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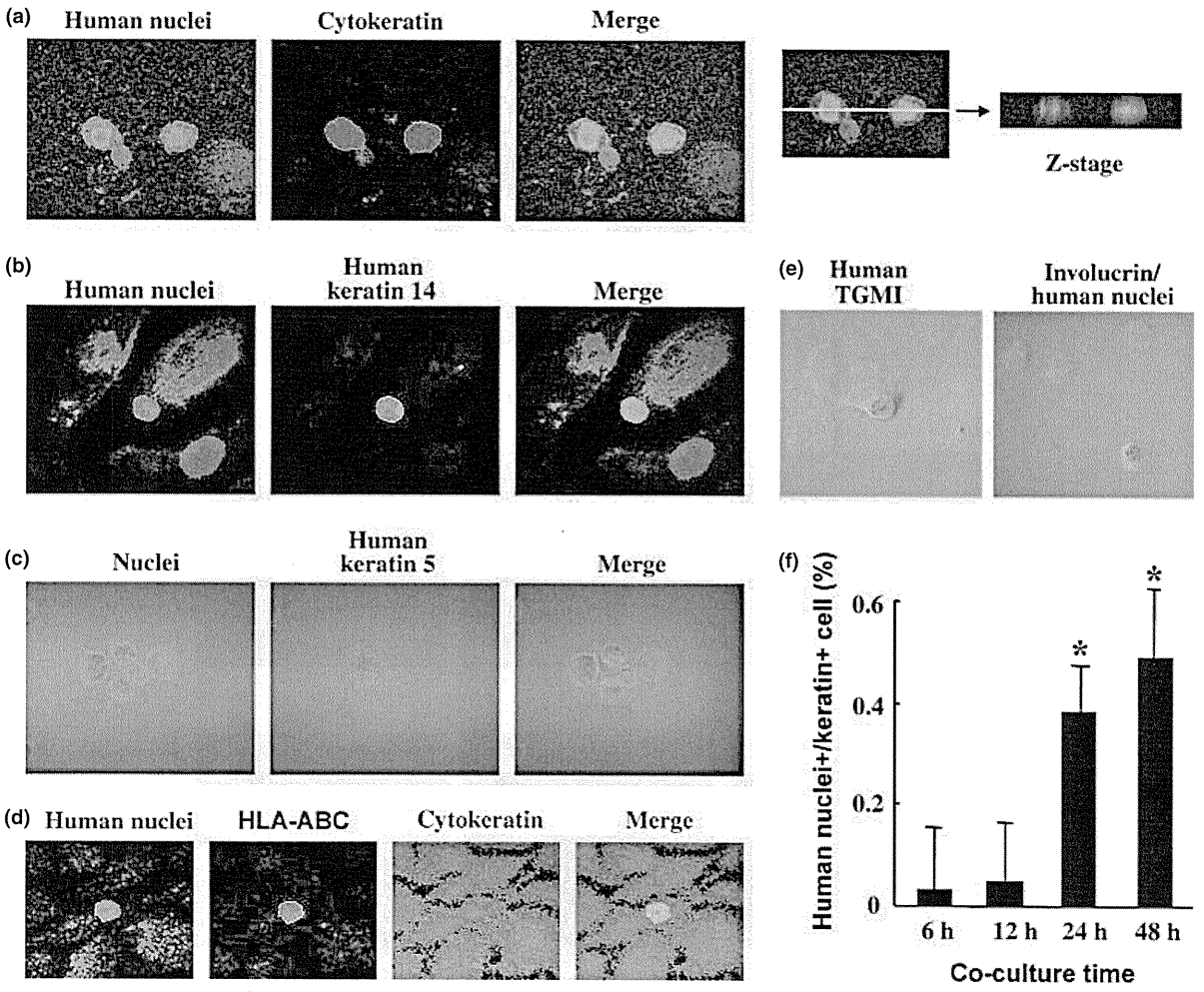

Figure 1 Coculture of human haematopoietic stem cells (hHSCs) and a mouse keratinocyte cell line, Pam212. (a) Expression of human nuclei (green) and cytokeratin (red) after 2 days in coculture, and cross-section analysis of the same cells (Z-axis). (b) Expression of human nuclei (green) and human cytokeratin 14 (red) after 2 days in coculture. (c) Expression of human cytokeratin 5 (green) and nuclei (propidium iodide staining, red) after 2 days in coculture. (d) Expression of human nuclei (green), human leucocyte antibody-ABC (red) and cytokeratin (blue). (e) Left: expression of human transglutaminase I (green) with transmission after 2 days in coculture; right: expression of involucrin (green) and human nuclei (red) with transmission after 2 days in coculture. (f) Percentages of hHSCs expressing keratin after 6, 12, 24 and 48 h in culture. *$P < 0.05$ vs. 6 h.

epidermal stem cells, playing an important role in differentiation.[16,17] Blocking antibodies during coculture of hHSCs and fixed NHEK with NHEK-conditioned medium did not influence the keratinocyte conversion (data not shown).

It is possible that the humoral induction of keratinocyte differentiation is mediated by a specific growth factor such as KGF and IGF.[18] However, we did not observe hNCs with exposure of hHSCs to KGF or IGF, which are secreted exclusively from keratinocytes (data not shown). These findings suggest that soluble factors other than KGF and IGF in keratinocyte supernatant may mediate HSCs differentiation.

Discussion

We have shown that hHSCs differentiate into keratinocytes in the presence of factors secreted from keratinocytes, without cell fusion. In this study, hHSCs converted into keratinocytes when cocultured with keratinocytes. By contrast, hHSCs cocultured with fixed keratinocytes were found never to convert into

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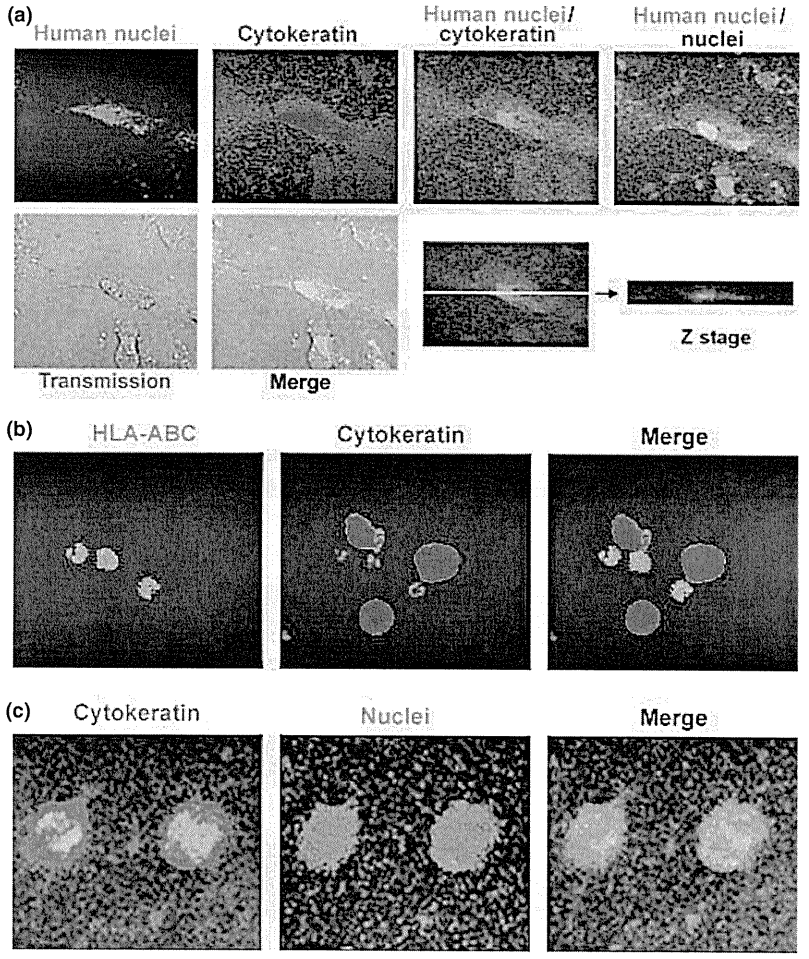

Figure 2 Coculture of human haematopoietic stem cells (hHSCs) and Pam212 cells fixed with 0.5% paraformaldehyde, and culture of hHSCs in conditioned medium of Pam 212 cells. (a) Expression of human nuclei (green), mouse nuclei (blue) and cytokeratin (red) after 2 days in coculture of hHSCs and fixed Pam212 cells, and analysis of same cells by Z-axis or transmission. (b) Expression of human leucocyte antibody-ABC (green) and cytokeratin (red). (c) Expression of cytokeratin (blue) and human nuclei (green) in culture of hHSCs in the conditioned medium of Pam 212 cells.

Table 1 Frequency of cytokeratin-positive cells derived from human haematopoietic stem cells (hHSCs).

Treatment	CK-positive cells, *n**
Coculture with Pam 212 cells	49
Coculture with fixed Pam 212 cells	0
Coculture with mouse fibroblasts	0
Culture in Pam 212 CM	9
Culture with fixed Pam 212 in Pam-212 CM	29
Culture in NHEK CM	35
Culture with fixed NHEKs in NHEK CM	40

CK, cytokeratin; CM, conditioned medium; NHEK, normal human epidermal keratinocyte. *In 10^4 hHSCs.

keratinocytes, and hHSCs cultured with keratinocyte-conditioned medium expressed keratinocyte-specific markers. These data support the existence of factors secreted from keratinocytes or the existence of relatively paraformaldehyde-sensitive cell surface molecules that induce hHSCs to differentiate into keratinocytes.

We did not observe differentiation after exposure of hHSCs to the growth factors KGF or IGF, which suggests that other soluble factors might mediate HSC differentiation. Indeed, a previous report on hepatocyte differentiation showed that the specific growth factors hepatocyte growth factor and fibroblast growth factor

4 failed to mediate such conversion.[10] Further investigation is required to identify specific soluble factors that affect differentiation of HSCs to keratinocytes.

Recently Mortier *et al.*[19] succeeded in generating a skin equivalent model from human cord blood cells, which contains heterogeneous cells including hHSCs and MSCs. Although the origin of the induced keratinocytes was not investigated, we propose that most of these cells are mesenchyme-derived, as our observation showed that purified hHSCs seldom convert to keratinocytes.

Murine BMSCs can contribute to the regeneration of injured adult tissues of various organs, including brain, liver and heart tissue, after bone-marrow transplantation.[1,3,20] These unexpected events were initially attributed to BMSC transdifferentiation, supporting the emerging idea of extended plasticity of adult stem cells. The alternative hypothesis of spontaneous cell fusion has also been proposed as the primary cause of unexpected cell-fate switches of BMSCs into various cell lineages.[21,22]

We found that the number of fused multinucleate cells (which are unlikely to undergo further cell division) in the skin was very low. Conversely, Fujino *et al.*[23] reported the observation of fused functional hepatocytes after hHSC injection into immunodeficient mice. Taking these results into consideration, it is likely that both cell fusion and conversion from HSCs play some role in the repair of damaged tissue.

Previously, we reported that CTACK/CCL27 accelerates skin regeneration via accumulation of BMDCs.[7] Furthermore, bone-marrow transplantation improves type XVII collagen-knockout epidermolysis bullosa (EB) mice, in which the deficient type XVII collagen, a cutaneous structure protein produced by keratinocytes, was restored by BMSCs.[8] Because there have been ethical and safety concerns in using embryonic stem cells and induced pluripotent stem cells, therapies using HSCs are thought to be safer.[24] In the near future, stem cell therapies might be a candidate for the treatment of severe eEB, for which there is no effective treatment other than palliative care.[25]

Conclusion

When exposed to skin tissue, hHSCs are capable of taking on many characteristics of the skin cell types, and this is mediated by the plasma environment rather than by direct cell–cell interactions, including the specific gene and/or protein expression and function of the cells.

