FOXO1 promotes wound healing through the up-regulation of TGF-β1 and prevention of oxidative stress

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Keratinocyte mobilization is a critical aspect of wound re-epithelialization, but the mechanisms that control its precise regulation remain poorly understood. We set out to test the hypothesis that forkhead box O1 (FOXO1) has a negative effect on healing because of its capacity to inhibit proliferation and promote apoptosis. Contrary to expectations, FOXO1 is required for keratinocyte transition to a wound-healing phenotype that involves increased migration and up-regulation of transforming growth factor β1 (TGF-β1) and its downstream targets, integrin-α3 and -β6 and MMP-3 and -9. Furthermore, we show that FOXO1 functions in keratinocytes to reduce oxidative stress, which is necessary to maintain cell migration and prevent cell death in a TGF-β1-independent manner. Thus, our studies identify a novel function for FOXO1 in coordinating the response of keratinocytes to wounding through up-regulation of TGF-β1 and other factors needed for keratinocyte migration and protection against oxidative stress, which together promote migration and decrease apoptosis.

Introduction

Cutaneous wound healing is a highly coordinated multistep process that involves inflammation, re-epithelialization, granulation tissue formation, remodeling of basement membrane and extracellular matrix, and dermal and epidermal maturation. The initial inflammatory response stimulates the release of growth factors and chemokines that initiate the later phases of wound repair (Singer and Clark, 1999; Martin and Leibovich, 2005; Li et al., 2007; Raja et al., 2007). The process of wound re-epithelialization requires efficient coordination of multiple events, including the formation of a provisional wound bed matrix, the migration of epidermal keratinocytes into the wound, the proliferation of keratinocytes, and the differentiation of new epithelium into stratified epitherm (Raja et al., 2007).

Keratinocyte migration is critical for re-epithelialization and is tightly regulated by various signaling pathways (Ridley et al., 2003). After an injury, the basal and suprabasal keratinocytes migrate from the wound edge to re-epithelialize the wounded tissue (Martin, 1997). However, the transcription factors that activate and initiate keratinocyte mobilization in response to wound healing have not been well established. Keratinocyte migration during wound healing is influenced by several factors (Martin, 1997). An impaired keratinocyte migration, but not defects in proliferation or differentiation, is associated with chronic healing defects and is a limiting factor in wound healing (Raja et al., 2007). Keratinocyte migration is initiated by various growth factors including transforming growth factor β1 (TGF-β1). TGF-β1 is one of the most extensively studied molecules and its role in promoting wound healing is well established (Tsuboi et al., 1992; Bennett and Schultz, 1993; Werner and Grose, 2003). In contrast, some reports suggest that TGF-β1 signaling in epidermal keratinocytes negatively affected wound healing (Ashcroft et al., 1999; Guasch et al., 2007). Activation of TGF-β1 leads to phosphorylation and nuclear translocation of its downstream targets.
signaling molecules SMAD2/3, which in turn induces target genes involved in cell proliferation and migration (Klass et al., 2009). TGF-β1 promotes keratinocyte migration by stimulating the expression of various integrins including integrin β6 (Gailit et al., 1994; Zambruno et al., 1995; Margadant and Sonnenberg, 2010).

Accumulating evidence suggests that reactive oxygen species (ROS) such as hydrogen peroxide (H2O2) and superoxide (O2−) are important regulators of wound healing (Schäfer and Werner, 2008). Wound healing induces a small increase in ROS, which are removed by protective antioxidant defense mechanisms. Low levels of ROS are essential to stimulate wound healing (Nishio and Watanabe, 1997; Rodríguez et al., 2008; Guo and Dipietro, 2010), whereas high levels result in epithelial cell damage and impaired wound repair (Xu et al., 2009).

The forkhead box O1 (FOXO1) transcription factor belongs to a large family of forkhead transcription factors that share a highly conserved forkhead DNA-binding domain. FOXO1 participates in a wide range of cellular processes including cell cycle arrest, DNA repair, apoptosis, and oxidative stress resistance (Myatt and Lam, 2007; Ho et al., 2008). FOXO1 controls cell cycle progression by regulating target genes such as p27Kip1 and p21 (Medema et al., 2000), apoptosis by regulating target genes such as Fas ligand and Bim (Dijkers et al., 2000), and protects against oxidative stress by up-regulating oxygen radical scavengers, such as manganese superoxide dismutase (Ponugoti et al., 2012). Although FOXO1 has been shown to be up-regulated in wounds (Siqueira et al., 2010), its role in wound healing has not been examined.

We investigated the functional impact of FOXO1 deletion in normal wound repair by generating keratinocyte-specific FOXO1-deficient mice in vivo and by RNAi in primary cultures of dermal keratinocytes in vitro. Because FOXO1 inhibits proliferation and promotes apoptosis we hypothesized that FOXO1 would negatively regulate wound healing. Contrary to our expectations, our results show that FOXO1 is needed to orchestrate the cellular events critical to wound healing by promoting keratinocyte migration and wound healing primarily through up-regulation of TGF-β1, but also by protection against oxidative stress through a TGF-β1–independent mechanism. Thus, a FOXO1 agonist may be an important therapeutic means to enhance the wound-healing response.

**Results**

**Keratinocyte-specific FOXO1 deletion delays wound closure**

To determine the role of FOXO1 in wound healing, we generated mice with deletion of FOXO1 in keratinocytes by breeding floxed FOXO1 mice with keratin 14 (K14) Cre-expressing mice. Small excisional wounds of 2.0 mm were made in the scalp of 16-wk-old K14.Cre−.FOXO1L/L mice and K14.Cre−.FOXO1L/L mice. Real-time PCR analysis of wounded mouse skin demonstrates an 80% loss of FOXO1 expression in the skin of K14.Cre−.FOXO1L/L mice compared with control K14.Cre−.FOXO1L/L mice (P < 0.05; Fig. 1 A). Immunofluorescence with FOXO1-specific antibody with histological sections from K14.Cre−.FOXO1L/L and K14.Cre−.FOXO1L/L mice establish an 80% reduction of FOXO1 expression specifically in the epidermis of K14.Cre−.FOXO1L/L compared with littermate control mice (Fig. 1, B and C). In contrast, there was little difference observed in the connective tissue (Fig. 1 B), demonstrating lineage-specific deletion in keratinocytes. FOXO1 activation in vivo was assessed by nuclear translocation. In keratinocytes from normal unwounded tissue, FOXO1 was in the inactive state with ~10% of keratinocytes exhibiting FOXO1 nuclear localization. Upon wounding, FOXO1 nuclear localization was increased over threefold (Fig. 1 D). In contrast, deletion of FOXO1 by keratin 14–driven Cre-recombinase reduced its nuclear localization by 85% and 82% in keratinocytes of wounded and normal epithelium, respectively (Fig. 1 D). For most wounds, thickened epithelium and FOXO1 expression returned to basal levels within 2.0 mm of the wound edge.

