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Limbal Stem Cells: Identity, Developmental Origin and Therapeutic Potential

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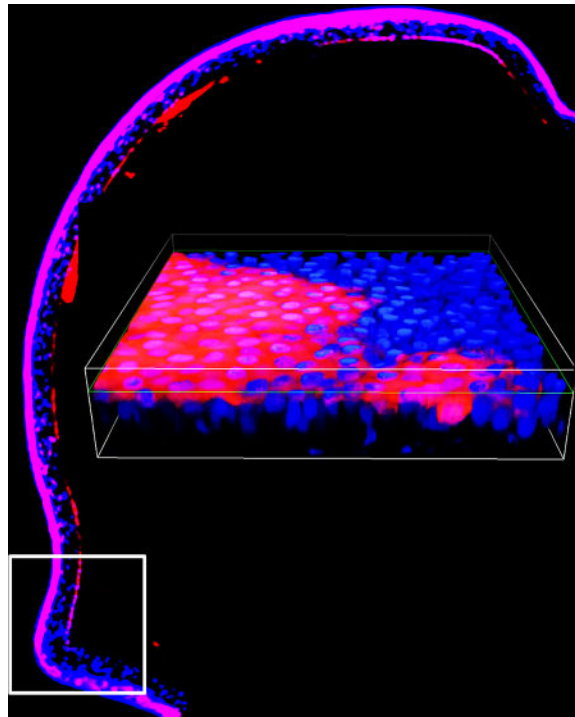
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Abstract

The cornea is our window to the world and our vision is critically dependent on corneal clarity and integrity. Its epithelium represents one of the most rapidly regenerating mammalian tissues, undergoing full turnover over the course of approximately one to two weeks. This robust and efficient regenerative capacity is dependent on the function of stem cells residing in the limbus, a structure marking the border between the cornea and the conjunctiva. Limbal stem cells (LSC) represent a quiescent cell population with proliferative capacity residing in the basal epithelial layer of the limbus within a cellular niche. In addition to LSC, this niche consists of various cell populations such as limbal stromal fibroblasts, melanocytes and immune cells as well as a basement membrane, all of which are essential for LSC maintenance and LSC-driven regeneration. The LSC niche's components are of diverse developmental origin, a fact that had, until recently, prevented precise identification of molecularly defined LSC. The recent success in prospective LSC isolation based on ABCB5 expression and the capacity of this LSC population for long-term corneal restoration following transplantation in preclinical *in vivo* models of LSC deficiency (LSCD) underline the considerable potential of pure LSC formulations for clinical therapy. Additional studies, including genetic lineage tracing of the developmental origin of LSC will further improve our understanding of this critical cell population and its niche, with important implications for regenerative medicine.

Graphical abstract

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Visual Abstract. Contribution of LSC to corneal epithelial development and homeostasis.

Immunofluorescent image of corneal epithelium from a 1 month-old Abcb5/Cre/tdTomato mouse depicting tdTomato-positive Abcb5-derived progeny cells within the entire adult mouse corneal epithelium. The white square on the left indicates the location of the limbus of which a high magnification image is shown on the right.

Limbal Stem Cell Identity

The cornea is essential for normal vision due to its multiple roles that include light refraction and transmission as well as protection of underlying eye structures from environmental injuries. The cornea consists of three layers, i.e. the epithelium, stroma and endothelium, which are separated by two membranes: Bowman's membrane, located between the epithelial and stromal layers, and Descemet's membrane, located between the stromal and endothelial layers. A hallmark feature of the corneal epithelium is its high regenerative potential and its capacity for rapid ocular surface repair through proliferation and centripetal migration of progenitor cell populations residing at the border of the cornea and the sclera in a location called limbus (1–3) (Figure 1).

Limbal stem cells (LSC) represent a quiescent cell population with high proliferative potential, which enables efficient corneal regeneration and repair (4–14). LSC do not express markers of differentiated mature corneal epithelium (2, 15). This constellation of features led to a decades-long search for a *bona fide* LSC marker that would enable prospective LSC isolation for therapeutic applications. In 1971, Davanger and Evensen (1) proposed that LSC reside in the palisades of Vogt (POV), a series of radially oriented fibrovascular ridges that are observed in the human limbus (16, 17) and can be detected by the optical coherence

tomography (18, 19). In 2005, based on histological examination of the human limbus, Dua et al. reported the presence of limbal epithelial crypts (LEC) and proposed that they also harbor LSC (20). LEC are more frequently detected in the superior or inferior limbus compared to the temporal or nasal limbus (21, 22). In non-human species, only porcine limbus has been reported to share the structure of the human limbus with regard to the location and topography of POV and LEC, while no evidence of POV has been found in the other animals (21, 23). In mice, LSC were first identified as slow-cycling label-retaining cells located in the basal layer of limbal epithelium (5). Despite the lack of the POV structures in mice, lineage-tracing studies clearly have shown that murine corneal stem cells exist in the limbus and that they are capable of producing daughter cells with centripetal migration during corneal regeneration (24–28).

It has been widely accepted that *bona fide* LSC are defined by their ability to establish and maintain long-term restoration of the corneal epithelium, i.e. properties that are only demonstrated by transplantation experiments (29). Numerous potential LSC markers have been proposed (Table 1), but for most, evidence for successful prospective enrichment of cells capable of long-term corneal restoration is currently lacking. In 2001, Pellegrini et al. proposed that the transcription factor p63 identifies human LSC (30). Following this discovery, Rama et al. evaluated the clinical effectiveness of autologous mixed limbal cell transplants grafted onto patients with unilateral LSC deficiency (LSCD) (29). They concluded that success of the transplants was dependent upon the number of p63+ cells contained within grafts, suggesting that p63 identifies LSC among mixed limbal cultures.

In these studies, limbal epithelial cultures used for transplantation generally contained up to 10% p63+ cells, with significant variability observed between individual grafts. When grafts contained less than 3% p63+ cells, the transplants failed; when grafts contained between 3–6% of p63+ cells, a partial transplant success was achieved; and when grafts contained between 5–10% of p63+ cells, the transplants were successful. These findings indicated that human LSC express p63, however, because of the nuclear expression of p63, further enrichment of the limbal grafts for p63 purity was not feasible, leaving unanswered the question whether a pure p63+ population could have resulted in more universal therapeutic success, as might be expected of an autologous LSC graft. Subsequently, several additional potential human LSC markers were described based on their anatomical and immunohistochemical association with p63, including positive selection markers Lgr5 (31), Tcf4 (32), CD157 (33), CD71^{low}/Integrin α 6^{high} (34), TrkA (35), N-Cadherin (36), Abcg2 (37, 38) and Cytokeratin15(39), and negative selection markers Cytokeratin 3 (2), ALDH^{dim} (40), RHAMM^{bright} (40) and Connexin-43 (41) (Table 1).

