Conditionally Immortal Slc4a11−/− Mouse Corneal Endothelial Cell Line Recapitulates Disrupted Glutaminolysis Seen in Slc4a11+/− Mouse Model

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PURPOSE. To establish conditionally immortal mouse corneal endothelial cell lines with genetically matched Slc4a11+/− and Slc4a11−/− mice as a model for investigating pathology and therapies for Slc4a11 associated congenital hereditary endothelial dystrophy (CHED) and Fuchs’ endothelial corneal dystrophy.

METHODS. We intercrossed H-2Kb-tsA58 mice (Immortomouse) expressing an IFN-γ dependent and temperature-sensitive mutant of the SV40 large T antigen (tsTAg) with Slc4a11+/− and Slc4a11−/− C57BL/6 mice. The growth characteristics of the cell lines was assessed by doubling time. Ion transport activities (Na+/H+ exchange, bicarbonate, lactate, and Slc4a11 ammonia transport) were analyzed by intracellular pH measurement. The metabolic status of the cell lines was assessed by analyzing TCA cycle intermediates via gas chromatography mass spectrometry (GC-MS).

RESULTS. The immortalized Slc4a11+/+ and Slc4a11−/− mouse corneal endothelial cells (MCECs) remained proliferative through passage 49 and maintained similar active ion transport activity. As expected, proliferation was temperature sensitive and IFN-γ dependent. Slc4a11+/− MCECs exhibited decreased proliferative capacity, reduced NH3/H+ transport, altered expression of glutaminolysis enzymes similar to the Slc4a11−/− mouse, and reduced proportion of TCA cycle intermediates derived from glutamine with compensatory increases in glucose flux compared with Slc4a11+/+ MCECs.

CONCLUSIONS. This is the first report of the immortalization of MCECs. Ion transport of the immortalized endothelial cells remains active, except for NH3/H+ transporter activity in Slc4a11−/− MCECs. Furthermore, Slc4a11+/− MCECs recapitulate the glutaminolysis defects observed in Slc4a11−/− mouse corneal endothelium, providing an excellent tool to study the pathogenesis of Slc4a11 mutations associated with corneal endothelial dystrophies and to screen potential therapeutic agents.

Keywords: Slc4a11 knockout, corneal endothelium, glutamine, ammonia

SLC4A11 mutations are associated with congenital hereditary endothelial corneal dystrophy (CHED). Fuchs’ endothelial corneal dystrophy, Harboyan syndrome (CHED plus perceptive deafness), and Peters anomaly1,4 Up to 80 distinct mutations in 17 of the 19 exons of SLC4A11 have been identified in individuals with CHED,5,6,7 which is characterized at or soon after birth by bilateral diffuse corneal edema without other significant developmental abnormalities of the anterior segment.8,10 Histologically, the diffusely edematous corneal stroma accounts for the marked increase in corneal thickness observed clinically.10 In addition, CHED is associated with a uniform thickening of Descemet’s membrane and vacuolization of corneal endothelium.9,10 The Slc4a11−/− C57BL/6 mouse recapitulates the human CHED-related defects, exhibiting a similar ground-glass diffuse corneal edema, increased corneal thickness, vacuolated corneal endothelial cells, and uniformly thickened Descemet’s membrane.21,22 Furthermore, similar to human CHED,23 endothelial cell density in Slc4a11−/− C57BL/6 mice is not significantly affected at early age.22 Based on these observations, both Han et al.22 and the authors of this study concluded that this Slc4a11−/− C57BL/6 mouse can serve as a good animal model for human CHED.

Recent functional studies of SLC4A11 indicate that it is permeable to H+24–26 and can act as an NH3/H+ cotransporter.24–26 We recently demonstrated that this ammonia permeability is essential for human corneal endothelial cells, as these cells produce ammonia as a by-product of glutamine catabolism, which is required to maintain a high level of ATP production.21 Furthermore, we found that Slc4a11−/− mouse corneal endothelium has disrupted expression of enzymes involved in glutamine metabolism.21 However, only a very limited amount of corneal endothelial material can be obtained from mice, constraining further cellular, molecular, and metabolic studies.

Of neural crest origin, differentiated corneal endothelial cells are arrested in the G1 phase of the cell cycle, and studies in both mice and humans have revealed that these cells have very low proliferative potential in vivo.20 When cultured in
vitro, corneal endothelial cells manifest limited passaging ability with rapid senescence and epithelial-to-mesenchymal (EMT) transition. This limited proliferative potential makes obtaining sufficient corneal endothelial sample a significant challenge for studying the molecular mechanisms that underlie corneal physiology and the pathophysiology in corneal endothelial diseases.