Deletion of FOXO1 in keratinocytes markedly reduced the rate of wound healing (Fig. 1, E and F). Wound area was three-fold larger in K14.Cre−.FOXO1L/L mice compared with K14.Cre−.FOXO1L/L mice on day 3 after wounding (P < 0.05). By day 7 all the wounds in control mice were healed, but were still open in K14.Cre−.FOXO1L/L experimental mice. Moreover, most of the control mice showed a high degree of healing on day 4 whereas most of the K14.Cre−.FOXO1L/L experimental mice did not show the same degree of healing until day 7, demonstrating considerably delayed healing (Fig. 1 G).

**Loss of FOXO1 leads to reduced keratinocyte migration but not proliferation**

We performed experiments using an in vitro wound-healing assay as described in Liang et al. (2007) to assess the direct effect of FOXO1 on keratinocyte wound-healing behavior using primary normal human epithelial keratinocytes (NHEKs). FOXO1 knockdown by FOXO1 siRNA was verified by real-time PCR (Fig. 2 A) and Western blot analysis (Fig. 2 B). The closure of the scratch wound was significantly slower in FOXO1-silenced keratinocytes (Fig. S1 A). At each time point examined, FOXO1 knockdown caused a 42–70% reduction in the number of keratinocytes filling the denuded wound gap compared with cells transfected with scrambled siRNA, which was statistically significant (P < 0.05; Fig. 2 E and Fig. S1 A). In contrast, knockdown of a related FOXO transcription factor, FOXO3, had no effect (P > 0.05; Fig. 2, C–E and Fig. S1 A) at any time point under the same conditions, nor did scrambled siRNA. Thus, FOXO1 reduction in in vitro “wounds” exhibited the same deficit as in vivo wounds with FOXO1 deletion. In addition, gain of function by over-expression of FOXO1 improved the number of keratinocytes filling the wound gap significantly compared with keratinocytes transfected with empty vector alone (Fig. 2 F).

Epithelial closure of wounds is facilitated by keratinocyte proliferation and migration and reduced by apoptosis. Each parameter was examined separately. Silencing FOXO1 resulted in an 80% decrease in keratinocyte migration in a transwell assay (P < 0.05; Fig. 2 G and Fig. S1 B). Quantitative real-time PCR revealed that FOXO1 knockdown significantly decreased mRNA...
Figure 1. Keratinocyte-specific FOXO1 deletion delays wound closure. (A) Relative fold change of FOXO1 mRNA expression levels normalized to ribosomal protein L32 mRNA expression levels in the scalp wounds of control K14.Cre−.FOXO1L/L and K14.Cre+.FOXO1L/L mice as measured by qRT-PCR. (B) FOXO1-immunostained sections (red) were counterstained with DAPI (blue). Bar, 100 µm. (C) Relative intensity measurements of FOXO1 immunostaining in the epithelium. (D) Quantification of FOXO1 nuclear localization in the wounded epithelium and normal epithelium on FOXO1-immunostained sections. (E) Representative photographs of scalp wounds on day 4 and 7 from K14.Cre−.FOXO1L/L and K14.Cre+.FOXO1L/L mice. (F) Wound-healing process was analyzed at different time points after scalp wounding. Average wound area was presented as percentage of the wound area on day 0 (100%). (G) K14.Cre−.FOXO1L/L and K14.Cre+.FOXO1L/L mice were stratified into three groups: (1) high degree of healing (covering >70% of the original wound surface), light bars; (2) moderate (covering 30–70%), gray bars; or (3) little to no healing (covering >30%), dark bars. EP, epidermis; CT, connective tissues; White dashed lines demarcate the epidermis from the dermis. Asterisks indicate significant increase or decrease compared with control mice (P < 0.05). Error bars represent mean ± SEM, n = 6–9 per group.
levels of genes involved in cell migration, including TGF-β1 by 61%, integrin α3 by 60%, integrin β6 by 84%, MMP-3 by 82%, and MMP-9 by 50% (P < 0.05; Fig. 2, H–L). We also noticed a 33% decrease in ECM remodeling protein collagen IV (Fig. S5 A). In contrast, FOXO1 knockdown in human keratinocytes had no effect on proliferation (P > 0.05; Fig. S2, A–C).

**TGF-β1 treatment rescues the migration defect of keratinocytes with FOXO1 knockdown**

To establish whether FOXO1 regulation of TGF-β1 played a critical role in keratinocyte migration, a transwell migration assay was performed under conditions where FOXO1 was knocked down and TGF-β1 rescue was performed. TGF-β1 treatment completely reversed the migration defect when FOXO1 was knocked down (P > 0.05; Fig. 3 A and Fig. S1 C). Furthermore, we determined whether TGF-β1 could rescue the effect of silencing FOXO1 in the in vitro wound-healing assay. At each time point TGF-β1 treatment rescued the wound closure defect in FOXO1-silenced keratinocytes (P < 0.05; Fig. 3 B and Fig. S1 D), demonstrating that one of the principle mechanisms through which FOXO1 affects re-epithelialization in vitro is due to its impact on keratinocyte migration mediated by TGF-β1.