Learning points

- It is known that HSCs have the potential for conversion into keratinocytes.
- Several mechanisms, including direct cell–cell interaction between HSCs and damaged skin, and involvement of paracrine-regulated soluble factors from the organ have been speculated; however, there have been no reports identifying the precise mechanism involved.
- In this study, we found that the conversion of HSCs into keratinocytes is mediated by the plasma environment rather than by direct cell–cell interactions.

Acknowledgements

We are grateful to Ms Yuika Osaki for her excellent technical assistance. This work was supported in part by grants-in-aid for scientific research (No. 13357008 to HS and no. 15790563 to RA) and by the Project for Realization of Regenerative Medicine (to HS) from the Ministry of Education, Science, Sports and Culture of Japan and by the Health and Labor Sciences Research Grants (No. H13-Measures for Intractable Disease-02 HS) from the Ministry of Health, Labor and Welfare of Japan.

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Macrophage Migration Inhibitory Factor Is Essential for Eosinophil Recruitment in Allergen-Induced Skin Inflammation

Yoko Yoshihisa[1,3], Teruhiko Makino[1,3], Kenji Matsunaga[1], Ayumi Honda[2], Osamu Norisugi[1], Riichiro Abe[2], Hiroshi Shimizu[2] and Tadamichi Shimizu[1]

Macrophage migration inhibitory factor (MIF) is a pluripotent cytokine that has an essential role in the pathophysiology of experimental allergic inflammation. Recent findings suggest that MIF is involved in several allergic disorders, including atopic dermatitis (AD). In this study, the role of MIF in allergic skin inflammation was examined using a murine model of AD elicited by epicutaneous sensitization with ovalbumin (OVA). We observed the number of skin-infiltrating eosinophils to significantly increase in OVA-sensitized MIF transgenic (Tg) mice compared with their wild-type (WT) littermates. On the other hand, eosinophils were virtually absent from the skin of MIF knockout (KO) mice and failed to infiltrate their skin after repeated epicutaneous sensitization with OVA. The mRNA expression levels of eotaxin and IL-5 were significantly increased in OVA-sensitized skin sites of MIF Tg mice, but were significantly decreased in MIF KO mice in comparison with the levels in WT littermates. Eotaxin expression was induced by IL-4 stimulation in fibroblasts in MIF Tg mice, but not in MIF KO mice. These findings indicate that MIF can induce eosinophil accumulation in the skin. Therefore, the targeted inhibition of MIF might be a promising new therapeutic strategy for allergic skin diseases.

Journal of Investigative Dermatology (2011) **131,** 925–931; doi:10.1038/jid.2010.418; published online 30 December 2010

INTRODUCTION

Atopic dermatitis (AD) is a chronic, relapsing inflammatory disease of the skin with significant morbidity and an adverse impact on patient well-being (Morar *et al.*, 2006). AD is considered to result from a dysregulation of the normal interactions between the environment and genes, defects in skin barrier function, and systemic and local immunological responses (Leung *et al.*, 2004). The contribution of the immune response to the pathogenesis of AD has been attributed largely to abnormalities in adaptive immunity, with key roles being played by T-helper 1(Th1)/Th2 cell dysregulation, IgE production, dendritic cell signaling, and mast-cell hyperactivity, leading to the pruritic, inflammatory dermatosis that characterizes AD (Leung *et al.*, 2004). In addition, accumulation of eosinophils is characteristic of the inflammation associated with AD (Honma *et al.*, 2000).

Macrophage migration inhibitory factor (MIF) was the first lymphokine reported to prevent random migration of macrophages (Bloom and Bennett, 1966). As the molecular cloning of MIF complementary DNA (Weiser *et al.*, 1989), MIF has been re-evaluated as a proinflammatory cytokine and pituitary-derived hormone that potentiates endotoxemia (Bernhagen *et al.*, 1993; Bucala, 1996). MIF has an important role in delayed-type hypersensitivity (Bernhagen *et al.*, 1998). Recently, it has been demonstrated that MIF also upregulates the expression of Toll-like receptor-4, which mediates lipopolysaccharide binding and activation of macrophages (Roger *et al.*, 2001). MIF is now recognized as a cytokine that exhibits a broad range of immune and inflammatory activities, including induction of inflammatory cytokines, and regulation of macrophage and lymphocyte proliferation. Furthermore, MIF induces the endothelial expression of E-selectin, ICAM-1, vascular cell adhesion molecule-1, IL-8, and monocyte chemoattractant protein-1, thus resulting in leukocyte recruitment (Gregory *et al.*, 2004, 2006; Cheng *et al.*, 2010). MIF originates from multiple cellular sources such as activated T lymphocytes, monocytes, eosinophils, and keratinocytes (Rossi *et al.*, 1998; Shimizu *et al.*, 1999; Yamaguchi *et al.*, 2000). MIF has also been shown to

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Abbreviations: AD, atopic dermatitis; KO, knockout; MIF, macrophage migration inhibitory factor; Tg, transgenic; WT, wild type

Received 9 September 2010; revised 2 November 2010; accepted 16 November 2010; published online 30 December 2010

exacerbate human allergic and inflammatory diseases, such as asthma (Rossi *et al.*, 1998) and acute respiratory distress syndrome (Donnelly *et al.*, 1997).

We recently reported excessive expression of MIF mRNA and protein in inflammatory skin lesions and in sera from AD patients (Shimizu *et al.*, 1999; Shimizu, 2005). We also showed that the serum MIF levels decrease as the clinical features of this disease improve, thus suggesting that MIF has a pivotal role in the inflammatory response in AD (Shimizu *et al.*, 1997). These studies raise the possibility that MIF is an important component of Th2-mediated immunopathology in general, and might therefore be relevant to chronic inflammatory allergic conditions.

Eosinophils may aggravate the inflammatory response in the skin of AD patients. Spergel *et al.* (1998, 1999) reported a murine model of allergic skin inflammation elicited by epicutaneous sensitization with ovalbumin (OVA). This model displays many of the features of human AD, including elevated total and specific IgE, dermatitis characterized by infiltration of the dermis by $CD4^+$ T cells and eosinophils, and increased local expression of mRNAs for the cytokines IL-4, IL-5, and IFN-γ. In our present study, MIF transgenic (Tg) mice and MIF knockout (KO) mice were used to assess the potential role of MIF in the pathogenesis of AD in this murine model of allergic skin inflammation. We also investigated the effects of MIF on eotaxin expression of dermal fibroblasts.

RESULTS

The expression of MIF was increased in bone marrow and skin from MIF Tg mice

MIF Tg mice exhibited no lethal or prominent pathological lesions in the organs examined. A northern blot analysis revealed the MIF mRNA expression in bone marrow and skin from MIF Tg mice to be ~10 times higher than that in wild-type (WT) mice (Figure 1a). MIF protein was also increased in the skin from MIF Tg mice compared with that from WT mice, as demonstrated by western blotting (Figure 1b).

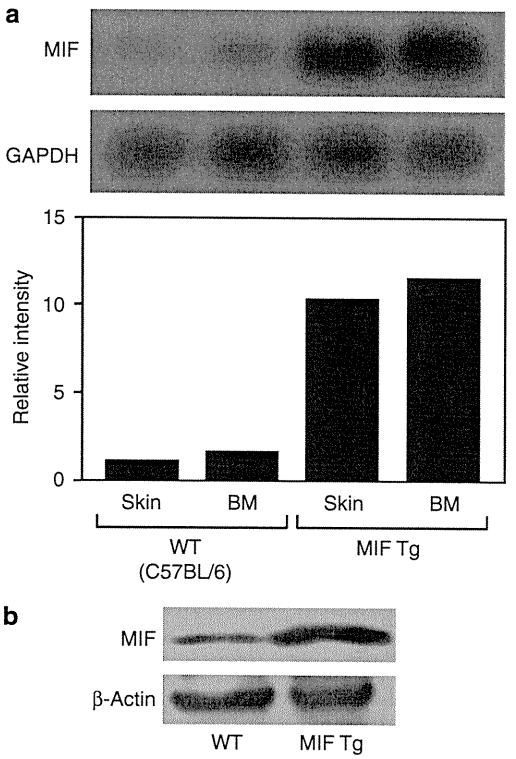

Figure 1. Expression of macrophage migration inhibitory factor (MIF) in tissues from MIF transgenic (Tg) mice. (**a**) Bone marrow (BM) and skin specimens were harvested from MIF Tg and wild-type (WT) mice, and the total RNA levels were determined by northern blot analysis as described in the Materials and Methods. The density of MIF bands was normalized to the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) signals. BM and skin from MIF Tg mice showed an ~10-fold higher level of MIF mRNA expression than those from WT mice. (**b**) Western blot analysis of skin from MIF Tg mice showed that the MIF protein level was also higher in MIF Tg mice than in WT mice.

OVA-sensitized skin sites of MIF Tg mice showed marked eosinophil infiltration

To examine the role of MIF in eosinophilic infiltration, MIF Tg and WT mice were subjected to epicutaneous OVA sensitization. Only a few eosinophils were present in saline-sensitized skin from MIF Tg and WT mice, while eosinophilic infiltration of the dermis was significantly increased following epicutaneous sensitization with OVA. The mean number of eosinophils after OVA sensitization was 13.6 ± 2.84 in MIF Tg mice, but only 4.8 ± 1.37 in WT mice ($P<0.001$; Figure 2a). Figure 2b shows the histological features of OVA-sensitized skin sites in MIF Tg and WT mice. The epidermis was slightly thickened, and numerous eosinophils and mononuclear cells infiltrated the upper dermis around the vessels, in the OVA-sensitized skin of MIF Tg mice.

Eosinophil numbers were not increased in the OVA-sensitized skin of MIF KO mice

To further clarify the roles of MIF in eosinophilic infiltration, MIF KO mice were subjected to epicutaneous OVA sensitization. The mean number of eosinophils after OVA sensitization was 2.0 ± 0.94 in MIF KO mice, and did not differ from that after saline sensitization. Furthermore, this value was significantly lower than that of WT mice (4.8 ± 1.37, $P<0.05$; Figure 3a). Histological features also confirmed only a few eosinophils to be present in the dermis after OVA sensitization in MIF KO mice (Figure 3b).

