

HIF-1 α in Epidermis: Oxygen Sensing, Cutaneous Angiogenesis, Cancer, and Non-Cancer Disorders

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Besides lung, postnatal human epidermis is the only epithelium in direct contact with atmospheric oxygen. Skin epidermal oxygenation occurs mostly through atmospheric oxygen rather than tissue vasculature, resulting in a mildly hypoxic microenvironment that favors increased expression of hypoxia-inducible factor-1 α (HIF-1 α). Considering the wide spectrum of biological processes, such as angiogenesis, inflammation, bioenergetics, proliferation, motility, and apoptosis, that are regulated by this transcription factor, its high expression level in the epidermis might be important to HIF-1 α in skin physiology and pathophysiology. Here, we review the role of HIF-1 α in cutaneous angiogenesis, skin tumorigenesis, and several skin disorders.

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INTRODUCTION

Since the mid-nineteenth century, skin atmospheric oxygen uptake has been documented in vertebrates. Whereas amphibians use skin as a major respiratory surface and fish take up 60% of their oxygen through the skin, transcutaneous oxygen uptake in human adult skin, accounting for 0.4% of the lung epithelium uptake, covers most epidermal needs (Stucker *et al.*, 2002). The importance of oxygen sensing by keratinocytes is already known in premature babies in whom oxygenation through skin has been used as a surrogate to the respiratory route (Carlidge and Rutter, 1988). Moreover, it has been recently shown that oxygen sensing by keratinocytes in a mouse model affects systemic oxygen delivery to other organs (Boutin *et al.*, 2008). These data among others suggest that epidermis has had a leading role in the adaptation of the organism to environmental oxygen pressure during evolution through its oxygen-sensing capacity.

Metazoan species have evolved a highly conserved key protein, hypoxia-

inducible factor-1 α (HIF-1 α), to regulate oxygen delivery to tissue. Originally discovered as the regulator of oxygen homeostasis through the control of erythropoietin, HIF-1 α was then found to drive the expression of hundreds of genes (Wenger *et al.*, 2005; Semenza, 2007) involved in many biological processes, including neovascularization, angiogenesis, cytoskeletal structure, survival/apoptosis, adhesion, migration, invasion, metastasis, glycolysis, and metabolic bioenergetics (review in Semenza, 2003; Pouyssegur *et al.*, 2006).

Quantitative evaluation of tissue oxygenation has shown that physiological oxygen pressure in epidermis is low compared with other tissues (Table 1; Evans and Naylor, 1967; Stewart *et al.*, 1982; Distler *et al.*, 2004; Bedogni *et al.*, 2005; Evans *et al.*, 2006). Although dermal oxygen partial pressure is 10% (corresponding to 76 mm Hg), the pressure corresponding to the epidermis ranges between 0.2 and 8% (Evans *et al.*, 2006). Indeed, epidermal oxygenation, which

occurs mostly through atmospheric oxygen (Stucker *et al.*, 2002), results in a mildly hypoxic microenvironment. Consistent with this constitutive low epidermal oxygenation, an accumulation of the hypoxia-detection agent, nitroimidazole/EF5, as well as high levels of nuclear HIF-1 α have been detected in both human and mouse epidermis, especially in the basal layer (Figure 1; Distler *et al.*, 2004; Bedogni *et al.*, 2005; Boutin *et al.*, 2008). Considering the broad spectrum of HIF-1 α effects, its high level of expression in epidermis could reflect an important role in local and systemic adaptation to environmental stresses. In this review, we highlight the role of HIF-1 α in cutaneous angiogenesis, skin tumorigenesis, and other skin disorders.

HIF-1 α : STRUCTURE, REGULATION, AND TARGET GENES

Structure of the HIF-1 α protein

HIF-1 is related to the family of basic-helix-loop-helix transcription factors. It comprises two subunits, HIF-1 α , which is tightly regulated, and the

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Abbreviations: AKT, protein kinase B (PKB); ECM, extracellular matrix; HIF-1 α , hypoxia-inducible factor; ROS, reactive oxygen species; SCC, squamous cell carcinoma; VEGF, vascular endothelial growth factor; VEGFR, VEGF receptor; XP, xeroderma pigmentosum

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Table 1. Oxygen level in different human tissues

Tissue	Oxygen (%)	Reference
<i>Skin</i>		Evans <i>et al.</i> 2006
Dermis	>7	
Epidermis	0.2–8	
Hair follicles	0.1–0.8	
Sebaceous gland	0.1–1.3	
Vessels	4–14	Saltzman <i>et al.</i> 2003
Heart	5–10	Roy <i>et al.</i> 2003
Brain	0.5–7	Hemphill <i>et al.</i> 2005; Nwaigwe <i>et al.</i> 2000
Kidney	4–6	Welch and Wilcox, 2001

Atmospheric air contains about 20.9% O₂, which represents a partial atmospheric pressure of 160 mm Hg. The qualitative terms physiological, modest hypoxia, moderate hypoxia, severe hypoxia, and anoxia are used to designate 10–14, 2.5, 0.5, 0.1, and 0% O₂, respectively. These percentages are assigned to partial oxygen pressures of 75–100, 19, 3.8, 0.76, and 0.0 mm Hg, respectively (Evans *et al.*, 2006).

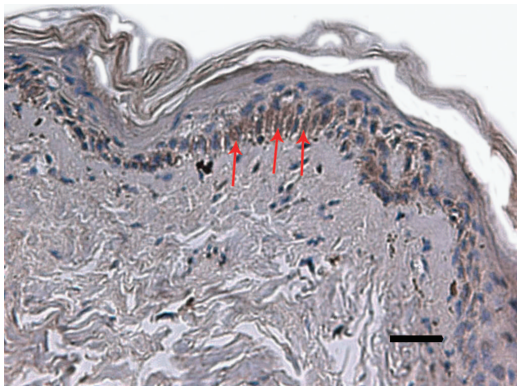


Figure 1. Hypoxia-inducible factor-1 α (HIF-1 α) expression in skin. Human skin immunolabeled using a specific anti-HIF-1 α antibody, followed by envision + horseradish peroxidase reagent, revealed with diaminobenzidine and counterstained with hemalun. HIF-1 α -positive cells appear brown. Bar = 100 μ m.

constitutively expressed aryl hydrocarbon nuclear translocator ARNT also called HIF-1 β (Figure 2a; reviewed by Maxwell, 2004; Metzen and Ratcliffe, 2004). Three isoforms of the α -subunit, named HIF-1 α , HIF-2 α (also referred to as EPAS-1, MOP2, HLF, and HRF), and HIF-3 α , have so far been identified in the human genome (Maynard *et al.*, 2003).

