MINIREVIEW

Molecular Responses to Hypoxia-Inducible Factor 1 α and Beyond

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ABSTRACT

Cellular response to changes in oxygen tension during normal development or pathologic processes is, in part, regulated by hypoxia-inducible factor (HIF), an oxygen-sensitive transcription factor. HIF activity is primarily controlled through post-translational modifications and stabilization of HIF-1 α and HIF-2 α proteins and is regulated by a number of cellular pathways involving both oxygen-dependent and -independent mechanisms. Stabilization of HIF-1 α activates transcription of genes that participate in key

pathways in carcinogenesis, such as angiogenesis, dedifferentiation, and invasion. Since its discovery more than two decades ago, HIF-1 α has become a hot topic in molecular research and has been implicated not only in disease pathology but also in prognosis. In this review, we will focus on recent insights into HIF-1 α regulation, function, and gene expression. We will also discuss emerging data on the involvement of HIF in cancer prognosis and therapeutic interventions.

Introduction

Oxygen (O₂) is an indispensable component of eukaryotic metabolic processes. When oxygen demand exceeds its cellular supply, cells and tissues often become hypoxic. Hypoxia is an important factor in the pathology of a number of human diseases, including cancer, diabetes, aging, and stroke/ischemia (Melvin and Rocha, 2012; Semenza, 2012). Hypoxia can also lead to the production of oxygen radicals in a variety of experimental systems via electron attack of molecular oxygen in the inactive mitochondria (Favaro et al., 2010; Kolamunne et al., 2011; Selivanov et al., 2011). The roles of these mitochondrial-generated free radicals are especially important in hypoxia signaling pathways, which have important implications for cancer, inflammation, and a variety of other diseases (Poyton et al., 2009).

Hypoxic regions can often be found in cancer tissue due to high cellular proliferation rates coupled with the development of abnormal vasculature. Solid tumors, for example, often become hypoxic because the normal tissue vasculature can

only support tumor growth within a diameter of ~2 mm (Folkman, 1971). Cellular response to changes in oxygen tension during normal development or pathologic processes is in part regulated by hypoxia-inducible factor (HIF). HIFs are DNA-binding transcription factors that mediate cellular responses to reduced oxygen availability through transcriptional activation of a multitude of genes that encode proteins needed for oxygen delivery to tissues and energy metabolism (Manalo et al., 2005; Elvidge et al., 2006). HIFs are basic helix-loop-helix-PER-ARNT-SIM proteins that form heterodimers, composed of an oxygen-labile α -subunit (HIF α) and a stable β -subunit [HIF β , also known as aryl hydrocarbon nuclear translocator (ARNT)]. Together, these subunits bind hypoxia-responsive elements (HREs), which are similar to Enhancer box (E-box) motifs and have the consensus sequence G/ACGTG. In humans there are three distinct HIF α isoforms: HIF-1 α , encoded by *HIF1A*; HIF-2 α , encoded by *EPAS1*; and HIF-3 α , which is expressed by multiple HIF3a splice variants (Ke and Costa, 2006). HIF-1 α , HIF-2 α , and HIF-3 α splice variants 1–3 possess an oxygen-dependent degradation domain (ODDD) and a N-terminal transactivation domain, whereas HIF-1 α and HIF-2 α possess a C-terminal transactivation domain (Ke and Costa, 2006). HIF activity is primarily controlled through post-translational modifications and stabilization of HIF-1 α and HIF-2 α proteins.

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ABBREVIATIONS: 4E-BP, 4E-binding protein; Akt, protein kinase B; BEZ235, 2-methyl-2-[4-[3-methyl-2-oxo-8-(quinolin-3-yl)-2,3-dihydroimidazo[4,5-c]quinolin-1-yl]phenyl]propionitrile; E3, Elongin BC/Cul2/pVHL; E-box, Enhancer box; FIH, factor inhibiting hypoxia-inducible factor; HAF, hypoxia-associated factor; HIF, hypoxia-inducible factor; HRE, hypoxia-responsive element; HSP90, heat-shock protein 90; mTOR, mammalian target of rapamycin; ODDD, oxygen-dependent degradation domain; PHD, prolyl-hydroxylase domain; PI3K, phosphoinositide-3-kinase; pVHL, von Hippel-Lindau tumor suppressor protein; PX-478, (S)-4-(2-amino-2-carboxyethyl)-N,N-bis(2-chloroethyl)aniline oxide dihydrochloride; REDD1, DNA damage-inducible transcript 4; RUNX, runt-related transcription factor; SP600125, dibenzo[cd,g]indazol-6(2H)-one; Top I, topoisomerase I; VEGF, vascular endothelial growth factor; YC-1, 5-[1-(phenylmethyl)-1H-indazol-3-yl]-2-furanmethanol.

