



Role of Hypoxia-Inducible Factor (HIF) in the Initiation of Cancer and Its Therapeutic Inhibitors

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Abstract

The inadequate oxygen (O₂) supply to a large extent alters the cellular microenvironment and results in hypoxia or even anoxia. Hypoxia-inducible factor (HIF) facilitates the cellular response to hypoxia. HIF, a heterodimer composed of two subunits, the subunit α and subunit β , is involved in several signaling pathways which involves both survival and death pathways, their activation and regulation. HIF is believed to be the best molecular target in the treatment of cancer, and also numerous inhibitors for HIF-1 α are available today. This chapter explains the HIF-1 α role in cancer and its therapeutic applications that potentially target HIF pathway.

Keywords

Cancer · Hypoxia · Hypoxia-inducible factor (HIF) · HIF-1 α inhibitors · Angiogenesis · Small molecule inhibitors

10.1 Introduction

Constant supply of O₂ is required for all the cells to carry out oxidative phosphorylation in the mitochondria for the generation of ATP by oxidative phosphorylation. Under normal regularized conditions, with the normal supply of oxygen, the cells

The original version of this chapter was revised. The book was inadvertently published without Abstracts and Keywords, which are now included in all the chapters. An erratum to this chapter can be found at https://doi.org/10.1007/978-981-10-6728-0_39

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divide in an orderly way and are replaced with new cells when they die, are worn out, or are damaged. In contrast, in an inadequate supply of oxygen, the lack of oxygen leads the cells to enter into abnormal and stressful conditions, where the regulated cell division becomes irregular and thereby activating several mechanisms in the process to sustain their viability. The inadequate supply of oxygen (O₂) in large extent alters the cellular microenvironment and results in hypoxia or even anoxia leading to the cellular transformation [56]. Under the hypoxic conditions, the transformed cells divide rapidly and result in the formation of tumors by crowding out the normal cells. In such condition, the energy requirement and production are the most important aspects to understand the differences between the proliferating and nonproliferating cells [91]. The heterogenous cells in a complex structure of tumor are undergoing different stresses, e.g., low oxygen levels in the interior, so often the core of a tumor is necrotic [32, 60, 71, 94].

Under the hypoxic conditions, due to nonavailability of oxygen, tumor cells generate energy by non-oxidative breakdown of glucose, followed by fermentation of lactic acid in cytosol [25, 28, 32, 36, 47, 91]. In such conditions, hypoxia plays a major role at different stages of cancer (initiation, accumulation, angiogenesis, and metastasis) by initiating the changes in the microenvironment, altering the oncogenic genes and normal metabolism, and in the development of new blood vessels, thereby inducing the metastasis. The cellular response to hypoxia is mainly mediated by the HIF. HIF is found in mammalian cells grown under hypoxic condition. It is stimulated in response to intratumoral hypoxia leading to genetic alterations by activating the oncogenes and inactivating the tumor suppressor genes. HIF plays an important role in adapting the cancer cells to low oxygen condition by triggering the transcription of over 100 target genes that regulate the tumor survival and progression [122–125].

10.2 HIF Structure

Hypoxia-inducible factor (HIF) is a heterodimer composed of two subunits, the subunit α and subunit β . The HIF-1 α subunit is oxygen sensitive and is a cytoplasmic protein. It is degraded by the ubiquitin–proteasome system continuously in well-oxygenated cells. The HIF-1 β subunit is also known as aryl hydrocarbon receptor nuclear translocator (ARNT), a nuclear protein, independent to oxygen tension and a heterodimeric partner of aryl hydrocarbon receptor (AhR). HIF-1 β is constitutively expressed to levels within the nucleus that remain relatively constant and binds to AhR and facilitates its translocation. These two subunits (α and β) belong to the family of basic helix-loop-helix (bHLH) and PER-ARNT-single-minded protein (SIM) (PAS) transcription factors. The characteristic feature of these family proteins is that they have recognizable domains and can regulate their own transcription. Among all the family members, the PAS domain was the only domain that is conserved. The N-terminal region of this PAS domain is essential to mediate DNA binding and interaction with HIF-1 β subunit [118].

The subunit α has three different isoforms, HIF-1 α , HIF-2 α , and HIF-3 α . Analogs of α subunits of HIF-1 α and HIF-2 α are more comprehensively studied and were compared to HIF-3 α . HIF-3 α is less analyzed when compared with the other HIF- α homologs. The inhibitory PAS domain protein (IPAS), a spliced variant of HIF-3 α discovery, led practical information about HIF-3 α . It functions as dominant-negative regulator of hypoxia-inducible gene expression and does not show any intrinsic transactivation activity as compared to the COOH-terminal transactivation domain (C-TAD) of HIF-1 α and HIF-2 α [111, 148].

The analogs of HIF-1 α and HIF-2 α share high percentage sequence identity (48%) and can heterodimerize with HIF-1 β subunit. These two analogs when heterodimerized with HIF-1 β subunit have distinct tissue-specific expression. The ubiquitously expressed HIF-1 α is constantly expressed and degraded in presence of induced hypoxic conditions. However, HIF-2 α distribution is restricted to specific tissue origins like vascular endothelial cells, the kidney, catecholamine-producing cells, renal interstitial fibroblasts, and some glomerular cells [95].

HIF-1 α in its C-terminal has two transactivation regions: the N-terminal transactivation region or N-TAD (AA 531–575) and the C-terminal transactivation region or C-TAD (AA 786–826) (Fig. 10.1). HIF-1 α transcriptional activity is mostly dependent upon these two domains. Under hypoxia conditions the transcription of HIF-1 α is modulated by C-TAD whereas stabilization by N-TAD. The requirement of C-TAD or N-TAD for different gene sets regulation is completely dependent on oxygen tension. N-TAD, also known as an oxygen-dependent degradation domain (ODDD), is responsible for stabilizing HIF-1 α against degradation as hydroxylation of conserved prolyl residues resides in this region. This domain is also important in mediating oxygen regulation stability. Prolyl-4-hydroxylases (PHDs), 2-oxoglutarate-dependent oxygenase superfamily enzymes, mediate this hydroxylation and promote the subunit degradation [77].

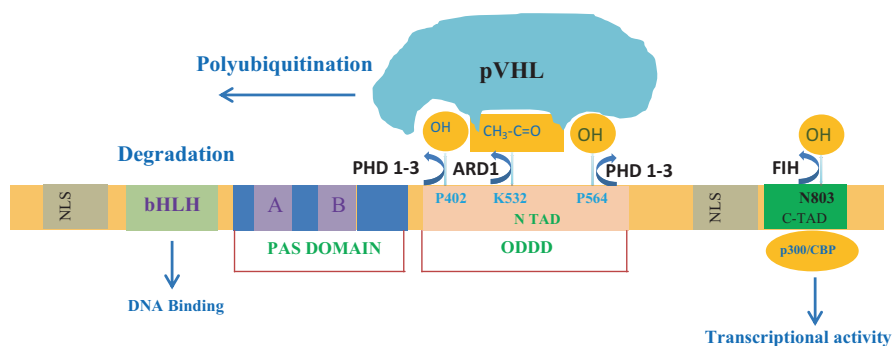


Fig. 10.1 Oxygen-dependent regulation of HIF-1 α activity (This figure is adapted from [95, 121] with modifications)

HIF-1 α hydroxylation does not occur in hypoxic conditions. In this condition α subunit along with other cofactors acts as transcription factor and thereby migrates to nucleus and dimerizes with β subunit and initiates its transcriptional program [18]. The resultant active protein that is HIF-1 is a messenger which is translocated to the nucleus to induce transcriptional responses to hypoxia [171].

