Review

The role of hypoxia-inducible factors in cancer

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Abstract. Hypoxia-inducible factor (HIF) is a heterodimeric transcription factor that mediates the adaptive responses to hypoxia by effecting the transcription of numerous hypoxia-inducible genes. HIF is frequently overexpressed in solid tumors, and the transactivation of HIF targets in transformed cells provides a distinct survival advantage. Accordingly, the upregulation of HIF correlates with increased

prognosis. In addition to the induction of HIF by hypoxia, its expression is induced by the loss of tumor suppressors VHL, PTEN, TSC1/2, PML, and SDH, as well as by the increased activity of PI3K and/or MAPK signaling pathways, underscoring the significance of HIF in oncogenesis.

progression or aggressiveness of the cancer and poor

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Expression of HIFs

Hypoxia-inducible factors (HIFs) are heterodimeric transcription factors of the basic helix-loop-helix PAS (Per/ARNT/Sim) family of DNA-binding proteins that induce the transcription of a diverse array of genes to effect the hypoxic response. HIFs are composed of an α subunit and a β subunit of which the most ubiquitously expressed is the aryl hydrocarbon receptor nuclear translocator (ARNT) [1, 2]. HIF activity is regulated at the level of the α subunit, with ARNT being constitutively expressed and stable [3]. There are three HIF- α genes in humans: HIF- 1α , HIF- 2α , and HIF- 3α . There are multiple splice variants of HIF-1 α and HIF-3 α , with dominantnegative protein products being produced in some tissues [4–9]. The role of the different HIF- α subunits has been investigated in development and in disease processes such as cancer where they are frequently overexpressed. In mice, knockout of HIF-1α or HIF- 2α is embryonic lethal, while the mouse knockout of HIF-3 α has not yet been addressed. HIF-1 α -/embryos die by day E10.5 of cardiac and vascular malformations [10, 11] and HIF- 2α –/– embryos die by day E16.5 of failed cardiac function due to decreased release of catecholamines [12]. In human tissues, HIF-1α messenger RNA (mRNA) expression is generally ubiquitous with high expression in the kidneys, while HIF-2α mRNA is predominantly expressed in the heart, placenta, and lungs [13, 14]. HIF- 2α may play a role in development of the tubular system and vascular remodelling as it is also expressed in endothelial cells [15–18]. Human HIF-3α mRNA expression has been found to be highest in the heart, placenta, lung, and skeletal muscle [6].

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HIF expression in cancer

HIFs are frequently upregulated in cancer and their metastases because transcription of their downstream target genes can promote growth and survival. Increased expression and activity of HIF-α in cancer may occur by loss of tumor suppressors such as VHL, activation of oncogenes, and increased activity of the PI3K and MAPK signalling pathways discussed below. High levels of HIF-1 α have been positively correlated with tumor progression and poor prognosis in patients with brain, non-small cell lung carcinoma (NSCLC), breast, oesophageal, stomach, fibrosarcoma, colorectal carcinoma (CRC), prostate, ovarian, uterine, and cervical tumors [19-34]. Overexpression of HIF- 2α has been correlated with tumor progression and poor prognosis in patients with NSCLC, head and neck squamous cell carcinoma (HN-SCC), CRC, and VHL-/- clear cell-renal cell carcinoma (CC-RCC) [31, 32, 34–38]. HIF-3 α expression is detectable in several human cancer cell lines [6, 39], and while expression of the dominant-negative HIF-3α inhibits endogenous HIF-1-mediated transcription [6, 8], the significance of the full-length HIF-3α for tumor progression is unknown. Generally, HIF overexpression promotes tumorigenesis, but there are several examples to the contrary. Knock-down of HIF-2α in rat glioma tumors reduced apoptosis, and overexpression of HIF-2 α reduced growth of these tumors [40], while in VHL-/- CC-RCC xenograft assays, overexpression of HIF-1α inhibited tumor growth and overexpression of HIF-2α promoted tumor progression [37].

