Complex role of HIF in cancer: the known, the unknown, and the unexpected

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Abstract: Tumor hypoxia has long been recognized as a driving force of malignant progression and therapeutic resistance. The discovery of hypoxia-inducible transcription factors (HIFs) has greatly advanced our understanding of how cancer cells cope with hypoxic stress by maintaining bioenergetics through the stimulation of glycolysis. Until recently, however, it remained perplexing why proliferative cancer cells opt for aerobic glycolysis, an energy-inefficient process of glucose metabolism. Furthermore, the role of HIF in cancer has also become complex. In this review, we highlight recent groundbreaking findings in cancer metabolism, put forward plausible explanations to the complex role of HIF, and underscore remaining issues in cancer biology.

Keywords: cancer biology, hypoxia, metabolism, oncogenic signaling

Introduction
Cellular adaptation to O2 deprivation – hypoxia – is a physiological response during the course of normal development and aging in metazoans, and is critical for continued growth and survival of the organism. Central to this adaptive response is hypoxia-inducible factor 1 (HIF-1), a transcription factor that orchestrates global responses to hypoxia in gene expression.1 HIF-1 is a heterodimer composed of HIF-1α (gene symbol HIF1A) and aryl hydrocarbon receptor nuclear translocator (gene symbol ARNT, and also known as HIF-1β).2 Both subunits possess a basic helix-loop-helix domain capable of dimerization and binding to the promoters of hundreds of target genes through the recognition of hypoxia-responsive elements that contain the core sequence RCGTG.3-7

As the regulatory subunit of HIF-1, the O2-labile HIF-1α stabilizes in response to hypoxia, leading to heterodimerization, DNA binding, and recruitment of the transcription co-activators p300 and CBP.8-10 HIF-1α uses a hydrophobic interface including Cys800 to interact with p300 and CBP.11-14 Interestingly, in normoxia, HIF-1 target genes are transcriptionally active but paused for RNA polymerase II elongation; hypoxia-activated HIF-1α employs CDK8-Mediator and the super elongation complex to alleviate the pausing for elongation.15 Numerous HIF-1 target genes are activated by this canonical mechanism of transcription, such as those involved in angiogenesis, metabolic reprogramming, cell survival and proliferation, and migration and metastasis (Figure 1).16-18 Also contributing to these cancer biological processes is HIF-2α (gene symbol EPAS1),19,20 a paralog of HIF-1α, which shares similar biochemical properties, regulatory mechanisms, and target genes, even though distinct, and even opposing, functions of HIF-2α have begun to be appreciated.21
HIF-1α is sensitive to O2, owing to the presence of an O2-dependent degradation domain that mediates ubiquitin-proteasomal proteolysis.22 The von Hippel-Lindau (VHL) protein is a part of the E3 ubiquitin ligase,23,24 which recognizes two highly conserved proline residues (Pro402 and Pro564 in HIF-1α, Pro405 and Pro531 in HIF-2α) for polyubiquitination; however, hydroxyl modification of these proline residues is a prerequisite for VHL recognition.25–27 Prolyl hydroxylation is catalyzed by three prolyl hydroxylase domain-containing (PHD) proteins of the Fe(II)- and 2-oxoglutarate (2OG)-dependent dioxygenase family: PHD1, PHD2, and PHD3 (gene symbols EGLN2, EGLN1, and EGLN3, respectively), which use molecular O2 for sensing and signaling.28–34

Likewise, the factor inhibiting HIF-1 (FIH1, gene symbol HIF1AN)35 is another type of hydroxylase that modifies Asn803 in the HIF-1α transactivation domain to block p300 interaction, thereby providing an additional mechanism for modulating HIF-1α activity.36,37 Although FIH1 is a dioxygenase that uses molecular O2 for substrate modification, its in vivo role for HIF-1α regulation requires further investigation because mice with a Hif1an-null mutation demonstrated no alterations of Hif-1 function but exhibited a hypermetabolic state with hyperventilation and decreased body mass, which was regulated systemically by the nervous system.38

Besides hydroxylation, numerous modulatory mechanisms have been identified, adding the complexity of HIF regulation. These include oncogenes and tumor-suppressor genes, acetylation and SUMOylation, reactive oxygen species and nitric oxide, and microRNAs. These regulatory mechanisms have been extensively reviewed.19