The active HIF-1 protein activates transcription of target genes by adhering to specific hypoxic response elements (HRE) which comprises A/GCGTG consensus motif. Similarly HIF-2 and HIF-3 are resultant active heterodimers of HIF-2 α or HIF-3 α with ARNT [119]. The presence of two nuclear localization signals in bHLH domain (17–33 amino acids) and COOH-terminal regulatory domain (718–721 AA) results in translocation of HIF-1 α into nucleus [110].

The interaction of C-TAD with coactivators CBP/p300 results in the change in transcription of HIF-1 α under hypoxia. This interaction is governed by the CH1 region of p300/CBP and also improved by SRC-1, and synergistic effect was observed at limited concentrations. Phosphorylation of p300 by the MAPK pathway increases the HIF-1 α /p300 complex formation and thereby increases the transcriptional activity of HIF-1. Upon blocking of HIF-1 α /p300 CH1 interaction, HIF-1 transactivation is inactivated as the p300-CH1 interacting protein and p35srj (for serine–glycine-rich junction) bind to p300/CBP. C-TAD interaction with p300/CBP does not occur in normal conditions. This is due to oxygen-dependent hydroxylation of N803 residue in the carboxyl-terminal transactivation domain (CAD) of HIF-1 α by factor-inhibiting HIF (FIH-1), a 2-oxoglutarate-dependent dioxygenase enzyme [77]. It prevents the interaction of HIF-1 α with transcriptional coactivators, p300 and CBP (cAMP response element-binding protein). Small redox protein thioredoxin-1 (Trx-1) under both normoxic and hypoxic conditions has been reported to enhance the binding of CBP/p300 to the C-TAD of HIF-1 α . This leads to the expression of HIF-1 α and its downstream target VEGF and improved angiogenesis [39]. Transactivation of HIF-1 by Ref-1 leads decrease of a cysteine residue in the C-TAD of HIF-1 α . But, the useful status of this cysteine residue and the consequence of CBP/p300 remains doubtful [59, 77].

The PHD enzymes (prolyl hydroxylase-domain protein) hydroxylate the proline 402 and 564 residues that are present in LXXLAP amino acid motif of ODDD of HIF-1 α subunit under normal oxygen conditions. This allows modified HIF-1 α at prolyl sites to bind to the von Hippel–Lindau (VHL) tumor suppressor protein. Only modified HIF-1 α is able to bind to the VHL protein whose binding may also be promoted by acetylation of K532 residue by the arrest-defective-1 (ARD1) acetyltransferase [42]. This VHL protein is a recognition component of an E3 ubiquitin-protein ligase. This ligase finally targets the HIF-1 α for proteasomal degradation by 26S proteasome. OS-9 is another factor that impacts on the degradation of HIF-1 α . OS-9 interacts HIF-1 α directly, and the prolyl hydroxylases PHD2 and PHD3 and forms a ternary complex. This complex formation stabilizes the interaction between HIF-1 α and PHDs, thus helping HIF-1 α hydroxylation and pVHL-mediated ubiquitination, and finally leads to degradation of HIF-1 α [34].

The HIF-1 activity depends on the regulation of its subunits (α and β) at several levels including transcription, translation, ubiquitin-mediated protein breakdown, and nuclear translocation. The loss of this activity decreases the vascularization, tumor growth, and energy metabolism. HIF-1, by employing transcriptional coactivators, controls the expression of many genes. The HIF-1 expression directly regulates the tumor growth. The overexpression of HIF-1 promotes the tumor growth by increasing HIF-1 transcription factor activity. The protein products play important roles in the severe and long-lasting adaptation to hypoxia, including angiogenesis, erythropoiesis, and pH regulation glycolysis. Pulse-chase studies of MCF-7 breast cancer cells stimulated with heregulin increase HIF-1 α synthesis but do not activate transactivation-region function that was stopped by rapamycin in PC-3 prostate cancer cells. In another study when Rat-1 fibroblasts and breast cancer cells (MCF7) were overexpressed with BNIP3 (BCL2/adenovirus E1B 19 kDa interacting protein 3) and NIX (BNIP3 homolog) at the transcriptional level, it induced apoptosis. The cell death induced by BNIP3 is mediated by binding of BNIP3 to anti-apoptotic proteins Bcl-2 and Bcl-xL and inhibiting those proteins. This hypoxia-induced apoptosis may be HIF-1 α dependent because BNIP3 promoter contains HRE [46].

10.2.1 Glucose Metabolism

The glycolytic rates in normal cells when compared to cancerous cells are very high even in the presence of oxygen, and energy required for cancerous cells is generated by glycolysis followed by fermentation of lactic acid in cytosol rather than oxidation of pyruvate in mitochondria, also defined as “aerobic glycolysis” [25, 28, 32, 36, 47, 91].

The aerobic glycolysis is an important pathway by which cells in the body could generate energy using glucose as main fuel source, whereas glutamine becomes the secondary fuel source for carcinogenic cells [91]. Glucose, the primary fuel source after entering the cell, is metabolized to pyruvate by a multistep set of reactions called glycolysis [32]. In typical normal cells, this pyruvate undergoes oxidative phosphorylation (OXPHOS) in mitochondria through Krebs cycle (TCA cycle) to generate energy (ATP) in order to meet the energy demands of the cell; however if oxygen levels are low, pyruvate is converted into lactate in cytoplasm through the action of lactate dehydrogenase (LDH) enzyme [28, 44]. In glycolysis one glucose molecule is broken down into two molecules of pyruvate thus generating two ATPs by consuming NAD⁺, whereas in OXPHOS one glucose molecule produces 30 ATPs by oxidation of NADH and FADH₂, clearly stating that OXPHOS is more efficient than glycolysis [36, 139]. The main difference between cancer and normal cells dwells here. In cancer cells the pyruvate is converted into lactate even when an ample amount of oxygen is available [28]. For creation of new biomass such as nucleotides, lipids, amino acids, and nonessential amino acids, cancer cells require more nitrogen. The excess glucose that is generated is deviated to produce

nucleotides through pentose phosphate stunt (PPS) [32]. In multiple steps, PPS pathway by the action of malic enzyme generates NADPH reducing equivalents to produce more pyruvate. These NADPH reducing equivalents are required to produce acetyl CoA from citrate through the action of ATP-citrate lyase (ACL) in cytosol [25]. This production leads to synthesizes of fatty acids that are required for membrane production. Glutamine an essential metabolite acts as an intermediate in the bloodstream to transport reduced nitrogen and is also required for cell growth. This metabolite is utilized by tumor cells as secondary energy source because it plays a crucial role in uptake of essential amino acids and can replenish the TCA cycle by supplying carbon, and also through the action of malic enzyme, it can produce more pyruvate [24]. More NADPH in PPS pathway is produced by transactivation of TP-53-induced glycolysis and apoptosis regulator (TIGAR) by p53 oncogene. PI3K/Akt and Ras are activated through RTKs by stimulation of growth factor. RTK signaling to C-Myc activates many genes that are involved in lactate production and glycolysis [25, 28, 32, 47, 91].

The sequence initiation of angiogenesis and glycolysis in differentiating cells is arbitrated partly by triggering HIF-1. HIF-1 target genes are mainly the genes that are intricate in the glucose uptake and glycolysis. HIF-1 controls expressions of phosphoglycerate kinase 1, aldolase A, and pyruvate kinase M in the glycolytic pathway, as well as expression of the glucose transporters (GLUT1 and GLUT3), which facilitate uptake of glucose by the cells [62]. It also induces adaptive responses to ensure that the cells should have sufficient energy levels and thus allowing their survival in a hostile environment [77, 140].

