

# Hypoxia Contributes to Melanoma Heterogeneity by Triggering HIF1 $\alpha$ -Dependent Phenotype Switching

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We have previously reported a model for melanoma progression in which oscillation between melanoma cell phenotypes characterized by invasion or proliferation is fundamental to tumor heterogeneity and disease progression. In this study we examine the possible role of hypoxia as one of the microenvironmental influences driving metastatic progression by promoting a switch from a proliferative to an invasive phenotype. Immunohistochemistry on primary human cutaneous melanoma biopsies showed intratumoral heterogeneity for cells expressing melanocytic markers, and a loss of these markers correlated with hypoxic regions. Furthermore, we show that the downregulation of melanocytic markers is dependent on hypoxia inducible factor 1 $\alpha$  (HIF1 $\alpha$ ), a known regulator of the hypoxic response. *In vitro* invasion assays showed that a hypoxic environment increases the invasiveness of proliferative melanoma cell cultures in a HIF1 $\alpha$ -dependent manner. In contrast, invasive phenotype melanoma cells showed no increase in invasive potential upon exposure to hypoxia. Thus, exposure of proliferative melanoma cells to hypoxic microenvironments is sufficient, in a HIF1 $\alpha$ -dependent manner, to downregulate melanocytic marker expression and increase their invasive potential.

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## INTRODUCTION

Melanoma is a growing public health burden because it is one of the few cancers still escalating in incidence (Jemal *et al.*, 2009). Despite advances in understanding the molecular nature of melanoma in recent decades, few treatment options are available for metastatic melanoma that only marginally increase overall patient survival (Lui *et al.*, 2007; Bollag *et al.*, 2010; Hodi *et al.*, 2010; Joseph *et al.*, 2010; Chapman *et al.*, 2011; Robert *et al.*, 2011; Flaherty *et al.*, 2012). One reason why melanoma is difficult to treat is its heterogeneity (Fidler, 1978). The source of this heterogeneity is unclear, but evidence suggests that it is driven by microenvironmental factors (Postovit *et al.*, 2006).

In the process of studying melanoma heterogeneity, we described different subtypes of melanoma cells *in vitro* (Hoek *et al.*, 2006) that can be distinguished by gene-expression analysis (Widmer *et al.*, 2012). These differences in gene

expression correlate with alterations in *in vitro* cell morphology, proliferation rate, invasion, transforming growth factor- $\beta$  susceptibility, and *in vivo* tumor growth kinetics (Hoek *et al.*, 2006; Hoek *et al.*, 2008a). These experiments have identified a proliferative phenotype and an invasive melanoma cell phenotype. Previous work showed that primary and metastatic lesions are commonly composed of a mixture of both phenotypes (Eichhoff *et al.*, 2010, 2011). We subsequently hypothesized that melanoma cells, responding to changes in microenvironmental conditions, change their transcription programs to switch back-and-forth between proliferative and invasive states and thereby drive metastatic progression (Hoek *et al.*, 2008a).

As other cancers, melanoma tumors include regions of hypoxia and anoxia caused by an imbalance in both oxygen supply and consumption. It has long been known that the perfusion of tumors is heterogeneous resulting in a wide range of pO<sub>2</sub> levels both within and between tumors (Chaplin *et al.*, 1986). It is estimated that the proportion of solid tumors with hypoxic (or anoxic) areas is up to 50–60% (Vaupel and Mayer, 2007). The negative impact of tumor hypoxia has been studied extensively. Early studies have shown that hypoxia-induced gene amplification can lead to resistance to treatment (Rice *et al.*, 1987; Luk *et al.*, 1990). In many cancer types, the induction of an epithelial-to-mesenchymal transition (EMT)-like process by exposure to an intralesional hypoxic microenvironment is currently under investigation. Tumor hypoxia is known to reduce the sensitivity of solid tumors to radiation therapy and can negatively influence treatment outcome and patient survival in multiple cancer types (Hockel *et al.*, 1996; Vergis *et al.*, 2008).

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Abbreviations: EMT, epithelial-to-mesenchymal transition; GLUT1, glucose transporter 1; HIF1 $\alpha$ , hypoxia inducible factor 1 $\alpha$ ; MTF, microphthalmia-associated transcription factor; qRT-PCR, quantitative real-time reverse-transcriptase-PCR; siRNA, silencing RNA

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Two recent studies of hypoxia in melanoma demonstrate a role for hypoxia in downregulating the master regulator of melanocyte differentiation, microphthalmia-associated transcription factor (MITF). A study by Cheli *et al.* (2012) showed that hypoxic conditions lead to a decrease in MITF expression and that a deletion of MITF is sufficient to increase the metastatic potential of mouse and human melanoma cells *in vivo*. They identified BHLHE40 (BHLHB2, DEC1) as a mediator of the observed hypoxia inducible factor 1 $\alpha$  (HIF1 $\alpha$ )-dependent inhibitory effect on MITF. In another study also published in 2011, the authors (Feige *et al.*, 2011) found BHLHE40 to be responsible for hypoxia-induced downregulation of MITF.