The expression of eotaxin and Th2-type cytokines increased in the OVA-sensitized skin of MIF Tg mice, but decreased in the OVA-sensitized skin in MIF KO mice

We next examined the expression of mRNAs for eotaxin and cytokines in OVA-sensitized skin specimens from MIF Tg, MIF KO, and WT mice. The expression levels of eotaxin and Th2-type cytokines, especially IL-5, were increased in the OVA-sensitized skin of MIF Tg mice compared with WT mice. However, IFN-γ, a Th1-type cytokine, did not differ between MIF Tg and WT mice. Conversely, low eotaxin mRNA expression was observed in the OVA-sensitized skin of MIF KO mice compared with WT mice. Similarly, the mRNA expression of the Th2-type cytokines, including IL-4,

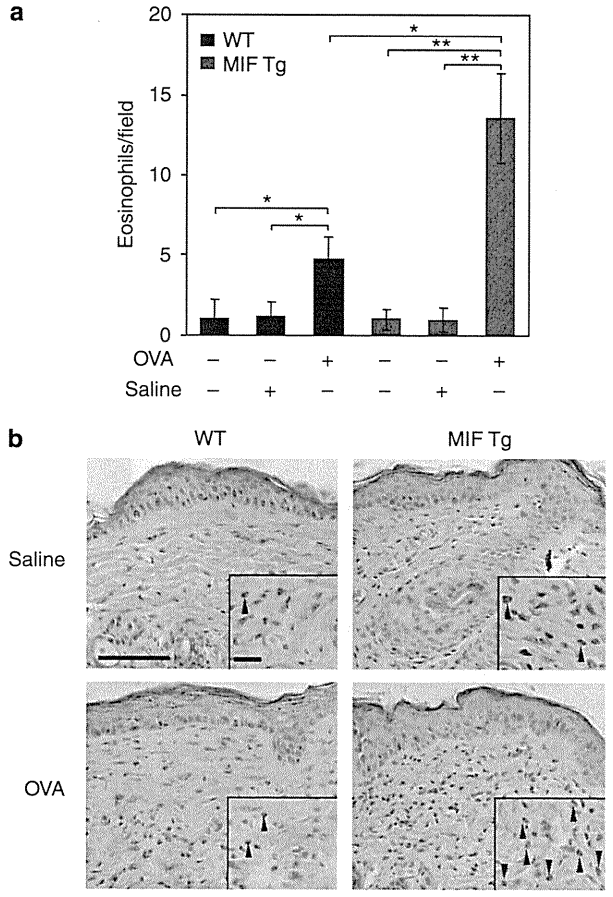

Figure 2. Eosinophil infiltration into ovalbumin (OVA)-sensitized skin sites of macrophage migration inhibitory factor (MIF) transgenic (Tg) mice. (**a**) The number of eosinophils in OVA-sensitized skin sites of MIF Tg mice was compared with the wild-type (WT) mice. Each value represents the mean ± SD ($n = 5$; $^*P < 0.001$, $^{**}P < 0.0001$). (**b**) Histological features of OVA-sensitized skin sites in MIF Tg mice and WT mice. Scale bar for large panels = 50 μm; scale bar for small panels = 10 μm; hematoxylin and eosin section. Arrowheads point to eosinophils. The experiments were repeated three times and similar results were obtained.

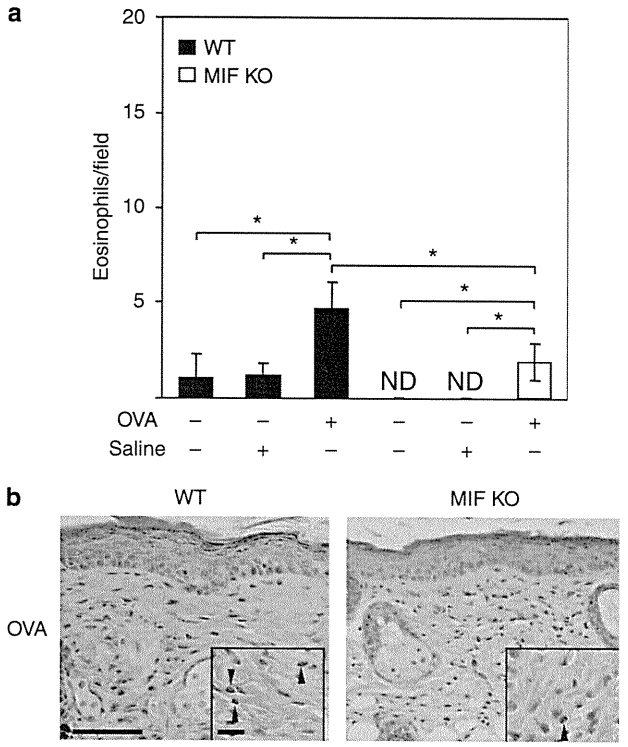

Figure 3. Eosinophil infiltration induced in ovalbumin (OVA)-sensitized skin sites of macrophage migration inhibitory factor (MIF) knockout (KO) mice. (**a**) The number of eosinophils in OVA-sensitized skin sites of MIF KO mice was compared with wild-type (WT) mice. Each value represents the mean ± SD ($n = 5$, $^*P < 0.05$). (**b**) Histological features of OVA-sensitized skin sites in MIF KO and WT mice. Scale bar for large panels = 50 μm; scale bar for small panels = 10 μm; hematoxylin and eosin section. Arrowheads point to eosinophils. The experiments were repeated three times and similar results were obtained each time.

IL-5, and IL-13, were low in the OVA-sensitized skin of MIF KO mice compared with WT mice (Figure 4).

The expression and production of eotaxin in cultured fibroblasts from MIF Tg mice and from MIF KO mice

To clarify the role of MIF in the expression of eotaxin, we performed *in vitro* experiments. A previous report described that IL-4 could dose-dependently induce the expression of eotaxin mRNA in dermal fibroblasts from humans and mice (Mochizuki *et al.*, 1998). Using this protocol, we analyzed the eotaxin expression in cultured fibroblasts from MIF Tg, MIF KO, and WT mice by stimulating them with IL-4. Unstimulated fibroblasts from these mice barely expressed eotaxin mRNA. However, fibroblasts from MIF Tg mice showed dramatically increased eotaxin mRNA after stimulation with 5 ng ml^{-1} of IL-4 (Figure 5a). To evaluate whether there was an accompanying change in eotaxin protein production, the amount of eotaxin in fibroblast supernatants was also analyzed. Eotaxin proteins in the culture supernatant of fibroblasts from MIF Tg mice were also significantly increased compared with those from WT mice ($^*P < 0.005$). However, fibroblasts from MIF KO mice showed minimal expression of eotaxin mRNA even when stimulated with 10 ng ml^{-1} of IL-4. Eotaxin production in the culture supernatant of fibroblasts from MIF KO mice was barely detectable (Figure 5b).

Recombinant MIF restored the expression and production of eotaxin in dermal fibroblasts from MIF KO mice

In dermal fibroblasts from WT mice, stimulation with IL-4 significantly induced the expression of eotaxin mRNA compared with unstimulated fibroblasts (Figure 6a). Addition of recombinant MIF significantly enhanced this increase in eotaxin expression. This suggests that the eotaxin expression in dermal fibroblasts from MIF Tg mice was markedly increased by IL-4 stimulation. A significant amount of eotaxin was also produced by combined stimulation with IL-4 ($^*P < 0.005$, $^{**}P < 0.05$; Figure 6b). Although the fibroblasts from MIF KO mice showed minimal induction of eotaxin mRNA expression in response to stimulation with IL-4, both the expression of eotaxin mRNA and the production of eotaxin protein were restored by addition of recombinant MIF

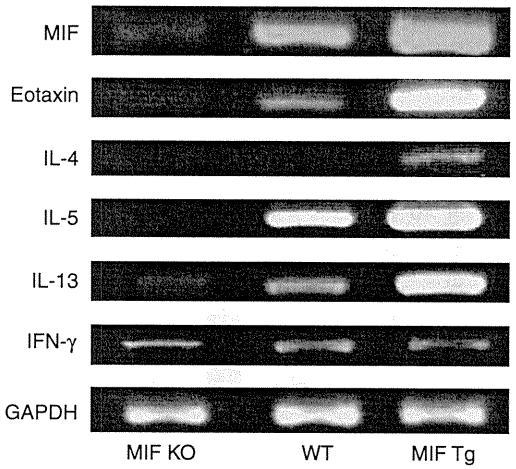

Figure 4. Expression levels of eotaxin and Th2-type cytokines in ovalbumin (OVA)-sensitized skin from macrophage migration inhibitory factor (MIF) transgenic (Tg) mice and MIF knockout (KO) mice. Reverse transcriptase-PCR analyses of eotaxin, IL-4, IL-5, IL-13, and IFN-γ levels in skin sites of MIF Tg and WT mice sensitized with OVA were performed. Eotaxin, IL-4, IL-5, and IL-13 mRNA expression levels were increased in OVA-sensitized MIF Tg; however, both eotaxin and Th2-type cytokines were markedly decreased in OVA-sensitized MIF KO mice, compared with WT mice. The experiments were repeated three times and similar results were obtained. GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

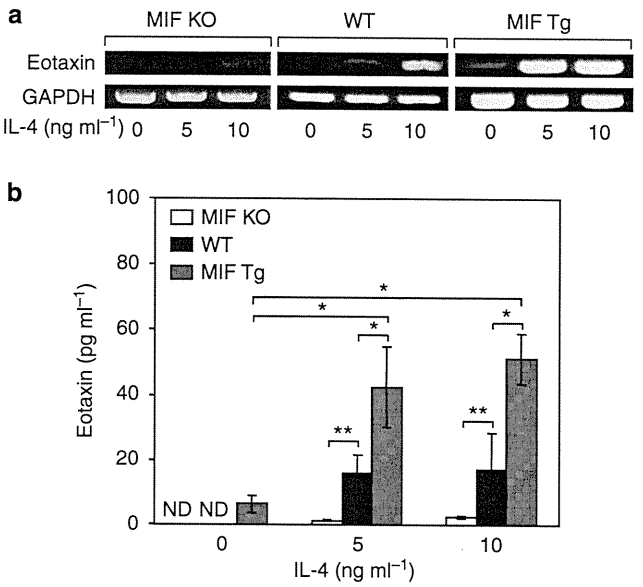

Figure 5. IL-4 induced eotaxin expression and production by fibroblasts from macrophage migration inhibitory factor (MIF) transgenic (Tg) and MIF knockout (KO) mice. Fibroblasts from MIF KO, MIF Tg, and wild-type (WT) mice were stimulated with IL-4 (5 or 10 ng ml^{-1}) for 24 hours. (**a**) RNA was extracted from the cells and the abundance of eotaxin mRNA was evaluated by reverse transcriptase-PCR. Data are from a representative experiment that was repeated three times and yielded similar results. (**b**) The eotaxin content of cultured supernatants was analyzed for eotaxin by ELISA. Each value represents the mean ± SD of five specimens. *P<0.005, **P<0.05. ND, not detected.

(Figure 6a and b). The levels of eotaxin production in MIF KO mouse fibroblasts exposed to MIF were similar to the levels in WT fibroblasts stimulated with IL-4 (Figure 6b).

DISCUSSION

There is growing evidence that the eosinophil is an important effecter cell in allergic inflammatory diseases, such as asthma and AD. Accumulation of eosinophils in the skin is characteristic of inflammation associated with AD (Leiferman, 1989; Kapp, 1995). This study explored, for the first time, the significant increase in eosinophil infiltration in the skin of MIF Tg mice after OVA sensitization, compared with WT mice. However, in MIF KO mice, eosinophils failed to infiltrate the skin after repeated epicutaneous sensitization with OVA. Eosinophils accumulate at inflammatory sites and release numerous mediators capable of initiating and maintaining allergic inflammation. Yamaguchi *et al.* (2000) reported eosinophils to be an important source of MIF in allergic inflammatory diseases. The number of eosinophils was reported to be significantly decreased in lung tissue and in bronchoalveolar lavage fluid from MIF KO mice after stimulation with OVA, compared with those from WT mice (Mizue *et al.*, 2005; Magalhães *et al.*, 2007; Wang *et al.*, 2009). In an allergic rhinitis model, eosinophil recruitment into the nasal submucosa was also suppressed in MIF KO mice (Nakamaru *et al.*, 2005). Consistent with these findings, our current evidence indicates that MIF is essential for the infiltration of eosinophils into the OVA-sensitized skin.