10.3 HIF-Associated Pathways

Although HIF-1 α transcription is constant, the mRNA translation and transactivation activity of HIF-1 α are induced by associated pathways and cell surface receptors of tyrosine kinases and G protein-coupled receptors. In pseudohypoxia circumstances, HIF-1 α subunits are stabilized by a variety of oxygen-independent signaling and cellular stress events. In hypoxia condition, in response to growth factor stimulation, the HIF-1 α levels increase in a specific manner. If hypoxia is associated with decreased degradation of HIF-1 α , growth factors, cytokines, and other signaling molecules stimulate synthesis of HIF-1 α through stimulation of the phosphatidylinositol 3- kinase (PI3K) or mitogen-activated protein kinase (MAPK) pathways [98].

Activation of phosphatidylinositol-4, 5-bisphosphate-3-kinase (PI3K)/AKT pathway has been shown to upregulate the HIF-1 α protein translation. Under non-hypoxic conditions, due to extremely short half-life, HIF-1 α protein expression is particularly sensitive to changes in the rate of synthesis. In the phosphatidylinositol-3-kinase (PI3K) pathway, binding of a growth factor (e.g., insulin-like growth factor 1, IGF-1) to its cognate tyrosine kinase receptor activates PI3K by phosphorylation and stimulates the downstream serine/threonine kinase Akt (protein kinase B). This

stimulation subsequently phosphorylates mammalian target of rapamycin (mTOR), providing a link between the microenvironment and HIF signaling [118, 120]. mTOR increases protein translation and mediates its action by phosphorylation of the mRNA cap-binding protein eukaryotic initiation factor 4E (eIF4E)-binding protein (4E-BP1). mTOR provide a potential mechanism for increasing HIF-1 α levels under normoxic conditions by disrupting the integrity of 4E-BP1, which is essential for inhibiting cap-dependent mRNA translation. In hypoxic conditions mTOR may increase HIF-1 α levels by the mechanism in which it occurs independently without eIF4E. Alternatively, mTOR induces protein translation by phosphorylation of p70 S6 kinase (S6K) which promotes ribosomal protein S6 phosphorylation, a substrate. This pathway is upset by a tumor suppressor protein (PTEN) which backs the phosphorylation of PI3K products.

In MAPK pathway, certain growth factors are involved in activation of RAS; this activation in turn stimulates RAS/RAF/MEK/ERK kinase cascade and induces HIF-1 α transactivation-domain function. Growth factors activate the mitogen-activated protein kinase (MAPK) to phosphorylate MAPK (extracellular signal-regulated kinase, ERK). Activated ERK is then capable of phosphorylating p70S6K1, 4E-BP1, S6K, and MAP kinase interacting kinase (MNK) [107, 161]. MNK can also phosphorylate eIF-4E directly that activates the translation initiator factor together with mTOR by inhibiting the 4E-binding protein (4E-BP). These signaling events result an increased rate of HIF-1 α protein synthesis through its effects on eIF4E. ERK and p70S6K1 are essential factors that are required for HIF-1 α mRNA translation. ERK regulates HIF-1 α synthesis and also plays a pivotal role in its transcriptional activation. ERK phosphorylates the coactivator CBP/p300, hence increasing HIF-1 α /p300 complex formation, and thus stimulates its transcriptional activation function (Fig. 10.2) [7, 26, 67, 70, 97].

The von Hippel–Lindau protein (pVHL) pathway along with p53, a tumor suppressor gene which induces apoptosis by regulating proteins such as Bax, regulates the levels of HIF-1 α . In environmental stress or DNA damage, p21 mediates p53 to cause growth arrest (Fig. 10.2). The murine double minute 2 (Mdm2) ubiquitin-protein ligase mediates ubiquitination and proteasomal degradation of HIF-1 α . Direct binding of the p53 tumor suppressor gene to the ODD domain of HIF-1 α causes the ubiquitination and degradation [46]. It is evident that absence of p53 tumor suppressor gene in certain types of tumor cells enhances HIF-1 α levels. In hypoxic tumors, mutations in tumor suppressor genes cancel the Mdm2-mediated degradation of HIF-1 α . It was studied that Hsp90 inhibitors such as geldanamycin (GA) could nullify HIF-1 α levels even in cell lines lacking von Hippel–Lindau protein (pVHL) regardless of the availability of oxygen. Mutation of prolyl residues (p⁴⁰² and p⁵⁶⁴) in HIF-1 α does not protect HIF-1 α from geldanamycin (GA)-induced degradation, suggesting that Hsp90 degradation involves a novel E3 ubiquitin ligase [46, 131, 140].

Redox (reduction-oxidation)-dependent processes displays a vital role in the control of HIF-1 α . Some studies have shown that generation of ROS can start both MEK/ERK and PI3K/Akt signaling pathways. This activation leads to enhanced HIF-1 α expression in human cancers such as ovarian, prostate, and breast cancer

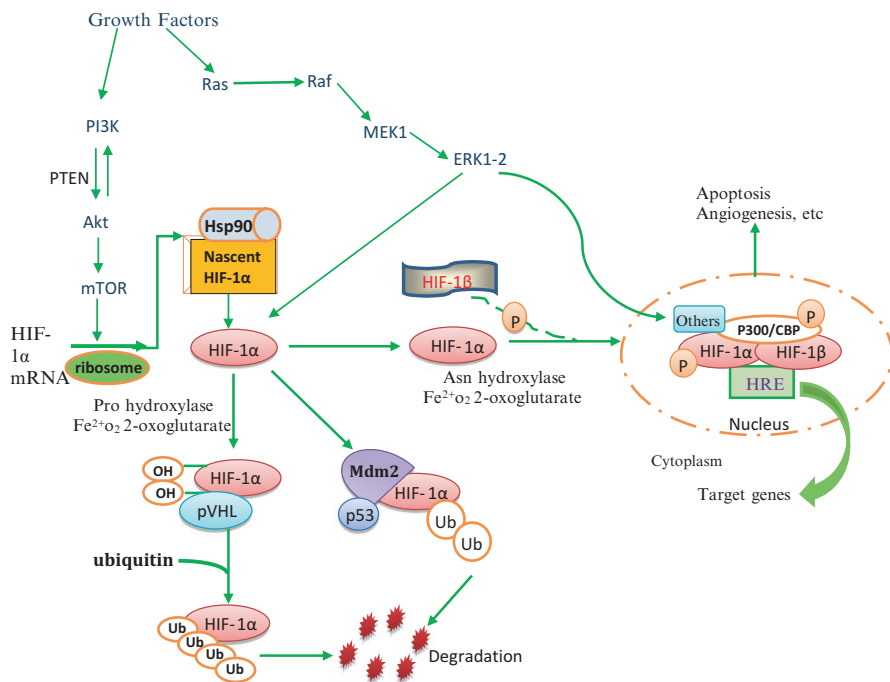


Fig. 10.2 Regulation of HIF-1 α activity at different levels (This figure is adapted with some modifications from [95, 153])

[34, 171]. Breast carcinoma is characterized by persistent ROS generation. In human prostate cancer cells, carcinogens such as vanadium and arsenate were shown to elevate ROS and induce HIF-1 α and VEGF expression through p70S6K1 activation. In human ovarian cancer cells, it is shown that p70S6K1 activation is stimulated by elevated epidermal growth factor (EGF) and its receptor (EGFR) which triggers H₂O₂ production.