In addition, both HIF-1α and HIF-2α employ crosstalk mechanisms to regulate cell proliferation, DNA repair, mitochondrial biology, and cell stemness.40,41 These noncanonical mechanisms of HIF-1α and HIF-2α actions seem independent of ARNT and direct DNA binding; rather, they require protein–protein interactions (Figure 1). HIF-1α and HIF-2α regulate cell-cycle genes in an opposing fashion; HIF-1α inhibits cell-cycle progression by suppressing c-Myc activity, whereas HIF-2α does the reverse.42–44 By similar mechanisms, HIF-1α represses, whereas HIF-2α stimulates, DNA repair genes.45–47 HIF-1α engages in the Notch signaling pathway to block cell differentiation, and the β-catenin signaling pathway to regulate embryonic and adult cell proliferation, albeit in an opposite way.46,51 Finally, HIF-1α also inhibits DNA replication through direct interaction with the adenosine triphosphatase Cdc6.52 Further studies are required to elucidate detailed mechanisms of noncanonical actions of HIF-1α and HIF-2α.

HIF-1α, HIF-2α, and cancer

Solid cancers frequently harbor hypoxic regions where HIF-1α and HIF-2α become overexpressed and activated.53 Furthermore, oncogenic signaling and growth factor stimulation lead to the activation of the phosphotidylinositol 3-kinase (PI3K)/Akt/mammalian target of rapamycin (mTOR) and mitogen-activated protein kinase (MAPK) pathways, thereby stimulating HIF-1α and HIF-2α synthesis.16,17,54–56 As a result, increased expression of both HIF-1α and HIF-2α has been observed in a wide variety of human cancers and, in general, is associated with poor prognosis.17,57 Likewise, numerous studies support the notion that HIF-1α and HIF-2α promote tumor angiogenesis and growth.17,18,57 Furthermore, rare somatic, gain-of-function mutations in EPAS1 have been identified to be associated with paraganglioma with pancytopenia and pheochromocytoma.59

It has been recognized, however, that HIF-1α expression is also associated with favorable prognosis, eg, in patients with neuroblastoma and renal cell carcinomas.21,60 Forced expression of HIF-1α in renal cell carcinoma cell lines retarded tumor growth in xenografts,61,62 suggesting a tumor-suppressing role
for HIF-1α. Conversely, it is suggested that Hif-1α is not required for renal cyst development in conditional Vhl-null mice.\textsuperscript{63} Furthermore, rare somatic, loss-of-function HIF1A mutations have been identified in the specimens of clear-cell renal carcinoma,\textsuperscript{64,65} and common focal, homozygous deletions have been detected in cell lines of VHL-deficient renal cell carcinomas.\textsuperscript{66} Despite this cogent evidence, the mechanism by which HIF-1α acts as a tumor suppressor remains unclear, and how cancer cells might escape from HIF-1α suppression needs to be addressed, especially in majority of renal cell carcinomas where HIF-1α is commonly overexpressed. What may explain retarded tumor growth in the xenograft studies, however, is that HIF-1α inhibits cell proliferation.\textsuperscript{40} Consistently, renal cell carcinomas with HIF-1α expression are statistically much smaller than those without, and intriguingly seem more metastatic.\textsuperscript{67} Therefore, the role of HIF-1α in malignant progression and metastasis cannot be ruled out in VHL-deficient renal cell carcinomas.

HIF-2α, on the other hand, is believed to be a major contributor to VHL-deficient renal carcinogenesis.\textsuperscript{59} However, in other experimental settings, HIF-2α seems to be a tumor suppressor; HIF-2α increases apoptosis in glioma\textsuperscript{68} and inhibits oncogenic signaling and activates a tumor-suppressor gene in non-small-cell lung cancer.\textsuperscript{58} Clearly, the role of HIF-1α and HIF-2α in cancer biology is complex, and their biological functions are likely context dependent.