This study also demonstrated that the expression of both eotaxin and IL-5 is markedly increased in the OVA-sensitized

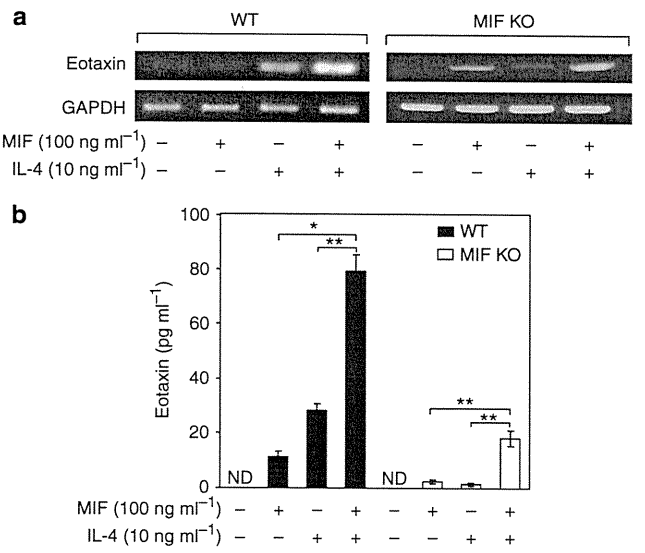

Figure 6. Recombinant macrophage migration inhibitory factor (MIF) restored eotaxin expression and production by IL-4 stimulation in dermal fibroblasts from MIF knockout (KO) mice. The fibroblasts were stimulated with IL-4 (10 ng ml^{-1}), MIF (100 ng ml^{-1}), or both IL-4 and MIF for 24 hours. (**a**) RNA was extracted from cells, and the abundance of eotaxin mRNA was evaluated by reverse transcriptase-PCR. Data are from a representative experiment that was repeated three times showing similar results. (**b**) The eotaxin contents of cultured supernatants were analyzed for eotaxin by ELISA. Each value represents the mean ± SD of six specimens. *P<0.005, **P<0.05. GAPDH, glyceraldehyde-3-phosphate dehydrogenase; ND, not detected.

skin sites of MIF Tg mice skin. The other Th2-type cytokines, IL-4 and IL-13, were also slightly increased in MIF Tg mice. On the other hand, the expression levels of eotaxin and Th2-type cytokines were markedly decreased in the OVA-sensitized skin sites of MIF KO mice. Acute AD involves a systemic Th2 response with eosinophilia, and marked infiltration of Th2 cells into skin lesions. These infiltrating T cells predominantly express IL-4, IL-5, and IL-13. Furthermore, the roles of cytokines in the induction of migration and the accumulation of eosinophils into an inflamed tissue have been extensively studied in recent years. Some of the important eosinophil chemoattractant cytokines include IL-5, IL-8, eotaxin, RANTES (regulated on activation, normal T cell expressed and secreted), and monocyte chemoattractant protein-3 (Lampinen *et al.*, 2004). Among these, eotaxin (CC chemokine ligand-11) is one of the most important eosinophil-selective chemoattractants (Jose *et al.*, 1994; Garcia-Zepeda *et al.*, 1996). Eotaxin is secreted by several cell types: epithelial cells, fibroblasts, and activated infiltrating leukocytes such as eosinophils (Garcia-Zepeda *et al.*, 1996; Ponath *et al.*, 1996; Uguccioni *et al.*, 1996). Eotaxin is reportedly related to the eosinophilia in allergic diseases, including AD and asthma (Ying *et al.*, 1997; Yawalkar *et al.*, 1999). IL-5 also has an important role in eosinophil development and differentiation (Sanderson, 1992). IL-5 KO mice had virtually no eosinophils in either saline-sensitized skin or in OVA-sensitized skin (Spergel *et al.*, 1999). Recently, Magalhães *et al.* (2009) reported that MIF was involved in IL-5-driven maturation of eosinophils and in tissue eosinophilia associated with *Schistosoma mansoni* infection. In addition, several earlier studies demonstrated that MIF KO mice failed to develop tissue eosinophilia, and that eotaxin, IL-4, and IL-5 were not induced in either allergic lung tissues or bronchoalveolar lavage fluid (Mizue *et al.*, 2005; Wang *et al.*, 2006). Accordingly, our results suggest that MIF is important in regulating both eotaxin and IL-5 in OVA-sensitized inflamed skin tissue.

In support of these *in vivo* observations, this study demonstrated that the expression of eotaxin was significantly increased after stimulation with IL-4 in fibroblasts from MIF Tg mice compared with WT fibroblasts, but not in fibroblasts from MIF KO mice. However, eotaxin expression in fibroblasts from MIF KO mice was restored by addition of recombinant MIF. These observations suggest that MIF is crucial to the expression of eotaxin, and antigen-induced eosinophil infiltration is suspected to be induced by eotaxin mainly by MIF, in addition with IL-5 production involved in MIF. Previous observations have shown that either IL-4 or IL-13 can increase eotaxin expression, and that they function synergistically with proinflammatory cytokines, such as tumor necrosis factor-α, to increase the production of eotaxin in epithelial cells and fibroblasts (Mochizuki *et al.*, 1998; Nakamura *et al.*, 1998; Li *et al.*, 1999; Stellato *et al.*, 1999; Fujisawa *et al.*, 2000; Terada *et al.*, 2000). Increases in both IL-4 and IL-13 in the inflamed skin of MIF Tg mice might involve enhancing the tissue eosinophilia. Furthermore, tumor necrosis factor-α secretion induced by MIF also has the ability to increase eotaxin expression in MIF Tg mice, on the basis of the known capacity of MIF to trigger the secretion of several inflammatory cytokines, including tumor necrosis factor-α (Donnelly *et al.*, 1997). It was recently elucidated that MIF activates an extracellular signal-regulated kinase-1/2–mitogen-activated protein kinase signaling through its receptor CD74 (Leng *et al.*, 2003) and c-Jun N-terminus kinase–mitogen-activated protein kinase signaling through CD74/CXCR4 (Lue *et al.*, 2011), in addition to the endocytic pathway described previously (Kleemann *et al.*, 2000); however, the receptor-mediated mechanism involved in MIF-mediated IL-4-induced eotaxin release is unclear. This mechanism should therefore be an important focus of research in association with MIF-mediated skin allergy.

Finally, we suggest that the inhibition of MIF might be an effective treatment for AD, suppressing both eosinophil infiltration and eotaxin expression in the skin. We recently demonstrated that in murine models of AD, MIF–DNA vaccination elicited the production of endogenous anti-MIF antibodies, producing rapid improvement of AD skin manifestations (Hamasaka *et al.*, 2009). Our previous data and the current findings therefore hold promise for the development of MIF inhibitors as a therapeutic strategy for allergic diseases.

MATERIALS AND METHODS

Materials

The following materials were obtained from commercial sources: a mouse eotaxin-specific ELISA kit from Genzyme TECHNE (Cambridge, MT); Isogen RNA extraction kit from Nippon Gene (Tokyo, Japan); M-MLV reverse transcriptase from GIBCO (Grand Island, NY); Taq DNA polymerase from Perkin-Elmer (Norwalk, CO); nylon membranes from Schleicher & Schuell (Keene, NH); Ficoll-Plaque Plus and Protein A Sepharose from Pharmacia (Uppsala, Sweden); recombinant mouse IL-4 from R&D systems (Minneapolis, MN). Recombinant rat MIF (this recombinant MIF crossreacts with that of mice) was expressed in *Escherichia coli* BL21/DE3 (Novagen, Madison, WI) and was purified as described previously (Shimizu *et al.*, 2004). All other chemicals were of analytical grade.

Mice

The MIF-overexpressing Tg mice were established after complementary DNA microinjection. Physical and biochemical characteristics, including body weight, blood pressure, and serum cholesterol and blood sugar levels, were normal, as reported previously (Sasaki *et al.*, 2004). The transgene expression was regulated by a hybrid promoter composed of the cytomegalovirus enhancer and the β-actin/β-globin promoter, as reported previously (Akagi *et al.*, 1997). The strain of the original MIF Tg mice was ICR, which were backcrossed with C57BL/6 for at least 10 generations. Tg mice were maintained by heterozygous sibling mating. Aged MIF Tg mice of 12 months or older developed neither skin allergies nor diseases. The MIF-deficient (KO) mice were established by targeted disruption of the *MIF* gene as described previously (Honma *et al.*, 2000), using a mouse strain bred onto a C57BL/6 background. MIF Tg, MIF KO, and WT mice were maintained under specific-pathogen-free conditions at the Institute for Animal Experiments of the Graduate School of Medicine and Pharmaceutical Sciences, University of Toyama. All experiments were performed on 8-week-old female adult mice.

Epicutaneous sensitization

Epicutaneous sensitization of mice was performed as described previously (Spergel *et al.*, 1998). Briefly, each mouse was anesthetized with 10% nembutal (Hospira, Osaka, Japan), then shaved with a razor. One hundred mg of OVA (Sigma, St Louis, MO) in 100 μl of normal saline were placed on a 1 × 1 cm patch (Alcare, Tokyo, Japan), which was secured to the skin with a transparent bio-occlusive dressing (ALCARE). The patch was left in place for 1 week and then removed. At the end of the second week, an identical patch was reapplied to the same skin site. Each mouse had a total of three 1-week exposures to the patch, separated from each other by 2-week intervals. Inspection confirmed that the patch was still in place at the end of each sensitization period. Skin biopsies from treated areas were obtained for RNA isolation and histological evaluation. Six-micrometer thick skin sections were stained with hematoxylin and eosin (H&E). Eosinophils were counted under a microscope at a magnification of ×400 and expressed as the mean number of the cells in five random fields (one section per mouse, five mice per group).

Northern blot analysis

Bone marrow cells were isolated from the femurs of MIF Tg or WT mice, and 1×10^6 cells ml^{-1} was collected. Total RNA was isolated from bone marrow cells and skin from mice using an Isogen RNA extraction kit according to the manufacturer's protocols. Twenty μg of RNA from control and test samples were loaded onto a formaldehyde-agarose gel and the RNA was transferred onto a nylon membrane. RNA fragments obtained by restriction enzyme treatment for MIF and glyceraldehyde-3-phosphate dehydrogenase were labeled with [α-^{32}P]deoxycytidine triphosphate using a DNA random primer labeling kit (Enzo Life Sciences International, Farmingdale, NY). Hybridization was carried out at 42 °C for 24–48 hours. Post-hybridization washing was performed in 0.1% SDS with 0.2 × standard saline citrate (1 × standard saline citrate: 0.15 M NaCl, 0.015 M sodium citrate) at 65 °C for 15 minutes. The radioactive bands were visualized by autoradiography on Kodak X-AR5 film (Tokyo, Japan) and quantitatively analyzed using the NIH Image system (Bethesda, MD). The results were normalized by compensating for the glyceraldehyde-3-phosphate dehydrogenase mRNA levels.

Reverse transcription-PCR analysis

Total RNA was extracted from each mouse skin specimen. RNA reverse transcription was performed with M-MLV reverse transcriptase using random hexamer primers and subsequent amplification using Taq DNA polymerase. PCR was carried out for 35–40 cycles with denaturation at 94 °C for 30 seconds, annealing from 46 to 64 °C for 1 minute and extension at 72 °C for 45 seconds using a thermal cycler (PE Applied Biosystems Gene Amp PCR system 9700, Life Technologies Japan, Tokyo, Japan). The primers used in this study are described in Supplementary Table S1 online. After PCR, the amplified products were analyzed by 2% agarose gel electrophoresis.