Under hypoxia, mitochondrial ROS and intracellular secondary messengers such as CaM (calcium binding protein) levels increase and stimulate the accumulation of HIF-1 α . CaM targets proteins (CaM kinase II, calcineurin, and actin) involved in the stimulation of transcriptional activity of HIF-1 α expression. Thus, the inhibition of Ca₂p/CaM by a CaM-dominant mutant, Ca₂p/CaM antagonist such as HBC, or Ca₂p chelator downregulates the transcriptional activity of HIF-1, and subsequently angiogenesis is suppressed. The ROS levels in mitochondria increase through transfer of electrons from ubisemiquinone to molecular oxygen at the Q_o site of complex III electron transport chain (ETC). HIF-1 α activation is modulated by inhibiting its hydroxylation by the prolyl and asparaginyl hydroxylases. Mitochondrial ROS also induces signaling components of HIF-1 α (ERK and p38 MAP kinase pathways) under hypoxic conditions. The activated ERK2 phosphorylates HIF-1 α and increases its transcriptional activity [34, 42, 110].

10.3.1 HIF and Cell Cycle

Under hypoxia, there are different adaptive responses to lessen oxygen and nutrients for hypoxia-/hypoglycemia-regulated genes, which are involved in the cell cycle regulation. These genes are either HIF-1 α dependent (p53, p21, Bcl-2) or HIF-1 α independent (p27, GADD153). Hypoxia causes a HIF-1-dependent escalation in the expression of the cyclin-dependent kinase (CDK) inhibitors p21Cip1 and p27Kip1 and hypophosphorylation of retinoblastoma protein (Rb). Decreased activity of CDK complexes and hypophosphorylation of retinoblastoma protein regulate the cell cycle progression in response to hypoxia. HIF-1 α activation may serve as a primary gatekeeper at the G1/S transition through at least two distinct mechanisms – the action of CKIs and another by cyclin E regulation. HIF-1 α regulates cyclin E, not the cyclin A protein levels, but both may bind CDK2 and control its kinase activity dependent upon phase of cell cycle [15, 42, 43].

10.3.2 HIF and Cancer

HIF α is expressed in various types of cancers that include colorectal, liver, gastric, pancreatic, renal, gastrointestinal (IBD), esophagus, and many others. But mechanism and the factors that regulate the HIF1 α expression remains poorly understood in cancer. Several studies demonstrated the associated mechanisms that activate the HIF α and their upstream or downstream factors. In this context, we explore recent updates on the impact of HIF α in different types of cancers.

HIF-1 α and HIF-2 α play a significant role and have overlapping and distant functions in inflammatory bowel disease (IBD) [154, 158]. IBD, a chronic inflammatory disease of the intestine, is characterized by repeated mucosa wounding and losing of intestinal epithelial barrier functions. It comprises two distinct pathological entities, ulcerative colitis (UC) and Crohn's disease (CD) [157, 158]. Immunohistochemical and immunostaining studies of surgical specimens from patients with IBD revealed higher vascular density in diseased tissue than in normal tissue [40].

Studies revealed that HIF was essential for restoration and intestinal barrier integrity [63]. Mouse models and cell studies demonstrated distinct functions for HIF-1 α and HIF-2 α and regulate diverse sets of genes to modulate the epithelial barrier [41, 92, 132, 154]. Regulation of HIF-1 α and HIF-2 α by different subset of genes also promotes disruption of intestinal tight junctions and increased barrier permeability. HIF-1 α is a critical transcriptional factor in intestinal epithelial cells and is beneficial in regulating the epithelial barrier following inflammation. HIF-1 α activation in intestinal epithelial cells decreases proinflammatory cytokines. Two mouse models of colon cancer, a sporadic and a colitis-associated colon cancer model, were assessed and proved that activation of HIF-1 α in intestinal epithelial cells did not result in spontaneous tumor formation. HIF-2 α activates several proinflammatory mediators and is important in wounding response, whereas its activation increases inflammation [157, 158, 168].

Pharmacologic inhibition of prolyl hydroxylases (PHDs) primes more vigorous activation of HIF-1 α rather than HIF-2 α . PHD inhibitors activate HIF-1 α and HIF-2 α in pulsatile manner and protect acute colitis in murine models. DMOG, a pan-hydroxylase inhibitor, activates the HIF pathway by mimicking hypoxia through the inhibition of hydroxylase activity, leading to stabilization and transactivation of HIF-1 α [22]. AKB-4924, a HIF-1-specific prolyl hydroxylase inhibitor (PHDi), enhances innate immunity by robustly activating HIF-1 α [61]. FG-4497, a novel PHD inhibitor, provides a protective adaptation in murine TNBS colitis [114].

HIF-1 α is a critical protein in the development of colorectal cancer (CRC) [84]. Various studies have reported the role of HIF-1 α in angiogenesis and tumor progression via regulation of VEGF in human colorectal carcinoma [75]. In colon cancer HIF isoforms have different cellular functions. In human colon cancer tissues, expression of HIF-1 α and, to a lesser extent, HIF-2 α was linked to upregulation of VEGF and tumor angiogenesis [52]. Overexpression of HIF-1 α was found in the tissue of stage III and stage IV lymph nodes and liver metastases [13]. HIF-1 α expression was strongly observed in the epithelium around the necrosis region of tumor compared to normal mucosa suggesting a significant correlation of HIF-1 α expression along with CXCR4, VEGF, and microvessel density. Immunohistochemical studies of tumor cells in colon cancer cases by Wu et al. [152] also indicated that HIF-1 α expression correlates with tumor TNM stage, lymph node status, tumor invasion, and distant metastases. JMJD2B upregulates hypoxia-inducible genes involved in cancer cell proliferation, apoptosis, cell cycle arrest, and invasion through specifically demethylating the H3K9me3 on their promoters. Study by Fu et al. [33] suggested a significant role of JMJD2B in CRC tumorigenesis and progression in HIF-1 α -dependent manner under hypoxia. Activation of HIF-1 α results in increasing transcription of STAT-3 and HSP90 in the CRC cell lines. This interaction between HIF-1 α and STAT-3 in the CRC cell lines is dependent on the presence of an active HSP90 [35]. HSP90 in HCC cells regulated the levels of HIF-1 α by inhibiting the ubiquitination and proteasomal degradation of HIF-1 α . Further studies also analyzed a positive correlation between HSP90 and HIF-1 α , with statistical significance, showing they may exert a synergistic effect on the occurrence, development, invasion, and metastasis of colorectal cancer [88, 155]. The results by Zhang et al. [167] and Zhang et al. [169] suggest that HIF-1 α enhances EMT and cancer metastasis by binding to ZEB1 promoter in CRC and proposed a novel molecular mechanism for HIF-1 α -inducing epithelial–mesenchymal transition (EMT) and cancer metastasis. LRG1 plays a crucial role in the progression of CRC by regulating HIF-1 α expression thereby inducing VEGF-A expression and EMT markers of E-cadherin, VDR, N-cadherin, α -SMA, vimentin, and Twist1. In human CRC cells, HIF-1 α under hypoxia induces B-cell CLL/lymphoma 9 protein (BCL-9) expression, an important underlying mechanism for increased BCL-9 expression [135].

