The Role of the miR-21/SPRY2 Axis in Modulating Proangiogenic Factors, Epithelial Phenotypes, and Wound Healing in Corneal Epithelial Cells

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Purpose. Subconjunctival injection of antagomir-21 attenuates the progression of corneal neovascularization. We examined the underlying mechanism by investigating the regulation of microRNA (miR)-21 expression and the involvement of miR-21 in the homeostasis of corneal epithelial cells.

Methods. Corneal epithelial cells were cultured with TGF-β1 and/or under hypoxia conditions. miR-21 expression was measured by quantitative PCR. The direct targets of miR-21 were validated by the 3′-UTR luciferase reporter assay. Alterations of proangiogenic signaling and the epithelial-mesenchymal transition (EMT) phenotype after miR-21/Sprouty2 (SPRY2) knockdown were examined by Western blotting. The effect of conditioned medium on angiogenesis was assessed using the tube formation assay. Wound healing was evaluated by the migration and scratch assays.

Results. TGF-β1 or hypoxia upregulated miR-21, and miR-21 silencing abolished TGF-β1/hypoxia-induced hypoxia inducible factor (HIF)-1α and VEGF expression. miR-21 inhibited SPRY2 by directly targeting its 3′-UTR. Simultaneous silencing of miR-21 and SPRY2 significantly upregulated p-ERK, HIF-1α, and VEGF and promoted angiogenesis. Induction of miR-21 or inhibition of SPRY2 reduced the levels of cytokeratin (CK)-3 and CK-12 and promoted EMT. Transwell and wound healing assays indicated that miR-21 promoted cell migration.

Conclusions. TGF-β1 or hypoxia induced miR-21 and inhibited SPRY2, thereby enhancing proangiogenic signaling, suppressing the epithelial phenotype, and promoting wound healing in corneal epithelial cells.

Keywords: corneal epithelial cell, miR-21, SPRY2, proangiogenic, epithelial markers, corneal wound healing

The corneal epithelium is the outermost layer of the cornea and acts as a barrier that protects the corneal interior from infection by noxious environmental agents.[1,2] The corneal epithelium accounts for 10% of corneal depth and is sustained by a relatively acellular, dense stroma of tightly packed collagen fibers in an environment that lacks blood vessels.[3,4] Invasion of the corneal epithelium by vessels decreases the function of the cornea leading to loss of vision.[5] In a previous study, we showed that microRNA-21 (miR-21) was significantly upregulated in the alkali-burned cornea compared to the healthy cornea. In vivo administration of antagomir-21 drastically inhibited the expression of hypoxia inducible factor (HIF)-1α and VEGF-A, leading to a significant reduction in neovascularization progression.[6] However, the detailed underlying mechanism including the regulation of miR-21 remains largely unclear. Hypoxia upregulates the expression of miR-21 in pancreatic cancer cells,[7] and miR-21 induces tumor angiogenesis by upregulating HIF-1α in human prostate cancer cells.[8] HIF-1α is a key hypoxia marker and regulates many angiogenic

genes. Overexpression of HIF-1α is largely responsible for the aberrant activation of VEGF and subsequent angiogenesis.[9,10] Several lines of evidence indicate that HIF-1α is present in the human corneas during neovascularization and angiogenesis. Silencing of corneal HIF-1α inhibits corneal neovascularization.[11,12] TGF-β1 is involved in the response to corneal injury, and neovascularization can be suppressed by blocking Smad3/TGF-beta signaling in a corneal alkali burn model.[13] TGF-β1 promotes the proliferation and trans-differentiation of scar fibroblasts by upregulating miR-21.[14] However, whether TGF-β1 or hypoxia regulates miR-21expression in corneal epithelial cells remains unknown.

The Sprouty (SPRY) family of proteins is a target of miR-21 in various cells and tissue types.[15–17] The SPRY family of proteins are well characterized negative regulators of p-ERK. miR-21-mediated downregulation of Spry1 enhances ERK-MAP kinase activity in the fibroblasts of the failing heart.[15] Kuracha et al.[18] reported that Spry1 and Spry2 are necessary for lens vesicle separation and corneal differentiation. We previously showed

TABLE. Antibody Information in Western Blot

Name of Antibody	Company	Catalog Number	Dilution
HIF-1α	Abcam (Cambridge, UK)	ab2185	1:500
VEGF-A	Abcam	ab46154	1:2000
Tubulin	Cell Signaling Technology (Beverly, MA, USA)	#2148	1:2000
SPRY1	Cell Signaling Technology	#13013	1:1500
SPRY2	Cell Signaling Technology	#13264	1:1000
SPRY4	Pierce (Rockford, IL USA)	PA531401	1:1000
p-ERK1/2	Cell Signaling Technology	#4370	1:2000
CK3	Abcam	ab77869	1:1000
CK12	Abcam	ab185627	1:1000
vimentin	Abcam	ab20346	1:1000

that SPRY2 and SPRY4 are downregulated in alkali-burned cornea, and their levels are restored in antagomir-21–treated corneas compared to the negative controls (antagomir-NC).[6] However, whether the expression of HIF-1α or VEGF is affected by the SPRY family of proteins in corneal epithelial cells remains to be determined.

We showed that miR-21 was induced by TGF-β1 or hypoxia and directly targeted SPRY2 in corneal epithelial cells. We found that miR21/SPRY2 signals were involved in the regulation of p-ERK, HIF-1α, VEGF, and corneal epithelial markers including cytokeratin (CK)-3 and CK-12, as well as cell migration.

