

Cancer and the Cellular Response to Hypoxia

Maria Adamaki*, Anastasia Georgountzou and Maria Moschovi

First Department of Pediatrics Hematology-Oncology Unit, National University of Athens, Aghia Sofia Children's Hospital, Athens, Greece

Abstract

Hypoxia is defined as the reduction of oxygen levels below normal (normoxia), i.e. below 5% and may occur naturally in certain physiological processes such as normal embryo development, stem cell function and angiogenesis [1-6]. However, hypoxia also plays a major role in many human pathological conditions, including cancer, inflammation, vascular disease and chronic kidney disease [7-10]. When an organism or tissue is exposed to hypoxia, a series of events takes place within that organism or tissue so as to reinstate oxygen homeostasis. Even though the physiological responses to hypoxia are well-documented, the molecular changes taking place at the cellular level are still being investigated to this very day. Detection of hypoxia by the cell is achieved through oxygen sensor relays residing inside the cell, a class of deoxygenases called PHDs (prolylhydroxylases), which activate special transcription regulators that lead to changes in the gene expression profile of the cell [11]. The changes in gene expression are mainly commanded by a family of hypoxia-responsive transcription factors called HIFs (hypoxia-inducible factors) which, since their discovery in the early 1990s [12] have greatly facilitated molecular research in the field; research on HIFs has led to the discovery of other hypoxia-responsive transcription factors, as well as additional molecular processes that take place following hypoxia, which play a very distinctive role in the transcriptional outcome of the cell. Overall, hypoxia causes a cell cycle arrest at the G1 phase [13] and ultimately, a hypoxia-responsive mechanism for the remodelling of chromatin leads to the activation or repression of specific downstream target genes, to changes in the translational profile of the cell and even to epigenetic post-translational modifications in the cell [14-17].

Introduction

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this microenvironment presents an obstacle to conventional anti-cancer therapies [20], thus increasing the likelihood for malignant progression and metastasis. Therefore, tumour hypoxia is seriously considered in the prognosis and treatment of cancer patients, whereas therapeutic strategies for targeting the hypoxic cancer microenvironment are well underway.

In this article we give an overview of the current knowledge on the cellular response to hypoxia, including a summary of the transcription factors regulating it and the molecular processes resulting from it. We will give particular emphasis on the role of hypoxia in cancer development and treatment, with respect to changes in the transcriptional and translational profile of the cancer cell. Finally, we will discuss the present therapeutic modalities in overcoming hypoxia-mediated drug resistance and the progress in the pharmacological design of hypoxia inhibitors as new cancer chemotherapeutics. Overall, since our field of expertise is pediatric oncology, we will at the same time attempt to present this information in relation to pediatric cancers.

The Cellular Response to Hypoxia

The HIF transcription factors

The HIF family of transcription factors are highly conserved heterodimeric proteins composed of α and β subunits. HIF- α consists of three isoforms: HIF-1 α , HIF-2 α and HIF-3 α , whereas HIF- β , also known as ARNT (aryl hydrocarbon receptor nuclear translocator), has

*Corresponding author: Maria Adamaki, First Department of Pediatrics, University of Athens, Oncology Research Laboratory, "Aghia Sofia" Children's Hospital, Thivon & Levidias Street, 11527 Goudi, Athens, Greece, Tel: 0030-210-7452172; Fax: 0030-7795538, E-mail: madamaki@med.uoa.gr

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only one isoform, HIF-1 β [21]. The α subunits are similar in structure and contain basic helix-loop-helix (bHLH) and PAS (PRE-ARNT-SIM) domains, in addition to an ODD (oxygen-dependent degradation) domain that renders them labile in the presence of oxygen [11]. The HIF-3 α isoform lacks the C-terminal transactivation domain that the other two possess, thus suggesting an inhibitory role on HIF-1 α and HIF-2 α [22]. Interestingly, the PAS domain, due to its primitive origin and involvement in circadian rhythms, is believed to suggest a link between the circadian light-dark cycle and oxygen availability [23,24]. Overall, ARNT is essentially a constitutively expressed subunit not regulated by oxygen levels, whereas HIF- α subunits are actively involved in conferring oxygen homeostasis [25]. Under normoxic conditions ($\geq 5\%$ O₂), the special sensors called PHDs catalyse the hydroxylation (hence prolyl hydroxylation) of the ODD domain in the HIF- α and act as a signal for HIF- α recognition by the VHL (von Hippel-Lindau) tumor suppressor protein [26]. The VHL, in turn, acts as an E3 ligase substrate recognition component and promotes ubiquitination of HIF- α , thus marking it for rapid degradation by the proteasome [27]. In addition, a second type of hydroxylation of HIF- α may take place, the so-called asparaginyl hydroxylation, catalysed by a class of deoxygenases called FIHs (factors inhibiting HIF). FIHs negatively regulate the transactivation domain of HIF- α by preventing it from binding to its co-activators p300 and CBP, thus repressing its transcriptional activity [28]. In other words, normoxia results in HIF- α being either transcriptionally repressed or degraded by hydroxylation. On the other hand, in an acutely hypoxic environment, where oxygen-dependent hydroxylation is inhibited, HIF- α translocates to the nucleus where it dimerizes with ARNT, thus avoiding degradation and increasing in stability [29]. Consequently, the HIF- α /ARNT complex recruits the necessary co-activators p300/CBP (and/or p160/SRC in the case of ARNT) in order to modify chromatin structure via histone acetylation and to be able to bind to target genes via its recognition sequence 5'-(A/G)CGTG-3', thus increasing transcription of the target sequences [30,31]. Figure 2 diagrammatically represents the regulation of gene expression by HIF-1. Several hundreds of genes have been recognised as direct targets of HIF binding and transactivation, the most important ones regulating erythropoiesis, angiogenesis, glycolysis, vascular development, mitochondrial function, metabolism, cellular proliferation, cell migration and cancer. Examples include erythropoietin (*Epo*), vascular endothelial growth factor (VEGF), platelet-derived growth factor (PDGF), glucose transporter-1 (Glut-1), GAPDH, lactate dehydrogenase A (LDHA), p53 and MYC [24,32,33]. Recent evidence shows that HIF-1 α preferentially binds to loci that have been transcriptionally active prior to the onset of hypoxia, further implying that the pre-existing differences in the basal gene expression of the cell may be responsible, at least in part, for the cell-type specificity in the response to hypoxia, as well as the promiscuity of certain genes to transactivation by the HIFs [34].

HIF-independent response to hypoxia

In addition to the HIFs, there are several other transcription factors and pathways that show altered activity as a result of hypoxia. These are outlined below.

Mammalian target of rapamycin (mTOR): Being a main regulator of cellular energy, mTOR's normal function is to phosphorylate the ribosomal protein S6 kinase (S6K) and the eIF4E-binding protein 1 (4E-BP1) and to promote the translation of mRNAs that are essential for cell growth and survival [35]. Under hypoxic conditions, however, mTOR phosphorylation of S6K and 4E-BP1 is

markedly suppressed, thus inhibiting ribosomal biogenesis and cap-dependent protein translation, respectively, in order to save cellular energy (ATP consumption) in the oxygen-limiting environment [36]. More specifically, hypoxia inhibits mTOR activity via the hypoxia-inducible gene REDD1, through the TSC1/TSC2 tumour suppressor complex and the constitutive activation of S6K promotes cell death [37]. On the other hand, it has been suggested that in a hypoxic tumour microenvironment inhibition of the mTOR pathway might induce new energy conservation strategies in cancer cells and thus be critical for maintaining their malignant phenotype via growth retardation and accumulation in the G1 phase [36,38]. This could have major implications in the way we regard cancer therapy, as attempts towards a forced activation of mTOR signalling are already proving more effective than mTOR suppression in inhibiting cancer growth in studies with mice [39].

Endoplasmic reticulum (ER): Under conditions of hypoxic stress, in order to maintain protein quality or to induce cell death, the ER activates the unfolded protein response (UPR), a coordinated cell-survival program mediated by three resident regulator kinases: PERK, IRE1 and ATF6. More specifically, upon hypoxic exposure, the ER induces phosphorylation of the eukaryotic initiator factor 2 alpha (eIF2 α) on Ser51 via activation of PERK, resulting in the rapid down-regulation of protein synthesis [40]. Inactivation of PERK or inhibition of eIF2 α phosphorylation has a negative effect on cell survival and tumour cells possessing these properties show a higher apoptotic rate than tumours with a normal functioning UPR [41]. In addition, activation of the IRE1 kinase has been found to promote the splicing of the X-box binding protein (XBP1) pre-mRNA, resulting in hypoxic tolerance and tumour growth in vitro [42].

Nuclear factor-kappa B (NF- κ B): This is essentially a family of seven transcription factors, encoded by the following five genes: RelA(p65), RelB, c-Rel, NF- κ B1(p50/p105) and NF- κ B2(p52/p100), all of which share an N-terminal DNA-binding and dimerisation domain, the Rel homology domain (RHD) [43]. Apart from being one of the most important regulators in the immune system and in inflammatory responses, the NF- κ B pathway is also known for its implication in cell cycle progression and cancer [44,45]. Under hypoxic conditions, down-regulation of PHD2 directs an increase in NF- κ B levels and up-regulates the expression of IL-8 and angiogenin genes, thus causing angiogenesis [46]. The exact mechanism for the hypoxia-mediated induction of NF- κ B has not been fully elucidated but a dual and opposing mode of action has been well established. For example, even though NF- κ B acts as a survival signal on most cell systems, it has a pro-death effect on neuronal cells [47-49], a property currently subject to intense scrutiny in the research field. Recent studies have shown NF- κ B to directly modulate HIF-1 α transcriptionally as a response to hypoxic stress [50,51]. Subsequent studies will reveal which subunits are involved in HIF activation and whether a reciprocal relationship exists.