**Critical role of HIF-1α in metabolic switch from oxidative phosphorylation to anaerobic glycolysis**

Among the first recognized biological functions of HIF-1α was metabolic adaptation to decreased O\textsubscript{2} availability, resulting from transcriptional upregulation of multiple genes involved in glucose transport and glycolysis, such as those encoding aldolase A (ALDOA), phosphoglycerate kinase 1 (PGK1), lactate dehydrogenase A (LDHA), and glucose transporters (SLC2A1 and SLC2A3).\textsuperscript{69} Genetic deletion of Hif1α gene in mouse embryonic cells confirmed the critical role for HIF-1α in glycolysis and lactate production.\textsuperscript{69,70}

Under normal O\textsubscript{2} tensions, glycolysis catabolizes glucose to pyruvate, which is converted to acetyl-CoA by pyruvate dehydrogenase for oxidative phosphorylation in the tricarboxylic acid (TCA) or Krebs cycle. Under hypoxia, cells decrease oxidative phosphorylation in the mitochondria and adopt anaerobic glycolysis and conversion of pyruvate to lactate. As a key regulator of this process, HIF-1α actively suppresses mitochondrial O\textsubscript{2} consumption by transcriptionally upregulating both pyruvate dehydrogenase kinases 1 and 3 (PDK1 and PDK3, respectively),\textsuperscript{76–78} which subsequently inactivate pyruvate dehydrogenase to block pyruvate conversion and flux of acetyl-CoA into the TCA cycle. Moreover, HIF-1α has been shown to inhibit oxidative phosphorylation by inhibiting mitochondrial biogenesis.\textsuperscript{74}

In addition to the critical role in the metabolic switch from oxidative phosphorylation to anaerobic fermentation – the Pasteur effect, HIF also stimulates energy storage for hypoxic cell survival through the induction of glycogen and lipid synthesis.\textsuperscript{73} Primarily, HIF-1α promotes glycogen accumulation through transcriptional activation of several genes involved in glycogen biosynthesis, such as GYS1, PPP1R3C, and PGM1.\textsuperscript{76–78} HIF-1α also upregulates expression of the peroxisome proliferator-activated receptor γ (gene symbol PPARγ), thereby increasing fatty acid uptake and triglyceride biosynthesis in cardiac hypertrophy.\textsuperscript{79} Additional HIF-1α target genes responsible for lipid accumulation include HILPDA and LPIN1.\textsuperscript{80,81} Interestingly, conditional deletion of murine Vhl in hepatocytes indicates a role for Hif-2α, rather than Hif-1α, in lipid synthesis, oxidation, and storage,\textsuperscript{82} another example of context dependence for HIF function.

**HIF-1α diverts glycolytic metabolites into biosynthesis by blunting pyruvate production**

In comparison to oxidative phosphorylation, glycolysis is inefficient in energy generation. Consistent with the role of HIF-1α in energy maintenance and conservation,\textsuperscript{83} it stands to reason that cancer cells adopt glycolysis under low O\textsubscript{2} tensions for survival. However, cancer cells generally manifest characteristics of increased proliferation associated with high glucose uptake and lactate production even in the presence of O\textsubscript{2} – aerobic glycolysis or the Warburg effect.\textsuperscript{84–86} Until recently, the significance of aerobic glycolysis remained debatable because it was unclear why cancer cells prefer energy-inefficient glycolysis to support proliferation, notwithstanding the recognition of the role of HIF-1α in aerobic glycolysis.\textsuperscript{87}

A reinterpretation of the Warburg effect is that aerobic glycolysis is not merely employed for bioenergetics but, more importantly, for biosynthesis of macromolecules (nucleotides, amino acids, and lipids) necessary for cell proliferation.\textsuperscript{85,86,88} This view has integrated oncogenic signaling (PI3K-AKT-mTOR and c-Myc) with regulation of metabolic pathways, biosynthesis, and cell proliferation. Recent studies have
pointed out the M2 splice isoform of pyruvate kinase (PKM2, a splice variant of the PKM gene) as a metabolic switch for aerobic glycolysis and tumorigenesis. In normal adult tissues, the splice variant PKM1 catalyzes the final step of glycolysis by transferring the phosphate from phosphoenolpyruvate to adenosine diphosphate, thereby yielding pyruvate and adenosine triphosphate, whereas PKM2 is expressed primarily in lung tissues and proliferating cells including stem cells and cancer cells. The transcription factor c-Myc promotes PKM2 splicing by inducing the expression of three heterogeneous nuclear ribonucleoproteins (hnRNPs). It has been shown that oncogenic signaling converges on the activation of mTOR to increase HIF-1α levels for PKM transcription and concomitantly c-Myc levels for PKM2 splicing (Figure 2).

