Corneal integrity and transparency are indispensable for good vision. Cornea homeostasis is entirely dependent upon corneal stem cells, which are required for complex wound-healing processes that restore corneal integrity following epithelial damage. Here, we found that leucine-rich repeats and immunoglobulin-like domains 1 (LRIG1) is highly expressed in the human holoclone-type corneal epithelial stem cell population and sporadically expressed in the basal cells of ocular-surface epithelium. In murine models, LRIG1 regulated corneal epithelial cell fate during wound repair. Deletion of Lrig1 resulted in impaired stem cell recruitment following injury and promoted a cell-fate switch from transparent epithelium to keratinized skin-like epidermis, which led to corneal blindness. In addition, we determined that LRIG1 is a negative regulator of the STAT3-dependent inflammatory pathway. Inhibition of STAT3 in corneas of Lrig1–/– mice rescued pathological phenotypes and prevented corneal opacity. Additionally, transgenic mice that expressed a constitutively active form of STAT3 in the corneal epithelium had abnormal features, including corneal plaques and neovascularization similar to that found in Lrig1–/– mice. Bone marrow chimera experiments indicated that LRIG1 also coordinates the function of bone marrow–derived inflammatory cells. Together, our data indicate that LRIG1 orchestrates corneal-tissue transparency and cell fate during repair, and identify LRIG1 as a key regulator of tissue homeostasis.

Introduction
In mammals, most external information is accumulated through visual systems, and integrity of the cornea is well known to be indispensable for good vision (1). During evolution, nature has found a way to develop a well-ordered visual system to maintain corneal tissue transparency and homeostasis. The cornea is a unique avascular and transparent epithelial tissue that harbors stem cells that control homeostasis and tissue regeneration after injury (2, 3). However, the homeostatic turnover of corneal epithelial tissue can become disrupted depending on the severity of damage to the corneal epithelium, resulting in collagen chronic inflammation and impaired tissue repair (4, 5). These inflammation-associated processes reportedly interfere with corneal transparency and the cornea’s barrier function (6).

It is well known that stem cells work to maintain the self-renewal and repair of tissues and organs (7, 8). Under normal conditions, the corneal epithelial tissue accommodates the homeostatic turnover of corneal stem cells, which is essential for postinjury tissue regeneration. Previous studies have reported that corneal epithelial stem cells reside in the basal layer of the limbal zone of the peripheral cornea (9, 10). The corneal epithelial stem cell system is one of the most clearly defined systems and is therefore an ideal model for investigating the role of regulatory molecules associated with stem cell tissue repair (2, 3). However, the molecular interplay between corneal epithelial stem cells and other players with critical roles in the regulation of tissue repair has yet to be elucidated.

Barrandon et al. previously reported the existence of 3 types of epidermal keratinocytes with different self-renewal capacities (11). Similar behavior has subsequently been reported for corneal keratinocytes (12). Holoclones (stem cells) have the highest reproductive capacity, while in paraclones (transient amplifying cells), terminal differentiation is observed within a few generations. However, the molecular mechanism and gene expression profile of holoclone-type stem cells are entirely unknown.

Leucine-rich repeats and immunoglobulin-like domains 1 (LRIG1) is a transmembrane glycoprotein recently reported as a potential master regulator of epidermal and intestinal epithelial stem cells (13–17). However, there are no reports to date that address the tissue-specific function of LRIG1 in the cornea. The findings of this present study demonstrate that LRIG1 was highly expressed in the holoclone-type corneal epithelial stem cells and that it was essential for the cell-fate maintenance of corneal epithelium during tissue repair. Loss of Lrig1 impaired wound-induced corneal stem/progenitor cell replacement and resulted in a cell-fate change from corneal to keratinized epithelium. Intriguingly, we found that LRIG1 controlled the corneal cell fate during repair by negatively regulating the Stat3-dependent inflammatory pathway. Moreover, corneal cell fate during repair was not only maintained by corneal epithelial stem/progenitor cells, but

Conflict of interest: The authors have declared that no conflict of interest exists.
Citation for this article: /Clin Invest. 2014;124(1):385–397. doi:10.1172/JCI71488.
also by BM-derived inflammatory cells, whose functions are well-regulated by the LRIG1/STAT3 inflammatory pathway. Thus, the findings of this present study provide new insights into the underlying homeostatic regulation of corneal keratinocyte stem/progenitor cells by LRIG1.