Tumor suppressor p53: Encoded by the gene TP53, the p53 protein is so well-known for its tumour suppressor properties that it has been tagged "the guardian of the genome". The importance of p53 in preventing cancer is highlighted in the fact that the gene is mutated in over 50% of all the human cancers, whereas p53 null mice develop cancer very early in life [52,53]. Normally, p53 has a half-life of only a few minutes, as the Mdm2 ubiquitin ligase directly binds to it and mediates its proteolytic degradation; upon activation, however, p53 becomes subject to various post-translational modifications that disrupt the

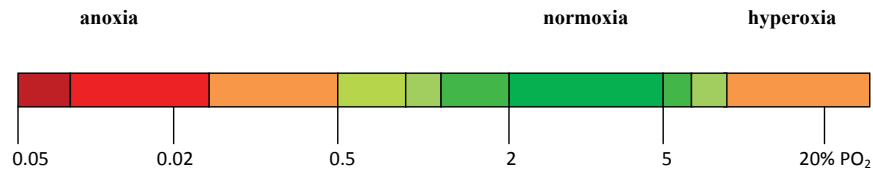


Figure 1: Diagrammatic representation of oxygen levels in adult brain cells. PO₂ (oxygen tension) varies with the cell type and the microenvironment of the respective organ. In the brain, physiological oxygen levels range between 2-5% whereas in the bone marrow physiological oxygen levels have been calculated to be highest (~5%) near the sinuses and lowest (1%) inside the cortical bone. Adapted from David M. Panchision (2009).

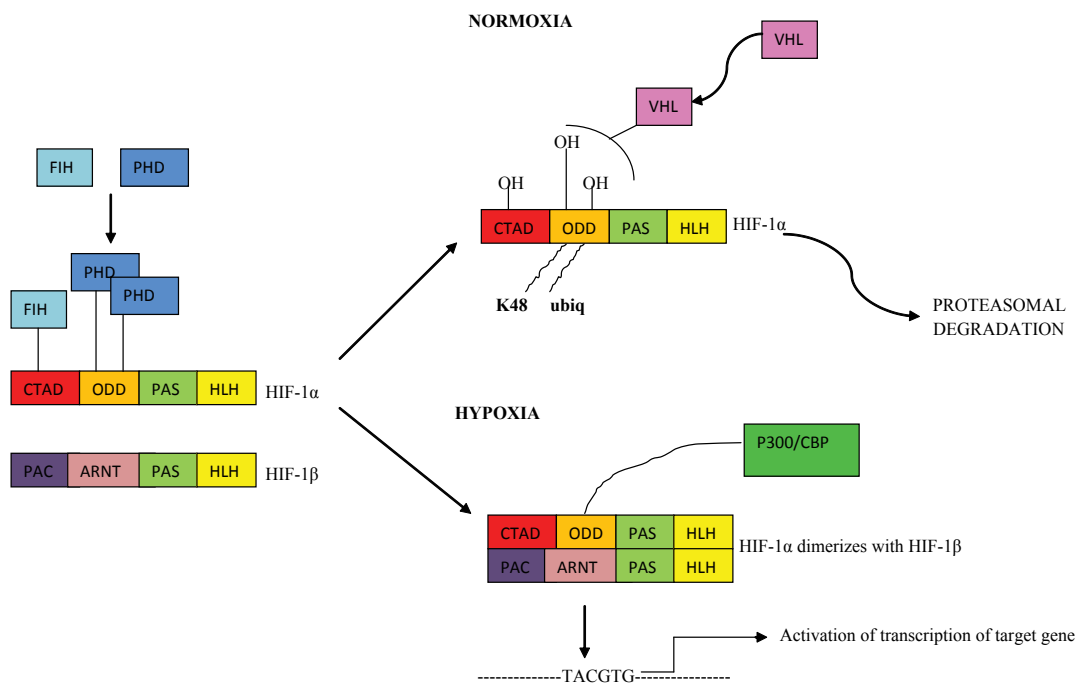


Figure 2: Regulation of gene expression by HIF-1α. In normoxic conditions, FIH and PHDs hydroxylate residues in the CTAD and ODD domains of HIF-1α, which in turn activates VHL binding and ubiquitination of HIF-1α, ultimately leading to its proteasomal degradation. Under hypoxic conditions, however, the lack of oxygen inhibits the action of FIH and PHDs, so HIF-1α is able to stabilise and dimerize with HIF-1β, ultimately activating target gene transcription through recruitment of co-activators. Adapted from Kenneth and Rocha (2008).

binding of Mdm2 and render p53 stable and transcriptionally active for a good few hours [54,55]. Activation is usually conferred as a response to DNA damage and results in either cell cycle arrest or apoptosis [53]; in particular, p53 interacts with the co-activator p300, as well as other transcription factors (eg. TFIID), so it is able to bind to damaged DNA in a sequence-dependent manner and to induce the transcription of downstream genes that are responsible for cell cycle inhibition or apoptosis [56,57]. Many studies have documented that p53 activation by hypoxia can be achieved by both HIF-1-dependent and HIF-1-independent mechanisms but it appears to be a very atypical response, in the sense that it does not induce the transactivation of the same set of genes as other stress signals, as for example in the case of Bnip3L [58-61]. Even though not all the p53 transcription targets have been defined so far, the role of p53 in hypoxia-induced apoptosis is profound. Under hypoxic conditions, p53 levels are believed to increase through an HIF-1 α-mediated decrease in Mdm2 [62] but others have speculated that p53 protein levels may also be influenced by the severity (i.e. 5.0-0.1% O₂) and duration of hypoxia (in hours versus days), as well as the cell type affected [63-65]. Like NF-κB, p53 also has a dual and opposing

mode of activity in that it can serve either as a pro-survival signal or as a pro-death signal. Under moderate hypoxia (± 1.0% O₂), p53 levels may be reduced so as to protect the cells from apoptosis, whereas under severe hypoxic conditions (≤ 0.1% O₂, reaching anoxia) the situation may reverse, in that HIF-1 may induce p53 stabilisation and lead to apoptosis [63,66].

MYC: This refers to a family of four transcription factors containing a bHLH/LZ (bHLH/Leucine Zipper) domain: c-Myc, N-Myc, L-Myc and S-Myc [67]. The Myc protein can bind DNA via its bHLH domain and form heterodimers with its partner transcription factor, Max, through the LZ domain. The Myc-Max heterodimers are able to bind to specific DNA sequences, the Enhancer Box Sequences (E-boxes), in the promoters of their target genes, recruit histone acetyltransferases (HATs) and activate transcription [68,69]. On the other hand, Myc can also act as a transcriptional repressor through displacing the p300 co-activator and binding to the Miz-1 transcription factor instead, hence inhibiting the expression of Miz-1 genes [70]. Overall, Myc proteins have essential functions in many biological processes, such as cell growth, proliferation, angiogenesis and genomic instability

[67,71]. The gene is frequently mutated in human cancers, resulting in its constitutive expression and leading to the unregulated expression of many other genes; a common example is the t(8;14) translocation, characteristic to the pathogenesis of Burkitt's Lymphoma [72]. Under normoxic conditions, Myc promotes cell growth and proliferation via the repression of cyclin-dependent kinase inhibitors; under hypoxic conditions however, Myc activity is compromised by the antagonistic relationship between Myc and HIF for the binding sites of target genes [13,73,74]. More specifically, in low oxygen levels, c-Myc is replaced by HIF-1 and so induces expression of the cyclin-dependent kinase inhibitor p21 and causes cell-cycle arrest [75]. Many reports have also shown that in hypoxic cells HIF-1 α can reduce the expression of Myc target genes and inhibit transformation via direct binding to Myc or to its partners [74-76]. Interestingly, HIF-2 α has the opposite effect and promotes hypoxic cell proliferation by inducing c-Myc activity; it does so via stabilization of the Myc-Max heterodimer, which allows it to activate the expression of its target genes [77]. Overall, both Myc and HIF are directly involved in angiogenesis and cancer development, while recent studies have also shown that HIF-1 α and c-Myc cooperation is essential in c-Myc-induced tumorigenesis [78,79]. Finally, HIF and c-Myc have been found to synergise for the induction of shared target genes VEGF, HK2 (hexokinase) and PDK1 (pyruvate dehydrogenase kinase 1), in a cell-type-specific manner [80], so speculations are also being made on additional functional relationships between other important transcription factors, such as p53 and NF- κ B.

Activator protein 1 (AP-1): This refers to any heterodimeric protein combination resulting from dimers between the Jun, Fos and ATF (activating transcription factor) families, so, depending on the cell type and microenvironment, the role of AP-1 is multifaceted and highly complex. Overall, AP-1 is able to respond to a variety of stimuli, including cytokines, growth factors, stress signals, infections and has been associated with many important biological processes, such as embryonic development, differentiation, proliferation, apoptosis and even tumorigenesis [81,82]. Activation of certain AP-1 dimer combinations (such as the c-Jun homodimer or the c-Jun/c-Fos heterodimer) induces the transcription of genes containing the TPA DNA recognition element (TRE; 5'-TGAG/CTCA-3') via site-specific binding [83]. It has been well documented that hypoxia induces AP-1 activity and mediates alterations in the gene expression of tyrosine hydroxylase, VEGF and endothelial nitric oxide synthase (eNOS) [84-86]. In addition, a functional cooperation seems to exist with other transcription factors in order to increase gene transcription; interestingly, AP-1 and HIF-1 cooperate to induce VEGF transcription, thus promoting vasculogenesis and angiogenesis [85,87,88]. AP-1 has also been shown to be strongly activated by hypoxia in a series of different tumour types, such as colon cancer, glioblastoma and malignant melanoma [89]. Last but not least, a synergistic relationship has also been reported between AP-1 and NF- κ B in the activation of common target genes, such as IL-8, contributing to the malignant progression of pancreatic cancer [90].

Other transcription factors: ATF-4 (activating transcription factor 4) is activated and stabilised independently of HIF by anoxia rather than hypoxia [91]; Egr-1 (early growth response 1), a transcription factor known for modulating the expression of genes involved in synaptic plasticity, cell growth and cell survival, is also up-regulated by hypoxia independently of HIF and is actively involved in the pathogenesis of pulmonary thrombosis and vascular remodelling [92-94]; Ets-1 is induced by hypoxia in an HIF-regulated manner and plays a very important role in angiogenesis and cancer invasion [95].

Other transcription factors responding to hypoxia via transcriptome regulation include RTEF-1 (related transcriptional enhancer factor-1), GATA-2, the STAT family, Mash-2 (mammalian achaete-scute homologous protein-2) and GADD153 (growth arrest and DNA damage-153) [94].

