Prolyl hydroxylase domain enzymes: important regulators of cancer metabolism

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Abstract: The hypoxia-inducible factor (HIF) prolyl hydroxylase domain enzymes (PHDs) regulate the stability of HIF protein by post-translational hydroxylation of two conserved prolyl residues in its α subunit in an oxygen-dependent manner. Trans-4-prolyl hydroxylation of HIFα under normal oxygen (O2) availability enables its association with the von Hippel-Lindau (VHL) tumor suppressor pVHL E3 ligase complex, leading to the degradation of HIFα via the ubiquitin-proteasome pathway. Due to the obligatory requirement of molecular O2 as a co-substrate, the activity of PHDs is inhibited under hypoxic conditions, resulting in stabilized HIFα, which dimerizes with HIFβ and, together with transcriptional co-activators CBP/p300, activates the transcription of its target genes. As a key molecular regulator of adaptive response to hypoxia, HIF plays important roles in multiple cellular processes and its overexpression has been detected in various cancers. The HIF1α isoform in particular has a strong impact on cellular metabolism, most notably by promoting anaerobic, whilst inhibiting O2-dependent, metabolism of glucose. The PHD enzymes also seem to have HIF-independent functions and are subject to regulation by factors other than O2, such as by metabolic status, oxidative stress, and abnormal levels of endogenous metabolites (oncometabolites) that have been observed in some types of cancers. In this review, we aim to summarize current understandings of the function and regulation of PHDs in cancer with an emphasis on their roles in metabolism.

Keywords: prolyl hydroxylase domain (PHD), hypoxia-inducible factor (HIF), metabolism, mouse models, hydroxylation, 2-oxoglutarate-dependent dioxygenases

Introduction

Low oxygen (O2) and nutrient availability are often encountered in solid tumors due to abnormal vasculature and rapid proliferation of cancer cells.1 Adaptation to these microenvironment changes involves alterations in the expression of genes that regulate cellular energy production, biosynthesis, cell growth, and redox homeostasis. This response is, in part, mediated by the transcription factor hypoxia-inducible factor (HIF), a key regulator of the mammalian hypoxia response. The HIF signaling cascade encompasses diverse cellular pathways, some of which also intersect with tumorigenic processes.2,3

HIF is a heterodimeric transcription factor comprised of an O2-sensitive α subunit and a constitutively expressed β subunit, both of which are basic helix-loop-helix Per-ARNT-Sim domain proteins.4 The stability of HIF is primarily regulated by post-translational prolyl hydroxylation of HIFα, a reaction catalyzed by the HIF prolyl hydroxylase domain proteins (PHDs), a group of enzymes that act as O2 sensors in metazoans.5 PHD enzymes were first described roughly 10 years after the
discovery of HIF. They are members of a large family of non-heme iron-dependent dioxygenases that utilize ferrous iron (Fe(II)) as a co-factor to catalyze the four-electron reduction of molecular $O_2$. They incorporate each $O_2$ atom, respectively, into the tricarboxylic acid (TCA) cycle metabolite 2-oxoglutarate (2OG) and the substrate polypeptide, forming succinate, carbon dioxide, and, in the case of PHDs, trans-4-hydroxylated prolyl products. The three main PHD isoforms, PHD1, PHD2, and PHD3 (also termed EGLN2, EGLN1, and EGLN3, respectively) have overlapping but unique tissue expression patterns. PHD2 is present in most tissues, whereas PHD1 is mainly in testes but also in brain, kidney, heart, and liver, and PHD3 showed highest expression in the heart. Both PHD2 and PHD3 are strongly induced by hypoxia. The three isoforms share high sequence homology in their C-terminal catalytic domains, but not in their $N$-termini, the function of which remains to be elucidated.

There are three HIF isoforms (HIF1$\alpha$, HIF2$\alpha$, and HIF3$\alpha$). HIF1$\alpha$ is ubiquitously expressed; HIF2$\alpha$ expression is more cell-specific, such as in endothelial, parenchyma, and interstitial cells, whereas HIF3$\alpha$ is less well studied and has multiple splice variants, some of which lack the transactivation domain present in HIF1$\alpha$ and HIF2$\alpha$. Under normal $O_2$ availability, HIF$\alpha$ is constantly expressed and hydroxylated by PHDs on two conserved prolyl residues (Pro-405 and Pro-531 in HIF1$\alpha$) present within an LXXLAP motif in its $O_2$-dependent degradation domain. Trans-4-prolyl hydroxylation confers a $>1,000$ fold increase in binding affinity to the protein pVHL (von Hippel-Lindau tumor suppressor), which is part of an E3-ubiquitin ligase complex that mediates ubiquitination and degradation of HIF$\alpha$ by the 26S proteasome. Because $O_2$ is an obligatory substrate for PHDs, HIF$\alpha$s escape PHD-dependent hydroxylation under hypoxic conditions, translocate to the nucleus and dimerize with the $\beta$ subunit (also termed ARNT), and through binding to hypoxia-response elements in promoter regions of target genes, activate the transcription of its target genes (Figure 1). Another layer of regulation is conferred through the hydroxylation of a specific asparaginyl residue (Asn-803 in HIF1$\alpha$) in the C-terminal activation domain of HIF$\alpha$, a post-translational modification catalyzed by another