Because of the central importance of the above mechanism we then determined whether treatment with TGF-β1 reversed the effect of FOXO1 knockdown on integrins that participate in migration. When FOXO1 was suppressed by RNAi, TGF-β1 stimulation led to a 130% increase in integrin α3 and 316% increase in integrin β6 expression in FOXO1-silenced keratinocytes (P < 0.05; Fig. 3, C and D). Taken together, these results
Figure 3. TGF-β1 treatment rescues the migration defect of keratinocytes with FOXO1 knockdown. NHEK cells were transfected with control or FOXO1 siRNAs for 48 h and then treated with vehicle or TGF-β1. (A) Transwell migration assay of cells transfected with control or FOXO1 siRNA; the migrated cells were stained with DAPI and photographed and counted. (B) Quantitative analysis of scratch-wound closure at the indicated time points in FOXO1 knockdown cells without or with TGF-β1. The mRNA levels of integrin α3 (C) and integrin β6 (D) were analyzed by real-time PCR. (E) Cell migration was assessed by transwell migration assay and the cells that have migrated across were stained with DAPI and photographed and counted. (F) ChIP assays for binding FOXO1 to the TGF-β1 promoter were performed and ChIP-enriched DNA was quantified by qPCR with the indicated primers, and values are expressed as percentage of input DNA. (G) NHEK cells were cotransfected with a control pcDNA vector or a vector that expresses constitutively active FOXO1 (FOXO1AAA), control siRNA, or siRNA specific to FOXO1, together with TGF-β1 reporter plasmid. Renilla luciferase reporter was used as an internal control. Luciferase activity was measured 36 h after transfection. Data show mean ± SEM of at least three independent experiments. *, P < 0.05 vs. scrambled siRNA; †, P < 0.05 vs. siFOXO1; ‡, P < 0.05 vs. control pcDNA vector.
a 2.6-fold decrease in TGF-β1 promoter activity (P < 0.05; Fig. 3 G). Taken together, these results indicate that FOXO1 directly binds and transactivates TGF-β1 promoter activity and confirms that TGF-β1 is a downstream target of FOXO1.

FOXO1 knockdown results in increased keratinocyte apoptosis

To investigate whether FOXO1 knockdown affects keratinocyte apoptosis in vitro, we performed TUNEL assays (Fig. 4). Apoptosis was 2.4-fold higher in FOXO1 knockdown keratinocytes compared with the controls, whereas scrambled siRNA had no effect (P < 0.05; Fig. 4 A and Fig. S4). Results were confirmed using cell death detection ELISA (Fig. 4 B). Given that FOXO1 silencing enhanced keratinocyte apoptosis, we tested whether increased apoptosis was linked with increased expression of apoptotic genes. FOXO1 silencing significantly increased genes that promote apoptosis such as Bim by 73%, FAS ligand by 68%, and caspase-6 by 32% (P < 0.05; Fig. 4, C–E), indicating that constitutive FOXO1 expression protected against apoptosis and that FOXO1 in these cells functioned to decrease mRNA levels of pro-apoptotic genes. This is somewhat surprising because FOXO1 expression is associated with pro-apoptosis in most cell types (Ho et al., 2008), but in some cells, as demonstrated here with keratinocytes, FOXO1 is needed to prevent apoptosis (Calnan and Brunet, 2008).

Figure 4. FOXO1 knockdown results in increased keratinocyte apoptosis. NHEK cells were transfected with control or FOXO1 siRNAs for 48 h. (A) Apoptotic keratinocytes were measured by TUNEL staining. Quantitative analysis of TUNEL-positive NHEK cells. The percentage of TUNEL-positive nuclei is reported as mean ± SD. (B) Apoptotic keratinocytes were confirmed by cell death detection ELISA. Real-time PCR analysis of Bim (C), FAS ligand (D), and caspase-6 (E) mRNA levels in FOXO1 knockdown keratinocytes. Data show mean ± SEM of at least three independent measurements. Asterisks indicate significant increase compared with cells transfected with siRNA control (P < 0.05).
FOXO1 silencing enhances the impact of oxidative stress to reduce keratinocyte migration and enhance apoptosis

FOXO1 has been reported to protect cells against ROS such as H$_2$O$_2$ by activating various ROS detoxifying enzymes (Storz, 2011). As shown in Fig. 5 A, loss of FOXO1 induced a 38% increase in ROS levels compared with controls. Incubation of keratinocytes with H$_2$O$_2$ enhanced ROS levels by 187% and silencing FOXO1 further enhanced H$_2$O$_2$-treated keratinocyte ROS levels by another 65%, whereas, treatment with N-acetyl-cysteine (NAC), a ROS inhibitor, markedly suppressed keratinocyte ROS levels (Fig. 5 A).

In contrast, TGF-$\beta_1$ expression in keratinocytes at day 2 (Fig. 5 B). ROS inhibitor NAC rescued 75% of the wound closure defect (Fig. S3). Furthermore, incubation of keratinocytes with NAC rescued the negative impact of FOXO1 knockdown on keratinocytes and silencing FOXO1 further decreased keratinocyte migration by another 18% (Fig. 5 C). Treatment of NAC reversed the inhibitory effect of H$_2$O$_2$ partially but significantly (Fig. 5 C). Consistent with the scratch-wound assay, TGF-$\beta_1$ treatment had no effect on H$_2$O$_2$-suppressed scratch-wound closure with or without FOXO1 silencing (P > 0.05; Fig. 5 B) and did not provide additional protection afforded by the antioxidant NAC (P > 0.05; Fig. 5 B). We further examined the effect of oxidative stress on keratinocyte migration by transwell migration assay. As shown in Fig. 2 D, silencing FOXO1 significantly impaired keratinocyte migration. Incubation with NAC rescued the negative impact of FOXO1 knockdown on keratinocyte migration (Fig. 5 C). Incubation of keratinocytes with low amounts of H$_2$O$_2$ resulted in a 71% reduced migration of keratinocytes and silencing FOXO1 further decreased keratinocyte migration by another 18% (Fig. 5 C). Treatment of NAC reversed the inhibitory effect of H$_2$O$_2$ partially but significantly (Fig. 5 C). Consistent with the scratch-wound assay, TGF-$\beta_1$ treatment had no effect on H$_2$O$_2$-suppressed keratinocyte migration (Fig. 5 C).

The effect of FOXO1 silencing and oxidative stress on keratinocyte apoptosis was examined. The antioxidant NAC rescued the pro-apoptotic effect of FOXO1 knockdown (P < 0.05; Fig. 5 D). H$_2$O$_2$ increased keratinocyte apoptosis twofold relative to controls (P < 0.05), which was enhanced another 3.7-fold by silencing FOXO1 (Fig. 5 D). TGF-$\beta_1$ had relatively little effect on keratinocyte apoptosis (Fig. 5 D). Taken together, these results indicate that FOXO1 has an important antioxidant role that protects keratinocytes against ROS, which is critical for maintaining keratinocyte migration as well as protection against apoptosis. Moreover, this protection is largely independent of TGF-$\beta_1$.

FOXO1 protects cells by stimulating antioxidant defense mechanisms such as glutathione peroxidases or inducing DNA repair enzymes such as GADD45$\alpha$. Silencing FOXO1 in keratinocytes significantly decreased mRNA levels of antioxidant genes such as glutathione peroxidase 2 (GPX-2) by 49% and cytoglobulin by 39%, as well as DNA damage repair gene GADD45$\alpha$ by 64% (P < 0.05; Fig. 5, E–G). Thus, the loss of FOXO1 expression in keratinocytes results in decreased expression of antioxidative genes and GADD45$\alpha$, which repairs oxidative damage.

