E4F1-mediated control of pyruvate dehydrogenase activity is essential for skin homeostasis

To cite this version:

HAL Id: inserm-02465232
https://www.hal.inserm.fr/inserm-02465232
Submitted on 11 Mar 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
E4F1-mediated control of pyruvate dehydrogenase activity is essential for skin homeostasis

Perrine Goguet-Rubia, Berfin Seyran, Laurie Gayte, Florence Bernex, Anne Sutter, Hélène Delpech, Laetitia Karine Linares, Romain Riscal, Cendrine Repond, Genevieve Rodier, Olivier Kirsh, Jawida Touhami, Jean Noel, Charles Vincent, Nelly Piroton, Guillaume Pavlovic, Yann Herault, Marc Sitbon, Luc Pellerin, Claude Sardet, Matthieu Lacroix, and Laurent Le Cam

*Institut de Recherche en Cancérologie de Montpellier, Montpellier F-34298, France; *INSERM U1194, Montpellier F-34298, France; *University of Montpellier, Montpellier F-34090, France; *Institut Régional du Cancer de Montpellier, Montpellier F-34298, France; *Équipe labellisée Ligue Contre le Cancer, 75013 Paris, France; *Réseau d’Histologie Experimen- tallel of Montpellier, BioCampus, CNRS-UMS3426, F-34094 Montpellier, France; *Institut de Génétique Moléculaire de Montpellier, CNRS-UMR5535, Montpellier 34293, France; *Département de Physiologie, University of Lausanne, 1005 Lausanne, Switzerland; *Epigenetics and Cell Fate, University Paris Diderot, Sorbonne Paris Cité, UMR7216 CNRS, Paris 75013, France; and *Institut de la Clinique de la Souris-Mouse Clinical Institute, PHENOMIN, CNRS-UMR7104, INSERM U964, Université de Strasbourg, Illkirch, France

Edited by Steven L. McKnight, The University of Texas Southwestern Medical Center, Dallas, TX, and approved August 5, 2016 (received for review February 18, 2016)

The multifunctional protein E4 transcription factor 1 (E4F1) is an essential regulator of epidermal stem cell (ESC) maintenance. Here, we found that E4F1 transcriptionally regulates a metabolic program involved in pyruvate metabolism that is required to maintain skin homeostasis. E4F1 deficiency in basal keratinocytes resulted in deregulated expression of dihydrolipoamide acetyltransferase (Dlat), a gene encoding the E2 subunit of the mitochondrial pyruvate dehydrogenase (PDH) complex. Accordingly, E4f1 knock-out (KO) keratinocytes exhibited impaired PDH activity and a redirection of the glycolytic flux toward lactate production. The metabolic reprogramming of E4f1 KO keratinocytes associated with remodeling of their microenvironment and alterations of the basement membrane, led to ESC mislocalization and exhaustion of the ESC pool. shRNA-mediated depletion of Dlat in primary keratinocytes recapitulated defects observed upon E4f1 inactivation, including increased lactate secretion, enhanced activity of extracellular matrix remodeling enzymes, and impaired clonogenic potential. Altogether, our data reveal a central role for Dlat in the metabolic program regulated by E4f1 in basal keratinocytes and illustrate the importance of PDH activity in skin homeostasis.

Significance

We found that the multifunctional protein E4 transcription factor 1 (E4F1) transcriptionally regulates a metabolic program involved in pyruvate metabolism that is required to maintain skin homeostasis. E4F1 deficiency in skin resulted in deregulated expression of dihydrolipoamide acetyltransferase (Dlat), a gene encoding the E2 subunit of the mitochondrial pyruvate dehydrogenase (PDH) complex. Accordingly, E4f1 knock-out (KO) keratinocytes exhibited impaired PDH activity and a metabolic reprogramming associated with remodeling of their microenvironment and alterations of the basement membrane, leading to epidermal stem cell mislocalization and exhaustion of the epidermal stem cell pool. Our data reveal a central role for Dlat in the metabolic program regulated by E4f1 in skin and illustrate the importance of PDH activity in skin homeostasis.