Chromatin modifications in hypoxia

The cellular response to hypoxia recruits special transcription factors to the promoters or enhancers of their target genes, where they bind to specific DNA sequences and ultimately alter the gene expression profile of the cell. Considering that DNA is packaged into dense structures of chromatin called nucleosomes, accessibility of the transcription factors to their target areas may not always be an easy task. Adjustment of the chromatin structure to accommodate for the accessibility of transcriptional activators or repressors seems to be an essential mechanism for the appropriate gene expression. Chromatin is distributed into euchromatic and heterochromatic regions corresponding to transcriptionally active or repressed regions, respectively, depending on how tightly the structure is packed. Heterochromatin is the higher-order packed chromatin, generally inaccessible to transcription factors. The nucleosome is the basic repeat unit of chromatin and consists of an octamer that has two molecules of each of the four histones H2A, H2B, H3, H4 and 146bp of DNA wrapped twice around it; the globular domains of the histones are enclosed in the nucleosome, whereas their N-terminal tails protrude from it and facilitate histone modifications [96]. Linker histones (such as H1 and H5) are used to connect the nucleosomes together and to be able to fold the DNA into more compact structures, such as the heterochromatin regions [97]. Overall, chromatin structure can be altered so as to allow for alterations in the regulation of transcription mainly via three basic mechanisms:

Post-translational modifications of the histones via their flexible tails: These refer to the covalent modifications of histones, such as phosphorylation, methylation, acetylation, ubiquitination, SUMOylation and poly(ADP-ribosyl)ation, that either alter the charge and structure of chromatin, or provide accessible DNA binding sites that are recognised by specific structural domains (eg. bromo- and chloro-domains) [98].

ATP-dependent nucleosome remodelling: This is essentially chromatin remodelling at the nucleosome level, via the utilisation of ATP as a source of energy by complexes such as the SWI/SNF, the ISWI and the MI-2/CHD [99]. These remodelling complexes create a shift of the DNA segments in the histone-DNA interactions and facilitate the disruption of the nucleosome structure [100].

Histone replacement modifications: This refers to the incorporation into nucleosomes of chromosome variants (mainly H2A and H3 variants) that are assembled and synthesized independently of DNA replication and which have profound epigenetic consequences in the transcriptional profile of the cell [101].

Under hypoxic conditions, the histone acetyltransferase (HAT) complex p300/CBP interacts with HIF and the acetylate histones in target genes, via inhibition of FIH-1, leading to an increase in localized histone acetylation and transcriptional activation of the target genes [17,30]. Other observations, however, have shown that the HIF-p300/CBP interaction is responsible for the altered expression of only 30-50% of the target genes, further demonstrating that not all of the hypoxia-responsive genes are transactivated by histone acetylation [102]. Histone deacetylases (HDACs) on the other hand, whilst

generally known for facilitating repression of transcription, in hypoxia can cooperate with HIF and regulate transcription either positively or negatively [14]. Accordingly, histone deacetylase inhibitors, which usually promote transcriptional activation, in the hypoxic environment turn into transcriptional repressors of HIF targets and promote HIF-regulated angiogenesis [103-105]. Changes in histone methylation are not an exception to the chromatin modification repertoire in the hypoxic environment. In a recent study it was observed that following exposure to hypoxia, the responsive promoters of the VEGF and Egr-1 genes displayed an increase of histone H3K4 trimethylation (usually associated with transcriptional activation) and a decrease in histone H3K27 trimethylation (generally associated with transcriptional repression), demonstrating a bivalent chromatin behaviour under hypoxic influence [15]. This may further suggest important epigenetic changes caused by modifications in the neighbouring *cis*- and *trans*-acting elements of the histones or even by the recruitment of different co-activators and co-repressors that are yet to be determined. In the context of ATP-dependent chromatin remodelling, the SWI/SNF complex also seems to contribute to the activation of HIF target genes in the hypoxic response. More specifically, the catalytic subunits of SWI/SNF enhance HIF-mediated activation of two highly homologous ATPases, an erythropoietin (Epo)-driven promoter and a synthetic 6XHRE-driven reporter; with the recruitment of HIF-1, these ATPases form two distinct remodelling complexes and target the promoters of two different genes, Epo and VEGF [106,107]. Even though both enzymes are recruited, along with HIF-1, to the promoters of these genes in a hypoxia-responsive manner and they induce transcriptional activation of Epo, they do not seem to be essential for the transactivation of VEGF [107]. This further demonstrates that chromatin remodelling due to the hypoxic response may be sufficient for the transcriptional activation of one gene but not for the successful transactivation of another. Further analysis of the cellular pathways involved in chromatin remodelling due to hypoxia will help to define the mechanisms that recruit specific transcription factors and their co-factors to specific hypoxia-responsive target genes.

The Role of Hypoxia in Cancer Development

Cancer development is a multistep process that requires the acquisition of a certain number of genetic or epigenetic mutations, resulting from genetic instability in the dividing cell. This instability is usually caused by defects in the mechanisms that control the cell cycle and normal cell differentiation and usually include: cell cycle arrest, resistance to DNA repair and to growth inhibition, evasion of immune surveillance and apoptosis, unlimited replication potential, angiogenesis, invasion and metastasis [108]. In addition, the carcinogenic microenvironment employs unique strategies so as to be able to overcome the suppressive effects of the normal surroundings and to facilitate disease progression, whilst also becoming resistant to conventional cancer therapies [109]. Hypoxia plays a very important role in both triggering the malignant transformation process and promoting adaptive cell responses within the tumor microenvironment. Most solid tumors contain regions with extremely low oxygen concentrations, a necessary prerequisite for cancer progression. Hypoxia in the tumor microenvironment usually occurs as a result of rapid cell proliferation, which distances cells from blood vessels, often occurring at a distance of 100-200µm from them. The newly formed vessels are usually aberrant and cannot meet the high nutritional demands of the proliferating cancer cells, or may become compressed or obstructed by tumor growth [110]. This forces the tumor cells to develop adoptive responses that will allow them to survive and

proliferate under hypoxic conditions. A central player in these adoptive responses is the HIF-pathway.

The HIF-pathway in cancer development

As mentioned in the previous section of this review, HIF-1 mediates the cellular adaptive response to hypoxia by increasing dramatically in transcriptional activity and inducing the transactivation of at least 100 hypoxia-responsive target genes. Many studies have demonstrated that most of the genetic alterations in tumor cells are synergistically interconnected with HIF-1 transcriptional activity, further highlighting the critical role of HIF-1 in cancer development. Indeed, HIF-1 is prevalent in many types of solid tumours and high expression usually correlates with poor clinical outcomes [111,112]. HIF-1 α expression is usually an aggressive marker for prostate, oropharyngeal, oesophageal, head and neck, lung, ovarian and breast cancer, whereas HIF-2 α is more frequently up-regulated in hepatic cancer, gliomas and neuroblastomas [113-116]. Hypoxia may additionally induce the expression of various growth factors that synergise with HIF-1 and promote cellular proliferation. Examples include EGF (epidermal growth factor), insulin, IGF-1 (insulin-like growth factor-1), IGF-2 and PDGF (platelet-derived growth factor) [117]. At the same time, in order to promote cancer cell proliferation and survival, certain growth-inhibitory events may also be mediated by the hypoxia-responsive genes; for example, mutations in the PTEN gene, a marked tumor suppressor, have been shown to promote tumor growth in glioblastoma cell lines in an HIF-1-coordinated manner [118]. On the other hand, certain animal model studies have shown that inhibition of HIF-1 decreases tumor growth, thus further supporting HIF-1-mediated cancer progression [119,120], while others have linked HIF-1 expression to higher apoptotic rates and increased patient mortality [121]. The latter, as mentioned earlier, is attributed to mechanisms such as the functional cooperation between HIF-1 and p53, which causes the activation of pro-apoptotic genes such as Bnip3L and hence promote hypoxia-induced apoptosis [60,122]. Overall, the finding that genetic and epigenetic alterations leading to oncogene activation and loss of tumor suppressor genes are correlated with increased HIF-1 activity, suggests that HIF over-expression represents a final common pathway in tumor pathogenesis, even if HIF activation is caused by conditions mimicking the effect of hypoxia [123]. To summarise, many studies have demonstrated the role of HIF-regulated gene expression in cancer development, including proliferation (MYC), angiogenesis (VEGF, PDGF), apoptosis (BNIP3), metabolism (PDK1, LDHA), DNA damage response (GADD45A), microRNAs (MIR210), extracellular matrix remodelling (LOX, MMP1), cell migration and invasion (CXCR4, SDF1) [124-127].

Hypoxia on cancer stem cells

Hypoxia seems to play an important role in maintaining the tumor stem cell (TSC) niche in the development of invasive cancer phenotypes, as shown from studies with cell cultures derived from pediatric patients. More specifically, it has been demonstrated through studies on pediatric neuroblastoma and rhabdomyosarcoma cell lines that the tumor stem cells, similar to normal stem cells, may share the unique property of migrating to the area of hypoxia and necrosis, where their highly tumorigenic fraction may be maintained and expanded [128]. In other studies with cancer stem cells, it was observed that hypoxia promotes the self-renewal capability of both the stem and the non-stem cell population; interestingly, the stem-like phenotype is induced more profoundly in the non-stem cell population and is accompanied by the upregulation of important stem cell factors, such as Oct4, c-Myc

and Nanog. This effect of hypoxia on cancer stem cells seems to be primarily mediated by HIF-2 α , since its loss seems to cause a decrease in the stem cell proliferation capacity and self-renewal [113,129]. All of these findings suggest that, in a restricted oxygen environment, the TSC fraction is enhanced via the acquisition of the stem cell state but at the same time it is critically dependent on the HIFs for survival, self-renewal and proliferation.

