

Oxygen Sensing: Hydroxylation of HIF-1

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Editorial

A fundamental trait of all metazoan cells is their ability to detect and respond to variations in oxygenation. Protein hydroxylation has been identified as a method by which variations in PO₂ are transduced to impact changes in gene expression, thanks to the discovery of the transcription factor HIF-1. The efficient synthesis of high-energy molecules by multicellular life on Earth is predicated on the usage of O₂, and O₂ consumption increases with the organism's mass and metabolic activity. However, due to the harmful effects of reactive oxygen species on cellular macromolecules, O₂ exposure must be minimized. As a result, all of a mammal's major physiological systems are involved in complicated homeostatic mechanisms that are meant to keep the O₂ concentration in each cell within a small range. Physiologists have been studying these systems for ages. These investigations have progressed to the cellular level throughout the last century. Finally, research over the last decade has revealed significant new information on the molecular mechanisms governing oxygen homeostasis in both prenatal and postnatal life.

Changes in gene expression are part of physiological reactions. The O₂-carrying capacity of the blood is maintained through the O₂-regulated synthesis of Erythropoietin (EPO), which boosts red blood cell progenitors' growth and survival. Hypoxia-inducible factor-1 was discovered, biochemically purified, and molecularly cloned after researchers studied the cis-acting regions required for enhanced transcription of the EPO gene in response to hypoxia (HIF-1). EPO is predominantly made by a rare cell type in the kidney. HIF-1, on the other hand, is expressed in all cell types and operates as a master regulator of oxygen homeostasis in both embryonic and postnatal physiology. HIF-1 has been found in all metazoan species studied, from *Caenorhabditis elegans* to *Homo sapiens* (organisms with cell counts that differ by more than 10 orders of magnitude), implying that HIF-1's presence was a necessary adaptation for metazoan evolution. HIF-1 is a heterodimeric protein made up of two subunits: HIF-1 α and HIF-1 β . Basic helix-loop-helix and Per-ARNT-Sim domains mediate heterodimerization and DNA binding in the amino-terminal half of each subunit. Two transactivation domains in the carboxy-terminal half of HIF-1 facilitate interactions with coactivators such as CREB binding protein (CBP) and p300. Both sequence-specific DNA binding proteins like HIF-1 and generic transcription factors like RNA Polymerase II interact with coactivators. Histone acetyltransferase activity is also present in coactivators, which is essential to make DNA embedded in chromatin accessible to the polymerase complex for transcription into RNA. HIF-1 is also involved in the pathophysiology of diseases such as ischemic cardiovascular disease and cancer, which are the leading causes of death in the United States.

As a result, HIF-1 has attracted a lot of attention as a potential therapeutic target for these diseases. Increased HIF-1 activity caused by HIF-1 gene therapy, small molecule inhibitors of prolyl hydroxylase activity, or inhibitors of HIF-1-VHL interaction may be used to accelerate neovascularization of ischemic tissue in the case of cardiovascular disease. Small-molecule inhibitors of HIF-1 activity, on the other hand, maybe useful as anticancer medicines. However, because HIF-1 is a global regulator of oxygen homeostasis, it may not be a good therapeutic target if it causes unanticipated and unpleasant side effects. Focusing on the products of HIF-1 target genes could be an alternate strategy. In patients with acute cerebral or myocardial infarction, erythropoietin treatment, for example, may prevent ischemia-induced apoptosis. The most difficult and vital task in this intriguing subject is to translate a fast-rising body of fundamental research data into therapeutic applications.