The authors declare no conflict of interest.

This article is a PNAS Direct Submission.

1P.G.-R. and B.S. contributed equally to this work.
2M.L. and L.L.C. contributed equally to this work.
3To whom correspondence may be addressed. Email: matthieu.lacroix@inserm.fr or laurent.lecam@inserm.fr.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1602751113/-/DCSupplemental.
inactivation in the epidermis results in ESC defects through a mechanism that involves, at least partly, the deregulation of the Bmi1–Arf–p53 pathway (7). Here, we show evidence supporting a major role for E4F1 in pyruvate metabolism that governs ESC maintenance and skin homeostasis.

Results

**E4f1 Inactivation in Basal but Not Suprabasal Adult Keratinocytes Leads to Epidermal Defects and Exhaustion of the ESC Pool.** Using E4f1 whole-body conditional KO mice (E4f1(K10): RERT), we previously identified an essential role for E4f1 in adult skin homeostasis (7). In this genetically engineered mouse model, E4f1 inactivation was achieved in the entire skin of adult animals, including the dermal compartment. To assess the cell of origin of these skin defects, we generated new mouse strains by crossing E4f1 conditional KO mice to transgenic animals expressing the tamoxifen (tam) -inducible CreER recombinase under the control of the keratin 14 (K14) or keratin 10 (K10) promoters [hereafter referred to as E4f1(K14)KO and E4f1(K10)KO strains], allowing acute inactivation of E4f1 in adult keratinocytes of the basal or spinous layers, respectively (20).

Molecular and histological analyses of adult back skin of 8- to 12-wk-old E4f1(K10)KO animals confirmed that topical skin applications of tam activated the Cre recombinase in suprabasal but not in basal keratinocytes (Fig. S1). Neither histological alterations nor differences in the expression pattern of the basal-cell specific K14 marker and of the differentiation markers K10 and involucrin were identified in skin samples harvested up to 4 mo upon regular tam administration (Fig. S2). In sharp contrast, K10 and involucrin were identified in skin samples harvested up to 2 wk after tam administration, E4f1(K14)KO mice resulted in skin phenotypes that recapitulated those originally observed in tam-treated E4f1(K14)KO mice (18, 22). Thus, 2 wk after tam administration, E4f1(K14)KO mice displayed epidermal hyperplasia (acanthosis), altered differentiation (dykeratosis), and a thicker and parakeratotic cornified layer (Fig. L4 and S3). Aberrant hyperproliferation and mislocalisation of basal keratinocytes was evidenced in E4f1-deficient epidermis by increased Ki67 staining, the presence of K14+ cells in suprabasal layers, and the expression of keratin 6 (K6) in the IFE (Fig. S4). At later time points (4–5 wk after tam administration), E4f1-deficient epidermis then became hypocoelular, whereas the hyperkeratosis remained evident (Fig. L4). In addition, impaired keratinocyte differentiation was illustrated by aberrant expression of K10 and involucrin (Fig. S4).

Consistent with our previous observations, ablation of E4f1 in adult basal keratinocytes altered ESC function and resulted in the definitive exhaustion of the ESC pool. Indeed, tam administration to E4f1(K14)KO mice led to the loss of expression of the bulge HF stem cell marker keratin 15 (K15) (Fig. 1B). Flow cytometry analysis of HF stem cells identified by the coexpression of CD34 and high levels of α6-integrin (CD34+/α6high) confirmed that tam-treated E4f1(K14)KO adult epidermis contained fewer HF stem cells compared with control epidermis (0.65% ± 0.15% vs. 2.25% ± 0.4%) (Fig. 1C). We also tracked ESCs in the IFE by analyzing the number of label retaining cells (LRCs) using an adaptation of an in vivo labeling protocol of multipotent ESCs located in the bulge area (BG) of the HF. (Scale bar, 100 μm.) (C) Number of follicular stem cells (FSC) in back skin epidermis prepared from the same mice as in B. FACS analysis of αCD34+CD34high FSC in back skin epidermis prepared from the same mice as in B (mean ± SEM, n = 10). (D) Number of label-retaining (EdU+) interfollicular stem cells (LRCs) detected by immunofluorescence (IF) on back-skin sections prepared from adult E4f1(K14)KO mice or E4f1(K14)CTR littermates, 5 wk after tam application. Histobars represent the mean value ± SEM of EdU+ cells per millimeter of epidermis (n = 5 animals per group). (E) Clonogenic assays performed with E4f1KO and CTRL primary murine keratinocytes cultured in presence or absence of 4OHT, as indicated (n = 5). Histobars represent the total number of colonies per well relative to control cells (expressed as percentages) determined after rhodamine B staining. ***p < 0.001; **p < 0.01; ns, not significant.

