, endothelial insulin resistance can also lead to increased oxidative stress via eNOS uncoupling by interrupting the metabolism of the NO-precursor arginine and co-factor BH₄, resulting in their decreased availability (203, 217, 251, 446, 498). Thus endothelial insulin resistance and hyperglycemia can both influence EC dysfunction via oxidative stress, however, while hyperglycemia causes a variety of both micro- and macrovasculopathies, insulin resistance primarily promotes cardiovascular disorders, including atherosclerosis (562).

D. Atherosclerosis

Representing more than 80% of the cardiovascular deaths in 2013, atherosclerosis is another leading cause of morbidity in the Western society (383). EC dysfunction is a main contributor to this chronic disease, which develops in large and small arteries of various organs (198, 322). The pathogenesis of atherosclerosis is a multistep process: upon activation, ECs increase the expression of adhesion molecules [i.e., intercellular adhesion molecule (ICAM-1), vascular cell adhesion molecule 1 (VCAM-1), E-selectin], which promotes monocyte recruitment within the vascular wall. Macrophages derived from these monocytes engulf modified lipoproteins, accumulate intracellular cholesterol, and become foam cells (121, 322). The ECs on the other hand become progressively more dysfunctional, causing uncontrolled generation of toxic ROS with a concomitant drop in the production of the anti-atherogenic cues NO and hydrogen sulfide (H₂S), further exacerbating vascular perturbation and inflammation, increasing oxidative stress and driving overall progression of the disease.

E. eNOS Uncoupling and Pro-atherosclerotic Effect of ROS Generation

As discussed above, NO is a master switch in cardiovascular homeostasis by virtue of its vasorelaxant, antihypertensive, and antithrombotic properties. NO causes vascular smooth muscle cells (SMCs) to relax and prevents a number of proatherosclerotic events like platelet aggregation, SMC proliferation and migration, leukocyte adhesion, and oxidative stress (182, 259, 318, 543). In atherogenesis, when NADPH and BH₄ are limiting, eNOS becomes “uncoupled” and switches from NO production (atheroprotective) to generation of superoxide anions and ONOO⁻, further amplifying eNOS uncoupling (36, 198) (FIGURE 10).

In the ApoE^{-/-} mouse model of atherosclerosis, supplementation with BH₄ indeed partially rescues the NO defect, decreases superoxide production, and improves endothelium-dependent vasodilation (36, 302). In ECs, BH₄ is generated via two pathways: de novo synthesis from GTP by GTP cyclohydrolase I (GTPCH-1) or regeneration from BH₂ by dihydrofolate reductase (DHFR). DHFR also converts dihydrofolate (DHF) to tetrahydrofolate (THF), thereby linking eNOS uncoupling to the folate one-carbon metabolism. Indeed, THF accepts one carbon from serine to generate 5,10-methylene-THF (meTHF) and glycine. Methylene tetrahydrofolate reductase (MTHFR) then reduces meTHF to 5-methyl-THF (mTHF), which gives a one-carbon unit to homocysteine to generate methionine (and to recycle THF) and the methyl donor S-adenosylmethionine (SAM) required for various methylation reactions (DNA, histone, other proteins) (36).

One peculiar target for methylation in this context is the eNOS substrate arginine itself. Arginine methylation yields

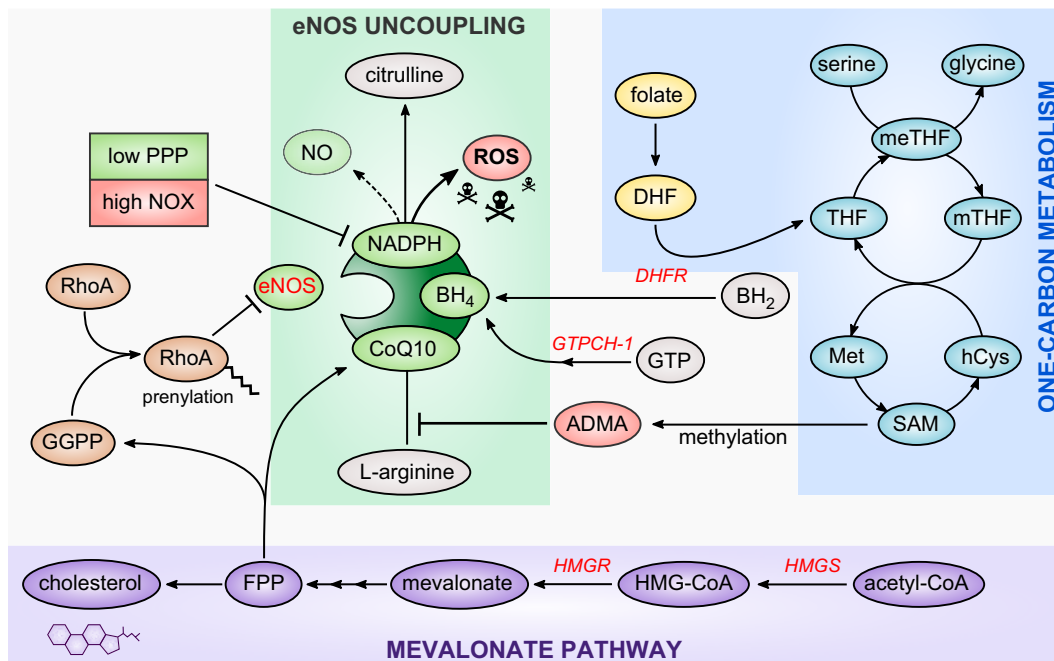


FIGURE 10. Metabolic aberrations in ECs in atherosclerosis. In atherosclerosis, ECs display prominent eNOS uncoupling leading to elevated ROS levels and reduced NO-mediated vasodilation. Underlying eNOS uncoupling are decreases in the levels of necessary cofactors (NADPH, CoQ10, BH₄) resulting from deregulated metabolic pathways or enzyme activities, and methylation of the eNOS substrate arginine (ADMA). Acetyl-CoA, acetyl-coenzyme A; ADMA, asymmetrical dimethyl arginine; BH₂, 7,8-dihydrobiopterin; BH₄, tetrahydrobiopterin; CoQ10, coenzyme Q10; DHF, dihydrofolate; DHFR, dihydrofolate reductase; eNOS, endothelial nitric oxide synthase; FPP, farnesylpyrophosphate; GGPP, geranylgeranyl pyrophosphate; GTPCH, GTP cyclohydrolase; hCys, homocysteine; HMG-CoA, hydroxymethylglutaryl coenzyme A; HMGs, 3-hydroxy-3-methylglutaryl-CoA reductase; HMGs, 3-hydroxy-3-methylglutaryl-CoA synthase; MET, methionine; meTHF, 5,10-methylene-methyltetrahydrofolate; mTHF, 5-methyltetrahydrofolate; MTHFR, methylenetetrahydrofolate reductase; NADPH, nicotinamide adenine dinucleotide phosphate; NO, nitric oxide; NOX, NADPH oxidase; PPP, pentose phosphate pathway; ROS, reactive oxygen species; SAM, S-adenosylmethionine; THF, tetrahydrofolate.

asymmetric/symmetric dimethylarginines (ADMA, SDMA) (FIGURE 10). Unlike arginine, ADMA and SDMA cannot be used by eNOS to generate NO, but rather compete with arginine for NO production, representing another level of eNOS uncoupling (40). Oxidative stress enhances ADMA accumulation by inactivating the ADMA eliminating enzyme dimethyl-arginine dimethyl-aminohydrolase (DDAH) (253, 435). Being elevated in atherosclerotic patient sera (up to 10-fold) (44), ADMA and more precisely the arginine-to-ADMA ratio is considered a cardiovascular risk factor (28, 394). Of note, SDMA induces oxidative stress and increases superoxide anion production in glomerular kidney ECs (166). Clinically, plasma levels of SDMA positively correlate with mortality in patients with stable coronary heart disease (502).

FoxO1 in ECs increases levels of the eNOS inhibiting ADMA in vivo through downregulation of the ADMA degrading enzyme DDAH, thereby adding an additional layer of FoxO-mediated regulation of endothelial NO levels (see above and FIGURE 9) (368). Furthermore, in the aorta from FoxO^{ECKO}/Ldlr^{-/-} mice, levels of NOXs are downregulated, suggesting a protective effect of FoxO ablation on the

endothelium (546). Moreover, in cultured HUVECs, FoxO1 induces the expression of the proapoptotic molecule BIM (327). Even though these data are in favor of therapeutically inhibiting endothelial FoxO1 in atherosclerosis, this will be extremely challenging given the above-mentioned crucial role for FoxO1 in fine-tuning EC metabolism (586). Furthermore, complete inhibition of FoxO1 might be harmful given its role in regulating endothelial oxidative stress and decreasing eNOS levels. Instead, fine-tuning FoxO1 levels by targeting posttranslational modifications (i.e., acetylation) might be an option that requires however further study (57, 440).

In methyltransferase reactions, SAM is converted to S-adenosylhomocysteine (SAH), which is further hydrolyzed to homocysteine and adenosine by SAH hydrolase (SAHH). Hyperhomocysteinemia (HHcy) causes EC dysfunction and is an independent risk factor for cardiovascular disease by reducing the levels of available NO and S-nitrosylated proteins important for EC homeostasis (80, 517). While the exact mechanism involved is not fully understood, HHcy causes accumulation of homocysteine-thiolactone and immunogenic and toxic N-homocysteinylated proteins. These

two compounds might mediate the pro-atherogenic effect of HHcy by altering gene expression in ECs. According to transcriptome analysis in HUVECs, they mainly affect the expression of genes in one-carbon, sulfur amino acid and lipid metabolism, and in epigenetic/chromatin organization regulation (211). Several studies reveal that plasma SAH and homocysteine levels are associated with DNA hypomethylation in atherosclerosis and vascular disease (623, 644). In line with this, increased SAH levels, again via modulation of histone methylation, cause ER stress, which plays an important role in EC dysfunction by inducing oxidative stress and inflammation (598, 600, 601). Furthermore, homocysteine-mediated ROS production promotes EC death by disturbing the mitochondrial membrane potential (an early event in apoptosis) leading to caspase activation (539, 548, 620). Taken together, SAH and homocysteine levels may serve as sensitive and comprehensive biomarkers for EC dysfunction in atherosclerosis (635).