In addition to being a glycolytic enzyme, PKM2 can function as a protein kinase for gene transcription in the nucleus. Activation of epithelial growth factor receptor induces extracellular signal-regulated kinase 2 (gene symbol MAPK1)-mediated phosphorylation and translocation of PKM2 into the nucleus. Nuclear PKM2 interacts with β-catenin to activate target genes such as CCND1 and MYC through phosphorylation of histone H3, which leads to the dissociation of HDAC3 and acetylation of histone H3. Accordingly, nuclear PKM2 promotes cell-cycle progression and cell proliferation by stimulating cyclin D1 and c-Myc expression. c-Myc further enhances PKM2 expression in a positive-feedback loop and also induces glycolytic gene expression. PKM2 can also phosphorylate signal transducer and activator of transcription 3 (gene symbol STAT3) to drive gene expression. In addition, PKM2 is a transcriptional coactivator of HIF-1α transcriptional activity. PKM2 can be hydroxylated by PHD3, and hydroxylated PKM2 enhances HIF-1α activity through direct interaction. Taken together, PKM2 stimulation of c-Myc and HIF-1α further promotes glycolysis.

So, is PKM2 essential to tumor growth and lactate production? On the contrary, mice with a conditional allele that abolishes Pkm2 but not Pkm1 expression show accelerated mammary tumor formation and heterogeneous Pkm1 expression. Pkm1 was detected in non-proliferating cells but not in those in proliferation, which suggests that active pyruvate kinase is required for non-proliferating, but not necessarily for proliferating, tumor cells. Interestingly, PKM2

![Figure 2](https://www.dovepress.com/)

**Figure 2** Role of hypoxia-inducible factor 1 (HIF-1) in regulating bioenergetics and biosynthesis through the induction of pyruvate kinase M2 (PKM2) in proliferating cancer cells.

**Notes:** Increased HIF-1 expression through oncogenic signaling not only promotes glucose uptake and glycolysis, but also cooperates with c-Myc to increase PKM2 expression through transcriptional upregulation of PKM and PKM2 splicing, respectively. PKM2 is present mainly in the nucleus as a dimer and acts as a protein kinase to drive gene transcription for cell-cycle progression. Its low activity as pyruvate kinase blunts the conversion of phosphoenolpyruvate (PEP) to pyruvate, thereby diverting upstream glycolytic metabolites into the biosynthesis pathways. Although PKM2 can also exist as a tetramer for glycolysis, its glycolytic activity is inhibited by oncogenic signaling.
found in tumor cells is usually dimeric with low enzymatic activity for glycolysis, whereas the tetrameric form in normal cells has a high activity.\textsuperscript{91} Furthermore, oncogenic signaling inhibits the tetrameric form of PKM2 through direct and selective binding to tyrosine-phosphorylated peptides, thereby enabling anabolism from glucose metabolites for tumor growth.\textsuperscript{99}

Thus, HIF-1α-mediated PKM2 expression provides a regulated, bifunctional protein that can act on the one hand as a tetrameric glycolytic enzyme for bioenergetics and lactate production but on the other as a dimeric transcriptional coactivator/protein kinase for cell proliferation. Most importantly, loss of glycolytic activity resulting from either a dimer or a tyrosine-phosphorylated peptides-bound tetramer diverts glycolytic metabolites into the anabolic pathways (Figure 2).

**Hereditary mutations in fumarate hydratase and succinate dehydrogenase**

Neither HIF-1α nor HIF-2α is known to transcriptionally regulate genes in the TCA cycle; rather, it is the intermediate metabolites including fumarate and succinate that have been shown to increase the activities of these transcription factors.\textsuperscript{108} Whereas germline mutation in the FH gene (encoding fumarate hydratase) predisposes individuals to hereditary leiomyomatosis and renal cell carcinoma, hereditary mutations in the genes encoding four subunits of succinate dehydrogenase (SDHA, SDHB, SDHC, and SDHD) and one cofactor (SDHAF2) are linked to familial pheochromocytomas and paragangliomas.\textsuperscript{100–102} These tumors are characterized by the induction of pseudo-hypoxia, ie, increased HIF activities and target gene expression in normoxia. At the molecular level, inactivation of fumarate hydratase and succinate dehydrogenase leads to the accumulation of fumarate and succinate, respectively,\textsuperscript{103} resulting in allosteric inhibition of prolyl hydroxylase PHDs and induction of HIF-1α and HIF-2α.\textsuperscript{104–106} Targeted inactivation of mouse Fhl1 confirmed the resultant activation of Hif-1α and Hif-2α and development of proliferative renal cysts.\textsuperscript{107} FH-deficient renal cancer cells also exhibit aerobic glycolysis and increased expression of HIF-1α.\textsuperscript{108} Additionally, accumulated fumarate produces succininated glutathione, resulting in increased mitochondrial reactive oxygen species and HIF-1α activation.\textsuperscript{109} In fact, it has been shown that fumarate can modify numerous proteins including mitochondrial aconitase 2 for the inhibition of aconitase activity in Fhl1-null mouse embryonic fibroblasts,\textsuperscript{110} even though reduced cytosolic, but not mitochondrial, aconitase activity is observed in FH-deficient renal cancer cells associated with iron deficiency.\textsuperscript{108}