To investigate the role of hypoxia in melanoma progression, we describe the effects of hypoxia on proliferative and invasive melanoma cell cultures. The results suggest that hypoxia, through HIF1 $\alpha$ , alters the gene-expression pattern of proliferative melanoma cells, making them more invasive in *in vitro* assays.

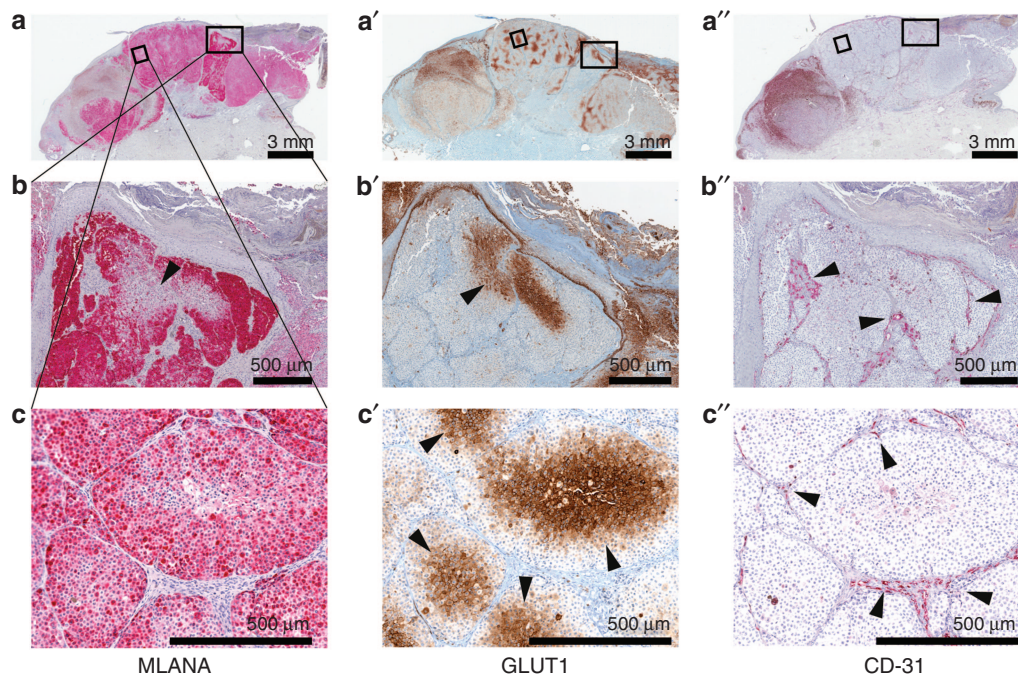
## RESULTS

To gain more insight into the nature of intratumor heterogeneity in patients, we stained Clark's level IV primary human cutaneous melanoma biopsies for key markers of melanocytic function, hypoxia response, proliferation, and vascularization. Immunohistochemical stainings show that the tumor is mostly composed of tumor cell nodules (Figure 1a''–c''), which are surrounded by stroma and endothelial cells (Figure 1c'', arrowheads). CD31 (*PECAM-1*), which is expressed constitutively on the surface of adult and embryonic endothelial cells

(Pusztaszeri *et al.*, 2006), was used to stain blood vessels. Glucose transporter 1 (GLUT1) (*SLC2A1*), a glucose transporter that has been shown to be upregulated in hypoxic tissue (Bashan *et al.*, 1992; Loike *et al.*, 1992), was upregulated with increasing distance from blood vessels in multiple regions of the tumor (Figure 1c', arrowheads). Panel a of Figure 1 shows that the majority, but not all, of the cells in the tumor express melanoma antigen recognized by T cells 1 (MLANA) that is involved in melanosome biogenesis and has been widely used to identify melanocytic lesions (Busam *et al.*, 1998). In the hypoxic areas, which are indicated by arrowheads in a', we found downregulation of the melanocytic marker MLANA (Figure 1a', arrowheads as compared with Figure 1b') and MITF (data not shown). To further illustrate the presence of hypoxia in the tumor, we co-stained tumor slides for HIF1 $\alpha$  and GLUT1 (Supplementary Figure S2 online). As proliferative phenotype cell cultures strongly express these melanocytic markers, whereas invasive phenotype cell cultures do not express them at all, their expression indicates a dedifferentiation of the melanoma cells and points toward a gain of invasive phenotype characteristics (Hoek *et al.*, 2006, 2008a; Eichhoff *et al.*, 2010, 2011; Zipser *et al.*, 2011). These data suggest that by exposure to a hypoxic microenvironment, melanoma cells downregulate melanocytic marker genes.