F. Mevalonate Pathway in ECs

In addition to one-carbon metabolism and folate/methionine cycling, the endothelial mevalonate or isoprenoid pathway (using acetyl-CoA to produce cholesterol) plays a significant part in atherogenesis (45, 160). In the mevalonate pathway, acetyl-CoA is first converted to 3-hydroxy-3-methylglutaryl (HMG)-CoA by HMG synthase, and then to mevalonate by HMG-CoA reductase (HMGR). Isoprenoid intermediates further downstream the pathway, such as geranylgeranylpyrophosphate (GGPP) and the cholesterol-backbone farnesylpyrophosphate (FPP), posttranslationally modify various proteins, including small GTPases such as RhoA and Rac1 (399). RhoA's activity to regulate cytoskeletal dynamics requires GGPP prenylation and subsequent EC plasma membrane localization, essential for EC homeostasis (236, 237). However, when active, RhoA also may contribute to EC dysfunction, in part by promoting the degradation of eNOS mRNA transcripts (301, 518) as well as by stimulating leukocyte recruitment and vascular inflammation during atherogenesis (374) (FIGURE 10). Serum lipid-lowering statins inhibit HMGR and are widely used to reduce cholesterol levels. A non-lipid-lowering effect of statins involves the reduction of GGPP pools and the subsequent inhibition of RhoA activation, preventing excessive inflammation and degradation of eNOS transcripts. However, these beneficial effects (reduced RhoA prenylation) have only been observed at doses far above clinical applicability. Furthermore, statins also lower FPP levels required to produce the mitochondrial cofactor CoQ10 (involved in eNOS coupling) and can therefore have adverse effects on the endothelium (83, 384, 544) (FIGURE 10).

G. NOX Control and NADPH Levels

As mentioned above, NADPH pools sustain eNOS coupling but can be depleted by ROS-generating NOXs (FIGURE 10),

which show prominent expressions in vascular diseases and are induced in atherosclerotic arteries exposed to turbulent blood flow (212, 249, 264, 472). Of the different isoforms expressed in ECs, NOX2 is a major source of ROS production (367). Its expression is upregulated in aortic endothelium of ApoE^{-/-} mice and occurs before the emergence of atherosclerotic plaques, whereas loss of NOX2 expression attenuates ROS generation in ECs and monocytes and increases NO availability (264, 558). Interestingly, the polyphenol drug resveratrol decreases NOX2 expression in cerebromicrovascular ECs (541) and protects against mitochondrial-derived ROS by upregulating PGC1 α (645) (see above in this section). Not all NOX-derived ROS are harmful; some can repress inflammation and lead to atheroprotection instead, as is the case for NOX4 (207, 300). Rather than indiscriminately inhibiting all NOXs, the development of isoform-specific NOX inhibitors will be the key in optimizing clinical applicability (534). As such, the peptidic NOX2 selective inhibitor gp91ds-tat reverses insulin resistance-induced reduction of EC-mediated vasorelaxation (519). Yet, the important role of NOX2 in the innate immune system might hinder further clinical applications of this inhibitor (256).

H. Cysteine Metabolism and H₂S Production

The gaso-transmitter H₂S has long been considered to lack any physiological function and to be no more than a highly toxic and malodorous gas. In contrast, H₂S is an important cue in the regulation of EC and cardiovascular homeostasis by inducing blood vessel relaxation and cardioprotection (439). H₂S is produced by ECs and SMCs by three enzymes using cysteine: cystathionine- γ -lyase (CSE), cystathionine- β -synthase (CBS), and the tandem of cysteine aminotransferase (CAT) and 3-mercaptopyruvate sulfurtransferase (3-MST). CSE is the predominant H₂S-producing enzyme in ECs and converts cysteine to pyruvate, ammonia, and H₂S (439, 571). CBS catalyzes two main reactions: first the direct transformation of cysteine to H₂S and homocysteine, and second the condensation of serine with the latter to generate cystathionine (571) (FIGURE 11).

The beneficial effects of H₂S on the vascular endothelium include 1) inhibition of vascular inflammation, via repression of the NF κ B pathway and the shear stress-induced binding of activated monocytes on vessel walls; 2) increased oxidative stress defense by favoring the production of reduced glutathione and by inducing antioxidant gene expression (i.e., catalase, MnSOD); 3) reduction of SMC proliferation; 4) increased angiogenesis and EC self-repair processes; and 5) reduced atherogenic modification of LDL and macrophage-derived foam cell formation (439, 571). Of interest, high-fat-fed mice with CSE deficiency suffer a higher risk to develop atherosclerotic lesions with high LDL and homocysteine levels, which is attenuated by treatment with the NaHS H₂S-donor (345, 605). Also in the context

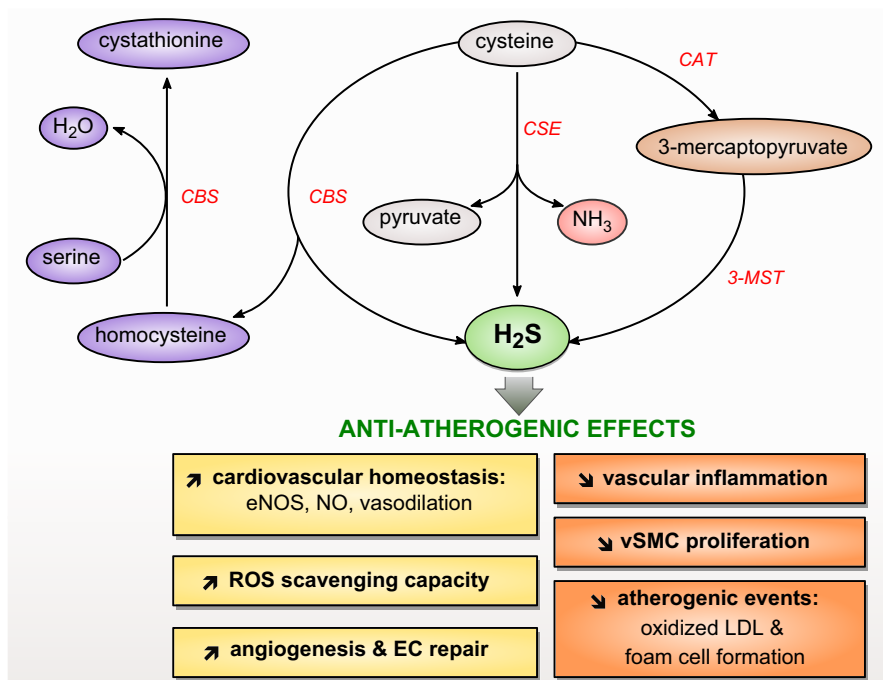


FIGURE 11. Endothelial cysteine to H₂S metabolism in atherosclerosis. The gasotransmitter H₂S is an important regulator of cardiovascular homeostasis and has anti-atherogenic effects. In ECs, H₂S can be produced from cysteine (via CSE or CAT and 3-MST activity) or in the condensation of cysteine and homocysteine to cystathionine (alternate action of CBS). The anti-atherogenic effects of H₂S are listed at the bottom of the image and are discussed in more detail in the main text. 3-MST, 3-mercaptopyruvate sulfurtransferase; CSE, cystathionine- γ -lyase; CBS, cystathionine- β -synthase; CAT, cysteine aminotransferase; eNOS, endothelial NO synthase; LDL, low-density lipoprotein; NH₃, ammonia; NO, nitric oxide; vSMC, vascular smooth muscle cell.

of atherosclerosis-associated HHcy, homocysteine is reported to inactivate CSE by homocysteinylolation, further aggravating the disease (439, 571) (FIGURE 11).

There is also a reciprocal interaction between H₂S and NO. Indeed, eNOS inhibition lowers H₂S-stimulated vasorelaxation, whereas CSE silencing abolishes NO-driven angiogenesis (91). This intertwined interaction is not fully understood, but is in part mediated by posttranslational modifications. By inducing eNOS S-sulphydration, H₂S facilitates eNOS dimerization and stabilization, leading to NO production (13, 91). Interestingly, the H₂S-dependent sulphydration of cysteine residues in pancreatic β -cells exposed to ER stress promotes aerobic glycolysis and reduces OXPHOS (185). Whether or not H₂S-driven sulphydration contributes to metabolic reprogramming towards glycolysis in sprouting ECs too is not known yet.

I. Blood Flow Influencing EC Metabolism

Atherosclerotic plaques preferentially develop in areas subject to low and turbulent shear stress, whereas arteries exposed to uniform laminar shear stress are less prone to plaque formation (522). The effect of shear stress can be attributed to mechano-activated signaling pathways that instruct ECs to react to the external milieu but, interestingly, also impact EC metabolism. The transcription factor KLF2 is upregulated in ECs subject to atheroprotective laminar shear stress (422, 477). Genetic overexpression of KLF2 causes ECs to adopt a more quiescent behavior through several mechanisms, including increased VE-cadherin expression (KLF2 induces expression of the mRNA binding protein quaking, which enhances VE-cadherin

mRNA translation) and tightening of the vascular barrier (115, 126), promotion of EC alignment in the flow axis (48), reduction of the pro-inflammatory state, and control of vascular homeostasis (395) (FIGURE 12). Of particular interest is how KLF2 links the biomechanical stimulus of shear stress to EC glucose metabolism. Indeed, increased KLF2 expression reduces glucose uptake and glycolysis, in part by repressing PFKFB3's promoter activity (126). Given that lowering glycolysis (by silencing PFKFB3) enhances EC quiescence (114), this KLF2-driven mechanism ensures that an adequate (lower) level of glycolytic flux sustains EC quiescence under laminar flow (FIGURE 12).

In atheroprone regions, low shear stress and oxidized LDL (oxLDL) induce miR-92a expression to repress endothelial KLF2 and phosphatidic acid phosphatase type 2B (PPAP2B) expression (81, 296, 333, 594) (FIGURE 12). Under normal atheroprotective flow, PPAP2B dephosphorylates lysophosphatidic acid (LPA) to prevent it from binding to its receptor (LPAR1) and inducing pro-inflammatory signaling (594). As such, EC-specific PPAP2B-deficient mice feature enhanced local and systemic inflammation associated with increased vascular permeability (412). Genome-wide association studies show that a single-nucleotide polymorphism (rs17114036) lowers PPAP2B expression in human ECs and is predictive of a higher risk for coronary artery disease independently of traditional risk factors, such as cholesterol and diabetes (484).