MATERIALS AND METHODS

Mouse Corneal Epithelial Cell Culture

All experimental protocols were approved by the animal care and use committee of Shanghai Tenth People's Hospital Affiliated to Tongji University in accordance with the ARVO Statement for the Use of Animals in Ophthalmic and Vision Research. Mouse corneal epithelial cells were harvested from the eyeballs of BALB/c mice (SLAC Animal, Shanghai, China). Briefly, epithelium was obtained by digestion with 0.2% collagenase IV (Sigma-Aldrich Corp., St. Louis, MO, USA) at 37°C for 2 hours. Single cells were obtained by digestion with 0.25% trypsin-EDTA (Sigma-Aldrich Corp.) at 37°C for 15 minutes, and cells were centrifuged and resuspended in keratinocyte serum-free medium (KSFM, Thermo Fisher Scientific, Waltham, MA, USA) supplemented with 0.3 M calcium chloride, 0.2 ng/mL epidermal growth factor, and 25 μg/ml brain pituitary extract. The cells were maintained at 37°C in 5% humidified CO_2 during routine passages, and the medium was changed every 2 days.

Treatment of Corneal Epithelial Cells With TGF-β1 and Hypoxia

TGF-β1 was purchased from PeproTech (Rocky Hill, NJ, USA). Corneal epithelial cells were seeded in 6-well plates at a density of 1×10^5 cells/well and maintained in culture medium for 24 hours. The culture medium then was removed and replaced with 10 ng/ml TGF-β1 in medium. Cells were cultured in a modular incubator equipped with an O_2 sensor (Eppendorf, Hamburg, Germany), which enabled the mixing of N_2 and air to achieve hypoxic conditions (1% O_2 and 5% CO_2 balanced with N_2).

Cell Transfection

The synthesized siRNA oligonucleotides against SPRY2, the miR-21 inhibitor, and the negative control for the miRNA inhibitor were purchased from RIBOBIO (Guangzhou, China). Cells were transfected with oligonucleotides using Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA) at a final concentration of 100 nM following the manufacturer's instructions.

Quantitative Real-Time PCR

Total RNA was extracted from samples using the TRIzol (Invitrogen) reagent according to the manufacturer's instructions. Aliquots of 0.5 μg RNA were reverse transcribed to cDNA using the PrimeScript RT reagent kit (Takara, Beijing, China). A stem-loop primer (5′-GTCGTATCCAGTGCAGGGTCCGAGG TATTCGCACTGGATACGACTCAACA-3′) was used for miR-21 reverse transcription, and a specific primer (5′-AACGCTTCAC GAATTTGCGT-3′) was used for reverse transcription of U6. Quantitative PCR (QPCR) was performed using the ABI 7500 Fast System (Applied Biosystems, Foster City, CA, USA). QPCR was performed using the SYBR PrimeScript RT-PCR kit (Takara), and the reaction mixtures were incubated at 95°C for 1 minute, followed by 40 cycles of 95°C for 15 seconds and 60°C for 1 minute. The following primers were used: miR-21 primers: forward 5′-CGGCGGTTAGCTTATCAGACTGA-3′, reverse 5′-CCAGTGCAGGGTCCGAGGTAT-3′. U6 primers: forward 5′-CTCGCTTCGGCAGCACA-3′, reverse 5′-AACGCTTCACGAATTTGCGT-3′. Experiments were performed at least three times.

Western Blot Analysis

Protein was extracted from the cells on ice for 15 minutes using RIPA lysis buffer (Beyotime, Haimen, China) supplemented with protease inhibitors and phosphatase inhibitors (Merck, Kenilworth, NJ, USA). The supernatants were collected following centrifugation at 12,000*g* at 4°C for 10 minutes. The protein concentration was determined using a BCA protein assay kit (Tiangen, Beijing, China), and whole lysates were mixed with 5× SDS loading buffer (125 mmol/l TrisHCl, 5% SDS, 20% glycerol, 100 mmol/l dithiothreitol [DTT], and 0.2% bromophenol blue) at a ratio of 1:4. The samples were heated at 100°C for 10 minutes and separated on SDS polyacrylamide gels. Proteins were transferred onto nitrocellulose membranes (Bio-Rad Laboratories, Hercules, CA, USA) and blocked with a 5% BSA solution. The membranes were incubated overnight at 4°C with antibodies listed in the Table. Specific bands were scanned and analyzed using ImageJ software (National Institutes of Health [NIH], Bethesda, MD, USA).