![Image](https://www.dovepress.com/20142/dovepress-hypoxia-20142-v01_93-2.gif)

**Figure 1** PHDs are 2OG-dependent dioxygenases that regulate the stability of HIF$\alpha$. In the presence of oxygen, PHDs post-translationally hydroxylate a prolyl residue in the NODDD and CODDD of HIF$\alpha$ subunits, which leads to its interaction with pVHL and ubiquitin-mediated degradation of HIF$\alpha$ by the 26S proteasome. Because PHDs have a low affinity for oxygen, they become inactive under hypoxic conditions, which allow HIF$\alpha$s to escape degradation, migrate to the nucleus, form a complex with the $\beta$ subunit and transcriptional co-activators p300/CBP and regulate the transcription of its target genes by binding to hypoxia-responsive elements in their promoter regions. Fumarate and succinate structurally mimics 2OG (succinate is also a product of the reaction) and can competitively inhibit PHD activities when present at elevated concentrations, as observed in some cancer cells. R-2HG can enhance PHD activity and promote HIF$\alpha$ degradation. In addition, ROS has also been suggested to modulate PHD activity.

**Abbreviations:** 2OG, 2-oxoglutarate; CODDD, C-terminal oxygen-dependent degradation; HIF, hypoxia-inducible factor; HRE, hypoxia-responsive element; NODDD, N-terminal oxygen-dependent degradation; p300/CBP, p300/CREB-binding protein; OH, hydroxyl group; PHDs, prolyl hydroxylase domain proteins; R-2HG, (R)-2-hydroxyglutarate; ROS, reactive oxygen species; Ub, ubiquitin; pVHL, von Hippel–Lindau tumor suppressor.
2OG-dependent dioxygenase termed factor-inhibiting HIF (FIH). β-hydroxylation of Asn-803 blocks the interaction of HIFα with its transcriptional co-activators CBP (cAMP response element-binding protein)/p300, thereby inhibiting HIF activity. Unlike FIH, which has a relatively tight affinity for O₂ (Kₘ value ~90 µM), PHDs bind O₂ loosely with Kₘ values of each isoform in the range of 230–250 µM. This concentration is well above observed physiological O₂ levels, making the PHDs sensitive to variations in local O₂ in tissues and thus acting as O₂ sensors. However, the multiple co-substrate and co-factor dependent nature of the PHDs raises the possibility that they also respond to metabolic alterations (Figure 1). Further, PHDs have been reported to have HIF-independent functions. In this review, we aim to summarize the current understandings of the roles of PHD enzymes in tumorigenesis with an emphasis on metabolism.

**HIF-dependent regulation of metabolism**

Elevated HIF1α and HIF2α levels have been observed in many human cancers and are often associated with poor prognosis. Particularly, a major proportion of clear cell renal cell carcinomas (ccRCCs) lose the function of VHL, which results in the inability to degrade HIFα in an O₂-dependent manner. HIF1α and HIF2α have both overlapping and non-redundant functions. Overall, HIF1α is associated with metabolism and energy production (Figure 2), whereas HIF2α has a more pro-proliferative effect that is advantageous to tumor growth.

**Glycolysis**

Many cancer cells exhibit enhanced capacity for anaerobic metabolism of glucose to produce lactate, even under sufficient O₂ availability. This phenomenon was first described by Warburg nearly a century ago, and also forms the basis of diagnostic cancer imaging using the labeled glucose analogue fluorodeoxyglucose in position emission tomography. A high glycolytic flux allows for continued adenosine triphosphate (ATP) production independent of oxidative phosphorylation in the mitochondria, reduces the generation of reactive oxidative species (ROS), and provides glycolytic intermediates that could be utilized by biosynthetic pathways to support growth. HIF1α is known to upregulate glycolysis by activating the transcription of enzymes on the glycolysis pathway, such as 6-phosphofructo-1-kinase, hexokinase 2, and fructose-bisphosphate aldolase A. Additionally, HIF1α also regulates the auxiliary processes to glycolysis, such as increasing glucose uptake by activating the glucose transporter 1, and facilitating glucose carbon efflux via lactate by upregulating lactate dehydrogenase and monocarboxylate carrier MCT4.

Pyruvate kinase (PK) catalyzes the final step in glycolysis, converting phosphoenolpyruvate (PEP) to pyruvate. The M2 isoform of pyruvate kinase (PKM2) is another glycolytic enzyme induced by HIF1α. PKM2 may be present as a highly active tetramer, or in a less active dimeric form, which is the case in many cancer cells. Due to the crucial position of PK on the glycolytic pathway, the presence of the inactive PKM2 dimer fine-tunes the glycolysis rate, causing accumulation of glycolytic intermediates, which can be channeled into biosynthetic pathways to produce nucleotides, phospholipids, and amino acids (reviewed by Vander Heiden et al). Thus, PKM2 has an anabolic effect by mediating glucose utilization in a manner that supports both bioenergetics and biosynthesis.