### Hypoxia-regulated EMT genes are differentially expressed between the two phenotypes

Intratumoral hypoxia has been shown to induce regulators of EMT and metastasis in breast-, colon-, prostate-, and non-small cell lung cancer (Luo *et al.*, 2006; Peinado and Cano,



**Figure 1. Immunohistochemistry of a primary cutaneous melanoma.** Overview pictures of a representative melanoma tumor are shown in the top row (a, b, c); boxes on the right-hand side of a, b, and c indicate regions of higher magnification shown in a', b', and c', and boxes on the left side highlight the magnified region in a'', b'', and c''. Staining for MLANA (a, a', and a'') shows regions with high expression and regions that have lost expression of this melanocytic marker (arrowhead). GLUT1 (b, b', and b'') stains hypoxic areas (arrowheads). CD31 shows blood vessels (c, c', and c'', arrowheads). Scale bars = 3 mm (a), 500  $\mu$ m (b), and 500  $\mu$ m (c). MLANA, melanoma antigen recognized by T cells 1.

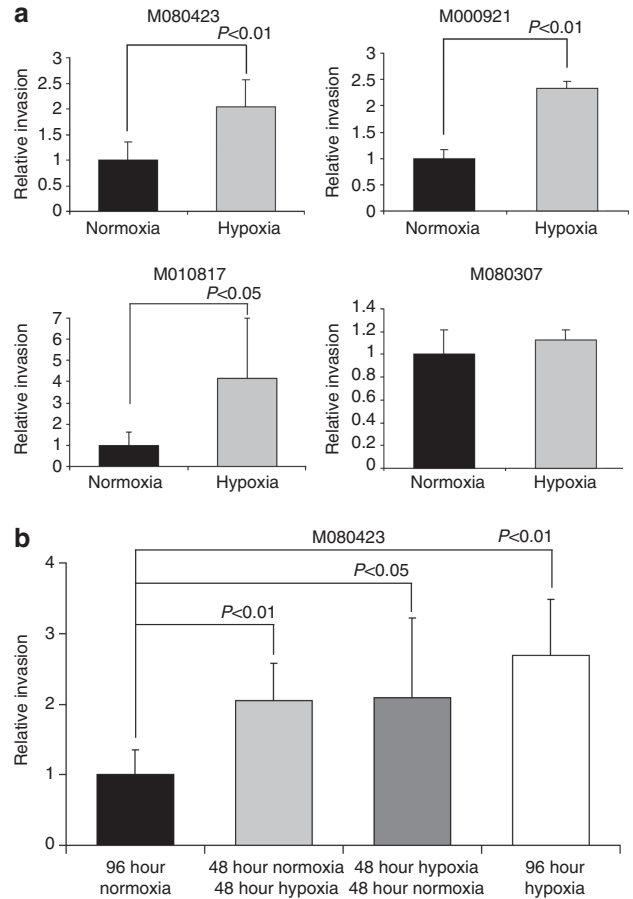
2008; Hung *et al.*, 2009; Jo *et al.*, 2009; Sipos and Galamb, 2012). An expression analysis of some of the genes known to be involved in this process shows a phenotype-specific expression pattern (Supplementary Figure S1 online). *LOX*, *ZEB1*, and *MMP2*, which are upregulated in the invasive phenotype, have been shown to be involved in EMT, but also in hypoxia-induced tumor invasiveness and metastasis (Ray and Stetler-Stevenson, 1994; Postigo and Dean, 1997; Hojilla *et al.*, 2003; Stamenkovic, 2003; Ertler *et al.*, 2006; Peinado *et al.*, 2008; Spaderna *et al.*, 2008; Baranwal and Alahari, 2009; Elloul *et al.*, 2010; Jia *et al.*, 2012; Xiong *et al.*, 2012). In development, as well as in the process of EMT and cancer progression, E-cadherin (CDH1) is repressed and leads to a loss of the extracellular matrix as well as of adherens and tight junctions (Peinado *et al.*, 2007). However, mesenchymal cadherins, such as N-cadherin (CDH2), are upregulated during EMT (Oda *et al.*, 1998; Peinado *et al.*, 2004). This cadherin switch can also be observed in proliferative and invasive melanoma phenotypes, with an upregulation of CDH1 in proliferative cells and an upregulation of CDH2 in invasive cells (Supplementary Figure S1 online). These findings suggest that an EMT-like process is involved in the switching of melanoma cells from proliferative to invasive phenotypes.