Two transactivation domains, N-terminal and C-terminal, have been identified in HIF-1 α . They interact with histone acetyltransferases, such as CBP, p300, and SRC-1, to activate the transcription of target genes. This association is regulated by both oxygen concentration and redox status. The basic-helix-loop-helix and Per-Arnt-Sim (PAS) domains are required for

dimerization of HIF-1 α with HIF-1 β as well as for DNA binding. In addition to the binding to DNA and coactivators, HIF-1 α interacts with factors regulating its stability such as heat shock protein-90 (Figure 2a; Brahimi-Horn *et al.*, 2005; Fandrey *et al.*, 2006).

Regulation of HIF-1 α

Under atmospheric oxygen pressure (termed normoxia), HIF-1 α is rapidly targeted for ubiquitination and proteasomal degradation after binding to the von Hippel-Lindau E3 ligase. The hydroxylation of HIF-1 α mediated by prolyl hydroxylases is a prerequisite for the association of HIF-1 α with von Hippel-Lindau (Maxwell *et al.*, 1999; Cockman *et al.*, 2000; Kamura *et al.*, 2000; Ohh *et al.*, 2000). Hydroxylation

by prolyl hydroxylase occurs on two specific prolines (P402 and P564 in human) present in the oxygen-dependent degradation domain of HIF-1 α in the presence of iron, oxygen, and 2-oxoglutarate (Ivan *et al.*, 2001; Jaakkola *et al.*, 2001; Masson *et al.*, 2001). Concurrently, hydroxylation of the asparagine residue 803 by an asparaginyl hydroxylase (also named FIH-1) prohibits binding of p300/CBP to the HIF-1 α subunit, which consequently abolishes transactivation of HIF-1 α (Mahon *et al.*, 2001). Reduction in prolyl hydroxylase activity under hypoxia results in stabilization and accumulation of HIF-1 α . Hypoxia-mediated reactive oxygen species (ROS) modulation and post-transcriptional modifications (e.g., phosphorylation, sumoylation, S-nitrosylation, and acetylation) of HIF-1 α have also been shown to be crucial in its stabilization and/or transcriptional activation process (Brahimi-Horn *et al.*, 2005; Fandrey *et al.*, 2006). When stabilized, HIF-1 α translocates to the nucleus, dimerizes with HIF-1 β , and binds to the hypoxia-response element (with an (A/G)CGTG core sequence) of target genes (Figure 2b and Table 2; Wenger *et al.*, 2005).

In addition to hypoxia, multiple oncogenic pathways, including growth factor signaling or genetic loss of tumor suppressors, can regulate HIF-1 α activity (Figure 2b; Semenza, 2002). Mitogen-activated protein kinases are required for the activation of the transcriptional activity and/or for HIF-1 α stabilization (Salceda *et al.*, 1997; Minet *et al.*, 2000; Hur *et al.*, 2001; Rezvani *et al.*, 2007). The loss of the tumor suppressor genes, von Hippel-Lindau or phosphatase and tensin homolog, upregulates HIF-1 α activity (Semenza, 2002). HIF-1 α stabilization could also be dependent on the phosphatidylinositol 3-kinase, protein kinase B (PKB/AKT), and its effector mammalian target of rapamycin (Paul *et al.*, 2004). Basic fibroblast growth factor, insulin, IL-1, hepatocyte growth factor, and heregulin induce the expression of HIF-1 α (Zhong *et al.*, 2000; Sodhi *et al.*, 2001; Tacchini *et al.*, 2001; Stiehl *et al.*, 2002; Kietzmann and Gorch, 2005). ROS, as second messengers, are other effectors found to