As an alternative mechanism, we examined whether the delayed scratch-wound closure in FOXO1-deficient keratinocytes is due to defects in glucose uptake or ATP production. However, we did not observe any changes in glucose uptake or ATP production in FOXO1-silenced keratinocytes compared with the controls (Fig. S2, D and E).

Decreased migration and proliferation, and increased apoptosis in keratinocytes isolated from FOXO1-deleted mice

To further establish the role of FOXO1 in regulating keratinocytes, experiments were performed with primary cells isolated from experimental K14.Cre$^{-}$FOXO1$^{L/L}$ and control K14.Cre$^{-}$FOXO1$^{L/L}$ mice. Western blot analysis showed that Cre recombination reduced FOXO1 expression in experimental compared with control keratinocytes (Fig. 6 A). Furthermore, Western blot analysis for TGF-$\beta_1$ demonstrates the loss of TGF-$\beta_1$ expression at the protein level when FOXO1 is deleted (Fig. 6 A). Similarly, TGF-$\beta_1$ signaling measured by phosphorylation of SMAD2/3 was found to be decreased in K14.Cre$^{-}$FOXO1$^{L/L}$ keratinocytes, while the total SMAD2/3 protein levels remained the same (Fig. 6 A), indicating that the delayed wound-healing phenotype observed in FOXO1-deleted mice was due to decreased TGF-$\beta_1$ expression.

The effect of FOXO1 deletion on cell migration, proliferation, and apoptosis in vitro was examined using primary dermal keratinocytes isolated from K14.Cre$^{-}$FOXO1$^{L/L}$ and K14.Cre$^{-}$FOXO1$^{L/L}$ mice. As shown in Fig. 6 B, deletion of FOXO1 resulted in a 50% decrease in cell migration compared with control keratinocytes. Deletion of FOXO1 also caused a twofold increase in apoptosis in keratinocytes isolated from experimental mice compared with control keratinocytes (Fig. 6 C). When proliferation was examined, FOXO1 deletion resulted in a small but significant 22% decrease in proliferation compared with wild-type keratinocytes (P < 0.05; Fig. 6 D). These results are very similar to those obtained by FOXO1 knockdown with specific siRNA.

Keratinocyte-specific FOXO1 deletion results in decreased keratinocyte migration and proliferation and increased apoptosis in vivo

Further investigation of the role of FOXO1 in delayed wound healing was performed by histological analysis of specimens obtained from small excisional wounds created in K14.Cre$^{-}$FOXO1$^{L/L}$ and K14.Cre$^{-}$FOXO1$^{L/L}$ mice. Wound closure was significantly reduced by FOXO1 deletion in keratinocytes in vivo (Fig. 7 A). The gap between the edges of the epithelium was $\approx$2.5-fold larger in day-4 wounds of experimental K14.Cre$^{-}$FOXO1$^{L/L}$ mice compared with matched K14.Cre$^{-}$FOXO1$^{L/L}$ control mice (P < 0.05; Fig. 7 B). This difference was fivefold on day 7 (P < 0.05; Fig. 7 F). Keratinocyte number was $\approx$1.5-fold higher in the wounds of control mice compared with experimental FOXO1-deleted mice (P < 0.05; Fig. 7,
To determine whether the effect of FOXO1 deletion in keratinocytes was due to altered migration, immunofluorescence was performed to measure the urokinase plasminogen activator receptor (uPAR), which is expressed in migrating keratinocytes. We observed a decrease in epithelial thickness by 25% (P < 0.05) in wounds of the FOXO1-deleted mice on day 4 (Fig. 7, E and I).

C and G), which increased the area of healing epithelium (Fig. 7, D and H). We also observed a decrease in epithelial thickness by 25% (P < 0.05) in wounds of the FOXO1-deleted mice on day 4 (Fig. 7, E and I).
keratinocytes and is a marker of keratinocytes that are in the process of migrating (Lund et al., 2006). The expression of uPAR in keratinocytes was reduced ~47% in the wounds of experimental K14.Cre−.FOXO1−/− mice compared with matched K14.Cre+.FOXO1+/+ control mice (P < 0.05; Fig. 8, A and B). The impact of FOXO1 on migrating keratinocytes during wound healing in vivo was similar to that observed in vitro. Previous studies suggest that hair follicles play important roles in normal wound healing (Lavker et al., 1993; Ito et al., 2005). Therefore, we examined the effect of keratinocyte-specific FOXO1 deletion on indicators of cell migration in hair follicles. The number of uPAR-positive cells in hair follicles was reduced 54% in FOXO1-deleted mice compared with the control mice, indicating that deletion of FOXO1 in the keratinocytes affects the number of migrating hair follicle cells (Fig. 8 B).

We next investigated the effect of keratinocyte-specific FOXO1 deletion on keratinocyte apoptosis and proliferation in vivo. The percentage of apoptotic keratinocytes increased by 1.6-fold in FOXO1-deficient wounds compared with control mice (P < 0.05; Fig. 8, C and D). In addition, we observed a 21% decrease in keratinocyte proliferation in the wound epithelium of FOXO1-deleted mice measured by the number of proliferating cell nuclear antigen (PCNA)–positive cells (Fig. 8, E and F; P < 0.05). We also observed a 36% decrease in the number of PCNA-positive hair follicle cells in FOXO1-deleted mice (Fig. 8 F).

**Loss of FOXO1 expression in keratinocytes leads to enhanced oxidative stress in vivo**

To examine whether there were changes in oxidative stress caused by FOXO1 deletion in keratinocytes in vivo we analyzed the expression of 8-hydroxy-2-deoxyguanosine (8-OHdG), a widely used marker of oxidative damage (Shigenaga et al., 1989). The number of 8-OHdG-positive keratinocytes increased 2.4-fold in healing wounds of K14.Cre+.FOXO1−/− mice compared with the control K14.Cre+.FOXO1+/+ mice (P < 0.05; Fig. 8, G and H). These results indicate that deletion of FOXO1 in keratinocytes in vivo enhances damage caused by oxidative stress. It is consistent with the in vitro studies (Fig. 5) supporting the notion that FOXO1 protection against oxidative stress is important in the cellular events of wound healing.

