

Hypoxia-regulated gene network in drug resistance and cancer progression

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Abstract

Hypoxia is a common phenomenon of solid tumors and contributes to aggressive phenotype and treatment failure. Hypoxia-inducible factor (HIF), a versatile transcription factor that regulates more than 5% of total human genes, not only plays important roles in controlling physiological processes, but is also a crucial mediator in hypoxia-induced tumor progression and chemoresistance. Overexpression of HIF-1 α is detected in a wide spectrum of cancers via different kinds of mechanisms, including reduced oxygen concentration, loss-of-function of tumor suppressor gene, activating mutation of oncogenes, and hyperactivation of protein kinase signaling pathways. HIF-regulated genes involve in many pathological processes such as metabolic switch, drug efflux, angiogenesis, cell proliferation, and anti-apoptosis, which ultimately leads to increased tumor growth and drug resistance. Due to the common failure of classic chemotherapeutic agents in treating hypoxic cancers, novel strategies have been developed to target tumors under hypoxic conditions including inhibition of HIF activity and administration of bioreductive drugs. These new strategies may provide more effective and specific methods in targeting hypoxic tumors.

Keywords: Drug resistance, hypoxia, metabolic switch, apoptosis, microRNA

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Introduction

Cancer is a primary factor leading to mortality and morbidity worldwide, mainly contributed by its invasion and metastasis. According to world health organization statistics, the incidence of 12.7 million new cancer cases in 2008 will rise to 21.4 million by 2030.¹ Although cancer development is a very complex, multi-step process with mechanisms largely unknown, hypoxia, no doubt, is one of the most important factors contributing to cancer progression and malignancy. When cancer cells start to grow, hypoxia occurs because of no adequate or normal microvasculature for the whole tumor develops concurrently.^{2,3}

Hypoxia-inducible factor (HIF) plays a central role to regulate transcription of numerous genes for adapting to hypoxia, maintaining oxygen homeostasis, and keeping cells alive.⁴ After HIF-1 α was first discovered by the identification of a hypoxia response element (HRE) in 1990s,^{5–7} scientists have proven it is a key regulator responsible for the induction of genes that facilitate adaptation and survival under low oxygen condition. Besides, HIF-1 activates the transcription of genes that are involved in pivotal aspects of cancer biology, including angiogenesis, survival, metabolism, and invasion. Intratumoral hypoxia and genetic

alterations can lead to HIF-1 α overexpression, which has been associated with tumor aggressiveness and treatment failure in many cancer types.^{7–11} In preclinical studies and clinical trial, inhibition of HIF-1 activity has marked effects on tumor growth.¹²

Although the molecular mechanisms of hypoxia-induced tumor progression and drug resistance remain elusive, recent studies have provided many new and exciting findings that will advance our understanding of this complicated pathological process. In this article, we will review the current understandings of the roles of hypoxia and HIFs in tumor pathogenesis and drug resistance. In addition, current developments in targeting hypoxia as a cancer therapeutic approach will also be reviewed.

HIF and HIF-regulated genes

Regulation of HIF

Regulation of cell functions in response to hypoxia is mainly mediated by two transcription factors, namely HIF-1 and HIF-2. HIF is a heterodimer composed of one α and one β subunit. The HIF heterodimer binds to DNA at HRE located in the promoter region, 5' untranslated region, or 3' untranslated region of numerous genes to regulate their

transcription under hypoxic status.^{13,14} In normoxia, HIF- α has very short half-life due to rapid degradation by ubiquitin-proteasome pathway^{15,16} (Figure 1). In the presence of oxygen molecules, HIF- α is hydroxylated by prolyl hydroxylase domain-containing protein (PHD) at two proline residues within the oxygen-dependent degradation domain.^{17,18} The proline-hydroxylated HIF- α is recognized by von Hippel-Lindau (VHL) protein, an E3 ubiquitin ligase. Binding of hydroxylated HIF- α by VHL initiates the process of polyubiquitination and protein degradation.^{19–23} In addition, the α subunit of HIF is also hydroxylated by factor-inhibiting HIF (FIH) at the C-terminal transactivation domain (asparagine residue) under normal oxygen level, which prevents its interaction with transcription coactivator, P300.^{24,25} Thus, the α subunit of HIF is constitutively transcribed, translated, and degraded under normoxic condition. Even with the presence of residual HIF protein, its transcription activity is markedly inhibited because of FIH-mediated hydroxylation of asparagine residue in the transactivation domain. In contrast, because both PHD and FIH require oxygen molecules to exert their enzymatic activity, the hydroxylation reaction cannot occur under hypoxia condition. Therefore, HIF- α protein level rapidly accumulates under hypoxia and binds to the β subunit of HIF (also known as aryl hydrocarbon receptor nuclear translocator, ARNT). The dimerized $\alpha\beta$

heterodimer then translocates to the nucleus and binds to HRE to regulate the expression of target genes.

Besides the absolute requirement of oxygen molecules, the enzyme PHD also needs 2-oxoglutarate and ferrous (Fe^{2+}) as two cofactors to exert its enzymatic activity. Therefore, the reduction of either one of these two cofactors leads to the inhibition of PHD's activity and stabilization of HIF- α . Iron chelators such as desferrioxamine and transition metal ions such as cobalt ion that deplete and compete with Fe^{2+} , respectively, are good inhibitors of PHDs. Dimethyloxaloylglycine, the 2-oxoglutarate analog, also inhibits PHD's enzyme activity. Therefore, desferrioxamine, cobalt chloride, and dimethyloxaloylglycine are often used as chemical hypoxia mimetics in biomedical research to cause the increase of HIF-1 α under normoxic condition.