However, HIF-1 α mRNA contains an internal ribosome entry site, the presence of which allows translation to be maintained under conditions that are inhibitory to cap-dependent translation, which occurs during hypoxia (Lang et al., 2002). In this review, we will focus on recent insights into HIF-1 α regulation, function, and gene expression. We will also discuss emerging data on the involvement of HIF in cancer prognosis and therapeutic interventions.

Oxygen-Dependent Regulation of HIF Signaling

2-Oxoglutarate-Dependent Dioxygenases. Under normal oxygen tension (normoxia), HIF α becomes hydroxylated on one (or both) of the two highly conserved proline residues within the ODDD domain by prolyl-hydroxylase domain (PHD)-containing enzymes. Hydroxylated HIF α is then recognized by the β -domain of von Hippel-Lindau tumor suppressor protein (pVHL) and ubiquitinated by the Elongin BC/Cul2/pVHL (E3) ubiquitin-ligase complex. The ubiquitination then marks HIF α for proteasomal degradation (Ke and Costa, 2006; Greer et al., 2012). There are three HIF-prolyl hydroxylases known in mammals, and they are encoded by separate genes: *PHD1*, *PHD2*, and *PHD3* (Myllyharju and Koivunen, 2013). Like all 2-oxoglutarate-dependent dioxygenases, PHDs require oxygen for hydroxylation, as well as tricarboxylic acid cycle intermediate, 2-oxoglutarate (α -ketoglutarate), iron (Fe²⁺), and ascorbate as cofactors (Schofield and Zhang, 1999). When oxygen levels are low, HIF α escapes PHD hydroxylation and recognition by the pVHL ubiquitin-ligase complex and translocates into the nucleus, where it transcriptionally activates hundreds of genes involved in erythropoiesis, angiogenesis, autophagy, and energy metabolism (Kaelin and Ratcliffe, 2008). Another dioxygenase that can influence HIF activity is the factor inhibiting hypoxia-inducible factor (FIH). When oxygen is available, FIH hydroxylates a conserved asparagine residue within the C terminus trans-activation domains of HIF α , creating a steric clash and preventing binding to coactivators such as p300/CBP, thus limiting HIF transcriptional activity (Ruas et al., 2005). FIH remains active at lower oxygen concentrations as compared with PHDs and is capable of suppressing the activity of HIF α subunits that escaped proteasomal degradation under moderate hypoxia (Dayan et al., 2006).

Given that PHDs and FIHs require α -ketoglutarate as a cosubstrate, they have been reported to be inhibited by several citric acid cycle metabolic intermediates, such as fumarate and succinate, which competitively inhibit all three PHDs with similar IC₅₀, and citrate and oxaloacetate, which competitively inhibit FIH (Koivunen et al., 2007). This inhibition of HIF hydroxylases may explain why highly vascular tumors develop in the absence of VHL mutations. Elevated levels of fumarate and succinate, in fumarate hydratase and succinate dehydrogenase-deficient tumors, were shown to inhibit all three PHDs, resulting in consequent stabilization/upregulation of HIF α and their product genes (Isaacs et al., 2005; Selak et al., 2005).

In addition to playing a vital role in tumorigenesis, FIH has been reported to be an essential regulator of metabolism and epithelial differentiation. *Fih1*^{-/-} mice displayed a range of metabolic phenotypes, such as decreased adiposity, hyperventilation, and increased insulin sensitivity. When placed on a high-fat diet, these animals were also less likely to develop

insulin resistance, weight gain, and hepatic steatosis (or fatty liver) (Zhang et al., 2010). FIH1 was shown to negatively regulate corneal epithelial glycogen metabolism in a HIF-1 α -independent manner, and suppression of miR-31 in human corneal epithelial keratinocytes led to increased FIH1 protein levels, decreased Notch activity, and diminished differentiation (Peng et al., 2012a,b). Moreover, *FIH1* expression was markedly increased in the epidermis of patients with psoriasis and in the corneal epithelium of patients with diabetic keratopathies (Peng et al., 2012a). Collectively, these data suggest that FIH may play a role in obesity and related diseases (i.e., diabetes and nonalcoholic fatty liver disease), making it a potential target of therapeutic intervention.