Western blot analysis

The epidermis of each mouse was homogenized with a Polytron homogenizer (Kinematica, Lausanne, Switzerland). The protein concentrations of the cell homogenates were quantified using a Micro BCA protein assay reagent kit (Thermo Fisher Scientific, Yokohama, Japan). Equal amounts of homogenates were dissolved in 20 μl of Tris-HCL, 50 mM (pH 6.8), containing 2-mercaptoethanol (1%), SDS (2%), glycerol (20%) and bromophenol blue (0.04%), and then were heated to 100 °C for 5 minutes. The samples were then subjected to SDS-PAGE and electrophoretically transferred onto a nitrocellulose membrane. The membranes were blocked with 2.5% non-fat dry milk powder in phosphate-buffered saline, probed with antibodies against MIF (Shimizu *et al.*, 1996) and subsequently reacted with secondary IgG antibodies coupled with horseradish peroxidase. The resultant complexes were processed for the ECL detection system (Amersham Biosciences, Buckinghamshire, UK). The relative amounts of proteins associated with specific antibodies were normalized according to the intensities of β-actin (Sigma).

Cell culture

Skin specimens were obtained from the dorsal surfaces of newborn MIF Tg, MIF KO, and WT mice. The skin specimens were cut into 3–5 mm pieces and placed on a large Petri dish with the subcutaneous side down, followed by tissue incubation for 1 week in a humidified atmosphere of 5% CO_2 at 37 °C. Once sufficient numbers of fibroblasts had migrated out of the skin sections, pieces of the skin were removed and the cells were passaged by trypsin digestion in the same manner as wound-harvested fibroblasts. Fibroblasts were grown in DMEM containing 10% fetal calf serum and 1% penicillin/streptomycin. After 3 passages, the fibroblasts were used for the experiments. The fibroblasts from MIF KO and WT mice were stimulated with MIF (100 ng ml^{-1}), IL-4 (10 ng ml^{-1}), or MIF (100 ng ml^{-1}) in combination with IL-4 (10 ng ml^{-1}) for 24 hours. We also stimulated the fibroblasts from MIF Tg, MIF KO, and WT mice with IL-4 (5 or 10 ng ml^{-1}) alone for 24 hours. The cells were analyzed using reverse transcriptase-PCR. Culture supernatants were analyzed for eotaxin by ELISA.

Statistical analysis

Values are expressed as the means ± SD of the respective test or control group. The statistical significance of differences between the control and test groups was evaluated by either Student's *t*-test or one-way analysis of variance.

CONFLICT OF INTEREST

The authors state no conflict of interest.

ACKNOWLEDGMENTS

This research was supported by a Grant-in-Aid for Scientific Research (Nos.11670813 and 13357008) from the Japan Society for the Promotion of Science.

SUPPLEMENTARY MATERIAL

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

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AKT Has an Anti-Apoptotic Role in ABCA12-Deficient Keratinocytes

Journal of Investigative Dermatology (2011) **131,** 1942–1945; doi:10.1038/jid.2011.132; published online 2 June 2011

TO THE EDITOR

Harlequin ichthyosis (HI) is a hereditary skin disorder characterized by severe hyperkeratosis and impaired skin barrier function (Moskowitz *et al.*, 2004; Akiyama *et al.*, 2005). We have identified the ATP-binding cassette transporter A12 (*ABCA12*) as the causative gene of HI and, furthermore, demonstrated that ABCA12 is essential for keratinocyte lipid transport (Akiyama *et al.*, 2005; Yanagi *et al.*, 2008). Loss of ABCA12 function causes lipid transport to be defective in keratinocytes of the upper spinous and granular layers, resulting in the deposition of numerous intracellular lipid droplets and malformation of intercellular lipid layers (Akiyama *et al.*, 2005; Yanagi *et al.*, 2010). Recently, we have shown that gangliosides accumulate in the differentiated keratinocytes of HI patients (Mitsutake *et al.*, 2010). On the basis of the evidence that lipid accumulation is involved in keratinocyte apoptosis (Wang *et al.*, 2001; Uchida *et al.*, 2010), we investigated apoptotic and anti-apoptotic parameters in skin samples from HI patients and *Abca12*$^{-/-}$ HI model mice.

We studied the skin of two HI patients and that of *Abca12*$^{-/-}$ mice. The *ABCA12* mutations of the two HI patients have been previously reported: one patient has the homozygous splice acceptor site mutation c.3295-2A>G and the other has the homozygous nonsense mutation p.Arg434X (Akiyama *et al.*, 2005). The procedure for generating *Abca12*$^{-/-}$ mice, the establishment of primary-cultured keratinocytes, immunofluorescence staining, immunoblotting, and real-time reverse transcriptase PCR analysis has been previously described (Yanagi *et al.*, 2008, 2010). First, we investigated the apoptosis of HI patient epidermis by hematoxylin–eosin stain and TUNEL assay (*In situ* Apoptosis Detection Kit, Takara Bio, Otsu, Japan). In the HI patients, the nuclei of the granular-layer keratinocytes were condensed (Figure 1b) and they show positive for TUNEL labeling (Figure 1d), although apoptotic nuclei are rare in the normal human epidermis (Figure 1a, c). The histopathological findings and results of TUNEL staining of the *Abca12*$^{-/-}$ mice were similar to those in the skin of the HI patients (Figure 1f and h). TUNEL staining in the epidermis of 18.5-day embryos indicated that the apoptosis of keratinocytes started during fetal skin development (Figure 1j).

We assessed the degree of AKT activation of *Abca12*$^{-/-}$ skin and keratinocytes using anti-AKT antibody #4691 and anti-phosphorylated AKT (Ser473) #4060 antibody (Cell Signaling, Danvers, MA). By immunoblot analysis, differentiated primary-cultured keratinocytes and the epidermis of *Abca12*$^{-/-}$ mice showed higher expression levels of Ser-473 phosphorylated AKT than those of the control wild-type mice (Figure 1o). Immunofluorescence staining detected phosphorylated AKT in the upper granular-layer keratinocytes of the *Abca12*$^{-/-}$ mouse skin (Figure 1l), but not in the skin of control wild-type mouse (Figure 1k). Cell proliferation was assessed by Ki-67 immunofluorescence (Figure 1). Ki-67 stain was similar in the wild-type and the *Abca12*$^{-/-}$ samples, indicating that the granular-layer keratinocytes of the *Abca12*$^{-/-}$ neonatal mice showed no excessive cell proliferation. To clarify whether AKT activation has

Abbreviations: ABCA12, ATP-binding cassette transporter A12; HI, harlequin ichthyosis; PPAR, peroxisome proliferator-activated receptor; RXR, retinoid X receptor

anti-apoptotic effects on *Abca12*$^{-/-}$ keratinocytes, we performed TUNEL staining of keratinocytes treated with AKT inhibitor, which blocks AKT phosphorylation (#124017; InSolution Akt Inhibitor VIII, Calbiochem, San Diego, CA). *Abca12*$^{-/-}$ keratinocytes incubated with 10 μM #124017 AKT inhibitor showed a notably greater number of TUNEL-positive cells than both wild-type keratinocytes with AKT inhibitor and *Abca12*$^{-/-}$ keratinocytes without AKT inhibitor (Figure 2). These results suggest that AKT activation helps *Abca12*$^{-/-}$ keratinocytes to avoid apoptosis. Furthermore, mRNA and protein levels of peroxisome proliferator-activated receptor (PPAR)-δ from *Abca12*$^{-/-}$ epidermis were shown to be significantly higher than those from wild-type epidermis (Taqman Gene Expression Assay, probe ID, Mm00803184_m1, Mm99999915_g1, Applied Biosystems, Carlsbad, CA; anti-PPAR-δ antibody H-74, Santa Cruz, Santa Cruz, CA; Supplementary Figure S1 online), which suggests upregulation of PPAR-δ as a candidate pathway for AKT activation.

Herein, we have suggested that apoptosis is involved in the pathomechanism of HI. Defective lipid transport due to loss of ABCA12 function leads to the accumulation of intracellular lipids, including glucosylceramides and gangliosides (Akiyama *et al.*, 2005; Mitsutake *et al.*, 2010). Studies by Wang *et al.* (2001) and Sun *et al.* (2002) showed that the elevation of ganglioside levels leads to keratinocyte apoptosis. Thus, we are able to speculate that the accumulation of gangliosides leads to the apoptosis of *Abca12*$^{-/-}$ keratinocytes, although the exact mechanism of apoptosis in *Abca12*$^{-/-}$ keratinocytes remains unclear.

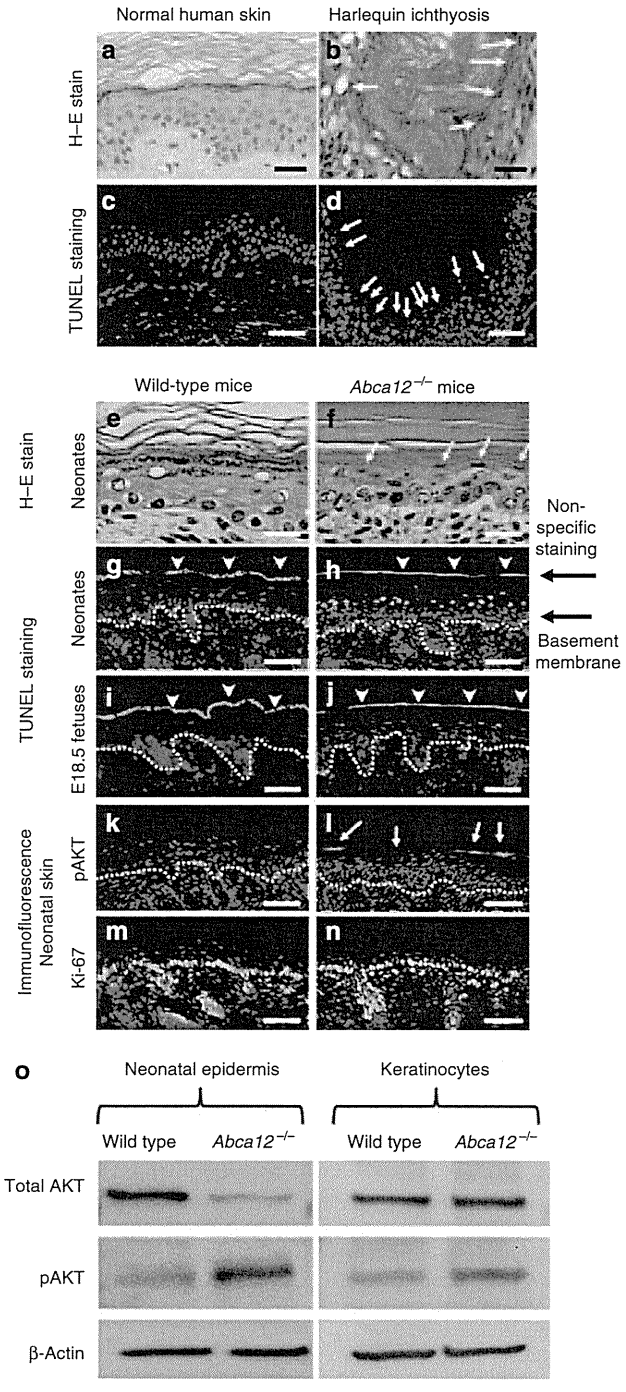

Figure 1. ATP-binding cassette transporter A12-deficient keratinocytes show TUNEL-positive nuclei and AKT activation. (**a**–**d**) In the harlequin ichthyosis patients, the nuclei of the granular-layer keratinocytes are condensed (**b**, white arrows) and they show positive TUNEL labeling (**d**, white arrows), although apoptotic nuclei are rare in the normal human epidermis (**a**, **c**). Data shown are representative of those from the two harlequin ichthyosis patients. (**e**, **f**) Granular-layer keratinocytes of *Abca12*$^{-/-}$ mice show more condensed nuclei (**f**, white arrows) than those of wild-type mice (**e**). (**g**–**j**) Granular-layer keratinocytes of *Abca12*$^{-/-}$ mice, a neonate (**h**) and an 18.5-day embryo (**j**), show TUNEL-positive nuclei. No TUNEL-positive cells are seen in the epidermis of the control wild-type mice (**g**, **i**). Dotted lines indicate the basement membrane. Nonspecific staining is seen on the skin surface (white arrowheads). (**k**, **l**) By immunofluorescence staining, AKT activation (Ser-473 phosphorylated AKT; green) is observed in granular-layer keratinocytes of *Abca12*$^{-/-}$ mice. (**m**, **n**) Immunofluorescence staining for the Ki-67-proliferation marker shows similar staining patterns of basal keratinocytes in wild-type (**m**) and *Abca12*$^{-/-}$ (**n**) samples. (**a**, **b**, **e**, **f**; hematoxylin–eosin (H–E) stain. Bars of **c**, **d**, **g**, **h**, **i**, **j**, **k**, **l**, **m**, **n** = 20 μm. Bars of **a**, **b**, **e**, **f** = 5 μm.) (**o**) Immunoblot analysis shows that levels of serine-473-phosphorylated AKT (pAKT) in neonatal epidermis and differentiated keratinocytes of *Abca12*$^{-/-}$ mice are higher than those of wild-type mice.