Genes regulated by HIF

Considering hypoxia controls numerous physiological and pathological processes, it is of interesting to identify hypoxia-regulated genes that govern diverse cellular functions. Hypoxia controls gene expression mainly through two distinct mechanisms: HIF-dependent and HIF-independent. In the HIF-independent pathway, hypoxia controls gene expression via influencing the activity of oxygen- and 2-oxoglutarate-dependent enzymes, the dioxygenases. It has been shown that under hypoxic condition,

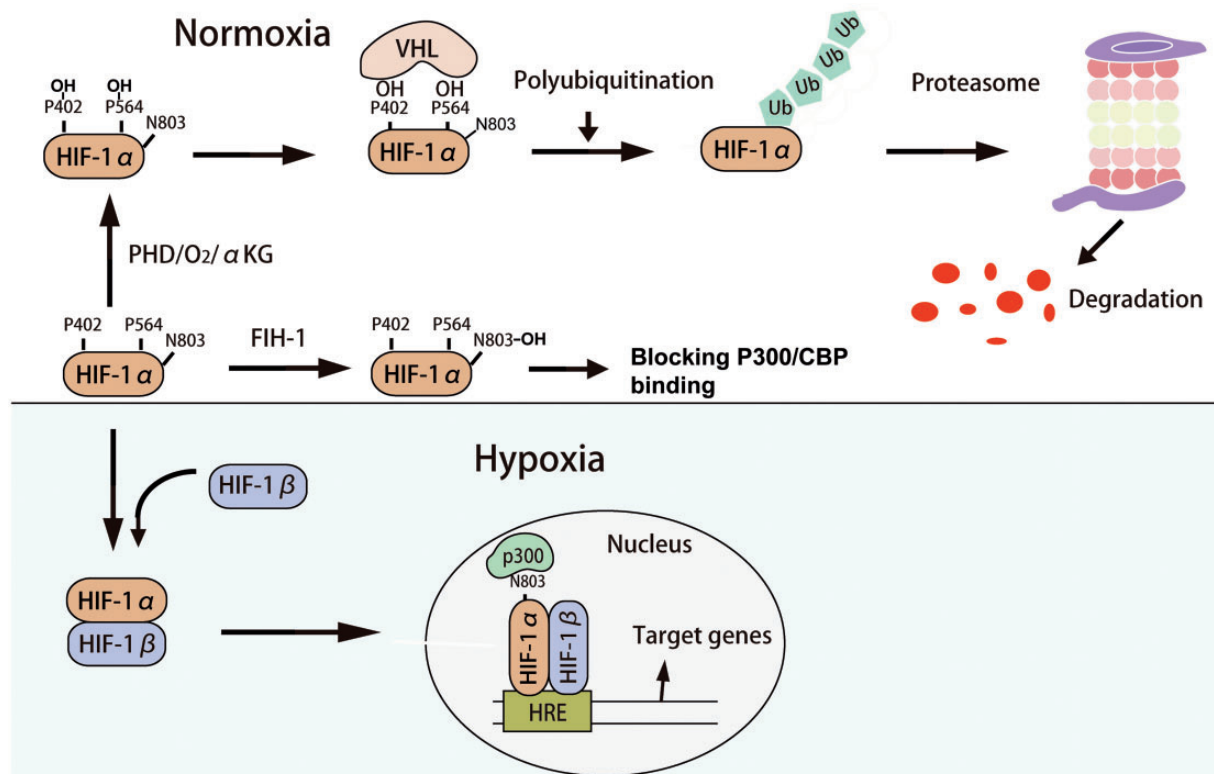


Figure 1 Regulation of hypoxia-inducible factors. In normoxia, HIF-1 α is hydroxylated by prolyl hydroxylase domain (PHD) protein and factor-inhibiting HIF (FIH), respectively. The proline-hydroxylated HIF-1 α is then recognized by von Hippel-Lindau E3 ubiquitin ligase (VHL) and subjected to be degraded via proteasome while the asparagine-hydroxylated HIF-1 α fails to interact with transcriptional activator such as P300 or CREB-binding protein (CBP). In hypoxia, HIF-1 α becomes stable and dimerizes with HIF-1 β . After translocation to the nucleus and recruitment of co-activators (e.g. CBP/p300), the HIF heterodimer binds the hypoxia response element (HRE) of target genes to regulate transcription. O_2 : oxygen, α -KG: α -ketoglutarate. (A color version of this figure is available in the online journal.)

some transcription factors such as nuclear transcription factor (NF)- κ B, CXXC finger protein 5, coiled-coil-helix-coiled-coil-helix domain 2, activation transcription factor (ATF)-3, and ATF-4 are upregulated due to loss of function of dioxygenase.^{26–30} Alternatively, hypoxia may lead to phosphorylation of c-MYC transcription factor via PI3K pathway.³¹ Upregulation or activation of these transcription factors results in induction of their downstream target genes independent of HIF transcription activity.

In contrast to the HIF-independent regulation, the majority of genes regulated by hypoxia are mediated directly by HIF-dependent transcriptional activation or repression. HIF-1 α or HIF-2 α dimerizes with HIF-1 β , the constitutively expressed isoform, and recognizes the HRE motif. It is reported that the HRE motif consists of a core element, 5'-RCGTG-3'³²; nevertheless, experimental data prove that this core HRE is necessary but not sufficient to determine the responsiveness of a gene to HIF transcription factors.³³ Therefore, it is reasonable to hypothesize that the sequences flanking the core element are important to determine the binding specificity. Indeed, recent studies by bioinformatic predictions^{34–37} and genomewide screenings^{38–41} reported that the flanking sequences, though not as conserved as the core element, are important for the binding of HIFs to their target genes.