Metabolism in hypoxic cells

Under physiological normoxic conditions (~ 5% O₂), cells convert glucose into energy (in the form of ATP) via the consecutive processes of glycolysis and oxidative respiration. The glycolytic enzyme pyruvate kinase (PK) catalyses the final step of glycolysis, i.e. the production of pyruvate from phosphoenol pyruvate (PKP), which is then shuffled from the cytoplasm into the mitochondria for oxidative respiration to take place (Figure 3). In highly proliferating cells, such as cancer cells and in anaerobic conditions, pyruvate is converted to lactate and is actively excreted from the cells [130]. As a matter of fact, many

cancer cells seem to prefer the much less efficient glucose fermentation and lactate production, instead of oxidative respiration and pyruvate production, as a means of meeting their energy demands, even in the presence of oxygen, a condition described as the Warburg effect [131,132]. Therefore, in the absence of oxygen, additional and highly inter-connected to the HIF-1 pathway in mediating tumorigenesis is the altered intrinsic glucose metabolism of the cell, i.e. the adaptive shift from oxidative to glycolytic metabolism [133,134]. In this procedure, carbonic anhydrases and in particular CA9, seem to relieve hypoxic tumor cells from intracellular acidosis that has been caused by the increased glycolysis and lactate production, hence contributing to their survival [135]. In particular, HIF-1 seems to mediate this metabolic switch via inhibition of pyruvate dehydrogenase, which in turn down-regulates cell-cycle activity and mitochondrial oxygen consumption [136,137]. More recently, evidence has come forward demonstrating that inhibition of PK, apart from down-regulating pyruvate production, also mediates redox balance in cells by activating the pentose phosphate pathway (Figure 3); this activation consequently

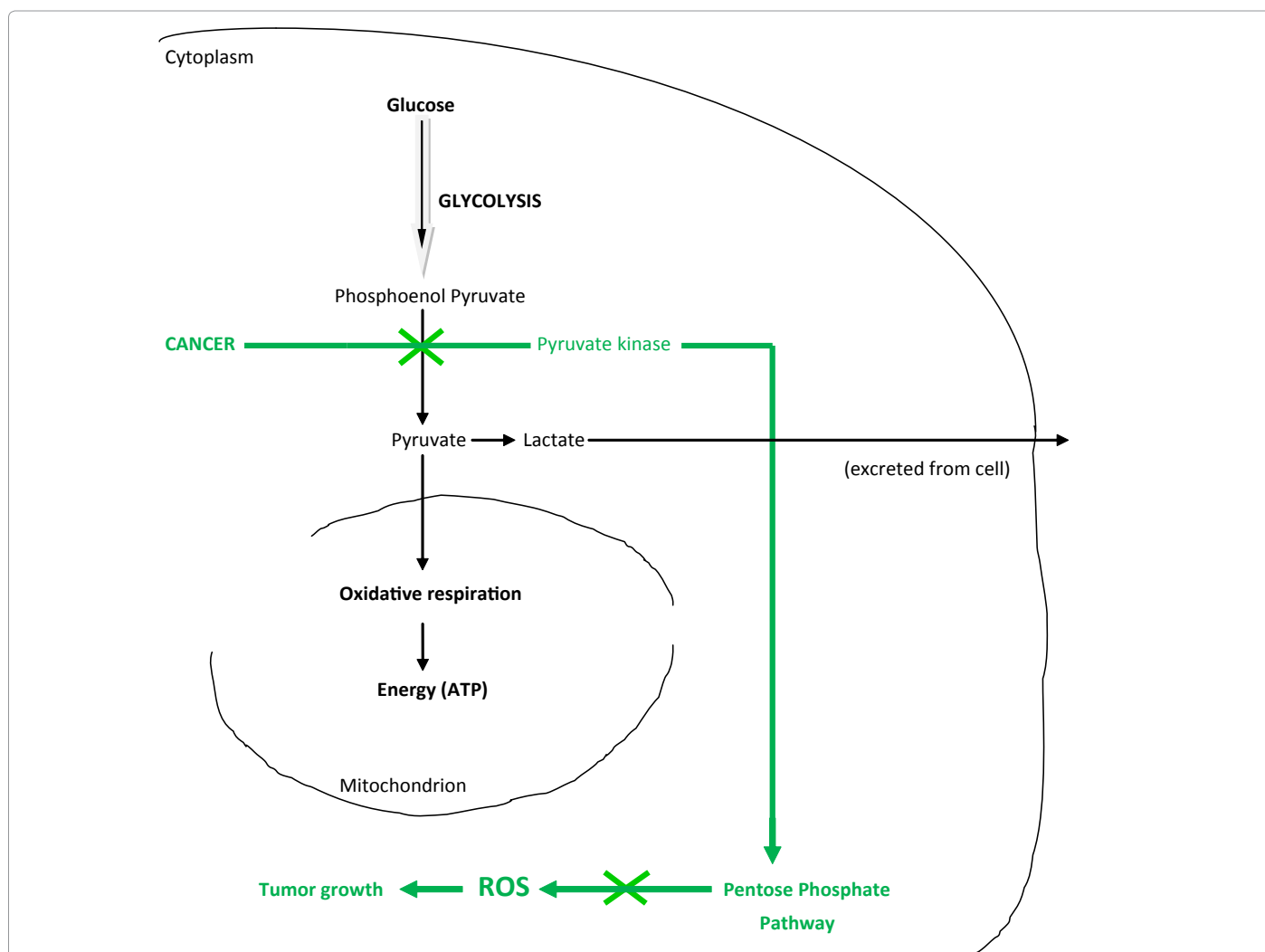


Figure 3: The cellular metabolic response to hypoxia. Under normal oxygen levels, glucose is converted into pyruvate through the process of glycolysis and then enters the mitochondrion and generates energy (in the form of ATP) through the process of oxidative respiration. Under hypoxic conditions, and in highly proliferating cells, however, pyruvate is converted into lactate which is actively secreted from the cell. In cancer, the reduced activity of the catalytic enzyme pyruvate kinase induces the pentose phosphate pathway which in turn limits ROS accumulation, diminishes oxidative damage and so promotes tumour growth. Adapted by Grüning and Ralser (2011).

limits the accumulation of mitochondrial reactive oxygen species (ROS) and oxidative stress, thus saving cancer cells from death due to oxidative damage and facilitating tumor growth [138]. In addition, it was also recently revealed that in human lung cancer cells, the activation of PK splice variant M2 (or PKM2) is inhibited via the oxidation of PKM2 residue Cys³⁵⁸ by acute increases in the production of intracellular ROS and diverts the glucose flux into the pentose phosphate pathway [19]. As a consequence, sufficient reducing potential is generated for the detoxification of ROS. However, when endogenous PKM2 was replaced by a PKM2 oxidation-resistant mutant that had Cys³⁵⁸ replaced by Ser³⁵⁸, the cells exhibited increased sensitivity to oxidative stress and impaired tumor formation in a xenograft model, further highlighting the therapeutic potential of this metabolic reconfiguration [19]. More importantly, this latest finding adds new understanding to the Warburg effect (i.e. that cancer cells prefer the inefficient glycolysis even in the presence of oxygen), as it appears that the maintenance of the redox balance can be more limiting to tumor growth than insufficient energy levels. Interestingly, another recent report has demonstrated that PKM2 acts as a co-activator of HIF-1, interacting directly with the HIF-1 α subunit and greatly enhancing its transcriptional activity [139]. In particular, it was shown that the PHD3-mediated phosphorylation of PKM2 promotes the transactivation of HIF-1 target genes by enhancing HIF-1 α DNA binding and p300 recruitment to hypoxia-responsive elements. Even more specifically, it was shown that the PKM2-HIF-1 α interaction is mediated by exon 10 of PKM2 (a region not present in the PKM1 variant), which contains the specific sequence motif responsible for the hydroxylation of HIF-1 α by PHD2 and another two hydroxylated proline residues that appear mutated when the PKM2-HIF-1 α interaction is lost [139,140]. In addition, a link was established between PHD3, PKM2 and HIF-1-mediated glycolysis from the observation that depletion of either PHD3 or PKM2 downregulates the transcription of HIF-1 metabolic target genes and reverses the Warburg effect [139,141]. Therefore, PKM2 expression in tumors appears to participate in a positive feedback loop that promotes alteration of gene expression via HIF-1 transactivation and reprograms glucose metabolism in cancer cells. This metabolic response to hypoxia is also accompanied by an increased expression of the genes coding for glycolytic enzymes and glucose transporters, which permits tumor cells to maintain a sufficient level of ATP energy for survival and proliferation [142,143]. Furthermore, HIF-1 α induces over-expression of many glycolytic protein isoforms, such as glucose transporters GLUT-1 and GLUT-2 which, under hypoxic conditions, suppress apoptosis via inhibition of the stress-activated protein kinase pathway and promote cell migration [144,145]. In particular, it has been reported that, via the induction of GLUT-1, hypoxia protects rhabdomyosarcoma and Ewing sarcoma cells from apoptosis due to glucose deprivation in an HIF-1 α -dependent manner [146]. Glycolysis may also be increased via repression of c-Myc, as shown by studies with VHL-deficient renal cell carcinoma [147], with the functional collaborations of HIF-1 α with both c-Myc and mTOR having well-established roles in cancer [78,148]. In relation to pediatric cancer, experimental data from Wilms' tumors have shown over-expression of CA9 and HIF-1 α , with concomitant high expression of VEGF and GLUT-1, further highlighting the importance of the functional relationship between the four hypoxia markers in cancer development [149].

Evasion of immune surveillance

Tumor cells commonly escape elimination by innate and adaptive immune responses using strategies such as the active suppression

of effector immune cells. Under hypoxic conditions, through the activation of HIF-1 and HIF-2, tumor cells produce chemoattractants and soluble factors (eg. CSFI, VEGF and TGF- β) that stimulate and recruit monocytes and macrophages to tumor sites [150]. Following recruitment, macrophages mature into tumor-associated macrophages (TAMs) and hypoxia induces the secretion of potent immunosuppressive factors, such as prostaglandin E₂ and IL-10; these inhibit the TAMs immunosuppressive effect by repressing their ability to present antigens to T-cells and to phagocytose dead cells [114,151,152]. HIF-1 α in particular, inhibits T-cells from undergoing activation-induced cell death and thus protects tumor cells from immune attack in the hypoxic environment [153,154]. A recent study has linked the hypoxia-induced transactivation of HIF-1 α with an increase in the expression of metalloproteinase ADAM10 and a decrease in the surface MHC class I chain-related (MIC) levels, further highlighting the resistance of tumor cells to innate immune-mediated lysis [155]. Expression of HIF-2 α , on the other hand, is associated with an unfavourable prognosis when found in the TAMs of breast and cervical cancers, whereas HIF-2 α deletion from the myeloid cells in animal models of hepatocellular carcinoma and colitis-associated colon carcinoma correlates with a decreased recruitment of TAMs to tumor sites and a reduced tumor grade [156-158].