**Hypoxia changes *in vitro* invasive potential in proliferative melanoma cells in a dose-dependent manner**

To further test if hypoxia drives proliferative cells to a more invasive state, we treated proliferative phenotype cells with 1% O<sub>2</sub> for 48 hours and tested their invasiveness *in vitro* by performing Boyden chamber experiments. The proliferative cell cultures treated with hypoxia showed a significant increase in invasion compared with the non-treated control cells (Figure 2a). The relative invasion increased by 2-fold for M080423, 2.3-fold for M000921, and even 4.2-fold for M010817. However, invasive phenotype cells (i.e., M080307) in identical treatment conditions did not show any change in invasiveness (*P*-value = 0.399) (Figure 2a). To test if the gain of invasive ability required the continued lack of oxygen, we returned the cells to normoxia for 48 hours after a hypoxia treatment period of 48 hours. In Figure 2b (dark gray bar), we show that the effect remained significant after cells were returned to normoxia 48 hours before testing invasion. When the cells were exposed to hypoxia for 96 hours, the effect was intensified (Figure 2b, white bar). However, proliferative melanoma cells in hypoxic conditions do not alter their proliferation rate (Supplementary Figure S3 online).

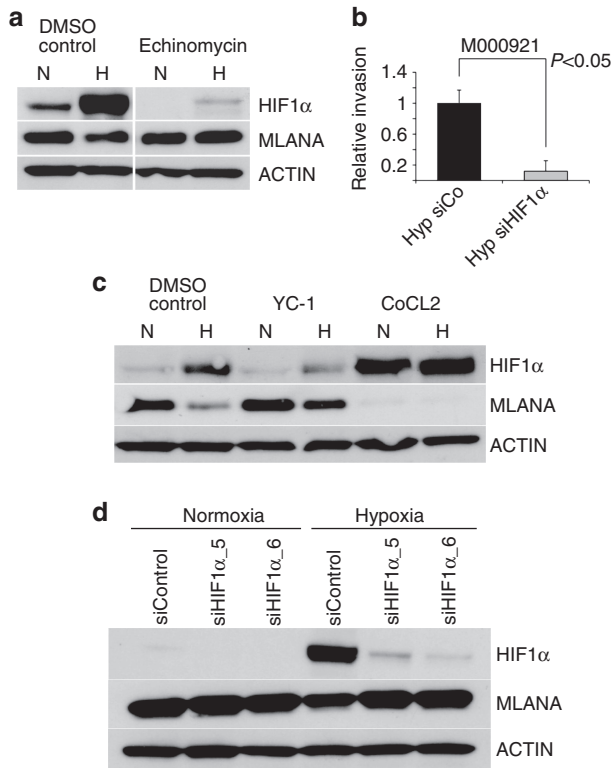
**Downregulation of *MLANA* during hypoxia is mediated by *HIF1α***

The inverse correlation of hypoxic areas with the expression of melanocytic markers like *MLANA* (Figure 1) raises the question whether the decrease in the expression of this protein is mediated by *HIF1α*, a known regulator of the hypoxic response. To test this possibility, we treated proliferative phenotype melanoma cells (i.e., M000921) with chemical compounds to either suppress or activate signaling through



**Figure 2. Hypoxia increases *in vitro* invasion in proliferative melanoma cells.** *In vitro* invasiveness of proliferative (M080423, M010817, and M000921) and invasive (M080307; *P*-value = 0.399) phenotype melanoma cell cultures (a). Hypoxia treatment of a proliferative melanoma cell culture (M080423) induces increased invasiveness in a dose-dependent fashion (b). Light gray bar: incubated in normoxia for 48 hours and subsequently analyzed in a Boyden chamber assay in hypoxia for 48 hours; dark gray bar: vice versa. The *P*-values are calculated by a *t*-test; the error bars represent the s.d.

*HIF1α*. To inhibit *HIF1α* transcriptional activity, we treated the cells with Echinomycin during exposure to hypoxia (1% O<sub>2</sub> for 72 hours) (Kong *et al.*, 2005). The induction of *HIF1α* as well as the downregulation of *MLANA* could be inhibited under hypoxia (Figure 3a), and the hypoxic induction of *in vitro* invasion (Figure 2a) could be significantly abrogated by about 8-fold through *HIF1α* knockdown (Figure 3b). The same results on marker expression could be seen when we enhanced *HIF1α* degradation with the chemical compound YC-1 (Chun *et al.*, 2001) (Figure 3c). CoCl<sub>2</sub> stabilizes *HIF1α* by inhibiting proline hydroxylases, leading to *HIF1α* expression also under normoxic conditions (Epstein *et al.*, 2001), leading to downregulation of *MLANA* (Figure 3c). Because these compounds might have off-target effects and because their specificity is unclear, we also performed silencing RNA (siRNA)-mediated knockdown of *HIF1α* using two different siRNAs against the *HIF1α* transcript (Figure 3d). The results confirm a *HIF1α*-dependent downregulation of *MLANA* in