Although both HIF-1 α and HIF-2 α recognize the same DNA motif, more and more experimental data demonstrate that HIF-1 α and HIF-2 α regulate a distinct subset of genes.^{39,40,42,43} Therefore, it is believed that these two homologs exert evolutionally diverse physiological and pathological functions instead of just a pair of redundant genes. Further study is necessary to carefully dissect the regulation and function of these two transcription factors in order to paint better pictures of hypoxia-mediated biological processes.

Functional roles of HIF in cancer biology

Metabolism reprogramming

It has been known that cellular metabolism in the neoplasm is quite different from its surrounding normal tissue. The rapid growth and proliferating cancer cells demand large amount of different nutrients to provide ATP and building blocks to maintain cellular structure and morphology. In normal cells, the majority of ATP and building blocks are derived from oxidative phosphorylation of glucose. One molecule of glucose can generate 38 ATPs through cytoplasmic glycolysis followed by mitochondrial oxidative phosphorylation. Besides, the intermediate metabolites of tricarboxylic acid (TCA) cycle can serve as building blocks for the synthesis of cellular components. However, the oxidative phosphorylation requires large amount of oxygen molecules as fuel. Because the oxygen supply, which heavily depends on the availability of blood vessels, is limited, cancer cells have to develop a different approach to metabolize glucose. In cancer cells, glucose is mainly catalyzed via the glycolytic pathway without going through the TCA cycle, the so-called Warburg effect.⁴⁴ Although Warburg effect has been proposed by Otto Warburg in 1920s, detailed mechanism was not elucidated until 2006. Two studies

reported that pyruvate dehydrogenase kinase 1 (PDK1) was markedly upregulated under hypoxia in a HIF-1 α -dependent manner.^{45,46} Upregulation of PDK1 phosphorylates pyruvate dehydrogenase (PDH) leading to the inhibition of its catalytic activity. As a result, pyruvate cannot be converted to acetyl-CoA, the initiated molecule to enter TCA cycle. Instead, accumulated pyruvate was converted by another hypoxia-inducible enzyme, lactate dehydrogenase A (LDHA), to become lactic acid (Figure 2). Later, it was reported that another member of PDK family, PDK3, is also a target of HIF-1 α .³⁵ Induction of PDK3 also results in blockage of PDH enzyme activity. The same study carefully dissects molecular mechanism responsible for induction of PDK1 and PDK3. PDK1 is induced by both HIF-1 α and HIF-2 α while PDK3 only induced by HIF-1 α .³⁵ Further study demonstrated that PDK3 but not PDK1 was elevated in colon cancer and elevation of PDK3 promotes metabolic switch, increases drug resistance, and is correlated with colorectal cancer malignancy and poor prognosis.^{35,47}

Although cytoplasmic glycolysis is not limited by oxygen availability, it produces less than 6% of ATP per molecule of glucose compared to mitochondrial phosphorylation. Since cancer cells actually rely more on ATP production for the rapid proliferation, they need to uptake much more glucose than normal cells do. This is achieved by overexpression of glucose transporters and glycolytic enzymes including glucose transporters (GLUT1 and GLUT3), hexokinase (HK1 and HK2), aldolase A (ALDA), phosphoglycerate kinase-1 (PGK1), enolase (ENO1), glyceraldehyde 3-phosphate dehydrogenase (GAPDH), pyruvate kinase M (PKM), and LDHA.^{48–51} As expected, these glucose transporters and glycolytic enzymes are induced by HIF-1 α .

How tumor cells sustain TCA cycle and building blocks for cellular components during hypoxia? Glutamine, one of the most abundant amino acid in plasma, plays an important role here. Glutamine, which is transformed to α -ketoglutarate, provides a carbon source for TCA cycle and nitrogen for phospholipids, amino acid, and nucleotides biosynthesis. Cancer cells overexpress a series of enzymes, including glutaminase, glutamate dehydrogenase, and transaminase that convert glutamine to α -ketoglutarate to maintain TCA cycle.^{52,53} Interestingly, c-MYC, an oncogenic transcription factor that is activated by hypoxia, enhances mitochondrial glutaminase expression and causes glutamine addiction in tumor cells.^{54,55}

An important issue accompanied with metabolic switch is the production of lactate and H⁺. Excessive H⁺ accumulation within the cytoplasm impairs cellular function and leads to cell death. Hypoxic cancer cells overcome this problem by upregulation of monocarboxylate transporter 4⁵⁶ and sodium-hydrogen exchanger 1⁵⁷ to pump lactate and H⁺, respectively, out of the cell. In addition, hypoxia induces carbonic anhydrase 9, which also contributes to net efflux of H⁺ from cancer cells.⁵⁸ As a result, the intracellular environment is more basic, which promotes proliferation, and the extracellular space is more acidic, which promotes invasion.