Evasion of apoptosis

To date, the exact mechanisms of apoptosis regulation under hypoxic conditions are not fully elucidated. Hypoxia is however known to induce apoptosis in both normal and cancer cells, with the latter developing mechanisms that allow them to increase their resistance and escape HIF-1-mediated apoptosis. More specifically, hypoxia has been found to increase the transcriptional activity of anti-apoptotic genes IAP-2, Bcl-2 and Bcl-XL, to activate the PI-3k/Akt survival pathway, a major regulator of cell survival and proliferation and to increase cell resistance to apoptosis via over-expression of the p53 negative regulator MDM2 [10,18,159]. Experimental data have also shown that hypoxia-induced apoptosis can be mediated by tumor necrosis factor-related apoptosis-inducing ligand (TRAIL), a potent apoptosis inducer that specifically limits tumor growth without damaging normal cells and tissues *in vivo* [159]. In particular, hypoxia dramatically inhibits TRAIL-induced apoptosis by blocking Bax translocation from the cytosol to the mitochondria, hence blocking a pivotal signaling molecule for the effective induction of apoptosis [159]. Last but not least, human cancer cells may acquire the property of immortalization through the maintenance of telomere lengths, which is dependent on expression of the hTERT and hTR telomerase genes [160]. Indeed, several studies have demonstrated that cells with increased telomerase activity can divide beyond the Hayflick limit (the number of times a normal cell population can divide before it stops) without entering senescence or apoptosis and this leads to unlimited proliferative capacity, i.e. cellular immortalization [161-163]. It has also been shown that telomerase can synergize with certain oncogenes and convert normal human epithelial cells and fibroblasts into cancer cells [164] and hypoxia may contribute to the immortality of cancer cells by increasing telomerase activity via transcription in the promoters of both gene variants, with active involvement of HIF-1 α [165,166].

Genomic instability and hypoxia

Several reports have linked hypoxia to increased genomic instability, which may also contribute into cancer formation. More specifically, it has been reported that hypoxia is responsible for increasing mutagenesis via down-regulation of the DNA mismatch

repair (MMR) system, which normally maintains genomic integrity by correcting replication errors [167,168]. In other words, the genomic destabilization seen in tumor cells is responsible for the cellular changes that confer progressive transformation on cancer cells and is further promoted by the hypoxic stress in the tumor microenvironment [169]. According to recent experimental evidence, hypoxia down regulates the expression of key genes within the MMR and homologous recombination (HR) pathways, such as MLH1 and MSH2, leading to increased mutagenesis, while suppressing the transcription of many critical HR-mediators, such as BRCA1, BRCA2 and RAD1, leading to down-regulation of recombinatorial repair and hence genomic instability [170,171]. In addition to this, a link has been made between genetic instability and HIF-1 α , with HIF-1 α inhibiting the expression of genes responsible for recognizing and repairing DNA base mismatches (such as MSH2, MSH6 and NBS1), despite notions from previous reports that repression of MMR and HR is HIF-independent [172,173]. On the other hand, several reports support the notion that “physiological” normoxia (O₂ levels about 5%, similar to natural niches), is protecting cells from falling into “genomic instability”, as compared to the atmospheric oxygen level (about 20%), also enhancing stem cell clonal recovery and reducing chromosomal abnormalities [174,175]. Others have also shown that neural stem cells (NSCs) exist within a “physiological” hypoxia (1-5% O₂) in both embryonic and adult brains and that hypoxia can promote the growth and survival of NSCs *in vitro* (Figure 1) [176]. In addition, *in vivo* studies have shown that hypoxia can positively influence the production and differentiation of NSCs, as well as that of other types of stem cell [176-179]. Furthermore, there is enough evidence to suggest that hypoxia can initiate and promote the process of malignant transformation when a low percentage of cells overcome and escape cellular senescence [180]. As hypoxia causes the progressive elevation in mitochondrial ROS production (chronic ROS), this leads to oxidative DNA damage due to the continuously accumulating ROS; HIF-2 α expression represses the DNA repair mechanisms in the hypoxic cells, enabling them to survive with sustained levels of elevated ROS along with the mutations that drive the malignant transformation [181]. In addition, it has recently been speculated that optimal “physiological” ROS levels confer minimal DNA damage due to adequate DNA repair, whereas both reduced and excessive ROS levels lead to genomic instability due to deficient DNA repair and oxidative DNA damage, respectively [182].

Angiogenesis

Hypoxia can promote angiogenesis via the activation of a number of angiogenic factors, such as VEGF, VEGF receptor-1, IL-8, platelet-derived growth factor (PDGF), adrenomedullin, angiopoietin-2, cyclooxygenase-2, endothelin-1 and -2, fibroblast growth factor-3, hepatocyte growth factor, histone deacetylase, monocyte chemoattractant protein-1, nitric oxide synthase, osteopontin, placental growth factor, Tie-2 (an angiopoietin receptor) and transforming growth factors [110]. Since VEGF is a major component of the blood vessel formation procedure in hypoxic tissues, it is only logical to accept that it also plays a major role in the pathological angiogenesis of tumor development. It has long been reported that the hypoxia-mediated HIF-1 α activation leads to VEGF up-regulation, which in turn triggers angiogenesis while at the same time suppressing angiogenic inhibitors, such as thrombospondin 1 [183,184]. Others support the notion that hypoxia is not responsible for the initiation of angiogenesis, that the initiation takes place via non-hypoxia-mediated mechanisms such as the activation of certain oncogenes and that hypoxia only contributes in accelerating the process [10]. Experimental data from glioblastoma mouse models show that

HIF-1 α , the direct effector of hypoxia, promotes neovascularization in glioblastomas via activation of VEGF; notably, when VEGF activity is impaired by ablation of either HIF-1 α or matrix metalloproteinase-9 (MMP-9) and angiogenesis is disabled, tumor cells invade deeper into the brain in the perivascular compartment, thus being characterized by a more invasive phenotype [185]. Up to date, no studies have been conducted exclusively on pediatric cancers so only a few referrals exist on the role of hypoxia-promoted angiogenesis in childhood tumors or tumors found in both adults and children. Nonetheless, significantly elevated levels of VEGF secretion have been found in hypoxic tumor stem cells from malignant gliomas, including a pediatric glioblastoma xenograft [186]. Recently it was reported that in the highly vascularized human rhabdomyosarcoma tumors, in addition to VEGF, hypoxia induces the up-regulation of IL-8 both at the mRNA and protein level, thus highlighting its implication in promoting angiogenesis [187]. Last but not least, another group demonstrated that HIF-1 α activity is a necessary prerequisite for hypoxia microRNA-16 (mir-16) down-regulation, which in turn induces VEGF expression in anaplastic lymphoma kinase (ALK)-positive anaplastic large-cell lymphomas, thus strongly suggesting the importance of mir-16 in regulating VEGF expression and angiogenesis [188].

Invasion and metastasis

As already mentioned in previous sections of this review, hypoxia induces the activation of a number of genes responsible for increased aggressiveness, invasion and metastasis of tumors, which subsequently leads to poor patient prognosis. Semenza [123,189] has already summarized the HIF-1 target genes, whose products actively contribute to cancer invasion and metastasis and regrouped the immunohistochemical studies in which increased levels of HIF-1 α (or HIF-2 α) protein in diagnostic tumor biopsies were associated with a decrease in patient survival. In search of data linking HIF expression to childhood cancers, we have found that HIF-1 α protein accumulation has been associated with poor patient survival in oligodendroglioma, whereas HIF-2 α over-expression is linked to increased patient mortality in childhood neuroblastoma and astrocytoma [124,190]. In a study conducted on both children and adult patients with osteosarcoma, HIF-1 α expression significantly correlated with surgical stage, percentage of dead cells and microvessel density (MVD), as well as with shorter overall survival (OS) and disease-free survival (DFS) [191]. More recently, still in the context of pediatric tumors, the effects of hypoxia on primary Ewing’s sarcoma family tumor (ESFT) cells were studied *in vitro* and were found to enhance the cells’ malignant properties by stimulating the invasiveness and soft-agar colony formation; as expected, the Ewing’s sarcoma oncoprotein EWS-FLI1 was up-regulated by hypoxia in a HIF-1 α dependent manner [192]. Generally speaking, the recent literature supports the notion that the hypoxia-induced tumor aggressiveness is associated with the expansion of the cancer stem cell marker CD133+ in pancreatic cancer cells in a predominantly HIF-1 α -dependent manner and that this might also play a key role during the transition from *in situ* to invasive breast cancer [193,194]. In explaining how hypoxia favors metastasis, it has been described that, through HIF activation, hypoxia facilitates the disruption of tissue integrity through the repression of the transmembrane molecule E-cadherin, therefore promoting tumor invasion and metastasis [195]. In the same study, it was also concluded that hypoxia enhances proteolytic activity at the invasive front, through upregulation of urokinase-type plasminogen activator receptor (uPAR) and alters the interactions between integrins and components of the extracellular matrix, thereby enabling cellular invasion through the basement membrane and the underlying stroma

[195]. It is believed that epithelial-mesenchymal transition (EMT), referring to the conversion of well-polarized, adhesive epithelial cells to non polarized mesenchymal cells, may be one of the initial steps involved in metastasis; both hypoxia and HIF-1 α overexpression have been shown to promote EMT [10]. In addition, it has been observed that neuroblastoma cells can adjust to a hypoxic environment by losing their differential gene expression patterns and by developing stem cell-like phenotypes [196]. Seeing that there is a correlation in neuroblastoma between low stage of differentiation and high (aggressive) clinical stage, it can easily be assumed that hypoxia-induced dedifferentiation of neuroblastoma cells in hypoxic tumor regions contribute to the tumor heterogeneity and increased malignancy [196]. Finally, hypoxia-induced hepatocyte growth factor (HGF)-MET is known to increase cell motility, promoting cell migration towards the blood or lymphatic microcirculation, while hypoxia-induced VEGF promotes angiogenesis and lymphangiogenesis in the primary tumor and induces changes in vascular integrity and permeability, providing the necessary routes for dissemination [195,197].