Recently, it has been shown that HIF1α also physically interacts with the PKM2 protein, resulting in increased transcriptional activity. Additionally, PHD3 catalyzes the hydroxylation of PKM2 on two prolyl residues at moderately hypoxic conditions, which strengthens the PKM2–HIF1α interaction and enhances HIF activity, forming a positive feedback loop for regulating glucose metabolism. A further layer of complexity is added by the fact that accumulation of the PKM2 substrate PEP promotes PEP-dependent histidine phosphorylation and thereby enhances the activity of phosphoglycerate mutase. Phosphoglycerate mutase is a glycolytic enzyme that catalyzes the conversion of 3-phosphoglycerate to 2-phosphoglycerate. 2-phosphoglycerate can stimulate the activity of phosphoglycerate dehydrogenase, the first and key regulatory enzyme in the serine biosynthesis pathway, whereas elevated 3-phosphoglycerate competitively inhibits the pentose phosphate pathway enzyme 6-phosphogluconate dehydrogenase, placing phosphoglycerate mutase at an important position in glucose metabolism.

In addition to promoting glycolysis, HIF also inhibits the oxidation of glucose carbon in the mitochondria by up-regulating pyruvate dehydrogenase kinase-1 and -3, which phosphorylates and thereby inactivates pyruvate dehydrogenase (PDH), the mitochondrial enzyme responsible for converting pyruvate to acetyl-CoA to prevent glycolysis-derived pyruvate from entering the tricarboxylic acid (TCA) cycle. Under hypoxia, mitochondrial respiration generates increased ROS, reasoning the diversion of pyruvate away from the TCA cycle, but perhaps another crucial advantage of metabolizing pyruvate through the lactate axis instead is the inherent need for the regeneration of co-factor nicotinamide...
adenine dinucleotide (NAD)$^+$ in order to sustain a continued high glycolytic flux.

**Mitochondrial activity**

In addition to limiting pyruvate availability to the TCA cycle, HIF also regulates mitochondrial activity in a manner that decreases $O_2$ consumption and promotes $O_2$ conservation in order to maximize respiratory efficiency and limit ROS generation under low $O_2$ tension. For example, HIF1α transcriptionally activates the mitochondrial protein NDUF4L2 (NADH dehydrogenase [ubiquinone] 1 alpha subcomplex 4-like 2), which decreases $O_2$ consumption by inhibiting electron transport chain Complex I activity.\(^{32}\) HIF also modulates cytochrome $c$ oxidase (electron transport chain complex IV) by activating transcription of cytochrome $c$ oxidase subunit IV-2 and ATP-dependent protease La, a mitochondrial protease that specifically degrades the cytochrome $c$ oxidase subunit IV-1 isoform, leading to optimized respiration efficiency under hypoxia.\(^{33}\) Further, HIF1 regulates the expression of micro-RNA mir-210, causing downregulation of the Complex I subunit NDUFA4 (NADH dehydrogenase [ubiquinone] 1 alpha subcomplex), Complex II subunit SDH (subunit D of succinate dehydrogenase [SDH] complex), the iron-sulfur cluster scaffold proteins 1/2 and the cytochrome $c$ oxidase assembly protein COX10.\(^{34,35,36,37}\) Finally, the HIF target gene BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 impairs mitochondrial bioenergetics and promotes mitophagy, thereby conferring hypoxia tolerance.\(^{38,39}\)
Glycogen and lipid metabolism

Significant lipid and glycogen accumulation occurs in some types of cancer, such as the VHL-defective ccRCC, giving its clear cell phenotype. HIF can enhance glycogen synthesis under hypoxia, leading to increased glycogen stores in both non-cancer and cancer cells. Both HIF1α and HIF2α induce the first enzyme in glycolysis, phosphoglucomutase 1, whereas HIF1α also upregulates other glycogenic enzymes, including glycogen synthase 1, glucose-1-phosphate uridylyltransferase and 1,4-α glucan branching enzyme.

HIF can also influence lipid metabolism. For example, HIF1α specifically induces the phosphatidate phosphatase isoform lipin 1, which is an enzyme involved in triglyceride biosynthesis. Hypoxia induces the transcriptional factor sterol regulatory-element binding protein-1 through phosphorylation of protein kinase B and activation of HIF1α, leading to upregulation of fatty acid synthase. HIF1α upregulates peroxisome proliferator-activated receptor-γ to activate fatty acid uptake and glycerolipid biosynthesis, whereas constitutive activation of HIF2α resulted in severe hepatic steatosis associated with impaired β-oxidation, decreased lipogenic gene expression, and increased lipid storage capacity. Interestingly, in VHL-mutant RCC cells, HIF2α promoted glutamine catabolism to fuel lipid synthesis through the reductive carboxylation pathway, by which glutamine-derived 2OG is converted to citrate by the NADPH-dependent isocitrate dehydrogenase isoforms 1 or 2 (IDH1/2) and aconitase. Hif1α expression also induced reductive carboxylation in mouse neonatal epithelial kidney cells. Mechanistically, it was proposed that HIF expression induces low intracellular citrate levels, which enhances glutamine utilization through the reductive flux of the TCA cycle to support lipogenesis.