**E4F1 Controls Pyruvate Metabolism in Keratinocytes Through Transcriptional Regulation of the E2 Subunit of the Pyruvate Dehydrogenase Complex Dlat.** Using a pan-genome ChIP approach combined with next-generation sequencing (ChIP-seq), we identified E4F1 binding sites at the whole-genome level in primary mouse embryonic fibroblasts and embryonic stem cells (18, 22). Functional annotation of E4F1 direct target genes indicated a significant enrichment in genes implicated in metabolism, including a set of five genes encoding core components or regulators of the mitochondrial pyruvate dehydrogenase (PDH) complex (PDC), a multicimeric complex that converts pyruvate into Acetyl-CoA (AcCoA). In embryonic stem cells, this set of E4F1-controlled genes includes the E2 and E3 subunits of the PDH complex, dihydrolipoamide acetyltransferase (Dlat) and dihydrolipoyl dehydrogenase (Dld), the regulatory subunit of the PDH phosphatase complex (Pdp1), the pyruvate transporter of the inner mitochondrial membrane Brp44l/Mpc1 (23, 24), and the mitochondrial transporter Slc25a19 that transports the PDH cofactor thiamine pyrophosphate (25). These results prompted us to evaluate whether E4F1 also controlled this set of PDH-related genes in primary keratinocytes. First, we confirmed by quantitative ChIP that endogenous E4F1 was recruited to the promoter of Dlat, Dld, Slc25a19, and Brp44l in cultured primary murine keratinocytes (Fig. 2A). Similarly to E4f1KO fibroblasts and muscle cells, E4F1-deficient keratinocytes displayed a marked decrease of Dlat mRNA level. However, the expression of Dld, Pdp1, Slc25a19, and Brp44l/Mpc1 remained unchanged upon E4f1 inactivation, suggesting that other E4F1-independent mechanisms contribute to their expression in keratinocytes (Fig. 2B). The mRNA levels of other PDH-related genes, including Pdhb1, which encodes the E1
subunit of the PDC, the PDH -kinases 1/4 (Pdk1, Pdk4) and -phosphatas 1/2 (Pdp1, Pdp2) remained unchanged in E4f1-deficient keratinocytes (Fig. S5). Decreased Dlat expression was confirmed at the protein level, as shown by immunostaining of skin samples prepared from E4f1(K14)KO animals, 1 wk after tam-administration. This decrease was further confirmed by immunoblotting both in tam-treated E4f1(K14)KO epidermis and in cultured E4f1KO primary keratinocytes (Fig. 2 C–E). Consistent with DLAT deregulation, altered PDH enzymatic activity was detected in these cells (Fig. 2 F and G and Fig. S6A). Taken together, these data indicate that the E2 subunit of the PDC Dlat is a major direct transcriptional target of E4f1 in basal keratinocytes.