C-reactive protein (CRP) also participates in atherogenic effects of lipoproteins. Indeed, as shown in vitro in HU-VECs, CRP increases the transcytosis of LDL across ECs, thereby enhancing LDL retention in vascular walls and

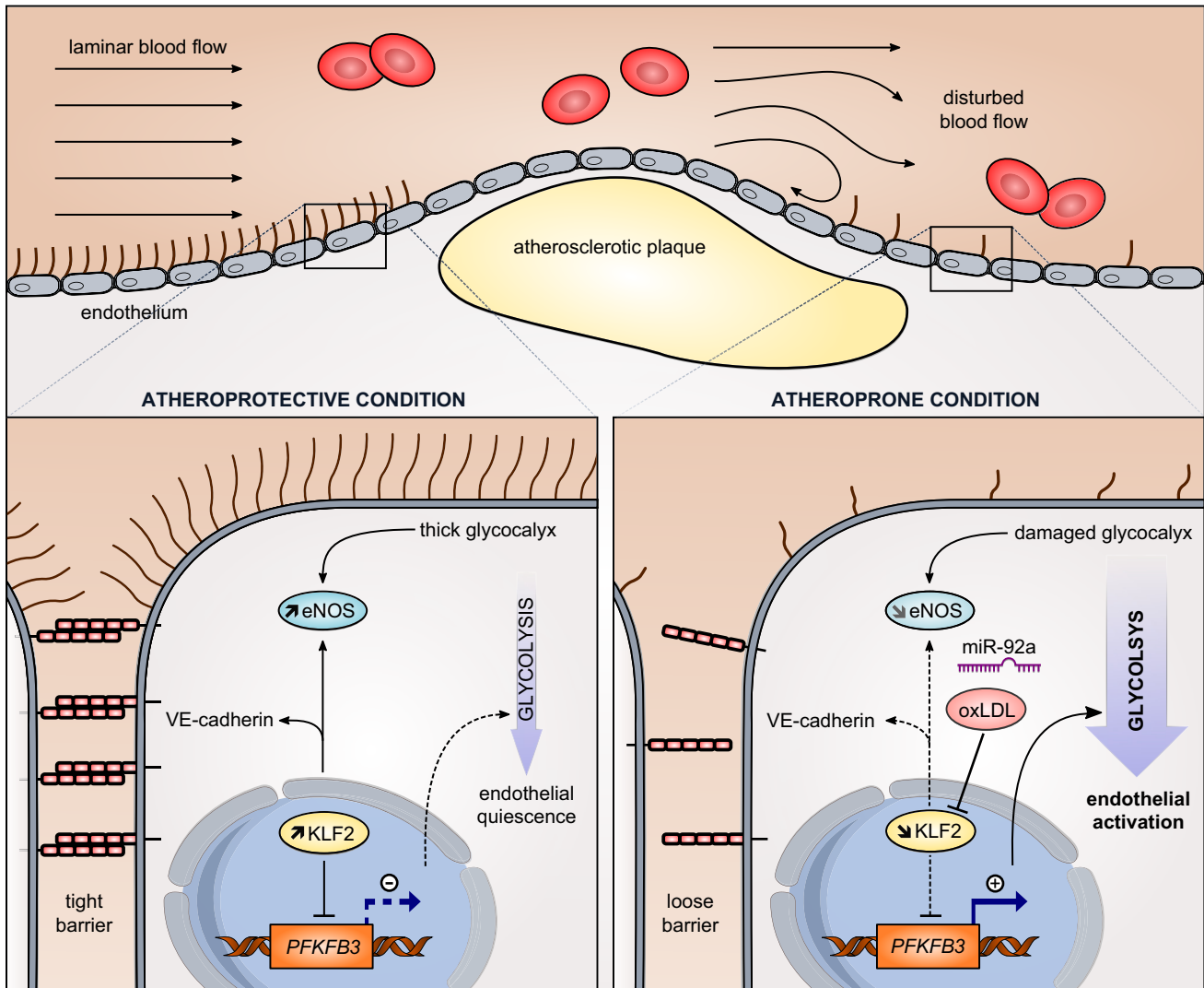


FIGURE 12. Impact of atheroprone versus atheroprotective flow on EC metabolism. Blood flow dynamics critically influence EC metabolism and behavior. Normal atheroprotective blood flow increases the activity of the flow-responsive transcription factor KLF2 which, in addition to increasing VE-cadherin expression and barrier function, transcriptionally represses PFKFB3 expression and lowers glycolytic rates to sustain EC quiescence. Atheroprone turbulent flow lowers KLF2 activity and VE-cadherin levels as well as releases the brake on PFKFB3 expression causing increased glycolysis and EC activation. Additionally, in atheroprone regions, low shear stress and oxLDL induce miR-92a expression to lower KLF2 levels. Finally, normal blood flow sustains a functional EC glycocalyx with protective function. However, atheroprone insults reduce thickness of this glycocalyx through mechanisms discussed in more detail in the main text. PFKFB3, 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase-3; KLF2, Krüppel-like factor 2; oxLDL, oxidized low-density lipoprotein; VE-cadherin, vascular endothelial cadherin; miR-92a, microRNA-92a.

ROS generation (42). Moreover, the pro-atherogenic effect of CRP has also been demonstrated in ApoE^{-/-} mice (173). CRP therefore represents an important cardiovascular disease risk factor (154, 173, 254). Interestingly, the inflammatory cytokine IL-6 is a major inducer of CRP in ECs in vitro, in mice models of thrombosis, and in patients with cardiovascular disease (97, 460, 473). Furthermore, IL-1 β can induce CRP levels, directly or indirectly via induction of IL-6 (62, 277). In atherosclerotic lesions, macrophages secrete IL-6 and IL-1 β , dependently on glycolytic activity (499). Moreover, glycolytic enzymes such as the pyruvate kinase M2 (PKM2) also control IL-1 β induction in macro-

phages (410). Therefore, targeting glycolysis in endothelium and/or in atherosclerotic-plaque infiltrating immune cells might offer new opportunities.

Another mechanism linking blood flow to EC metabolism relates to the endothelial glycocalyx layer (EGL), a thick gel-like layer composed of glycoproteins, sulfated proteoglycans (e.g., syndecan-1), and associated glycosaminoglycans (GAGs) at the luminal surface of ECs (110, 532). If intact, the EGL is atheroprotective; in ECs, the EGL constituent glypican-1 (GPC1) colocalizes with eNOS in caveolae and lipid rafts to mediate its activity in response to

shear stress (143). Moreover, the EGL tightens the endothelial barrier and limits vascular permeability and prevents thrombosis and vessel wall inflammation (through inhibition of respectively platelet and leukocyte adhesion to ECs) (110). Laminar shear stress promotes EGL deposition. In contrast, pro-atherosclerotic insults like hyperglycemia, ox-LDL, and ROS drive EGL damage and shedding (30, 280, 409, 503) (FIGURE 12). At the clinical level, patients with acute coronary syndrome display EGL damage with elevated levels of plasma syndecan-1, reminiscent of EGL shedding (371). Conversely, EGL degradation also promotes ROS generation, sustaining a vicious circle (295). Given that the EGL consists of glycoproteins and glycosaminoglycan chains (such as hyaluronan), its production is likely somehow linked to EC glucose metabolism. As discussed above, the HBP pathway produces UDP-GlcNAc for protein glycosylation. In addition, the GAG hyaluronan is made up by disaccharide units of glucuronic acid (GlcUA) and GlcNAc (122). Hyaluronan synthases use UDP-GlcUA and UDP-GlcNAc as rate-limiting substrates, synthesis of which is an energy-consuming process requiring glycolytic intermediates (560). Indeed, the uronic/glucuronate pathway is an alternative pathway for glucose oxidation that uses the glycolytic metabolite G6P to produce UDP-GlcUA, while the HBP uses the glycolytic intermediate (F6P) to produce UDP-GlcNAc (see section III and FIGURE 3). How ECs regulate these metabolic pathways to produce the EGL in response to atheroprotective/susceptible flow requires further study.

VIII. ENDOTHELIAL CELL METABOLISM IN VASCULAR DISORDERS: EXCESS ANGIOGENESIS

While diabetes and atherosclerosis are tainted by vascular complications as a result of early EC dysfunction, other life-threatening diseases including cancer and pulmonary arterial hypertension are mainly characterized by excessive angiogenesis, which likewise appears to be driven by endothelial metabolic aberrations.

A. Cancer

Excess angiogenesis in cancer is caused by 1) aberrant angiogenic growth factor signaling due to gene mutations in cancer cells, 2) angiogenic growth factor secretion by infiltrating immune cells and stromal cells, 3) a pro-angiogenic make-up of the tumor microenvironment due to aberrant cancer cell metabolism, and 4) dysfunctional blood vessels and amplification of hypoxia and low pH due to a lack of oxygen supply and waste removal.

Activation of oncogenes or inhibition of tumor suppressor genes (e.g., k-Ras, v-Src, v-Raf, and p53) leads to aberrant secretion of pro-angiogenic factors by cancer cells and con-

sequently stimulates the growth of new blood vessels into the tumor (448). In addition, infiltrating platelets, immune cells, and stromal cells secrete factors that promote angiogenesis. As such, the tumor microenvironment is enriched with pro-angiogenic factors, including VEGF, bFGF, chemokines, and PDGF (581). Nutrient and oxygen deprivation contributes to the induction of tumor angiogenesis. Even tumors of <1 mm in size can show substantial levels of hypoxia (321). The subsequent stabilization of HIF-1 α and induction of its target genes leads to further excessive secretion of VEGF and other angiogenesis promoting factors, and incites ECs to sprout and form new vessels (222). Once tumors grow to a diameter of 1–4 mm, hypoxia is reduced, because tumors become vascularized (321). Still, the excess production of pro-angiogenic signals leads to continuous stimulation of aberrant, even nonproductive tumor angiogenesis resulting in abnormal vessels. Pericytes, which promote maturation and vessel stabilization, associate with tumor endothelium but more loosely and to a far lesser extent than with normal endothelium (19, 176). The vessel walls of the tumor vasculature are spotted with gaps due to irregular shape and size of ECs, abnormal tight junction formation, and EC hyperproliferative activity and motility, leading to reduced blood flow and vessel perfusion. These properties amplify aggressive tumor growth and create a nutrient-deprived microenvironment, from where cancer cells attempt to escape; the leaky tumor vascular barrier facilitates cancer cell dissemination and metastatic spread (137).