Recently, our laboratories demonstrated that ATP-binding cassette (ABC) superfamily member ABCB5 identifies LSC with the ability to restore and maintain the corneal epithelium upon transplantation to preclinical models of LSCD (42). Specifically, our studies showed that prospectively isolated human ABCB5-positive LSC, but not ABCB5-negative limbal epithelial cells, possessed the capacity to fully restore the corneal epithelium upon grafting to LSC-deficient mice in xenogeneic or syngeneic transplantation models (42). ABCB5 was found in those studies to be preferentially expressed on label-retaining LSC in mice, and on Np63 α -positive cells in humans. Consistent with these findings, ABCB5+

LSC frequency was significantly reduced in LSC-deficient patients. Importantly, *Abcb5* loss of function in *Abcb5* KO mice caused depletion of quiescent LSC due to enhanced proliferation and apoptosis, and resulted in defective corneal differentiation and wound healing, demonstrating that ABCB5 not only marks LSC, but is required for LSC function. These results from gene knockout studies, LSC tracing and transplantation models, as well as phenotypic and functional analyses of human biopsy specimens, provided robust evidence that ABCB5 identifies mammalian LSC. Since this original report, additional studies by independent laboratories have confirmed the presence of ABCB5+ LSC in human and mouse limbal epithelium (43–48). Moreover, our most recent studies utilizing genetic lineage tracing in *Abcb5*/Cre reporter mice crossed with tdTomato (B6;129S6-*Gt(ROSA)26Sor^{tm14(CAG-tdTomato)Hze/J}*) mice (49), aimed at further dissecting the origin of LSC and their progeny cell fate, identified tdTomato-positive ABCB5-derived progeny within the entire adult mouse corneal epithelium (Figure 2), identifying at the level of genetic lineage tracing an ABCB5-expressing precursor cell that gives rise to self-renewing corneal epithelium during development and regeneration, consistent with the LSC phenotype.

Developmental Origin of LSC and Their Niche

The LSC niche is one of the few active mammalian stem cell niches preserved in adulthood that enables continuing regeneration and repair of high turnover tissues (50). In addition to LSC themselves, this niche consists of various cell populations such as limbal stromal fibroblasts, melanocytes, immune cells including Langerhans cells, macrophages, vascular endothelial cells, and a basement membrane (36, 51–53) with diverse developmental origins. Limbal stromal fibroblasts originate from neural crest (54), express the mesenchymal stem cell (MSC) markers CD73, CD90 and CD105 (55–57) and possess the ability to differentiate into adipocytes, osteocytes, keratinocyte, vascular endothelial cells, pericytes and cornea-like epithelium *in vitro* (56, 58–60). While in culture limbal stromal fibroblasts can be induced to express ABCG2 and ABCB5 (48), however, there is no evidence that limbal stromal fibroblasts can give rise to LSC or corneal epithelium *in vivo*. Nevertheless, it has been shown that stromal stem cells possess the ability to remodel pathological stromal tissue by suppressing inflammation and restoring transparency (57, 61). The role of melanocytes located in close proximity to LSC still remains unclear. It is hypothesized that they protect LSC from oxidative DNA damage and contribute to the maintenance of LSC quiescence (36, 62, 63). Similar to limbal stromal fibroblasts, melanocytes are also derived from neural crest cells (64). The limbal basement membrane consists of specific components such as $\alpha 1$, $\alpha 2$ chains of collagen IV, collagen XVI, laminin $\alpha 1$, laminin $\gamma 3$, agrin and tenascin C (65–69). Previous studies have suggested that the limbal basement membrane may facilitate stem cell adhesion required for LSC homeostasis and harbor and provide critical LSC growth factors and cytokines released from limbal niche cells (53, 65, 67, 68). In addition to these components, lymphocytes, stromal nerves and blood vessels contribute functionally to the LSC niche (65, 70)

Due to the complexity and heterogeneity of the LSC niche and the relative elusiveness, until recently, of the cellular identity of *bona fide* LSC, the developmental origin of LSC remains currently enigmatic. To date, it has been established that at least two embryonic layers, the

surface ectoderm and the periocular mesenchyme, contribute to the formation of the corneo-limbal-scleral junction, i.e. the area where LSC reside (Figure 3). The surface ectoderm, which separates from neuroectoderm during early eye field formation, gives rise to the corneal epithelium (71). An early eye field transcription factor, PAX6, can be first detected in the surface ectoderm of the developing mouse at embryonic (E) 8 stage (72), and is subsequently expressed in the developing corneal epithelium at E12.5 (73). Recent genetic lineage tracing studies in *Pax6/Cre* (P0–3.9-GFP^{Cre}) mice crossed to *ROSA^{mT/mG}* reporter mice showed GFP expression in the entire corneal epithelium suggesting that Pax6-expressing progenitors contribute to corneal epithelial generation and regeneration during development and adulthood (73), which raised the possibility that Pax6⁺ cells within the surface ectoderm represent the cells of origin of LSC. This possibility is also supported by findings in Pax6^{+/-} mice that revealed that Pax6 haploinsufficiency results in reduced expression of the corneal epithelial differentiation marker Krt12 and increased corneal vascularization consistent with a LSCD phenotype (74).