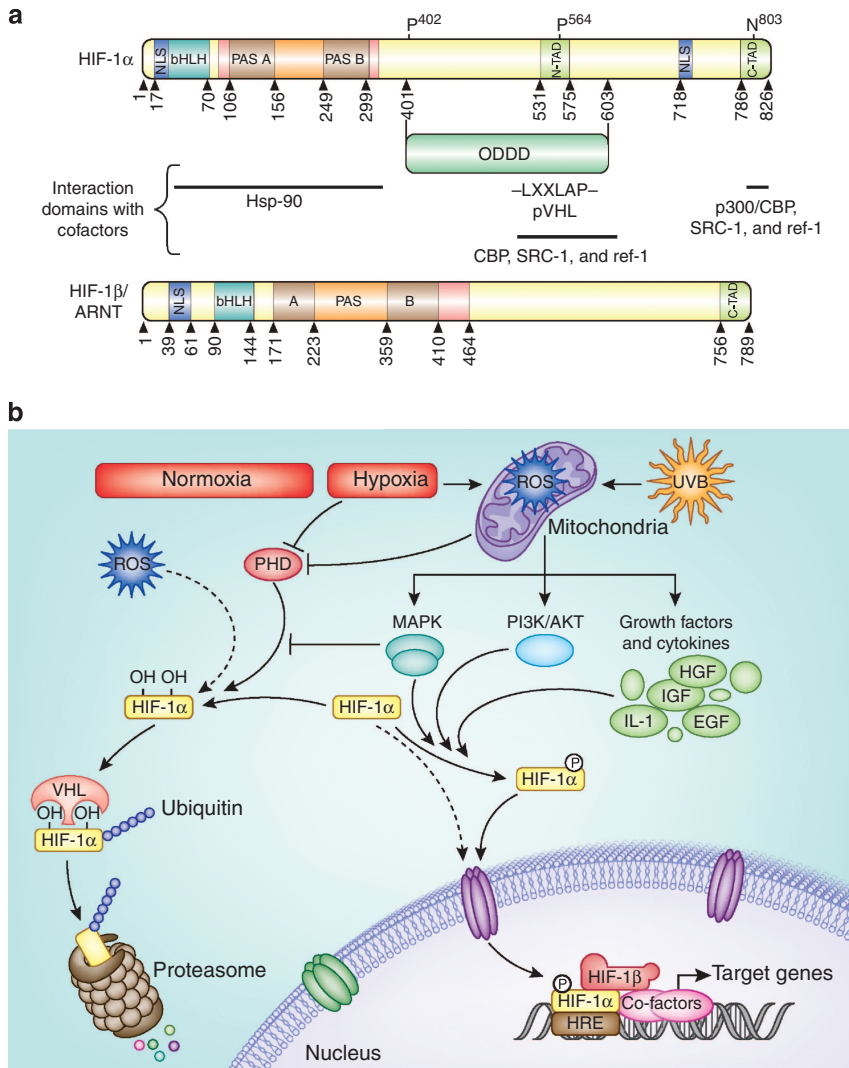


Figure 2. Structure and regulation of hypoxia-inducible factor-1 α (HIF-1 α) under different stimuli. (a) Schematic representation of human HIF-1 α and HIF-1 β . Both proteins are related to the basic-helix-loop-helix-Per-Arnt-Sim (bHLH-PAS) transcription factor family that contains an N-terminal bHLH domain and two PAS domains. HIF-1 α contains an oxygen-dependent degradation domain (ODDD) that mediates oxygen-regulated stability, and a C-terminal transactivation domain (C-TAD) whose transcriptional repression in normoxia is controlled through hydroxylation of the asparagine 803 by the factor-inhibiting HIF-1. Interaction domains with von Hippel-Lindau (VHL) and other cofactors are indicated, as well as amino-acid numbers for each domain. (b) Under normoxia, HIF-1 α is subjected to oxygen-dependent hydroxylation on proline 402 and 564 in ODDD. Ubiquitination by the VHL targets HIF-1 α to proteasomal degradation. Under conditions of hypoxia, UVB irradiation, or upon activation of some growth factor signaling pathways, HIF-1 α is stabilized, translocates to the nucleus, interacts with hypoxia-responsive elements (HREs), and finally promotes the activation of target genes. It is important to note that growth factors, cytokines, and AKT activation can also induce HIF-1 α protein synthesis or coactivator recruitment. AKT, protein kinase B; HGF, hepatocyte growth factor; Hsp-90, heat shock protein-90; LXXLAP, the motif that is required for interaction with prolyl hydroxylase (PHD) and VHL, and conserved from *Caenorhabditis elegans* to human; MAPK, mitogen-activated protein kinase; NLS, nuclear localization signal; N-TAD, N-terminal transactivation domain; PI3K, phosphatidylinositol 3-kinase; pVHL, protein VHL; ROS, reactive oxygen species.

modulate HIF-1 α activation positively or negatively (Gerald *et al.*, 2004; Kietzmann and Gorlach, 2005; Rezvani *et al.*, 2007; Galanis *et al.*, 2008).

HIF-1 α targets

Many HIF-1 α target genes are important in skin physiology (Table 2). These include genes that encode proteins

involved in cell growth and/or apoptosis (e.g., transforming growth factor- β 3, connective tissue growth factor, and Noxa), cell adhesion and migration (e.g., integrin- β 1 and laminin-332), DNA repair (e.g., xeroderma pigmentosum C (XPC) and XPD), melanogenesis (e.g., stem cell factor), angiogenesis and wound healing (e.g., vascular endothelial growth factor (VEGF), placental growth factor, and platelet-derived growth factor), extracellular matrix (ECM) formation and turnover (e.g., plasminogen activator inhibitor-1), chemotaxis (stromal cell-derived factor-1), and chemokine receptors (C-X-C chemokine receptor type 4; Liu *et al.*, 1995; Forsythe *et al.*, 1996; Takahashi *et al.*, 2000; Fink *et al.*, 2002; Kelly *et al.*, 2003; Pennacchietti *et al.*, 2003; Staller *et al.*, 2003; Ceradini *et al.*, 2004; Choi *et al.*, 2004; Higgins *et al.*, 2004; Kim *et al.*, 2004; Nishi *et al.*, 2004a; Patel *et al.*, 2005; Erler *et al.*, 2006; Bosch-Marce *et al.*, 2007; Fitsialos *et al.*, 2008; Keely *et al.*, 2009; Rezvani *et al.*, 2010a). HIF-1 α also mediates glucose uptake and metabolism by binding to promoter of genes encoding several glucose transporters and glycolytic enzymes (such as glucose transporter-1, hexose kinase-1, and 6-phosphofructo-2-kinase/fructose-2,6-bisphosphate-3; Semenza *et al.*, 1994; Ebert *et al.*, 1995; Okino *et al.*, 1998; Fukasawa *et al.*, 2004; Obach *et al.*, 2004; Roth *et al.*, 2004), which are important in metabolic reprogramming from oxidative to glycolytic metabolism (i.e., the Warburg effect) during carcinogenesis (Rezvani *et al.*, 2011a, b).