The metabolic profile of tumor tissues is most frequently characterized by low glucose concentrations (even as low as 0.12 mM) (234) and high lactate concentrations (as high as 40 mM) (568). The second most increased metabolite in tumor tissue is glutamate, derived from extracellular glutamine (205). Moreover, tumors are acidic, partly caused by higher glycolytic activity, in addition to higher general metabolic activity leading to increased CO₂ and H⁺ production, and lack of metabolic waste removal due to insufficient blood perfusion (363). Most of these characteristics have been described to promote tumor angiogenesis. As such, VEGF transcription and/or secretion are increased by glucose deprivation and acidic pH (631, 636). Increased lactate stimulates angiogenic growth, since high intracellular lactate concentrations in ECs stimulate 1) a pro-angiogenic, autocrine NF κ B/IL8 loop (557) and 2) normoxic stabilization of HIF-1 α , thereby promoting VEGFR2 expression, VEGF-A secretion, and EC migration and sprouting (243, 506). This occurs through competition of lactate with 2-oxoglutarate, a cofactor for the prolyl hydroxylase domain protein 2 (PHD2); as a result, degradation of HIF-1 α in normoxia is inhibited (116, 557). ECs import lactate via monocarboxylate transporter 1 (MCT1), expressed in tumor-associated vasculature (286), and can be targeted to reduce tumor angiogenesis.

In general, tumor ECs (TECs) can display cytogenetic abnormalities (6, 229, 230) and have a different epigenetic profile (336) and gene expression signature than normal ECs (NECs) (336, 407, 486, 510, 553, 615). TECs are more angiogenic, more responsive to paracrine and autocrine pro-angiogenic signaling, have better survival strategies than NECs (14, 60, 298, 358, 615), and are often more resistant to chemotherapeutic and anti-angiogenic drugs (7, 9, 228, 231). Furthermore, TECs can be heterogeneous within one and the same cancer type (231, 232, 398). For example, TECs from high-metastatic melanomas have higher pro-angiogenic capacities than those from low-metastatic melanomas (398). Additionally and in contrast to those in low-metastatic melanoma, TECs from high-metastatic melanoma secrete biglycan, which further promotes metastasis (339). TECs can also adopt cancer cell-specific characteristics through horizontal DNA transfer (147); they can share certain genomic aberrations with cancer cells (641, 646) or even derive directly from cancer stem-like cells, as shown for glioblastoma (458).

TEC metabolism has long remained uncharted territory. Several features point towards a hyperactive glycolytic metabolism of TECs: 1) their overstimulated angiogenic behavior, 2) the partial resemblances they bear to cancer cells at least in certain aspects (147, 458, 646), and 3) the observation that they overexpress the glucose transporter GLUT1 (486). RNA sequencing analyses of TECs isolated from B16 melanoma-infested livers shows that TECs and NECs have distinct metabolic gene signatures (66), with the TEC metabolic gene signature indeed confirming a hyperglycolytic phenotype leading to increased glucose-dependent biomass production, which is further validated by *in vitro* studies involving [¹⁴C]glucose and [¹³C]glucose tracing techniques (66). EC-specific heterozygous deletion of the glycolytic activator PFKFB3 (PFKFB3^{+/ Δ EC}) in tumor-bearing mice reduces the hyperglycolysis in TECs, even though not more than by 15–20%. While primary tumor size is not affected, cancer cell intravasation and metastatic spread are substantially reduced. Strikingly, tumor vessels in PFKFB3^{+/ Δ EC} mice are enlarged and better covered with pericytes, display better perfusion dynamics, and have increased VE-cadherin junctions than in controls, all hallmarks of a normalized vasculature. Indeed, morphologically, PFKFB3^{+/ Δ EC} tumor vessels appear regular and orderly formed, in contrast to the typically chaotic appearance of tumor vasculature in control mice (66) (**FIGURE 13**).

Mechanistically, glycolysis inhibition reduces the amount of ATP required for VE-cadherin endocytosis, leaving more VE-cadherin at the plasma membrane and thereby increasing endothelial barrier integrity (66). Furthermore, lowering glycolytic flux decreases intracellular lactate levels and attenuates NF κ B signaling (66), thereby counteracting the lactate-dependent, pro-angiogenic signaling loop described

above (557). This decrease in NF κ B signaling lowers expression of cancer cell adhesion molecules in TECs, preventing cancer cells from transmigrating (66). Of note, glycolysis inhibition in pericytes renders these mural cells more quiescent and adhesive by upregulating N-cadherin levels, allowing them to better cover and support newly formed vasculature favoring tumor vessel normalization (66).

Importantly, tumor vascularization can also occur via non-angiogenic mechanisms, in which cancer cells use preexisting blood vessels, rather than inducing the growth of new ones. The process of vessel co-option, for it is less dependent on pro-angiogenic signaling, is associated with resistance to anti-angiogenic therapy in patients with colorectal liver metastasis (178, 293). Whether ECs of co-opted vessels change their metabolic phenotype to maintain functionality when associated with cancer cells will be an exciting avenue to pursue.

B. Pulmonary Arterial Hypertension

Pulmonary arterial hypertension (PAH) is a progressive and life-threatening pathology characterized by lung EC dysfunction and adverse vascular remodeling. Excessive angiogenesis in the form of excessive EC proliferation and suppressed apoptosis (141, 355), resulting in aberrant vascular remodeling and lumen-obliterative pulmonary vascular lesions (311), are now considered to underlie the pathophysiology of PAH, rather than only vasoconstriction (another PAH characteristic) as thought previously (521). Such aberrant lung endothelial phenotypes lead to increased pulmonary arterial pressure (>25 mmHg) at rest and heightened pulmonary vascular resistance (162, 364, 537), ultimately leading to right ventricular cardiac failure and premature death.

PAH is no longer considered a disease exclusively affecting pulmonary arteries, but involves several other (extrapulmonary) organs as well (reviewed in Refs. 426, 521). PAEC dysfunction, typified by excessive proliferation, decreased apoptosis, and an obliterative vascular repair program, is considered as an early event in the pathogenesis of PAH; however, at later stages of the disease many more vascular cell types, such as SMCs, pericytes, and (myo)fibroblasts, become involved as well (457, 521). One key feature of PAH-associated vascular cells studied is mitochondrial remodeling resulting in suppressed glucose oxidation and secondary upregulation of glycolysis (described further below) (426, 521). The latter is in line with the increased proliferative phenotype, considering that under physiological conditions, glycolysis stimulates angiogenesis (114). Finally, the infiltration and presence of activated inflammatory and immune circulating cells indicate that inflammation may also play a significant role in PAH's pathogenesis (537). It becomes clear that the pathogenesis of PAH involves multiple pathways rather than one single mechanism. Despite