Luciferase Reporter Assay

Corneal epithelial cells were seeded in 24-well plates the day before transfection. Cells were cotransfected with 100 ng of wild-type or mutant psiCHECK2-mouse Spry2-3′-UTR and miR-21 mimic (50 nM) or mimic negative control (50 nM) or miR-21 inhibitor (100 nM) or inhibitor negative control (100 nM) using
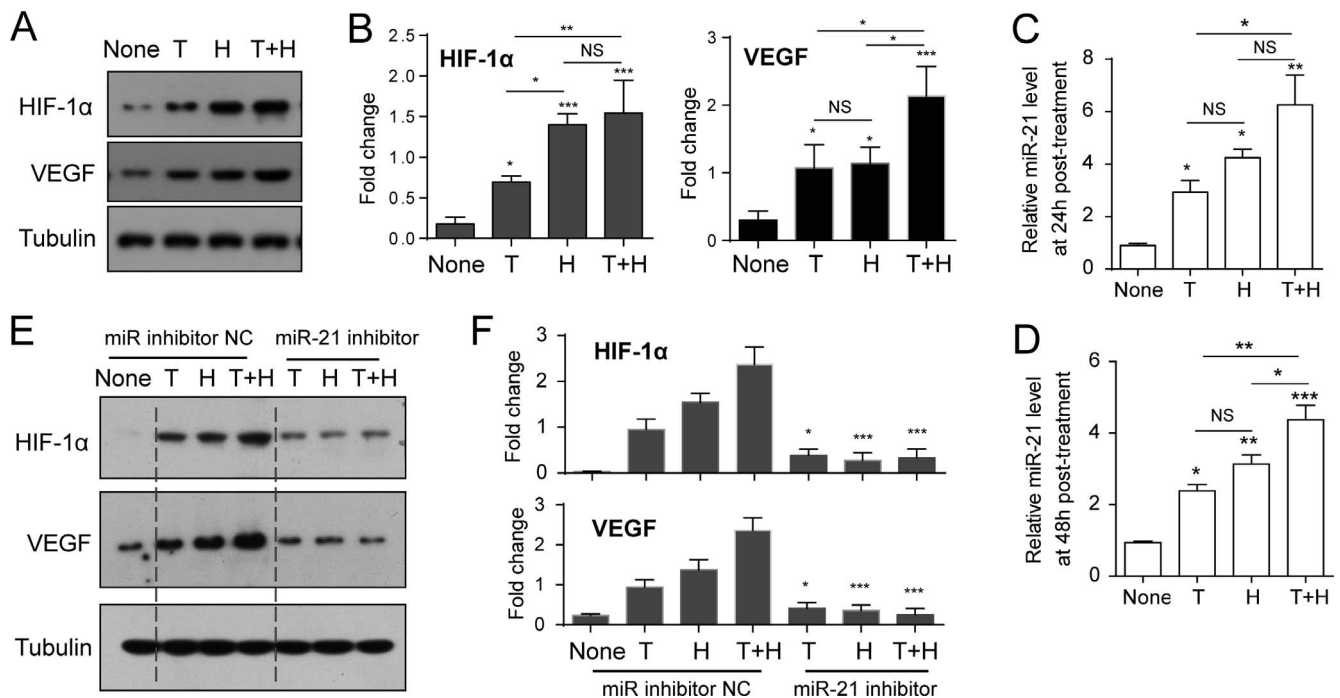
FIGURE 1. miR-21 is critical for the proangiogenic phenotype of corneal epithelial cells under TGF-β1 and/or hypoxia treatment. (A–D) Corneal epithelial cells were exposed to TGF-β1 (T), 1% O_2 (H), or TGF-β1 plus 1% O_2 (T+H). The protein levels of HIF-1α and VEGF were determined by Western blotting (A) followed by densitometry analysis using ImageJ software. (B) Tubulin was used as the loading control. The expression of miR-21 at 24 (C) or 48 (D) hours after the indicated treatments was determined by qPCR. (E, F) Corneal epithelial cells were treated with miR-21 inhibitor combined with TGF-β1 (T), 1% O_2 (H), or TGF-β1 plus 1% O_2 (T+H), and the protein levels of HIF-1α and VEGF were determined by Western blotting (E) followed by densitometry analysis using ImageJ software (F). Values represent the mean and standard deviation. *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, versus the untreated group (B–D) or inhibitor NC group (F). Western blot experiments were performed in triplicate and PCR experiments were performed in quadruplicate.

Lipofectamine 2000 (Invitrogen). At 36 hours after transfection, luciferase activity was measured using the Dual Luciferase Reporter Assay System (Promega, Madison, WI, USA). All experiments were performed in triplicate.

Tube Formation Assay

The 96-well plates were filled with 75 μL Matrigel (Corning Matrigel Basement Membrane Matrix; Corning, Inc., Corning, NY, USA) and allowed to solidify at 37°C. Then HUVECs (2 × 10^4 cell) were gently seeded on top of the gel in the presence of conditioned medium of corneal epithelial cells. After 16 hours of incubation, tube-forming structures were analyzed. The average number of tubules was calculated from three fields in each sample.

Scratch Wound Closure Assay

Corneal epithelial cells were seeded in 24-well plates at a density of 5 × 10^4 cells/cm² and incubated for 24 hours in medium to form a confluent monolayer. Two liner defects were produced by a silicone needle in monolayer cells. The scratch-wounded corneal epithelial cells were washed with 1× PBS to remove any cell fragments. Still images were acquired at two independent points in each defect under a Zeiss Observer Z1 microscope (Carl Zeiss Meditec, Jena, Germany) equipped with a CCD camera at 12 and 24 hours. The remaining wound area was measured using ImageJ software (version 1.48, NIH).

Transwell Migration Assay

Migration experiments were performed using a 24-well Transwell chemotaxis chamber technique. Briefly, the Transwell membrane was precoated with 30 μL of Matrigel, the lower chamber was filled with Dulbecco's modified Eagle medium (DMEM) containing 10% fetal bovine serum (ScienCell Research Laboratories, Carlsbad, CA, USA), and a total of 1 × 10^6 cells in 200 μL medium were seeded into the upper chamber. Chambers were incubated for 24 hours at 37°C. The cells remaining on the upper surface of the membrane were removed followed by PBS washes, and those on the undersurface of the membrane were fixed and stained with crystal violet. Fields on the membrane were counted under a ×20 objective. Each assay was performed in triplicate.

Statistical Analysis

Results were analyzed statistically using 1-way ANOVA and paired-sample t-tests. The tube formation data are expressed as the mean and each data point represents an individual sample. All other data are expressed as the average ± SD. $P < 0.05$ was considered statistically significant.

RESULTS

TGF-β1 and Hypoxia Induce the Expression of Proangiogenic Factors in Corneal Epithelial Cells by Upregulating miR-21