HIF-1 α EXPRESSION IN CUTANEOUS ANGIOGENESIS

A fine-tuned balance between angiogenic and antiangiogenic factors drives the angiogenic process. Once the balance is disrupted, the vasculature rapidly responds by triggering an angiogenic response, the angiogenic switch (Hanahan and Folkman, 1996). The process occurs universally in both physiological and pathological contexts. Physiological examples of cutaneous angiogenesis include cutaneous blood flow, wound healing, and the hair follicle cycle. Cutaneous

Table 2. HIF-1 α target genes with an important function in skin physiology

Major effects	Genes	Reference
<i>Cutaneous angiogenesis</i>		
Re-epithelialization, granulation tissue formation, and ECM synthesis and remodeling	VEGF	Forsythe <i>et al.</i> 1996; Liu <i>et al.</i> 1995
	PLGL	Kelly <i>et al.</i> 2003; Patel <i>et al.</i> 2005
	PDGF	Kelly <i>et al.</i> 2003; Patel <i>et al.</i> 2005
	TGF- β 3	Nishi <i>et al.</i> 2004a
	CTGF	Higgins <i>et al.</i> 2004
	IGFBP-1	Tazuke <i>et al.</i> 1998
SDF-1		Ceradini <i>et al.</i> 2004
Vascular tone	iNOS	Melillo <i>et al.</i> 1995
	HO	Lee <i>et al.</i> 1997
	ET1	Hu <i>et al.</i> 1998
ECM metabolism	PAI-1	Fink <i>et al.</i> 2002
	Lysyl oxidase	Erler <i>et al.</i> 2006
	Collagen prolyl-4 hydroxylase	Takahashi <i>et al.</i> 2000
Cell proliferation, motility, and migration	Integrin- β 1	Keely <i>et al.</i> 2009
	Laminin-332	Fitsialos <i>et al.</i> 2008
<i>Skin tumorigenesis</i>		
DNA repair	XPC	Rezvani <i>et al.</i> 2010a
	XPD	Rezvani <i>et al.</i> 2010a
	CSB	Filippi <i>et al.</i> 2008; Rezvani <i>et al.</i> 2010a
Cell growth/apoptosis	MSH-2	Koshiji <i>et al.</i> 2005
	BNIP3	Bruick, 2000; Kothari <i>et al.</i> 2003
	Noxa	Kim <i>et al.</i> 2004
	MCL-1	Piret <i>et al.</i> 2005
Metabolism	Tert	Nishi <i>et al.</i> 2004b; Yatabe <i>et al.</i> 2004
	GLUT1	Ebert <i>et al.</i> 1995; Okino <i>et al.</i> 1998
	HK1	Roth <i>et al.</i> 2004
	PFKFB3	Fukasawa <i>et al.</i> 2004; Obach <i>et al.</i> 2004
	Phosphoglycerate kinase-1	Semenza <i>et al.</i> 1994
	Lactate dehydrogenase A	Firth <i>et al.</i> 1995
	ENO1	Semenza <i>et al.</i> 1996
Xenobiotic transporter	GAPDH	Graven <i>et al.</i> 1999; Lu <i>et al.</i> 2002
	MDR1	Comerford <i>et al.</i> 2002
<i>Others</i>		
Hematopoiesis and melanogenesis	SCF	Bosch-Marce <i>et al.</i> 2007
Protooncogene, re-epithelialization, and melanogenesis	C-MET (HGFR)	Choi <i>et al.</i> 2004; Pennacchietti <i>et al.</i> 2003

Abbreviations: BNIP3, BCL2/adenovirus E1B 19-kDa-interacting protein; CSB, Cockayne syndrome B; CTGF, connective tissue growth factor; ECM, extracellular matrix; ENO1, enolase-1; ET1, endothelin-1; GAPDH, glyceraldehyde phosphate dehydrogenase; GLUT1, glucose transporter-1; HGFR, hepatocyte growth factor receptor; HIF, hypoxia-inducible factor; HK1, hexose kinase-1; HO, heme oxygenase; IGFBP-1, IGF-binding protein-1; iNOS, inducible nitric oxide synthase; MCL-1, myeloid cell leukemia sequence-1; MDR1, multidrug resistance-1; MSH, melanocyte-stimulating hormone; PAI-1, plasminogen activator inhibitor-1; PDGF, platelet-derived growth factor; PFKFB3, 6-phosphofructo-2-kinase/fructose-2,6-bisphosphate-3; PLGL, placental growth factor; SCF, stem cell factor; SDF-1, stromal cell-derived factor-1; Tert, telomerase reverse transcriptase; TGF- β 3, transforming growth factor- β 3; VEGF, vascular endothelial growth factor; XPC, xeroderma pigmentosum C; XPD, xeroderma pigmentosum D.

Only those genes were included in which binding of HIF-1 α to the target DNA sequence in a DNA-binding assay or functional transactivation of reporter gene expression have been reported.

angiogenesis is also involved in inflammation and cancer. A myriad of angiogenic factors are involved in the angiogenic response of various tissues (Bouis *et al.*, 2006; Laquer *et al.*, 2009; Nguyen *et al.*, 2009). Among these factors, HIF-1 α has a critical role by regulating angiogenesis through the modulation of several key factors, such as VEGF-A, fibroblast growth factor-2 (Calvani *et al.*, 2006; Black *et al.*, 2008), or the VEGF receptors (VEGFR1, 2, and 3; Gerber *et al.*, 1997). Moreover, inducible nitric oxide synthase, an enzyme producing nitric oxide (NO) that induces cutaneous vasodilatation in response to local heat, injury, or hypoxia (Harbrecht, 2006; Houghton *et al.*, 2006), is a target of HIF-1 α (Melillo *et al.*, 1995).

HIF-1 α in cutaneous vascular blood flow

Cutaneous blood flow is regulated by vasodilation and vasoconstriction of blood vessels close to the skin surface, and it controls physiological parameters such as body heat (Minson, 2003; Charkoudian, 2010), as well as ions, water, and gas exchange across the skin (Christensen, 1975; Mahany and Parsons, 1978; Malvin and Hlastala, 1989; Gniadecka *et al.*, 1998). Both neuronal and hormonal regulations of cutaneous vasculature are involved in cutaneous blood flow (Langley, 1911; Krogh *et al.*, 1922; Smith, 1976). Overproduction of the HIF-1 α target gene *VEGF* in keratinocytes induces the formation of leaky blood vessels and skin ulcerations (Larcher *et al.*, 1998; Thurston *et al.*, 1999), whereas overexpression of stabilized HIF-1 α itself in keratinocytes expands skin dermal vasculature without any vascular leakage, edema, or inflammation phenotype (Elson *et al.*, 2001; Kim *et al.*, 2006). Furthermore, an increased number of dilated blood vessels have been observed in these mice (Elson *et al.*, 2001). These data indicate an important regulatory effect of HIF-1 α expression in keratinocytes upon cutaneous blood vessel growth and dilation.