Despite these findings, whether activation of HIF pathway has a causal effect on renal cyst formation was questioned.\textsuperscript{111} Indeed, in mouse genetic studies, Fhl1\textsuperscript{−/−}-associated renal cyst formation was independent of Hif-1α and Hif-2α, and was further exacerbated by inactivation of Hif-1β but not Hif-2α.\textsuperscript{112} In fact, FH-deficient cysts and tumors were associated with upregulation of the KEAP1-NRF2 antioxidant pathway (Figure 3A), resulting from derepression of nuclear factor erythroid 2-like 2 (NRF2, gene symbol NFE2L2) upon fumarate inhibition of the negative regulator kelch-like ECH-associated protein 1 (gene symbol KEAP1) by succination. Consistently, upregulation of antioxidant response genes through the KEAP1-NRF2 axis is a distinct feature of type 2 papillary renal cell carcinoma caused by FH mutation, in contrast to those of clear cell carcinomas arising from SDH or VHL mutation.\textsuperscript{113} Furthermore, NRF2 apparently decreases HIF-1α levels by reducing reactive oxygen species in FH-deficient cells.\textsuperscript{109} The NRF2-mediated antioxidant and detoxification program is involved in oncogene-induced tumorigenesis.\textsuperscript{114} Intriguingly, NRF2 has also been shown to promote biosynthesis by redirecting glucose and glutamine into the anabolic pathways in the presence of activated PI3K-AKT signaling.\textsuperscript{115} Despite the lack of involvement of Hif-1α in Fhl1\textsuperscript{−/−}-associated renal cyst development, upregulation of HIF-1α remains essential to glycolytic metabolism and oncogenic growth of FH-deficient renal cancer,\textsuperscript{108} consistent with the aforementioned role of HIF-1α in glycolysis and anabolism.

Although mutations in SDHD is linked to hereditary paraganglioma,\textsuperscript{116} heterozygous deletion of Sdhd in mice develops no tumor but subtle glomus cell hypertrophy and hyperplasia.\textsuperscript{117} Succinate accumulation has been shown to specifically inhibit PHD3 apoptotic activity, thereby blocking the apoptosis of sympathetic neuronal precursor cells during development and contributing to the pathogenesis of familial pheochromocytoma (Figure 3A).\textsuperscript{118} Interestingly, mice with germline deletion of Egln3 also exhibited reduced apoptosis and increased cell numbers in the superior cervical ganglia, adrenal medulla, and carotid body.\textsuperscript{119} Furthermore, a combined heterozygous deletion of Eps1l rendered sympathetic neurons more sensitive to induced apoptosis, indicating an anti-apoptotic role of HIF-2α in this setting. Conversely, as mentioned above, rare somatic, gain-of-function mutations in EPAS1,\textsuperscript{58,59} as well as germline mutations in FHI\textsuperscript{120} have been associated with malignant paragangliomas and
pheochromocytomas. Furthermore, hypermethylation has also been identified in tumors with SDH and FH mutations. Methylosome analysis of a large cohort of paraganglioma patients has revealed a hypermethylation phenotype similar to that in gliomas. Sdhb deletion in mouse chromaffin cells led to DNA hypermethylation, resulting from succinate inhibition of the JmjC domain-containing histone demethylases and DNA hydroxylases (Figure 3B). Finally, DNA hypermethylation has also been identified in tumors with FH mutations.