Results

Gene expression profile of holoclone-type corneal keratinocyte stem cells. In order to gain insight into the mechanisms responsible for the homeostasis within epithelial stem cells, we performed gene expression profiling of holoclone-type and paraclonal-type human corneal keratinocytes. This led to the identification of 15 genes that were upregulated at least 5-fold in holoclone-type corneal keratinocytes. This led to the identification of 15 genes that were upregulated at least 5-fold in holoclone-type corneal keratinocytes for the homeostasis within epithelial stem cells, we performed gene expression profiling of holoclone-type corneal keratinocytes. For the homeostasis within epithelial stem cells, we performed gene expression profiling of holoclone-type corneal keratinocytes. For the homeostasis within epithelial stem cells, we performed gene expression profiling of holoclone-type corneal keratinocytes.

Inflammation is a known clinical feature of keratinization-associated blindness, and tissue-intrinsic inflammatory responses recruit hematopoietic cells, as they drive epithelial hyperproliferation via a reciprocal signaling loop (19, 20). Characterization of the inflammatory infiltrates in remodeling tissues of LRIG1-KO corneal stroma (12 months) showed pronounced recruitment of CD31-, F4/80-, GR1-, and CD3-positive cells (Figure 3B), while these were completely absent in the normal WT corneal stroma (12 months). This implies that the loss of LRIG1 results in the intensive infiltration of BM-derived inflammatory cells.

Loss of LRIG1 impairs wound-induced corneal stem cell turnover. Corneal homeostasis is maintained by stem cells, which are responsible for physiological cell turnover and the wound-healing response (2, 3). We hypothesize that the cell-fate switch observed in the LRIG1-deficient corneal epithelium is a consequence of an abnormal tissue repair process following injury. To investigate this theory, we performed mechanical corneal-epithelial debridement (2 mm) under a microscope. After wounding the cornea once per week for 3 weeks, all of the KO corneas (3 months) developed intensive inflammation and subsequent corneal opacity, in contrast with the WT corneas (3 months) with normal phenotypes (Figure 4A). The examination revealed extensive thickening and pathologic keratinization of the corneal epithelium, with inflammation of the underlying corneal stroma (Figure 4A).

To determine the biological characteristics of the corneal epithelial cells, we performed immunohistochemistry for cornea-specific keratin 12 and epidermis-specific loricrin (Figure 3A). While the epithelia of the WT corneas (3, 8, and 12 months) specifically expressed keratin 12, that of the LRIG1-KO corneas (3, 8, and 12 months) had gradually lost keratin 12 (Supplemental Figure 2) and gained loricrin expression. These changes were also associated with increased proliferation, as determined by BrdU labeling. This suggests that loss of LRIG1 results in a cell-fate change from corneal to keratinized epithelium, which leads to the thickening of the epithelium.

KO mouse corneas elicited abnormal phenotypes, as observed both macroscopically and histologically (Figure 2A). However, corneal epithelial stratification, the number of conjunctival goblet cells, and BrdU-labeled cell ratios (in vitro) tended to be slightly higher in the KO specimens, thus suggesting that LRIG1 plays a role even in steady-state homeostasis (Supplemental Figure 1). After a latency period of 6 months, LRIG1-KO corneas gradually formed corneal plaques with massive neovascularization and intense infiltration of inflammatory cells. Finally, approximately 70% of the LRIG1-KO mice developed abnormal corneal phenotypes within 24 months (Figure 2B). Histological examination revealed extensive thickening and pathologic keratinization of the corneal epithelium, with inflammation of the underlying corneal stroma (Figure 2A).