Glycolytic Isoenzyme Pyruvate Kinase-M2. Another enzyme that has been recently implicated in HIF-1 α regulation is pyruvate kinase (ATP: pyruvate 2-*O*-phosphotransferase, EC 2.7.1.40), which is the final enzyme in glycolysis. It catalyzes the transfer of a phosphate group from phosphoenolpyruvate to ADP to create pyruvate and ATP. There are several different isoenzymes of pyruvate kinase, as follows: pyruvate kinase isoenzyme type L, which is expressed in tissues with gluconeogenesis, such as liver, kidney, and intestine, and pyruvate kinase isoenzyme types M1 and M2 (Mazurek, 2011). In tumors, M2 variant is the predominant form of pyruvate kinase that is expressed, and HIF-1 α has been reported to activate *PKM2* transcription (Christofk et al., 2008; Luo et al., 2011). Specifically, PHD3-mediated hydroxylation of PKM2 increased the HIF-1 α binding to HREs at target genes, recruitment of coactivator p300, histone acetylation, and subsequent transactivation of HIF-1 target genes (Luo et al., 2011). PHD3 knockdown inhibited PKM2 coactivator function, reduced glucose uptake and lactate production, and increased O₂ consumption in cancer cells. Moreover, PKM2 hydroxylation did not appear to be affected by 1% O₂, suggesting that PHD3 is still active under hypoxic conditions. PKM2-stimulated expression of HIF-1 α target genes promoted the shift from oxidative phosphorylation to glycolytic metabolism and increased expression of vascular endothelial growth factor (*VEGF*) gene (Luo et al., 2011). PKM2, therefore, may play a more extensive role in promoting HIF-mediated cancer progression than previously thought.

Runt-Related Transcription Factors. HIF-1 α is known to be an important regulator of angiogenesis. HIF-1 α regulation and stability during angiogenesis are mediated by the runt-related transcription factor (RUNX). *RUNX* genes (*RUNX1*, *RUNX2*, and *RUNX3*), also known as the acute myeloid leukemia, are developmental regulators and play a role in human cancers (Ito, 2004). All three *RUNX* genes appear to be involved in HIF-1 α regulation and stability during angiogenesis. *RUNX1* and HIF-1 α proteins were demonstrated to directly interact with one another, primarily via the Runt homology domain of *RUNX1*, with dual effects. *RUNX1* overexpression inhibited DNA-binding and transcriptional activity of HIF-1 α protein with reduced expression of the HIF1-targeted gene, *VEGF*, whereas silencing of *RUNX1* expression by specific small interfering RNA significantly increased transcriptional activity of HIF-1 α protein, suggesting that *RUNX1* inhibited transcription-dependent functions of HIF-1 α (Peng et al., 2008). *RUNX2* was reported to compete with VHL tumor suppressor protein, by directly binding to HIF-1 α ODDD and significantly inhibiting the ubiquitination of HIF-1 α , without changing its hydroxylation status. Moreover, overexpression of *RUNX2*

enhanced in vitro and in vivo angiogenesis through enhanced secretion of VEGF (Lee et al., 2012).

The effect of RUNX3 on HIF-1 α stability was also recently investigated. RUNX3 overexpression was found to attenuate HIF-1 α stability under normoxic and hypoxic conditions in gastric cancer cells. Under hypoxic conditions, RUNX3 was shown to regulate the stability of HIF-1 α at the post-translational level. Treatments by 5-aza-2-deoxycytidine, an inhibitor of DNA methyltransferase, and by trichostatin A, a histone deacetylase inhibitor, resulted in the recovery of RUNX3 and suppression of both HIF-1 α and VEGF. Furthermore, RUNX3 was shown to directly interact with the C-terminal activation domain of HIF-1 α and PHD2, potentiate proline hydroxylation, and subsequently promote the degradation of HIF-1 α . RUNX3 overexpression also markedly inhibited hypoxia-induced angiogenesis in vitro and in vivo (Lee et al., 2013). Ultimately, RUNX3 suppresses hypoxia-mediated angiogenesis by destabilizing HIF-1 α protein via promoting its proline hydroxylation.