Drug resistance

As mentioned at the beginning of this section, tumor hypoxia, acting through direct and indirect mechanisms, has long been recognized as a major factor involved in the resistance to radiotherapy and many chemotherapeutic agents and is thus linked to a poorer clinical outcome [198]. Radiosensitivity rapidly declines when tumor pO₂ is <25–30 mmHg and it has been found that radiation therapy is about two to three times less effective in destroying hypoxic cells than normoxic cells [199,200]. Oxygen increases DNA damage either through the formation of oxygen-derived free hydroxyl radicals, after the interaction of radiation with intracellular water, or by enhancing the stabilization (“fixation”) of the highly reactive hydroxyl radicals that cause DNA damage. Since oxygen contributes in reducing the ability of the tumor cells to repair their damaged DNA after radiation therapy, it is believed that hypoxia can protect some malignant cells from radiation damage, subsequently causing local disease recurrence. Interestingly, this may occur after even a single fraction of radiation treatment but it may also explain to a certain extent the radioresistance following fractionated therapy. Taking into consideration that between the radiotherapy sessions the patterns of re-oxygenation of tumor cells are variable, it is possible that some cells remain hypoxic and are thus still protected. In addition, hypoxia may promote radioresistance indirectly, by inducing proteomic and genomic changes. Hypoxic stress can lead to the selection of a number of tumor cells with diminished apoptotic potential and influence the cell cycle, slowing proliferation and increasing the number of cells in the G₀ phase, thus reducing tumor radiosensitivity. It also leads to the increased transcriptional production of repair enzymes or resistance-related proteins, such as heat shock proteins, allowing cells to survive otherwise lethal conditions [200]. Radiotherapy is an important component of the treatment of many pediatric tumors, but very few studies refer to the role of hypoxia in radioresistance in children. Experimental data, however, have shown that both non-interrupted and cycling hypoxia pre-treatment significantly increases cell resistance to ionizing radiation compared with normoxic controls in U87 glioma xenografts and that cycling hypoxia treatment, through increased HIF-1 synthesis and stabilization, has a greater effect in increasing radiation resistance compared with non-interrupted hypoxia treatment [201]. Other groups have documented that the antitumor activity of ionizing radiation in U87 glioma xenografts is enhanced by improving intra-tumoral oxygenation [202]. On the other hand, acute hypoxia, resulting from

poor and fluctuating blood flow in irregular newly formed tumor blood vessels, as well as chronic hypoxia, which is due to increased diffusion distances, can result in the diminished and uneven distribution of chemotherapeutic agents, subsequently affecting their therapeutic efficacy [198]. Hypoxia can also directly limit the chemotherapy induced DNA damage by reducing the generation of free radicals and this has been proposed as the mechanism of chemoresistance for agents such as bleomycine and anthracyclines. In particular, hypoxia induces the elevation of glutathione levels and DNA-repair enzymes seem to favor resistance to alkylating agents, bleomycin and platinum compounds [200]. Others have shown that hypoxia is able to induce 4-HPR (the chemopreventive retinoid *N*-(4 hydroxyphenyl) retinamide) resistance in Molt-4 cells (ALL cell line) and the potential mechanism may be the inhibition of 4HPR-induced regulation of mitochondrial pathway-related proteins associated in signaling apoptosis [203]. In addition, hypoxia mediates cycle cell modification and especially G₁/S-phase arrest can be incriminated for the resistance to vinca alkaloids and methotrexate [204]. Increased glycolysis with extracellular acidosis, a common feature in hypoxic tumor regions, may also favor chemoresistance by affecting the transport of drugs across the cell membrane, the intracellular drug accumulation (e.g. anthracyclines, bleomycin) and drug activity (e.g. vinblastine, doxorubicin, bleomycin). Some chemotherapeutic agents, such as cyclophosphamide, carboplatin and doxorubicin have been shown to be oxygen dependent under both *in vivo* and *in vitro* conditions [200]. In recent years, the contribution of HIF-1 to drug resistance has been observed in a wide spectrum of neoplastic cells [20]. One of the first reported molecular mechanisms explaining this contribution was that HIF-1 α is able to activate the multidrug resistance 1 (MDR1) gene in response to hypoxia, coding for a membrane glycoprotein and finally leading to the decrease of intracellular concentration in a range of chemotherapeutic drugs, such as vinca alkaloids, anthracyclines and paclitaxel [205]. HIF-1- mediated changes in drug efflux have been shown to promote chemoresistance in many tumor cell lines, including glioblastoma cell resistance to adriamycin [205]. As mentioned earlier, HIF-1 α is also linked to defective apoptosis and/or changes in cell cycle regulation, a phenomenon initially attributed to the HIF-1 α anti-apoptotic target genes, but recent data have proposed additional mechanisms such as the suppression of p53 apoptosis by HIFs [206]. Overall, apoptosis inhibition is highly related to drug resistance in many adult tumor studies, but again little is known about the importance of hypoxia in pediatric tumors. However, a group have reported that hypoxia, in an HIF-1 α -dependent manner, promotes resistance to apoptosis by etoposide and vincristine in neuroblastoma cells derived from pediatric patients [207]. As for the changes in cell cycle control promoting chemoresistance, more *in vivo* data are needed, since the functional importance of HIF appears to be variable, depending on the cell-type and the context. HIF activation due to hypoxia may, however, lead to chemoresistance through gene mutations that lead to the inhibition of DNA damage, as well as through the suppression of mitochondrial activity, which is strongly connected to the activation of cellular death pathways [20].

Implication of hypoxia in childhood cancer

In contrast to the well-investigated impact of hypoxia and HIFs in adult malignancies, their role in pediatric tumors has remained largely unaddressed. A great portion of our knowledge comes from tumors affecting both adults and children but the studies referring to cancer types that occur mostly among pediatric patients are scarce. We sought to collect the available data regarding the implication of hypoxia and

HIF activation in childhood cancer and, from our point of view, its clinical significance is becoming increasingly apparent. (Available data summarized in Table 1). First of all, hypoxia is a significant regulator at the level of the TSC niche. Researchers have found that a highly tumorigenic fraction of neuroblastoma and rhabdomyosarcoma cell lines is localized in the hypoxic zones *in vivo* and that this fraction is further increased by hypoxia [128]. Others report elevated levels of VEGF secretion, further induced by hypoxia, by TSC from malignant gliomas, including a pediatric GBM xenograft, while conditioned medium from the TSC increases endothelial cell migration *in vitro* [186]. Moreover, several studies highlight the importance of hypoxia as an adverse feature in almost every step of the cancerous procedure in pediatric tumours, mainly suggested by the presence of hypoxia-related markers/surrogate markers, such as HIF-1 α , VEGF, the facilitative glucose transporter Glut-1 and carbonic anhydrase IX (CA IX). In relation to cellular adaptations, hypoxia has been shown to induce glycolytic activity in hepatomas. Gwak et al report an HIF-1 α -dependent induction of hexokinase II expression and others an almost 3-fold increase in hexokinase II promoter activation [208,209]. Experimental data from Wilms' tumours has shown over-expression of CA9 and HIF-1 α , with concomitant high expression of VEGF and GLUT-1 [149], whereas GLUT-1 and aldolase induction are also reported to take place in an HIF-1 α -dependent manner, in rhabdomyosarcoma and Ewing sarcoma cells [146]. Finally, the expression of lactate

dehydrogenase 5 (LDH5), the major LDH isoenzyme sustaining the anaerobic transformation of glycolysis, is highly upregulated in B-cell non-Hodgkin lymphomas, in direct relation to the expression of HIFs [210]. With angiogenesis being regarded a very important step in tumor development, VEGF is the most studied hypoxia-related factor in childhood malignancies. Patients with osteosarcoma, Ewing's sarcoma, neuroblastoma, rhabdomyosarcoma and Wilms' tumor were found to have increased serum levels of VEGF and the highest levels were associated with metastatic disease [210]. Evidence of elevated VEGF levels is linked to hypoxia and/or HIF activation in Wilms' tumor [149,211], rhabdomyosarcoma, [187], anaplastic large-cell lymphoma [188], neuroblastoma [212,213], as well as in cell lines and in hypoxic tumor stem cells from malignant gliomas and a pediatric glioblastoma xenograft [186]. Evasion of apoptosis as directly related to hypoxia has been shown in rhabdomyosarcoma and Ewing sarcoma cell lines, where it was speculated that the HIF-1 α -mediated increase in glucose uptake plays an important role in conferring apoptosis resistance and indirectly in hepatomas, where inhibition of hexokinase II (found to be upregulated by hypoxia) led to apoptotic cell death [146,208]. More extensive appear to be the pediatric data linking hypoxia to tumor aggressiveness, invasion, metastasis and, consequently, prognosis. Degradation of the extracellular matrix implicated in tumor invasion is achieved partly through the proteolytic activity of matrix metalloproteinases (MMP), found to be up-regulated in an HIF-1 α -

Tumorigenic implication	Cancer type	HIF mediation	Effect	Reference
TSC niche	Neuroblastoma		↑Tumorigenic fraction	Das et al. [128]
	Rhabdomyosarcoma			
	GBM xenograft		↑ Endothelial cell migration	Bao et al. [186]
Cellular adaptations	Hepatoma	HIF-1 α	↑Hexokinase II	Gwak et al. [208] Mathupala et al. [209]
	Wilms tumors	HIF-1 α	↑GLUT-1, CA9	Dungwa et al. [149]
	Rhabdomyosarcoma	HIF-1 α	↑ GLUT-1, aldolase	Kilic et al. [146]
	Ewings' sarcoma	HIF-1 α		
	B-cell non-Hodgkin lymphomas	HIF1 α , HIF2 α	↑ LDH5	Giatromanolaki et al. [210]
Angiogenesis	Wilms' tumor	HIF-1 α	↑ VEGF	Karth et al. [211] Dungwa et al. [149]
	Rhabdomyosarcoma	no	↑ IL-8	Wysoczynski et al. [187].
	Anaplastic large-cell lymphoma	HIF-1 α	↑ VEGF	Dejean et al. [188]
	Neuroblastoma		↑ VEGF	Rössler et al. [212] Jögi et al. [213]
	GBM xenograft TSC		↑ VEGF secretion	Bao et al. [186]
Apoptosis evasion	Rhabdomyosarcoma	HIF-1 α	↑ Glucose uptake	Kilic et al. [146]
	Ewings' sarcoma	HIF-1 α		
	Hepatoma	HIF-1 α	↑ Glucose uptake	Gwak et al. [208]
Invasion and metastasis	Glioma	HIF-1 α	↑Proteolytic activity of matrix metalloproteinases degradation of the extracellular matrix	Fujiwara et al. [214]
	Hepatoma			Miyoshi et al. [215]
	Glioma	HIF-1 α	↑ Cell migration	Zagzag et al. [216]
	Ewings' sarcoma	HIF-1 α	↑ Invasiveness and soft-agar colony formation	Aryee et al. [192]
	Neuroblastoma		Cell dedifferentiation, tumor heterogeneity , increased malignancy	Jogi et al. [196]
	Medulloblastoma	HIF-1 α	Activation of the Notch signaling pathway, ↑ stem cell viability and expansion	Pistollato et al. [217]