HIF-1 α in wound healing

Wound healing, a well-defined cascade of events activated following

cutaneous injury to seal the skin defect, is an interactive process involving soluble mediators, blood cells, ECM, and parenchymal cells (Singer and Clark, 1999; Barrientos *et al.*, 2008).

Following acute injury, the micro-environment of the skin wound becomes more hypoxic due to vascular disruption and high oxygen consumption by cells at the edge of the wound (Hunt *et al.*, 1972; Niinikoski *et al.*, 1972; Varghese *et al.*, 1986). This acute hypoxia, which has a positive role in early skin wound healing, is gradually normalized following neovascularization and completion of wound healing (Tandara and Mustoe, 2004). One of the mechanisms underlying the beneficial effects of acute hypoxia on improvement of the wound healing process could be increased HIF-1 α expression (Elson *et al.*, 2000; Albina *et al.*, 2001). In support of the positive role of HIF-1 α in wound healing improvement, Loh *et al.* (2009) demonstrated impaired wound healing concomitant to decreased HIF-1 α in ageing mice. Moreover, using an epidermal HIF-1 α -deficient mice model, we have recently found that loss of HIF-1 α in keratinocytes results in a significant delay in wound healing in aged mice (Figure 3a; unpublished data). In fact, HIF-1 α could affect the wound healing process in many ways (Figure 3b):

(i) HIF-1 α is known to activate many angiogenic factors (growth factors, chemokines, and cytokines) at the transcriptional level, including VEGF, placental growth factor, angiopoietins 1 and 2, platelet-derived growth factor-B, stromal cell-derived factor-1, transforming growth factor- β , and stem cell factor within various cells involved in wound healing (Forsythe *et al.*, 1996; Kelly *et al.*, 2003; Ceradini *et al.*, 2004; Tandara and Mustoe, 2004; Tang *et al.*, 2004; Patel *et al.*, 2005; Bosch-Marce *et al.*, 2007; Simon *et al.*, 2008). These angiogenic factors bind to cognate receptors (e.g., VEGFR1/VEGFR2/VEGFR3, platelet-derived growth factor receptor- α/β , C-X-C chemokine

receptor type 4, and C-KIT), which are expressed on the surface of vascular endothelial cells and vascular pericytes/smooth muscle cells. Receptor-ligand interaction activates these cells and promotes the formation of new capillaries from existing vessels. In agreement, gene therapy by overexpression of HIF-1 α has recently been found to improve wound healing in diabetic mice (Mace *et al.*, 2007; Botusan *et al.*, 2008; Liu *et al.*, 2008).

(ii) Besides activation of cells in existing vessels, HIF-1 α could promote angiogenesis and vascular remodeling in wound healing by mobilizing angiogenic cells from distant sites (including bone marrow and pericytes and endothelial cells from other tissues) to home to the wound (Ceradini *et al.*, 2004; Bosch-Marce *et al.*, 2007; Chang *et al.*, 2007; Sarkar *et al.*, 2009). Expression of a constitutively active form of HIF-1 α in mouse skin is sufficient to mobilize circulating angiogenic cells and to improve healing of wounds in diabetic mice (Liu *et al.*, 2008). By contrast, decreased expression of HIF-1 α in HIF-1 α heterozygous-null mice is associated with impaired recruitment of circulating angiogenic cells to the wound and deficiency of wound vascularization and healing (Zhang *et al.*, 2010).

(iii) HIF-1 α could improve wound healing by affecting skin cell motility and proliferation, which are essential factors in the re-epithelialization phase. HIF-1 α was found to promote human dermal fibroblast and keratinocyte migration, both *in vitro* and *in vivo*, through addressing the intracellular heat shock protein-90 α into the extracellular environment (Li *et al.*, 2007; Woodley *et al.*, 2009). HIF-1 α has been shown to modulate cell motility and migration by regulating the expression of ECM proteins and their receptors. Laminin-332, one of the major

keratinocyte-secreted ECM protein involved in cell migration during wound healing (Ryan *et al.*, 1994; Nguyen *et al.*, 2000), has been found to be regulated by HIF-1 α (Fitsialos *et al.*, 2008). Interaction of laminin-332 with its receptors (integrins- $\alpha3\beta1$ and - $\alpha6\beta4$), activates signaling pathways that subsequently promote proliferation, survival, and migration of keratinocytes (Rousselle and Aumailley, 1994; Murgia *et al.*, 1998; Nguyen *et al.*, 2000; Nikolopoulos *et al.*, 2005). The effect of HIF-1 α on epithelial cell adhesion and migration could go beyond its effect on laminin-332 expression. HIF-1 α has also been shown to regulate the expression of integrin- $\beta1$ (Keely *et al.*, 2009) as well as that of various metalloproteinases (Semenza, 2003; Shyu *et al.*, 2007; Lee *et al.*, 2010). Finally, HIF-1 α functions as an upstream player in the p21-mediated growth arrest of keratinocytes (Cho *et al.*, 2008), suggesting a role in the regulation of keratinocyte proliferation.

ROLE OF HIF-1 α IN UV RESPONSE AND SKIN TUMORIGENESIS

HIF-1 α and keratinocyte responses to UV irradiation

Solar UVB radiation is the primary environmental risk factor responsible for the induction of skin cancers, including basal cell carcinoma, squamous cell carcinoma (SCC), and melanoma. A major deleterious effect of UVB is the induction of well-defined structural alterations in DNA (Ravanat *et al.*, 2001). UVB-induced DNA damage sets in motion a highly complex well-coordinated series of responses whereby DNA damage and stalled replication forks can be detected. This, in turn, can trigger DNA repair, cell cycle delay, or apoptosis (Latonen and Laiho, 2005). The ultimate fate of cells with damaged DNA is dependent on the type and extent of damage, DNA repair capacity, and UVB-induced apoptotic signaling pathways (Kulms and Schwarz, 2002; Assefa *et al.*, 2005).