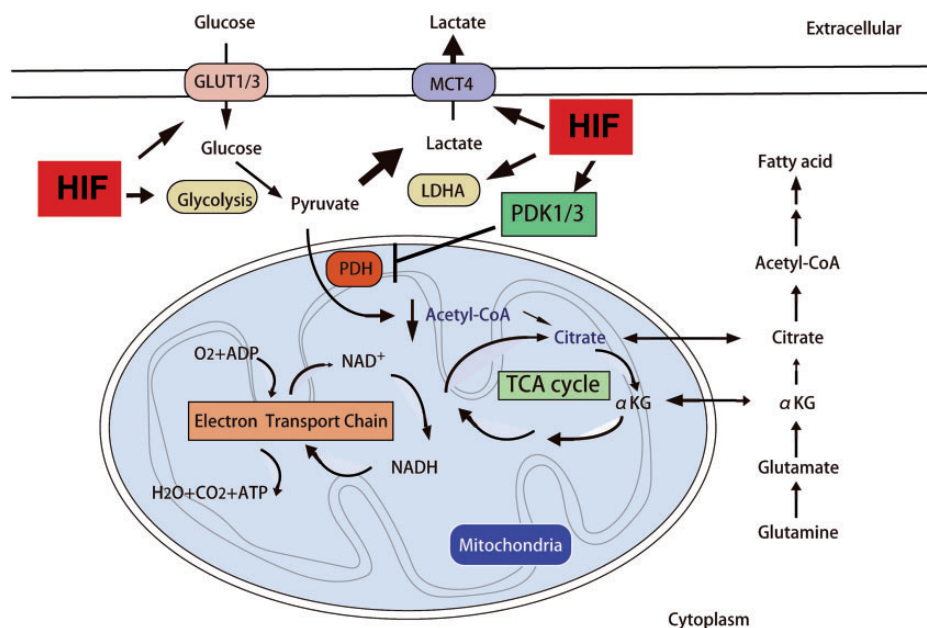


Figure 2 HIF-1 regulates the glucose metabolism. Under well oxygenated condition, glucose is metabolized to pyruvate. Then pyruvate dehydrogenase (PDH) converts pyruvate to acetyl-CoA for the entry into TCA cycle. Under hypoxia, HIF-1 targets and activates many glycolytic enzymes and lactate dehydrogenase A (LDHA) to increase lactate production. Besides, HIF1 promotes pyruvate dehydrogenase kinase 1/3 (PDK1/3) to inactivate PDH which prohibits the conversion of pyruvate to acetyl-CoA. In addition, glutamine is converted to α -ketoglutarate to provide intermediates for TCA cycle and fatty acid synthesis. (A color version of this figure is available in the online journal.)

Cell proliferation and survival

For cancer cell proliferation, increase expression of growth factors for autocrine signaling is needed (Figure 3). Indeed, it has been reported that various growth factors such as vascular endothelial growth factor (VEGF), fibroblast growth factor-9 (FGF9), transforming growth factor- α (TGF- α), platelet-derived growth factor B (PDGFB), insulin-like growth factor-2 (IGF-2), erythropoietin (EPO), and endothelin 1 (ET-1) are regulated by HIF in different cancer cells.^{59–63} It is of interest to know that hypoxia regulates these mitogenic factors not only at the transcriptional level but also at the translational level. Recent studies reveal that hypoxia induces translational switch from cap-dependent to cap-independent manner to maintain production of critical survival proteins.^{63–65} In addition to peptide growth factors, HIF also induces cell proliferation via activation of extracellular signal-related kinase (ERK) signaling. Suppression of dual specificity phosphatases-2 (DUSP2), an ERK-specific phosphatase, by HIF-1 α prolongs ERK phosphorylation and thus results in promoting cancer cell proliferation.⁶⁶

Keeping cell proliferating is the first priority besides trying to maintain survival when facing an unfavorable condition such as hypoxia. A group of anti-apoptotic genes such as B-cell lymphoma 2 (BCL2), B-cell lymphoma-extra-large (BCL-xL), myeloid cell leukemia sequence 1 (MCL-1), NK- κ B, and survivin are upregulated by HIF-1 α under hypoxic condition to enhance cell survival.^{67,68} Autophagy, the process that occurs for compensating hypoxia, nutrient depletion, and metabolic stress, is a means for cells to avoid apoptosis or necrosis and

counteracts the potentially deleterious effects caused by mitochondrial dysfunction and reactive oxygen species.^{69,70} Under hypoxic condition, HIF activates BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 (BNIP3) and BNIP3-like (BNIP3L) proteins to induce mitochondrial-selective autophagy.^{71,72} Upregulation of BNIP3 and BNIP3L has been shown to protect cancer cells from apoptosis.⁷²

Angiogenesis

It is necessary for tumor cells to have adequate blood flow to gain nutrients and remove metabolic waste during rapid growth. Angiogenesis is a complex process that involves multiple gene products expressed by different cell types. Nonetheless, genes involved in different steps of angiogenesis are independently responsive to hypoxia. These include VEGF and its receptors, placental growth factor (PGF), PDGFB, angiopoietin 1 and 2 (Ang1 and Ang2), stromal-derived factor-1 (SDF-1), matrix metalloproteinases (MMPs), plasminogen activator receptors (uPAR) and inhibitors (PAI), and procollagen prolyl hydroxylase.^{73–77} Since angiogenesis is the hallmark of cancer and VEGF is the signature gene regulating angiogenesis, anti-VEGF antibody has been used in combination with chemotherapy for treating various cancers.^{78–80} For example, fluoropyrimidine-based chemotherapy plus the anti-VEGF antibody, bevacizumab, is standard first-line treatment for metastatic colorectal cancer, and treatment with bevacizumab has been shown to have significant impact on progression-free survival and overall survival for those patients.^{79,81}