Table 1: Summary of pediatric data linking hypoxia to childhood malignancies.

dependent manner in gliomas and hepatomas [214,215]. In addition to this, in glioma cells, inhibition of HIF-1 α by geldanamycin has been found to reduce cell migration *in vitro*, thus hinting at a potential role for HIF-1 α in glioma cell invasion [216]. In osteosarcoma, HIF-1 α expression significantly correlates with surgical stage, percentage of dead cells and microvessel density (MVD), as well as with shorter overall survival (OS) and disease-free survival (DFS) [191]. In primary Ewing's sarcoma family tumor (ESFT) cells hypoxia has been found to enhance the cells' malignant properties by stimulating the invasiveness and soft-agar colony formation through an HIF-1 α -mediated manner [192]. In neuroblastoma cells, the hypoxia-induced de-differentiation of hypoxic tumor regions has been found to contribute to the tumor heterogeneity and increased malignancy [196]. In medulloblastoma cells, hypoxia, through HIF-1 α and by activation of the Notch signalling pathway (maintaining Notch1 in its active form) has been found to promote stem cell viability and expansion [217]. It has also been reported that HIF-1 α protein accumulation is associated with poor patient survival in oligodendroglioma, whereas HIF-2 α over-expression is linked to increased patient mortality in childhood neuroblastoma and astrocytoma [124,190,218]. Finally, hypoxia has been reported to contribute to chemoresistance and radioresistance in some pediatric malignancies. For example, hypoxia has been shown to protect rhabdomyosarcoma (A204 RMS) and Ewing's sarcoma (A673ES) cells against doxorubicin-, vincristin-, actinomycin D-induced apoptosis in a time- and dose-dependent manner [146]. In neuroblastoma cell lines (SH-EP1 and SH-SY5Y) short periods of hypoxia (1% O₂) of up to 16 hours appears to have no effect on drug-induced apoptosis to the clinically relevant drugs vincristine, etoposide and cisplatin, whereas prolonged hypoxia of 1 to 7 days results in the reduction of vincristine- and etoposide-induced apoptosis [207]. HIF-1-mediated chemoresistance to adriamycin has also been found in many tumor cell lines, including glioblastoma cells [205]. Certain experimental data have shown that both non-interrupted and intermittent hypoxia contribute to cell resistance to ionizing radiation in U87 glioma xenografts, while others have documented that the antitumor activity of ionizing radiation in U87 glioma xenografts is enhanced by improving intra-tumoral oxygenation [201,202].

Hypoxia Targets as New Cancer Chemotherapeutics

Hypoxic cells are genetically unstable, resistant to apoptosis, invasive and metastatic. These properties make them more resistant to ionizing radiation and chemotherapy, so the way we regard cancer diagnosis and treatment today is highly associated with approaches that target tissue hypoxia [219]. At the same time advances in hypoxia research are beginning to unravel the molecular mechanisms responsible for the hypoxic tumor microenvironment, so the signalling molecules of the hypoxic cascade are becoming potential targets for cancer therapy.

General hypoxia-based therapeutic strategies

The most logical strategy to employ in enhancing radio- and chemo-sensitivity is the administration of high pressure oxygen. At the same time, the development of hypoxia-based radio-sensitizers is proving very promising in targeting tumor cells in their hypoxic microenvironment.

Hyperbaric Oxygen Therapy (HBO): This is the administration of pure oxygen at a pressure higher than 1 atmosphere to the tumor sites; studies have shown that intermittent HBO therapy increases the radio-curability and life expectancy in many cancers, especially head

and neck cancer, but it also sensitizes chemotherapy by increasing tumor perfusion and cellular sensitivity, as seen in *in vitro* studies with doxorubicin and taxol [220-222].

Radio-sensitizers: These are agents that simulate the action of oxygen, thus compensating for the low oxygen concentration and the increase in radiation-induced damage. Despite the initial disappointment in the use of nitroimidazoles as active compounds, it was later shown that, in association with radiotherapy, nimorazole induces a higher cancer-related survival in head and neck carcinomas, whereas misonidazole increases 1-year survival by 8% in astrocytomas [223,224]. More recently, molecular research has focused on the development of bi-functional hypoxic cell radio-sensitizers, thus allowing for the simultaneous inhibition of certain tumor hypoxia responses, such as angiogenesis and metastasis. Many new agents, including p53-inhibiting agents, are currently being tested in clinical trials in the hope that they can be effectively used in the development of bi-functional radio-sensitizers for cancer therapy [225-229].

ARCON (Accelerated Radiotherapy with Carbogen and Nicotinamide): This is a method additional to radio-sensitizing, in which radiotherapy is administered in association with inhaling hyperoxic gas so as to decrease diffusion-limited hypoxia and nicotinamine so as to decrease perfusion-limited hypoxia [222]. Despite the lack of response in clinical studies with non-small cell lung cancer, ARCON has shown some promising results in xenograft models of breast cancer and preliminary studies of bladder cancer [230-232].

Hypoxic cytotoxins: With tirapazamine being the most widely studied compound of this group, hypoxic cytotoxins are bio-reductively activated in tumor cells and give rise to cytotoxic DNA breaks, thus potentiating the anti-tumor effects of radiation and chemotherapy [233,234]. Despite having no effect when administered together with paclitaxel and carboplatin, the combination of tirapazamine and cisplatin has been shown to increase response rate and overall survival in clinical trials of non-small cell lung cancer; in addition, the combination with cisplatin and radiation in locally advanced squamous cell carcinoma of the head and neck has proved far more effective in terms of survival rates than fluorouracil, cisplatin and radiation together [235-237].

Recombinant anaerobic bacteria: This is essentially the injection of non-pathogenic strains of bacteria, such as *Clostridium*, in the form of spores, in tumor areas. These spores only become activated and grow in the hypoxic environment, exerting either direct anti-tumor activity or carrying enzymes that can be manipulated for anti-tumor activity. The strain *C.oncolyticum*, in particular, has been genetically modified to express cytosine deaminase, an E.coli enzyme able to metabolise the non-toxic 5-fluorocytosine to the toxic anti-tumor 5-fluorouracil and shows potent activity in many animal studies [238,239].

Erythropoietin (Epo): Recombinant human Epo (rHuEpo) has shown great potential as a therapeutic tool in cancer patients, as many studies have shown that it may improve the radio- and chemo- tumor sensitivity by increasing oxygenation, as well as oxygen-sensitization of other chemotherapeutic drugs [240,241].

HIF-based therapeutic targets

Since HIF-1 is such an important regulator of the cellular response to hypoxia, two strategies really stand out when it comes to targeting hypoxia for therapeutic purposes:

Inhibition of the signalling pathways that regulate HIF-1 function

mTOR inhibitors: Rapamycin is well-known for its anti-proliferative effect in many human and animal cell lines, as well as for its strong inhibitory effects on tumor growth and angiogenesis [242-247]. Temsirolimus, or CCI-779 (Wyeth), an ester analogue of rapamycin, has been shown to inhibit HIF-1 α -mediated VEGF endothelial proliferation in a breast cancer line, as well as mTOR-dependent angiogenesis and tumor growth in rhabdomyosarcoma xenograft models under hypoxic conditions [248,249]. Everolimus, or RAD001 (Novartis), an orally available rapamycin analog, was found to inhibit cell proliferation in lymphoid and smooth muscle cells, whilst at the same time exhibiting immunosuppressive effects in human T-cell clones; hence it is now clinically used both as an immunosuppressant in autoimmune disorders and as a tumor suppressor drug in cancer treatment [250-252]. Deforolimus, or AP23573 (Ariad Pharmaceuticals), a phosphorous rapamycin analog, has shown strong anti-proliferative effects in tumor cell lines *in vitro* and mouse xenografts *in vivo* [253]. Current efforts are focusing on the development of selective mTOR inhibitors, i.e. ones that compete with ATP in the catalytic site of mTOR, in the hope that these will be more effective in blocking cell proliferation than rapamycin; these include: PP242, PP30, Torin1, Ku-0063794, WAY-600, WYE-687 and WYE-354 [254]. Finally, dual specificity inhibitors of both mTOR and PI3K signaling pathways are also being investigated for their potentiality as cancer therapeutics and include: GNE477, NVP-BEZ235, PI-103, XL765 and WJD008 [254].

EGFR inhibitors: Gefitinib (Iressa) and Erlotinib (Tarceva) are both small molecule inhibitors already used in the treatment of non-small cell lung cancer but they have also been found to inhibit VEGF expression in squamous cell carcinoma *in vitro* [255]. Cetuximab, or C225 (Erbix), a monoclonal antibody that was shown to inhibit HIF-1 α protein levels, has been approved for the treatment of metastatic colorectal carcinoma and squamous cell carcinoma of the head and neck [256]. Trastuzumab (herceptin), on the other hand, is a humanized monoclonal antibody that targets the human EGF receptor 2 (Her2) and prevents it from inducing activation of HIF-1 α and VEGF in breast cancer cells, hence promoting anti-angiogenesis [257-259].

VEGF inhibitors: Bevacizumab, an anti-VEGF neutralizing antibody currently in clinical use for cancer therapy, has shown strong anti-angiogenic activity *in vivo* and the ability to suppress the growth of xenografts derived from stem cell-like glioma cells [186].

Tyrosine kinase inhibitors: Imatinib mesylate, or Gleevec (Novartis), the small molecule inhibitor of the oncogenic fusion BCR-ABL used in the treatment of leukemias, has also been found to inhibit induction of HIF-1 α and VEGF expression in small cell lung cancer cell lines [260].

Microtubule disrupting agents: Being a natural estrogen metabolite, 2ME2 (2-methoxyestradiol) promotes microtubule disruption via inhibition of tubulin polymerisation and causes mitotic arrest [261]. In pre-clinical models 2ME2 has shown increased anti-tumor activity in association with decreased HIF-1 α protein levels and a newly formulated version, Panzem[™], already approved in the treatment of rheumatoid arthritis, is currently in phase II clinical trial for cancer patients [262,263].