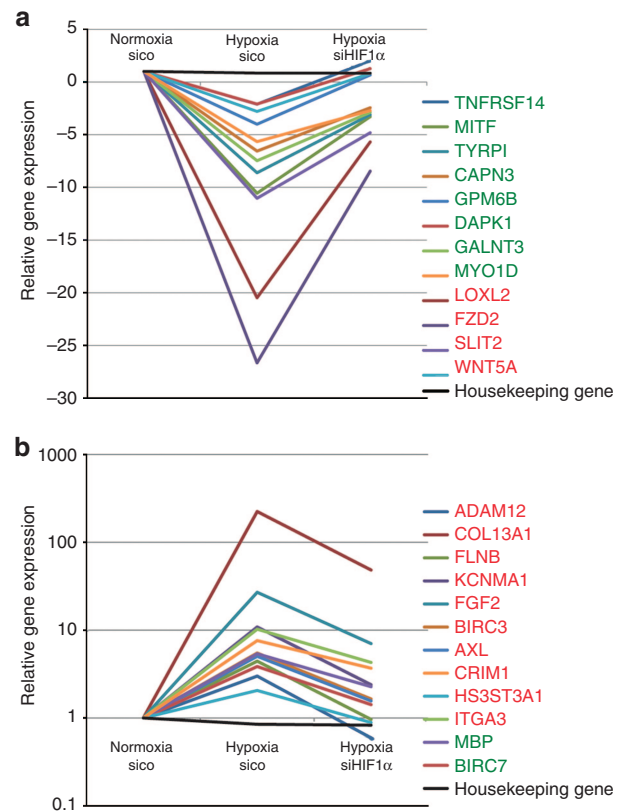


**Figure 3. Downregulation of MLANA and upregulation of *in vitro* invasion upon hypoxia treatment is hypoxia inducible factor 1α (HIF1α) dependent.** Echinomycin enhances HIF1α degradation under hypoxic conditions (a). Relative invasion under hypoxic culture conditions and treatment with silencing RNA (siRNA) against HIF1α (Hyp siHIF1α) and control siRNA (Hyp siCo), *P*-value < 0.05, done in quadruplicate (b). Treatment of proliferative melanoma cell cultures with YC-1 decreases HIF1α levels. CoCl<sub>2</sub> stabilizes HIF1α under normoxic conditions (c). Under normoxia, no HIF1α could be detected (d). Treatment with siRNA against HIF1α (siHIF1α\_5/6) and control siRNA (siControl). The *P*-value is calculated by a *t*-test; the error bars represent the s.d. MLANA, melanoma antigen recognized by T cells 1.

hypoxia, as well as a HIFα-dependent hypoxic induction of invasive properties, suggesting a role for HIF1α in the phenotype switch induced by tumor hypoxia.

#### Hypoxia regulates a phenotype-specific gene set through HIF-1α

It is likely that there are intermediate factors acting downstream of HIF1α that repress *MLANA* gene expression. To find HIF1α targets that might repress *MLANA*, we performed siRNA knockdown of HIF1α followed by quantitative real-time reverse-transcriptase-PCR (qRT-PCR) analysis. We tested 90 genes that have been previously identified to be differentially expressed between a large number of proliferative and invasive phenotype melanoma cell lines (Widmer *et al.*, 2012). These genes were assembled on a custom qRT-PCR array. This array was used to find genes that are downregulated when treated with hypoxia, but rescued when *HIF1α* is knocked down. The results show 12 genes that are at least 2-fold downregulated upon hypoxia treatment (hypoxia sico) (Figure 4a) and at least 2-fold upregulated when *HIF1α* was knocked down under hypoxic conditions (hypoxia siHIF1α) compared with normal hypoxia (hypoxia sico).



**Figure 4. qRT-PCR using RNA from hypoxia- and/or siHIF1α-treated proliferative phenotype melanoma cell cultures.** Genes that were at least 2-fold downregulated when grown in a hypoxic environment (hypoxia sico), but at least 2-fold upregulated when *HIF1α* was knocked down (hypoxia siHIF1α) (a). Genes that were at least 2-fold upregulated when grown in a hypoxic environment (hypoxia sico), but at least 2-fold downregulated when *HIF1α* was knocked down. This experiment was performed in duplicates with two different siRNAs against *HIF1α* (b). Gene names in green highlight genes that were upregulated in the proliferative phenotype melanoma cell cultures. Gene names in red indicate genes that were upregulated in the invasive phenotype cell cultures.

Of the 12 genes, 8 were upregulated in the proliferative phenotype cell cultures (Figure 4a, gene names in green) and 4 were upregulated in invasive phenotype cell cultures (Figure 4a, gene names in red). We were also interested in genes that were upregulated at least 2-fold upon hypoxia treatment (hypoxia sico), but had an at least 2-fold decreased expression when HIF1α is knocked down under hypoxic conditions (hypoxia siHIF1α) compared with normal hypoxia (hypoxia sico). Of the 12 genes fulfilling these criteria, 10 were upregulated in the invasive phenotype cells (Figure 4b, gene names in red), whereas 2 genes were upregulated in the proliferative phenotype cell cultures (Figure 4b, gene names in green). The results show that 18 (75%) out of the 24 genes regulated by HIF1α were differentially regulated between the proliferative and invasive phenotype melanoma cell lines in such a way that proliferative genes were downregulated and invasive genes are upregulated by HIF1α (i.e., genes with green text in Figure 4a, and genes with red text in Figure 4b).