### Somatic mutations in isocitrate dehydrogenase

There has been rapid expansion of knowledge in recent years of single somatic mutations in cytosolic isocitrate dehydrogenase 1 (gene symbol IDH1), and these mutations were identified initially in \( \geq 70\% \) WHO grade II–III gliomas and secondary glioblastomas. Tumors lacking mutations in IDH1 often had single mutations in IDH2, a mitochondrial gene in the TCA cycle for interconversion of isocitrate and 2OG. Similar mutations have also been found in \(< 23\% \) acute myeloid leukemia, albeit mainly in IDH2. Interestingly, all the mutations are heterozygous and affect the same active site of the enzyme at a single arginine residue (Arg132 of IDH1 and Arg172 of IDH2), thereby reducing the intracellular concentration of 2OG, a cosubstrate of the HIF prolyl hydroxylases. Accordingly, it was found that mutant IDH1 forms a catalytically inactive heterodimer with the wild type, resulting in a decrease of PHD activity and an increase of HIF-1α levels in human gliomas harboring an IDH1 mutation.

This loss-of-function theory was only part of the story, however, because a wild type allele of IDH1 or IDH2 always remains in these tumors, raising the possibility of gain of function as result of mutations. Indeed, both mutant IDH1 and mutant IDH2 acquire the ability to catalyze the nicotinamide adenine dinucleotide phosphate-dependent reduction of 2OG to \((R)-2HG\) and \((R)-enantiomer of 2-hydroxyglutarate ((R)-2HG). Accordingly, elevated levels of \((R)-2HG\) are detectable in IDH mutant gliomas and acute myeloid leukemias.

So, is \((R)-2HG\) an oncometabolite stimulating hypoxic signaling for tumorigenesis? On the contrary, it has been suggested that \((R)-2HG\) downregulates HIF-1α and HIF-2α levels by increasing PHD1 and PHD2 activity to promote transformation of immortalized human astrocytes (Figure 3A). This finding was supported by the evidence that \((R)-2HG\) can substitute 2OG for PHD enzymatic activity in a cell-free reaction, and this finding is correlated with diminished expression of HIF-1α and HIF-2α in IDH1 mutant cells and reduced HIF target gene expression in IDH1 mutant gliomas. Furthermore, decreased HIF-1α expression is conducive to transformation by mutant IDH1. Moreover, \((R)-2HG\) is sufficient to promote leukemogenesis by inducing cytokine independence and blocking hematopoietic differentiation, whereas the
(S)-enantiomer of 2-hydroxyglutarate, despite being a more potent inhibitor of 2OG-dependent dioxygenases,\textsuperscript{129-131} fails to do so owing to its inhibition of PHD activity to increase, rather than decrease, HIF-1α levels.\textsuperscript{132}

The notion that (R)-2HG inhibits HIF signaling seems at odds with the genetic evidence of mouse studies; increased Hif-1α protein levels and target gene transcription were observed in the embryo of brain Idh1 (R132H) knock-in mice where high levels of (R)-2HG were produced,\textsuperscript{133} and no alteration of Hif-1α signaling was found in the hematopoietic stem cells and progenitor cells from the knock-in mice of the myeloid lineage.\textsuperscript{134} Although the mechanisms by which HIF-1α prevents astrocyte transformation and leukemogenesis remain unclear, a lower level of HIF-1α expression in IDH1 mutant cells might be conducive to tumor initiation because HIF-1α also upregulates histone demethylases,\textsuperscript{135,136} which have been shown to be inhibited by (R)-2HG for transformation.

In addition to PHDs, (R)-2HG is a potent inhibitor of other 2OG-dependent dioxygenases,\textsuperscript{137} including the TET family of 5-methylcytosine hydroxylases, which convert 5-methyl-cytosine to 5-hydroxymethylcytosine for DNA demethylation.\textsuperscript{138,139} In fact, IDH1 somatic mutations in glioblastomas and lower-grade gliomas have a CpG island methylator phenotype, displaying DNA hypermethylation at a large number of loci.\textsuperscript{141,142} Similarly, acute myeloid leukemias with IDH1 or IDH2 mutations also exhibit genome-wide DNA hypermethylation with a specific signature shared with those harboring mutations in TET2,\textsuperscript{125} a member of the TET protein family. Consistently, expression of IDH mutants was found to impair TET2 catalytic function, and mutations in IDH1 and IDH2 were mutually exclusive with those in TET2 in a large cohort of acute myeloid leukemias.\textsuperscript{125}