**E4f1KO Results in Metabolic Reprogramming of Keratinocytes.** Next, we characterized the metabolic consequences of impaired PDH activity in E4f1-deficient keratinocytes. We postulated that decreased PDH activity in E4f1-deficient keratinocytes triggered a decrease of glucose-derived AcCoA production and the redirection of the glycolytic flux toward lactate production (Fig. 3A). Consistent with this hypothesis and the role of AcCoA as a direct substrate for acetylation reactions, E4f1KO keratinocytes exhibited decreased histone H4 acetylation, as shown by immunoblotting using an anti-pa-acetyl lysine histone H4 antibody (Fig. 3B). Moreover, in line with increased pyruvate metabolism by the NADH-dependent lactate dehydrogenase (LDH), E4f1KO keratinocytes displayed an increased NAD+/NADH ratio (Fig. 3C). Increased expression of the glucose transporter GLUT1 suggested that glucose uptake increased upon E4f1 inactivation in keratinocytes (Fig. S6B). These cells also exhibited increased expression of the monocarboxylate transporter MCT4 that favors the efflux of lactate outside the cell (Fig. 3 D and E). Accordingly, increased lactate secretion by E4f1KO keratinocytes was evidenced by a change in their extracellular acidification rate (ECAR) (Fig. 3F). Other metabolic changes were observed in E4f1-deficient keratinocytes, as illustrated by increased fatty acid oxidation (FAO) (Fig. 3G). This adaptive metabolic response was likely sufficient to sustain mitochondrial respiration because no significant difference was observed in oxygen consumption upon E4f1 inactivation in keratinocytes cultured in complete medium (Fig. S6D). Analyses of tam-treated E4f1(K14)KO mice and control littermates confirmed that E4f1-deficient keratinocytes underwent the same metabolic

![Fig. 2. E4f1 inactivation in basal keratinocytes results in decreased Dlat expression and impaired PDH activity. (A) ChIP-qPCR assays performed with anti-E4f1 or control (CTR) antibodies in cultured primary keratinocytes on the promoter region of Dlat, Did, Mpc1brp44L, Pdpr, and Slc25a19. A gene-poor noncoding region of chromosome 6 (NC2) and the Pdha1 promoter region (TSS, transcription start site) were used as controls. Enrichments are represented as percentages of input (mean value ± SEM; n = 3). (B) mRNA levels of E4f1, Dlat, Did, Brp44L, Mpc1, Pdpr, and Slc25a19 in the epidermis of E4f1(K14)KO mice or E4f1(K14)CTR littermates, 1 wk after tam administration. Histobars represent the mean value ± SEM (n = 5) determined by RT-qPCR. (C) Protein levels of E4f1, Dlat, PDHA1, and α-actin (loading control) determined by immunoblotting in (C) total protein extracts prepared from epidermis of E4f1(K14)KO mice and control littermates, 1 wk after tam administration, or (D) E4f1KO or CTR cultured primary keratinocytes. (Non-specific band. (E) Immunostaining of DLAT in skin sections prepared from the same mice as in C. Sections were counterstained with DAPI. Scale bar, 50 μm.) (F and G) PDH activity measured in protein extracts prepared (F) from epidermis of E4f1(K14)KO and CTR mice, 1 wk after tam administration, or (G) from cultured primary keratinocytes of the indicated genotype using Colorimetric Assay kit (Biovision) (mean ± SEM, n = 5). All analyses in cultured primary keratinocytes were performed after 4 d of culture in the presence of 40μT. **P < 0.001; ***P < 0.001; *P < 0.05; ns, not significant.

![Fig. 3. Metabolic reprogramming of E4f1-deficient keratinocytes. (A) Schematic representation of the metabolic reprogramming in E4f1KO keratinocytes including the redirection of the glycolytic flux toward lactate production. (B) Protein levels of acetylated-lysine histone H4 and α-actin (loading control) determined by immunoblotting in total protein extracts prepared from epidermis of E4f1(K14)KO mice (Upper) or from E4f1KO cultured primary keratinocytes (Lower) and match control (CTR) samples. (C) NAD+/NADH ratio in E4f1KO and CTR cultured primary keratinocytes (mean ± SEM; n = 9). (D and E) MCT4 expression was determined by IF (D) and by immunoblotting (E) in E4f1KO and CTR cultured primary keratinocytes. (Magnification: 40x.) (F) ECAR of E4f1KO and CTR primary keratinocytes in basal conditions or after addition of glucose (mean ± SEM; n = 5). (H) Relative level of FAO measured upon incubation of E4f1KO and CTR cultured keratinocytes with 3H-palmitate (mean ± SEM of n = 5 samples per group). (K) Chorionic assays performed with E4f1KO and CTR primary keratinocytes in presence or absence of acetate, as indicated (n = 3). **P < 0.001; ***P < 0.001; *P < 0.05; ns, not significant. TCA, tricarboxylic acid cycle.
reprogramming in vivo. Thus, immunohistochemistry (IHC) analyses of skin samples prepared from these animals indicated that E4f1 inactivation in basal keratinocytes resulted in increased expression of GLUT1, MCT4, and of CD147/BASIGIN, a chaperone required for MCT4 relocalization at the cytoplasmic membrane (Fig. 3H and Fig. S6C). Strikingly, E4f1(K14)KO mice exhibited lactacidemia and increased level of circulating ketone bodies, a by-product of FAO (Fig. 3 I and J). Moreover, the clongenic potential of E4f1/KO keratinocytes was partly rescued by addition of exogenous acetate that can replenish AcCoA pools (Fig. 3K), confirming that the profound metabolic reprogramming of E4f1-deficient keratinocytes impinged on their biological functions.