Another ectodermal transcription factor, p63, has been detected in the adult human LSC niche and was proposed to mark LSC (30, 75). During embryonic development, p63 expression can be observed in the surface ectoderm at the mouse E6 stage, and, at the time of birth, it is found in the basal cells of the stratified skin and its appendages (76). Comparison of Pax6 and p63 expression in the developing mouse cornea showed that p63 was preceded by Pax6 by two days and, unlike Pax6, was not restricted to the developing eye (73). While loss of function of p63 in knockout mice results in failure of epithelial stratification and marked inhibition of normal limb, tail, facial, and external genital development (76, 77), p63 knockout does not result in LSCD. Human patients with Ectrodactyly-Ectodermal Dysplasia-Clefting syndrome caused by p63 mutations display skeletal malformations, and lacrimal and meibomian gland defects, which, in some cases, are also associated with corneal clouding (78). Genetic lineage tracing studies using *Np63^{+/-}/Cre* mice crossed to *ROSA26^{EYFP}* mice showed selective EYFP expression in developing glandular and stratified epithelia expressing Np63 (e.g. skin, thymus, salivary gland, esophagus and trachea) (79). In findings by the same authors, evaluating this lineage-tracing model in the adult cornea, Np63-derived EYFP-positive progeny cells were detected throughout the corneal epithelium (including the apical layer) and Np63 protein expression was observed in the basal corneal epithelial cell compartment, but was not restricted to the limbus (Pignon, JC and Signoretti, S; personal communication). Consistent with other findings (29, 42), these results show that p63 is expressed by LSC (42), but indicate that it may not represent a specific LSC marker and may not be required for normal LSC function.

As opposed to a possible surface ectodermal origin, LSC might alternatively originate from the periocular mesenchyme. During embryonic development, the periocular mesenchyme gives rise to multiple corneal structures, including the corneal stroma and endothelium, Schlemm's canal, and the trabecular meshwork. Using a transgenic system allowing distinct binary labeling of mesodermal and neural crest progenitors, Gage et al. showed that both somatic mesoderm and the neural crest contribute to the formation of periocular mesenchyme (54). The majority of cells in the corneal endothelium and stroma hereby appeared to be of neural crest origin. Within the limbal region, the endothelial lining of

Schlemm's canal and the iris stroma were derived mostly from mesoderm, whereas ciliary muscles and trabecular meshwork contained a majority of cells of neural crest origin (54). Mesoderm and neural crest derivatives also exhibited distinct eye transcription factor expression patterns, with PITX2 and FOXC1 preferentially expressed by neural crest-derived progenitors, and PITX1 and MYOG by mesoderm-derived cells. Using a temporal gene knockout approach, Gage et al. demonstrated that neural crest-expressed PITX2 is required for corneal morphogenesis and cell fate specification within the surface ectoderm and the mesenchymal primordia, and is also essential for establishing of the angiogenic privilege of the cornea (80). In addition, Seo et al. reported that neural crest deletion of FOXC1 leads to aberrant vessel growth in the normally avascular mouse cornea due to inhibition of the anti-angiogenic activity of sVEGFR-1 (81, 82). These studies highlight the potential critical role of neural crest derivatives in establishing angiogenic privilege of the central cornea and suggest the possibility that LSC might be of neural crest origin. This notion is also supported by studies of Du et al., which showed that a subpopulation of human corneal neural crest-derived stromal cells expressed mesenchymal stem cell markers and exhibited multipotent differentiation potential (59). Of note, the LSC marker ABCB5 (42) also identifies cells of mesenchymal stem cell molecular phenotype in other tissues (83) suggesting a possible neural crest origin of ABCB5+ LSC. Additional genetic lineage and transplantation studies using clonal cell populations will help to further define the developmental origin of LSC.

LSC in Corneal Homeostasis and Wound Healing – Therapeutic Potential

It has been widely accepted that LSC give rise to transient amplifying cells (TAC), and that TAC migrate centripetally and anteriorly to generate differentiated corneal epithelial cells, which will eventually be shed from the corneal surface, as proposed in the X-Y-Z hypothesis (84, 85) (Figure 4A). Although acute wound healing in the central cornea can be achieved by proliferation and migration of central corneal epithelial cells (86), LSC are essential for corneal homeostasis and normal wound healing (4, 5, 87, 88). The critical role of LSC in corneal repair is further supported by recent studies showing impaired corneal wound healing in *Abcb5* knockout mice (42) and suggested by findings of impaired corneal wound healing in diabetic mice with diminished expression of the LSC-expressed genes *ABCG2*, *Np63 α* and *Krt15* (89–92). Lineage-tracing methods have also suggested involvement of LSC in corneal homeostasis and wound healing (24–28). Specifically, Amitai-Lange et al. reported that while central corneal cells had the ability to contribute to mild corneal wound repair, larger corneal injuries required the involvement of LSC (24).

While the significance of the limbus as an anatomical niche for corneal epithelial stem cells (i.e., LSC) is relatively established, Majo et al., using a genetic tracing model, identified the existence of additional stem cells capable of corneal and conjunctival regeneration residing in the entire corneal epithelium (93). Consequently, they proposed an alternative theory of corneal regeneration describing the limbus as a zone of equilibrium in which the expanding conjunctival and corneal epithelia are confronted in a mechanism reminiscent of tectonic plates and suggesting that rupture of the corneo-conjunctival equilibrium results in migration of LSC onto the cornea (93) (Figure 4B). The LSC paradigm and this hypothesis advanced

by Majo et al. do not appear to be mutually exclusive as recently reported by Lobo et al. (28).

A number of cell signaling pathways have been shown to play a critical role in corneal wound healing (Figure 5). In the diabetic cornea, disease-associated impaired wound healing can be accelerated by overexpression of the hepatocyte growth factor (HGF) receptor c-MET, and by silencing of MMP-10 and cathepsin F (94, 95). Additionally, inhibition of miR-146a, which is pathologically induced in diabetic mice, leads to increased expression of phosphorylated p38 and epidermal growth factor receptor (EGFR) by LSC, resulting in normalization of epithelial wound healing (96). Keratinocyte growth factor (KGF) secreted by limbal fibroblasts increases the mitotic activity of LSC, that express KGF receptor (KGFR), leading to acceleration of corneal epithelial wound healing (97–99). Ciliary neurotrophic factor (CNTF) promotes migration of corneal epithelial stem/progenitor cells through activation of Akt signaling mediated by matrix metalloproteinases (100, 101). In the setting of corneal injury, LSC proliferation can also be stimulated by epidermal growth factor (EGF) and fibroblast growth factor- β (FGF- β) produced by the damaged corneal epithelium (102), whereas LSC differentiation is driven by insulin-like growth factor-I (IGF-I), which induces expression of IGF receptor on LSC (102). A number of EGF family members are expressed by the limbal epithelium, including transforming growth factor- α (TGF- α), hepatocyte binding epidermal growth factor (HB-EGF), epiregulin (EREG) and amphiregulin (AREG) (103). Epiregulin expression is restricted to limbal basal epithelial cells, and is thought to contribute to the high proliferative capacity of these cells in the setting of wound healing (104, 105).