In esophageal squamous cell carcinoma, HIF-1 α expression levels significantly correlates with the expression of VEGF protein and with initial response to concurrent CRT. HIF-1 α expression strongly apparent within nuclei and/or cytoplasm of

tumor cells and its expression are also found to be different in two separate tumor microenvironments: SCCs and ACs of the esophagus cancer proposing a different mechanism for HIF-1 α expression in esophagus cancer [45, 96, 106].

Under hypoxic conditions, ERK1/2 phosphorylates and activates HIF-1 α in pancreatic cancer cells. This activation contributes the ABCG₂ expression by inducing binding of HIF-1 α to target promoter region for transcription [51]. Recent findings in pancreatic cancer patients indicated that HIF-2 α induces cell migration, invasion *in vitro*, and regulated E-cadherin and MMPs protein expression; these are vital to epithelial–mesenchymal transition (EMT). It is regulated by binding of Twist2 protein to E-cadherin promoter; this indicates HIF-2 α may act as an effective therapeutic target for prevention of pancreatic cancer [159].

HIF-1 α is an important mediator and also acts as potential target for treatment of gastric cancer. The overexpression of HIF-1 α in human gastric cancer proves the fact of it being a potential target. While regulating VEGF expression in cancer cells, it also plays a major role in the formation of complex proangiogenic microenvironment in tumors, and thereby affecting vessel morphology and vessel function. The *in vitro* studies in metastatic human gastric cancer cells evidenced that HIF-1 α was not required for cellular proliferation. The inactivation of the HIF-1 α activity by 2ME significantly reduced migratory, invasive, and adhesive features of gastric cancer cells. Inhibition of its function has proven the antitumor efficacy in rodent models and angiogenesis. In human gastric cancer cells, inhibition of HIF-1 α activity by transfection with a construct expressing a dominant-negative mutant version of HIF-1 α (pHIF-1 α DN) that dimerizes with HIF-1 β to form HIF-1 complexes that cannot activate transcription leads to impaired gastric tumor growth, angiogenesis, and vessel maturation [115, 131]. HIF-1 α also regulates transcription factors (NF- κ B1, BRCA1, STAT3, STAT1) and their corresponding network genes (MMP1, TIMP1, TLR2, FCGR3A, IRF1, FAS, and TFF3) that were associated with hypoxia, inflammation, and immune disorder in gastric cancer [145]. In the recent study, it is revealed a novel mechanism in three GC cell lines, 44As3, 58As9, and MKN45, and the integrity of mitochondrial autophagy (mitophagy) might determine the aggressiveness of cancer via the mitochondrial ROS (mtROS)/HIF-1 α interplay under hypoxic conditions [127]. Relative mRNA expression of miR-421 (microRNAs), a crucial factor in carcinogenesis, was found to be upregulated by HIF-1 α in gastric cancer tumor tissues [38]. Low expression of microRNA-186 (miR-186) facilitates aerobic glycolysis and suppresses cell proliferation induced by HIF-1 α in gastric cancer cell lines. The *in vivo* xenograft tumor studies demonstrate that the miR-186/HIF-1 α axis has an antioncogenic role in gastric cancer [86]. The *in vitro* and *in vivo* results revealed that dextran sulfate (DS) may reduce tumor metastasis through inhibition of HIF-1 α and ITG β 1 expression in gastric cancer cells [156]. In hypoxic gastric cancer cells, angiopoietin-like protein 4 (ANGPTL4), a hypoxia-inducible gene expression, is independent of HIF-1 α [73]. Expression of HSP60 or HIF2 α serves as predictive marker for diagnosis of gastric cancer. In gastric cancer cells, HSP60 or HIF2 α inhibition induce apoptosis and suppresses cell mobility by negative relation of MEK/ERK signaling [138].

10.3.3 HIF Pathway Inhibitors

Research is currently focused to target HIF involved pathways, and several drugs have been developed by considering the fundamental role of HIF and the analogs in the activation of various pathways involved in tumor progression in several cancers. Based on the mechanism of action, HIF inhibitors can be divided into the agents that modulate HIF1 α (1) mRNA expression, (2) protein translation, (3) protein degradation, (4) DNA binding, and (5) transcriptional activity. The inhibitors representing each group are depicted in Fig. 10.3 and discussed below and listed in Table 10.1.

In diverse human cancer cell lines, the elevation of HIF-1 α protein is by PI3K/Akt/mTOR signaling pathway. Various compounds for inhibiting PI3K/Akt/mTOR signaling pathway are under the exploitation stage, and few compounds are in clinical trials. Inhibitors *wortmannin*, *LY294002*, *GDC-0941*, and *PI-103* specifically inhibit PI3 kinase in dose-dependent manner [105]. FDA-approved drugs like *rapamycin* and its chemical derivatives (*temsirolimus* and *everolimus*) have more potency to target mTOR and inhibit the protein translation of HIF-1 α at cellular levels [113].

Glyceollins, a set of phytoalexins present in soybean, potentially inhibit the HIF-1 α synthesis and decrease stability by blocking the PI3K/AKT/mTOR pathway and interaction of Hsp90 with HIF-1 α [81].

TSL-1, an agent in aqueous extracts of *Toona sinensis* (TS) leaves, which induces apoptosis via mitochondria-dependent pathway. TSL-1 stops cell division in G0/G1 phase via the decrease in cyclin D1, cyclin-dependent kinases (CDK2 and CDK4), and induced p53 expression. TSL-1 suppresses progression of cell cycle and motility through phosphorylation inhibition of JAK2/stat3, Akt, MEK/ERK, and mTOR. TSL-1 also inhibits p21, HIF-2 α , *c-Myc*, VEGF, and MMP9 expressions and its anti-migration activity [19].

EZN-2968, an antisense oligodeoxynucleotide that precisely targets HIF-1 α . A trial with administered EZN-2968 in patients with advanced solid tumors observed modulation of HIF-1 α mRNA, protein, and its target genes [55]. In MCF-7 xenografts, *aminoflavone*, a potential therapeutic target for several human diseases, inhibited HIF-1 α protein accumulation and expression of target genes [137].

GL 331, a topoisomerase II inhibitor, suppresses tumor-induced angiogenesis. In CL1-5 cells treated with GL331 downregulates HIF-1 α expression through transcriptional repression. It also exerts cytotoxic effects on the glioma cells [16, 20].

Camptothecins (CPTs) analogs, topotecan and irinotecan, are active in different human tumors and shown significant anticancer activity against various tumors by inhibiting DNA topoisomerase I. *Topotecan* is the approved agent using in the treatment of lung cancer [37]. *Irinotecan* is a cytotoxic drug used for the patients suffering with colorectal cancer (CRC) in advanced stage. *SN-38* (10-hydroxy-7-ethyl-camptothecin) is the active metabolite of irinotecan prevents re-ligation of single-stranded DNA breaks induced during the DNA synthesis [37, 90]. These agents have shown the antitumor activity in xenograft model by inhibiting HIF-1 α

