Candidate Genes for the Hypoxic Tumor Phenotype

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Abstract

In this study, we have analyzed changes induced by hypoxia at the transcriptional level of genes that could be responsible for a more aggressive phenotype. Using a series of DNA array membranes, we identified a group of hypoxia-induced genes that included plasminogen activator inhibitor-1 (PAI-1), insulin-like growth factor-binding protein 3 (IGFBP-3), endothelin-2, low-density lipoprotein receptor-related protein (LRP), BCL2-interacting killer (BIK), migration-inhibitory factor (MIF), matrix metalloproteinase-13 (MMP-13), fibroblast growth factor-3 (FGF-3), GADD45, and vascular endothelial growth factor (VEGF). The induction of each gene was confirmed by Northern blot analysis in two different squamous cell carcinoma-derived cell lines. We also analyzed the kinetics of PAI-1 induction by hypoxia in more detail because it is a secreted protein that may serve as a useful molecular marker of hypoxia. On exposure to hypoxia, there was a gradual increase in PAI-1 mRNA between 2 and 24 h of hypoxia followed by a rapid decay after 2 h of reoxygenation. PAI-1 levels were also measured in the serum of a small group of head and neck cancer patients and were found to correlate with the degree of tumor hypoxia found in these patients.

Introduction

Within solid tumors, hypoxia develops at distances beyond the diffusion capacity of oxygen from blood vessels (typically 100–150 μm; Ref. 1). In addition, hypoxia can develop in areas of a tumor with compromised blood flow due to aberrant vasculature formation and high interstitial pressure (2). The tumor microenvironment is a critical component that influences the behavior of transformed cells and their response to therapeutic interventions. Evidence from recent laboratory studies suggests that tumor hypoxia contributes to the progression of a more malignant phenotype by selecting for cells with a diminished apoptotic potential. Hypoxic conditions will also reversibly inhibit cell-cycle progression under certain growth conditions (3). Because cells exposed to low oxygen conditions are relatively resistant to conventional radiotherapy and chemotherapy, this population of cells significantly impacts clinical response to anticancer therapies.

Tumor hypoxia has been directly measured in a variety of human cancers including head and neck carcinomas, cervical carcinomas, and soft tissue sarcomas. Brizel et al. and Nordsmark et al. showed that, in head and neck carcinomas, hypoxia correlated with a lower probability of disease-free survival (4, 5) and that, in soft tissue sarcomas, hypoxia was associated with increased incidence of distant metastases (6). Hockel et al. (7) also found that hypoxia in cervical carcinomas resulted in increased local and distant failures. Interestingly, hypoxia predicted for distant failure not only in patients treated with radiotherapy but also in those treated with surgery alone. These studies suggest that hypoxia alters fundamental, physiologically important pathways that result in more aggressive tumor behavior in a wide variety of tumors.

We hypothesized that the development of an increased malignant phenotype can at least partially be attributed to changes in hypoxic gene expression. Under hypoxic conditions, the major transcription factor affecting gene regulation is HIF-1α (8). This factor regulates a diverse family of genes including VEGF (9), the urokinase receptor (10), tyrosine hydroxylase (11), endothelin 1 (12), nitric oxide synthase (13), erythropoietin (14), and numerous glycolytic enzymes (15). HIF-1 binds as a heterodimer consisting of an oxygen-sensitive HIF-1α (helix-loop-helix protein, HLH) subunit (16–18) and a constitutively expressed oxygen insensitive ARNT/HIF-1β (aryl hydrocarbon receptor nuclear translocator) subunit (17, 18). HIF-1α-deficient embryonic stem (ES) cells that are null at this locus fail to induce HIF-1 target genes when exposed to hypoxia (19, 20). The HIF-1 heterodimer binds to a 6-bp (5′-ACGTG/C/G-3′) hypoxia responsive element (HRE) that functions as a transcriptional enhancer in hypoxia-responsive genes (21). Although the majority of hypoxia-regulated genes are dependent on HIF-1, other transcription factors such as nuclear factor κB (22, 23), AP-1 (24, 25), and c/EBPβ (26, 27) as well as Egr-1 (28) are also activated by hypoxia.

We sought to characterize global transcriptional changes in tumor cells after exposure to hypoxic stress with the goal of determining how hypoxia influences the regulation of defined sets of genes involved in metabolic regulation, cell-cycle control, angiogenesis, and tissue invasion. We used cDNA array membranes containing 588 genes and compared gene expression under normoxic and hypoxic conditions in a squamous cell carcinoma-derived cell line. These studies resulted in the identification of nine hypoxia inducible genes that were subsequently confirmed by Northern blot analysis to be hypoxia-inducible.