**Metabolic Reprogramming of E4f1-Deficient Keratinocytes Associates with Remodeling of the Microenvironment and Loss of Adhesion of the ESC with the Basement Membrane.** In many tumors, increased lactate secretion has been linked to the remodeling of the extracellular matrix (ECM) and degradation of the basement membrane (BM) by ECM-remodeling enzymes (26). To further characterize the consequences of the metabolic reprogramming of E4f1-deficient keratinocytes, we performed histological analyses of E4f1(K14)KO skin. Electron microscopy analyses indicated that E4f1 inactivation in basal keratinocytes resulted in dysfunction of the BM, which appeared either diffused with thinner lamina densa or focally disrupted (Fig. S7A). Alterations of the BM in E4f1KO skin was confirmed upon staining of skin sections by the Gomori reticulin method, which stains the argyrophilic (silver staining) fibrous structures present in the BM (Fig. S7B). Immunostaining of skin samples prepared from E4f1(K14)KO mice with anti-laminin V antibody showed that the expression pattern of this essential component of the BM was diffused and focally discontinuous in E4f1KO skin sections compared with its defined and continuous pattern in control samples (Fig. 4A). This defect also correlated with an abnormal expression pattern of integrin β4 (Igβ4). In areas showing broad disruption of the BM, Igβ4 expression was not restricted to the basal pole of keratinocytes but was also detected at the apical or lateral sides of both basal and suprabasal keratinocytes (Fig. 4A). Remodeling of the ECM within the dermal compartment was also evidenced by picro-Sirius red staining of collagen fibers on skin sections prepared from tam-treated E4f1(K14)KO mice (Fig. S7C). These results led us to investigate whether the massive remodeling of the ECM and alterations of the BM observed upon E4f1 inactivation resulted from increased activity of ECM-remodeling enzymes. Increased matrix metalloproteinase 9 (MMP9) and cathespin activities were detected by gelatin-zymography in protein extracts prepared from total skin samples of tam-treated E4f1(K14)KO mice (Fig. 4B and Fig. S7D). Moreover, increased MMP2, MMP9, and cathespin activities were also evidenced in the culture medium of E4f1KO primary keratinocytes (Fig. 4 C and D). Addition of the LDH-inhibitor oxamate in the culture medium decreased cathepsin activities in these cells (Fig. 4D). Moreover, stable expression of ectopic TIMP1, a broad MMP inhibitor, in feeder cells partly rescued the clongenic potential of E4f1KO ESC (Fig. 4E). Improved clonogenicity of E4f1-deficient ESC was also observed upon incubation with GM6001, a pharmacological MMP inhibitor with broad spectrum (Fig. 4F). Taken together, these data indicate that the induction of ECM remodeling enzymes in E4f1-deficient keratinocytes is a consequence of their metabolic reprogramming and impinges on their clongenic potential.