Oxygen-Independent Regulation of HIF Signaling

Although HIF regulation has primarily been thought to be subject to oxygen tension, multiple studies have also reported that HIF-1 α can undergo oxygen-independent regulation. As noted earlier, the oxygen-dependent degradation of the HIF-1 α subunit is mediated by PHDs, VHL, Elongin C/Elongin B E3 ubiquitin-ligase complex, and the proteasome. However, inhibition of heat-shock protein 90 (HSP90) was shown to lead to oxygen/PHD/VHL-independent proteasomal degradation. Receptor for the activated protein kinase C is a HIF-1 α -interacting protein that competes with HSP90 for binding to HIF-1 α and is required for O₂-independent and HSP90 inhibitor-induced degradation of HIF-1 α (Liu et al., 2007). Hypoxia-associated factor (HAF), a novel E3-ubiquitin ligase, was also reported to bind to HIF-1 α , resulting in its proteasomal degradation irrespective of cellular oxygen tension (Koh et al., 2008). HAF and HIF-1 α interact in vitro and in vivo through binding of HAF residues 654–800 to HIF-1 α residues 296–400, and this binding is not oxygen dependent and does not require prolyl hydroxylation (Koh et al., 2008). Therefore, HAF is capable of negatively regulating HIF-1 α levels under conditions in which the pVHL-E3 ligase complex is inactive, like hypoxia.

HIF-1 α and Gene Expression

HIFs are the key regulators in the major transcriptional cascade involved in the cellular response to changes in oxygen tension. Recently, several groups have used chromatin immunoprecipitation coupled to next-generation high-throughput sequencing to examine the binding of HIF α subunits across the genome (Tanimoto et al., 2010; Schödel et al., 2011). Analysis of HIF-binding motifs confirmed the 5'-RCGTG-3' (where "R" denotes a purine residue) core-binding sequence (Simon and Keith, 2008) and revealed no additional absolute sequence requirement for HIF binding (Xia et al., 2009a; Schödel et al., 2011). HIF and several other basic helix-loop-helix transcription factors bind to the E-box binding site, CACGTG. When a cytosine precedes the HIF consensus site, the E-box site is formed (Benita et al., 2009). Moreover, these analyses also revealed that the HIFs bind to ~500 high-affinity target sites

across the genome, many of which are located at considerable distances (>100 kb) away from the genes that they regulate (Tanimoto et al., 2010; Schödel et al., 2011). The Nucleosome-Seq and chromatin immunoprecipitation coupled to next-generation high-throughput sequencing analyses of histone modifications (H3K4me3, H3Ac, and H3K27me3) and binding status of RNA polymerase II revealed that the chromatin formed an open structure in regions surrounding the HIF-1 α binding sites, but this event occurred prior to the actual binding of HIF-1 α (Tanimoto et al., 2010). DNase I hypersensitivity also revealed that HIFs appear to be recruited to genes that are already expressed under normoxic conditions, indicating that it is unlikely that they direct the hypoxia-induced changes in the chromatin structure of target genes. Therefore, epigenetic regulation of chromatin may have a central role in defining the hypoxic response (Schödel et al., 2011). The limited concordance (40–60%) between the HIF binding sites detected in breast cancer (MCF7) and renal cell carcinoma cell lines may indicate that the range of HIF target genes may largely be determined by the underlying cell type-specific patterns of chromatin structure (Schödel et al., 2011).