Antioxidative effect

Both HIF isoforms have been reported as upstream regulators of an antioxidative response in different cell types. HIF1α reduces mitochondria-dependent generation of ROS under hypoxia by promoting anaerobic metabolism of glucose. Increased flux through the pentose phosphate pathway, in part mediated by PKM2, produces NADPH, essential for countering oxidative stress. Hif2α-deficient mice exhibited multiple-organ dysfunctions and enhanced oxidative stress, and Hif2α was shown to regulate antioxidant enzymes, including superoxide dismutase 1, superoxide dismutase 2, glutathione peroxidase 1, and catalase. HIF2α knockdown in human lung adenocarcinoma cells also led to lower expression levels of antioxidant enzymes, including heme oxygenase 1, ceruloplasmin, crystallin, peroxiredoxin 3, and glutathione peroxidase 8.

HIF-independent regulation by PHDs

Although HIF is the most well-known substrate, PHDs have been suggested to have other direct or indirect targets. Here we summarize a few findings in current literature that may be associated with tumorigenic processes.

Nuclear factor kappa-light-chain-enhancer of activated B cells pathway signaling

The transcription factor nuclear factor kappa-light-chain-enhancer of activated B cells (NF-κB), which is involved in inflammatory and innate immune responses, is constitutively activated in some cancers. PHD1 and PHD3 can inhibit IκB kinase β (IKKβ), leading to decreased NF-κB signaling. It has been suggested that the regulation of IKKβ occurs via PHD-dependent hydroxylation of a putative LXXLAP motif present in the IKKβ proteins. However, PHD3 may also inactivate IKKβ by blocking its interaction with the heat shock protein 90 in a hydroxylation-independent manner. In line with this, PHD2 has been shown to downregulate angiogenesis and vasculogenesis by inhibiting angiogenin and interleukin 8 via the NF-κB pathway. Further, haplo-deficient Phd2 mice exhibited activation of NF-κB signaling in tissue-resident M2-like macrophages, causing increased collateral arteriogenesis (Table 1).

Activating transcription factor 4

Activating transcription factor 4 (ATF4) is a transcription factor that regulates genes involved in redox balance, amino acid metabolism, autophagy, and angiogenesis, promoting tumor survival under hypoxic and nutrient-deprived environments. It has been shown that ATF4 upregulation under hypoxia is dependent on PHD3 but independent of VHL-mediated ubiquitination. Another report demonstrated that both PHD1 and PHD3 interact with ATF4, and co-expression with either PHD isoform repressed ATF4 transcription activity. However, the authors also showed that ATF4 did not serve as a hydroxylation substrate for either PHD1 or PHD3 in vitro.

PHD3 and apoptosis

Kinesin-like protein KIF1B regulates neuronal apoptosis, and its loss-of-function mutations have been identified in neuroblastomas and pheochromocytomas.
Phenotype improved hypoxia tolerance in hepatocytes that protects them against ischemia/reperfusion.

Exposure to 75% oxygen caused significant degradation of retinal Hif proteins, accompanied by massive losses of retinal microvessels in neonatal Phd2/−/− mice. Phd2/−/− mice significantly stabilize Hif1α, and to some extent Hif2α, in neonatal retinal tissues, and protected retinal microvessels from oxygen-induced obliteration.

Phd2/−/− mice displayed preformed collateral arteries that preserved limb perfusion and prevented tissue necrosis in ischemia. Regulation of arteriogenesis and artery homeostasis occurs by Phd2-dependent control of a specific differentiation state in macrophages.

No gross abnormalities were observed in cardiac filament structure or function, though knockout mice had significantly increased cardiac capillary area and smaller areas of necrosis post ligation of the left anterior descending artery. This correlated with a decreased number of apoptotic cells in the infarcted myocardium and significantly improved cardiac function 3 weeks after myocardial infarction.
Phd3 plays an important role in prolonging neutrophil survival during hypoxia, distinct from other hypoxia-associated changes in neutrophil function and metabolic activity. This selective defect in neutrophil survival occurred in the presence of preserved Hif transcriptional activity but was associated with upregulation of the proapoptotic mediator Siva1 and loss of its binding target Bcl-xL.