To determine the biological characteristics of the corneal epithelial cells, we performed immunohistochemistry for cornea-specific keratin 12 and epidermis-specific loricrin (Figure 3A). While the epithelia of the WT corneas (3, 8, and 12 months) specifically expressed keratin 12, that of the LRIG1-KO corneas (3, 8, and 12 months) had gradually lost keratin 12 (Supplemental Figure 2) and gained loricrin expression. These changes were also associated with increased proliferation, as determined by BrdU labeling. This suggests that loss of LRIG1 results in a cell-fate change from corneal to keratinized epithelium, which leads to the thickening of the epithelium.
delayed and incomplete wound healing in the absence of \textit{Lrig1} (Figure 4B). This finding suggests that the loss of \textit{Lrig1} impairs the recruitment of stem/progenitor cells after wounding.

\textit{Loss of Lrig1 causes the proinflammatory state in the cornea.} Once a tissue senses invading insults, various types of innate resistance are initiated to limit the tissue damage. Inflammation is generally associated with altered cytokine and chemokine expression, and proinflammatory mediators are increased and then decayed by positive and negative feedback mechanisms (20). Surprisingly, \textit{Lrig1}-KO corneas (2–3 months) prior to wounding tended to display elevated levels of inflammatory cytokines, even in the absence of gross morphological changes (Figure 5). After injury, the levels of cytokines regulating innate lymphoid cells (ILC) and T lymphocyte subsets, such as TH1, TH2, and TH17, tended to be higher in the KO corneas as compared with the WT corneas (Figure 5). These findings suggest that the loss of \textit{Lrig1} confers a proinflammatory state in the cornea, thus accelerating the wound-induced inflammatory responses.

\textit{Lrig1 operates as a negative regulator of the Stat3-dependent inflammatory pathway.} Chronic inflammation reportedly stimulates ErbB, Wnt, and Notch signaling proteins (14–17, 19–21). Analysis of \textit{Lrig1}-KO and WT corneas (3 and 12 months) showed no apparent difference in these signaling pathways (Supplemental Figure 3). A subset of cytokines are reportedly involved in the progression and resolution of tissue inflammation signals via the JAK/STAT pathway (22–27). Examination of \textit{Lrig1} WT and \textit{Lrig1}-KO corneas (3 months) showed elevated expression levels of Stat3 in the KO tissues (Figure 6A). Moreover, Stat3 luciferase reporter assays, using both mouse conjunctival fibroblasts and keratinocytes, showed elevated responsiveness to IL-6 upon loss of \textit{Lrig1} (Figure 6B). This implies that \textit{Lrig1} affects, directly or indirectly, transcriptional activation downstream of Stat3. Next, we analyzed the expression of Stat3 and phosphorylated Stat3 (pStat3, activated) in \textit{Lrig1} WT and \textit{Lrig1}-KO corneas (3 months). Under normal conditions, Stat3 was detected in both WT and KO corneal epithelium, yet we did not detect pStat3 (Figure 6C). Three weeks after single wound
stimulation, nuclear pStat3 was readily detected only in the Lrig1-KO’s corneal epithelium and stroma, suggesting that Lrig1 negatively regulated the Stat3 activation (Figure 6C). SOCS proteins are critical negative feedback regulators of the cytokine/JAK/STAT pathway and represent early processors of STAT signaling (28–30). The expression of gp130 was unchanged in the WT and KO corneas (3 months), but RNA expression of SOCS3 tended to be elevated in the Lrig1-KO tissues, both during steady-state homeostasis and upon wounding, in line with the increased STAT signaling (Figure 6D). In striking contrast, the expression of JAK1/2 tended to be downregulated in Lrig1-KO corneas with wound stimulation (Figure 6D). This strongly implies that Lrig1 operates as a negative regulator of the Stat3-dependent inflammatory pathway.

Activation of Stat3 represents the pathological phenotypes evident in Lrig1-KO corneas. In order to reveal whether epithelial activation of Stat3 sufficiently mimics the loss-in-function observed in the Lrig1-KO cornea, we examined the tissues from a Tg mouse model (6 months); these tissues express constitutively active Stat3 (K5 Stat3 Tg) in the basal layer of the epithelium (26). It is noteworthy that the Tg mice developed corneal plaques with neovascularization that, phenotypically, closely resembled that in the Lrig1-KO cornea (Figure 7A). Histological examination revealed pathological keratinization of the corneal epithelium, with extensive remodeling of the underlying stroma showing F4/80<sup>+</sup> and CD3<sup>+</sup> inflammatory infiltrates (Figure 7, B and C). This finding is also associated with cell-fate switching from keratin 12 to loricrin expression (Figure 7C), and demonstrates that activation of Stat3 recapitulates the pathological phenotypes evident in Lrig1-KO corneas.