The effect of TGF-β1 or hypoxia on the expression of proangiogenic factors was assessed by exposing mouse corneal epithelial cells to TGF-β1 and/or 1% O_2 (hypoxia) for 48 hours. As shown in Figures 1A and B, TGF-β1 and 1% O_2 upregulated HIF-1α and VEGF. Although the two treatments had similar
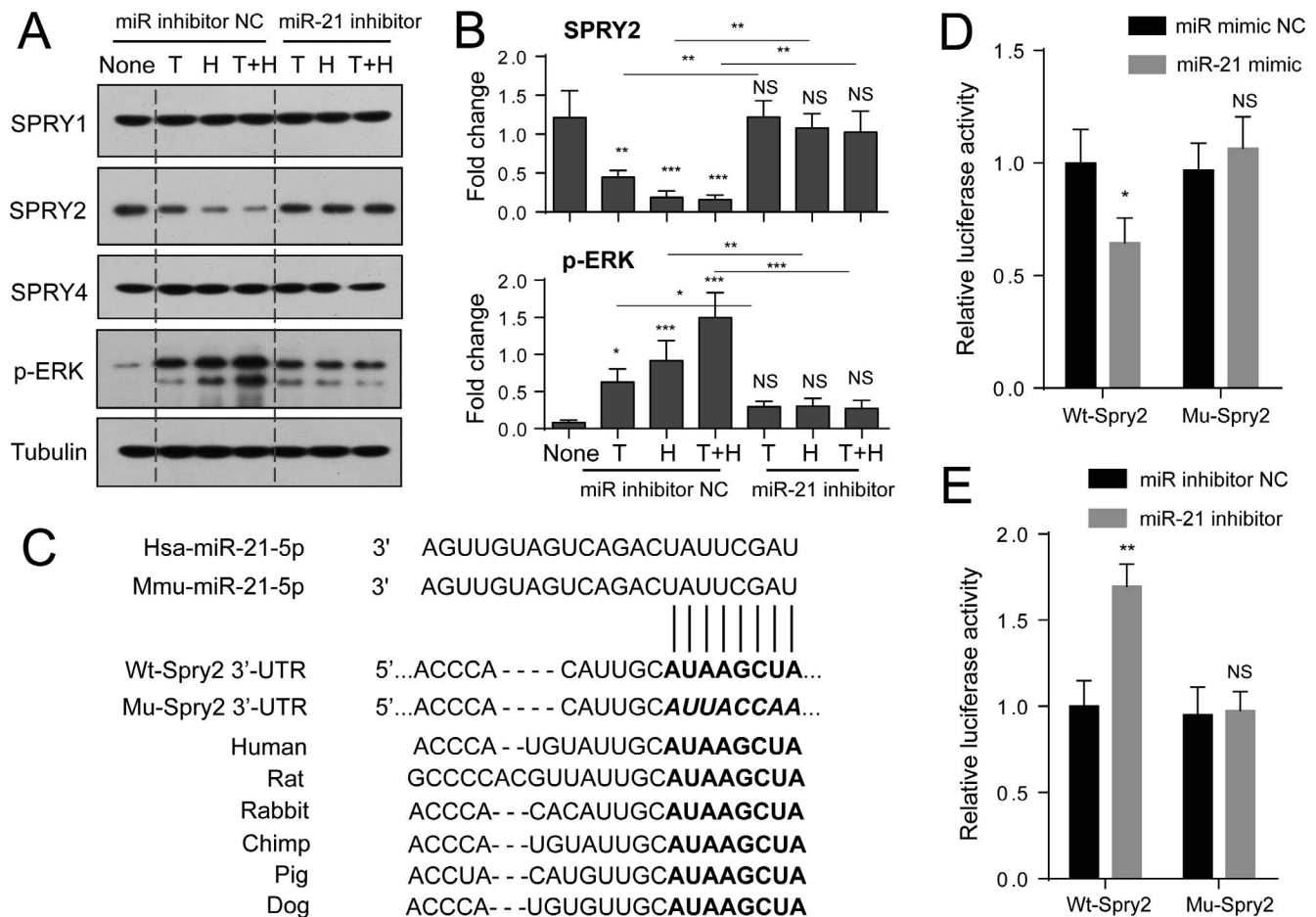
FIGURE 2. SPRY2 is a direct target of miR-21 in corneal epithelial cells. Corneal epithelial cells were treated with miR-21 inhibitor and exposed to TGF-β1 (T), 1% O_2 (H), or TGF-β1 plus 1% O_2 (T+H). The protein levels of SPRY1, SPRY2, SPRY4, and p-ERK, were determined by Western blotting (**A**) followed by densitometry analysis using ImageJ software (**B**). Tubulin was used as the loading control. (**C**) miR-21 and its putative binding sequences in the mouse 3′-UTR of Spry2. The binding sequences in the complementary sites were replaced by the indicated nucleotides to produce mutant Spry2 3′-UTR luciferase reporter constructs. Marked sequences represent the conserved complementary nucleotides of the miR-21 binding sequence in humans and various mammals. (**D, E**) Luciferase activity of the wild-type and mutated 3′-UTR of Spry2 treated with miR-21 mimic (**D**) or inhibitor (**E**). *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, versus the untreated group (**B**) or mimic NC (**D**) or inhibitor NC group (**E**). Experiments were performed in triplicate.

effects on VEGF induction, HIF-1α levels increased more dramatically in response to 1% O_2 than TGF-β1 treatment.

Simultaneous treatment with TGF-β1 and 1% O_2 had a stronger effect on upregulating VEGF than single agent treatment, indicating a synergistic action. We previously showed that miR-21 expression is increased in the alkali-burned cornea compared to the healthy cornea.[6] Here, we showed that TGF-β1 or 1% O_2 for 24 and 48 hours upregulated miR-21, and the effect was stronger at 24 hours (Figs. 1C, 1D). Combination treatment resulted in a higher miR-21 induction at 24 hours (Fig. 1C).

To elucidate the biologic function of miR-21, we next inhibited the expression of miR-21 in the presence of TGF-β1 or under hypoxia conditions. Silencing of miR-21 drastically downregulated HIF-1α and VEGF protein expression, restoring VEGF expression to basal levels (Figs. 1E, 1F). These results supported that miR-21 induces the proangiogenic phenotype of corneal epithelial cells in the presence of TGF-β1 treatment and/or hypoxia.

MiR-21 Directly Targets SPRY2 in Corneal Epithelial Cells

Previously, we found that SPRY1/2/4, which are candidate targets of miR-21, were significantly inhibited in the alkali-

burned cornea at 4 days post injury compared to their expression in the normal cornea.[6] Based on these results, we examined whether miR-21 upregulation is required for the downregulation of the SPRY family of proteins under TGF-β1 or hypoxia treatment in corneal epithelial cells. The results showed that SPRY2, but not SPRY1 or 4, was significantly suppressed in response to TGF-β1 or hypoxia treatment, whereas p-ERK, which is negatively regulated by the SPRY family of proteins, was activated (Figs. 2A, 2B). Inhibition of miR-21 rescued SPRY2 expression and inhibited p-ERK to basal levels. The levels of SPRY1/4 remained unchanged (Figs. 2A, 2B).