HIF-1 α and Jumonji Domain-Containing Histone Demethylases

Multiple groups have also reported that HIF-1 α can bind to and regulate the expression of multiple Jumonji domain-containing histone demethylases. JmjC domain lysine demethylases are members of the dioxygenase superfamily of enzymes, which contain iron and are 2-oxoglutarate-dependent enzymes (Klose et al., 2006). Many of these histone demethylases have HREs in their promoters and are induced by HIF-1 α (Yang et al., 2009). For example, *JARID1B* (*KDM5B*), *JMJD1A* (*KDM3A*), *JMJD2B* (*KDM4B*), and *JMJD2C* (*KDM4C*) are known to be direct HIF-1 α target genes with robust HIF-1 α binding to HREs in their promoters and upregulated expression under hypoxic conditions (Pollard et al., 2008; Sar et al., 2009; Krieg et al., 2010; Guo et al., 2012). Under hypoxia, cells ectopically expressing *JARID1B* had decreased levels of histone 3 lysine 4 methylation (Xia et al., 2009b). Furthermore, *JMJD1A* was shown to regulate a subset of hypoxia-induced genes, including *ADM* and *GDF15*, by maintaining a lower level of histone 3 lysine 9 dimethylation at their promoter regions. *JMJD1A* was also important for tumor growth in the hypoxic microenvironment of tumor xenografts (Krieg et al., 2010). In addition to upregulating the expression of certain demethylases, hypoxia can also directly inhibit their enzyme activity because they require oxygen, α -ketoglutarate, and ascorbate as cofactors to carry out their enzymatic function. Demethylases are not completely inactive during hypoxia. Their enzymatic activity is less, so an increased amount of the enzyme is needed (Chen and Costa, 2009). Moreover, in human cancer cell lines and tumors, miR-210, a robust target of HIF and master micro RNA of the hypoxia response, was found to target the mitochondrial iron-sulfur scaffold protein, down-regulation of which was the major cause of formation of reactive oxygen species in hypoxia (Favaro et al., 2010). Therefore, the hypoxia-induced production of free radical oxygen species may also diminish demethylase activity by depleting ascorbate levels or oxidizing iron necessary for the demethylase activity.

HIF-1 α and Cancer Prognosis

Increased expression of HIF-1 α has been observed in a broad range of human cancers, often correlating with poor prognosis (Table 1). HIF-1 α and VEGF status were significantly associated with tumor stage, lymph nodes, and liver metastases in patients with colorectal cancer. Patients with positive HIF-1 α and VEGF tumors tended to have a poorer prognosis and shorter survival time (Cao et al., 2009). HIF-1 α overexpression was also positively correlated with colorectal liver metastasis and phosphoinositide-3-kinase catalytic subunit alpha mutation status and served as an independent risk factor for malignancy recurrence after curative resection of colorectal liver metastasis (Shimomura et al., 2013). Elevated expression of HIF-1 α was associated with vascular invasion and a poor prognosis for patients with hepatocellular carcinoma (Zheng et al., 2013). In patients with esophageal squamous cell carcinoma, high HIF-1 α expression was also associated with lymph node metastasis, serosa infiltration, tumor stage, and overall survival time in esophageal squamous cell carcinoma patients (Chai et al., 2013). HIF-1 α expression was also correlated with angiogenesis and unfavorable prognosis in bladder cancer, gastrointestinal stromal tumor of the stomach, early-stage invasive cervical cancer, pancreatic cancer, head and neck cancer, nonsmall cell lung cancer, melanoma, and breast and ovarian cancers (Birner et al., 2000; Giatromanolaki, 2001; Giatromanolaki et al., 2001, 2003; Koukourakis et al., 2002; Shibaji et al., 2003; Takahashi et al., 2003; Theodoropoulos et al., 2004; Winter et al., 2006; Klatte et al., 2007; Sun et al., 2007a; Daponte et al., 2008; Yamamoto et al., 2008). The above studies indicate that increased expression of HIF-1 α proteins in tumor cells, whether induced by hypoxia or aberrant oncogenic signaling, is responsible for driving tumor growth and progression, most likely by regulating the expression of crucial target genes that are involved in carcinogenesis.

Whereas increased HIF-1 α levels are often correlated with poor prognosis, some studies have shown the opposite to be true. Fillies et al. (2005) found that HIF-1 α overexpression provides a better prognosis for patients with early stage squamous cell carcinoma of the oral floor. In a study by Lidgren et al. (2006), high HIF-1 α levels in renal cell carcinoma were associated with a better prognosis.

TABLE 1
Correlation of prognosis and HIF-1 α expression in human cancers

Cancer Type	Prognosis	Reference
Colorectal	Poor	Cao et al., 2009 Shimomura et al., 2013
Hepatocellular	Poor	Zheng et al., 2013
Esophageal	Poor	Chai et al., 2013
Bladder	Poor	Theodoropoulos et al., 2004
GIST	Poor	Takahashi et al., 2003
Cervical	Poor	Birner et al., 2000
Head and neck	Poor	Winter et al., 2006
NSCLC	Poor	Giatromanolaki et al., 2001 Giatromanolaki et al., 2003
Melanoma	Poor	Koukourakis et al., 2002
Breast	Poor	Yamamoto et al., 2008
Ovarian	Poor	Daponte et al., 2008
Pancreatic	Poor	Sun et al., 2007 Shibaji et al., 2003
RCC	Poor	Klatte et al., 2007

GIST, gastrointestinal stromal tumor; NSCLC, nonsmall cell lung cancer; RCC, renal cell carcinoma.