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<td>Simultaneous genetic deletion of Phd1, Phd2, and Phd3 in osteoblastic niches of the bone marrow microenvironment elevated Epo expression in bone and increased hematocrit.</td>
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<td>Phd2+/−</td>
<td>Combined loss of Phd2 in stromal and cancer cells sensitized tumors to chemotherapy whereas loss of Phd2 protected healthy organs against chemotherapy-induced oxidative damage. Loss of Phd2 in healthy organs triggered a Hif-mediated anti-oxidative response.</td>
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<td>Phd2+/− Rosa26-CreERT2</td>
<td>P294R knock-in mutation was introduced into the mouse Phd2 locus to model the first reported human PHD2 mutation (P317R). Phd2+/− mice displayed a degree of erythrocytosis equivalent to that seen in Phd2+/− mice and the associated erythrocytosis was reversed by intercrossing with Hif2α−/− but not Hif1α−/− mice. Erythrocytosis was also induced by homozygous and heterozygous knockout of Phd2 in renal cortical interstitial cells or by homozygous knockout of Phd2 in hematopoietic progenitors.</td>
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<td>Phd1+/−</td>
<td>Mice exposed to chronic hypoxia for 7 days manifested an exaggerated HVR, which was similarly exaggerated in Phd2−/− mice. Carotid body volume increased in Phd2−/− mice. HVR in Phd1+/− and Phd3−/− mice was similar to littermate controls. Acute exposure to a small molecule PHI did not mimic the ventilatory response to hypoxia though 7-day administration of the PHI induced only modest increases in HVR and carotid body cell proliferation, despite marked stimulation of erythropoiesis. This was in contrast with chronic hypoxia, which elicited both exaggerated HVR and cellular proliferation.</td>
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<td>Phd1+/−</td>
<td>Conditional Phd2 inactivation in renal Epo producing cells, neurons, and astrocytes displayed excessive erythrocytosis due to severe overproduction of Epo, exclusively driven by Hif2α. In contrast, Hif1α served as a protective factor. Simultaneous inactivation of Phd2 and Hif1α resulted in drastic Phd3 reduction and overexpression of Hif2α-related genes, neurodegeneration, and lethality.</td>
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<td>Phd2+/−</td>
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<td>Phd2+/− LysM-Cre+/−</td>
<td>Eight- to 10-week-old mice were given N(G)-nitro-L-arginine methyl ester (L-NAME), a nitric oxide synthase inhibitor, and Ang II infusion. L-NAME/Ang II comparably increased systolic blood pressure in control and Phd2+/− LysM-Cre+/− mice; the latter exhibiting less aortic medial and adventitial thickening, and macrophage infiltration. Cardiac interstitial fibrosis and myocyte hypertrophy were also significantly ameliorated in Phd2+/− LysM-Cre+/− mice. Transforming growth factor-β and collagen expression were decreased in the aorta and heart from Phd2+/− LysM-Cre+/− mice and left ventricular hypertrophy and reduced ejection fraction induced by L-NAME/Ang II treatment in control mice were not observed in Phd2+/− LysM-Cre+/− mice. These beneficial features were inhibited by digoxin, which inhibits Hifα synthesis.</td>
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induction is dependent on PHD3 hydroxylase activity, though it is unclear whether KIF1Bβ is a direct substrate for hydroxylase.61 Recently it has been shown that HCLK2 (human homologue of the Caenorhabditis elegans biological clock protein Cik2) is hydroxylated by PHD3. HCLK2 hydroxylation activates the ataxia telangiectasia and Rad3-related checkpoint kinase 1 pathway and subsequent apoptosis in response to DNA damage.62 Another reported substrate for PHD3 is beta(2)-adrenergic receptor, a prototypic G-protein coupled receptor whose induction has been associated with apoptosis.63–65 Hydroxylation of beta(2)-adrenergic receptor leads to its interaction with the VHL-E3 ligase complex and ubiquitin-mediated degradation.66

**RNA polymerase II**

PHD1 and PHD3 also hydroxylate the large subunit of RNA polymerase II (Rpb1) on Pro-1465 located within an LXX-LAP motif, which is necessary for phosphorylation of Ser5 in the C-terminal domain of Rpb1.67 Hydroxylation leads to non-degradative ubiquitination and is necessary for oxidative stress-induced recruitment of Rpb1 to the chromatin-engaged fraction of VHL-positive RCC cells. Although PHD2 also interacted with Rpb1, it had an inhibitory effect on hydroxylation in this case. Hydroxylation of Pro-1465 was suggested to have an oncogenic effect as expression of wild-type Rpb1 stimulated kidney tumor growth, whereas expression of the P1465A mutant prevented it.68

**Isoform specific effect of PHDs**

Germline mutations in PHDs are not considered a frequent cause of hereditary pheochromocytoma or RCC,69 in which HIF upregulation is frequently demonstrated.70,71 Interestingly, PHD3 protein is undetectable in ccRCC primary tumors compared to pheochromocytoma and colorectal cancers,72 indicating context-dependent roles of PHD isoforms. Not surprisingly, Phd knockout mice also display some isoform-specific phenotypes (Table 1). Phd1 deficiency lowers O2 consumption and induces hypoxia tolerance in skeletal muscle by altering glucose metabolism from oxidative to anaerobic, thereby reducing ROS genera-
tion whilst maintaining a basal mitochondrial respiration rate. This protects Phd1-deficient myofibers against lethal ischemia. 