Bioinformatics analyses identified a putative miR-21 binding site in the 3′-UTR of Spry2 that was conserved across species (Fig. 2C). The results of the 3′-UTR reporter assay showed that the luciferase activity of the wild-type Spry2 3′-UTR construct was significantly inhibited by miR-21 mimic (Fig. 2D). Conversely, suppression of miR-21 increased the luciferase activity of the wild-type construct (Fig. 2E). miR-21 expression had no significant impact on the luciferase activity of the mutant Spry2 3′-UTR (Fig. 2C–E). Taken together, these results suggested that miR-21 directly targeted the 3′-UTR of Spry2 and inhibited its expression in corneal epithelial cells.
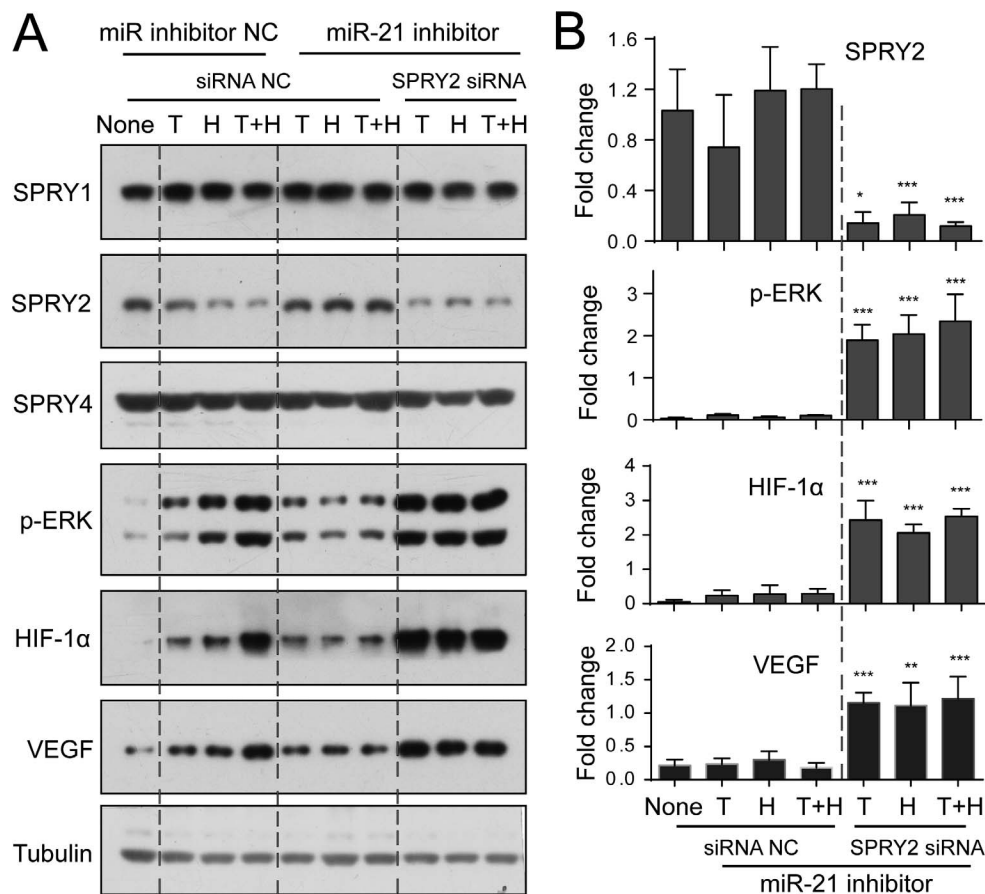
FIGURE 3. The miR-21/SPRY2 axis promotes the proangiogenic phenotype of corneal epithelial cells. Corneal epithelial cells were treated with miR-21 inhibitor in the presence or absence of siRNA against miR-21 and SPRY2, and exposed to TGF-β1, 1% O_2 or TGF-β1 plus 1% O_2. The protein levels of SPRY1/2/4, HIF-1α, p-ERK, and VEGF were determined by Western blotting (**A**) followed by densitometry analysis using ImageJ software (**B**). Tubulin was used as the loading control. Experiments were repeated three times.

The miR-21/SPRY2 Axis is Vital for the Proangiogenic Phenotype of Corneal Epithelial Cells

We showed that TGF-β1 or hypoxia downregulated SPRY2 and upregulated p-ERK, HIF-1α, and VEGF, and these effects were reversed by silencing miR-21.

To examine the biologic significance of the miR-21-mediated downregulation of SPRY2, we simultaneously knocked down miR-21 and SPRY2 in corneal epithelial cells. SPRY2 siRNA specifically decreased SPRY2 level without altering SPRY1/4 levels. Knockdown of Spry2 abolished the effect of miR-21 inhibition on downregulating p-ERK, HIF-1α, and VEGF. Silencing of SPRY2 almost completely reversed the effects of miR-21 inhibition, suggesting that high levels of SPRY2 are essential for the suppression of p-ERK, HIF-1α, and VEGF (Fig. 3). These data confirmed that miR-21 promoted p-ERK activation and the proangiogenic phenotype of corneal epithelial cells by suppressing SPRY2.

Since proangiogenic factors were induced in corneal epithelial cells in response to TGF-β1 or 1% O_2 treatment, we hypothesized that this treatment also may induce angiogenesis. A tube formation assay was performed to evaluate the effect of conditioned medium from corneal epithelial cells on the angiogenesis of HUVECs in Matrigel. The results showed that conditioned medium from TGF-β1 and/or hypoxia-treated cells promoted the development of tubes at a rate 2.01- to 3.19-fold higher than that in cells exposed to untreated conditioned medium. However, the effect of conditioned medium from miR-21 inhibitor-treated cells was comparable to that of medium from untreated cells. Inhibition of SPRY2 notably induced angiogenesis of HUVECs, whereas miR-21 levels were largely reduced (Fig. 4).