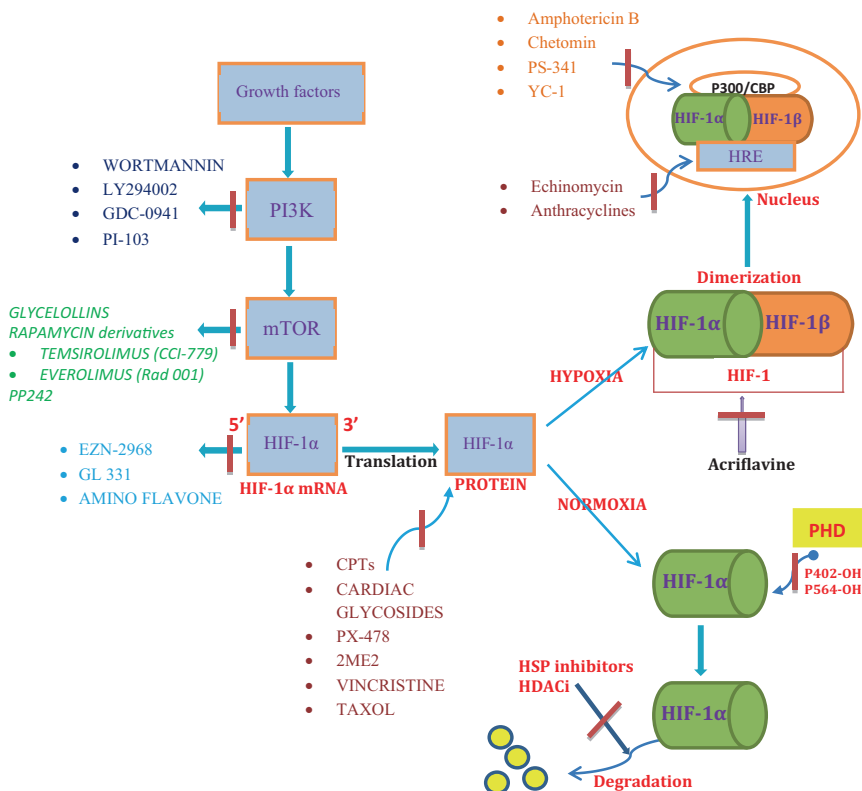


Fig. 10.3 Inhibitors that modulate different HIF-1α pathways

Table 10.1 Classification of HIF-1α pathway inhibitors and their molecular targets

Inhibitory mechanism	Target	Compound
PI3/AKT/mTOR inhibitors	PI3K	Wortmannin
		LY294002
		GDC-0941
		PI-103
	AKT/mTOR, Hsp90	Glyceollins <i>Toona sinensis</i> (TSL-1)
	mTOR	Rapamycin derivatives • Temsirolimus (CCI-779) Everolimus (Rad 001) PP242
mRNA expression	HIF-1α mRNA	EZN-2968
		GL 331
		Amino flavone
Protein translation	Topoisomerase I (top-1) inhibitor/ HIF-1α accumulation inhibitor	Camptothecins (CPTs)
		• Topotecan (NSC-609699)
		• (PEG-SN 38)
		• SN-38
		Irinotecan

(continued)

Table 10.1 (continued)

Inhibitory mechanism	Target	Compound	
	Topoisomerase II inhibitor	GL-331	
	HIF-1 α /mTOR-independent mechanism	Cardiac glycosides <ul style="list-style-type: none"> • Digoxin • Ouabain • Proscillaridin Strophanthidin glycoside	
	HIF-1 α /pVHL and p53-independent mechanism	PX-478	
	Disrupts tumor interphase microtubules	2ME2 (2-methoxy-estradiol) derivatives <ul style="list-style-type: none"> • ENMD-1198 • ENMD-1200 • ENMD-1237 Vincristine Taxol	
HIF-1 α degradation	HSP90 inhibitors	Geldanamycin derivatives <ul style="list-style-type: none"> • 17-AAG • 17-AG • 17-DMAG Radicicol derivatives <ul style="list-style-type: none"> • KF58333 • Apigenin IPL-504 (retaspimycin) Y-632	
		FIH	YC-1
		Farnesyl transferase inhibitor	SCH66336
		Histone deacetylase inhibitors (HDACi)	Sirtuin1 (SIRT1)
			FK228 (romidepsin)
	Trichostatin A (TSA)		
	TRX-1 signaling (thioredoxin-1)	LW6	
		LAQ824	
		LBH589	
		PX-12	
HIF- α /HIF-1 β dimerization inhibitors	HIF-1 α /2 α PAS B-domain	Acriflavine	
	HIF-2 α PAS B-domain	PT-2385	
Transcriptional activity	p300 recruitment	Chetomin	
		Bortezomib (PS-341)	
	FIH interaction and p300 recruitment	Amphotericin B	
	Hsp70	Triptolide	
DNA binding	HRE	FM19G11	
		Echinomycin Anthracyclines derivatives Doxorubicin (DXR) Daunorubicin (DNR)	

accumulation. Clinical trials of these compounds are under progress to provide evidence as anticancer activity agents.

Cardiac glycosides, a group of natural products used in cardiac congestion and cardiac arrhythmias treatment. Recent studies suggested that cardiac glycosides have potential characteristic properties for the treatment of cancer [100]. Cardiac glycosides also inhibit cancer cell proliferation at nanomolar concentrations [117]. For example, *strophanthidin glycoside*, an organic solvent extract from *Crossosoma bigelovii*, showed the HIF-1 α translation inhibitory effect [68].

Digoxin, a cardiac glycoside extracted from the foxglove plant, having antitumor activity against many cancers including lung, colon, prostate, and ovary. It shows activity through Erk and stress response pathways [30]. It exerts antitumor properties through antiproliferative and apoptosis mechanisms in HepG2 cell line cultured with different concentrations of digoxin [133]. Digoxin when treated also has shown to prolong tumor latency and hampers tumor xenograft growth in mice. It also inhibits HIF-1 α expression and its target genes *VEGF*, *GLUT1*, *HK1*, and *HK2* [166]. Digitoxin in H1975 cells showed a significant cytotoxic effect by causing G2 phase arrest and suppressed microtubule polymerization through decreasing α -tubulin [170].

Ouabain is another cardiac glycoside used as novel anticancer HIF-1 α antagonist. It can regulate HIF-1 α translation and affects neither HIF-1 α mRNA levels nor protein degradation. Studies revealed that inhibitory effect of ouabain on HIF-1 α protein synthesis is by eIF4E rather than mTORC1, eIF2 α signaling, or Na(+)/K(+)-ATPase inhibition. Mechanistically, ouabain straightly binds to eIF4E and disrupts association between IF4E/eIF4G complex rather than eIF4E/mRNA complex both in vitro and in vivo, finally suppressing the intracellular CAP-dependent translation [14].

Proscillaridin A exerts its cytotoxic activity by targeting both topoisomerase I and II enzymes simultaneously. In human fibroblasts it elevates intracellular Ca²⁺ concentration, activates caspase-3, and induces apoptosis relatively at high concentration. It exerts the antiproliferative and apoptotic activity at nanolevel drug concentrations (30 and 100 nM) [10, 151].

PX-478 (*S*-2-amino-3-[4'-*N,N*-bis(chloroethyl)amino] phenyl propionic acid *N*-oxide dihydrochloride) decreases Hif-1 α levels in both in vitro and in vivo by suppressing mRNA and blocking translation. PX-478 inhibitory mechanism is independent of pVHL or p53. This drug inhibits HIF-1 α levels and transactivation in a variety of cancer cell lines including HT-29, PC-3, DU-145, MCF-7, Caki-1, and Panc-1. The effect of PX-478 is limited to hypoxia, as baseline levels of vascular endothelial growth factor is not altered under normoxic conditions [69, 149]. A recent study showed that PX-478 significantly decreased or inhibited extra skeletal bone formation by inhibition of Hif1 α . This finding indicates that Hif-1 α represents a promising target to prevent and treat pathologic extra skeletal bone or heterotopic ossification (HO) [2].