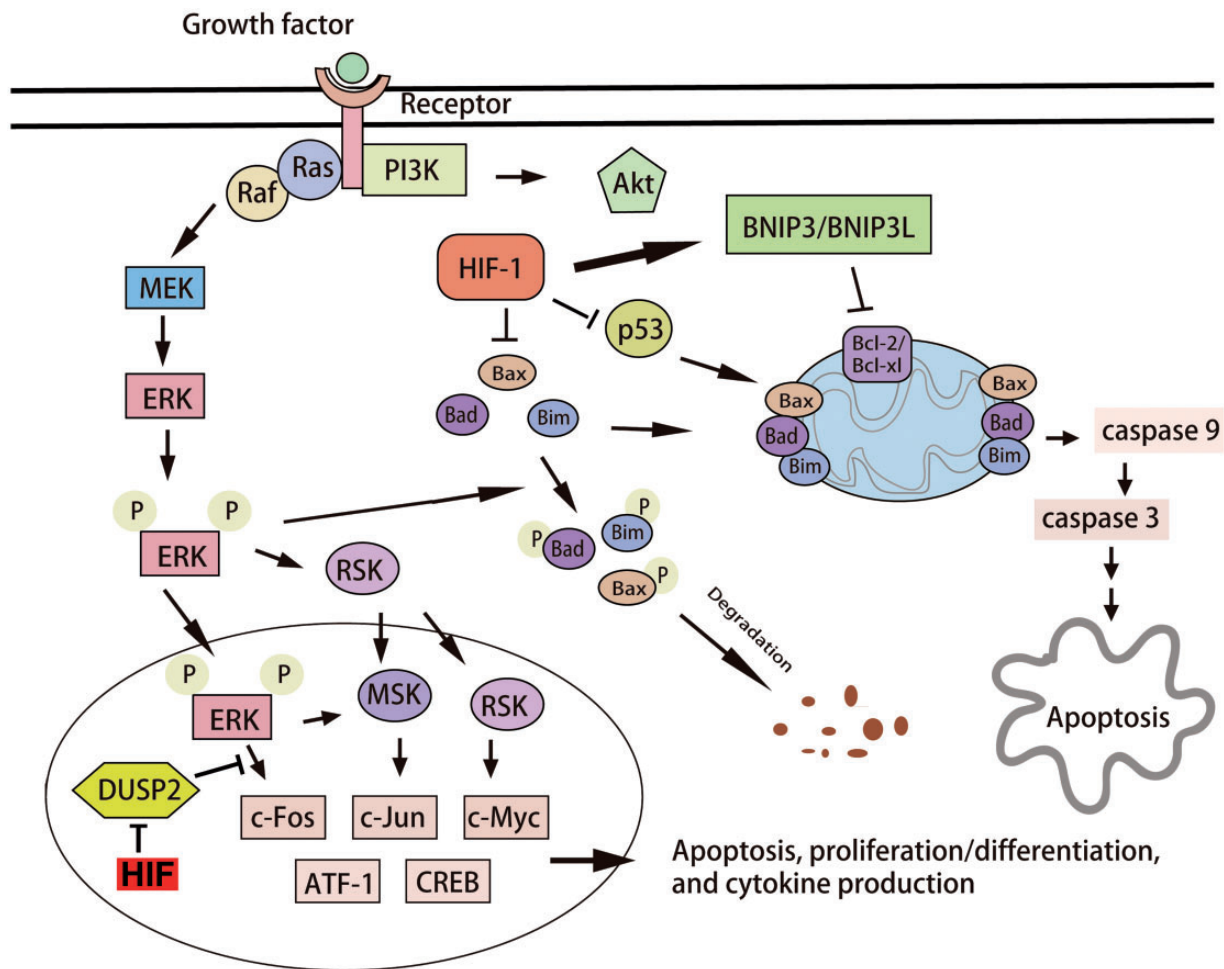


Figure 3 The pathways of HIF-1-modulated signaling in cell proliferation and anti-apoptosis under hypoxia. Hypoxia upregulates growth factors and their receptors to trigger signals through Ras-Raf-MEK-ERK cascades resulting in (1) induction of target genes to inhibit apoptosis and/or promote cell proliferation and survival, and (2) phosphorylation and inactivation of Bim, Bax, BAD, and caspase 3 to block apoptosis. HIF-1 α further inhibits the expression of dual specificity phosphatase 2 (DUSP2) and thus enhances ERK phosphorylation and gene expression. CREB: c-AMP response element-binding protein, ATF1: activating transcription factor 1. (A color version of this figure is available in the online journal.)

Invasion and metastasis

Epithelial-mesenchymal transition (EMT) is thought to be the most important step of cancer invasion and metastasis initiation. HIF induces various transcriptional regulators to cause EMT, including Twist1, Snail 1 and 2, TGFA, zinc finger E-box-binding homeobox 1 and 2 (ZEB1 and 2), and transcription factor 3.^{82–84} In addition, HIF inhibits E-cadherin and other proteins involved in maintaining epithelial cells characteristics while upregulates genes with functions in promoting mesenchymal phenotypes such as N-cadherin and vimentin.⁸⁵ After EMT, primary cancer cells need to go through multiple steps such as detachment from original site, extracellular matrix modulation, intravasation, circulation, extravasation, and homing to finally colonize on other distant organs. Among all these sequential processes, detachment from neighboring cells and extracellular matrix represent the first step of metastasis. Cell-cell and cell-matrix adhesion is strengthened by expression of members of tetraspanin superfamily including CD9 and CD151.⁸⁶ Expression of CD151 is downregulated under hypoxia but is restored after re-oxygenation, which

perfectly facilitates cancer cells to detach from the hypoxic primary site and attach to the secondary site.⁸⁷ Upregulation of lysyl oxidase (LOX) and lysyl oxidase-like (LOXL) enzymes by HIF-1 α is also a critical process to remodel extracellular matrix for cancer cell migration.⁸⁸ The induction of metalloproteases including MMP1, MMP3, and membrane type-1 MMP by HIF-1 α and HIF-2 α is associated with metastasis.^{89,90} VEGF and Ang2 help cancer cells migrate into blood vessel while L1 cell adhesion molecule and other proteins may promote cancer cells invasion and metastases.⁹¹ Furthermore, induction of monocarboxylate transporter 4 (MCT4) to efflux lactate and sodium hydrogen exchanger 1 (NHE-1) to pump H⁺ outside cancer cells by hypoxia results in extracellular acidification, which is of beneficial for cancer cell invasion and metastasis.^{56,57,92}