Regulation of HIF-α by PHDs and VHL

HIF activity is regulated at the level of the α subunit by mechanisms affecting its protein expression, stability, and transcriptional activity. The most well characterized regulatory mechanism for HIF-α is its degradation in the presence of oxygen [1]. Oxygen-dependent hydroxylation by a family of prolyl-hydroxylase domain-containing proteins, or PHDs 1-3 [41, 42], at a conserved residue in the oxygen-dependent degradation (ODD) domain mediates binding to the von Hippel Lindau (VHL) tumor suppressor protein, pVHL [6,43–48]. pVHL is the substrate-docking interface for an E3 ubiquitin ligase complex that polyubiquitylates HIF-α, targeting it for degradation by the common 26S proteasome [46-48]. Under conditions of reduced oxygen availability PHDs do not hydroxylate HIF- α [41,42], the VHL E3 ligase does not recognize the α subunit, and it is no longer targeted for ubiquitin-mediated destruction by the 26S proteasome [46–48]. Patients with VHL disease have inherited an inactivating mutation in one allele of VHL and have a subsequent somatic mutation of the remaining allele [49]. CC-RCC-causing mutations in VHL patients that prevent VHL from recognizing HIF- α or those that disrupt the formation of a functional E3 ligase complex result in the failure to target HIF-α for efficient oxygen-dependent degradation and a loss of tumor suppressor function for VHL in the kidney [50, 51]. In these VHL patients or individuals with somatic mutations of VHL in the kidney epithelium, patients develop CC-RCC and haemangioblastomas [52-56]. As mentioned, overexpression of HIF-α, particularly HIF-2α, has been implicated in the tumorigenesis of VHL-/- CC-RCC. Interestingly, mutations in tumor suppressors other than VHL may also disregulate HIF-α stability by affecting pVHL's ability to bind HIF-α. Loss of the succinate dehydrogenase (SDH) or fumarate hydratase (FH) tumor suppressors result in increased levels of succinate and fumarate, respectively, which inhibit PHD activity preventing hydroxylation of HIF- α [57].

Regulation of HIF-α protein levels by phosphorylation signalling cascades

Both phosphoinositol 3-kinase (PI3K) and mitogenactivated protein kinase (MAPK) signalling cascades can regulate HIF-1α protein levels in an oxygenindependent manner. Increased expression of HIF-1α via the PI3K signalling pathway may occur by gain-offunction mutations in upstream positive regulators such as receptor tyrosine kinases and Ras, or loss-offunction mutations in tumor suppressors such as tuberous sclerosis (TSC) 1 or 2 or phosphatase and tensin homolog (PTEN) [58–64]. The PI3K pathway can increase translation of HIF-1α mRNA by both mammalian target of rapamycin (mTOR)-dependent or mTOR-independent mechanisms [58, 61, 65, 66]. As part of a signalling complex, mTOR kinase regulates protein synthesis via S6 kinase-mediated phosphorylation of S6 ribosomal binding protein to increase expression of translational mediators and via activation of eukaryotic initiation factors to increase both cap-dependent and cap-independent translation [66]. The mTOR-dependent mechanism of increased HIF-1α translation is most active under low serum conditions and has been observed in TSC2-/- mouse embryonic fibroblast (MEF) cells and osteosarcoma U2OS cells with TSC2 knock-down [61], in neuroblastoma cells downstream of brain-derived growth factor (BDGF)-mediated activation of the TrkB receptor via PI3K [30], in IGF-2-overexpressing rhabdomyosarcoma cell lines [67], in the MCF7 breast cancer cell line via activation of the human epidermal growth factor receptor 2 (HER2) [58], and in PML-/– MEFs via loss of Ras homolog enriched in brain (Rheb) regulation [68]. PI3K can also upregulate translation of HIF-1α mRNA by a mechanism that is mTOR-independent and may be dependent on internal ribosomal entry sequence (IRES)-mediated translation instead of the cap-dependent translation potentiated by mTOR [66, 69].