Based on these results, we hypothesized that the observed disruption of the BM impacted on the maintenance of ESC within their normal microenvironment, leading to the definitive exhaustion of the ESC pool. To test this hypothesis, we analyzed EdU+ LRCs on skin sections prepared from tam-treated E4f1(K14)KO mice or control littermates 2 wk after tam administration and evaluated their localization within the epidermis. The same skin sections were also processed to assess MCT4 expression as a surrogate marker of the metabolic reprogramming of E4f1KO keratinocytes.
keratinocytes. Two weeks after tam administration, E4f1KO epidermis displayed approximately the same number of EdU+ LRCs than control epidermis (0.25 ± 0.05 vs. 0.23 ± 0.02 per millimeter, respectively). However, the number of E4f1KO LRCs in a suprabasal position was significantly increased compared with LRCs of control epidermis that remained, as expected, in the basal layer (suprabasal: 0.1 ± 0.04 vs. 0.01 ± 0.01; basal: 0.14 ± 0.03 vs. 0.21 ± 0.003 per millimeter, respectively) (Fig. 4G). Interestingly, this atypical feature of E4f1KO LRCs was particularly evident within focal epidermal lesions exhibiting MCT4 positivity, whereas LRCs remained in contact with the BM in the adjacent MCT4+ areas of the same epidermis (Fig. 4G). Five weeks after tam administration, the number of LRC diminished in E4f1KO epidermis, confirming that E4f1 inactivation finally ended in the exhaustion of the ESC pool (Fig. 1D). Thus, these data show that the metabolic reprogramming triggered by E4f1 inactivation in basal keratinocytes associates with the remodeling of their microenvironment and alterations of the BM, leading to the loss of attachment of the ESC within their normal niche and their definitive loss.

**Discussion**

Our analyses performed in different mouse models where E4f1 was genetically inactivated in the basal or the spinous layers of the epidermis show that the complex skin phenotypes observed upon E4f1 inactivation originate from defects in basal keratinocytes. Our results indicate that E4f1 deficiency in these cells leads to a metabolic reprogramming of keratinocytes that affects skin homeostasis and ended in the definitive exhaustion of the ESC pool. We found that this metabolic shift, which includes the redirection of the glycolytic flux toward lactate production, is a direct consequence of PDH deficiency. Moreover, our data identify DLAT, the E2 subunit of the PDC, as an essential component of this metabolic program regulated by E4f1 in keratinocytes.

Whether E4f1-mediated control of the PDC in keratinocytes is clinically relevant remains to be determined. It is worth noting, however, that a homozygous nonsynonymous mutation in the coding region of the E4f1 gene has been recently identified in a patient presenting clinical symptoms resembling those of Leigh syndrome patients (27). Although skin abnormalities have been reported only in some Leigh syndrome patients (28), they are part of the broad spectrum of clinical manifestations that are commonly observed in several mitochondrial disorders (29). Further investigations are necessary to evaluate whether E4f1-mediated control of mitochondrial activities, which likely extend beyond the control of the PDC, contribute to the skin manifestations observed in these patients.

Another pathological situation that has been associated with changes in PDH activity is cancer. Interestingly, the metabolic reprogramming of E4f1-deficient keratinocytes is reminiscent of the one observed in many cancer cells that display increased aerobic glycolysis, even in high oxygen conditions, an effect known as the Warburg effect. It is well established that PDH deregulation in cancer cells can result from posttranslational modifications of PDC subunits by inhibitory kinases (PDKs), activating phosphatases (PDPs), or the lipooamidase SIRT4 (30, 31). We failed to detect deregulation of Pdks and Pdps mRNA levels in E4f1KO keratinoocytes, and our data rather support the notion that transcriptional control of Dlat is the main mechanism by which E4f1 controls PDH activity in normal epidermal cells. It remains to be seen whether E4f1-mediated control of Dlat is an alternative regulatory mechanism of the PDC in skin cancer cells. Nevertheless, our data clearly show that the control of PDH activity by E4f1 in basal keratinocytes is essential for normal skin homeostasis.