To demonstrate the potential clinical applicability of hypoxic gene expression, we analyzed PAI-1 in the serum of patients with squamous cell carcinomas. Previous reports have suggested that PAI-1 plays a role in tissue invasion/remodeling and its up-regulation may contribute to the development of a more malignant tumor phenotype (29–31). Furthermore, increased expression of PAI-1 in some human tumors has been correlated with poor prognosis (32, 33). Most importantly, because it is a secreted protein, serum levels are readily detectable and may be useful as a molecular marker of hypoxia. We obtained serum samples from head and neck carcinoma patients and investigated whether PAI-1 levels correlated with the degree of tumor
hypoxia. The use of larger gene arrays may yield other secreted proteins and provide additional serum markers that reflect tumor hypoxia.

Materials and Methods

Cell Lines. Two cell lines obtained from American Type Culture Collection were used in this study. FaDu cells were established in 1968 from a punch biopsy derived from a hypopharyngeal tumor. The morphology of FaDu cells in vitro is epithelial. FaDu cells form well-differentiated epidermoid carcinomas when transplanted into immune deficient mice. SiHa cells were established in 1975 from tissue fragments derived from a squamous cell carcinoma of the cervix. The morphology of SiHa cells in vitro is epithelial. SiHa cells form poorly differentiated epidermoid carcinomas when transplanted into immune deficient mice. SiHa cells possess one to two copies of human papilloma virus type 16 integrated in their genomes and FaDu cells are human papilloma virus-negative. These two cell lines were chosen because they were both derived from squamous cell carcinomas, a tumor type in which hypoxia has been thought to be an important physiological modulator of malignant progression. Both of the cell lines were not used past 10 passages in cell culture.

Clontech Atlas cDNA Expression Array Membranes. Hybridizations were carried out according to the manufacturer’s specifications. The membranes were prehybridized at 68°C for 30 min in ExpressHyb solution. Message RNA was purified by binding to a poly(A) column and probe that was generated by reverse transcription in the presence of [α-32P]dATP. The membranes were then hybridized overnight with 0.5 × 10^6 cpm/ml probe at 68°C with continuous agitation. Membranes were washed twice with 2× SSC/1% SDS and twice with 0.1× SSC/0.5% SDS. All of the washes were carried out for 30 min at 68°C. The membranes were then visualized by phosphorimaging, and quantitation was performed with ImageQuant software. Counts were normalized to M(23,000 highly basic protein (Accession Number P40429) for loading controls.

Northern Blot Analysis. Total RNA was isolated with Trizol according to the manufacturer’s protocol. RNA samples (10 µg) were denatured in glyoxal for 1 h at 50°C and separated by agarose gel electrophoresis. The gel was then transferred by capillary action overnight to Nytran membrane and cross-linked by exposure to UV light. Probes were generated by reverse transcription PCR using the manufacturer’s primers (Clontech), gel-purified, and labeled with [32P] by random priming. Hybridization to [32P]-labeled probes was carried out at 65°C using ExpressHyb solution (Clontech) according to the manufacturer’s protocol and washed for 2 h to a stringency of 0.2× SSC/1% SDS. Equal loading and transfer between lanes was demonstrated by methylene blue staining of 28S and 18S ribosomal bands before probing. All of the membranes were exposed by phosphorimaging and quantitated with ImageQuant software.

Hypoxic Treatment. FaDu and SiHa cells were routinely cultured in DMEM + 10% FCS. Fresh media was exchanged 3–5 h before treating for varying amounts of time in a 37°C hypoxic incubator (Sheldon Manufacturing Inc.), which maintained an environment of less than 0.05% oxygen. The normoxic cells were maintained in a 37°C-incubator with 21% O2. All of the experiments were performed at 70–80% cell confluency and the pH of the media remained between 7.0–7.4 for the duration of the experiment.

Immunohistochemical Staining of Tissues for EF-5 Binding: Photogaphy and Analysis of Binding. The techniques used here were previously described (34, 35). For each patient, at least two tumor regions and two levels within each region (separated by 0.5 mm) were examined for regions of in situ EF-5 binding. The regions were imaged using a ×10 microscope objective (field size set electronically at 1.05 × 0.7 mm²), and typically nine fields were examined for each section. To provide multiple pixels per cell while improving camera sensitivity, each image field consisted of 600 × 400 pixels each of which was a 2 × 2-bin of the actual camera chip pixels, with 12-bit gray-scale resolution.