2-Methoxyestradiol (2ME2) is a natural estrogen metabolite having antiangiogenic, antiproliferative, and pro-apoptotic drug activities. It culminates induction of apoptosis by diverse cellular effects including microtubule disruption, commencement of signal transduction pathways, and generation of reactive oxygen species

[102]. 2ME₂ targets apoptosis in rapidly proliferating cells of both the tumor cell and endothelial cell compartments and inhibiting blood vessel formation. The ability of 2ME₂ to inhibit metastatic spread in several models adds to its therapeutic value for cancer treatment at various stages of the disease. Many genes regulating cell death and repression of growth/survival machinery were also induced transiently in multiple myeloma (MM) cells. Cells under normoxia and hypoxia conditions when exposed to 2-ME reduced mRNA expression of HIF-1 α and HIF-2 α were observed [4, 8]. 2ME₂ significantly induced apoptosis in HIF-1 α overexpressed AML cells by suppressing the expression HIF-1 α . In vivo 2ME₂ has been shown to downregulate HIF-1 α target genes, such as for VEGF, phosphoglycerate kinase, glucose transporter-1, GLUT1, and HO-1 [8, 172]. In clinical trials the 2ME₂ was noticed to target both tumor cells and neovasculature in preclinical models. The report of first Phase I trials of 2-methoxyestradiol, alone and in combination with docetaxel, was well tolerated in patients with metastatic breast cancer (MBC) [23, 53]. 2ME₂ analogs (*ENMD-1198*, *ENMD-1200*, and *ENMD-1237*) with superior properties have been identified [76, 109, 128].

Few compounds like *Taxol* and *vincristine* also inhibit protein translation of HIF-1 α by disrupting tumor interphase microtubules. Taxol induces static magnetic field (SMF) effect on microtubules to cause abnormal mitotic spindles that delay cell exit from mitosis [93]. Vincristine clinical trials in adults have demonstrated clinical activity without dose-limiting neurotoxicity. The safety, tolerability, and activity of vincristine might be reasons for FDA approval for adults with relapsed acute lymphoblastic leukemia [126].

Hsp90 antagonists induce degradation of HIF-1 α proteins because binding of HSP90 to HIF-1 α promotes HIF-1 α activity [95]. Heat shock protein 90 is a 90-kDa ATPase-dependent molecular chaperone which is a ubiquitously expressed and highly conserved. The expression of Hsp90 in cancer cells is generally higher than that in normal cells. The Hsp90 proteins include a wide variety of signal-transducing proteins that regulate cell growth and differentiation; these are like protein kinases and steroid hormone receptors [101]. Hsp90 inhibitors may be organ-specific and should be carefully monitored, and they have some effects on cell adhesion-associated molecules. Hsp90 has long been regarded as an emerging drug target for a wide spectrum of cancers. Heat shock protein inhibitors are a diverse group of agents which have been verified to have pro-apoptotic effects on malignant cells [3, 129]. The high sensitivity of the inhibitor in cancer cells is proposed due to the formation of the Hsp90-cochaperone-client super complex that is highly unstable and possesses high ATPase activity [89]. Initial development of hsp90 inhibitors, *geldanamycin* and *17-AAG* (17-N-allylamino-17-demethoxygeldanamycin), showed nearly 100-fold higher binding affinity in cancer cells than in normal cells. The effect is restricted by hepatotoxicity and need for solvent carrying agents. On the other hand, *retaspimycin*, or *IPI-504*, a derivative of geldanamycin and 17-AAG, is highly soluble in water and has shown promising activity in gastrointestinal stromal tumor in Phase I/II trials [28]. Currently, Phase I/II trials are underway in the evaluation of dosing schedules and activity for IPI-504 in breast cancer [49, 146].

Y-632, a novel pyrimidine derivative, Hsp90 function suppressed through induced thiol oxidation and disruption of Hsp90–Hsp70/Hsp90 organizing protein complex. This further induces inhibition of cell adhesion, G₀/G₁ cell cycle arrest, and apoptosis [147].

17-DMAG (17-dimethylaminoethylamino-17-demethoxygeldanamycin), another geldanamycin derivative of the HSP90 inhibitor, stalled the viability of human lung cancer cell lines via reduced expression of client proteins, including the proto-oncogene RAF-1. 17-DMAG treatment in human SCLC cell line SBC-5 inhibited the formation of metastatic sites in both liver and bone [134].

KF58333, a novel oxime derivative of radicicol, binds to Hsp90 and destabilizes its associated signaling molecules. KF58333, without altering the HIF-1 α mRNA expression, resulted in significant downregulation of HIF-1 α under hypoxic conditions. KF58333 also inhibited tumor angiogenesis and vascular endothelial growth factor (VEGF) secretion in a dose dependently [74].

Apigenin a naturally occurring flavonoid exhibits antiproliferative and antiangiogenic activities. Apigenin inhibits VEGF expression via degradation of HIF-1 α and interferes with the function of Hsp90 in endothelial cells of human umbilical artery. In pancreatic cancer cells, it inhibits HIF-1 α , GLUT-1, and VEGF mRNA and protein expression in both normoxic and hypoxic conditions [99, 108]. It inhibits the growth of UV-induced skin cancer and thyroid cancer cells by activating AMP-activated protein kinase (AMPK), leading to suppression of basal mTOR activity. This suppression of mTOR activity inhibits cell proliferation and arrests the cell cycle at G₂/M phase. Apigenin is shown to reduce CDK4 and cyclins D1 and A, but not the cyclin E, CDK2, and CDK6 protein expression. Its growth inhibitory effects are mediated by targeting signal transduction pathways and emerging as a promising anticancer agent [11, 163].

YC-1 [3-(5'-hydroxymethyl-2'-furyl)-1-benzyl indazole], a HIF-1 inhibitor, acts by reducing HIF-1 α expression [50, 104]. YC-1 inhibits HIF-1 α expression via the FIH-dependent CAD inactivation as well as protein downregulation [83]. YC-1 suppresses the hypoxic responses by posttranslationally inhibiting HIF-1 α accumulation and exhibits novel antiangiogenic anticancer agent properties [21, 160].

SCH66336, a small molecule farnesyl protein transferase inhibitor that shares a common tricyclic nucleus and competes with peptide/protein substrates for binding to farnesyl protein transferase [87]. It also inhibits the interaction between HIF-1 α and Hsp90 to inhibit VEGF production in NSCLC and HNSCC cells [48].

Under hypoxia, histone deacetylase (HDAC) inhibitor enhances p53 and von Hippel–Lindau expression and thereby stimulates angiogenesis. This stimulation leads to downregulation of HIF-1 α and VEGF thus promoting HIF-1 α degradation [65]. Stress-responsive genetic regulator, sirtuin 1 (Sirt1) gene expression, increases in a HIF-dependent manner, and loss of HIF signaling affects Sirt1 deacetylase activity during hypoxia [17]. SIRT1 downregulation was due to decreased NAD levels; this allowed the acetylation and HIF-1 α activation. SIRT1 deacetylase and the HIF-1 α transcription factor act as redox and oxygen sensors, respectively, whereas hypoxic HIF-1 α stabilization requires SIRT1 activation [85]. Sirt1 regulates HIF-1 α and HIF-2 α by deacetylating Lys674 of HIF-1 α and HIF-1 α K674 and

HIF-2 α K741 by PCAF and CBP, respectively. HIF-1 α deacetylation blocks the recruitment of p300 to HIF-1 α . This blockade consequently inactivates HIF-1 α ; represses HIF-1 target genes including VEGF, GLUT1, and MMP2; and finally promotes cancer cell invasion [58, 165].