Targeting the HIF-1 α -responsive genes and transcription factors

Topoisomerase-I inhibitors: Topotecan, the best characterized molecule of this group, is a potent inhibitor of HIF-1 α that causes DNA damage and cytotoxicity by reversibly binding and stabilising the Topoisomerase-1 enzyme on the DNA [264]. Whilst already approved for second line therapy of small cell lung cancer and ovarian cancer, topotecan has also been shown to inhibit tumor growth with a concomitant HIF-1 α protein level reduction in glioma xenograft models [222,265]. Furthermore, a recent study has demonstrated that topotecan inhibits VEGF-mediated angiogenic activity induced by hypoxia in human neuroblastoma cells [266].

PX-478: being one of the most potent HIF-1 α inhibitors, PX-478 has shown anti-tumor activity which positively correlates with HIF-1 α levels in both cell lines and large xenograft models [267]. PX-478 has completed Phase I clinical trial for advanced solid tumours and lymphomas, where it was associated with stable disease and dose-dependent inhibition of HIF-1 α [268].

YC-1 (3-(5'-hydroxymethyl-2'-furyl)-1-benzylindazole): This is a pharmacological agent initially formulated for circulatory disorders, acting as an inhibitor of platelet aggregation and vasodilation via activation of soluble guanylate cyclase (sGC) [269,270]. YC-1 has shown significant anti-tumor activity with concomitant reduction of HIF-1 α protein levels in hepatoma cells and five xenograft models [271,272].

Heat-shock protein 90 (Hsp90) inhibitors: Hsp90 is a chaperone protein involved in the conformation, stability, maturation and function of many other proteins, mainly transcription factors and signalling kinases, including regulation of HIF-1 α activation and cell cycle control [273]. Geldanamycin (GA) is a naturally occurring Hsp90 inhibitor that works by competing with Hsp90 for its ATP binding site, causing ubiquitination and proteasome-mediated degradation of the associated proteins; interestingly, GA has been found to cause the degradation of HIF-1 α in renal cell carcinoma and prostate cancer cell lines, so GA analogs are currently being tested in clinical trials for their efficacy in treating renal tumors, metastatic breast cancer, malignant melanoma, thyroid carcinoma and lymphoma [222,274,275]. Similarly, other Hsp90 inhibitors have shown promising results in xenograft models and clinical trials of hypoxia in that they inhibit HIF-1 α activity and VEGF expression; examples include radicicol, KF58333, SCH66336 and apigenin [275-279].

Histone deacetylase inhibitors (HDACI): Studies have shown that HDACI (especially HDAC-6 and HDAC-4) are actively implicated in the proteasome-dependent degradation of HIF-1 α , either by a VHL- and ubiquitin-independent pathway mediated by an HDAC-6-dependent hyperacetylation of Hsp90, or by an increased acetylation and poly-ubiquitination pathway mediated by the direct interaction between the HDACI and HIF-1 α [280,281]. Vorinostat (ZOLINZA[™], Merck) is an FDA-approved HDACI for the treatment of cutaneous T-cell lymphoma (CTCL), while several other HDACI are currently being tested in phase I/II studies for their efficacy as cancer therapeutics; examples include: valproic acid (also used as an anticonvulsant and mood stabilizing drug in epilepsy and bipolar disorder), MGCD0103, FK228, LBH589, Trichostatin A, AR-42 and CUDC101 [282].

Thioredoxin inhibitors: Since redox protein thioredoxin (Trx-1) over-expression has been found to correlate with increased HIF-1 α protein levels and VEGF production in many human cancers, the next logical step is to design inhibitors that will prevent Trx-1 signalling

[283]. Examples include PX-12 and pleurotin, already showing encouraging results in decreasing HIF-1 α levels and expression of HIF-1 α -responsive genes *in vitro* [284].

Chetomin: Being a metabolite of the fungus *Chaetomium* with anti-microbial properties, chetomin has also shown strong potency in disrupting the interaction of HIF-1 α with p300, hence inhibiting hypoxia-mediated transcription and tumor growth in xenograft models [285].

Echinomycin: Despite disappointing results when extensively tested in phase I/II clinical trials in the 1990s, echinomycin, essentially an antibiotic, has shown strong potency in inhibiting HIF-1 α activity *in vitro*, paradoxically hinting at a possible therapeutic efficacy if exploited accordingly [286-288].

Miscellaneous: Ascorbate, Fara-A (nucleotide analog) and certain anti-inflammatory drugs such as ibuprofen and indomethacin have been found to inhibit HIF-1 α activity and angiogenesis in both normal and cancer cells *in vitro* [289-292]. On the other hand, flavopiridol, a protein kinase inhibitor, has demonstrated strong potency in inhibiting VEGF and HIF-1 α expression in human monocytes and glioma cells [293,294]. Recently, the development of a synthetic polyamide especially designed to inhibit the binding of the HIF-1 α /ARNT heterodimer to its cognate DNA sequence and its successful delivery in mammalian cells has shed new light in the mechanisms regarding HIF-1 α inhibition [295,296]. Considerations are also being made for the development of proteasome inhibitors as HIF-1 α transcriptional inhibition-mediated tumor therapeutics [297], whereas natural products such as curcumin (component of spice turmeric), berberin (Chinese herb component), resveratrol (found in grapes) and certain flavonoids such as genistein are also being screened for their ability to inhibit HIF-1 α activity in certain human cell lines and xenograft models [298-302]. Finally, recent studies have demonstrated that zinc supplementation downregulates HIF-1 α activity and protein levels in highly invasive and angiogenic prostate cancer and glioblastoma cells, resulting in the inhibition of VEGF expression and in the prevention of angiogenesis and tumor invasiveness, thus indicating that zinc could become a useful HIF-1 α inhibitor in anti-cancer therapies [303,304].

PHD-based therapeutic targets

Since PHDs are actively implicated in the proteasome-mediated degradation of HIF-1 α in the normoxic environment, as discussed at the beginning of this review, strategies employing their activation are well under consideration. Examples include:

Cyclosporin A: Essentially an immunosuppressive agent used in organ transplantation, cyclosporine A has also been found to inhibit the HIF-1 α -mediated cellular response to hypoxia via induction of PHD activation in glioma cells *in vitro* [222,305].

R59949: This agent has shown potent activity in inhibiting HIF-1 α protein accumulation via activation of PHD *in vitro* and therefore is a promising candidate for further *in vivo* testing [306].

Antioxidants: Such as ascorbic acid, N-acetylcysteine and vitamin C have been shown to decrease HIF-1 α protein levels, possibly by maintaining the reduced active state of the catalytic ferrous ion of PHD and by inducing VHL-mediated HIF-1 α degradation [307].

Clinical setbacks in the field of anti-angiogenic cancer therapy

Despite the FDA approval of several VEGF blockers for cancer therapy and the reported prolonged survival of the responsive cancer

patients, recent findings show that progression-free survival (PFS) is very short, usually in the order of a few months and not always followed by overall survival (OS) [308,309]. Similarly, approvals of oral small molecule anti-angiogenic receptor tyrosine kinase inhibitors (TKIs) have also been associated with a number of failures in randomized phase III trials, whether administered alone or with chemotherapy [310,311]. The anti-VEGF neutralizing antibody bevacizumab, in particular, has produced extremely disappointing results in preclinical testing and in colorectal cancer phase III trials, with worse clinical outcomes appearing in patients who received bevacizumab plus chemotherapy compared to just chemotherapy [312,313]. Even though such therapeutic strategies may initially elicit a beneficial response by reducing tumor size, they can also result in hypoxia and hence eventually enhance tumor aggressiveness by reducing drug efficacy due to HIF-1 α expression. As a result, hypoxia might select for the malignant metastatic cells that expand to more invasive metastatic disease, ultimately leading to shorter life expectancy [312,314,315]. Several mechanisms have been proposed to explain the aforementioned setbacks, mostly regarding changes in the tumor cells, as is for example the tumor microenvironment, where VEGF blockade induces hypoxia as a result of reducing tumor microvasculature, tumor vessel blood flow and blood perfusion [315,316]. Should other angiogenic factors be upregulated at a more advanced tumor stage, as for example PIGF, FGFs, chemokines and ephrins, not only will VEGF-blockade as cancer therapy no longer be effective, but tumor vascularisation will be rescued, leading to tumor invasiveness and metastasis [317]. Notably, depending on the cell type affected, certain tumor types may be less sensitive to VEGF blockade, as is for example pancreatic cell carcinoma, due to its hypovascular stroma structure [315]. As a consequence, there is an urgent need for devising strategies that will allow the anti-angiogenic drugs to be effectively combined with chemotherapy in targeting tumor hypoxia and HIF-1 α expression. One such strategy could be metronomic chemotherapy, i.e. repetitive, low doses of chemotherapeutic drugs designed to minimise toxicity and target the tumor stroma, as opposed to targeting the tumor itself. It has already been shown that combining anti-angiogenic drugs with metronomic chemotherapy produces more potent anti-tumor effects *in vitro*, whereas a randomized phase II clinical trial of metronomic cyclophosphamide/capecitabine in combination with bevacizumab for the treatment of metastatic breast cancer has shown a significant enough overall clinical benefit so as to move the treatment forward to phase III clinical trial testing [318-321].

Conclusions/Future Perspectives

To summarize, hypoxia induces the activation of many pathways within the cell, some being HIF-mediated and some HIF-independent, which interconnect and cooperate with each other in response to the hypoxic stress. Chromatin remodelling, changes in gene expression and altered translational processes are all aspects of the cellular response to hypoxia and are actively involved in cancer formation. The research and development of novel chemotherapeutic targets based on these features of the hypoxic response has been the subject of intense scrutiny in the past 20 years. Despite the fact that many hypoxia-based therapeutic agents show promising results *in vitro* and *in vivo*, with some of them having successfully passed onto Phase I/II clinical trials, we still haven't fully deciphered the molecular mechanisms interconnecting the various signalling pathways involved in the hypoxic response or gained enough insight into how gene expression affects the malignant phenotype. In addition, very little data exists on the effect of hypoxia on childhood tumorigenesis, so current therapeutic modalities are almost

exclusively based on data acquired from studies in adults. Future research in this area will lead to a better understanding of how the hypoxic cascade affects cancer progression in this particularly fragile patient population and hopefully lead to better and more effective therapeutic and prognostic outcomes.

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