Eppendorf pO2 Histogramy and PAI-1 Determination. Eppendorf electrode measurements were taken through three tracks of neck nodes of patients with squamous cell carcinoma of the head and neck. Each pass with the probe recorded 50–100 measurements of oxygen concentration along the track. Measurements were also taken through one track of s.c. tissue of an uninvolved area in the neck to serve as a control. Serum levels of PAI-1 protein were measured using ELISA kits from biopool International (Ventura, CA) according to the instructions of the manufacturer. The PAI-1 ELISA has a detection limit of 0.5 ng/ml and measures latent (inactive) PAI-1, active PAI-1, and PAI-1 complexed with tPA/PAI and uPA/PAI. Using this assay and the manufacturer’s protocol, the range of PAI-1 values found in individuals without pathophysiological conditions or in the third trimester of pregnancy is 4–43 ng/ml All of the human serum samples were obtained with the subjects’ informed consent and were used for research purposes only. Total tumor burden (primary tumor and nodes) as assessed from computed tomography and magnetic resonance imaging scans indicated that there was no relationship between tumor burden and PAI-1 levels. Tumor burden ranged from 12.7 cm² to 60 cm². However, a relationship between median pO2 values and PAI-1 levels in the serum was found. The graph represents data from eight patients with pathologically verified squamous cell carcinoma of the head and neck before any form of treatment.

Results

Fig. 1 shows a series of multiple gene array membranes that illustrate gene expression changes induced by hypoxia in a squamous cell carcinoma cell line (FaDu) originally derived from a pharyngeal wall tumor. These membranes were prepared with 588 known genes categorized into six groups: (a) regulators of cell cycle; (b) apoptosis/tumor suppressors/oncogenes; (c) DNA damage/development; (d) cell...
adhesion/angiogenesis; (e) regulators of invasion/cell-cell interaction; and (f) growth factors/cytokines. Cells were exposed to 6 or 18 h of hypoxia prior to mRNA isolation, and gene expression was then compared with cells cultured under normoxia. Quantitative analysis of these membranes was performed with ImageQuant software.

Because numerous investigators have shown that VEGF mRNA levels are exquisitely sensitive to hypoxia, we used this level of gene induction as a cutoff point for assessing hypoxia-induced genes. We only analyzed genes that demonstrated a greater level of induction than found with VEGF. Using this criteria, we identify nine genes (Table 1) that exhibited a greater than 3-fold induction under hypoxic conditions. Interestingly, the level of mRNA induction as determined by gene array analysis did not always correlate with the level of induction as determined by Northern blot analysis (Table 1). However, all of the genes that we initially identified based on their hypoxic induction as determined by Northern blotting (Table 1) that exhibited a greater than 3-fold induction under hypoxic conditions. Interestingly, the level of mRNA induction as determined by gene array analysis did not always correlate with the level of induction as determined by Northern blot analysis (Table 1). However, all of the genes that we initially identified based on their hypoxic inducibility when compared with VEGF were found to be induced by hypoxia as assessed by Northern blotting (Table 1).

Fig. 2 is a composite of Northern blots that demonstrates the increase in mRNA expression of the seven most-hypoxia-inducible genes derived from membrane analysis. In this figure, we compared the induction of each gene in two different squamous cell carcinomas.

Table 1. Analysis of candidate genes

<table>
<thead>
<tr>
<th>Gene</th>
<th>Accession number</th>
<th>Fold induction by array analysis</th>
<th>Fold induction by northern analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td>MIF</td>
<td>25639M</td>
<td>9.3</td>
<td>2 to 3</td>
</tr>
<tr>
<td>BIK</td>
<td>X89986</td>
<td>7.6</td>
<td>2 to 3</td>
</tr>
<tr>
<td>PAI-1</td>
<td>X04429</td>
<td>7.4</td>
<td>&gt;10</td>
</tr>
<tr>
<td>Collagenase-3 (MMP13)</td>
<td>X75308</td>
<td>6.3</td>
<td>&lt;2</td>
</tr>
<tr>
<td>LDL receptor-related protein</td>
<td>X13916</td>
<td>6.0</td>
<td>5 to 10</td>
</tr>
<tr>
<td>IGFBP-3</td>
<td>M31159</td>
<td>5.6</td>
<td>5 to 10</td>
</tr>
<tr>
<td>FGF-3 (INT-2)</td>
<td>X14445</td>
<td>5.6</td>
<td>&lt;2</td>
</tr>
<tr>
<td>Endo-2</td>
<td>M65199</td>
<td>4.4</td>
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</tr>
<tr>
<td>GADD45</td>
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<td>&lt;2</td>
</tr>
<tr>
<td>VEGF</td>
<td>M32977</td>
<td>3.3</td>
<td>&gt;10</td>
</tr>
</tbody>
</table>

Fig. 2. Kinetics of PAI-1, IGFBP-3, Endo-2 (endothelin-2), LBP (LDL Rec Rel Protein), MIF, BIK, and VEGF induction by hypoxia. The times for mRNA analysis were chosen so that membrane hybridization and Northern blotting could be directly compared. Northern blot analysis for two different squamous cell carcinoma cell lines, FaDu and Siha, is shown. In addition, the induction of each gene by the hypoxia mimetic agent DFO (6 h) is also included to further support the hypoxia-inducibility of each gene.