Although both forms of 2-HG have been shown to be competitive inhibitors of multiple 2OG-dependent dioxygenases, including the JmjC domain-containing histone demethylases and the TET family of 5-methylcytosine hydroxylases as well as PHDs,\textsuperscript{130} the half-maximal inhibitory concentration of (R)-2HG for histone demethylases is 200-fold less than for PHD2, indicating more important effects of IDH mutations on chromatin remodeling.\textsuperscript{131} In keeping with this, IDH mutation has been shown to inhibit histone demethylation and induce DNA hypermethylation in cell culture and animal model, thereby blocking cell differentiation.\textsuperscript{134,143,144} Furthermore, targeted inhibition of mutant IDH2 with the small molecule AGI-6780 induces differentiation of established erythro-leukemia cells and primary human acute myeloid leukemia cells in vitro.\textsuperscript{145} The small-molecule inhibitor of mutant IDH1 (AGI-5198) also promotes differentiation of glioma cells harboring IDH1 mutation and inhibits the growth of tumor xenografts.\textsuperscript{146} Interestingly, AGI-5198 induces histone demethylation and expression of genes associated with glial differentiation without appreciable changes in genome-wide DNA methylation, suggesting additional mechanisms of IDH1 mutation for glioma growth.

**Conclusion**

It took nearly two decades to appreciate that HIF-1α stimulation of glycolysis is not merely to maintain bioenergetics for cell survival, but equally importantly is to promote biosynthesis of macromolecules for cell proliferation. HIF-1α does the latter by blunting the glycolytic pathway through the induction of PKM2. PKM2 engages in various mechanisms as a dimer to drive cell proliferation\textsuperscript{147} and as a glycolytic enzyme in tetramer is further suppressed by oncogenic signaling. Although how PKM2 oscillates between dimer and tetramer is not well understood, receptor tyrosine kinase-mediated activation of the PI3K-AKT-mTOR pathway seems essential in orchestrating cellular biosynthesis of nucleotides, amino acids, and lipids that involves multiple pathways including HIF-1α and c-Myc signaling, and glutamine-dependent anaplerosis for cell proliferation.\textsuperscript{148}

Yet, rapid cell proliferation induces hypoxia, which is known to suppress mTORC1 through multiple mechanisms.\textsuperscript{21} In fact, HIF-1α is known to inhibit mTORC1 activity through transcriptional upregulation of DDIT4 (encoding REDD1), a negative regulator of mTORC1 activity,\textsuperscript{149,150} whereas HIF-2α, unrelated to aerobic glycolysis, stimulates mTORC1 activity by transcriptionally upregulating SLC7A5 (encoding an amino acid transporter).\textsuperscript{151} So, how do cancer cells escape from these mechanisms for proliferation? One possible answer to this conundrum is to inactivate HIF-1α, as mentioned above, albeit rarely, which implies the benefit of keeping HIF-1α expression in cancer cells. Alternatively, cancer cells may decrease expression of the stress-sensor protein ATM (ataxia telangiectasia mutated, gene symbol ATM), which is required for transcriptional activation of REDD1 through HIF-1α phosphorylation,\textsuperscript{152} or they may attempt to maintain mTORC1 activity by relying on exogenous desaturated lipids from serum for survival.\textsuperscript{153} Lastly, they may adopt a “stop-and-go” mechanism by entering cell-cycle arrest while promoting an angiogenic response to alleviate hypoxic stress for continued proliferation.\textsuperscript{154}

By altering the intracellular or intercellular context, cancer cells can adopt aberrant ways of maintaining survival and proliferation. Therefore, the selection of NRF2 signaling
for detoxification and anabolism, rather than anti-proliferative HIF-1α signaling, might be beneficial to renal cyst development at the early stage in FH-mutant cells. Similarly, an initial decrease in HIF-1α levels may facilitate DNA hypermethylation in cells harboring FH, SDH, or IDH mutations, because HIF-1α does the opposite by inducing histone demethylases and DNA demethylation, as also observed in metastasis of VHL-deficient renal cancer.\textsuperscript{155} It is also noteworthy that none of the FH, SDH, and IDH mouse models has recapitulated a corresponding phenotype of the human diseases, suggesting the requirement of additional genetic/epigenetic alterations for tumorigenesis. Further studies are warranted to elucidate the mechanisms underlying these changes and the logistics of utilizing various signaling pathways to cancer’s best advantage. Understanding of these dynamic processes is expected to provide more unexpected answers to the mystery of cancer.

Acknowledgments

This work was supported in part by an NIH Grant CA084563 from the National Cancer Institute. We thank K Kraus for editorial assistance.

Disclosure

The authors have no conflicts of interest in this work.

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The authors have no conflicts of interest in this work.

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