MicroRNA expression

MicroRNAs (miRNA) are small noncoding transcripts ranging from 19 to 24 nucleotides long and have been found to play key roles in physiological and pathological processes, including cancer development, proliferation, and

metastases.^{93,94} The altered expression of miRNAs is associated with clinical prognosis of tumor, resistance to chemotherapy and radiation therapy, and tumor recurrence.⁹⁵ For most updated information regarding effects of hypoxia-regulated miRNAs in cancer development and drug resistance, please read the recent review by Liao et al.⁹⁶

Role of HIF in drug resistance

HIF has been reported to participate in drug and radiotherapy resistance in cancer treatment. Radiotherapy (ionizing radiation) causes DNA damage directly and indirectly. Ionizing radiation and some chemotherapeutic drugs cause intracellular/tissue water ionizing to produce free radical (to impair DNA). Lack of oxygen reduces the cytotoxic effects of drugs and radiotherapy directly. Therefore, areas of hypoxic tumor tissue are more resistant to treatment and are associated with a poor clinical prognosis.⁹⁷ In addition to the direct effect of lack-of-oxygen molecules on chemo- and radio-reactivity, hypoxia also induces therapeutic resistance via gene upregulation. It has been shown that HIF induces drug resistance of cancer cells, which can be reversed after blocking HIF under normoxia or hypoxia.⁹⁸ As mentioned above, hypoxia/HIF can modulate at least hundreds of genes to control cell proliferation, survival, metabolism, and drug efflux, which ultimately leads to drug resistance (Figure 4). In the following sections, we will discuss drug resistance induced by hypoxia-controlled genes through different pathways.

Hypoxia-induced drug resistance through metabolic alteration

As described earlier, one of the hall marks of cancer cells is the elevated glucose uptake and the switch of cellular metabolism from oxidative phosphorylation to aerobic glycolysis, the so-called Warburg effect. The Warburg effect is not only a critical cellular metabolic adaptation to cyclic hypoxia, it is also an obviously beneficial trade-off for cancer cells to increase chemoresistance, mutation rate, and invasion/metastatic ability.⁹⁹ Recent data revealed that expression of PDK1 and PDK3 is upregulated by HIF-1 α -dependent hypoxic stress and is linked to increased drug resistance in cell culture system.^{35,45,46} However, upregulation of PDK3, but not PDK1, is associated with colon cancer malignancy and early recurrence.⁴⁷

Despite their roles in energy biogenesis, mitochondria also play an important role in the control of cell death. Mitochondria regulate cell death pathways not only through control of intrinsic apoptotic pathways but also the generation of reactive oxygen species.¹⁰⁰ It has been shown that chemotherapy induces cell death and, at least in part, is mediated through the generation of reactive oxygen species. The generation of reactive oxygen species is suppressed in tumor cells under hypoxia by HIF-1 α ,¹⁰¹⁻¹⁰³ thus conferring the drug resistance of tumor cells.

Hypoxia-induced drug resistance through increased drug efflux

The ATP-binding cassette (ABC) transporter, a membrane-resident P-glycoprotein encoded by multidrug resistance 1