Discussion

When tumor cells are exposed to hypoxic stress, transcription of a discrete set of genes is initiated to serve a variety of cellular functions. It has been proposed that within solid tumors, hypoxia functions as a selective pressure leading to an apoptosis-resistant population of cells (38). In addition, other investigators have demonstrated that hypoxia increases the ability of tumor cells to metastasize (39, 40). These laboratory studies suggest that hypoxia influences tumor development by modulating gene transcription. This hypothesis is also supported by clinical data that correlates hypoxic tumors in soft tissue sarcomas,
head and neck carcinomas, and cervical carcinomas with worse overall survival (4–7). In this study, we sought to characterize gene expression changes that occur in response to hypoxia because we hypothesized that changes in gene expression might be responsible in part for the more aggressive phenotype of the hypoxic tumor cell.

With the use of a multiple gene array membrane, we screened 588 genes that had previously been identified to play a role in oncosogenesis, for their response to changes in oxygenation. Because hypoxia had been previously shown to be a potent transcriptional activator of VEGF, we chose to use it as a cutoff point for identifying additional hypoxia-regulated genes. Using this criteria, we found nine genes that demonstrated greater hypoxic induction than VEGF as determined by ImageQuant analysis. The level of hypoxic induction when analyzed by Northern blot did not always correlate with the level of induction by array analysis because of differences in both the quantitative and qualitative aspects of probe and target gene hybridization. Such differences have been previously reported for p53-regulated genes (41). Furthermore, although the gene array screening was performed in FaDu cells, a similar level of induction was found by Northern blot analysis in Siha cells. It is noteworthy that Table 1 is not an exhaustive list of hypoxia-induced genes because the squamous carcinoma cells do not express or express at varying levels the genes on the array membrane. The gene array represents only a small fraction of expressed genes, and we analyzed only genes that were more-hypoxia-inducible than VEGF.

Table 1 is a ranked list of hypoxia-inducible genes that compares their induction by gene array analysis and Northern blot analysis. These genes can be broadly categorized into two groups: those involved in apoptosis (BIK and IGFBP-3) and those involved in local tissue/tumor response (MIF, PAI-1, Endo-2, MMP-13, FGF-3, LRP, and VEGF).

BIK and IGFBP-3 are both proapoptotic genes (42, 43) that are transcriptionally up-regulated during hypoxia. Apoptosis is a complex process that reflects a shift in the delicate balance between pro- and antiapoptotic genes. During the time in which these genes are induced, we did not see any significant increase in apoptosis, which makes the function of these genes during hypoxia unclear. Perhaps other antiapoptotic pathways have become activated during hypoxia, which then negates the effects of these pro-apoptotic genes, or these genes may play other roles in growth regulation under hypoxic conditions.

The second and larger category of genes that we have identified by gene array analysis are involved in tissue remodeling and invasion. Young et al. have demonstrated that when tumor cells are exposed to hypoxia and reoxygenation, it results in an increased rate of metastasis as determined by lung colony formation of metastatic foci (39). Studies presented here and elsewhere suggest that many of the genes involved in the breakdown of the basement membrane and the eventual establishment of metastatic tumor foci are hypoxia-inducible (10, 44). Thus, the induction of tissue-remodeling genes by hypoxia undoubtedly contributes to the development of a more malignant phenotype.

A more detailed analysis of PAI-1 revealed that its regulation is exquisitely sensitive to hypoxia. Under normoxic conditions, there are undetectable levels of PAI-1 and between 2–24 h of hypoxia there is a gradual increase in PAI-1 mRNA. Reoxygenation of 2–6 h under normoxic conditions results in a marked decrease in PAI-1 expression to near-normoxic levels. Several groups have reported that PAI-1 is hypoxia-inducible in cell lines in vitro (45, 46). Furthermore, analysis of the 5’ genomic sequence from the transcriptional start site of the PAI-1 gene reveals a putative hypoxia responsive element (HRE) that provides a possible mechanism for PAI-1 regulation by hypoxia.

As discussed above, increased PAI-1 staining of tumor sections has been correlated with a worse prognosis. However, the link between PAI-1, tumor hypoxia, and outcome has yet to be made. Because PAI-1 is a secreted protein, its serum levels can be easily measured and may serve as a surrogate marker of tumor hypoxia. Although we found a relationship between serum PAI-1 levels in head and neck cancer patients and the extent of hypoxia found in the tumors of these patients, a more thorough study is warranted to investigate whether other genes involved in plasminogen metabolism are also associated with tumor aggressiveness. It is also important to note that other pathophysiological conditions may elevate serum PAI-1 including pregnancy, cardiac ischemia, and blood clotting disorders, making a thorough clinical examination a necessity. In summary, PAI-1 represents but one hypoxia-regulated secreted protein that may eventually aid in cancer diagnosis, prognosis, and surveillance.

References


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HYPOXIA-INDUCED GENES

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