Loss or deficiency of LSC causes destruction of corneal homeostasis and results in abnormal wound healing (3, 106), a condition known as LSCD. LSCD leads to conjunctival epithelial ingrowth, neovascularization of the corneal stroma, corneal opacification and vision loss (3, 106). The major causes of acquired LSCD are Stevens-Johnson syndrome, ocular cicatricial pemphigoid, chemical or thermal burns and contact lens over-wear (107–110). Limbal tumors, severe corneal infections and iatrogenic causes are more rare etiologies of LSCD (107, 108, 110). In recent decades, significant advances have been made in the development of LSC-based therapies for the treatment of LSCD. First, in 1997, Pellegrini et al. described the use of autologous cultured limbal epithelial cells (CLET) for the treatment of unilateral LSCD (111). In this study, cellular grafts were generated from limbal biopsies of healthy eyes contralateral to the diseased eyes of unilateral LSCD patients and the biopsies were enzymatically digested and expanded as holoclones *in vitro*, to generate corneal epithelial sheets for transplantation. This cell-based therapeutic approach, containing p63-positive LSC at varying concentrations, recently received conditional approval by the European Medicinal Agency (EMA) based on a reported success rate of 60–70% (29). In another, similar approach, enzymatically digested limbal biopsies cultured on human amniotic membrane were transplanted to patients with unilateral LSCD, with therapeutic success ranging from 50% to 83% (112–114). While these techniques have resulted in long-term restoration of the corneal epithelium, they are, for the most part, only applicable to patients with unilateral disease, but not to the much more frequent group of patients with bilateral disease. Additionally, since such grafts contain variable numbers of LSC, estimated by the expression of p63 in companion cultures (29), they do not represent pure LSC grafts. Thus,

there exists a need to further improve LSC-based therapeutic approaches to unilateral and bilateral LSCD therapy. Additionally, several regulatory and logistical barriers need to be overcome in order to further advance widespread approval, availability and acceptance of stem cell-based LSCD therapies: (i) A somatic cell therapeutic should possess a defined composition and purity of the biologically active ingredient for appropriate dosing and potentially required dosing intervals, and prevention of unwanted side effects; (ii) current protocols employ the transfer of non-LSC populations contained within grafts that may be biologically inactive, or might produce unwanted side effects through inauthentic reconstitution of the LSC niche and/or the corneal stroma; and (iii) neither holoclones nor cell/matrix compositions consisting of limbal cells grown on amniotic membrane have been shown to be cryopreservable, presenting considerable challenges in manufacturing, storage, transport, and local transplantation logistics of such therapeutic compositions that have prevented wide-spread availability and adoption of these techniques. We posit that prospective isolation and purification of LSC, for example through use of a cell surface marker such as ABCB5, might have the potential to overcome these obstacles, leading to easier fulfillment of current regulatory requirements and likely further improvements of therapeutic outcomes.

In contrast to unilateral LSCD, treatment of patients with bilateral LSCD poses even greater challenges. Clinical studies using allogeneic limbal tissue transplants provide, at best, transient restoration of the cornea. The failure of these allograft transplants is most likely due to alloantigen-specific immune-mediated rejection of the donor graft. The central cornea is a well-known and established “immune privileged” tissue that allows the survival of fully allogeneic corneal transplants in low-risk recipient patients (115). In contrast, the limbus does not represent the same immune-privileged microenvironment encountered in the central cornea. It contains, in addition to LSC with immune-suppressive roles (116), other cell types such as Langerhans cells, macrophages, and dendritic cells capable of potent induction of rejection responses when grafted to allogeneic recipients. Therefore, such immunogenic cell types contained within mixed limbal allografts that lack purity for relatively non-immunogenic LSC might be primarily responsible for immune-mediated rejection of grafts currently employed for the treatment of patients with bilateral LSCD. Thus, it is very likely that transplantation of purified LSC populations (such as, for example, isolated through the newly available marker ABCB5 (42)) that are devoid of accompanying immunogenic cell populations, might significantly reduce LSC allograft rejection, and hence improve therapeutic outcomes in bilateral LSCD treatment.

It is well established that immune tolerance and privilege, including in allotransplantation, are significantly controlled by negative costimulatory pathway mechanisms, including the molecular interaction of programmed cell death 1 receptor (PD-1) with its ligands, PD-L1 and PD-L2 (117). In experimental model systems of allograft rejection in the cornea, previous studies by Hori et al. (118) and Watson et al. (119) revealed that PD-1 is similarly required for prolonged allograft survival. Specifically, corneal allografts survived when transplanted onto wild-type recipient mice, but were rejected when transplanted onto PD-L1 knock-out recipient mice, validating the critical role of PD-1 in corneal immune privilege (120). Intriguingly, ABCB5+ stem cells derived from other tissues have already been found to express PD-1 and to exhibit immune-privilege with a capacity to engraft across fully

mismatched allogeneic barriers (83), warranting examination whether ABCB5+ LSC exhibit similar tolerogenic properties. If so, they might represent a particularly promising cell source for treatment not only of unilateral LSCD, but also as LSC allograft for the treatment of bilateral LSCD.

In addition to the above-mentioned studies, a number of promising therapeutic approaches to LSCD utilizing advanced cell reprogramming techniques have been reported in preclinical models. Corneal epithelial-like cells could be induced from embryonic stem cells (ESCs) (121) and from induced pluripotent stem cells (iPSCs) (122, 123). In this regard, Hayashi et al. created a self-formed ectodermal autonomous multi-zone (SEAM) of ocular cells using human iPSCs from which they successfully isolated corneal epithelial stem/progenitor cells capable of long-term corneal regeneration (122). Other groups showed that corneal epithelial-like cells could be also derived through direct reprogramming of the other cell types such as bone marrow mesenchymal stem cells (BM-MSCs), hair follicle stem cells (HFSCs), skin epithelial stem cells, fibroblasts and oral mucosal epithelial cells (124–128), dental pulp stem cell sheet (129) and nasal mucosal epithelial cell sheet (130) suggesting that these approaches might represent novel options for treatment of LSCD in the future.