This prompted us to investigate whether Stat3 blocking would inhibit the pathological phenotypes found in Lrig1-KO corneas. After corneal wounding, a Stat3 inhibitor, STA21 (31, 32), was topically applied on the corneal surface 4 times a day. Seven days after wounding (7 d), WT and Lrig1-KO corneas (3 months) that received STA21 exhibited transparent corneas without inflammation, whereas Lrig1-KO corneas without STA21 exhibited corneal opacity (Figure 7D). Seven days after a second wound (14 d), WT corneas without STA21 still maintained transparency; however, Lrig1-KO corneas without STA21 exhibited corneal plaques with intensive inflammation and sometimes hypopyon (Figure 7, E and F). Together, these findings demonstrate that blocking Stat3 rescued the incidence of pathological phenotypes observed in the Lrig1-KO corneas.

Lrig1 coordinates BM-derived inflammatory cells. The intensive infiltration of inflammatory cells into the Lrig1-KO cornea suggests the possibility that Lrig1 may play a critical role in stem cell-related
tissue repair in the corneal epithelium. To demonstrate the contribution of BM-derived cells in the role of LRIG1, we performed the corneal wound experiment twice (days 0 and 7) in BM chimeric mice. Validation of BM reconstitution revealed a successful hematopoietic reconstitution of primary and secondary lymphoid organs, with myeloid and lymphoid cells in all BM chimeras (Supplemental Figure 4). Before wounding (10 weeks after BM transplantation [BMT]), no mice (WT or KO) showed the abnormal corneal phenotypes. Seven days after wounding, WT (donor)→WT (recipient) mice, and KO→WT mice showed transparent corneas and no abnormal corneal phenotypes, suggesting that only KO-derived BM cells were not enough to induce the corneal phenotype (Figure 8, A–C). As expected, KO→KO mice exhibited corneal plaque with inflammatory features 21 days after wounding. However, in WT→KO mice, inflammatory features and the formation of corneal plaques were reduced, as observed both macroscopically and histologically, suggesting that WT-derived BM cells could rescue the corneal pathological phenotypes in Lrig1-KO corneas and that both corneal and BM cell abnormalities are needed to trigger LRIG1 pathogenesis (Figure 8, C and D). These results imply that Lrig1 may coordinate, albeit in part, BM-derived inflammatory cells, which are essential for corneal maintenance during wound healing.

Discussion
The results of this study demonstrate that loss of Lrig1 during corneal repair resulted in the cell-fate switch from transparent...
The corneal epithelium to keratinized skin-like epidermis, leading to corneal blindness. This pathological skin-like epithelium differed from the physiological mouse epidermis, as it showed epithelial hyperproliferation and invaginations into the underlying corneal stroma. A previous report indicated that LRIG1 expression defines a distinct multipotent stem cell population in mammalian epidermis and normally contributes to the interfollicular epidermis and sebaceous glands (15). Our findings show that Lrig1-KO corneas with wounding formed corneal plaques with massive neovascularization and intense infiltration of inflammatory cells. However, the findings of a previous report from a member of our group illustrated that Lrig1-KO mice, with or without minor wound stimulation on the trunk skin, did not develop any epidermal hyperplasia (psoriasiform skin changes), suggesting that more continuous wounding might be needed to induce the phenotypes in the areas covered with thick hair (13).

In a normal situation, tear film is essential for maintaining the stability of ocular surface epithelium; therefore, eyelids, including meibomian glands, have a critical role in corneal homeostasis. The other findings of a previous report from a member of our group demonstrated that Notch1 deficiency results in loss of meibomian glands, causing the loss of tear film, and microlesions of the corneal epithelium (19). We thus examined the morphology of eyelids in Lrig1-KO mice and found that there were no abnormal phenotypes in them (data not shown). Further investigation regarding Notch1 and LRIG1 interaction is needed to clarify this point.