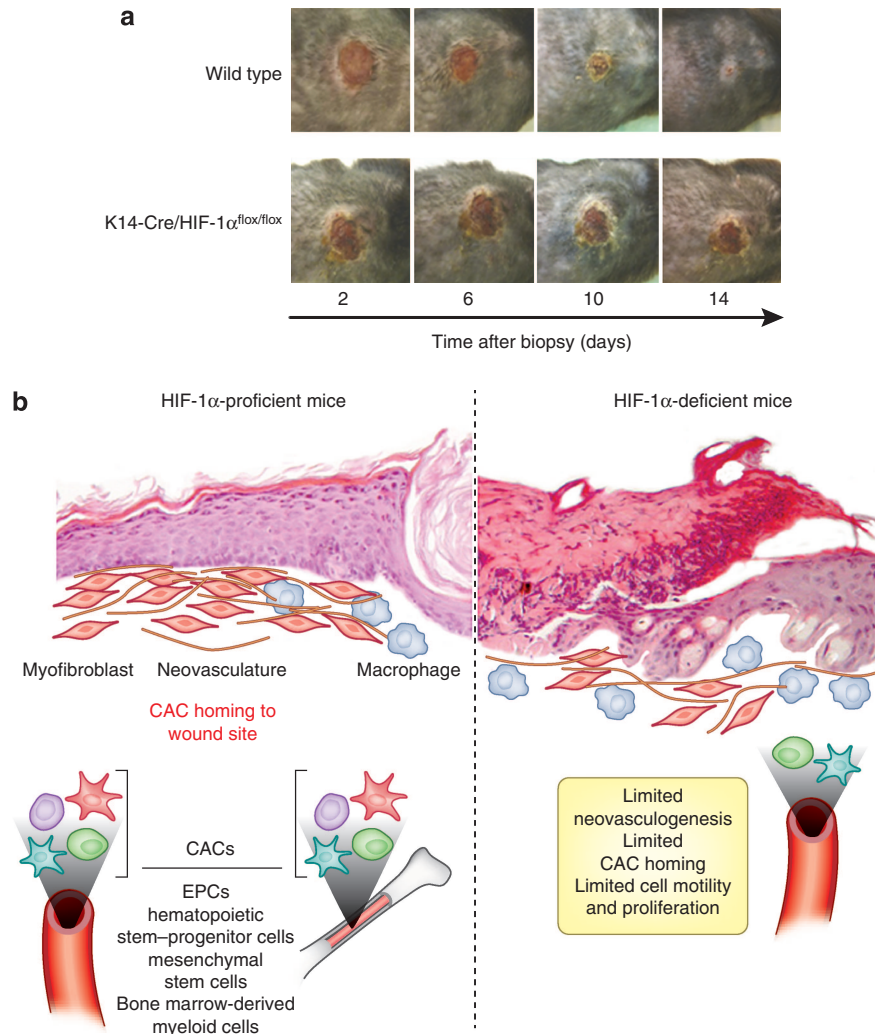


Figure 3. Role of hypoxia-inducible factor-1 α (HIF-1 α) in wound healing. (a) Wound healing is delayed in K14-Cre/HIF-1 $\alpha^{flox/flox}$ -aged mice. Wound healing assay was performed using standardized 8-mm biopsies on the back of the mice. As compared with control wild-type mice, there was a significant impairment of wound healing in K14-Cre/HIF-1 $\alpha^{flox/flox}$ mice. The time course of wound healing in two representative wild-type and HIF-1 α -deficient mice shows dramatic impairment of skin regeneration in the absence of HIF-1 α expression in keratinocytes. (b) A model outlining the effects of HIF-1 α in wound healing. The acute wound healing process is derived through interaction among keratinocytes, fibroblasts, endothelial cells, and macrophages. During wound healing, in HIF-1 α -proficient mice (left), numerous chemokines released from keratinocytes, such as vascular endothelial growth factor and stromal cell-derived factor-1, trigger the mobilization of circulating angiogenic cells (CACs) at the wound site. In mice with depletion of HIF-1 α in keratinocytes (right), the mobilization of CACs and consequently neovascularization are impaired, resulting in limited wound healing. For more explanations, see the text. EPC, endothelial progenitor cell.

We and others have shown that HIF-1 α expression is modulated after UVB exposure and that HIF-1 α has an important role in the regulation of cellular responses to this type of genotoxic stress (Rezvani *et al.*, 2007; Turchi *et al.*, 2008; Wunderlich *et al.*, 2008). UVB induces ROS, which in turn have a biphasic effect on HIF-1 α expression. Whereas rapidly produced cytoplasmic ROS downregulate HIF-1 α expression, delayed mitochondrial ROS production results in its upregulation (Rezvani *et al.*, 2007). It is likely that spatiotemporal

repression and activation of HIF-1 α has a substantial influence on the regulation of keratinocyte responses to UVB irradiation. In fact, downregulation of HIF-1 α protein expression immediately after UVB irradiation has been found to be important to release keratinocytes from UVB-induced cell cycle arrest (Cho *et al.*, 2009). Late HIF-1 α upregulation, which is regulated by mitogen-activated protein kinase (Rezvani *et al.*, 2007; Nys *et al.*, 2010), phosphatidylinositol 3-kinase/AKT (Wunderlich *et al.*,

2008), and/or ATF3 (Turchi *et al.*, 2008), has a proapoptotic effect in UVB-irradiated keratinocytes (Rezvani *et al.*, 2007; Turchi *et al.*, 2008; Nys *et al.*, 2010) through upregulation of proapoptotic genes (such as *Noxa*, *BCL2*/adenovirus E1B 19-kDa-interacting protein (*BNIP3*), or tumor necrosis factor-related apoptosis-inducing ligand (Turchi *et al.*, 2008; Nys *et al.*, 2010) and interaction with p53 (Rezvani *et al.*, 2007). Affecting DNA repair efficiency is the other means by which HIF-1 α can modulate keratinocyte responses to UVB (Rezvani *et al.*,

2010a). Biphasic variation of HIF-1 α upon exposure of keratinocytes to UVB was also found to regulate the removal rate of 6-4 photoproducts and cyclobutane pyrimidine dimers, the most frequent types of UVB-induced lesions primarily removed by nuclear excision repair. This study showed that the effect of HIF-1 α on the nuclear excision repair machinery relies on the transcriptional regulation of XPC, XPD, XPB, XPG, and Cockayne syndrome A and B expression by direct HIF-1 α binding to the hypoxia-response elements of these genes in their promoter region (Rezvani *et al.*, 2010a).