Conclusions

Amongst adult stem cell populations that sustain high-turnover mammalian tissues, LSC represent a relatively well-studied entity with proven clinical relevance in human regenerative medicine, based on their capacity for corneal restoration following transplantation to LSCD patients. Recent advances in the identification of LSC markers now promise not only to further enhance their therapeutic potential, but also to allow further dissection of their developmental origin, differentiation plasticity and contributions to the LSC cell niche, as such markers can now be deployed in genetic lineage tracing models capable of documenting ever more primitive precursors and potentially identifying additional cell fates beyond the corneal epithelial lineage alone. Further studies in these respects are urgently needed, as they will refine our current understanding of anterior eye development and homeostasis. In particular, such genetic lineage tracing studies, combined with single cell transplantation studies, will serve to answer the question of identity of a common progenitor for anterior eye chamber development and what its developmental lineage may be. Moreover, further study of LSC and their molecular markers will shed light on the cellular and molecular mechanisms involved in their preservation of undifferentiated phenotype, their high proliferative potential throughout adulthood, their maintenance, replenishment and immunoregulatory functions, thereby informing not only promising novel LSC-based clinical approaches to corneal disease, but also more broadly, based on potential relevance to other adult stem cell niches, the field of adult regenerative medicine as a whole.

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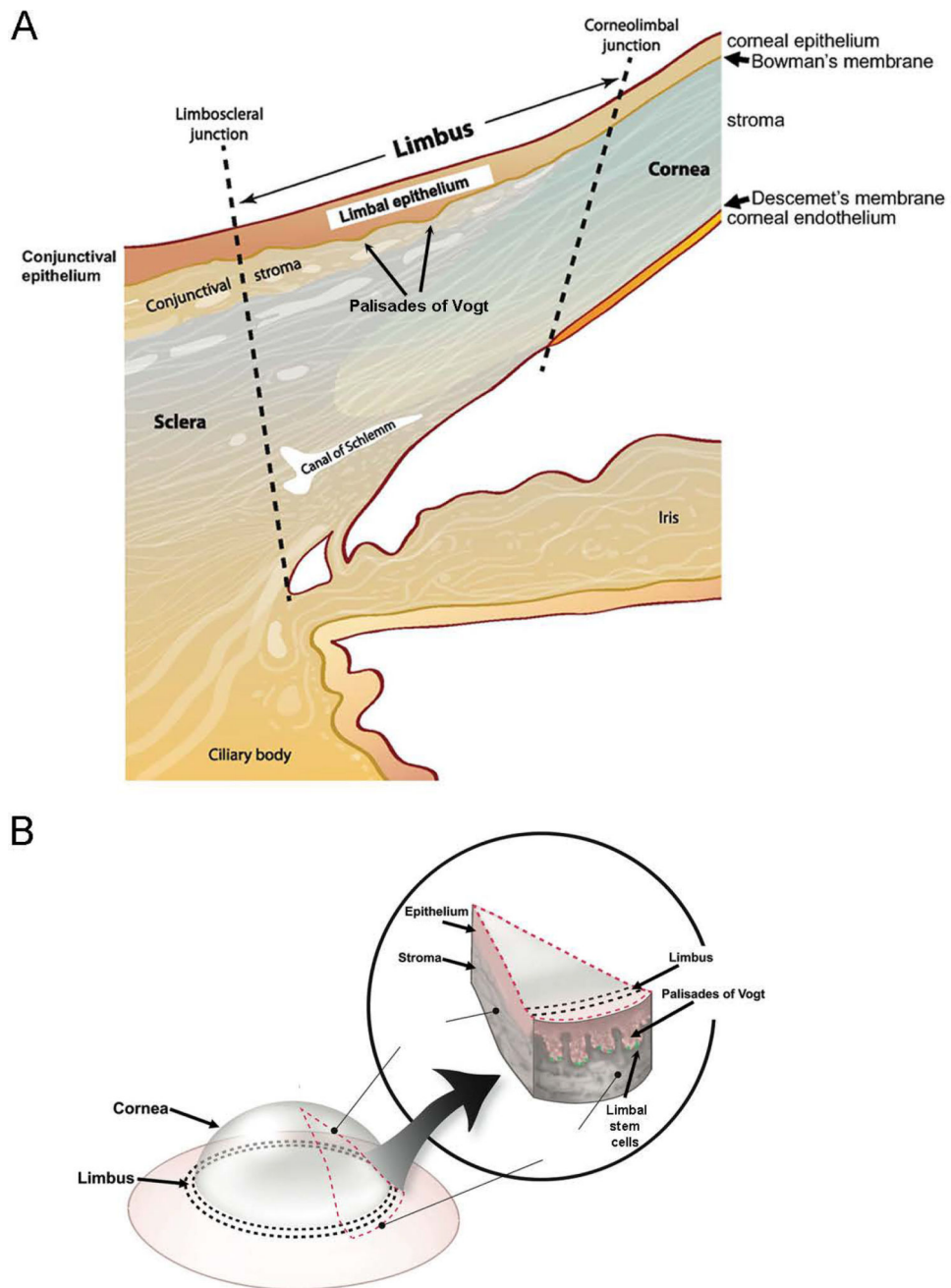
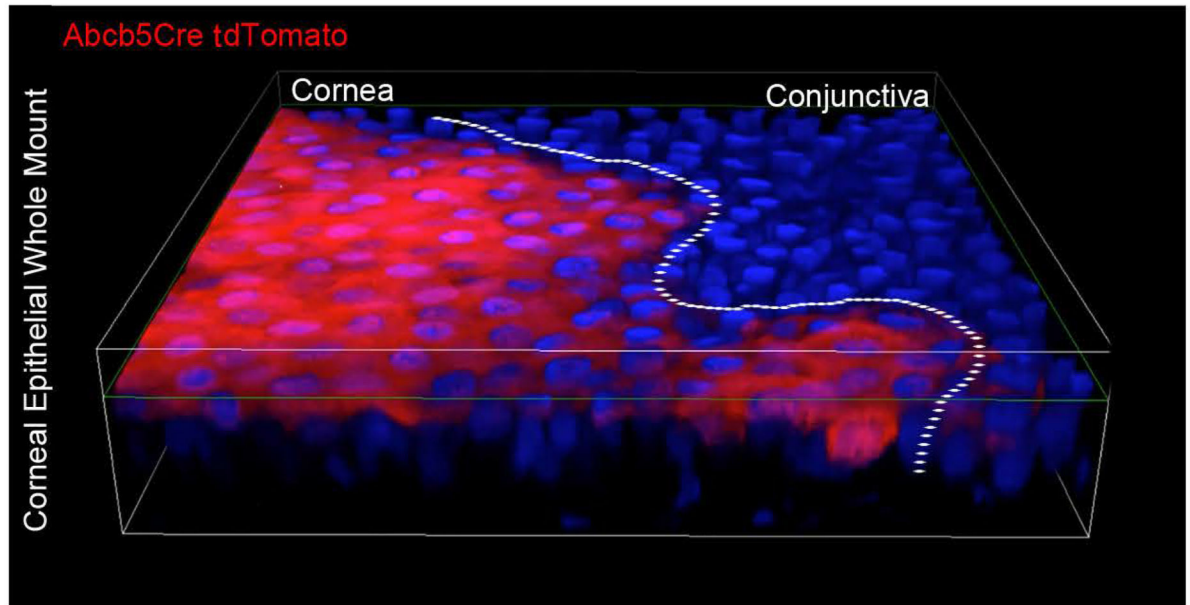