**Loss of FOXO1 expression in keratinocytes leads to down-regulation of TGF-β1 and reduced SMAD signaling**

TGF-β1 plays a critical role in re-epithelialization and wound repair (Werner and Grose, 2003). Experiments were performed to determine whether loss of FOXO1 in keratinocytes had an effect on the expression of TGF-β1 in healing wounds of K14.Cre−.FOXO1−/− and K14.Cre+.FOXO1−/− keratinocytes. BrdU incorporation was determined by measuring absorbance at 450 nm. Data show mean ± SEM of at least three independent experiments. *, P < 0.05 vs. K14.Cre+.FOXO1+/+ keratinocytes.
controls the cellular events of wound healing. A summary of the cellular events regulated by FOXO1 in keratinocytes in vitro and in vivo are shown in Table 1.

Discussion

FOXO1 has been shown to play an important role in cellular processes that are linked to repair, particularly inhibiting proliferation, increasing apoptosis, and reducing oxidative stress. However, its role in regulating keratinocytes and keratinocyte behavior in wound healing has not been investigated. Based upon the effects of FOXO1 we anticipated that deletion of FOXO1 would enhance wound healing by increasing proliferation and reducing apoptosis. To test this we performed wound-healing experiments both in vivo using a conditional deletion of FOXO1 in a keratinocyte lineage as well as in vitro. Unexpectedly, mice with FOXO1 deletion in keratinocytes exhibited impaired wound closure in vivo and also displayed very similar either recombinant TGF-β1 or vehicle. TGF-β1 treatment enhanced wound closure. On day 4, wounds were 58% larger in the vehicle-treated compared with the TGF-β1–treated in K14.Cre+ FOXO1L/L mice (P < 0.05; Fig. 10, A and B). On a histological level TGF-β1 treatment rescued the wound-healing defect in FOXO1-deleted mice by decreasing the size of the epithelial gap by 75% and enhancing the size of the healing epithelium measured by epithelial length and thickness (Fig. 10, C–G). FOXO1-deleted mice treated with TGF-β1 also had a 2.4-fold increase in the number of migrating cells in the wounded epithelium and a twofold increase in the number of migrating cells in hair follicles (Fig. 10, H and I). However, there was no significant difference in proliferating keratinocytes when TGF-β1–treated wounds were compared with vehicle-treated wounds in FOXO1-deleted mice (P > 0.05; Fig. 10 J). Thus, the negative effect of FOXO1 deletion was rescued by TGF-β1 treatment in vivo as was also noted in vitro. This further links the functional importance of FOXO1 regulation of TGF-β1 as a mechanism by which FOXO1 controls the cellular events of wound healing. A summary of the cellular events regulated by FOXO1 in keratinocytes in vitro and in vivo are shown in Table 1.
Figure 8. Loss of FOXO1 expression in keratinocytes results in decreased keratinocyte migration and proliferation and increased apoptosis. Paraffin-embedded cross sections from K14.Cre−FOXO1L/L and K14.Cre+FOXO1L/L mice were analyzed by immunofluorescence using an anti-uPAR antibody (A), anti-PCNA antibody (E), or anti-8-OHdG antibody (G), and by TUNEL assay (C). Quantification of uPAR-positive migrating keratinocytes (B), TUNEL-positive apoptotic keratinocytes (D), PCNA-positive proliferative keratinocytes (F), and 8-OHdG–positive keratinocytes (H). Bars: [A and G] 100 µm; [C and E] 200 µm. EP, epidermis; CT, connective tissues. White dashed lines demarcate the epidermis from the dermis. Each value is the mean ± SEM for n = 6–9 mice per group. Asterisks indicate significant changes compared with control mice (P < 0.05).
Figure 9. **Reduced TGF-β1 and phospho-SMAD2/3 expression in the FOXO1-deleted mice keratinocytes.** Paraffin-embedded cross sections from K14.Cre−.FOXO1L/L and K14.Cre+.FOXO1L/L mice were analyzed by immunofluorescence using (A) anti–TGF-β1 antibody, (C) phospho-SMAD2/3 antibody, and (E) anti-SMAD2/3 antibody. Quantitative analysis of (B) TGF-β1–positive keratinocytes, (D) phospho-SMAD2/3–positive keratinocytes, and (F) SMAD2/3-positive keratinocytes. Bar, 100 µm. EP, epidermis; CT, connective tissues. White dashed lines demarcate the epidermis from the dermis. Each value is the mean ± SEM for n = 6–9 mice per group. Asterisks indicate significant changes compared with control mice (P < 0.05).

results in an in vitro model of wound healing. Delayed wound healing caused by FOXO1 deletion was primarily caused by a decrease in migrating keratinocytes both in the wounded epithelium and in hair follicles. We determined that a primary downstream event regulated by FOXO1 was TGF-β1 expression and that wound healing impaired by FOXO1 deletion could be rescued by treatment with TGF-β1 in vivo and in vitro. Thus, FOXO1 is required for the up-regulation of TGF-β1 in wound
Figure 10. TGF-β1 treatment rescues impaired wound closure in FOXO1-deleted mice. (A) Representative photographs of scalp wounds on day 4 and day 7 from K14.Cre-FOXO1<sup>L/L</sup> and K14.Cre-FOXO1<sup>L/L</sup> mice treated with vehicle or TGF-β1. (B) Wound-healing process was analyzed at different time points after wounding. Average wound area was presented as percentage of the wound area on day 0 (100%). (C) Hematoxylin and eosin staining of K14.Cre-FOXO1<sup>L/L</sup> and K14.Cre-FOXO1<sup>L/L</sup> mice wound biopsies on day 7 after wounding. Bar, 500 µm. WC, wound center; WE, wound epithelium; Normal, normal epithelium. The quantification of epithelial migration and re-epithelialization in the day-7 scalp wounds of K14.Cre-FOXO1<sup>L/L</sup> and K14.Cre-FOXO1<sup>L/L</sup> mice were treated with either vehicle or TGF-β1 and were analyzed by immunofluorescence using an anti-uPAR antibody and anti-PCNA antibody. Percentage of uPAR-positive migrating keratinocytes was quantified in normal and wound epithelium (H) as well as in hair follicles (I). (J) PCNA-positive proliferative keratinocytes in wound epithelium. EP, epidermis; CT, connective tissues; *, P < 0.05. Error bars represent mean ± SEM, n = 4–6 mice per group.
Table 1. Effect of FOXO1 deletion or knockdown