Mechanistically, loss of Phd1 activates the Pparz pathway, which upregulates pyruvate dehydrogenase kinase isozyme 4 (Pdk4) in a primarily Hif2α-dependent manner. Pdk4 restricts entry of glycolytic intermediates into the TCA cycle, reducing mitochondria respiration and resulting in hypoxia tolerance.

Germline Phd2 knockout causes embryonic lethality due to placental and heart defects. 

Conditional deletion of Phd2 results in increased angiogenesis, polycthyemia, and congestive heart failure in mice. Phd2 inactivation redirects endothelial tip cells to a more quiescent cell type to facilitate restoration of O2 supply, which is in part dependent on Hif2α-mediated upregulation of soluble vascular endothelial growth factor receptor-1 and vascular endothelial cadherin.

Haploinsufficiency of Phd2 normalized endothelial lining and vessel maturation in mouse stroma, and led to activation of the NF-κB pathway in macrophages, causing enhanced collateral arteriogenesis that prevented tissue necrosis in ischemia. Further, reduced Phd2 activity in hearts and kidneys amplifies the antioxidative response of both Hif isoforms and protects normal organs functions from side toxicity of chemotherapy-induced ROS.

Conditional Phd2 knockout studies in the hematopoietic system revealed that Phd2 regulates hematopoietic stem cell maintenance under the steady state and stressful conditions. Neuronal-specific Phd2 knockout pre-conditions the forebrain against hypoxic/ischemic insults by inducing neuroprotective Hif target genes. In another study, neuronal Phd2 deletion led to impaired synaptic signaling in the hippocampus. Phd2 deletion in cardiomyocytes also protected mice from acute myocardial ischemic injury, potentially due to Hif1α-dependent tissue protection effects.

Phd3 knockout in mice resulted in a hypofunctional sympathoadrenal system and reduced blood pressure. Acute deletion of Phd3 in the liver improved glucose tolerance and insulin sensitivity by specifically stabilizing Hif2α, which augments the expression of insulin receptor substrate-2 and leads to an increase in insulin-stimulated phosphorylation of protein kinase B and transcription factor Forkhead box protein O1. Loss of Phd3 activity also increased pro-inflammatory activity of macrophages through Hif1α- and NF-κB-dependent enhancement of the innate immune response, leading to premature organ dysfunction in septic Phd3-deficient mice. Further, Phd3-deficiency led to increased neutrophil apoptosis during hypoxia, an effect associated with the upregulation of the proapoptotic mediator Siva1 and loss of its binding target Bcl-xL.

Regulation of PHDs activity

PHDs depend on multiple co-substrates and co-factors for activity, and therefore are potential targets of regulation not only by O2, but also by other factors including 2OG availability, oxidative stress, and abnormal levels of endogenous metabolites that are structural mimics of 2OG. In addition to being a co-factor to dioxygenases, 2OG is also a key TCA cycle metabolite and is involved in intracellular nitrogen transport by acting as the nitrogen acceptor in transamination reactions. Gottlieb et al showed that amino acid starvation led to 2OG depletion and thereby inactivation of PHDs, the activity of which is required for amino acid-induced signaling of the mammalian target of rapamycin complex 1, raising the possibility that PHDs are also cellular nutrient sensors. On the other hand, it has been shown that purified PHD enzymes have a relatively tight affinity for 2OG. The $K_m$ values for 2OG are 1–2 μM for PHD1/2 and 12 μM for PHD3 in vitro, which are significantly lower than 2OG levels generally detected under normal physiology. The discrepancies in reported $K_m$ values of PHDs for 2OG may partly arise from the presence of endogenous 2OG that are pre-bound to the recombinant enzymes during purification. Therefore further evidence may be needed to support whether oscillations of intracellular 2OG concentration significantly alters PHD activities.

The activity of PHDs can also be modulated by oncometabolites. SDH and fumarate hydratase (FH) catalyze sequential steps in the TCA cycle, and their inactivation results in accumulation of succinate and fumarate, respectively, both of which are structural analogues of 2OG (succinate is also a product of the 2OG-dependent dioxygenase-catalyzed reactions) and have been shown to inhibit the PHD enzymes at pathophysiological concentrations.

Loss-of-function mutations in SDH are detected in paragangliomas and pheochromocytomas, as well as a number of other malignancies, whereas FH inactivation occurs primarily in hereditary leiomyomatosis and RCC. HIF stabilization is often observed in these tumors, potentially due to fumarate or succinate-mediated inhibition of PHDs. However, it has also been argued that, because PHDs have a tight binding affinity for 2OG, the activation of HIF in the SDH- or FH-deficient settings is likely to be due to inactivation of PHDs by oxidative stress, which is generated as a result of mitochondrial dysfunction.