Figure 1. Schematic illustration of the human cornea and limbus

(A) Cross section illustrating the location and cellular layers of the cornea and limbus. **(B)** The Palisades of Vogt located at the corneo-limbal-scleral junction of the eye.

A



B

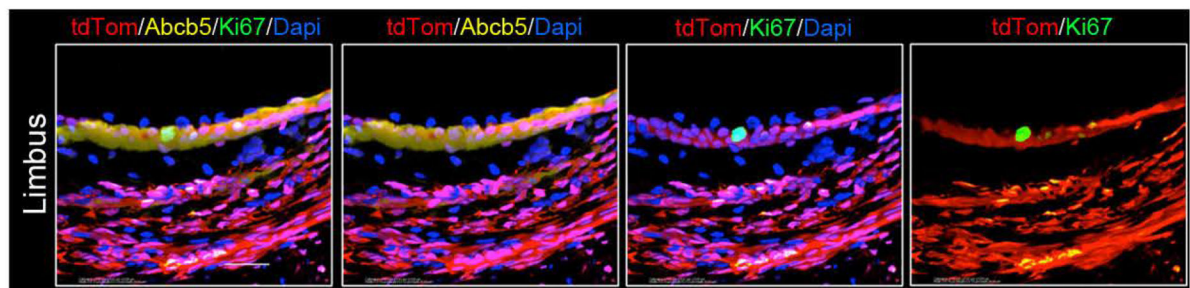


Figure 2. Contribution of ABCB5+ stem cells to corneal epithelial development and homeostasis (A) Immunofluorescent image of corneal epithelium from a 1 month-old *Abcb5*/Cre/*tdTomato* mouse (whole-mount cornea). *Abcb5*/Cre transgenic mice were generated by insertion of an IRES-Cre cassette in the *Abcb5* 3'UTR downstream of the STOP codon located in exon 30. *Abcb5*/Cre mice were crossed with *tdTomato* (B6;129S6-*Gt(ROSA)26Sortm9(CAG-tdTomato)Hze/J*) mice for genetic lineage tracing studies. Whole-mount cornea preparations from *Abcb5*/Cre/*tdTomato* mice identified *tdTomato*-positive *Abcb5*-derived progeny cells within the entire adult mouse corneal epithelium. (B) Immunofluorescent ($\times 60$ magnification) images of *tdTomato* (red), *Abcb5* (yellow) and *Ki67* (green) co-expression in the limbus of *Abcb5*/Cre/*tdTomato* mice. The nuclei are stained with Dapi, 4',6-diamidino-2-phenylindole (blue).