Regulation of HIF-α expression by other mechanisms

There is also some evidence that reactive oxygen species can increase HIF-driven gene expression by modulating both HIF- α levels and transcriptional activity [70]. Recently it was shown that nitric oxide synthase expression in oral squamous cell carcinoma is responsible for accumulation of HIF-1 α [71] and that NADPH oxidase 4 (NOX4) expression in CC-RCC is required for endogenous HIF-2 α mRNA and protein expression [72].

Regulation of HIF transactivation

HIFs bind to hypoxia-responsive elements (HREs) in the enhancers of target genes, which requires the basic helix-loop-helix, PAS, and PAS-associated C-terminal (PAC) domains at the amino-termini of the α subunits [73]. Two transactivation domains mediate gene transcription by HIF-1 α and HIF-2 α : the N-terminal transactivation domain (N-TAD), which partially overlaps with the ODD domain, and the C-terminal transactivation domain (C-TAD) [74, 75]. HIF-3α has an N-TAD but does not possess the C-TAD of HIF-1 α and HIF- 2α [6, 39, 76]. Although HIF- 3α may have weaker transactivation activity at hypoxia-responsive elements than HIF-1 and HIF-2 [39, 76], its novel Cterminus may have additional uncharacterized transactivation properties [6, 39]. The C-TAD of HIF-1α and HIF-2α bind to p300/CREB binding protein (CBP), steroid receptor co-activator-1 (SRC-1), and transcription intermediary factor-2 (TIF-2) as coactivators to effect transcription [75, 77-80]. For HIF-2α, the C-TAD may not be necessary for transcription of all HIF-mediated genes such that the N-TAD alone appears to sometimes suffice [81]. The mechanism of transactivation by the N-TAD is not well characterized, and although p300/CBP can potentiate its activity, there is no evidence for a direct interaction between the N-TAD and p300/CBP as there is for the C-TAD [77-79, 82, 83]. The binding of coactivators to the C-TAD is regulated by posttranslational hydroxylation and cysteine reduction

events. Hydroxylation of a conserved asparagine residue in the C-TAD in the presence of oxygen by factor inhibiting HIF-1 (FIH-1) prevents binding of p300/CBP to the C-TAD [84]. Under hypoxia, the C-TAD is no longer hydroxylated, and p300/CBP may be recruited by HIF-1 α [84]. The HIF-2 α C-TAD appears to be resistant to FIH1-mediated inhibition under normoxia [81]. To promote C-TAD-mediated transactivation, reduction of a conserved cysteine residue in the C-TAD of HIF- 1α and HIF- 2α by REF-1 in conjunction with transferrin potentiates binding of p300/CBP and SRC-1 to this domain [77]. Interestingly, knockout of the C-TAD-interacting CH1 domain of p300 and CBP in mouse has revealed that less than 50% of HIF-1-inducible genes in MEFs are dependent on this interaction [85]. Most HIF-1 regulated/CH1-dependent genes were sensitive to histone deacetylase (HDAC) inhibitors, and some required both HDAC activity and p300/CBP [85]. HIF- 1α has been shown to interact with HDACs 4, 6, and 7, and these interactions have also been shown to stabilize and potentiate transcription by HIF-1 α [86, 87]. The role of direct acetylation of HIF-1 α in regulating it's stability and transcription activity is controversial and will not be discussed [88–92]. Phosphorylation of HIF-1 α and p300 also regulates transactivation. P300 phosphorylation by the MAPK pathway improves the recruitment of p300/CBP to the C-TAD of HIF-1α [93]. Direct phosphorylation of HIF-1α by the MAPK pathway has been shown to potentiate transactivation by HIF-1 of target genes [94, 95], and may involve protecting the subunit for

A differential role for the N-TAD and C-TAD in HIF transcription

exportin-dependent nuclear export [96].