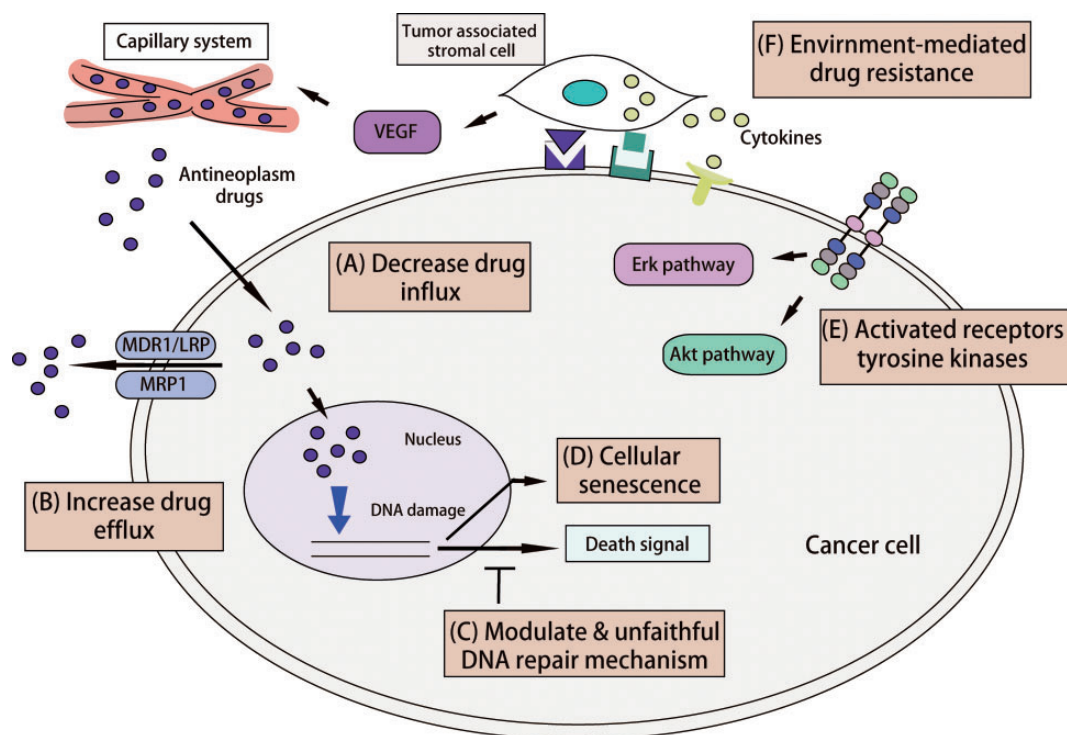


Figure 4 An overview of hypoxia-related chemoresistance. (A color version of this figure is available in the online journal.)

(MDR1) gene, is upregulated by hypoxia.¹⁰⁴ By acting as a drug efflux pump, MDR1 decreases the intracellular concentrations of chemotherapeutic drugs to cause drug resistance. An induction of MDR1 by HIF-1 α has been reported in cancers of breast, colon, glioma, and stomach.^{105–109} Multidrug-resistance-associated protein, another ABC transporter, was also reported to be involved in HIF-1 α -mediated drug efflux and chemoresistance.^{106,109,110} EGR-1 is an important transcription factor that increases cell survival and is overexpressed in a wide spectrum of human cancers.^{111–113} Recent data demonstrated that hypoxia-induced prolonged ERK activation induces the overexpression of EGR-1 and MDR1.⁶⁶ Taken together, these data demonstrate that HIF-1 α can directly and indirectly upregulate MDR1 to increase the drug efflux ability of cancer cells.

Hypoxia-induced drug resistance through inhibition of apoptotic pathways

DNA damage is sensed by DNA damage response pathway,¹¹⁴ which aims to prevent the transmission of damaged DNA and confer the genome stability. Typically, DNA damages are sensed by ATM/ATR kinases, which phosphorylate p53 to induce cell cycle arrest and apoptosis.^{115,116} The classic chemotherapeutic agents that were designed to cause DNA damage of fast-growing cancer cells would kill most tumor cells but also give selective advantages to cells bearing mutations in genes involving in DNA repair pathway, leading to more aggressive phenotype and development of drug resistance. In addition to this colony selection phenomenon, it also has been shown that hypoxia could attenuate DNA damage-induced cell cycle arrest and apoptosis.

Deregulation of apoptosis and cell cycle under hypoxic condition are pivotal causes of tumor progression and drug resistance. Cancer cells display different response to hypoxia by expressing a subset of anti-apoptotic genes such as BCL2, BCL-xL, MCL-1, NF- κ B, and survivin in a HIF-1-dependent manner.^{67,68} Upregulation of these genes protects cancer cells from hypoxia-induced cell death and confers cancer cells the ability to resist chemotherapies. It has been shown that functional interference of HIF-1 α results in enhanced apoptosis upon chemotherapeutic treatment in different cancer types. Through regulation of those anti-apoptotic genes, HIF-1 α plays a crucial role in inhibition of apoptosis and promoting tumor cell survival upon chemotherapy.

Hypoxia-induced drug resistance through hyperactivation of ERK pathway

Sustained activation and nuclear translocation of ERK are prerequisites for controlling cell proliferation, differentiation, and survival.^{117,118} Constitutive activation of ERK pathway is associated with malignancy in many cancers^{119–121}; however, no activating mutation in ERK has been detected in human cancer.¹²² Phosphorylation of ERK depends on activating mutation of upstream signaling kinases or loss-of-function of downstream phosphatases. It is evident that activating mutations of upstream molecules such as epidermal growth factor receptor, RAS, and RAF

would result in constitutive ERK phosphorylation.^{123–129} Nevertheless, aberrant activation of ERK has also been found in many cancers without detectable activating mutations of these genes,^{119,120,130} suggesting that loss-of-function of the downstream phosphatases also plays important roles in causing ERK activation. The downstream phosphatases that specifically inactivate ERK signaling are members of DUSP family. Downregulation of DUSP2 and DUSP4 thus leading to prolonged ERK activation has been found in various cancer types.^{66,131} Intriguingly, reduced expression of DUSP2 and DUSP4 is mediated by HIF-1 α , which results in increasing chemoresistance and malignancy in human cancer cells.^{66,132} In-depth investigation reveals that knockdown of DUSP2 upregulates several important genes downstream of ERK such as MDR1, EGR-1, CCN1, glucose response protein 78, and osteopontin,⁶⁶ which had been reported to confer drug resistance and aggressive tumor phenotypes.^{133–135} Taken together, these findings suggest that hypoxia-dependent, DUSP-mediated ERK activation is an important pathway that increases drug resistance via several different pathways.