HIF-1 α in skin cancer

The effects of HIF-1 α in cancer are not straightforward. On one hand, HIF-1 α can contribute to solid tumor progression via multiple mechanisms, including promotion of angiogenesis, modulation of metabolism through regulation of glycolysis flux and oxidative phosphorylation, and inhibition of apoptosis (Maxwell *et al.*, 1997; Ryan *et al.*, 2000; Hockel and Vaupel, 2001). Elevated levels of HIF-1 α protein are often associated with a poor prognosis in several human cancers (Birner *et al.*, 2000; Talks *et al.*, 2000; Zhong *et al.*, 2000; Beasley *et al.*, 2002; Koukourakis *et al.*, 2002).

On the other hand, in certain cancer cells, such as renal or lung cancers, HIF-1 α directly and indirectly inhibits *c-Myc* function, resulting in either p21-mediated cell cycle arrest or apoptosis (Savai *et al.*, 2005; Gordan *et al.*, 2007). Direct or indirect interaction of HIF-1 α and p53 also contributes to the regulation of tumor development (Hammond and Giaccia, 2006). Induction of the proapoptotic target genes such as *BINP3* may also explain the tumor suppressor capability of HIF-1 α (Sowter *et al.*, 2001). Considering the many functions and effects of HIF-1 α (Semenza, 2003), it is likely that its contribution in tumor progression is complex and dependent on the cell origin and status of other activated or inactivated genes.

HIF-1 α expression in non-melanoma skin cancer

HIF-1 α expression has not yet been studied in basal cell carcinoma, and

little is known about the role of HIF-1 α in skin SCC. HIF-1 α gain of function in keratinocytes results in an increased number of papillomas, a benign neoplasm that sometimes converts to a premalignant lesion, after chemical carcinogenesis induction (Scortegagna *et al.*, 2009). This observation can partially be explained by HIF-1 α overexpression-mediated increased angiogenesis, which was documented to be an early event in papilloma development (Bolontrade *et al.*, 1998; Elson *et al.*, 2001; Scortegagna *et al.*, 2009). Although these papillomas appear earlier, their proliferation is lower and their cells are more differentiated, suggesting suppression of epithelial-mesenchymal transition. Furthermore, conversion of these papillomas to SCCs is largely inhibited compared with those formed in control mice (Scortegagna *et al.*, 2009). The effect of HIF-1 α upregulation on SCC differentiation may be related to HIF-1 α -mediated upregulation of p21, which has a key role in the onset of keratinocyte growth arrest and differentiation upon different stimuli (Missero *et al.*, 1995; Todd and Reynolds, 1998). Consistently, the intradermal injection of HIF-1 α small interfering RNA was recently found to diminish p21 expression in rat epidermis and to induce skin hyperplasia (Cho *et al.*, 2008, 2010).

In addition to the role of HIF-1 α in SCC formation, it may have another role in tumoral invasion for the following reasons: (1) several angiogenic factors, namely, VEGF, fibroblast growth factor-2, platelet-derived growth factor, and angiopoietin are expressed in SCCs (Czubayko *et al.*, 1997; Strieth *et al.*, 2000; Hawighorst *et al.*, 2002; Bran *et al.*, 2009); (2) HIF-1 α regulates the expression of numerous angiogenic factors and metalloproteinases; and (3) VEGF can increase HIF-1 α mRNA translation into protein via phosphoinositol-3 kinase and AKT (Semenza, 2000; Kilic *et al.*, 2006). Consistently, overexpression of VEGF-A in immortalized keratinocytes leads to invasive and malignant SCCs following xenografting into immunodeficient mice (Lederle *et al.*, 2010), whereas the metastatic ability of transfected VEGF-null keratinocytes is

completely abolished (Mirones *et al.*, 2009). Although the incidence and angiogenic status of chemically induced SCCs in mice overexpressing the angiogenesis inhibitor endostatin in keratinocytes is comparable to the incidence in control mice, both lymph vessels and lymphatic metastases are highly reduced in tumors carrying these keratinocytes, indicating an inhibitory role for endostatin in the aggressiveness of the tumor (Brideau *et al.*, 2007).

HIF-1 α and melanoma

This cancer has a high propensity to metastasize early, which results in high mortality. Alteration of several signaling pathways, such as NRAS, BRAF, phosphatase and tensin homolog/phosphatidylinositol 3-kinase/AKT, and p16/ARF, occurs in melanoma and leads to acquisition of growth advantages, resistance to apoptosis, and invasive/metastatic behavior (Cannon-Albright *et al.*, 1996; Demunter *et al.*, 2001; Davies *et al.*, 2002; Stahl *et al.*, 2004).

Constitutive activation of AKT characterizes a high percentage of human melanomas and is associated with a poor prognosis. AKT has been shown to transform melanocytes only when cells are grown in a hypoxic environment in an HIF-1 α -dependent manner (Bedogni *et al.*, 2005, 2008). Melanomas harboring the BRAF mutation, BRAF^{V600E}, have higher expression of HIF-1 α (Kumar *et al.*, 2007). Enhanced HIF-1 α expression in these melanoma cells results in a higher cell survival in hypoxic conditions, suggesting that the effects of the oncogenic BRAF^{V600E} mutation may be partially mediated by the HIF-1 α pathway (Kumar *et al.*, 2007). However, melanocytic nevi, the pigmented lesions that are usually quiescent/senescent and rarely progress to melanoma, also comprise cells with the BRAF^{V600E} mutation (Garraway *et al.*, 2005), suggesting that these melanocytes have to acquire additional alterations to escape senescence and become cancerous. Amplification of microphthalmia-associated transcription factor might be one of these modifications. In fact, microphthalmia-associated transcription factor has been shown to be amplified in a large number of melanomas containing the

BRAF mutation (Garraway *et al.*, 2005). It has been found that microphthalmia-associated transcription factor can regulate HIF-1 α expression by binding directly to the HIF-1 α promoter, and that overexpression of HIF-1 α has prosurvival effects on melanoma cells (Busca *et al.*, 2005).