In our observation series, Lrig1-KO corneas gradually formed corneal plaques and, finally, approximately 70% of the Lrig1-KO mice developed abnormal corneal phenotypes within 24 months. Although we breed the mice under specific pathogen–free conditions and we only observed the corneal phenotype in Lrig1-KO mice, not in the WT mice, caged mice often receive repeated small wounds to the epithelial surface and it seems highly likely that these events might precipitate the phenotype in older mice.

One of the most striking findings is that the loss of Lrig1 confers a proinflammatory state in the cornea, and after wound stimulation, Lrig1-KO corneas exhibited extensive cellular infiltration and inflammation. The cornea is a unique transparent epithelial tissue in the body, and nature has found a way to provide the cornea with an antiinflammatory system that greatly reduces the threat of inflammation-induced visual loss (6). Tissue-intrinsic inflammatory responses recruit hematopoietic cells that amplify the response through their innate receptors, triggered by endogenous ligands present in the inflamed tissue. Thus, the remodeling of corneal stroma was characterized by the existence of blood vessels (neovascularization), infiltration of inflammatory cells, morphological changes of collagen fibrils, and abnormal corneal keratocytes (Supplemental Figure 5). Immunohistochemistry revealed that hematopoietic cell markers were distinctly expressed in the remodeling stroma of the Lrig1-KO corneas, whereas no or limited expression was observed in the Lrig1 WT corneas. In view of these findings, it is clear that

<table>
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<tr>
<th>Cytokine</th>
<th>Prewound</th>
<th>Early wound</th>
<th>Chronic wound</th>
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<tr>
<td>TNF-α</td>
<td>3.01</td>
<td>2.98</td>
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<td>MCP-1</td>
<td>15</td>
<td>13.95</td>
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<td>IL-10</td>
<td>1.50</td>
<td>4.10</td>
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Figure 5
Loss of Lrig1 causes the proinflammatory state in the cornea. Cytokine profiles (TNF-α, MCP1, IFN-γ, TSLP, and IL-5/10/13/17/25/33) of Lrig1 WT and Lrig1-KO corneas (2–3 months) in the prewound, early wound, and chronic wound stage by real-time PCR (n = 4 corneas mixed). Numbers show relative mRNA expression.
LRIG1 modulates the ocular antiinflammatory system and may have some role in maintaining corneal transparency.

It has been reported that cell-fate decision depends on the surrounding microenvironment (niche) and that stem cells and niche cells exchange specific signals with one another (7, 8). Interestingly, development of corneal plaques in Lrig1-KO mice was always accompanied by the remodeling of the corneal stroma. The kinetic study revealed that cell-fate changes in the Lrig1-KO cornea were preceded by changes within the underlying corneal stroma. The loss of Lrig1 in the corneal epithelium resulted first in the upregulation of various kinds of cytokines regulating ILC and T cell subsets. Subsequently, they recruited inflammation-inducible hematopoietic cells to the cornea, finally leading to the remodeling of the corneal stroma. Only after formation of this microenvironment did the Lrig1-KO corneal cells undergo the phenotype switch. These findings suggest that the microenvironment must provide tissue-specific signals that allow corneal epithelial cells to change their phenotypes. The mechanism of the cell-fate switch...
of the Lrig1-KO cornea after wounding seems to be the result of tissue-intrinsic inflammatory responses.

In chronically inflamed murine tissues, several factors, including NF-κB, TGF-β1, bone morphogenetic proteins, and Wnt, Notch, and ErbB signaling proteins, are upregulated in the context of inflammation, thus leading to mesenchymal differentiation and a strong inductive signal for stem-cell proliferation (14–17, 19–21). In Lrig1-KO corneas, we were unable to confirm any distinction in the expression of these factors from those in the WT corneas. Various cytokines are involved in the progression and resolution of tissue inflammation, and most cytokines utilize the so-called JAK/STAT pathway (22–27). Therefore, we next focused on the JAK/STAT pathway as a potential target for further investigations.