It has been suggested that as oxygen concentration decreases during hypoxia, inhibition of PHD-mediated hydroxylation of the ODD domain may occur before inhibition of FIH-1-mediated hydroxylation of the C-TAD [97]. This would lead to activation of the N-TAD before the C-TAD, and perhaps selective regulation of some genes in a positive manner by the N-TAD, but negatively once cofactors can be recruited to the C-TAD [97].

HIF transcriptional targets in the development and progression of cancer

Many of the genes regulated by HIF-1 and HIF-2 to allow a cell and tissue to adapt to hypoxic conditions also promote the survival of a tumorigenic phenotype in cancer. HIF-1 can upregulate more than 60 targets, including those involved in angiogenesis, anaerobic glucose metabolism, metastasis, cell motility, iron metabolism, growth and survival, apoptosis, telomere maintenance, and drug-export mechanisms. Several of these processes and the relevant HIF targets will now be discussed.

The most notable protein induced by HIF-1 and HIF-2 involved in angiogenesis is vascular endothelial growth factor (VEGF)-A [16, 98-100], the potent endothelial cell mitogen highly expressed in many solid tumor types. Angiogenesis is required for a tumor to grow beyond the size accommodated by diffusion from the existing vasculature alone [101]. Interestingly, increased angiogenesis in solid tumors does not result in the tumor losing the induction of the hypoxic response if HIF can be targeted for degradation because the tumor vasculature is highly irregular allowing for regions of hypoxia to persist [102–104]. HIF-1 has also been shown to increase the expression of transforming growth factor (TGF)-β3, leptin, and endoglin to promote angiogenesis [10, 98, 99, 105-107]. In addition, HIF-1 can increase the permeability and dilation of the vasculature by inducing the expression of VEGF-A, nitric oxide synthase 2, haem oxygenase-1, endothelin-1, and the $\alpha_{1\beta}$ -adrenergic receptor [98, 99, 108–113]. HIF-2 has also been shown to transactivate VEGF receptor-2 (VEGFR2) and the endothelial receptor tyrosine kinase Tie-2 [16, 18, 114].

To adapt to reduced oxygen availability and subsequent decreased oxidative phosphorylation, HIF-1 upregulates the enzymes of glycolysis and glucose transporters (GLUTs) 1 and 3 to maintain cellular ATP pools [115, 116]. This switch to anaerobic metabolism is also another trademark of solid tumor biology. Interestingly, the glucose metabolites pyruvate and oxaloacetate appear to regulate normoxic HIF-1 α expression in cancer cell lines by inhibiting PHD-mediated hydroxylation of HIF-1 α [117, 118]. Therefore, there may be a role for glycolysis in a positive feedback loop of sustained HIF-1 α activation in cancer [117, 118].

Increasing the invasive potential of a cell and changing the extracellular environment to promote migration is required for tumor spreading and metastasis. HIF-1 regulates autocrine motility factor (AMF), TGF-α, urokinase-type plasminogen activator receptor (uPAR), matrix metalloproteinase-2 (MMP-2), E-cadherin (negatively), lysyl oxidase, and chemokine (C-X-C motif) receptor 4 (CXCR4) to potentiate migration and invasion of cancer cells [34, 112, 119–128]. E-cadherin, a homophilic adhesion molecule of epithelial cells, was recently identified as being positively regulated by VHL in a HIF-dependent

manner (HIF induces the expression of inhibitory regulators of transcription) [124-126]. Loss of Ecadherin expression occurs early in pre-neoplastic lesions and potentiates migration and invasion of VHL-/- CC-RCC cells [124, 129]. Lysyl oxidase promotes metastasis of breast cancer tumors by promoting focal adhesion kinase activity and cell-tomatrix adhesion [123]. Induction of CXCR-4 and its ligand stromal cell-derived factor-1alpha (SDF-1 α) by HIF-1 and HIF-2 promotes invasiveness of VHL-/-CC-RCC cells locally and metastasis distally to organs expressing SDF-1α ligand [34, 127, 128]. Deposition of vimentin, which is also regulated by HIF-1, an extracellular matrix (ECM) component, leads to a dedifferentiated ECM (instead of the more differentiated keratin-rich ECM) that promotes increased motility of cancer cells [122].