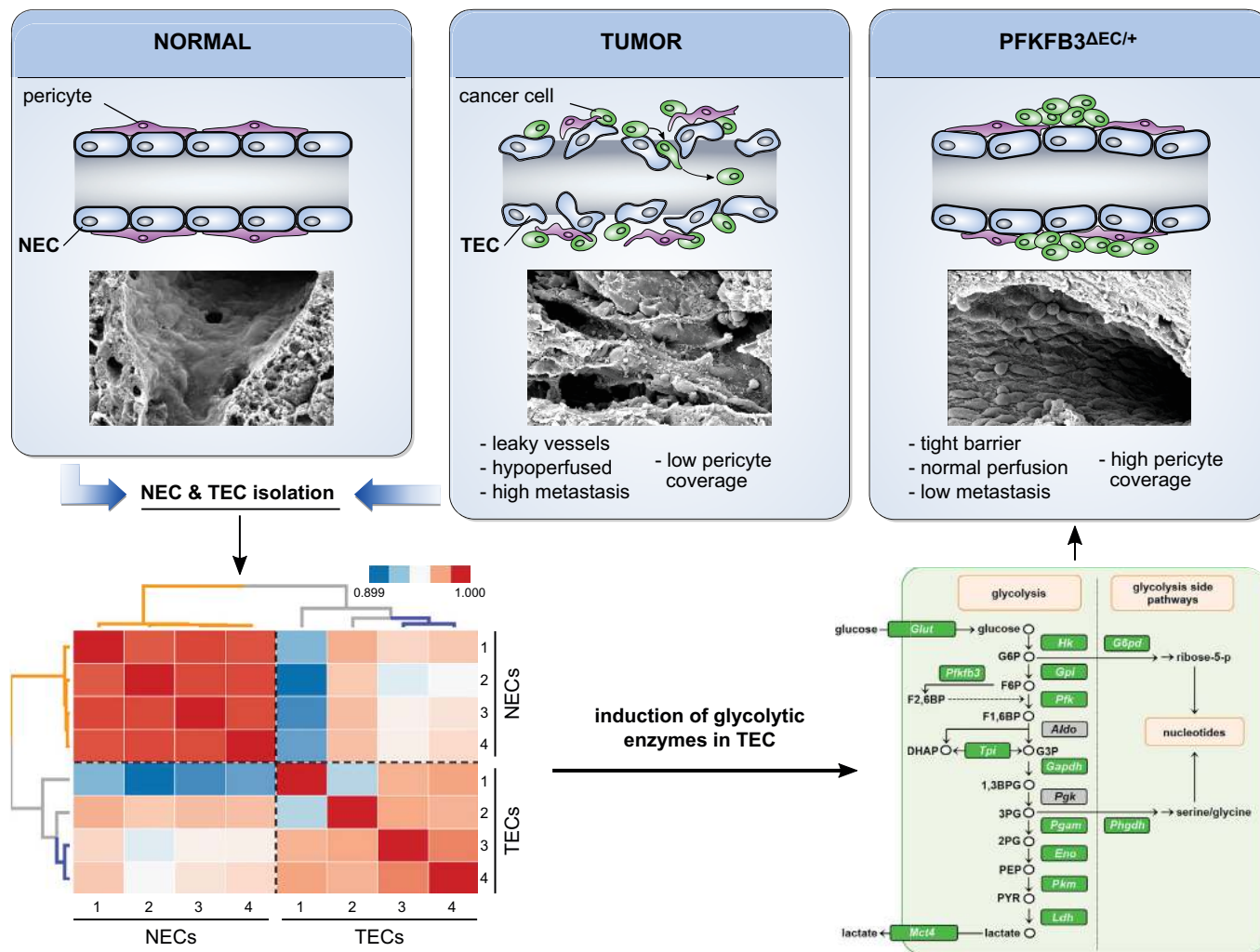


FIGURE 13. Reduction of hyperglycolysis in tumor ECs normalizes tumor vessels. Normal, mature blood vessels (*top left*) have a highly organized endothelial lining to ensure optimal blood flow and barrier function and are stabilized through pericyte coverage. In contrast, tumor vessels (*top middle*) are highly abnormal and tortuous and have a severely disorganized endothelium and reduced pericyte coverage. As a result, blood flow through these vessels is reduced, leading to a hypoperfused and consequently more aggressive, metastasis-prone tumor. In addition, tumor vessels are leaky which grants cancer cells easy access to the systemic circulation to establish distant metastases. Transcriptomic analysis of ECs isolated from normal vessels (normal ECs or NECs) versus ECs from tumor vessels (tumor ECs or TECs) and subsequent correlation heatmap analysis and hierarchical clustering of 1,255 metabolic genes (*bottom left*, color coding: high degree of correlation in red; lower degree of correlation in blue; numbers at the bottom and on the right indicate individual samples) shows differential metabolic wiring between NECs and TECs. Further analysis revealed that specifically glycolysis is induced in TECs and has the highest percentage of upregulated enzymes of all central metabolism pathways analyzed (*bottom right*, green coding indicates increased expression; gray coding indicates unaltered expression levels). Reverting hyperglycolysis in TECs in endothelial PFKFB3 haplodeficient mice leads to tumor vessel normalization featuring restored endothelial barrier function, increased pericyte coverage, and normalized blood flow which sustains tumor perfusion and renders the tumor more benign and less metastasis-prone (*top right*). [Correlation heatmap (*bottom left*) and pathway analysis (*bottom right*) as well as scanning electron microscopy images in the *top panels* are adapted from Cantelmo et al. [66], with permission from Elsevier.]

the role of PAECs early on in the pathogenesis of PAH, SMCs have been most extensively investigated, leaving questions on how metabolic aberrations specifically affect PAECs in PAH largely unanswered.

eNOS is the key regulator of basal vessel tone in the lungs (74, 159). As mentioned above in the sections on diabetes

and atherosclerosis, aberrant production of eNOS-derived NO is a hallmark of EC dysfunction present in several vasculopathies and results in overall oxidative stress and vasoconstriction. Oxidative stress also plays a central role in vascular remodeling in PAH (53, 354, 578). Total body and pulmonary bioavailability of NO is reduced in PAH patients (87, 163, 200, 337, 606), while levels of the potent

vasoconstrictor ET-1 are increased (197, 444, 463). Previously, contradictory reports on eNOS expression levels in lungs of PAH patients made it unclear as to how eNOS-derived NO concentrations were lower in PAH patients than healthy controls (196, 353, 606). However, it was recently reported that this reduction in NO is due to increased threonine (T495) phosphorylation of eNOS via PKC with inhibitory functional consequences for eNOS, rather than decreased eNOS expression levels (194, 520). ET-1 is responsible for eNOS uncoupling by PKC-mediated phosphorylation at T495 and translocation of eNOS from the plasma membrane to mitochondria, where the eNOS-derived superoxide and ONOO⁻ reduce respiratory capacity and as such disrupt mitochondrial bioenergetics in PAECs. Furthermore, the mitochondrial ROS induces HIF-1 activity and the subsequent switch to glycolysis (520). β -Blockers, pharmacologically inhibiting PKC activity, have been shown to restore NO bioavailability in PAH-associated pulmonary ECs (194). Interestingly, administration of eNOS-transduced endothelial progenitor cells to rats with established PAH resulted in regeneration of pulmonary endothelium and markedly improved their survival (640).

Decreased levels of arginine and BH₄ may be another cause of diminished eNOS-derived NO bioavailability in this disease. While there are sufficient levels of the eNOS cofactor BH₄ (194), others previously reported higher arg II expression and lower NO production in pulmonary ECs derived from PAH patients, indicating aberrant arginine metabolism (606). Similar results were reported *in vitro* in pulmonary ECs under hypoxic conditions (as a model for PAH), implicating hypoxia as well in the pathophysiology of PAH and vascular remodeling (69, 290). Even though arg II inhibitors are commercially available, their use should be addressed with caution as PAECs have elevated protein levels of arg II upon its pharmacological inhibition, partially due to increased protein half-life (289).

Increased EC mitophagy is a critical initiating event in PAH pathogenesis and results in EC loss due to inadequate biosynthesis of new mitochondria (225). This is in line with reports on early PAH-associated EC apoptosis and subsequent selection for ECs with excessive proliferative and apoptosis-resistant phenotypes (474). A decrease in EC mitochondrial biogenesis [also characterized by decreased PGC1 α expression (225)] and subsequent reduction in the number of fully functional endothelial mitochondria may provide an explanation for the PAH-associated metabolic phenotype, *i.e.*, a shift from oxidative phosphorylation (glucose oxidation) to glycolysis. Furthermore, PAH-associated ECs display increased expression and activity of HIF-1 α , caused by oxidative stress (via decreased mitochondrial MnSOD expression) and lower levels of NO, ultimately downregulating the number of mitochondria (170, 607). The increased HIF-1 α levels, even under normoxic condi-

tions, induce transcription of hypoxia-responsive genes (46, 344) and thereby contribute to the metabolic shift from oxidative to glycolytic metabolism. Transcriptomic and metabolomic analysis of PMVECs from PAH patients confirmed increased gene expression of key glycolytic enzymes and GLUT1 and global activation of the glycolytic pathway (169).

However, increased glycolysis alone seems insufficient to sustain the total metabolic needs of a hyperproliferative phenotype. Indeed, the hyperproliferative phenotype of PAH-associated ECs has also been attributed to upregulation of the PPP, nucleotide salvage pathway, and the mitogenic polyamine biosynthesis pathway (169, 381). Moreover, stiffening of the pulmonary vascular extracellular matrix in PAH induces upregulation of glutaminase 1 (GLS1), pyruvate carboxylase (PC), and lactate dehydrogenase A (LDH-A) metabolic enzymatic activity, in part to promote glutamine metabolism in addition to glycolysis to meet the metabolic demands of increased proliferation and vascular remodeling (39). Finally, PAH-associated pulmonary ECs also display decreases in carnitine and FAO pathways, further highlighting their reduced oxidative metabolic nature (169). Noteworthy, PAH has recently been characterized further by intracellular lipid accumulation (upregulation of FA transporter molecule CD36) and reduced FA consumption in myocardium of PAH patients, due to reduced FAO, resulting in right ventricular lipotoxicity and ultimately right cardiac failure and death (55, 525, 526). Whether similar lipotoxicity also occurs in ECs specifically has not been reported yet.

C. Ocular Neovascularization

Ocular neovascularization is a feature of many eye diseases with diverse etiologies and is characterized by excess angiogenesis in one of the ocular tissues (retina, cornea, optic disk, and iris). Much like tumor vessels (see above in this section), the neovessels are structurally abnormal and leaky with blinding hemorrhages and fibrosis as a final outcome (307). In proliferative diabetic retinopathy (PDR) for example, excess angiogenesis occurs in response to hypoxic lesions that result from EC dysfunction and lack of efficient blood supply (449, 561). The resulting retinal neovessels are nonfunctional, lack pericyte coverage, and display increased vessel leakiness and as such aggravate the vascular undersupply of the retina and affect vision due to frequent vitreous hemorrhaging (451). The metabolic maladaptations in diabetic dysfunctional ECs have been discussed above and should further be explored as therapeutic targets, given that PDR accounts for ~5% of blindness cases worldwide.

Retinopathy of prematurity (ROP) is a blinding disorder that affects premature infants and involves excess oxygen-induced retinal neovascularization. In the mouse ROP

model, mice are exposed to increased oxygen tension, for a limited amount of time during which the retinal vasculature is still developing (P7–P12), causing retinal vaso-obliteration. Upon exposure to room air, the retina of the mice then becomes relatively hypoxic, leading to activation of angiogenesis and pathological vascular tuft formation (485). PFKFB3 blockade by 3PO in ROP mice at P12–17 attenuates vascular tuft formation (483). Likewise, treatment of ROP pups with etomoxir to inhibit FAO reduces vascular tuft formation (481) (FIGURE 14).

The novel concept of targeting EC metabolism has also been applied in other preclinical models for pathological ocular neovascularization. Mouse choroidal neovascularization (CNV) is a preclinical model of wet age-related macular degeneration (AMD) and can be induced in mice by laser injury of the Bruch's membrane. CNV in wet AMD is initiated by hypoxia and local inflammation and can be inhibited by targeting the angiogenic growth factors VEGF and PIGF (554). Experimental evidence shows that glycolytic flux is a determining factor in CNV in mice, since treatment of mice with 3PO reduces CNV lesions (483) and even amplifies the efficiency of VEGFR2 inhibition (483). Together, these findings illustrate the importance of EC me-

tabolism in different aspects of ocular diseases characterized by excessive neovessel formation.

IX. METABOLIC MEMORY OF ENDOTHELIAL CELLS: ENDOTHELIAL CELL METABOLISM AND EPIGENETICS

A peculiar trait of EC metabolism is the presumed existence of a so-called “metabolic memory.” In the context of diabetes, both biological and clinical data suggest that hyperglycemia-induced oxidative stress exerts long-lasting detrimental effects on vascular function, even after restoration of glycemic levels. In addition to the role of additional diabetes-related factors, a metabolic/hyperglycemic memory [with hyperglycemia driving stable molecular modifications, via (aberrant) epigenetic mechanisms, and perpetuating EC dysfunction despite normalization of glucose levels] may explain the poor reversibility of hyperglycemia-induced metabolic modifications (75, 98, 99, 470). Accumulating evidence supports such hypothesis that hyperglycemic stress (constant or transient), driven by a self-sustaining cycle of oxidative stress, has persistent effects on the vasculature (reviewed in Refs. 245, 246, 271, 419).