The controversy regarding HIF-1 α levels and prognosis is best illustrated in a study by Vleugel et al. (2005). The group examined HIF-1 α concentrations in invasive breast cancers with two overexpression patterns as follows: 1) HIF-1 α overexpressed in perinecrotic regions, and 2) diffusely overexpressed HIF-1 α . They found that the perinecrotic expression patterns were associated with the expression of hypoxia-associated genes carbonic anhydrase IX (CAIX) and glucose transporter 1 (GLUT1)—and this correlated with poor prognosis. Tumors with HIF-1 α diffusely expressed were not associated with CAIX and GLUT1 expression, and these patients had a better prognosis (Vleugel et al., 2005). The contradicting conclusions predicting HIF-1 α 's role in cancer prognosis further emphasize the complexity of HIF's involvement in cancer.

HIF-1 α and Therapeutic Interventions

Given its wide-scoping role in the pathology of human disease, HIF-1 α -targeting therapeutic agents have gained considerable traction and attention among the medical and scientific community. A number of potential cancer therapeutic agents have recently been shown to function by directly or indirectly interacting with mammalian target of rapamycin (mTOR) signaling cascade. mTOR is a serine/threonine protein kinase that regulates protein synthesis, cell growth, and cell survival and is involved in both positive and negative feedback loops with HIF-1 α (Demidenko and Blagosklonny, 2011). Phosphorylation of mTOR and its downstream effectors 4E-binding protein (4E-BP)1 and p70S6K was reported to raise cellular levels of HIF-1 α by stimulating its translation. Specifically, HIF-1 α was shown to bind with HIF-1 β and activate transcription of growth factors and cytokines that stimulated the receptor tyrosine kinase–phosphoinositide-3-kinase (PI3K)–protein kinase B (Akt) pathway, which resulted in further activation of mTOR (Finlay et al., 2012; Agani and Jiang, 2013). HIF-1 α was also shown to stabilize DNA damage-inducible transcript 4 (REDD1). Once stabilized, REDD1 can bind and activate tuberous sclerosis protein 2, resulting in an indirect inactivation of mTOR (Horak et al., 2010; Kucejova et al., 2011). Below, we will discuss several drugs that inhibit mTOR and/or HIF-1 α , and this information is presented in Table 2. We note in this work that this is not a comprehensive list of all HIF-1 α -inhibiting drugs, and the reader is referred to reviews (Xia et al., 2012; Hu et al., 2013; Tang and Yu, 2013) for more information on this topic.

Inhibition of HIF-1 α protein synthesis via suppression of the PI3K-Akt-mTOR pathway appears to be a common mode of action for a number of the recently characterized anticancer drug candidates (i.e., magnolol, sorafenib, YC-1 (5-[1-(phenylmethyl)-1H-indazol-3-yl]-2-furanmethanol), and BEZ235 [2-methyl-2-[4-[3-methyl-2-oxo-8-(quinolin-3-yl)-2,3-dihydroimidazo[4,5-c]quinolin-1-yl]phenyl]propionitrile]). In human bladder cancer cells, the phenolic compound magnolol was shown to suppress the PI3K-Akt-mTOR pathway and subsequently reduced HIF-1 α accumulation by inhibiting hypoxia-induced reactive oxygen species and VEGFR2, two known activators of the PI3K-Akt pathway (Chen et al., 2013). Sorafenib, like magnolol, was also reported to decrease synthesis of HIF-1 α but mediated its effects by decreasing phosphorylation of mTOR and its downstream effectors p70S6K and 4E-BP1 (Liu et al., 2012). YC-1 prevents HIF-1 α translation by suppressing the PI3K-Akt-mTOR-4E-BP pathway. YC-1 also inhibited nuclear factor κ B,