The miR-21/SPRY2 Axis Regulates the Expression of Corneal Epithelial Markers and Induces EMT

To evaluate whether the miR-21/SPRY2 axis regulates the expression of corneal epithelial markers as well as the epithelial-mesenchymal transition (EMT) process, the levels of CK3, CK12, and vimentin were measured in the presence of miR-21 inhibitor and/or SPRY2 siRNA. The results showed that TGF-β1 and/or 1% O_2 inhibited the expression of CK12, whereas only TGF-β1 and 1% O_2 suppressed CK3 and increased vimentin expression. Inhibition of miR-21 abolished the downregulation of epithelial markers and upregulation of vimentin. Coinhibition of miR-21 and SPRY2 downregulated CK3 and CK12 and upregulated vimentin level (Fig. 5). These results indicated that corneal epithelial markers, such as CK3, CK12, and EMT, were regulated by the miR-21/SPRY2 axis under TGF-β1 treatment or hypoxia conditions.
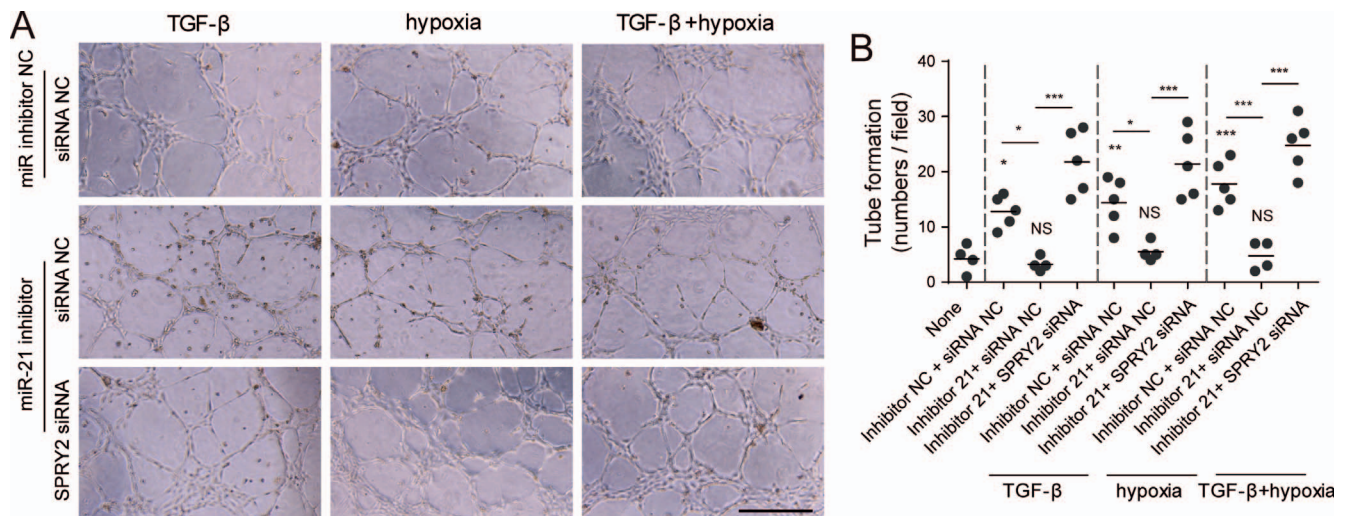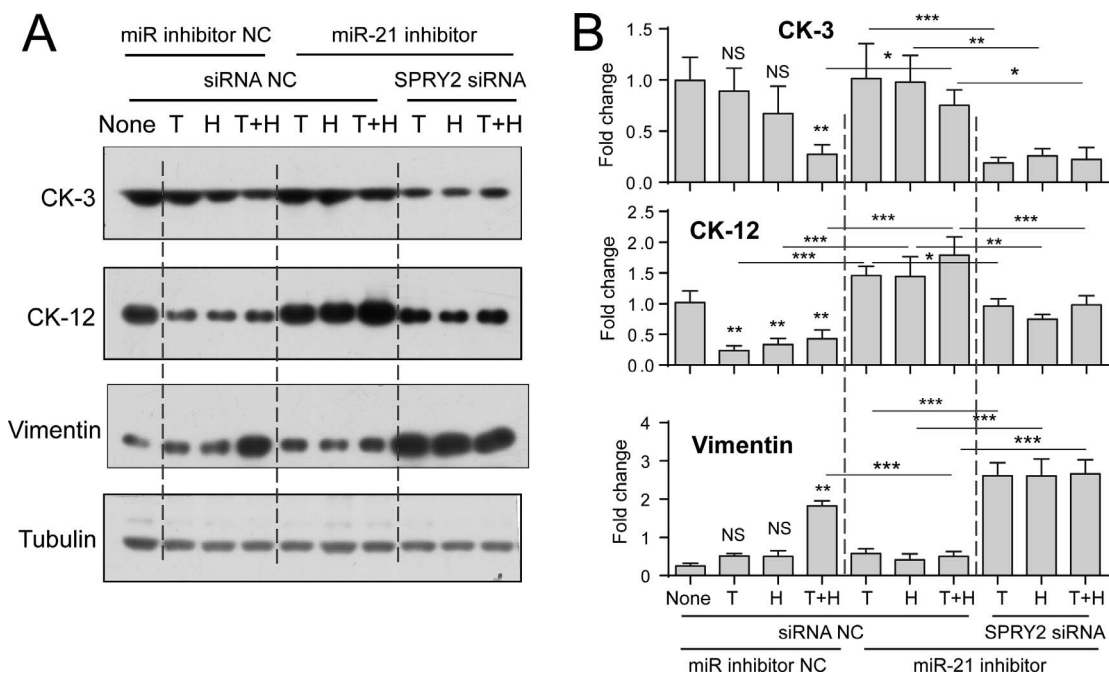
FIGURE 4. Conditioned medium from corneal epithelial cells affected angiogenesis of HUVECs. (**A, B**) Corneal epithelial cells were treated with miR-21 inhibitor in the presence or absence of siRNA against SPRY2, and subsequently exposed to TGF-β1, 1% O$_2$, or TGF-β1 plus 1% O$_2$. The conditioned medium from each group was added to HUVEC culture. Tube formation was photographed (**A**) and counted (**B**). The experiment was repeated three times, and each sample was tested in triplicate. *Scale bar*: 500 μm.
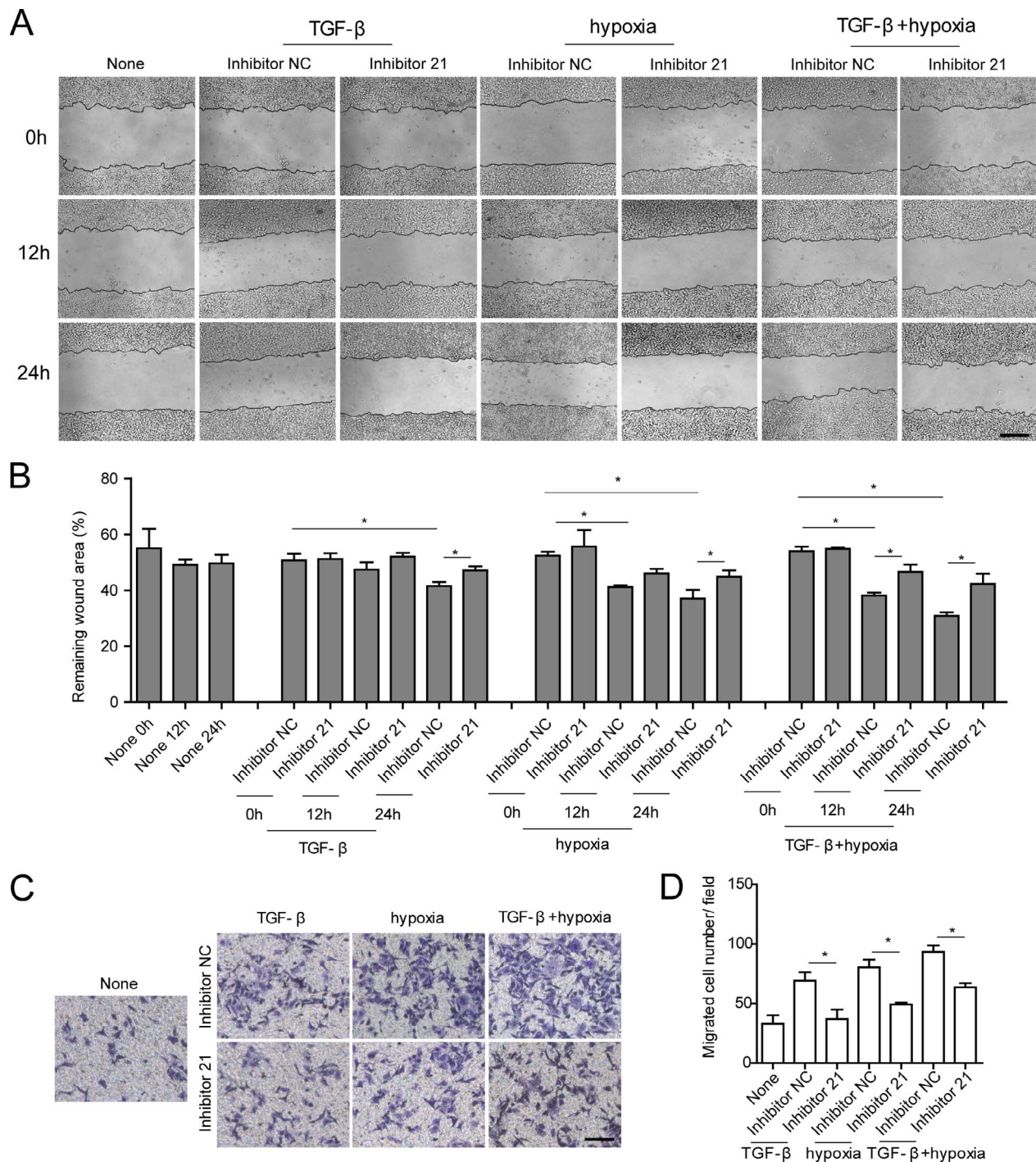
miR-21 Promotes the Migration of Corneal Epithelial Cells and Increases Wound Healing