## DISCUSSION

The characterization of different subsets of melanoma cells in a tumor lesion is of major clinical relevance, because all the subpopulations of melanoma cells need to be killed for successful therapeutic intervention. The exceptional transcriptional and phenotypic plasticity of melanoma cells has so far hampered the discovery of single prognostic factors or target molecules appropriate for general melanoma therapy. In our previous work, we demonstrated that invasive phenotype melanoma cells are less susceptible to MAPK inhibition and that proliferative phenotype melanoma cells temporarily switch their phenotype to one with more invasive features during drug treatment (Zipser *et al.*, 2011). Furthermore, immunotherapy targeting melanocytic markers will not eradicate the invasive phenotype cells, because these markers are downregulated upon phenotype switching.

Recently published studies have shown inter- and intratumoral heterogeneity for driver mutations like *BRAF* or *KIT*, suggesting a limited scope for current therapies in personalized medicine that target specifically mutated serine or tyrosine kinases (Sakaizawa *et al.*, 2012; Yancovitz *et al.*, 2012). Not only is intrinsic genetic heterogeneity of importance as a basis for tumor progression, but acquired heterogeneity that is induced by microenvironmental factors may also lead to therapeutic resistance. To overcome intrinsic as well as acquired resistance, it is imperative to understand tumor heterogeneity at the genetic and transcriptional levels.

We have previously shown that melanoma cells with high MITF and MLANA expression are only weakly invasive *in vitro*, whereas melanoma cells with no MITF and MLANA expression are highly invasive (Hoek *et al.*, 2006; Eichhoff *et al.*, 2011; Zipser *et al.*, 2011). Immunohistochemical stainings of melanoma tumors show regions with high GLUT1 expression, indicating hypoxic regions which anti-correlate with the melanocytic markers MITF and MLANA (Figure 1). These results suggest that in a hypoxic microenvironment, melanocytic markers are downregulated, which is a sign of cell dedifferentiation that is also evident in invasive phenotype cells. These data confirm the results of an earlier study in which proliferative markers (i.e., MLANA and MITF) were anti-correlated with invasive markers (WNT5A) and hypoxia (GLUT1) in melanoma (Eichhoff *et al.*, 2010). Conversely to what Eichhoff *et al.* reported, we also observed GLUT1 expression in many nested, nicely organized tumor regions (Figure 1). Although the staining for CD31 suggests the presence of blood vessels around the tumor cell nests, it seems that either the nests are too large or the blood vessels are not fully functional so that the melanoma cells become hypoxic.

To identify the role that hypoxia might have in melanoma progression, we measured the effect of hypoxic conditions on the *in vitro* invasive potential of proliferative melanoma cells by performing Boyden chamber invasion assays. The results showed a significant increase in invasion from 2- to more than 4-fold for all tested proliferative cell cultures (Figure 2a). An invasive cell line (i.e., M080307) did not display such an increase in invasive potential (Figure 2a). We also showed that the higher *in vitro* invasiveness observed in proliferative

melanoma cultures is dose dependent, lasts at least 48 hours, and increases with longer exposure time up to 96 hours (Figure 2b).

Because one of the mediators of hypoxic responses in many cell types is the HIF1 $\alpha$  protein, we modulated its expression level and could show that the hypoxic downregulation of MLANA is HIF1 $\alpha$  dependent (Figure 3). We demonstrate that a knockdown of HIF1 $\alpha$  under hypoxic conditions decreases *in vitro* invasion by about 8-fold, thereby suggesting a requirement for HIF1 $\alpha$  in the hypoxic-induced invasive ability of proliferative melanoma cell cultures (Figure 3b). Possible mediators for this effect were identified by qRT-PCR analysis of 90 genes, which are differentially expressed between the proliferative and invasive melanoma phenotypes (Widmer *et al.*, 2012). Analysis of these data showed 12 genes to be downregulated by hypoxia treatment, but not when *HIF1 $\alpha$*  is knocked down (Figure 4). Of these, eight genes are commonly downregulated in the invasive melanoma cell cultures and therefore potentially involved in the switch from a proliferative to an invasive phenotype. Interestingly, *MITF* and its target tyrosinase-related protein 1 are among these genes (Figure 4). Also, *TNFRSF14*, *CAPN3*, *GPM6B*, and *DAPK1*, which are potential targets of *MITF* that we have previously identified (Hoek *et al.*, 2008b), are differentially expressed. This suggests an important role for HIF1 $\alpha$ -regulated *MITF* in the process of hypoxia-induced phenotype switching. Furthermore, two of these genes are known to have a pro-apoptotic function: calpain 3 (*CAPN3*) (Moretti *et al.*, 2009) and death-associated protein kinase 1 (*DAPK1*) (Lin *et al.*, 2007). In addition, glycoprotein M6B (*GPM6B*) has been shown to be downregulated in highly invasive melanoma cells versus poorly invasive lines (Seftor *et al.*, 2002).