STATs are a family of latent cytoplasmic proteins involved in transmitting extracellular signals to the nucleus (22–24). Most surprisingly, continuous activation of Stat3 resulted in the reproduction of pathological phenotypes evident in Lrig1-KO corneas. Stat3 reportedly plays a critical role in various biological activities,
including cell proliferation, survival, and migration. Sano et al. previously reported that Stat3 is activated in keratinocytes of human psoriatic lesions, and Tg mice expressing a constitutively active form of Stat3 in keratinocytes developed skin lesions, either spontaneously or in response to wounding, that closely resemble human psoriasis (26). Itami et al. also reported that loss of Lrig1 resulted in psoriasiform epidermal hyperplasia and that Lrig1 expression was apparently downregulated in human psoriatic lesions (13). Using a mouse model, we clearly demonstrate that activation of Stat3 reproduced the pathological phenotypes observed in Lrig1-KO corneas and abrogation of Stat3 function inhibited the corneal phenotype switch, thus suggesting that Lrig1 and Stat3 molecules are closely linked with one another, both clinically and biologically. In addition, we have performed immunohistochemistry for pStat3 in pathologically keratinized corneal tissues in patients with severe ocular surface disease and have found that pStat3 was sporadically expressed in them (data not shown). Thus, we presume that Stat3 inhibitor–based therapy might be effective for treating patients with most severe ocular surface diseases.

We demonstrated the interaction between LRIG1 and the Stat3 molecule, but its precise mechanism has yet to be determined. It has been reported that LRIG1 is a negative regulator of EGF and Met receptors and that LRIG1-mediated receptor ubiquitination and degradation may contribute to the suppression of these receptor functions (33–35). In view of these previous findings, it could also be possible that LRIG1 regulates the expression of these receptors, thereby limiting their activities. From our experiments, we only demonstrated that LRIG1, directly or indirectly, regulates Stat3 activation. Future extensive study is needed to clarify this point.

Tissue-intrinsic inflammatory responses recruit hematopoietic cells, and characterization of the inflammatory infiltrates in remodeling Lrig1-KO tissues obviously showed pronounced recruit-
Previous biological findings showed that LRIG1 controls the fundamental signal network within the epithelial area (13–17), and there are no reports to date that demonstrate the crosstalk between the epithelium and the surrounding microenvironment. The cellular microenvironment is crucial for the maintenance of stem cells as well as for cell-fate decision during tissue repair. BM-derived cells reportedly stabilize their surrounding tissue micro-environments by adapting different phenotypes as feed-forward mechanisms to maintain tissue homeostasis (36–42). Based on the results of our corneal wound experiment using BM chimera mice, we hypothesize that LRIG1 might regulate BM-derived cell behavior. However, its precise mechanism is a complex organismal process and remains to be determined.

Importantly, and based on the findings in the present study, ocular inflammation is incompatible with good vision, and corneal cell fate during repair is not only maintained by corneal epithelial stem cells, but also by BM-derived inflammatory cells, whose functions are well controlled by the Lrig1/Stat3 inflammatory pathway (Figure 9). In view of these and previous findings on the function of LRIG1 in epidermal and intestinal stem cells (13–17), we theorize that LRIG1 provides a general mechanism to control systemic tissue homeostasis and serves as a target for therapeutic exploitation.
**Methods**

*Mice. Lrig1-KO mice were regenerated from cryopreserved sperm (C57BL/6 background) (13). Genotyping was performed using 3 different primers (Supplemental Table 2; WT: 322 bp, KO: 400 bp). The K5 Stat3 Tg mice were as described previously (26). Mice were born with the expected ratio of Mendelian inheritance, and no changes in sex ratios were observed.

**Tissues.** All human cornea tissues were obtained from SightLife Eye Bank, and all corneas were stored at 4°C in storage medium (Optisol-GS; Bausch & Lomb).