Besides BRAF and AKT, increased ROS level, NF κ B activation (Kuphal *et al.*, 2010), and overexpression of endothelin B receptor (Spinella *et al.*, 2007) could all result in increased HIF-1 α expression and activity in melanomas. An endothelin-mediated increase in HIF-1 α expression can promote VEGF secretion and matrix metalloproteinase activation in melanoma cells, which in turn affects their invasion capacity (Spinella *et al.*, 2007). Altogether, these studies suggest a tumor-promoting effect of HIF-1 α in melanoma.

HIF-1 α IN NON-CANCER SKIN DISORDERS

HIF-1 α in microbial infection

In addition to serving as the body's outermost protective covering, the skin protects the body against infectious diseases by its innate immune responses, especially the production of antimicrobial peptides capable of inactivating many microorganisms (Boukamp *et al.*, 1988; Ganz, 2002; Braff and Gallo, 2006). It has been reported that HIF-1 α is upregulated in the skin upon infection with various bacterial, viral, fungal, or parasitic infections both *in vitro* or *in vivo* (Werth *et al.*, 2010). Using a keratinocyte-targeted deletion of HIF-1 α , it has been shown that HIF-1 α provides protection against necrotic skin lesions induced by bacteria via upregulation of cathelicidin, an antimicrobial peptide coded by the human *LL-37* gene (Peyssonnaud *et al.*, 2008). Interestingly, cathelicidin production is decreased in some inflammatory skin disorders such as atopic dermatitis (Ong *et al.*, 2002).

HIF-1 α in psoriasis

Several lines of evidence suggest that HIF-1 α could have an important role in psoriasis, a chronic skin disease characterized by keratinocyte

hyperproliferation, epidermal inflammation, and angiogenesis. In fact, pivotal angiogenic genes such as *VEGF* and its receptors are upregulated in psoriasis (Detmar *et al.*, 1994). Transgenic mice with VEGF upregulation in keratinocytes show inflammation and all the hallmarks of psoriasis, suggesting a causative role of VEGF in this disease (Xia *et al.*, 2003). On the other hand, transgenic delivery to the skin of inflammatory mediators, such as tumor necrosis factor- α or keratinocyte growth factors like transforming growth factor- α , did not completely reproduce the psoriatic phenotype (Vassar and Fuchs, 1991; Cheng *et al.*, 1992; Guo *et al.*, 1993; Carroll *et al.*, 1997; Schon, 1999), suggesting that VEGF upregulation is an early step in the pathophysiology of this disease (Detmar, 2004). HIF-1 α has been found to be upregulated in psoriatic epidermis, in an expression pattern similar to VEGF mRNA expression (Rosenberger *et al.*, 2007; Tovar-Castillo *et al.*, 2007; Ioannou *et al.*, 2009), thereby suggesting a possible application of HIF-1 α inhibitors in the therapy of psoriasis.

HIF-1 α in systemic sclerosis and keloids

Apart from infection and psoriasis, upregulation of HIF-1 α has been reported in systemic sclerosis and keloids. Systemic sclerosis is characterized by microvascular alterations and excessive fibrosis of the skin and the internal organs. Activation of HIF-1 α in dermal fibroblasts of systemic sclerosis patients might contribute to the progression of skin fibrosis (Hong *et al.*, 2006; Distler *et al.*, 2007) via upregulation of connective tissue growth factor, a cytokine expressed by the endothelium and fibroblasts (Hong *et al.*, 2006). Keloids are skin fibrotic conditions characterized by an excessive accumulation of ECM components in response to cutaneous injury. Upregulation of plasminogen activator inhibitor-1 in an HIF-1 α -dependent manner contributes to keloid pathogenesis (Zhang *et al.*, 2004). Metabolic analysis of keloid fibroblasts indicated a bioenergetics similar to that of most cancer cells, i.e., increased glycolysis and decreased oxidative

phosphorylation, which might be related to increased HIF-1 α expression (Vincent *et al.*, 2008).

In summary, growing evidence strongly supports an important role of HIF-1 α signaling in non-cancer skin pathophysiology, although the detailed mechanistic aspects and therapeutic applications remain relatively unexplored.

CONCLUSION AND PERSPECTIVES

Although fetal skin develops in a liquid milieu, adult epidermis is in contact with the atmospheric oxygen and its oxygenation depends heavily on atmospheric oxygen (Stucker *et al.*, 2002). Thus, the skin faces dramatically different environments between the fetal and neonatal periods. It is well known that skin barrier maturation is important immediately after birth in humans and that premature babies can be oxygenated through the skin (Fluhr *et al.*, 2010). Considering the functions of HIF-1 α , its role could be crucial in the context of neonatal adaptation to atmospheric conditions to increase the maturation of the epidermal barrier as well as to adapt neonatal dermal vascularization. Some of the HIF-1 α -regulated genes such as *XPD* (Rezvani *et al.*, 2010a) are involved in the transcriptional machinery, and their mutation can affect epidermal differentiation, which manifests at birth with a collodion membrane engaging the skin, as noted in the disease trichothiodystrophy (Morice-Picard *et al.*, 2009; Rezvani *et al.*, 2010b).

Besides the neonatal period, it is likely that HIF-1 α has an important role in the regulation of physiological skin responses to different stressors. By affecting the expression of various key cutaneous genes, HIF-1 α regulates cutaneous angiogenesis, controls inflammatory and innate immune responses, modulates skin responses to sunlight by affecting the DNA repair machinery, apoptosis, and lastly the tumorigenic processes. Thus, its importance in dermatology deserves closer attention.

CONFLICT OF INTEREST

The authors state no conflict of interest.

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