Gain of function mutations in IDH1 and IDH2 frequently occur in low-grade gliomas and acute myeloid leukemia, conferring a neomorphic enzyme activity that produces (R)-2-hydroxylutarate (R-2HG), which is postulated to promote, rather
than inhibit, the hydroxylase activities of PHD1 and PHD2, thereby diminishing HIF signaling (reviewed by Losman and Kaelin).103 Reduced HIF levels were associated with enhanced growth of IDH1 mutant human astrocytes.93 Consistent with this, PHD2 depletion in erythroleukemic cells transformed by the expression of IDH1 mutant abolished their growth factor independence and restored normal differentiation.72,105

ROS has also been assigned a role in regulating PHD activity. Potential mechanisms of ROS-induced PHD inactivation include oxidation of the ferrous iron (Fe[II]) to the ferric state (Fe[III]) or oxidation of active site residues.5 However, although peroxide treatment initially reduced PHD activity, prolonged exposure enhanced it.106 Bio-reductants such as ascorbate (vitamin C) or glutathione are necessary for maximal PHD activity in vitro, potentially through facilitating the reduction of ferric iron to its ferrous state.107,108 Treatment with ascorbate or the antioxidant N-acetylcysteine in vivo inhibited growth of Myc-mediated xenograft tumors by diminishing HIFα levels in a PHD2 and VHL-dependent manner.109 The ROS scavenging agent Se-methylselenocysteine also displayed an antitumor effect in ccRCC xenograft tumors by promoting PHD2 activity and reducing HIF1α.72,110

There is controversy, however, as to whether PHDs are direct physiological targets of ROS. Genetic and pharmacological inhibition of electron transport chain has been shown to stabilize HIF, supporting a direct role of mitochondrial ROS in HIF regulation.111-115 However, overexpression of thioredoxin reductase 1 blocked ROS generation under hypoxia but had no effect on HIF1α accumulation or transcriptional activity.116 In line with this, inhibition of mitochondrial ATP synthase increased mitochondrial ROS production but did not lead to HIF1α stabilization.117,118 Further, it has been shown that the HIF asparaginyl hydroxylase FIH is markedly more sensitive to exogenous peroxides than PHDs,119 raising the possibility of differential regulation of HIF protein stability and transcriptional activity by hypoxia and oxidative stress. An alternative model of PHD regulation proposes that increased mitochondrial O2 consumption reduces cytosolic O2 availability to the PHDs, which can inhibit PHD activity and lead to HIF accumulation.120

Nitric oxide (NO) has also been proposed to regulate PHD activity. Biochemical and biophysical studies suggested that NO may compete with O2 for binding to the active site Fe(II), and can potentially interact with multiple cysteine residues in PHD2 in vitro.121 Although acute exposure to high doses of NO stabilized HIF1α, prolonged exposure or low doses reduced HIF1α accumulation in cells, potentially by modulating co-substrate and co-factor availability to PHDs and HIF1α-mediated feedback expression of PHD2.122

PHDs are also subject to regulation at the protein level. The seven in absentia homology 2 (Siah2) E3 ligase ubiquitin protein has been shown to preferentially target PHD3 for polyubiquitylation and proteasomal destruction.123 Siah2-dependent degradation of PHD3 increased under hypoxia conditions, whereas Siah2 null fibroblasts displayed reduced HIF1α expression levels.124 On the other hand, the FK506-binding protein 38 has been shown to negatively regulate PHD2 protein stability through interaction with the N-terminal MYND (myeloid, Nervy, and DEAF-1) finger domain of PHD2 in an ubiquitin-independent proteasomal pathway.125

Other 2-oxxygenases and metabolism

The Fe(II) and 2O2-dependent dioxygenases are a large enzyme family comprised of over 60 members, many of which have yet unidentified functions. Here we summarize a few 2-oxxygenases that may have implications in cancer.

Chromatin modifying 2-oxxygenases

The ten-eleven translocation (TET) family of DNA modifying enzymes (comprising of TET1, TET2, and TET3) are 2O2-dependent dioxygenases that catalyse the hydroxylation of 5-methylcytosine to form 5-hydroxymethylcytosine,126 and the oxidation of 5-hydroxymethylcytosine to 5-formylcytosine and 5-carboxylcytosine.127,128 These reactions are considered intermediate steps in DNA demethylation, but interestingly, 5-hydroxymethylcytosine, 5-formylcytosine, and 5-carboxylcytosine also exhibit replication dependent dilution and each has specific "reader" proteins,129-131 suggesting that these modifications may be functional during development. TET2 mutations frequently occur in hematological malignancies,132,133 and TET1 can act as a tumor suppressor in prostate and breast cancers and as an oncogene in myeloid/lymphoid leukemia-rearranged leukemias.134-136 Intriguingly, somatic mutations in TET2 and IDH occur in acute myeloid leukemia in a mutually exclusive manner.137 Further, 2HG-producing IDH mutant cancers frequently display a DNA hypermethylation phenotype,138-140 whereas R-2HG has been shown to inhibit TET2 activity in vitro.141 This evidence points to TET2 being a pathological target of the oncometabolite R-2HG. Similarly, a hypermethylation phenotype has been observed in SDH- and FH-mutant malignancies,142,143 indicating that the TET-mediated epigenome remodeling is potentially an important oncogenic mechanism in SDH and FH-deficient cancers.144
The JmjC domain-containing histone H3 lysine 27 demethylase UTX and histone H3 lysine 4 demethylase JARID1C are both 2OG-dependent dioxygenases. Inactivating somatic mutations in UTX have been identified in multiple tumor types, including myeloid leukemias, RCCs, breast and colorectal cancers, and glioblastoma. Inactivating mutations in JARID1C were identified in ccRCC, together with the histone H3 lysine 36 methyltransferase SET domain containing 2. The evidence highlights the importance of chromatin modifying enzymes in cancer regulation.