We next set out to investigate the impact of TGF-β1 or hypoxia on corneal epithelial cell migration and proliferation. Corneal epithelial cells were exposed to TGF-β1 and/or 1% O$_2$ in the presence of miR-21 or control inhibitor for 0, 12, or 24 hours. The scratch wound closure assay was performed to measure cell migration. The results showed that wound closure was enhanced after 24 hours in TGF-β1–treated cultures and at 12 hours in response to 1% O$_2$ and combination treatment with TGF-β1 and 1% O$_2$ compared to vehicle controls (Figs. 6A, 6B). However, inhibition of miR-21 attenuated the overall wound healing rate (Figs. 6A, 6B). The Transwell assay was performed to examine the effects of miR-21 on migration, and the results showed that TGF-β1 and 1% O$_2$ increased the migration of corneal epithelial cells, whereas inhibition of miR-21 significantly decreased migration (Figs. 6C, 6D). Collectively, these results showed that miR-21 induced the migration of corneal epithelial cells.

FIGURE 5. EMT of corneal epithelial cells is regulated by the miR-21/SPRY2 axis under TGF-β1 treatment or hypoxia conditions. (**A, B**) Corneal epithelial cells were treated with miR-21 inhibitor in the presence or absence of siRNA against SPRY2 and exposed to TGF-β1 and/or 1% O$_2$. (**A, B**) Cells were subjected to Western blot analyses (**A**) of corneal epithelial markers (CK3 and CK12) and vimentin followed by densitometry analysis using ImageJ software (**B**). Tubulin was used as the loading control. Experiments were repeated three times.

FIGURE 6. miR-21 promotes the migration of corneal epithelial cells. (**A**) Representative images of the wound healing assay of corneal epithelial cells treated with TGF-β1, 1% O₂, or TGF-β1 plus 1% O₂ in the presence of miR-21 inhibitor or negative control. *Scale bar*: 300 μm. (**B**) The *summary bar graph* illustrates the rate of wound closure at the indicated time points during the scratch wound assay. (**C**) Corneal epithelial cells were treated with TGF-β1, 1% O₂, or TGF-β1 plus 1% O₂ in the presence of miR-21 inhibitor or negative control. Relative cell migration was examined using the Transwell migration assay. *Scale bar*: 50 μm. (**D**) The summary graph shows the results of the Transwell migration assay. *$P < 0.05$ vs. control. This experiment was repeated three times, and each sample was tested in triplicate.