**Antibodies.** For immunohistochemistry, the following antibodies were used: mouse mAb anti-β-catenin (610153, x200; BD Biosciences), rat mAbs anti-BrdU (ab6326, x200; Abcam Plc), anti-CD31 (550274, x200; BD Biosciences), anti-F4/80 (RM2900, x100; Life Technologies), anti-GR1 (553128, x100; BD Biosciences), and anti-CD3 (MAB4841, x100; R&D Systems, Inc.), rabbit polyclonal antibodies (pAbs) anti-LRIG1 (x200; provided by S. Itami, Osaka University), anti-loricrin (PRB-145P, x700; COVANCE), anti–keratin 12 (KR074, x200; Transgenic), anti-Stat3 (9132, x200; Cell Signaling Technology), anti–phospho-Stat3 (9131, x200; Cell Signaling Technology), anti–phospho-EGFR (ab40815, x200; Abcam), and anti–c-Met (sc-162, x50; Santa Cruz Biotechnology, Inc.), goat pAbs anti-LRIG1 (sc-50076, x200; Santa Cruz Biotechnology), anti-EGFR (E1282, x100; Sigma-Aldrich), and anti-Notch1 (sc-6014, x50; Santa Cruz Biotechnology Inc.). Second antibody included Alexa Fluor 488 anti-mouse, rat, rabbit, and goat IgG (x1500), and Alexa Fluor 594 anti-rat IgG (x1500) (Molecular Probes). Antibodies used for cell surface staining were phycoerythrin-conjugated and Green (11). Secondary cultures of human corneal epithelial cells were classified as paraclone. When all colonies were terminal or when no colonies formed, the clone was classified as a holoclone. When < 1% of the colonies were present, the clone was classified as a paracrine.

**Gene expression analysis.** Gene expression profiles were examined by use of a high-density oligonucleotide probe array, GeneChip, of Human Genome U133 Plus 2.0 (Affymetrix). Total RNA was extracted using the RNeasy kit (QIAGEN). cRNA preparation and target hybridization were performed according to the manufacturer’s instructions. The average value of duplicates from each transcript was used for comparison, and the expression levels of the individual transcripts were normalized by the expression level of β-actin. The primers that were used are shown in Supplemental Table 3.

**BrduLabeling.** According to the manufacturer’s protocol (Zymed Laboratories Inc.), we injected the Lrig1 mice (n = 3) and cultured corneal epithelial cells on amniotic membrane with BrdU-labeling reagent (1 ml/100 g). After 2 hours, the mice were sacrificed, and the eye and cultured cells were then embedded in Tissue-Tek OCT compound (Sakura Finetek Europe B.V.).

**3D culture.** Mouse corneal epithelial cells were cultured according to our previously reported system (43–46). Corneal epithelial explants, including the corneal limbus (n = 3), were cultured for 14 days with mitomycin C-inactivated 3T3 fibroblasts (2 × 10^4 cells/cm²). The culture medium consisted of a defined keratinocyte growth medium (KGM) (Gibco; Life Technologies) supplemented with 5% FBS. The cultures were incubated at 37°C in a 5% CO₂–95% air incubator, and the medium was changed daily.

**In vivo wound model.** Experimental mice (Lrig1 WT and Lrig1-KO, 8 weeks old, n = 4 each) were anesthetized by intraperitoneal injection of combined xylazine and ketamine. After an administration of topical oxybuprocaine eye drops (Santen Pharmaceutical Co.), central corneal epithelial debridement was performed, using a commercially available hand-held diamond-tipped glass engraver (IH-640; Ito Co.), under a stereomicroscope. Briefly, we used a 2-mm trephine to demarcate the margins of the wound (both single and repeated wounds) to avoid damaging the peripheral cornea and limbal areas. To perform the repeated wound, we first used fluorescein green staining to identify areas of intact epithelial tissue. If there was intact epithelium within the 2-mm demarked area, it was removed with the hand-held diamond-tipped glass engraver. At this point, we avoided damaging the corneal stroma as much as possible. The experimental mice were killed by an overdose of sodium pentobarbital, and the eyes were then enucleated and embedded in OCT compound. To observe the area of remaining epithelial defect at the different time points, fluorescein green staining was used.