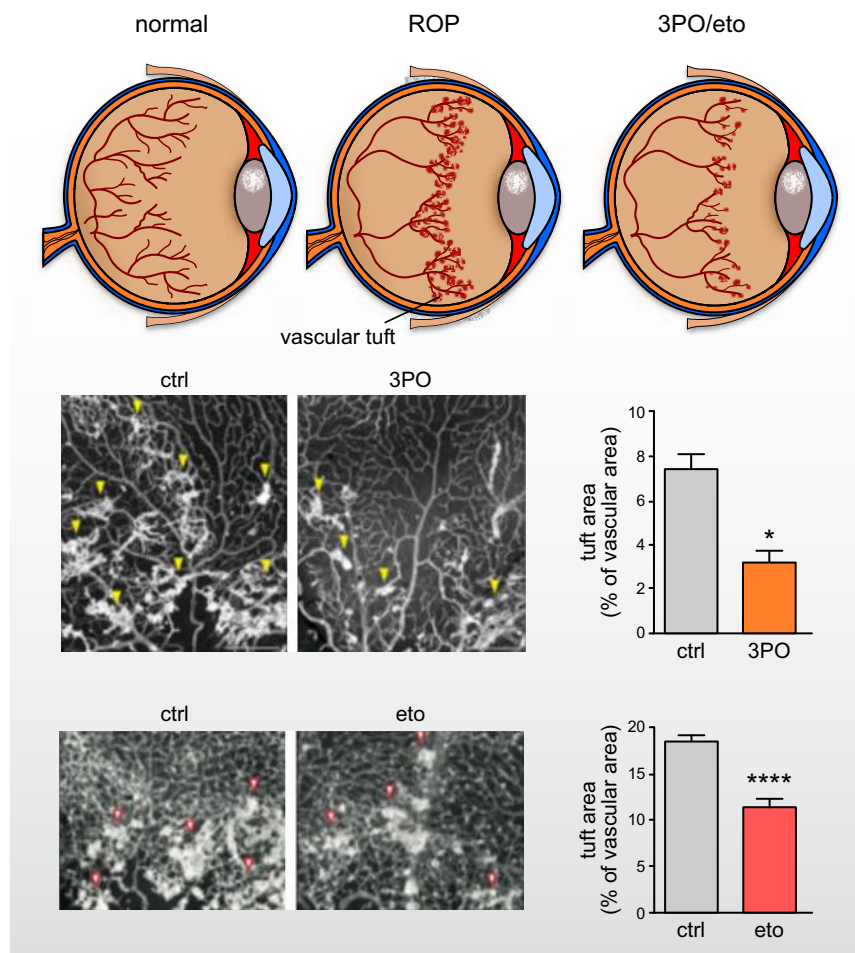


FIGURE 14. Blocking glycolysis or FAO mitigates pathological ocular neovascularization. In a mouse model for retinopathy of prematurity (ROP), treatment of the mice with 70 mg/kg of the PFKFB3 blocker 3PO significantly reduces the formation of pathological vascular tufts (yellow arrowheads). In the same model, blocking FAO with the CPT1a blocker etomoxir also attenuates tuft formation. The retinal microvasculature is stained with isolectin B4. Pictures and corresponding quantifications of vascular tuft area are from Schoors et al. (481), with permission from Macmillan Publishers Ltd., and Schoors et al. (483), with permission from Elsevier. The drawings at the top of this figure provide schematic overviews to recapitulate these findings. 3PO, 3-(3-pyridinyl)-1-(4-pyridinyl)-2-propen-1-one; eto, etomoxir.

Mitochondrial DNA damage, for example, persists despite restoration of normoglycemia (338). Moreover, hyperglycemia-induced oxidative stress promotes a pro-inflammatory memory in ECs, as elevated levels of PKC-activated NOX subunit p47phox persist upon lowering glucose levels (246). The mitochondrial adaptor protein p66^{Shc}, a key redox enzyme, plays a pivotal role in this oxidative stress-dependent metabolic and vascular memory. Its hyperglycemia-induced upregulation persists after glucose normalization and is associated with mitochondrial oxidative stress, reduced NO availability, and reduced ROS scavenging via MnSOD, NFκB-induced inflammation, and cellular death as well as insulin resistance in ECs (64, 78, 96, 415, 416, 418). The persistent upregulation of p66^{Shc} in ECs also sustains increased methylglyoxal levels and eNOS inhibition, thereby promoting endothelial dysfunction (100, 418, 643) (FIGURE 15). In line with this, deficiency of p66^{Shc} in mice (though not EC-specific) protects against hyperglycemia-induced endothelial dysfunction and high-fat diet-induced atherosclerosis (65, 637).

Hyperglycemic memory is closely linked to persistent epigenetic modification. As such, the sustained overexpression of p66^{Shc} upon glycemic normalization in ECs is dependent on promoter CpG hypomethylation and histone 3 acetylation (418). Increased acetylation of histone 3 in ECs exposed to high glucose can be relieved by overexpression of deacetylase SIRT1, thereby inhibiting p66^{Shc} expression and protecting against hyperglycemia-induced EC dysfunction in vitro and in vivo (419, 643). Overexpression of endothelial SIRT1 also restores hyperglycemia-perturbed activity and expression levels of AMPK and MnSOD, respectively (592, 642). In this context, it is also interesting to note that mice overexpressing SIRT1 in the endothelium show improved endothelial vasodilation and less atherosclerotic lesions on a high-fat diet (637, 643). Additional evidence reports that p53 may be a critical intermediate between SIRT1 and p66^{Shc} (272, 328). p53 gets acetylated and transcriptionally active upon reduction of SIRT1 deacetylase activity and has p66^{Shc} as one of its transcriptional targets (reviewed in Ref. 419). Overall, the SIRT1-p53-p66^{Shc} pathway may be responsible for the sustained EC dysfunction after glucose normalization. Interestingly, the methyltransferase Set7/9 is activated by hyperglycemic signals and inhibits SIRT1 activity. Set7/9 further leads to histone methylation of over 8,000 gene promoters, including the NFκB promoter leading to its activation and therefore contributing to endothelial dysfunction (271, 417). Taken together, epigenetic modification events seem to be critical for sustained EC dysfunction after glucose normalization and influence long-term complications of metabolic disease (FIGURE 15).

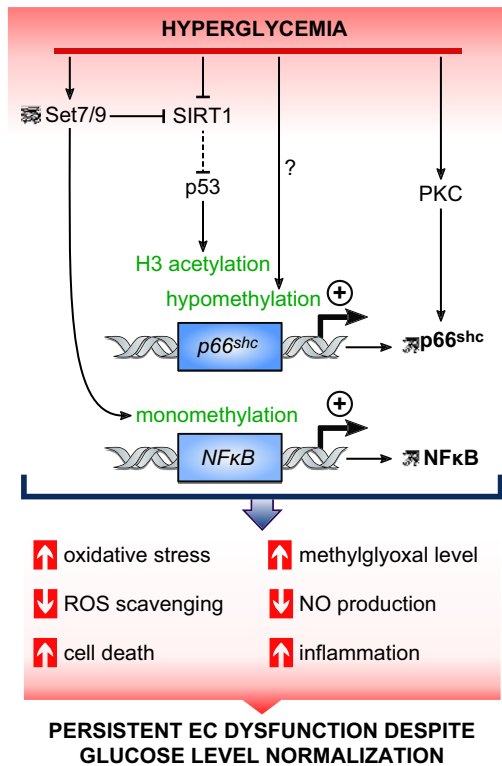


FIGURE 15. Molecular mechanisms underlying the hyperglycemic memory in ECs. Schematic and simplified scheme showing different (interconnected) molecular mechanisms and their contribution to a hyperglycemic memory in ECs. Hyperglycemic stimuli, even when followed by normal glucose restoration, act on different key mediators such as the methyltransferase Set7/9, the deacetylase SIRT1 and PKC which (epigenetically) change the expression levels/activity of NFκB and the mitochondrial adaptor p66^{Shc} to cause a persistent pro-inflammatory and increased oxidative stress state. More details on the intricate signaling leading to this hyperglycemic memory are provided in the main text. SIRT1, sirtuin 1; H3, histone 3; PKC, protein kinase C; NFκB, nuclear factor-kappa B; NO, nitric oxide; ROS, reactive oxygen species.

A body of evidence suggests that oxidative stress in the diabetic and atherosclerotic vasculature influences epigenetic modifications (150, 400, 413, 433, 524, 573), impacting expression of key pro-inflammatory and pro-atherosclerotic targets (VCAM-1, E-selectin, ICAM-1), and resulting in the self-maintenance of a harmful metabolic memory and EC dysfunction (172, 455). Furthermore, hyperglycemia and the diabetic state trigger a metabolic memory via epigenetic modulations in SMCs and macrophages (reviewed in Ref. 271), key cell types involved in the pathogenesis of atherosclerosis. Further investigating the mechanisms underlying this metabolic memory, including mapping the epigenome of diabetic ECs, and looking for means to revert this to the normal state, will be key in minimizing long-term diabetic vascular complications.

Of note, the anti-diabetic drug metformin was recently put forward as a promising therapeutic drug against the development of a metabolic memory, independent of its glucose-lowering activity via the following mechanism. Indeed, short-term high glucose treatment causes persistent EC se-

nescence (metabolic memory) by reducing SIRT1 deacetylase activity and inducing p300 acetyltransferase activity. Similarly to the findings described above, this causes p53 to become hyperacetylated and active, thereby driving p53/p21-mediated senescence. As a potent SIRT1 activator, metformin reduces the occurrence of this memory phenotype (634).