Interestingly, as with cancer cells, we show that the metabolic reprogramming of E4f1KO basal keratinocytes results in increased activity of ECM-remodeling enzymes, including MMPs and cathepsins. The exact molecular mechanism by which increased glycolysis activates MMP activity in cancer cells remains controversial. Previous studies have suggested that the MCT-chaperone CD147/BASIGIN increases MMP activity through a yet undefined mechanism (32). However, recent data contradict this working model (33). Whatever the mechanism, the high glycolytic profile and increased activity of tissue-remodeling enzymes, including MMPs and cathepsins, strongly suggest that E4f1KO keratinocytes recapitulate some features of cancer cells, including their ability to induce the focal degradation of the basement membrane and to remodel their microenvironment. Here, we show that these alterations impact on ESC maintenance within their niche, leading to their mechanical elimination and ending in the complete exhaustion of the ESC pool. Interestingly, we previously reported that the ability of E4f1 to control the Bmi1–ARF–p53 pathway partly contributes to ESC self-renewal (7). These data raise interesting questions regarding the connection between the metabolic reprogramming of E4f1-deficient keratinocytes and the deregulation of the p53 pathway in these cells. The potential cross-talk between PDH activity and the control of the p53 pathway is a promising hypothesis that warrants further investigation.
It was recently proposed that basal keratinocytes rely more on glycolysis to sustain their energetic demand than their differentiated progeny in which mitochondrial-reactive oxygen species trigger epithelial differentiation through Notch and β-catenin signaling (6). Our data do not necessarily contradict this model, but provide clear evidence that when glycolysis is further increased in basal keratinocytes, such as in E4F1-deficient cells, this profoundly alters epithelial homeostasis and ESC maintenance. Our results also question the mechanisms leading to the inhibition of keratinocyte differentiation observed in E4f1KO epidermis.

Altogether our results identify E4F1 as an essential regulator of the metabolic status of basal keratinocytes and stress the importance of a tight control of the PDH activity for epithelial homeostasis.

**Materials and Methods**

**Generation of Mouse Models and Experimental Treatment.** Generation of E4f1 KO and E4f1 KO mice was previously described (7, 19). These mice were intercrossed with K14CreER (20) or K10CreERT2 (5) mice to generate experimental groups (E4f1+/-flox, K14CreER, E4f1+/-flox, K14CreER, E4f1+/-flox, K10CreERT2, and E4f1+/-flox, K14CreER (referred to as E4f1K14C1TR, E4f1K14KO, E4f1K10C1TR, E4f1K10KO, respectively). Compound mice were maintained on a mixed genetic background (129Svl/DBA/C57Bl6) and housed in a pathogen-free barrier facility. Cre-mediated recombination of the E4f1+/- allele was induced by topical applications of tamoxifen (Sigma; diluted in ethanol, 2 mg/dl for 4 consecutive days) on the shaved skin of 8- to 12-week-old animals. Experiments were approved by the regional ethics committee for animal welfare (Comité éthique pour l’expérimentation animale du Languedoc Roussillon, protocol 12068). Oligonucleotides used for genotyping these animals are provided in **SI Materials and Methods**.

**Histology, IHC, and Immunolabeling of Skin Sections.** IHC and immunolabeling of skin sections were performed as previously described (7) using the following antibodies: anti-DLAT (sc-32925 Santa Cruz), MCT4 (sc-50329 Santa Cruz), BASIGIN (G-19 sc-9757, Santa Cruz), Laminin V (generous gift from C. Feral’s laboratory, University of Nice, Nice, France), Int54 (553745 BD Pharmingen), K14 (PRB-155P (Covance), K10 (PRB-155P Covance), Involucrin (sc-15230 Santa Cruz).

**Culture of Primary Keratinocytes.** Murine primary keratinocytes were isolated from newborn skin as previously described (7) and grown in calcium-free Eagle’s MEM (Bio-Whittaker; Lonza) supplemented with 8% (vol/vol) calcium-free serum (FBS), 1% (vol/vol) penicillin/streptomycin (Bio-Whittaker; Lonza) and 2 mM L-glutamine. Primary keratinocytes were cultured under standard conditions (103(4):392. (2015) The transcription factor E4F1 coordinates CHK1-dependent cell-cycle arrest and mitotic functions. Cell Rep 11(2):220–233.