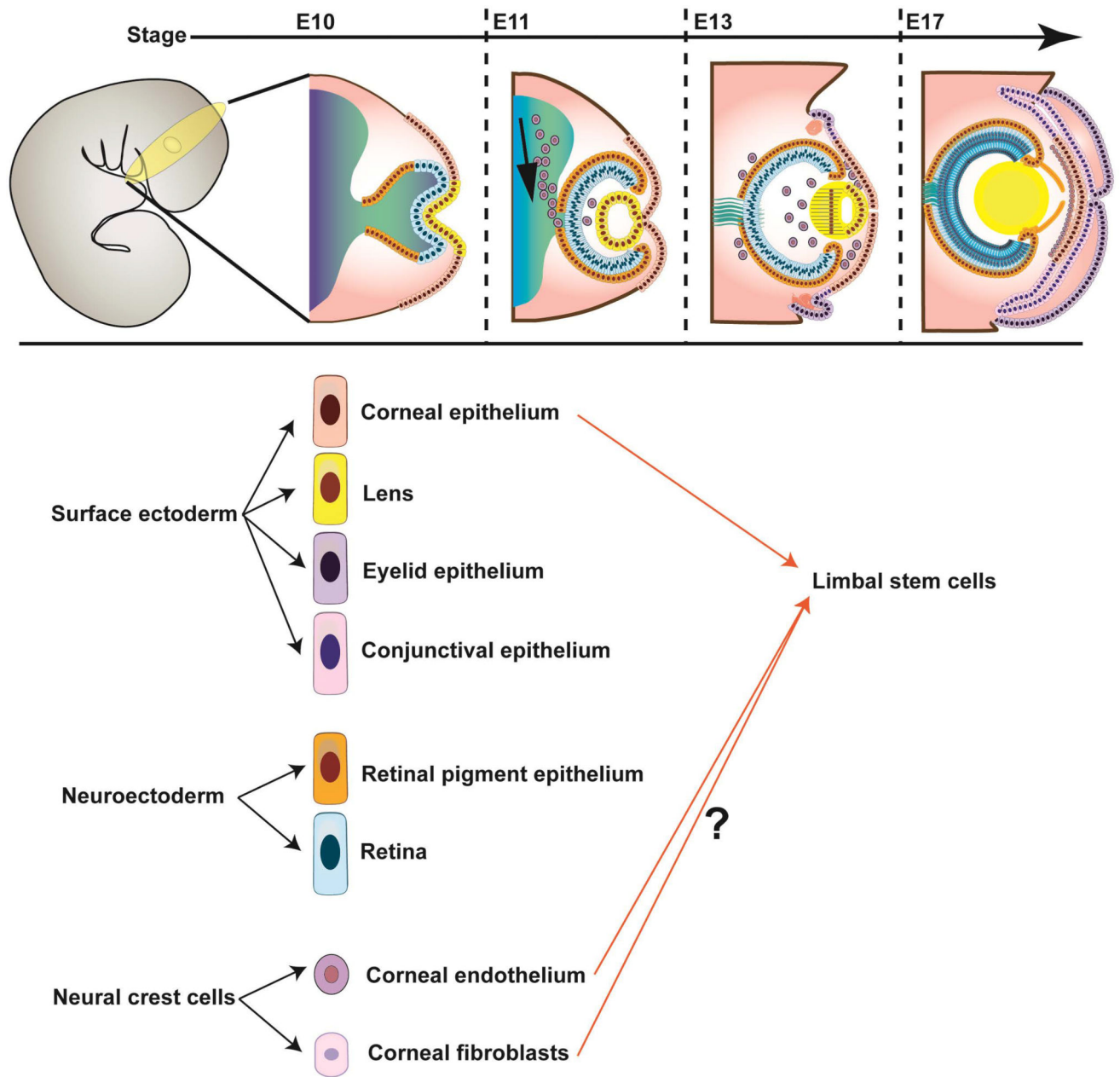


Figure 3. Developmental origin of LSC

(A) Schematic illustration of corneal development. From left to right: Extending neuroepithelium induces the surface ectoderm to form the lens, cornea, conjunctiva and eyelid. Migrating neural crest cells differentiate into corneal endothelium and stromal fibroblasts. (B) Contribution of diverse embryonic layers to the formation of the LSC niche. Current models suggest that LSC could be developmental descendants of the surface ectoderm as well as the periocular mesenchyme.

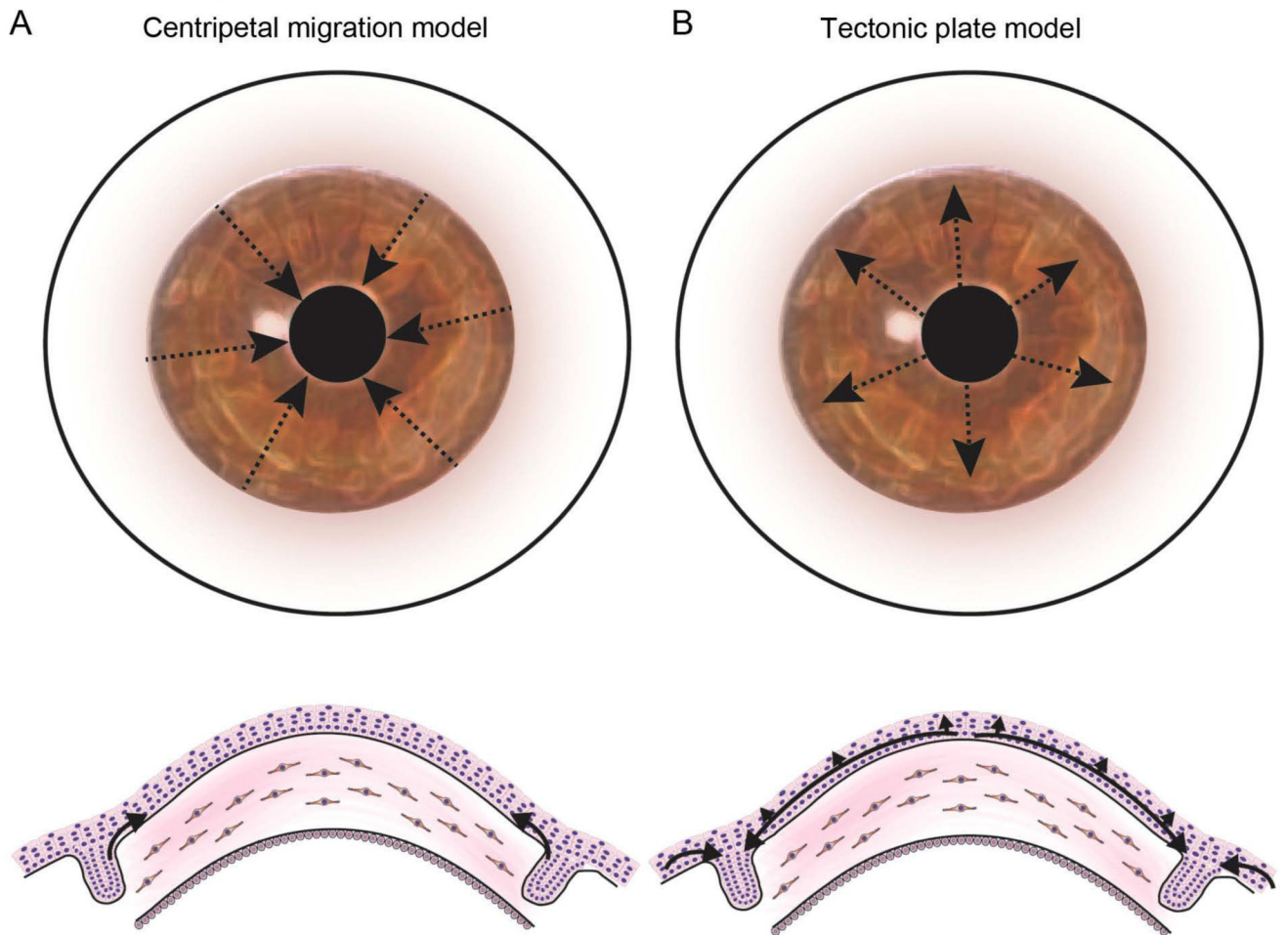


Figure 4. Current models of corneal epithelial migration and maintenance

(A) The Centripetal Migration Model, also known as the X-Y-Z hypothesis, of corneal regeneration. This model suggests that LSC located in the limbic region undergo centripetal migration and differentiation to maintain the corneal epithelium. (B) An alternative model suggests the existence of stem cells capable of corneal and conjunctival regeneration in the entire corneal epithelium. According to this model, the limbus represents a zone of equilibrium in which the expanding conjunctival and corneal epithelia are confronted in a mechanism reminiscent of tectonic plates; rupture of this equilibrium is suggested to result in migration of LSC onto the cornea.