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We examined alternative mechanisms by which FOXO1 could affect wound healing. The formation of reactive oxygen species and the level of oxidative stress are increased in healing wounds (Schäfer and Werner, 2008; Guo and Dipietro, 2010). When normal levels of ROS are exceeded, such as in diabetic wound healing, excessive oxidative stress occurs and causes a decrease in keratinocyte proliferation and migration and increased apoptosis (Nishio and Watanabe, 1997; Wenk et al., 1999; Deveci et al., 2005). We found that the loss of FOXO1 expression in keratinocytes in vitro increased ROS levels and deletion of FOXO1 in keratinocytes in vivo resulted in increased oxidative damage in healing wounds as measured by a marker of oxidative damage, 8-OHdG (Shigenaga et al., 1989). We showed two additional mechanisms through which elevated ROS levels caused by reduced expression of FOXO1 limits the wound-healing behavior of keratinocytes. The increased susceptibility to oxidative stress caused by FOXO1 deletion is directly linked to impaired cell migration because it can be rescued by treatment with an antioxidant, NAC. Under mild oxidative stress caused by deletion of FOXO1, TGF-β1 was also able to rescue impaired migration, but under more severe oxidative stress such as H2O2 combined with FOXO1 deletion it did not. Thus, FOXO1 affects keratinocyte migration through two mechanisms, regulation of TGF-β1 and protection against the anti-migratory effect of elevated ROS. In addition, FOXO1 protection against ROS is needed to reduce oxidative damage and reduce keratinocyte apoptosis. An increase in both is linked to impaired wound healing (Soneja et al., 2005; Sen and Roy, 2008).

FOXO1 activity protects cells against oxidative stress by activating antioxidant defense mechanisms such as MnSOD and glutathione peroxidases (van der Horst and Burgering, 2007; Storz, 2011). The expression of antioxidant genes such as glutathione peroxidase 2 and cytoglobulin were down-regulated in FOXO1-silenced keratinocytes in vitro. Another mechanism by which FOXO1 is protective is by modulating the expression of the DNA repair enzyme, GADD45α, which repairs DNA damaged by oxidative stress (Furukawa-Hibi et al., 2002; Tran et al., 2002). GADD45α had reduced expression in FOXO1-silenced keratinocytes. Collectively, these data indicate that loss of FOXO1 expression in keratinocytes results in increased ROS levels and decreased antioxidant defense mechanisms, leading to reduced keratinocyte migration and increased apoptosis. Although in a number of cell types FOXO1 promotes apoptosis, several lines of evidence suggest that FOXO1 plays a central role in cell survival during conditions of oxidative stress through up-regulation of antioxidant enzymes and regulation of cell survival pathways (Burgering and Medema, 2003; Tothova et al., 2007; Sengupta et al., 2011). Our results are in agreement with previous results that FOXO1 can protect against cellular oxidative stress (Ponugoti et al., 2012).

FOXO1 activity also increases the expression of antioxidants, such as MnSOD and glutathione peroxidases, which protect cells against oxidative stress. In keratinocytes, FOXO1 regulates the expression of these genes, leading to increased antioxidant activity and reduced cell death.

Keratinocyte migration requires the up-regulation of integrins and MMPs (Gailit et al., 1994; Zambruno et al., 1995; Hsieh et al., 2010). Our data demonstrate that FOXO1 deficiency in keratinocytes significantly attenuates the expression of integrins-β and -α3 needed for wound re-epithelialization (Huang et al., 1998). In addition, silencing of FOXO1 decreased mRNA levels of matrix metalloproteinases MMP-3 and MMP-9 in keratinocytes that facilitate keratinocyte migration and wound healing (Agren, 1999). Thus, FOXO1 is needed to maintain expression of integrins and MMPs that are required for optimal keratinocyte migration and wound healing. In addition, silencing FOXO1 reduced basement membrane protein collagen IV, indicating that deletion of FOXO1 could have direct or indirect effects on wound healing that are due to altered basement membrane protein production.
deletion caused a small reduction in keratinocyte proliferation in vivo. This suggests that FOXO1 has only a minor effect on regulating the cell cycle of keratinocytes in wound healing.

In summary, we unexpectedly found that FOXO1 promotes healing because it is needed for keratinocyte transition to a wound-healing phenotype that involves migration and up-regulation of TGF-β1 and its downstream targets, integrin-α3 and -β6 and matrix metalloproteinase-3 and -9. The negative effect of FOXO1 deletion both in vitro and in vivo was rescued by treatment with TGF-β1. The impact of FOXO1 deletion on keratinocyte migration in vitro was also reversed by an antioxidant in a TGF-β1–independent manner. Lastly, FOXO1 deletion increased susceptibility to ROS-mediated apoptosis. This change was linked to the up-regulation of genes that protect against oxidative damage and prevent apoptosis. Thus, treatment with FOXO1 agonists may represent a potential therapeutic target for enhancing tissue repair by mobilizing keratinocytes for rapid wound epithelialization and protecting them from oxidative stress.

Materials and methods

Mice

Mice expressing a floxed allele of FOXO1 were provided by R.A. DePinho (MD Anderson Cancer Center, Houston, TX) and have been previously described (Pak et al., 2007). The second major coding exon (encoding the C-terminal half of FOXO1) was targeted by the insertion of loxP sites and mice were backcrossed three times onto the FVBn background. Mice expressing keratin 14-Cre (strain Tg(KRT14-cre)1Amc/J) were obtained from the Jackson Laboratory. These mice were bred to generate experimental (K14.Cre+; FOXO1L/L) and control (K14.Cre+; FOXO1+/-) mice and experiments were performed using mice 16–20 wk of age. Mice with floxed allele of FOXO1, K14.Cre+; FOXO11/+, and K14. Cre−; FOXO11/+ developed normally and did not show any sign of disease. All mice were maintained in a regular 12-h day–night cycle. All the animal experiments were approved by the University of Pennsylvania Institutional Animal Care and Use Committee.

In vivo wound-healing experiments

Mice were anesthetized by i.p. administration of ketamine (80–100 mg/kg) and xylazine (5–10 mg/kg); the scalp hair was shaved, cleansed, and two excisional wounds of 2.0 mm were created in the scalp at the midline with 18-gauge needles. All wounds were performed with a 1:1 ratio of excisional wounds of 2.0 mm were created in the scalp at the midline with 18-gauge needles. All wounds were performed with a 1:1 ratio of PBS to warm sterile dermal punch as described previously (Siqueira et al., 2010). Wounds were treated with 150 µM H2O2, 1 mM N-acetylcysteine (NAC), 2 µg/ml TGF-β1, or various combinations of these agents. Experiments were performed at least three times.