X. METABOLIC CROSSTALK

Intra- and intercellular communications provide important cues to ensure adequate tissue biogenesis and orchestrate physiological processes. Upon external stimuli (e.g., inflammation, hypoxia, tumorigenesis), these interactions may derail and become implicated in the etiology and evolution of several pathologies. One of the most fundamental ways of metabolite-based communication between ECs and other cell types in the body is by controlling endothelial uptake and transport of nutrients such as glucose and FAs. Additionally, surrounding mural or immune cells produce a wide variety of external stimuli (i.e., Dll4/Notch, VEGF/VEGFR2, FGF/FGFR; see sects. II and III) that can alter EC metabolism. Subsequent alterations in the levels of endothelial lactate production and excretion, for example, then impact the surrounding cells creating a metabolic crosstalk loop. Whether other metabolic intermediates of glycolysis, the TCA cycle, or FA metabolism participate in an intercellular crosstalk remains largely to be elucidated.

With glycolysis being the primary metabolic pathway for energy production in ECs (114), and lactate being the major end product of glycolysis, ECs excrete large amounts of lactate (423). Physiological lactate concentrations range from 1.5 to 3 mM in blood and tissues at baseline conditions (508) and can rise to >10 mM in disease settings such as atherosclerosis, rheumatoid arthritis, and cancer (90, 214, 235). Endothelial production of lactate and extracellular export can act as a vasoactive signal for pericytes. This interaction appears to be dynamically regulated based on the cellular energy status: when energy supplies are low, lactate causes vasodilation, whereas when energy supplies are abundant, lactate acts as a vasoconstrictor (616). In addition, lactate has diverse functions in a variety of cell types, including direct regulation of global gene transcription in skeletal muscle and neurons (224, 622) and polarization of immune cells (90, 214). Lactate has further been shown to inhibit glycolytic activity in T-cells, possibly through downregulation of HK1 or direct inhibition of PFK, and to inhibit cytotoxic T-cell responses and cause chronic inflammation through enhanced IL-17A secretion, which activates Th17 cells (31). In cancer cells, lactate has various functions (235), including stimulating cell migration and progression (29, 47), promoting glutamine uptake and metabolism (428), and direct binding to n-MYC downstream-regulated gene 3 protein (NDRG3), a PHD2-binding protein, resulting in the stabilization and activation of

Raf-ERK1/2 signaling, thereby promoting hypoxia responses in cancer cells and angiogenesis (305). The wide variety of responses to lactate in other cell types warrants further investigation and consideration; strategies targeting EC glycolysis may yield secondary benefit through limiting lactate production (FIGURE 16).

Conversely, lactate produced by other cell types has been shown to have numerous effects on ECs. For example, lactate promotes an “angiogenic switch” in ECs, through the upregulation of VEGF and VEGFR2 (297), and promotes EC migration (32). Furthermore, lactate activates PI3K/Akt signaling in ECs via ligand-mediated activation of the tyrosine kinases Axl, Tie2, and VEGFR2, promoting angiogenesis (471) (FIGURE 16). In the tumor context (see above in this section), lactate influx in ECs through MCT1 leads to stimulation of the NF κ B/IL8 pathway in a ROS- and I κ B α -dependent manner, promoting tumor angiogenesis (557). Targeting MCT1 in ECs rescues lactate-mediated HIF1 α activation and reduces tumor angiogenesis (506). Further investigation on the efficacy of targeting EC lactate transporters in other disease settings will be of future interest.

Over the last decade, the study of extracellular vesicles (EVs) has received growing interest. This less conventional mode of communication involves a broad variety of cells and is particularly modulated by extracellular signals. EVs can contain a number of factors including metabolites, nucleic acids (mRNA, DNA, miRNA), and proteins (soluble and transmembrane), all of which can directly stimulate target cells (92). Cardiomyocytes and ECs, the two main cell types in the heart, directly influence each other, particularly upon glycemic changes. Indeed, under in vitro glucose starvation conditions, the EV content of cardiomyocytes is remodeled and stimulates angiogenesis and proliferation in recipient ECs (187). Starved cardiomyocyte-derived EVs enhance glucose transporter expression (GLUT1 and 4) along with the glycolytic activity in ECs (186). Interestingly, in response to these vesicles, ECs secrete pyruvate in their microenvironment, presumably to sustain cardiomyocyte function (187). Finally, given that the contents of EC-derived EVs may reflect cellular stress or disease state, it merits further attention whether these EVs could act as diagnostic markers in vascular disorders (FIGURE 16).

XI. THERAPEUTIC OPPORTUNITIES AND FUTURE PERSPECTIVES

As evidenced above, ECs rewire their central metabolism when becoming dysfunctional and during pathological vessel overgrowth. This obvious connection between metabolic maladaptation in ECs and illness calls for the exploration of novel metabolism-centric treatment strategies. Growing interest in and deeper understanding of the most detailed features of EC metabolism will advance translation into therapeutics. As such, by targeting ECs in their very core, metabolism-centric therapies might offer novel thera-

EC METABOLISM

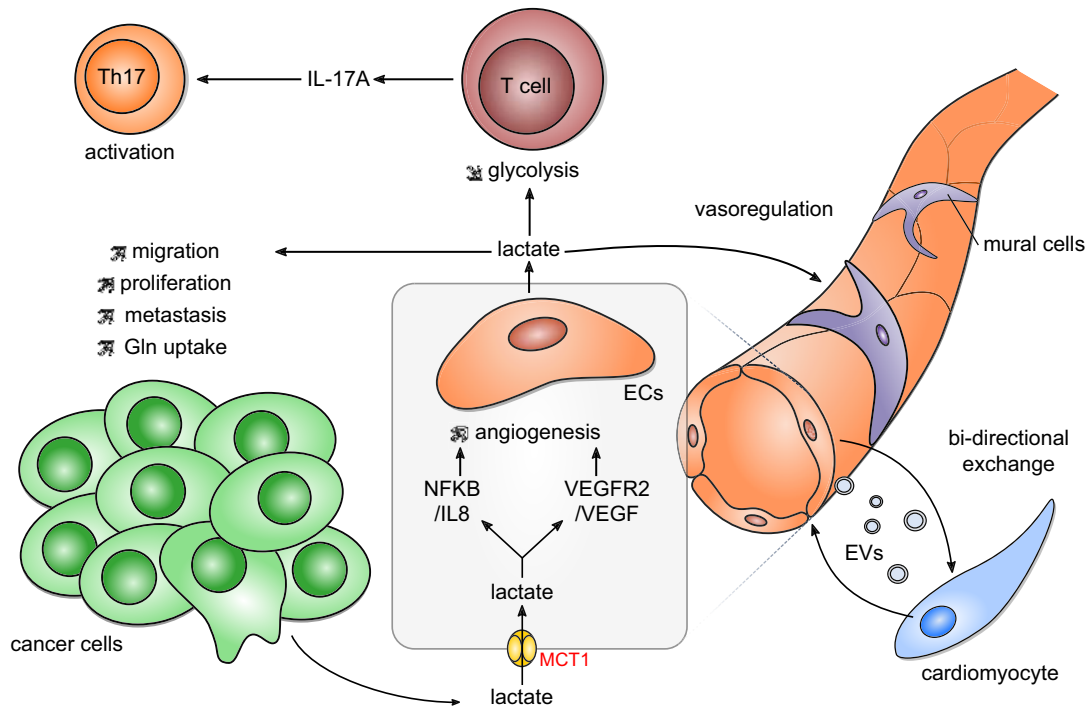


FIGURE 16. Two-way metabolic crosstalk between ECs and other cell types. Schematic and simplified view on possible metabolic crosstalk between ECs and other cell types. ECs use lactate, the end product of glycolysis, to signal to other cell types and thereby influence the immune compartment, cancer cell growth but also vasoconstriction/vasodilation (for details see main text). Conversely, lactate derived from other cell types, for example, cancer cells, can be taken up by ECs through the MCT1 transporter and drive (tumor-)angiogenesis by inducing VEGF/VEGFR2 or NFκB/IL8 signaling. Another way of crosstalk is through the exchange of EVs (containing metabolites, nucleic acids, and proteins) as exemplified here by the bidirectional exchange of EVs between ECs and cardiomyocytes (for more details, see main text). Gln, glutamine; EV, extracellular vesicles; IL8, interleukin 8; IL17A, interleukin 17A; MCT1, monocarboxylate transporter 1; NFκB, nuclear factor-kappa B; Th17, T helper 17 cell; VEGFR2, VEGF receptor 2.

peutic opportunities, as compared with current growth factor-centric anti-angiogenic approaches that suffer from acquired resistance and escape mechanisms (reviewed in Ref. 583). Also, unlike current anti-angiogenic therapies, which block a single target (such “targeted” strategies regularly fail in the clinic because of the induction of compensatory mechanisms), targeting EC metabolism is a more global approach, as angiogenic factors converge onto EC metabolism and ECs need energy, biomass, and redox control to form new vessel sprouts, and, as explained below in this section, it is possible to target key metabolic players without inciting compensatory feedback mechanisms.

Of utmost importance for future research is the quest for additional specific, perhaps even unique, metabolic features that distinguish ECs from other cell types. From a therapeutic point of view, such unique targets will be key to successful metabolism-centric anti-angiogenic strategies. As mentioned above (see sect. III), ECs are highly glycolytic and use FAO for a rather unique purpose (114, 481). Whether glutamine (or other amino acids) is used to serve a metabolic purpose that is unique for ECs, remains to be determined. Apart from unique traits, the search for synthetic lethality will most probably be in the limelight of future EC metab-

olism research. Inhibition of one particular metabolic target might cause ECs to re-route their metabolism and to overcome the initial blockade. Identification and subsequent targeting of the compensatory metabolic pathway creates opportunities for more efficient therapeutic strategies. Forward and unbiased metabolomics approaches (see further below in this section) should facilitate identification of such synthetically lethal metabolic rewiring.