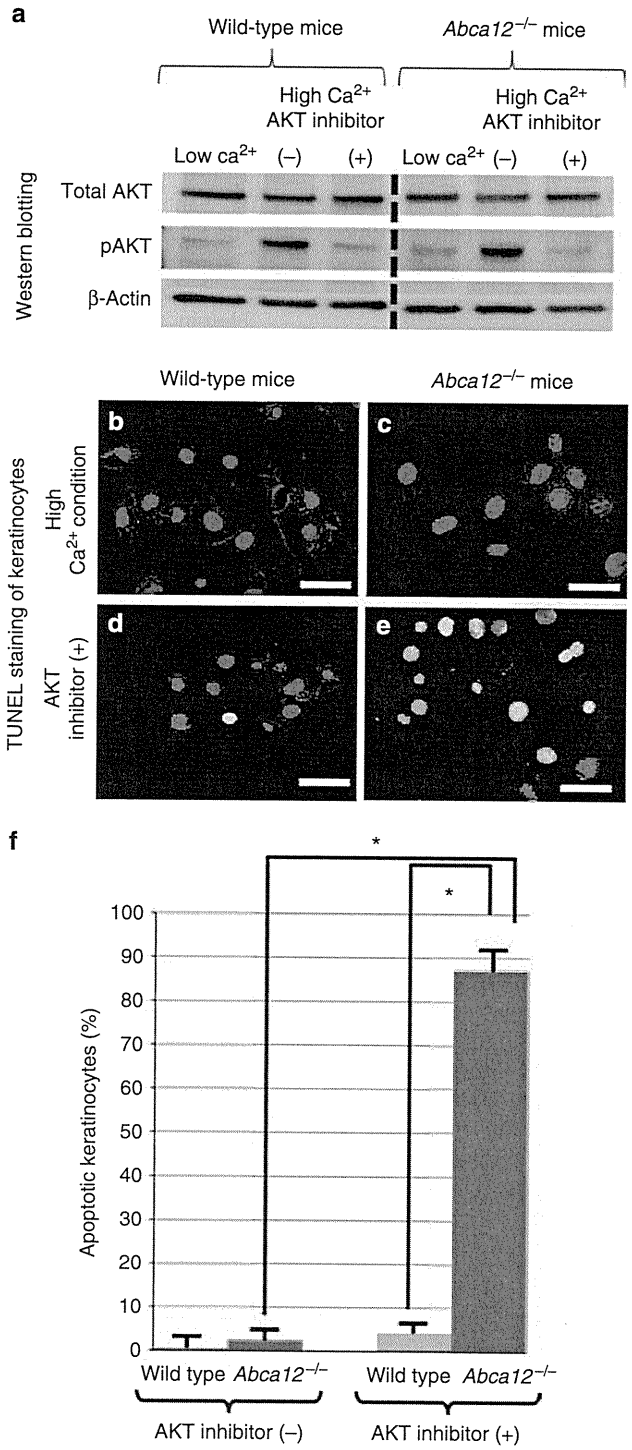

Figure 2. Inhibition of AKT activation leads to apoptosis of *Abca12*$^{-/-}$ keratinocytes. (**a**) Immunoblot analysis indicates that the AKT inhibitor can inhibit AKT activation (phosphorylated AKT (pAKT) synthesis) in differentiated keratinocytes. (**b–e**) TUNEL staining of keratinocytes cultured under high Ca^{2+} condition treated with/without the AKT inhibitor. Neither wild-type cells (**b**) nor *Abca12*$^{-/-}$ cells (**c**) are TUNEL positive. *Abca12*$^{-/-}$ keratinocytes with the AKT inhibitor (#124017; 10 μM) show many TUNEL-positive nuclei (**e**), although only a small number of wild-type cells with the AKT inhibitor are TUNEL positive (**d**). (Bars = 20 μm.) (**f**) Percentage of TUNEL-positive keratinocytes. *Abca12*$^{-/-}$ keratinocytes with AKT inhibitor shows a significantly greater number of TUNEL-positive nuclei than wild-type keratinocytes with/without the AKT inhibitor and *Abca12*$^{-/-}$ keratinocytes without the AKT inhibitor. ($n = 3$, mean ± SD, $^*P < 0.05$).

Although *Abca12*$^{-/-}$ granular-layer keratinocytes show characteristics of apoptosis, including condensed nuclei and positive TUNEL labeling, they are able to form epidermal stratification. In several disorders involving keratinocyte apoptosis, e.g., toxic epidermal necrolysis, the apoptotic epidermal keratinocytes show not only TUNEL-positive nuclei but also defective epidermal stratification (Abe *et al.*, 2003). Thrash *et al.* (2006) reported that AKT1 activation is an essential signal for keratinocyte cell survival and stratification, by experiments with gene silencing and three-dimensional cell cultures. Thus, we hypothesized that the AKT pathway might work as a compensatory mechanism against apoptosis in *Abca12*$^{-/-}$ keratinocytes. We have clearly shown that AKT activation occurs in *Abca12*$^{-/-}$ granular-layer keratinocytes, which suggests that AKT activation serves to prevent the cell death of *Abca12*$^{-/-}$ keratinocytes. By immunoblot analysis using anti-AKT1/2/3 antibodies (#2938/3063/3788, Cell Signaling), *Abca12*$^{-/-}$ epidermis showed expression of AKT1 and AKT2, but not AKT3 (Supplementary Figure S2 online). Compared with wild-type epidermis, *Abca12*$^{-/-}$ epidermis seemed to have more AKT1 than AKT2. From our data and the literature (Thrash *et al.*, 2006), we are able to speculate that AKT1 is the major isoform of phosphorylated AKT in *Abca12*$^{-/-}$ epidermis.

We have shown that PPAR-δ is a candidate molecule in the upstream of the AKT activation pathway in *Abca12*$^{-/-}$ keratinocytes. Di-Poi *et al.* (2002) reported that PPAR-δ has an anti-apoptotic role in keratinocytes via transcriptional control of the AKT1 signaling pathway. PPAR-δ also regulates the expression of ABCA12 (Jiang *et al.*, 2008). From these studies, we can speculate that upregulation of PPAR-δ is in response to apoptosis or decreased ABCA12 expression. To ascertain the function of PPAR-δ, we performed the experiments using a PPAR-δ-specific antagonist (GSK0660, Santa Cruz). Differentiated *Abca12*$^{-/-}$ keratinocytes treated with 1 μM GSK0660 for 48 hours showed TUNEL-positive nuclei, from which we are able to speculate an anti-apoptotic role for

PPAR-δ in *Abca12*$^{-/-}$ keratinocytes (Supplementary Figure S1 online). From our studies and the literature (Di-Poi *et al.*, 2002), PPAR-δ has been shown to have at least an anti-apoptotic role in *Abca12*$^{-/-}$ keratinocytes; however, it remains unclear whether the upregulation of PPAR-δ is in response to apoptosis or decreased ABCA12 expression.

Furthermore, we have measured the mRNA expression levels of other nuclear hormone receptors, including PPAR-α, PPAR-γ, retinoic acid receptor-α, liver X receptor-α, liver X receptor-β, RXR-α, and RXR-γ (Applied Biosystems). The mRNA level of RXR-α from *Abca12*$^{-/-}$ epidermis was shown to be significantly higher than that from wild-type epidermis (Supplementary Figure S1 online). The interaction between the upregulation of RXR-α and AKT activation in keratinocytes has not been reported. However, Wang *et al.* (2011) reported that RXR-α ablation in the epidermis enhances UV-induced apoptosis, which suggests that RXR-α has an anti-apoptotic function in keratinocytes. Thus, upregulation of RXR-α may also have an anti-apoptotic function in *Abca12*$^{-/-}$ keratinocytes.

In conclusion, the present data suggest that keratinocyte apoptosis is involved in the pathomechanisms of HI and that the AKT signaling pathway helps *Abca12*$^{-/-}$ keratinocytes to survive during the keratinization process. In light of this, activation of the AKT signal pathway may be to our knowledge, previously unreported strategy for treating keratinization disorders, including ichthyosis.

CONFLICT OF INTEREST

The authors state no conflict of interest.

ACKNOWLEDGMENTS

We thank Ms Aoyanagi for her technical assistance. This work was supported in part by a grant-in-aid from the Ministry of Education, Science, Sports and Culture of Japan (Kiban A 23249058: to MA), a grant from the Ministry of Health, Labor and Welfare of Japan (Health and Labor Sciences Research Grants; Research on Intractable Disease: H22-177: to MA), and a grant-in-aid from the Japan Society for the Promotion of Science Fellows (to TY).

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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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See related commentary on pg 1790

Interpretation of Skindex-29 Scores: Cutoffs for Mild, Moderate, and Severe Impairment of Health-Related Quality of Life

Journal of Investigative Dermatology (2011) **131,** 1945–1947; doi:10.1038/jid.2011.138; published online 19 May 2011

TO THE EDITOR

Health-related quality of life (HRQL) is commonly assessed by means of standardized questionnaires and expressed in domain and overall HRQL scores. An important challenge is to interpret these scores correctly. What does a given score really mean? Although there is no standard approach, several methods exist to facilitate the interpretation of HRQL scores.

In a recently published study (Prinsen *et al.*, 2010), we identified

Abbreviation: HRQL, health-related quality of life

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30 June 2010

doi:10.1016/j.jdermsci.2010.11.014

Letter to the Editor

New insight into genotype/phenotype correlations in *ABCA12* mutations in harlequin ichthyosis

Harlequin ichthyosis (HI) is a severe and often fatal congenital ichthyosis with an autosomal recessive inheritance pattern [1]. The clinical features include thick, plate-like scales with ectropion, eclabium and flattened ears. *ABCA12* mutations underlie HI [2,3] and it was clarified that HI is caused by severe functional defects in the keratinocyte lipid transporter ABCA12 [2]. To date, various *ABCA12* mutations have been reported in HI patients [4]. However, genotype/phenotype correlations in *ABCA12* mutations have been poorly elucidated. In order to obtain clues to understand genotype/phenotype correlations in *ABCA12* mutations, we report two HI patients from two independent Japanese families, who were compound heterozygotes for *ABCA12* mutations.