Real-time PCR

Real-time PCR was performed essentially as described previously (Siqueira et al., 2010). Total RNA was isolated from confluent NIH/3T3 cells following the manufacturer’s instructions (RNaseasy; Qiagen). 1 µg of total RNA was reverse transcribed using High Capacity RNAto-cDNA kit (Applied Biosystems), and real-time PCR was performed using the Universal Probe Library System (Roche). All primers were designed using the Universal Probe Library Primer Design Center (Roche). Results were normalized with mitochondrial ribosomal protein L32. Each experiment was performed 2–4 times with similar results.

Western blot

Epithelial cells were lysed with lysis buffer (Thermo Fisher Scientific) containing protease inhibitor cocktail and phosphatase inhibitor cocktail (Thermo Fisher Scientific). Protein concentration was measured using a protein assay with BSA as a standard (Bio-Rad Laboratories). 50 µg cell lysate was resolved in 4–20% SDS-PAGE (Bio-Rad Laboratories) and transferred onto PVDF membrane (Thermo Fisher Scientific). The membranes were incubated with primary antibodies against FOXO1 (Santa Cruz Biotechnology, Inc.), FOXO3 (Cell Signaling Technology, Inc.), p-TGF-β1 (Promega), p-STAT3 (Santa Cruz Biotechnology, Inc.), and STAT3 (Sigma-Aldrich) after blocking with 5% BSA. The samples were then incubated with horseradish peroxidase–labeled anti-rabbit IgG or anti-mouse IgG, and immunoreactive bands were detected with ECL Western blotting reagents (Thermo Fisher Scientific).

CHIP assays

CHIP assays were performed using CHIP-it Kit (Active Motif) following the manufacturer’s instructions, as described previously (Albowi et al., 2009). Isolated DNA was subjected to quantitative real-time PCR by using primers specific for the TGF-β1 promoter with a Universal Probe Library Probe (Roche). The TGF-β1 promoter primer sequences used were: set 1 (left, 5'-CCATGGTGAGC- GCCCTCC-3'; right, 5'-TAATCGGGGGGATGAGAC-3'), set 2 (left, 5'-TAAACACGGTGAGCCCTAGA-3'; right, 5'-GGCCGACGTCTTGCTTCC-3'). CHIP experiments were repeated three times with reproducible results.

strepavidin, and counterstained with DAPI. For immunohistochemistry, antibody was localized by incubation with avidin–biotin horseradish peroxidase complex using a biotinylated secondary antibody. To enhance the signal, tyramide signal amplification was used that enhances the chromogenic signal (PerkinElmer). Apoptosis was assessed by the DeadEnd Fluorometric TUNEL System (Promega).

Microscopy

Sections were observed with 4x and 20x objectives and images were acquired using a fluorescence microscope (Eclipse 90i; Nikon) and a CoolSnap EZ camera (Photometrics). All images were taken at room temperature with a TXRED or FITC filter. Image analysis was performed using Nikon AR image analysis software.

Cell culture and siRNA transfections

Primary cultures of human epidermal keratinocytes (NHEK) were purchased and maintained in KGM-2 growth medium (Lonza) supplemented with 0.1 ng/ml EGF, 5.0 µg/ml insulin, 0.5 µg/ml hydrocortisone, 0.15 mM calcium, 5 mg/ml epinephrine, 10 µg/ml transferrin, and 2 ml bovine pituitary extract. All cells were grown in a humidified atmosphere with 5% CO2 concentration. ON-TARGETplus SMARTpool siRNAs against FOXO1, FOXO3, TGF-β1, and control siRNA were obtained from Thermo Fisher Scientific. DNA transfections were performed using Lipofectin (Invitrogen) and siRNA transfections were performed using GeneMute siRNA transfection reagent (Signagen).

In vitro wound-healing and transwell migration assay

NHEK cells were transfected with FOXO1 or scrambled siRNA 48 h before assay. For in vitro wounds, confluent cells were “scratched” using a 200-µl pipette tip as described previously (Li et al., 2007) and photographs were taken as indicated to assess the number of keratinocytes that had migrated into the wounded area. For the migration assay, 2 × 104 cells were incubated in the upper chamber of a transwell (Corning Costar; Thermo Fisher Scientific) containing a polycarbonate membrane filter (6.5-µm diameter, 8-µm pore size). After 6 h, cells remaining in the upper surface of the membrane were removed and migrated cells on the lower surface of the membrane were counted after staining with DAPI. In some cases, cells were treated with 150 µM H2O2, 1 mM N-acetylcysteine (NAC), 2 µg/ml TGF-β1, or various combinations of these agents. Experiments were performed at least three times.

Histological analysis

The scalp and attached calvarial bone were fixed in 4% paraformaldehyde for 24 h, decalcified in 10% EDTA solution, embedded in paraffin, and sectioned at 5 µm. Sections were stained with hematoxylin and eosin (H&E) and histomorphometric analysis was performed with computer-assisted image analysis at the center of each lesion. We measured parameters such as epithelial gap, epithelial cell number, epithelial area, and epithelial thickness at the wound site.

Immunohistochemistry, immunofluorescence, and apoptosis in histological sections

Antigen retrieval was performed by heating slides in 10 mM sodium citrate (pH 6.0) for 5 min at 95°C. Sections were then incubated with primary antibody against FOXO1 (Santa Cruz Biotechnology, Inc.), proliferating cell nuclear antigen (PCNA; Santa Cruz Biotechnology, Inc.), urokinase-type plasminogen activator receptor (uPAR; Santa Cruz Biotechnology, Inc.), 8-hydroxydeoxyguanosine (8-OHdG; EMD Millipore), TGF-β (Abcam), phospho-SMAD2/3 (Santa Cruz Biotechnology, Inc.), and SMAD 2/3 (Santa Cruz Biotechnology, Inc.) or matched nonimmune primary antibody overnight at 4°C. For immunofluorescence, antibody was localized by a biotinylated secondary antibody and visualized using Alexa 546-conjugated streptavidin, and counterstained with DAPI. For immunohistochemistry, antibody was localized by incubation with avidin–biotin horseradish peroxidase complex using a biotinylated secondary antibody. To enhance the signal, tyramide signal amplification was used that enhances the chromogenic signal (PerkinElmer). Apoptosis was assessed by the DeadEnd Fluorometric TUNEL System (Promega).
Luciferase reporter assay
Luciferase activity was measured using the Dual Luciferase Reporter Assay kit (Promega) according to the manufacturer’s instructions. In brief, NHEK cells were cotransfected with plasmid DNA of TGF-β1-Luc, Renilla-Luc, pcDNA-FOXO1 AAA, scramble, or FOXO1 siRNA. Empty vector DNA was added as needed so that the same amounts of expression vector were present in each transfection. Transfection was performed using Lipofectamine (Invitrogen) in 24-well plates. 24 h after transfection, cells were lysed, and luciferase and Renilla activities were measured using a luminometer (Infinite M200; Tecan). Firefly luciferase activities were divided by Renilla activities to normalize for transfection efficiency. Experiments were performed three times with similar results.