Targeting hypoxia for cancer treatment

HIF targeting drugs

Since HIF controls many processes of tumorigenesis, it is reasonable to consider inhibiting HIF expression and/or activity for cancer treatment. There were many new developed agents to inhibit HIF-1 α protein expression by targeting different objectives (Table 1). Wortmannin, CCI-779, rapamycin, and LY294002 are inhibitors of PI3K-Akt-mTOR. Hsp90 inhibitors, histone deacetylase inhibitors, camptothecins analogs, topoisomerase I inhibitors, 2 ME2 and analogs, and RNA antagonist (e.g. EZN-2968) were proven to be effective to inhibit HIF-1 function preclinically or clinically. There are still many other molecules/drugs inhibiting HIF-1 function not only in reducing protein level but also inhibiting dimerization, DNA binding, and transcriptional activity. Acriflavine, a very old antibiotic, binds to PAS-B subdomain of HIF-1/2 α and thus interrupts binding with HIF-1 β to block HIF-dependent transcription. Doxorubicin and other anthracycline agents exert their ability to destroy HIF DNA binding activity and thus block transcription of genes required for tumor growth and vascularization. The FDA approved bortezomib, a proteasome inhibitor, binds to carboxyl-terminal transactivation domain of HIF-1 α to change the structure and disrupt the function of HIF-1 α -dependent transactivation. Inhibition of aldose reductase, an enzyme that catalyzes the reduction of lipid aldehydes and their glutathione conjugates, prevents increase of HIF-1 α and VEGF by regulating 26S proteasome-mediated protein degradation in human colon cancer cells.

Bioreductive drugs

Although some exciting results have been shown by targeting HIF, it needs to bear in mind that HIF is indispensable for maintaining normal physiological functions as well. Ablation of HIF protein or inhibiting HIF activity will generate severe adverse effects. Therefore, the concept of

Table 1 Overview of drugs related to HIF-1 activity inhibition

Mechanism	Target	Drug Name	Drug Class	Status	Ref.
Blockage of HIF-1 α protein synthesis	mTOR	Rapamycin; everolimus, temsirolimus	Allosteric binders to FKBP12- rapamycin binding domain	Approved	143-145
		WYE-125132	mTOR kinase inhibitor	Preclinical	146
	Topoisomerase I	Topotecan	Camptothecin analogues	Approved	147,148
	Topoisomerase II	Doxorubicin	Anthracycline	Approved	149,150
	Microtubule	2-methoxyestradiol (2ME); taxane; vinca alkaloid	Microtubule-targeting agent	Clinical trial (2ME); approved (Taxotere, Vincristine)	151
Disruption of HIF-1 α protein stability	Unknown	Digoxin	Cardiac glycoside	Approved	152
	HSP90	17-AAG	Benzoquinone ansamycin antibiotics	Clinical trial	153, 154
	Histone deacetylase	LAQ824; FK228(Romidepsin)	Histone deacetylase inhibitor	Suspended	155
Blockage of HIF heterodimerization	FIH1	YC-1	Guanylate cyclase activator	Approved	156,157
	PAS-B subdomain	Acrflavine	Antimicrobial agent	Preclinical	158,159
	DNA binding	Doxorubicin	Anthracycline	Preclinical	160
Blockage of DNA bindings	p300	Echinomycin	DNA intercalator	Approved	152
		Chetomin		Suspended	161
	Thioredoxin 1	PX12	Dithiodiketopiperazine	Preclinical	162
Inhibition of HIF-1 transactivation	26 proteasome	Bortezomib	Imidazole disulphide	Clinical trial	163
	FIH	Amphotericin B	Proteasome inhibitor	Approved	164,165
	GLUT1	Glufosfamide	Cyclooxygenase inhibitor	Approved	166
Inhibiting of HIF-1 target gene products	MCT1	Fasentin	Glucose isophosphoramidate mustard	Clinical trial	167
		α -cyano-4-hydroxycinnamate	Oxobutanilide	Preclinical	168
	VEGFR	Bevacizumab	Lactate transport inhibitor	Preclinical	169
Blockage of HIF-1 signal transduction	EGFR	Cetuximab	Monoclonal antibody	Approved	170,171
	BRAF	Sorafenib	Monoclonal antibody	Approved	172,173
	COX2	Celecoxib	ATP competitive kinase inhibitor	Approved	174
			COX2 inhibitor	Approved	175

17-AAG: 17-allylamino-gelatinamycin, COX2: cyclooxygenase 2, EGFR: epidermal growth factor receptor, FIH1: factor inhibiting HIF-1, GLUT1: glucose transporter 1, HSP90: heat-shock protein 90, MCT1: monocarboxylate transporter 1, PX12: 1-methylpropyl 2-imidazolyl disulfide, VEGFR: vascular endothelial growth factor receptor.

pro-drugs has been developed. There are five chemical moieties including nitro groups, quinones, aromatic N-oxides, and transition metals that could be metabolized by enzymatic reduction under hypoxic conditions, thus providing the basis for targeting hypoxic tumor.^{136–142} Most of those bioreductive drugs are reduced by cellular reductases and form the free radical intermediates. The re-oxidation of this intermediate is oxygen-dependent and thus the produced free radical cannot be eliminated in hypoxic cells. Such bioreductive pro-drugs can inhibit the growth of hypoxic cells with no or little effect on normoxic cells.

Conclusion

Malignancy, one of the leading causes of cancer-related death worldwide, is quite complicated and difficult in treatment. Despite receiving aggressive treatments, the mortality rate is still high. HIF, the product under hypoxia, is a predominant determinant in a wide range of cancer cell biology in mammal. Expression of HIF is correlated with cancer cell angiogenesis, proliferation, metastases, and treatment outcome. So, blocking any step of HIF-related pathway maybe helpful to win the battle against cancer. Clinically, some HIF-related inhibitors seem to have the potential to cure several types of cancers. However, the effectiveness is still not very high. And it should be very cautious in utility of HIF inhibitors due to its possibly wide range effects not only in cancer but also in normal cells. Therefore, detecting more underlying mechanisms of the HIF pathway and/or identifying more satisfying agents that targets molecules in the HIF pathway will be the first priority in the future.

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