Furthermore, a set of 12 genes is induced by hypoxia but not when *HIF1 $\alpha$*  is knocked down (Figure 4). Ten of these genes are upregulated in the invasive phenotype melanoma cell cultures and are therefore of particular interest (Figure 4). One of the most interesting genes encodes fibroblast growth factor 2, a mitogenic and angiogenic factor that can act as an autocrine growth factor for melanoma cells (Halaban *et al.*, 1988; Becker *et al.*, 1989). *AXL*, a receptor tyrosine kinase, has been shown to be expressed only in MITF-negative melanoma cells (Sensi *et al.*, 2011), confirming our own results (Hoek *et al.*, 2006; Widmer *et al.*, 2012). Sensi *et al.* also showed that *AXL* increases the motility and invasion of melanoma cells. *HIF1 $\alpha$*  appears also to induce the expression of multiple genes that encode proteins involved in interactions with the extracellular matrix, such as ADAM12, a disintegrin and metalloproteinase (COL13A1), a transmembrane collagen chain (ITGA3), an integrin alpha subunit, and FLNB, a filamin known to bind to the actin cytoskeleton (Prockop and Kivirikko, 1995; Takafuta *et al.*, 1998; Danen and Sonnenberg, 2003; Lendeckel *et al.*, 2005; Kveiborg *et al.*, 2008). The upregulation of *BIRC3*, a gene encoding an apoptosis inhibitor, is consistent with the downregulation of two pro-apoptotic genes (*CAPN3* and *DAPK1*). The potassium channel *KCNMA1*, which is also upregulated in the presence of hypoxia in a HIF1 $\alpha$ -dependent manner, could be regulated

by MITF over the microRNA miR-211 (Mazar *et al.*, 2010). Further studies have to determine if inhibition of one or more of these factors can abrogate the tumor-promoting effect of HIF1 $\alpha$ .

The data presented here suggest that hypoxia is a possible microenvironmental stimulus triggering a switch from a proliferative to an invasive melanoma cell phenotype. By down-regulating melanocytic genes, HIF1 $\alpha$  induces an EMT-like dedifferentiation to a more invasive type of melanoma cell. Upregulation of pro-angiogenic and pro-tumorigenic factors, as well as of extracellular matrix-modifying genes along with a downregulation of pro-apoptotic genes, may allow the invasive melanoma cells to contribute to melanoma progression.

## MATERIALS AND METHODS

### Cell culture

M-series primary melanoma cell cultures were set up from surplus material from cutaneous melanoma and melanoma metastases in our laboratory. Many of these lines have been previously published and have been shared with multiple international laboratories for *in vitro*, genomic, and xenografting assays (Lin *et al.*, 2008; Hoek *et al.*, 2008a; Eichhoff *et al.*, 2011; Zipser *et al.*, 2011; Kiowski *et al.*, 2012; Widmer *et al.*, 2012). Written informed consent was approved by the local IRB (EK647 and EK800). Clinical diagnosis was confirmed by histology and immunohistochemistry. Melanoma cells were brought into culture as previously described (Geertsens *et al.*, 1998). Melanoma cell cultures were grown in RPMI (Invitrogen, Carlsbad, CA) including 5 mM glutamine, 1 mM sodium pyruvate, and 10% heat-inactivated fetal bovine serum (GIBCO 10500; Invitrogen), and they were grown at 37°C and 5% CO<sub>2</sub>. The study was conducted according to the Declaration of Helsinki Principles.

### Quantitative real-time reverse-transcriptase-PCR

Total RNA was extracted from primary melanoma cell cultures using TRIzol according to the manufacturer's instructions (Invitrogen). Total RNA was used for cDNA synthesis using Promega's Reverse Transcription System (Promega, Madison, WI) or RT HT First Strand cDNA kit for the qRT-PCR arrays according to the supplied protocols. Gene expression was quantified using the FastStart Universal SYBR Green Master (ROX; 04913914001; Roche, Basel, Switzerland) and the Vii7 system from Applied Biosystems (Carlsbad, CA). The primers for MITF and WNT5A were purchased from Qiagen (Venlo, the Netherlands). The qRT-PCR arrays (Custom RT2 Profiler PCR Array (CAPI10586E-6)) were purchased from SA Biosciences (Qiagen, Venlo, the Netherlands).