**FIH**

In comparison to PHDs, whose catalytic activities are remarkably specific, FIH is a much more promiscuous enzyme, catalyzing the hydroxylation of not only HIF but also a large family of ankyrin repeat domain-containing proteins. In addition to being an asparaginyl hydroxylase, FIH can also catalyze the β-hydroxylation of aspartyl, histidinyl, serinyl, leucinyl, and isoleucinyl residues, although the biological significance of the non-asparaginyl substrates is unclear. Interestingly, the Fih null mice displayed a phenotype of dysregulated energy metabolism with no developmental defects or other classical features associated with canonical HIF functions. In another study, FIH inhibition or knockdown in VHL-defective RCC cells increased HIF-dependent apoptosis and promoted survival of these cells. Taken together, the effects of FIH on metabolism is context-specific and may be both HIF-dependent and HIF-independent.

**Fat mass and obesity-associated**

The 2OG-dependent dioxygenase fat mass and obesity-associated protein (FTO) catalyzes RNA and single strand DNA demethylation in vitro. The expression of FTO is associated with increased risk for obesity and type 2 diabetes. Mouse models of Fto suggest its deficiency leads to postnatal growth retardation, increased energy expenditure, and a lean phenotype, whereas its overexpression results in increased food intake and obesity in mice. Amino acid deprivation in mouse and human cell lines downregulated FTO mRNA and protein levels, whereas FTO-deficient cells display reduced mammalian target of rapamycin complex 1 signaling potentially due to the inability to sense amino acids. Recently, it has also been suggested that FTO may be implicated in melanoma independent of body mass index.

**Ribosomal hydroxylases**

Recently, a subset of 2-oxygenases has been shown to possess unprecedented enzymatic activities and catalyze post-translational hydroxylation of ribosomal proteins. The 2OG and Fe(II)-dependent oxygenase domain-containing protein 1 catalyzes the trans-3-prolyl hydroxylation of Pro-62 in the 40S ribosomal protein S23 and is postulated to have a role in the regulation of translation and growth. Jumonji domain-containing 4 is a 2-oxygenase that catalyzes the C4-lysyl hydroxylation of eukaryotic release factor 1 at Lys-63, a conserved residue located within its stop codon recognition domain, and eukaryotic release factor 1 hydroxylation has been suggested to promote translational termination efficiency. Myc-induced nuclear antigen with a molecular mass of 53 kDa (MINA53) and NO66 are known to interact with the Myc oncogenic pathway and are highly expressed in several cancers. Both MINA53 and NO66 have previously been assigned as histone lysine demethylases. However, direct evidence of their histone demethylase activity by mass spectrometry is lacking. Recently it was shown that MINA53 catalyzes the (2S,3S)-3-histidyl hydroxylation of the 60S ribosomal protein Rpl27a at His-39, whereas NO66 hydroxylates the 60S ribosomal protein Rpl8 at His-216 with the same stereochemistry. Whether they play regulatory roles in translation or ribosomal biogenesis in vivo remains to be determined.

**Conclusion**

The identification and function of 2-oxygenases has rapidly expanded over the last decade, though the PHDs have remained a primary focus within this class of enzymes. Though mainly associated with the regulation of HIF, many studies have identified diverse and often contrasting roles in cellular metabolism for both PHD-mediated HIF-dependent and HIF-independent metabolic regulation. This can be explained, at least in part, by the range in specificity for HIF subunits and other substrates combined with tissue-specific expression and cellular localization of the different PHD isoforms. Both genetic and biochemical inhibition of the PHDs have been demonstrated to be of benefit in a plethora of clinical applications, including protective roles in ischemia/reperfusion injury, neural protection, support of macrophage function, enhanced neutrophil survival, protection against inflammatory bowel disease, and enhanced expression of epithelial barrier protection genes. Many of these functions are mediated by HIF1α, which plays a key role in the reprogramming of metabolism by activating the transcription of genes encoding glucose transporters and...
glycolytic enzymes. In contrast, PHD3-mediated regulation of HIF2α regulates hepatic lipid and glucose metabolism and provides a direct link between hypoxia and insulin signaling in diabetes. Further, HIF2α regulates erythropoietin responses to hypoxia in anaemia inferring an important role in iron homeostasis.169–172

In summary, targeting of PHDs provides a feasible method of therapeutic intervention in cancer metabolism and has traction outside oncology. However, given the cell- and tissue-specific roles of the PHDs and their main substrate HIF, multiple factors should be considered in the design of either small compound inhibitors or genetic targeting, such as drug efficacy, toxicity, pharmacokinetics, and accurate delivery to the target tissue.

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