ROS assay
The cellular ROS levels were measured by using chloromethyl-2,7’-dichlorodihydrofluorescein diacetate acetyl ester (CM-H2DCFDA) following the manufacturer’s instructions (Invitrogen). NHEK cells were transfected with FOXO1 or scrambled siRNA for 48 h in 96-well plates and then treated with 150 µM H2O2, 1 mM NAC, 2 ng/ml TGF-β1, or various combinations of these agents. After 16 h, cells were incubated with 10 µM CM-H2DCFDA for 30 min at 37°C and fluorescent intensity was recorded by excitation at 492 nm and emission at 527 nm using a plate reader (Infinite M200; Tecan). Experiments were performed three times with similar results.

Apoptosis in vitro
Apoptosis was measured by TUNEL assay using the DeadEnd Fluorometric TUNEL System (Promega) according to the manufacturer’s instructions. The protein concentration was measured using the BCA Protein Assay kit (Thermo Fisher Scientific). The relative ATP levels were normalized with the protein concentration. Experiments were performed three times with similar results.

Glucose uptake assay
To measure glucose uptake, NHEK cells transfected with scrambled siRNA or FOXO1 siRNA were incubated with 200 µM [(7-nitrobenz-2-oxa-1,3-diazol-4-ylamino)-2-deoxyglucose (2-NBDG; Invitrogen) for 30 min, washed three times with cold PBS, followed by flow cytometric detection of fluorescence produced by the cells. For each measurement, a minimum of 10,000 events were collected using a FACSCalibur® flow cytometer (BD). Data analysis was performed using FlowJo software (Verity Software House). Experiments were performed three times with similar results.

ATP determination assay
The intracellular ATP levels were measured using the ATP Determination kit (Molecular Probes; Invitrogen) in a luminometer (Infinite M200; Tecan), following the manufacturer’s instructions. The protein concentration was measured using the BCA Protein Assay kit (Thermo Fisher Scientific). The relative ATP levels were normalized with the protein concentration. Experiments were performed three times with similar results.

Statistics
Statistical analysis between two groups was performed using two-tailed Student’s t-test. In experiments with multiple time points or treatments, differences between the wild-type and experimental groups were determined by one-way ANOVA with Scheffe’s post-hoc test. Results are expressed as the mean ± SEM. P < 0.05 was considered statistically significant.

Online supplemental material
Fig. S1 shows the images from scratch-wound and transwell migration assays of FOXO1 knockdown cells. Fig. S2 shows the effect of FOXO1 knockdown on proliferation, glucose uptake, or ATP production in keratinocytes. Fig. S3 shows that increased oxidative stress impairs keratinocyte migration of in vitro scratch wound. Fig. S4 contains images of TUNEL assay and shows that silencing FOXO1 results in increased apoptosis. Fig. S5 shows that silencing FOXO1 in keratinocytes results in decreased collagen IVA mRNA levels. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.201305074/DC1

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References


Figure S1. Effect of FOXO1/FOXO3 knockdown on keratinocyte migration in the absence and presence of TGF-β1. (A) Photomicrographs of scratch closure at the indicated time points in NHEK control cultures or FOXO1/FOXO3 knockdown cells after scratch wounding. Bar, 500 µm. (B and C) Cell migration was assessed by transwell migration assay; the cells that migrated across the transwells were stained with DAPI and the migrated cells were photographed. Bar, 200 µm. (D) Photomicrographs of scratch closure at the indicated time points in FOXO1 knockdown cells without or with TGF-β1 after scratch wounding. Bar, 500 µm. (E) NHEK cells were transfected with control or TGF-β1 siRNAs for 48 h. TGF-β1 levels were analyzed by real-time PCR. *, P < 0.05 vs. scrambled siRNA.
Figure S2. Effect of FOXO1 knockdown on proliferation, glucose uptake, or ATP production in keratinocytes. NHEK cells were transfected with control or FOXO1 siRNAs for 48 h. (A) Proliferative keratinocytes were determined by PCNA immunofluorescence or (B) BrdU ELISA. BrdU incorporation was determined by measuring absorbance at 450 nm. (C) Real-time PCR analysis of cyclin D1, cyclin D2, CDK1, CDK2, and CDK4 mRNA levels in FOXO1 knockdown keratinocytes. (D) Cells were incubated with 2-NBDG and the amount of NBDG uptake was measured by flow cytometry. (E) Intracellular ATP levels were measured using ATP determination kit. a.u., arbitrary units. Data show mean ± SEM of at least three independent measurements.
Figure S3. **Increased oxidative stress impairs keratinocyte migration of in vitro scratch wound.** NHEK cells were transfected with control or FOXO1 siRNA for 48 h and then treated with 150 µm H$_2$O$_2$, 1 mM NAC, 2 ng/ml TGF-β1, or various combinations of these agents after scratching. The number of cells in the scratched area was counted. Data show mean ± SEM of at least three independent measurements. *, P < 0.05 vs. scrambled siRNA; **, P < 0.05 vs. siFOXO1; #, P < 0.05 vs. H$_2$O$_2$-treated siFOXO1.

Figure S4. **FOXO1 knockdown results in increased keratinocyte apoptosis.** NHEK cells were transfected with control or FOXO1 siRNAs for 48 h. Apoptotic keratinocytes were measured by TUNEL staining. Green fluorescence indicates TUNEL-positive cells. Blue fluorescence indicates DAPI nuclear staining. Bar, 200 µm.
Figure S5. Silencing FOXO1 in keratinocytes results in decreased collagen IVα1 mRNA levels. NHEK cells were transfected with control or FOXO1 siRNAs for 48 h. (A) Real-time PCR analysis of collagen IVα1 mRNA levels in FOXO1 knockdown keratinocytes. *, P < 0.05 vs. scrambled siRNA.