HIF-1 and HIF-2 regulate the expression of many growth and survival factors for tumor maintenance and progression, including VEGF-A, transforming growth factor (TGF)-α, survivin, cyclooxygenase (COX)-2, platelet-derived growth factor (PDGF)-β, insulin-like growth factor (IGF-2), and insulin-like growth factor binding proteins (IGFBPs) 1–3 [16, 98– 100, 119, 130–135]. TGF- α is a powerful mitogen for renal proximal tubule epithelial cells (the suggested origin of CC-RCC) and VHL -/- CC-RCC cell lines, and signalling downstream of its receptor epithelial growth factor receptor (EGFR) may result in an autocrine signalling loop with PI3K further activating expression of HIF-1 and HIF-2 [119]. Expression of survivin, an anti-apoptotic factor, has been partly attributed to downstream signalling from the EGFR in breast cancer via HIF-1 [135]. Similarly, COX-2 expression by HIF-1 in CRC cells leads to production of the survival factor prostaglandin E2 (PGE2) and positive feedback on HIF-1 activity by activating the MAPK pathway [134].

HIF-1 also has the potential to induce several proapoptotic genes such as BCL2/adenovirus E1B 19-kDa interacting protein 3 (BniP3), BCL2/adenovirus E1B 19-kDa interacting protein 3-like (BNip3L), and DNA-damage-inducible transcript 4 (DDIT4) [136–138]. Mutation of p53 and epigenetic silencing, such as for the BNip3 promoter in CRC cancer cell lines [139], may explain the apparent contradiction of increased HIF-1 expression generally correlating with poor prognosis.

HIF-1 can contribute to radiotherapy and chemotherapy treatment resistance. It increases the expression of the P-gp drug efflux pump that is commonly overexpressed in cancer which confers resistance to chemotherapeutics [140]. It has also been implicated in double-strand break repair and transcriptionally upregulating expression of the catalytic subunit of

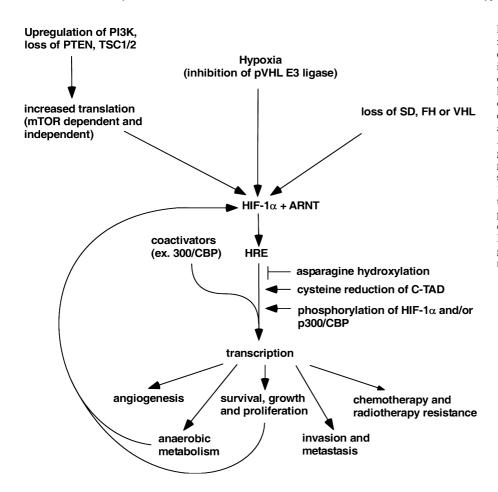


Figure 1. Deregulation of hypoxia-inducible factor (HIF) in cancer by oxygen-dependent and independent mechanisms. Loss of tumor suppressor proteins, hypoxia, and increased activity of phosphorylation signalling cascades increase the expression and/or stability of HIF in cancers. As well, positive feedback by the glycolytic metabolites growth factor signalling downstream of HIF-1 increase HIF-1α expression. HIF transactivation is tightly regulated by phosphorylation and hydroxylation events, and the upregulation of HIF-target genes promotes the growth and survival of tumor by multiple mechanisms.

telomerase, human telomerase reverse transcriptase (hTERT) [141–143]. Increased expression of hTERT is also a trademark of cancer allowing the number of cell divisions to be unhinged to telomere length of the chromosomes [144].