Trichostatin A (TSA), an antifungal antibiotic showing histone deacetylase (HDAC) activity. In vitro and in vivo studies in human breast cancer and squamous cell carcinoma cell lines assessed the antitumor efficacy and toxicity of TSA [141]. It induced caspase-dependent or caspase-independent apoptosis according to cell types. In gastric cancer cells, TSA increased TRAIL-induced apoptosis [82]. In HSC-3 cells, TSA enhanced the Bim protein expression levels by dephosphorylating ERK1/2 pathway. In Ca9.22 cells TSA damaged MMP and increased cytosolic apoptosis-inducing factor (AIF) [54].

LW6, a small compound, inhibits the HIF-1 α accumulation. LW6 degrades HIF-1 α via VHL expression, with modifications of P402A and P564A, at hydroxylation sites in the oxygen-dependent degradation domain (ODDD), without affecting the activity of prolyl hydroxylase (PHD) [78]. A recent data revealed that angiogenesis suppression through LW6 inhibited HIF-1 α stability via direct binding with calcineurin B homologous protein 1 (CHP1) [64].

LAQ824 and *LBH589*, the inhibitors of histone deacetylase (HDACi) and established cancer therapeutic agents. Both engage in the intrinsic apoptotic cascade which does not require p53. Mitochondrial damage is the key event for LAQ824 and LBH589 to mediate tumor cell death [31].

Thioredoxin-1 (Trx-1), a redox protein usually overexpressed in many human tumors. It increases aerobic and hypoxia-induced HIF-1 α protein in the cells and leads to expression of HIF-regulated genes. Trx-1 controls multiple aspects of cell growth and survival [57].

PX-12 (1-methylpropyl 2-imidazolyl disulfide), an irreversible inhibitor of Trx-1. This is currently under clinical development [5, 112]. PX-12 decreases plasma VEGF levels and contributes to the antitumor activity [6]. PX-12 acts independently and increases nuclear Nrf2; this one interacts with PMF-1 to increase SSAT1 expression, and further SSAT1 binds to HIF-1 α and RACK1, finally resulting in oxygen-independent HIF-1 ubiquitination and degradation [66].

Pleurotin, a growth inhibitory and antitumor agent shown to decrease HIF-1 α protein levels, HIF-1-*trans*-activating activity, VEGF formation, inducible nitric oxide synthase, and the expression of downstream target genes [150].

AJM290 and *AW464* (quinols), two novel anticancer drugs that inhibit Trx-1 function and also inhibit HIF-1 α CAD transcription activity and DNA binding. In contrast to other Trx inhibitors, these agents also inhibit HIF degradation [57].

Small molecules can inhibit HIF-1 dimerization and potentially inhibit the tumor growth and vascularization.

Acriflavine antagonizes HIF upon binding to the HIF- α PAS-B domain. It directly binds to HIF-1 α and HIF-2 α and suppresses dimerization of HIF-1 and transcriptional activity. It also induces cell death under hypoxic conditions and reduced the expression of the HIF-1 target genes *VEGF*, *PTGS2*, and *EDN1* [12, 80].

PT2385, HIF-2 α inhibitor allosterically binds to PAS-B domain of HIF-2 α , thereby preventing HIF-2 α dimerization with ARNT (aryl hydrocarbon receptor nuclear translocator, HIF-1 β). This results in decreased transcription and expression of HIF-2 α downstream target genes, many of which regulate tumor cell growth and survival. Blocking HIF-2 α reduces the proliferation of HIF-2 α -expressing tumor cells. PT2385 is currently under evaluation in Phase I clinical trials for the treatment of clear cell renal carcinoma [144].

In hypoxic conditions, HIF-1 α is translocated into nucleus, heterodimerizes with HIF-1 β , and binds to hypoxia response element (HRE) DNA sequence. *Chetomin*, a metabolite complex, produced by several fungi of the genus *Chaetomium*, disrupts the ability of tumors to adapt to hypoxia by blocking the HIF pathway and reduces hypoxia-dependent transcription. Chetomin targets transcriptional coactivator p300 by disrupting its CH1 domain and impairs the interaction of between HIF-1 α and p300 [130, 142].

Bortezomib, the first proteasomal inhibitor (PI) and also confirmed antitumor activity-containing agent in clinical setting. Bortezomib attenuates the transcriptional activity and impairs tumor growth only of HIF-1, and not HIF-2. Bortezomib inhibits HIF-1 α protein expression at the translational level under both normoxic and hypoxic conditions and its nuclear targeting through inhibition of PI3K/Akt/mTOR and MAPK pathways, respectively, by dephosphorylation of phospho-Akt, phospho-p70S6 K, and phospho-S6RP [1, 9].

Amphotericin B (AmB), an agent that interferes the HIF-1 α expression through CAD-FIH. AmB represses the C-terminal transactivation domain (CAD) of HIF-1 α , a target site of the factor-inhibiting HIF-1 (FIH). CAD-FIH interaction inhibits the recruitment of p300 through CAD of HIF-1 α [162].

Triptolide possesses anticancer, antiangiogenesis, and drug-resistance activities. Triptolide suppresses HIF-1 α through c-Myc-dependent mechanism. Triptolide treatment in SKOV-3 cells resulted in loss of function of HIF-1 α protein transcriptional activity and reduced mRNA levels of its target genes [29, 173].

FM19G11, an agent that inhibits HIF-alpha protein expression and suppresses target genes of two alpha subunits in several tumor cell lines. FM19G11 reduces overall histone acetylation with significant p300 repression and behaves as a target gene of HIF2alpha at nanomolar range of FM19G11 inhibiting transcriptional and translational expression of Oct4, Sox2, Nanog, etc. [103].

Echinomycin (NSC-13502), a small molecule that binds in a sequence-specific manner in the DNA and shows dual effect on HIF-1 activity under normoxic and hypoxic conditions. It inhibits binding of HIF-1 α and HIF-1 β proteins to a HRE sequence. It suppresses cell growth and induces apoptosis with decreased mRNA expression of HIF1 targets, glucose transporter-1 (GLUT1), and B-cell CLL/lymphoma-2 (BCL2). This agent has failed as anticancer agent due to its dual effect [72, 143, 164].

Anthracycline and its chemical derivatives (doxorubicin (DXR) and daunorubicin (DNR)) are the topoisomerase inhibitor family that suppresses hypoxia-inducible factor-1 (HIF-1) transcriptional activity by obstructing its binding to DNA. These

agents are using widely in the prevention of tumors [116]. Doxorubicin (DXR) weakens the transcriptional activity of the HIF by inhibiting the binding of the HIF heterodimer to the consensus – RCGTG – enhancer element and downregulated HIF target lysyl oxidase (LOX) family members [136]. Anthracyclines also inhibit the endogenous HIF-1 target gene expression. In hypoxic cells the VEGF and GLUT1 mRNA levels were significantly decreased by DNR, and DXR, in a dose-dependent manner [79].

10.3.4 Future Approaches

The thrust is continuously inundated in identifying the novel metastasis-associated oncogenes and tumor suppressor genes. Several therapeutic approaches that target HIF and its associated factors in tumor progression are emerging continuously. Further studies are needed for answering how the cells sense hypoxia and how HIF-1 α activation occurred along with other signaling pathways. In recent studies, researchers have focused on the determination of the pathways (pro-survival and apoptosis) activated in response to hypoxia in cancer cells, and further it is needed to analyze the hypoxia-response gene expression patterns to the levels such as apoptosis, angiogenesis, and metastasis in human cancer cells through microarray analysis and other high-throughput technologies.

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