### Western blot analyses

Cells were washed twice with cold phosphate-buffered saline and lysed at 4°C in RIPA protein lysis buffer as previously reported (Dissanayake *et al.*, 2007). Proteins were separated by SDS-PAGE using the NuPAGE SDS-PAGE Gel System (Invitrogen) on 4–12% Tris-glycine gels (Invitrogen) under reducing conditions according to the manufacturer's instructions and transferred onto nitrocellulose membranes (Invitrogen). Primary antibodies used were: HIF1 $\alpha$ : mouse monoclonal anti-HIF1 $\alpha$  1:1000 (610959; BD Biosciences, San Jose, CA); MLANA: mouse monoclonal anti-MLANA 1:1000, (ab3168; Abcam, Cambridge, UK); ACTIN: goat polyclonal anti-Actin 1:1000 (sc-1616; Santa Cruz Biotechnology, Dallas, TX). Secondary antibodies used were: rabbit polyclonal anti mouse IgG-HRP

(ab97046, Abcam) and Rabbit anti-goat IgG-HRP (sc-2768, Abcam). Bound antibodies were detected using ECL Western Blotting Detection Reagent (28906836; GE Healthcare).

### *In vitro* invasion assay (Boyden chamber assays)

*In vitro* invasion assays were performed using Matrigel-coated cell inserts (BD Biosciences; 354480) and uncoated cell inserts (BD Biosciences; 353097) according to the manufacturer's instructions. A total of  $5 \times 10^4$  cells in 500  $\mu$ l starving medium were seeded onto cell culture inserts. RPMI containing 10% fetal calf serum was used as chemoattractant. After incubation at 37°C for 48 hours, the cells on the membranes were fixed, stained, cut out, and mounted on a glass slide. The number of cells, which had moved through the pores to the other side of the membrane, was assessed by microscopy. Invasion values were calculated by dividing the number of cells migrating through Matrigel-coated inserts by the number of cells migrating through uncoated inserts.

### Proliferation assay

Melanoma cells were counted after 24, 48, and 72 hours, and doubling time was calculated.

### Immunohistochemical stainings

All tissue used for immunohistochemistry was fixed in 4% paraformaldehyde and embedded in paraffin. Sections were deparaffinized in xylene and rehydrated. Epitope retrieval was performed in antibody specific buffers. Staining was performed using kits supplied by Ventana (Tucson, AZ) or Dako (Glostrup, Denmark) REAL Detection System (kit 5005). Antigen-specific antibodies were applied and visualized with either the iVIEW DAB detection kit (Ventana) or the Chem-Mate detection kit (Dako). Slides were counterstained with haematoxylin. Antibodies used were: MLANA (Novocastra, Leica Biosystems, Nussloch, Germany; NCL-L-MLANA; EDTA; 1:50), GLUT1 (Cell Marque, Rocklin, CA; 355A-16; EDTA; 1:100), CD31 (Dako; M0823; Protein kinase K; 1:40), and Hif1 $\alpha$  (Abcam; mgc3, ab16066).

### Hypoxia treatment

Cells were cultured in a Modular Incubator Chamber (MIC-101; Billups-Rothenberg, Del Mar, CA), flushed with 20 l min<sup>-1</sup> (flow meter; RMA-23-SSV; Dwyer, Michigan City, IN) with certified premixed gas composed of 1% O<sub>2</sub>, 5% CO<sub>2</sub>, and 94% N<sub>2</sub> (Carbagas, Guemligen, Switzerland). The O<sub>2</sub> concentration inside the chamber was measured with an oxygen sensor (VTI-122, Disposable Polarographic Oxygen Cell, 100122; Vascular Technology, Nashua, NH). The hypoxia chamber was placed in an incubator at 37°C. Medium exchange and splitting of the cells was performed outside the hypoxic environment. To stabilize HIF1 $\alpha$  expression in melanoma cells under normoxic conditions, cells were treated with 100  $\mu$ M CoCl<sub>2</sub> (Sigma-Aldrich, St Louis, MO) for 24, 48 or 72 hours. To inhibit expression or stabilization of HIF1 $\alpha$  in melanoma cells under hypoxic conditions, cells were treated with 60  $\mu$ M YC-1 (Calbiochem, Merck, Darmstadt, Germany) or 5 nM of Echinomycin *Streptomyces* sp (Calbiochem).

### siRNA transfections

siRNA transfection of melanoma cells was carried out using INTERFERin transfection solution according to the manufacturer's protocol (Polyplus Transfection, Illkirch, France). Cells were transfected with

10 nM of siRNA (Qiagen) for 24, 48 or 72 hours before RNA or protein was extracted. As control siRNA, the All-Star negative siRNA sequence (Qiagen) was used. siRNA used were: Hs\_HIF1A\_5 (NM\_001530; S102664053, Qiagen FlexiTube) and Hs\_HIF1A\_6 (NM\_001530; S102664431, Qiagen FlexiTube).

#### CONFLICT OF INTEREST

The authors state no conflict of interest.

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#### SUPPLEMENTARY MATERIAL

Supplementary material is linked to the online version of the paper at <http://www.nature.com/jid>

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