Tissue specificity of HIF-1 and HIF-2 dependent transcription

An emerging area of research in hypoxia-mediated gene expression is the tissue-specific gene transcription profile of HIF-1 versus HIF-2. As mentioned, HIF-2 α plays an important role in the development and progression of VHL-/- CC-RCC. Support for the preferential expression of HIF-2 α in VHL-/- CC-RCC is from data demonstrating that HIF-2 appears to be responsible for activating transcription of the pro-tumorigenic genes such as TGF- α , VEGF, and cyclin D1, while HIF-1 upregulates the pro-apoptotic factor BNip-3 [37]. Another group has also reported similar results demonstrating HIF-2 α was predominantly responsible for VEGF, uPAR, and PAI-1 expression in VHL -/- CC-RCC [145]. However, this group found that in MCF-7 breast cancer cells, it

was HIF-1 α that primarily regulates VEGF and IGF-1 [145]. As well, HIF-2 and HIF-1 seem to negatively affect the expression of one another in both VHL-/– CC-RCC cell lines and MCF-7 [37, 145].

HIF-2 has unique targets additional to those of HIF-1. The VEGFR2 (Flk-1) is a HIF-2 regulated gene whose transcription is dependent on the interaction of the N-TAD of HIF-2 α with the E26 transformation-specific (ETS) transcription factors [114]. Several other genes have been reported to be HIF-2 driven in an ETSdependent manner as well, including CBP/p300interacting transactivator with ED-rich tail 2 (CITED2) and WNT1 inducible signaling pathway protein 1 (WISP1) in the MCF-7 cell line [146]. In the 11 genes identified as being HIF-2 regulated, almost all had an ETS-binding site adjacent to the HRE, and knock-down of ETS family member ELK-1 significantly reduced the expression of these genes [146]. The mechanisms of transcription for the HIF-2specific targets octomer binding transcription factor-4 (Oct-4) and erythropoietin are not as well understood and may involve interaction of HIF-2α with as of yet uncharacterized co-factors. Oct-4 is a transcription factor essential for maintaining stem cell pluripotency [147]. Significantly, knock-in expression of HIF-2 α in Oct-4–/– homozygous mouse embryos caused large embryonic-stem cell-derived tumors [147]. Erythropoietin (EPO) was first reported to be a HIF-1 regulated gene; it has now been shown that knockdown of HIF-2 α but not HIF-1 α by siRNA (small-interfering RNA) transfection significantly decreased the expression of EPO in Kelly neuroblastoma and Hep3B cell lines (the cell line that was used to identify EPO as a HIF-1 target) [148]. While the EPO HRE in isolation was responsive to both HIF-1 α and HIF-2 α knockdown and showed no cell-type specific expression, when the entire EPO enhancer was used, there was a significant difference in luciferase activation, suggesting an explanation for the earlier findings that EPO was a HIF-1-regulated gene [148].

Conclusion

Hypoxia-inducible gene expression is regulated by a family of HIF transcription factors of which HIF-1 is the most well characterized, HIF-2 has emerged as a non-redundant player, and the role of full-length HIF-3 is as of yet unknown. Oxygen-dependent regulation of the α subunit of these factors is well established, as is the role for both PI3K and MAPK signalling cascades (see Fig. 1). Deregulation of these pathways by loss of any one of several tumor suppressors leads to increased expression and/or activity of HIFs during tumorigenesis, providing a growth and survival advantage to the cells. Interestingly, drugs that have been shown to inhibit HIF have demonstrated significant activity in clinical trials, and in the case of kidney cancer, represent major advances in the treatment of these diseases. However, when treatments involve non-specific targeting of several HIF-α subunits, consideration should be given to the fact that the role of a given subunit is tissue-specific, and in some instances they can play an inhibitory role in tumorigenesis.

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