Initial proof-of-principle for metabolism-centric treatment of pathological angiogenesis is provided by (pharmacological) inhibition of PFKFB3 (482, 483, 608). Revoking the dogmatic view that successful antimetabolic therapies require complete and permanent glycolysis inhibition proved crucial in this matter. Indeed, the PFKFB3 inhibitor tool compound 3-(3-pyridinyl)-1-(4-pyridinyl)-2-propen-1-one (3PO) causes EC glycolysis only to drop transiently and by no more than 40%. In vivo, this matches the surplus in glycolysis needed for quiescent ECs to start forming new sprouts and apparently suffices to mitigate pathological angiogenesis (482, 483). ECs, especially tumor ECs, are so sensitive to partial glycolysis inhibition (because they are so glycolysis addicted and critically rely on this metabolic pathway, more than other cell types), which thereby also offers greater selectivity to paralyze ECs without neces-

sarily inducing toxic effects in other cell types. Complete glycolysis inhibition on the other hand affects healthy quiescent vessels as well as other cell types, relying on glycolysis too. In contrast to ECs, which cannot adapt to (deep) glycolysis blockade, other cell types can switch to other (oxidative) metabolic pathways to survive (482). More complete and sustained inhibition of glycolysis with 2DG indeed causes toxicity in ECs *in vitro* (483) and cancer patients under 2DG treatment present adverse effects and the disease still progresses (206, 442). The advantages 3PO brings over 2DG relate to dosing and mode of action and have been discussed previously (206, 483). PFK158, a novel, more potent derivative of 3PO (535), successfully made it through a phase 1 multicenter clinical trial in patients with solid malignancies (<http://www.advancedcancertherapeutics.com/clinical-trials.html>). Whether it can be used as a novel anti-angiogenic drug will need further investigation. Additional screens for novel PFKFB3 inhibitors have been undertaken (54), yet await further testing in (pre)clinical settings.

Other novel strategies can come from unexpected sources. Propranolol, a nonselective β -adrenergic receptor-blocking agent, is successfully being used to treat infantile hemangiomas (IH, most common vascular tumor in children) (304). A possible mechanism by which propranolol stops the growth and induces involution of IHs is the upregulation of PTEN and subsequent inhibition of AKT activity, as shown in the hemangioma-derived endothelial cell line XPTS-1 (316). Given that Akt activity affects glycolysis (and other metabolic pathways) (462), the potential impact of propranolol on EC metabolism could be exploited for therapeutic options in vascular disorders (with a hyperglycolysis component).

As discussed above, tumor vessels are abnormal and their ECs display a hyperglycolytic metabolism, a reduction of which through partial PFKFB3 inactivation normalized the affected vasculature, reduced metastasis, and improved chemotherapy, even of a standard dose (66). Overall, precisely because ECs are so glycolysis addicted and tumor ECs even more so, they also become more sensitive to glycolysis inhibition, even by very low amounts. In fact, available preclinical evidence suggests that the “less is more” principle might well be a key paradigm-shifting objective in treating pathological angiogenesis with perturbed vascular cell metabolism. In a way, the hyperglycolysis in TECs bears resemblance to an overheated car engine; it suffices to cool the overheated engine down to normal levels to prevent activated ECs to form excess vessels and restore normalized vessel structure and function. In addition, precisely because 3PO blocks an “activator of an activator” of glycolysis and lowers glycolysis by no more than 35% *in vivo*, this treatment regimen does not evoke metabolic compensatory mechanisms (114, 482, 483), although further clinical evaluation will be necessary. Since vascular pericytes are also highly glycolytic, like ECs, a low dose of 3PO rendered these mural cells also more quiescent and increased their

adhesiveness to ECs (by upregulating N-CAM adhesion molecule), thereby promoting pericyte coverage and tumor vessel normalization (66). Lastly, targeting endothelial PFKFB3 with 3PO may possibly be a valuable strategy in treating atherosclerosis too, as the resulting dampened glycolytic flux could maintain EC quiescence even under turbulent shear stress conditions, similar to atheroprotective KLF2-induced repression of PFKFB3 under uniform laminar shear stress conditions (126).

In vascular disorders with an endothelial hyperglycolysis component, metabolic inhibitors might offer an additional advantage in terms of routes of administration. Wet age-related macular degeneration (AMD), a leading cause of blindness in the elderly, is treated with anti-VEGF therapy administered by intraocular injection. This leaves the patient with local side effects and personal discomfort originating from the (repeated) needle injections in the eye, in addition to resistance in a formidable fraction of treated patients. In a preclinical mouse model for AMD, systemic delivery of the glycolytic inhibitor 3PO reduces choroidal neovascularization without any need for intraocular injections (483). Along the same lines, systemic treatment of mice with the FAO inhibitor etomoxir reduced pathological vascular tuft formation in an ROP model (see sect. VIII) and inhibited lymphatic neovessels from vascularizing the cornea after corneal cauterization (591), an established model for blinding corneal neovascularization (591). In line with the above discussed newly uncovered role for FAO-derived acetyl-CoA in histone acetylation in LECs and how this drives lymphangiogenesis, supplying the mice with acetate to restore acetyl-CoA fully abolished the inhibitory effects of etomoxir on lymphatic neovascularization (591). These *in vivo* findings may offer novel therapeutic opportunities towards blocking lymphangiogenesis in a cancer setting or conversely towards restoring lymphangiogenesis in lymphedema, for which currently no efficient therapies are available.

We have illustrated that metabolic adaptations resulting in EC dysfunction in both diabetes and atherosclerosis are mainly caused by oxidative stress. Despite the promising findings from studies targeting metabolic regulators [i.e., AMPK (72), PARP1 antagonists (133)] to decrease this oxidative stress, outcomes of clinical trials using antioxidant therapies have been rather disappointing (309). Also, dietary BH₄ and arginine supplementation to avert eNOS uncoupling showed no benefits in patients (106, 587). As such, a “prophylaxis rather than cure” approach or combination therapy may be required. A promising metabolic target is aldose reductase (enzyme converting excess glucose into sorbitol in the polyol pathway), which has several inhibitors currently undergoing clinical trials for diabetic vascular complications (208).

Even though specific targeting of the endothelium for therapeutic purposes remains challenging, some new strategies are arising. For instance, polymeric nanoparticles consisting of

low-molecular-weight polyamines and lipids deliver siRNAs to lung ECs without reducing target gene expression in hepatocytes or pulmonary/peritoneal immune cells (109). Taking advantage of diseased EC-specific gene expression to guide drug carriers towards the desired site of delivery might possibly become a promising approach, which, on top, would require lower drug concentrations. As such, nanoparticles equipped to recognize and bind EC-expressed inflammation markers might be a tool for delivering metabolic drugs specifically to the atherosclerotic region (reviewed in Ref. 329). Another example involves the higher expression of the apelin receptor APJ in tumor versus healthy ECs; apelin-conjugated liposomes were efficiently taken up by tumor ECs in tumor-bearing mice (269). Likewise, integrin $\alpha\nu\beta 3$ -targeted nanoparticles carrying cytotoxic doxorubicin accumulated at and induced apoptosis at integrin $\alpha\nu\beta 3$ expressing tumor vessels (386). In case these approaches become better validated and withstand scrutiny of clinical trials, loading the nanocarriers with metabolic inhibitors could become a means to specifically target derailed EC metabolism in disease.

Finally, the near future will bring a logic yet necessary change to the EC metabolism field in the way new metabolic targets will be identified. Indeed, genotype-to-phenotype studies, characterizing the angiogenic role of a preselected metabolic enzyme (reverse approach), have provided seminal insights into EC metabolism. Given that the metabolome represents the final product of the (epi)genome, and complements transcriptomics and proteomics (18, 140), increasingly more studies engage in unbiased and untargeted omics approaches (forward approach), using ECs from healthy and diseased tissues, also of patients (18, 205, 570, 648). The integration of such omics data, for example through *in silico* genome-scale metabolic modeling (GEM), enables a forward, data-driven, and all-encompassing omics approach to identify new metabolic targets as possible disease-drivers or -modifiers (49, 274, 629). In contrast to the cancer metabolism field, the EC metabolism field is in its early infancy and has yet to apply such forward approaches (189, 366). With the current advances in isolation and culturing techniques of ECs from different tissues and/or disease states (e.g., TEC vs. NEC, diabetes, atherosclerosis, and arterial hypertension; see sects. VII and VIII), the stage is all set to explore and exploit forward omics approaches (66). The advent and general applicability of techniques to study *in vivo* EC metabolism, for example by *in vivo* metabolic tracing and metabolic imaging (112, 226, 388), will greatly deepen our current understandings, especially given the substantial influence of the microenvironment on cellular metabolism (67, 112).

XII. CONCLUDING SUMMARY

Here, we comprehensively reviewed the existing literature on EC metabolism, both the more basic aspects by listing and describing the different metabolic pathways and its determinative role in developmental and pathological an-

giogenesis. Indeed, EC metabolism stretches far beyond the dogmatic view of simply fueling cell growth and activity. Several metabolic pathways act in parallel with genetic/growth factor signaling to sustain appropriate EC behavior. This concept substantially gains importance when derailed metabolism renders ECs dysfunctional and causes some of the most life-threatening disorders known to humans.

With seminal findings on endothelial glycolysis and FAO being translated towards possible targets in these disorders, other metabolic pathways still require further insight into their exact roles in angiogenesis. Does glutamine metabolism hold the key to further unlock EC metabolism-centric anti-angiogenic strategies? It is undoubtedly a highly attractive target both because of already gathered knowledge on its role in ECs (see sect. III) and the recent development of inhibitors with high specificity for rate-limiting enzymes in glutamine metabolism (361). What is the role of other AAs (like serine, asparagine, aspartate,...), the metabolism of which is hardly being studied in ECs, let alone in vessel sprouting?

Emerging evidence suggests that diseases affect EC subtypes in a vascular bed-specific pattern. For instance, diabetes causes EC dysfunction in skin, peripheral nerves, heart, and kidney but stimulates EC growth in the retina (see sects. VII and VIII). Yet, current anti-angiogenic therapies do not discriminate between different EC types in different vascular beds. This then raises the question if future anti-angiogenic therapy should be “tailored” to EC subtype and vascular bed. The observations that EC heterogeneity is indeed paralleled by differences in metabolism (see sect. VI) create both the opportunity and the formidable challenge to accomplish such “tailored” strategies.

Developing further knowledge on the most intricate aspects of EC metabolism such as metabolic compartmentalization, metabolic cross talk with other cell types, and EC subtype-specific metabolic traits is another future challenge in this young field and a prerequisite to the development of novel therapeutic strategies.

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DISCLOSURES

P. Carmeliet declares to be named as inventor on patent applications claiming subject matter related to findings reviewed in this manuscript. The other authors report no conflict of interest financial or otherwise.

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