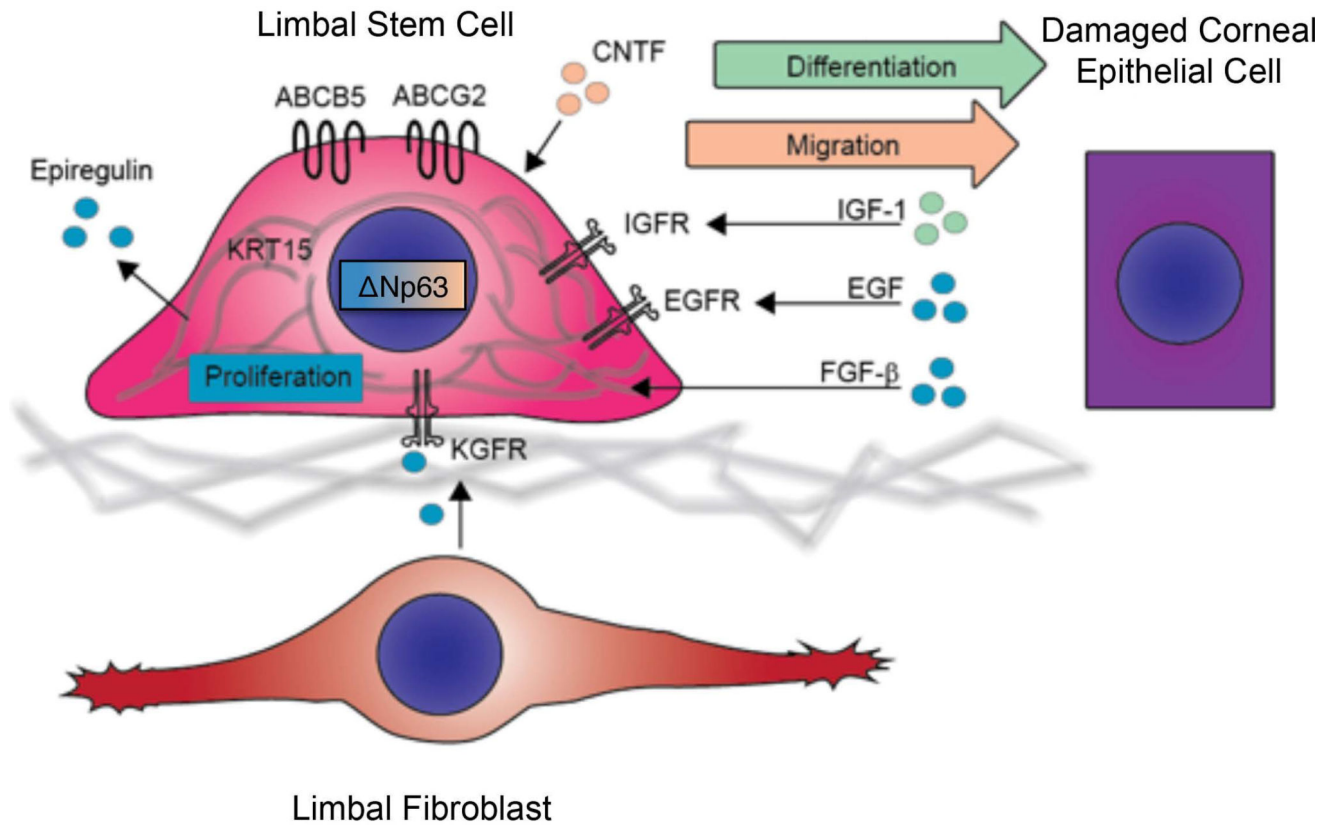


Figure 5. Factors affecting corneal epithelial wound healing

Normal corneal wound healing is dependent on proliferation (blue), migration (orange) and differentiation (green) of corneal progenitors. Attenuated expression of LSC markers, including ABCB5, ABCG2, Np63 α or K15, is associated with abnormal corneal wound healing, which may result in increased corneal fragility, ulceration and clouding. Limbal epithelial cell proliferation is supported by expression of Np63 α and epiregulin in limbal basal epithelial cells, by keratinocyte growth factor (KGF) secreted from limbal fibroblasts, and by epidermal growth factor (EGF) and fibroblast growth factor- β (FGF- β) produced by damaged corneal epithelium. Migration is promoted by expression of Np63 α and ciliary neurotrophic factor (CNTF). Differentiation is induced by insulin-like growth factor-I (IGF-I), rapidly produced by injured corneal epithelium upon injury. KGFR, KGF receptor; EGFR, EGF receptor; IGFR, IGF receptor.

Table 1

Putative LCS markers

Marker	Unseparated cells				Enrichment of marker positive cells			
	Species		Co-expression with Np63 α protein		Method of enrichment	Colony forming efficiency (CFE)	Restoration of corneal epithelium via transplantation	
	Non-human	Human	IHC	Flow			Frequency of holoclones	Short term
<i>Negative Selection</i>								
Cytokeratin 3 (2)	rabbit							
SSEA14 (131)		+			magnetic beads	+		
ALDH ^{lim} (40)		+	+		cell sorting	+		
RHAMM ^{bright} (40)		+	+		cell sorting			
Connexin-43 (41)		+	+	+	cell sorting			
<i>Positive Selection</i>								
Cytokeratin 15 (39)	mouse	+						
Lgr5 (31)		+	+					
Tcf4 (32)		+	+					
CD157 (33)		+	+					
SOD2/CK15 clusters (132)		+						
CD71 ^{low} /integrin $\alpha 6^{\text{high}}$ (34)		+	+		cell sorting	+		
TrkA (35)		+	+					
N-Cadherin (36)		+	+	+		+		
Hoechst efflux (133)	rat	+			side population			
Integrins $\beta 1$ - $\beta 4$ (22)	mouse		+					
Hoechst efflux (134)	rabbit				side population	+		
Abcg2 (37)	rabbit		+		side population	+		
Abcg2 (37, 38)		+	+		side population	+		
p63, Abcg2, Integrins (135)		+	+					

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Marker	Unseparated cells				Enrichment of marker positive cells			
	Species		Co-expression with Np63a protein		Method of enrichment	Colony forming efficiency (CFE)	Restoration of corneal epithelium via transplantation	
	Non-human	Human	IHC	Flow			Short term	Long term
ABC5 (42)	mouse	+	+	+	cell sorting		+	+