The Journal of Clinical Investigation

http://www.jci.org Volume 124 Number 1 January 2014

395
Luciferase promoter assay. Transferase of luciferase reporters into cul-
tured Lrig1 WT and Lrig1-KO mice conjunctival fibroblasts and keratino-
cyes followed our previous protocol (47). Both fibroblasts and keratino-
cyes were plated in 24-well culture plates and cultured in DMEM with 10% FBS (fibroblast) or defined KGM (keratinocyte) for 18 to 24 hours 
before transfection. A Stat3 Reporter Assay Kit (QIAGEN) was used to 
measure the transcription factor activity. Cells (3 x 10⁶) were cotransfected 
by Lipofectamine (fibroblast; Life Technologies) or FuGENE HD (kera-
tinocyte; Promega) for 24 hours, followed by cytokine treatment (IL-6; 
BioLegend Inc.) for 6 hours. The resultant cells were lysed with 100 µl 
Passive Lysis Buffer (Promega). Luciferase activity was read on a Veritas 
Microplate Luminometer (Promega).

Generation of BM chimera mice. BM chimeras were generated with 
5 x 10⁶ freshly isolated total BM cells from the femur and tibia of Lrig1 
WT or Lrig1-KO mice (donor, 10–12 weeks), respectively, following our 
previous protocol (48, 49). Isolated cells were intravenously injected 
either into lethally irradiated (900 cGy) Lrig1 WT or Lrig1-KO mice (host, 16–18 
weeks). A mechanical corneal wound was applied to the hosts 10 weeks 
before BM reconstitution. The efficiency of corneal wound healing and 
hematopoietic reconstitution of lymphoid organs of hosts by donor-
derived cells was assessed 13 weeks after BM transfer by genotyping tail, 
thymus, and BM DNA. Furthermore, lymphoid organs of reconstituted 
mice were analyzed by FACS as described below and were compared in 
statistical analysis to those of age-matched Lrig1 WT or Lrig1-KO mice.

Flow cytometric analysis. Single-cell suspensions of freshly isolated thyl-
mus, spleen, and total BM cells of the femur and tibia were subsequently 
icubated with αCD16/CD32 for 10 minutes, followed by staining with 
a combination of conjugated antibodies in FACS buffer (PBS + 4% heat-
activated FCS + 2 mM EDTA) for 30 minutes. Stained cells were analyzed 
on a FACS Canto II flow cytometer (BD Biosciences).

Statistics. The 2-tailed, unpaired Student’s t test was used to compare the 
differences between 2 groups, and P values of 0.05 or less than 0.01 were 
considered significant. The values are presented as mean ± SD. 
FACS data were analyzed with FlowJo software (TreeStar Inc.) and Graph-
Pad Prism software (GraphPad Software Inc.). Statistical significance 
was determined using a 2-tailed Mann-Whitney U test for paired samples 
or 1-way ANOVA and nonparametric tests for multiple groups. P < 0.05 was 
considered statistically significant.

Study approval. All animals used for this study were maintained and 
handled according to the protocols approved by the Kyoto Prefectural 
University of Medicine. All animal studies were approved by the Commit-
tee on Animal Research of Kyoto Prefectural University of Medicine. All 
experiments were performed in accordance with the tenets set forth in 
the Declaration of Helsinki.

Acknowledgments

We especially thank Kim B. Jensen for critical comments on the manuscript. We also thank Y. Hata, H. Saito, T. Horikiri, S. Mano, and K. Yamazaki for assisting with the experimental 
procedures, and J. Bush and A.W. Amici for reviewing the manuscript. 
This study was supported in part by Grants-in-Aid for scientific 
research from the Japanese Ministry of Education, Culture, Sports, 
Science and Technology (no. 23592621), the JST-ETH Strategic 
Japanese-Swiss Cooperative Program (HeiSei 20), the EPFL, the 
CHUV, OptiStem, and BBSRC (UK).

Received for publication June 11, 2013, and accepted in revised form 
on October 3, 2013.

Address correspondence to: Takahiro Nakamura, Department of 
Ophthalmology, Kyoto Prefectural University of Medicine, 
Kawaramachi Hirokoji, Kamigyo-ku, Kyoto 602-0841, Japan. 
Phone: 81.75.251.5578; Fax: 81.75.251.5663; E-mail: nakamur@
koto.kpu-m.ac.jp.