TABLE 2
HIF-1 α inhibitors and mechanisms of action

HIF-1 α Inhibitor	Mechanism	Reference
Magnolol	Suppresses PI3K-Akt-mTOR pathway	Chen et al., 2013
Sorafenib	Decreases phosphorylation of mTOR and its downstream effectors p70S6K and 4E-BP1	Liu et al., 2012
YC-1	Suppresses the PI3K-Akt-mTOR-4E-BP pathway	Sun et al., 2007
BEZ235	Inhibits both PI3K and mTOR by interacting with their ATP-binding clefts	Karar et al., 2012
Meformin ^a	Inactivates mTOR by increasing the levels of REDD1	Ben Sahra et al., 2011
Deferasiro ^a	Inactivates mTOR by increasing the levels of REDD1	Ohyashiki et al., 2009
SP600125 ^a	Inactivates mTOR by increasing the levels of REDD1	Jin et al., 2009
Topotecan	Prevents translation of HIF-1 α mRNA	Rapisarda et al., 2004
PX-478	1) Decreases HIF-1 α mRNA levels; 2) prevents HIF-1 α translation; and 3) prevents HIF-1 α deubiquitination	Lee et al., 2011

^aMay actually increase HIF-1 α levels.

a downstream target of Akt (Sun et al., 2007b). Moreover, a recent study by Karar et al. (2012) reported on the HIF-1 α inhibitory effects of BEZ235, an agent that inhibits both PI3K and mTOR by interacting with their ATP-binding clefts. BEZ235 proved to be a more efficient inhibitor of HIF-1 α synthesis than either a mTOR inhibitor or a PI3K inhibitor alone.

Other mTOR inhibitors, such as deferasiro and SP600125 (dibenzo[cd,g]indazol-6(2H)-one), which may be therapeutic in the treatment of cancer, function to inactivate mTOR by increasing the levels of REDD1, a HIF-1 α -stabilized protein (Jin et al., 2009; Ohyashiki et al., 2009). Given the implications of HIF-1 α in human cancers, it is likely that the mTOR inhibitors that function to reduce HIF-1 α levels are likely to have promising treatment effects. However, further research is needed to establish mTOR inhibitors as effective chemotherapeutics.

Some other notable drugs that have shown promising results for the inhibition of HIF-1 α in cancer therapy include topotecan and PX-478 [(S)-4-(2-amino-2-carboxyethyl)-N,N-bis(2-chloroethyl)aniline oxide dihydrochloride]. Topotecan is a topoisomerase I (Top I) inhibitor and has been shown to inhibit HIF-1 α . Top I is a monomeric enzyme that catalyzes the conversions of the different topological states of DNA. Topotecan stabilizes Top I on DNA and induces DNA damage during replication; however, topotecan has been shown to inhibit HIF-1 α in an S-phase-independent manner. Topotecan inhibits HIF-1 α accumulation by preventing translation of HIF-1 α mRNA, and Top I is required for this inhibition (Rapisarda et al., 2004). PX-478 is the first HIF-1 α inhibitor to be used at a clinical stage for the treatment of solid tumors. The drug inhibits HIF-1 α levels via a number of mechanisms, as follows: 1) decreasing HIF-1 α mRNA levels, 2) preventing HIF-1 α translation, and 3) preventing HIF-1 α deubiquitination. The drug significantly decreased expression of the HIF-1 α target genes, *VEGF* and *GLUT-1* (Lee and Kim, 2011). Although the inhibition of HIF-1 α appears to be a promising field of cancer research, only a few of the drugs have advanced past preclinical and clinical development, and further investigations are needed to establish these drugs as valid tools in chemotherapy.

Conclusion

HIF is a transcription factor that is regulated by a number of cellular pathways involving both oxygen-dependent and oxygen-independent mechanisms. Stabilized HIF-1 α activates transcription of genes that participate in angiogenesis,

dedifferentiation, and invasion—all of which are key pathways in carcinogenesis. Due to its large role in cancer and its association with poor prognosis, it is not surprising that HIF-1 α has become an important topic in molecular research. The complex mechanisms underlying the hypoxic microenvironment of solid tumors have yet to be fully characterized, but it is certain that HIF-1 α is a key mediator. Manipulating pathways and mediators, such as mTOR, that are known to regulate HIF-1 α may be of therapeutic value. Future research should attempt to unearth the missing links between HIF and cancer metabolism, as well as examine the therapeutic effects of small molecular inhibitors of HIF-1 α regulators.

Authorship Contributions

Wrote or contributed to the writing of the manuscript: Brocato, Chervona, Costa.

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