Patient 1 is the second child of healthy, unrelated Japanese parents. The skin of the baby girl was covered with white, diamond shaped plaques at birth (Fig. 1a). After therapy with oral retinoids and local application of white petrolatum, in a humid incubator, the scales gradually detached and passive and spontaneous mobility of the joints increased. Now at the age of 1 year and 7 months, her general condition is good, although she still has white to grey scales on a background of erythematous skin over her entire body. Patient 2 is the fourth child of healthy, unrelated Japanese parents. Her older brother had a history of congenital ichthyosis and died in early infancy. The skin of the newborn showed serious symptoms with thick, white, diamond shaped plaques, partly bordered by bleeding fissures (Fig. 1c). Although she had therapy with oral retinoids and local application of white petrolatum, in a humid incubator, her clinical symptoms failed to show any apparent improvement and she died when she was 5 months old.

Skin biopsies showed thick stratum corneum in both patients (Fig. 1d–g). In Patient 2, parakeratosis was observed in the epidermis and a sparse inflammatory cell infiltration was seen in the superficial dermis (Fig. 1e inset). Electron microscopy (Hitachi, Tokyo, Japan) revealed a large number of abnormal, variously sized lipid droplets that accumulated in the cornified cells of both patients' epidermis.

Mutational analysis of *ABCA12* was performed in both patients and their families. Each genomic DNA sample was subjected to PCR amplification, followed by direct automated sequencing. Oligonucleotide primers and PCR conditions used for amplification of all exons 1–53 of *ABCA12* were originally derived from the report by Lefèvre et al. [5] and were partially modified for the present study. The entire coding region including the exon/intron boundaries for both forward and reverse strands from the patients, their parents and 50 healthy Japanese controls were also sequenced. Both patients had the same paternal novel nonsense mutation p.Arg1515X (Fig. 1h) which leads to truncation of the first ATP-binding cassette within ABCA12 likely resulting in ABCA12 loss of function (Fig. 2a). On the other allele, Patient 1 had a maternal recurrent splice acceptor site mutation c.3295-2A>G (Fig. 1h). This splice site mutation was reported in an unrelated Japanese family with HI and was shown to lead to comparable amounts of 2 splice pattern variants [2]. The first mutant transcript would result in a 3 amino acids deletion (1099_1101delYMK). These 3 amino acids are located in the first transmembrane domain and are highly conserved (Fig. 2b). The second mutant transcript lost a 170-bp sequence from exon 24, which led to a frameshift. Expression of a small amount of ABCA12 protein, although mutated, was detected in the granular layer keratinocytes of the patient's epidermis and cultured keratinocytes by immunofluorescent staining [2]. Thus, it is possible that Patient 1 expresses some mutated ABCA12 protein with a partial function. This might be the reason why Patient 1 survived beyond the perinatal and neonatal period and is still alive although this might also be in part due to the prompt oral retinoid treatment.

Patient 2 carried a maternal missense mutation p.Gly1179Arg on the other locus (Fig. 1h). To confirm the presence of the mutation p.Gly1179Arg in Patient 2, we performed restriction enzyme digestion analysis using *BclI* (NEW ENGLAND BioLabs). Restriction enzyme digestion of PCR products was carried out according to the manufacture's protocols. The 255-bp PCR products from wild type alleles were not digested by *BclI*, although the PCR products from the allele with the mutation p.Gly1179Arg were digested into 173- and 82-bp fragments. The father's PCR product after *BclI* digestion showed a single 255-bp band, which indicated he had only normal alleles. In contrast, the PCR product after *BclI* digestion from the mother of Patient 2 showed 255-, 173- and 82-bp bands, which indicated that she was heterozygous for the p.Gly1179Arg missense mutation (supplementary Fig. S1). This mutation was reported in a

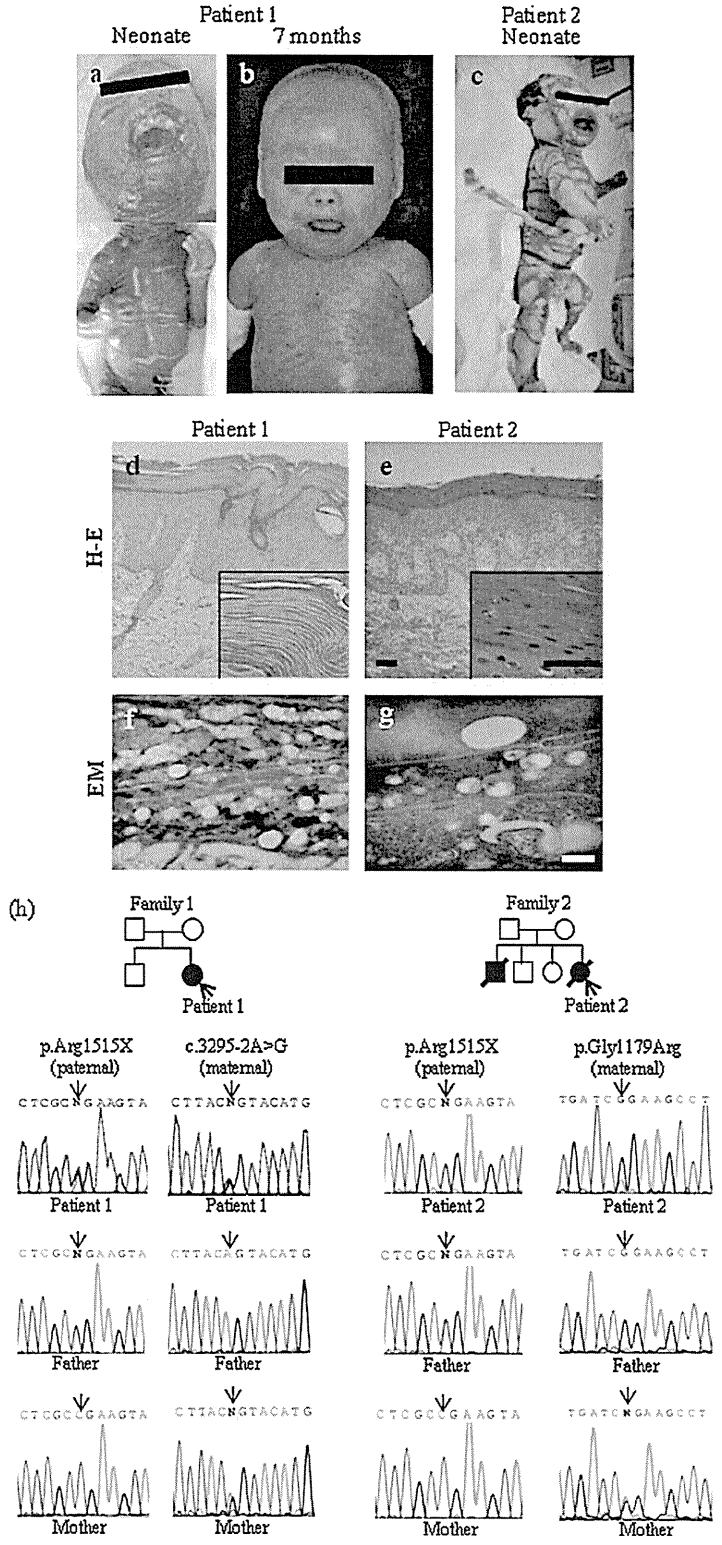
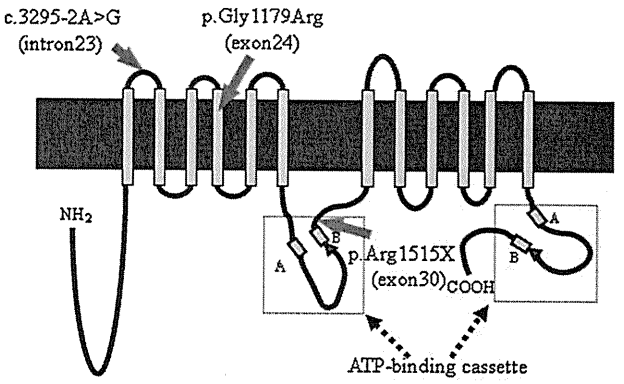


Fig. 1. (a–c) Clinical features of HI patients. Patient 1 showed the typical clinical phenotype of HI during the neonatal period, including the face and trunk (a). Her clinical symptoms remarkably improved at 7 months of age (b). Patient 2 showed more serious symptoms with thick plate-like scales and skin fissures in the neonatal period (c) and lived until the age of 5 months. (d–g) Histological features of the skin lesions of HI patients. Skin biopsies showed thick stratum corneum in both patients. Bars, 50 μm (d and e). In Patient 2, parakeratosis were observed (e, inset). By electron microscopy, abnormal variously sized lipid droplets had accumulated in the cornified cells of both patients' epidermis. Bars, 200 nm (f and g). (h) Families with HI and *ABCA12* mutations. Patient 1 was a compound heterozygote for two *ABCA12* mutations, a novel nonsense mutation p.Arg1515X and a recurrent splice site mutation c.3295-2A>G, and both her parents were heterozygous carriers. Patient 2 harboured two *ABCA12* mutations, p.Arg1515X and p.Gly1179Arg, and both her parents were heterozygous carriers of these defects.



c.3295-2A>G: 1099_1101delYMK

Homo sapiens	1089	VYEKDLRLHEYMKMMGVNSCSHF 1111
Rattus norvegius		VYEKDLRLHEYMKMMGVNSCSHF
Mus musculus		VYEKDLRLHEYMKMMGVNSCSHF
Gallus gallus		VQEKDLRLYEYMKMMGVNASSHF
Danio rerio		VHERELRLHEYMKMMGVNPISHF

p.Gly1179Arg

Homo sapiens	1165	ISVFFNNTNIAALIGSLIYIIAFFPFIVL 1193
Rattus norvegius		ISVFFNNTNIAALIGSLIYVIAFFPFIVL
Mus musculus		ISVFFNNTNIAALIGSLIYVIAFFPFIVL
Gallus gallus		ISVFFNNTNIAALVGSLVYILTFFPFIVL
Danio rerio		VSSFFDKTNIAGLSGSLIYVISFFPFIVL

Fig. 2. (a) Structure of ABCA12 protein and the three mutations in present HI families. Dark blue area, cell membrane; bottom of dark-blue area, cytoplasmic surface. Note the mutation shared between the two patients is a truncation mutation in the first ATP-binding cassette (p.Arg1515X). The other mutation in Patient 2 is just a missense mutation in the first cluster of transmembrane domains (p.Gly1179Arg). (b) ABCA12 amino acid sequence alignment shows the level of conservation in diverse species of the amino acids, 1099_1101delYMK and p.Gly1179Arg (red characters).

Laotian family [6]. The glycine 1179 is a highly conserved amino acid residue (Fig. 2b) located in the first transmembrane ABCA12 domain (Fig. 2a), and this mutation substitutes an uncharged polar glycine residue for a positively charged arginine residue. The presence of these mutations was excluded in 100 alleles of 50 normal unrelated Japanese individuals.

Determinants of genotype/phenotype correlations resulting from *ABCA12* mutations, typically demonstrate that homozygotes or compound heterozygotes with truncation *ABCA12* mutations lead to an HI phenotype. Only a few exceptional cases have been reported such as the present case. The mutation p.Gly1179Arg might result in major loss of ABCA12 function and/or structure, leading to the severe phenotype in Patient 2.