DISCUSSION

The normal cornea actively maintains avascularity, and the in-growth of new blood vessels into the cornea reduces visual acuity.[19] In a previous study, we showed that antagomir-21 attenuates the progression of corneal neovascularization, and this effect may be mediated by SPRY2/4 inhibition of p-ERK.[6]

Here, we investigated the role of miR-21 in corneal epithelial cells. The results showed that miR-21 was induced by TGF-β1 or hypoxia, and suggested that the miR-21/SPRY2 axis is vital for wound healing and the regulation of proangiogenic and epithelial markers in corneal epithelial cells.

We previously showed that miR-21 was significantly increased in the alkali-burned cornea compared to the healthy

cornea. TGF-β1 and hypoxia have important roles in the induction of neovascularization.[20,21] However, whether TGF-β1 and hypoxia induce the expression of miR-21 and neovascularization in corneal epithelial cells remains unknown. To address this question, we exposed corneal epithelial cells to TGF-β1 or hypoxia, and the results showed that TGF-β1 or hypoxia induced the expression of miR-21, HIF-1α, and VEGF and inhibited the expression of the corneal epithelial cell markers CK3 and CK12, which are critical for the maintenance of corneal transparency. Furthermore, the conditioned medium from TGF-β1- or hypoxia-treated cells induced angiogenesis. To determine whether the effects of TGF-β1 or hypoxia were mediated by miR-21, we inhibited the expression of miR-21 and found that the levels of HIF-1α and VEGF were reduced, and CK3 and CK12 levels were increased. The conditioned medium failed to induce tube formation. Taken together, these results indicated that TGF-β1 or hypoxia induced angiogenic factors and inhibited corneal epithelial cell markers in corneal epithelial cells by increasing the expression of miR-21.

SPRY proteins are downstream targets and negative feedback regulators of the FGF-Ras-ERK signaling pathway.[22,23] Kuracha et al.[18,24] reported that Spry1- and Spry2-mediated negative modulation of FGF–ERK signaling regulates lens vesicle separation and corneal epithelial proliferation. We previously reported that SPRY1/2/4 were significantly inhibited in the alkali-burned cornea 4 days after injury compared to normal corneas.[6] However, inhibition of SPRYs to determine their function was not performed previously. Here, we demonstrated that SPRY2, but not SPRY1 or 4, was suppressed in response to TGF-β1 or hypoxia treatment. Klein et al.[25] showed that different Sprouty genes are expressed in different tissue compartments (Spry2 in the epithelium and Spry4 in the mesenchyme) to prevent diastema tooth formation. We speculated that Spry2, but not Spry1/4, has a role in the corneal epithelium. The 3′-UTR reporter assay confirmed that miR-21 directly targets the 3′-UTR of Spry2 and inhibits its expression in corneal epithelial cells. Furthermore, we inhibited the expression of miR-21 and SPRY2 simultaneously, and the results showed that p-ERK, HIF-1α, and VEGF were significantly induced, and the corneal epithelial markers CK3 and CK12 were considerably reduced compared to those in cells treated with miR-21 inhibitor. These results implied that high levels of SPRY2 were essential for suppressing the expression of p-ERK, HIF-1α, and VEGF and maintaining the expression of CK3 and CK12. In agreement with our results, Impagnatiello et al.[26] reported that Spry1 and Spry2 are membrane-anchored proteins that negatively regulate angiogenesis-associated receptor tyrosine kinase signaling and inhibit angiogenesis. Taken together, our results indicated that the miR-21/SPRY2 axis is vital for the proangiogenic phenotype and regulation of EMT in corneal epithelial cells. To the best of our knowledge, our study represents the first attempt to elucidate the role of the miR-21/SPRY2 axis in the regulation of angiogenesis and the epithelial phenotype in normal epithelial cells.

Adequate control of corneal epithelial wound healing is crucial for the health of the cornea. Corneal epithelial wound healing is a complex process that involves cell proliferation, migration, and differentiation.[27,28] miRNAs have an important role in inducing corneal epithelial cell proliferation and migration. Several miRNAs, such as miR-18a, induce connective tissue growth factor (CTGF) and promote the proliferation and migration of sodium hyaluronate-treated human corneal epithelial cells.[28] miR-184 significantly suppresses the proliferation and migration of human corneal epithelial cells.[29] miR-204 inhibits the proliferation and migration of human corneal epithelial cells by targeting Sirtuin 1.[30] We previously showed that miR-184 and miR-204 are downregulated and miR-21 is upregulated after alkali-burn injury in corneal tissue.[6] miR-21 is a wound-related miRNA, and its role in wound healing was demonstrated in skin wound models.[31,32] In the immortalized human keratinocyte cell line HaCaT, TGF-β1–induced miR-21 can target PTEN and promote cell migration by regulating the EMT process.[32] Another study reported that miR-21 regulates the EMT phenotype of keloid keratinocytes by targeting PTEN,[33] thereby affecting keloid formation. Here, we speculated that miR-21 has a key role in the regulation of corneal wound healing. We found that inhibition of miR-21 downregulated mesenchymal markers and decreased migratory activity. These data indicated that miR-21 is essential for inducing the migration and proliferation of corneal epithelial cells. Consistent with our study, Wang et al.[34] reported that miR-21 positively regulates skin wound healing by promoting cell migration and proliferation.

In summary, our results showed that TGF-β1 or hypoxia induced the expression of miR-21, and the miR-21/SPRY2 axis was vital for the proangiogenic phenotype of corneal epithelial cells. The miR-21/SPRY2 axis modulated epithelial phenotypes, as indicated by CK3 and CK12 expression. In addition, we demonstrated that TGF-β1 or hypoxia promoted the migration of corneal epithelial cells and increased wound healing via miR-21.

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