Recently, long-term survival of patients with HI has been more frequently observed and documented [7,8]. The clinical symptoms of Patient 1 showed a remarkable improvement during infancy. In contrast, the symptoms of Patient 2 did not improve, and she died at the age of 5 months. The marked difference in the clinical severity of the two patients indicated that the p.Gly1179Arg has far bigger deleterious functional effects than c.3295-2A>G. The present study clearly demonstrates that some missense *ABCA12* mutations within highly conserved transmembrane regions are able to cause drastic changes in protein structure and function, leading to severe phenotypes, similar to truncation mutation patients. Further accumulation of similar cases is needed to confirm genotype/phenotype correlation in *ABCA12* mutations, especially in studies involving missense mutations underlying HI.

Acknowledgments

We thank Dr. James R. McMillan for proofreading the manuscript. This work was supported in part by a grant-in-aid from the Ministry of Education, Science, Sports and Culture of Japan (Kiban B 20390304: to M.A.), a grant from Ministry of Health, Labour and Welfare of Japan (Health and Labour Sciences Research Grants; Research on Intractable Disease: H22-177: to M.A.).

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.jdermsci.2010.11.010.

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Cell Stem Cell
Article

Hair Follicle Stem Cells Provide a Functional Niche for Melanocyte Stem Cells

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DOI 10.1016/j.stem.2010.11.029

SUMMARY

In most stem cell systems, the organization of the stem cell niche and the anchoring matrix required for stem cell maintenance are largely unknown. We report here that collagen XVII (COL17A1/BP180/BPAG2), a hemidesmosomal transmembrane collagen, is highly expressed in hair follicle stem cells (HFSCs) and is required for the maintenance not only of HFSCs but also of melanocyte stem cells (MSCs), which do not express *Col17a1* but directly adhere to HFSCs. Mice lacking *Col17a1* show premature hair graying and hair loss. Analysis of *Col17a1*-null mice revealed that COL17A1 is critical for the self-renewal of HFSCs through maintaining their quiescence and immaturity, potentially explaining the mechanism underlying hair loss in human *COL17A1* deficiency. Moreover, forced expression of *COL17A1* in basal keratinocytes, including HFSCs, in *Col17a1*-null mice rescues MSCs from premature differentiation and restores TGF-β signaling, demonstrating that HFSCs function as a critical regulatory component of the MSC niche.

INTRODUCTION

The stem cell microenvironment, or niche, is critical for stem cell maintenance (Li and Xie, 2005; Moore and Lemischka, 2006). Accumulating evidence has confirmed that cell-cell and cell-extracellular matrix adhesion within the niche is essential for the establishment and maintenance of niche architecture in different stem cell systems (Raymond et al., 2009). Adhesion to the underlying extracellular matrix has been suggested as an important factor in epidermal stem cell maintenance (Green, 1977; Watt, 2002), but a specific stem-cell anchoring matrix for stem cell maintenance has not yet been identified. Hair follicle stem cells (HFSCs) are found in the hair follicle bulge, a distinct area of the outer root sheath that overlies the basement membrane at the lower permanent portion in mammalian hair follicles (Blanpain and Fuchs, 2006; Cotsarelis, 2006). The HFSC population is composed of multipotent keratinocyte stem cells and is responsible for the cyclic regeneration of hair follicles as well as a transient supply of progeny to the interfollicular epidermis (IFE) and to sebaceous glands after wounding (Blanpain and Fuchs, 2006; Cotsarelis, 2006; Oshima et al., 2001). The HFSC population in the bulge area normally supplies a short-term reservoir to the secondary hair germ (subbulge area), which is located just below the bulge area but above the dermal papilla and corresponds to the lowermost portion of resting hair follicles (Figure S1A available online; Greco et al., 2009). Melanocyte stem cells (MSCs), which are originally derived from the neural crest, also reside in the follicular bulge-subbulge area (Figure S1A). MSCs supply pigment-producing melanocytes to the hair matrix during each hair cycle to maintain hair pigmentation (Nishimura et al., 2002). Therefore, the bulge-subbulge area houses at least two distinct stem cell populations with different origins. However, it is still unclear to what extent these two different stem cells interact to promote each other's maintenance.

Hemidesmosomes are multiprotein adhesion complexes that promote stable epidermal-dermal attachments. The transmembrane protein collagen XVII (COL17A1/BP180/BPAG2) is a structural component of the outer hemidesmosomal plaque, which projects beneath hemidesmosomes in epidermal basal keratinocytes into the underlying basement membrane to mediate anchorage (Masunaga et al., 1997; Nishizawa et al., 1993; Powell et al., 2005). In patients with *COL17A1* deficiency, a subtype of congenital junctional epidermolysis bullosa blistering disease, hemidesmosomes are poorly formed (McGrath et al., 1995; Nishie et al., 2007) and there is a characteristic premature hair loss (alopecia) with hair follicle atrophy (Darling et al.,

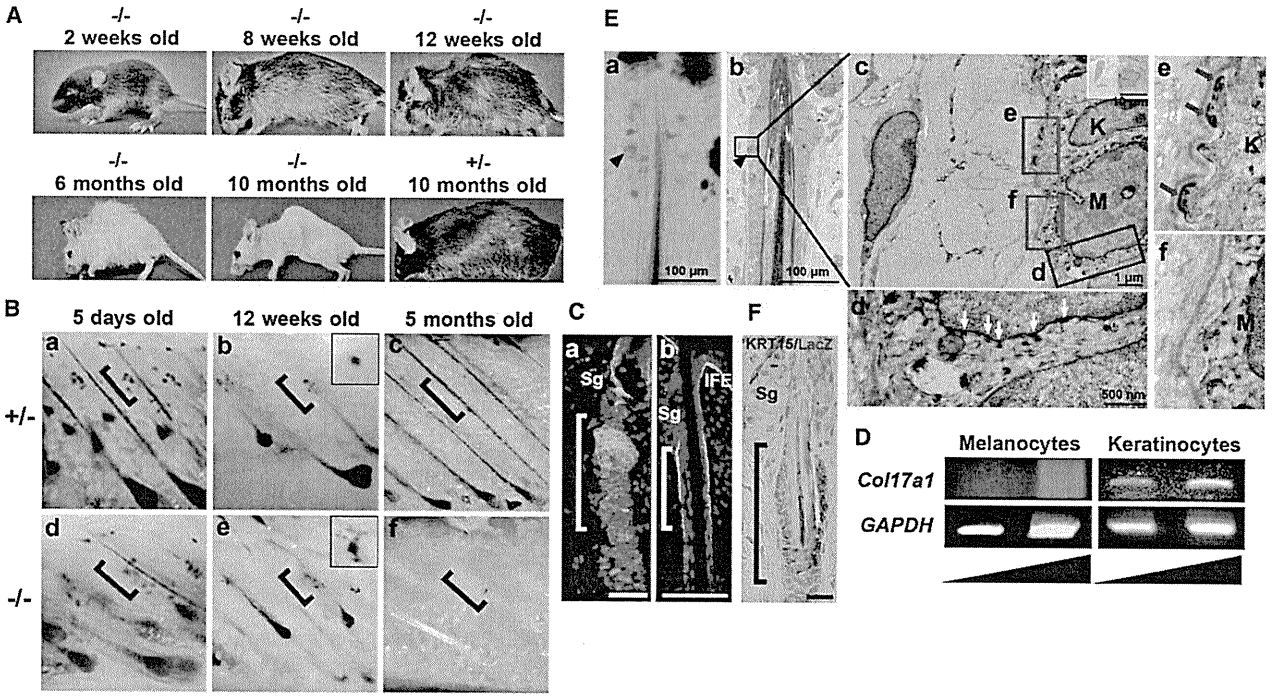

Figure 1. Hair Graying and Hair Loss Are Preceded by Depletion of MSCs in *Col17a1* Deficiency

(A) Macroscopic phenotype of *Col17a1*$^{-/-}$ mice at different times as noted and of *Col17a1*$^{+/-}$ littermates at 10 months of age.

(B) Deletion of *Col17a1* affects the maintenance of MSCs in the bulge-sububulge area. The distribution and morphology of *Dct-lacZ*-expressing melanoblasts is normal in the bulge-subbulge area of 5-day-old *Col17a1*$^{-/-}$ mice (a and d). At 12 weeks of age, abnormal melanocytes with dendritic morphology were found in the bulge area of *Col17a1*$^{-/-}$ anagen follicles (e). Inset in (e) shows magnified view of ectopically pigmented melanocytes in the hair follicle bulge-subbulge of *Col17a1*$^{-/-}$ mice. By 5 months of age, *Dct-lacZ*-expressing cells were lost both in the bulge-subbulge area and in the hair bulb (f). Bulge-subbulge areas are demarcated by brackets.

(C) COL17A1 expression in the bulge area (demarcated by brackets). (a) COL17A1 (a: red) is expressed in KRT15 (a: green)-expressing bulge keratinocytes and in basal cells of the IFE (b: green) in wild-type skin. (b) *Dct-lacZ*-expressing melanoblasts (b: red) are located close to COL17A1^{+} basal cells (b: green) in wild-type follicles. Scale bars represent 40 μm.

(D) RT-PCR analysis; the level of *Col17a1* mRNA is below the detection limit in flow cytometry-sorted GFP-tagged melanoblasts.

(E) Light and electron micrographs of *Dct-lacZ*-expressing melanoblasts in the bulge area (MSCs). The arrowheads in (a) and (b) point to *Dct-lacZ*-expressing melanocytes in the bulge areas in semithin sections of the skin. The ultrastructural high-power view is of the boxed areas shown in (b) and (c). X-gal reaction products accumulated in association with the nuclear membrane (d: white arrows). *Dct-lacZ*-expressing melanocytes lack hemidesmosome formation in the basement membrane zone (f), whereas adjacent keratinocytes form mature hemidesmosomes in the bulge area (e: red arrows).

(F) *Dct-lacZ*-expressing melanoblasts (blue) are in direct contact with keratin 15 (KRT15)-expressing keratinocytes in the bulge area (yellow brown). Scale bar represents 20 μm.

M, melanocytes in bulge; K, keratinocytes in bulge; Sg, sebaceous gland; IFE, interfollicular epidermis. See also Figure S1.

1997; Hintner and Wolff, 1982) that suggests that COL17A1 plays a role in hair follicle homeostasis. We previously reported premature hair loss in *Col17a1*-deficient mice (Nishie et al., 2007), although the precise underlying mechanism is unknown. In this study, we used *Col17a1* knockout mice and *COL17A1*-expressing transgenic mice to show that *Col17a1* plays essential roles in the maintenance of HFSCs, which provide a functional niche for MSCs.

RESULTS

Defective MSC Maintenance and Resultant Hair Graying in *Col17a1*-Null Mice

To understand the role of collagen XVII in hair follicle homeostasis, we performed a careful chronological analysis of *Col17a1*-deficient mice. As shown in Figure 1A, *Col17a1* null mice showed premature hair loss generally preceded by extensive hair graying. Conversely, heterozygous mice displayed a normal phenotype. The hair coats in *Col17a1*-null mice were indistinguishable from control littermates for 8 weeks after birth. However, progressive hair graying started from the snout at around 12 weeks of age and then became pronounced on their backs at around 4–6 months of age and was associated with a sparser hair distribution that was subsequently followed by progressive and more extensive hair loss (Figure 1A). It is notable that these hair changes were not accompanied or preceded by any apparent changes in the skin. Skin friction, such as attempting to artificially peel neonatal skin, can induce skin erosions in *Col17a1*-null mice (Nishie et al., 2007) but did not significantly accelerate hair graying or hair loss. Thus, it is unlikely that the hair changes are a secondary outcome of skin detachment but is more likely that the hair graying and hair loss are programmed through the