To overcome these limitations, we intercrossed the Sloc4a11+/+ and Sloc4a11−/− C57BL/6 mice with H-2Kb-tsA58 Immortomouse, which carries a temperature-sensitive mutant form of the simian virus-40 large T antigen. We used the resulting progeny to generate two conditionally immortal, genetically matched mouse corneal endothelial cell lines: Sloc4a11+/+ mouse corneal endothelial cells (Sloc4a11+/+ MCEC) and Sloc4a11−/− mouse corneal endothelial cells (Sloc4a11−/− MCEC). Here we report the successful establishment of these two genetically matched wild-type and Sloc4a11 knockout MCECs. We examined proliferative properties, transport activity, and Sloc4a11-related glutaminolysis activity. The resultant cells retain key endothelial transport function and the Sloc4a11-deficient cells show altered glutamine metabolism consistent with what was observed in Sloc4a11−/− mouse corneal endothelium. Overall, the generation of these cell lines establishes a valuable tool for studying aspects of corneal endothelial diseases that require a large number of cells.

**METHODS**

**Animal Genotyping**

All mice were housed and maintained in specific pathogen-free conditions and used in the experiments in accordance with institutional guidelines and the current regulations of the National Institutes of Health, the US Department of Health and Human Services, the US Department of Agriculture, and the ARVO Statement for the Use of Animals in Ophthalmic and Vision Research.

The H-2Kb-tsA58 transgenic Immortomouse (Charles River Laboratories, Wilmington, MA, USA) was intercrossed with Sloc4a11+/+ and Sloc4a11−/− C57BL/6 mice, respectively, to generate offspring bearing the Immortomouse transgene together with Sloc4a11+/+ or Sloc4a11−/−. Sloc4a11−/− C57BL/6 mice have a targeted deletion of exons 9 to 13 of the murine Slc4a11 gene. The offspring were genotyped by PCR of genomic DNA from ear-punch sections following protocols using QIAamp DNA Mini Kit (Qiagen). Primer sequences used were the same as the primers used for mouse genotyping listed above.

**Generation of MCEC Cultures of Sloc4a11+/+ and Sloc4a11−/− Genotypes**

MCECs were prepared from 12-week-old mice. Briefly, the globes were aseptically enucleated followed by corneal dissection and corneal endothelium peeling. Then corneal endothelial sheets with attached Descemet’s membrane were placed in OptiMEM-I medium (#51985; Thermo Fisher Scientific, Canoga Park, CA, USA) supplemented with 8% heat-inactivated fetal bovine serum (FBS) (#10082139; Thermo Fisher Scientific), EGF 5 ng/mL (#01-107; Millipore, Darmstadt, Germany), pituitary extract 100 µg/mL (Hyclone Laboratories, Logan, UT, USA), calcium chloride 200 mg/L, 0.08% chondroitin sulfate (#G6737; Sigma-Aldrich Corp., St. Louis, MO, USA), gentamicin 50 µg/mL (#15710072; Thermo Fisher Scientific), antibiotic/antimycotic solution diluted 1:100 (#15240062; Thermo Fisher Scientific) and 44 units/mL IFN-γ (#485-MI; R&D Systems, Minneapolis, MN, USA). IFN-γ was used to stimulate the MHC promoter for tsTAg expression. Cells were further selected based on morphology via single-cell cloning for colonies with corneal endothelial hexagonal shape and contact inhibition. Cells were incubated at 33°C with 5% carbon dioxide.

The two lines, Sloc4a11+/+ MCEC and Sloc4a11−/− MCEC, were genotyped by PCR following protocols using QIAamp DNA Mini Kit (Qiagen). Primer sequences used were the same as the primers used for mouse genotyping listed above.

**Cell Expansion and Continuous Propagation**

MCECs were cultured at 33°C (5% CO2) or 37°C (5% CO2) in OptiMEM-I medium (51985; Thermo Fisher Scientific) supplemented with 8% heat-inactivated FBS (10082139; Thermo Fisher Scientific), EGF 5 ng/mL (01-107; Millipore), pituitary extract 100 µg/mL (Hyclone Laboratories), calcium chloride 200 mg/L, 0.08% chondroitin sulfate (G6737, Sigma-Aldrich Corp.), gentamicin 50 µg/mL (15710072; Thermo Fisher Scientific), antibiotic/antimycotic solution diluted 1:100 (15240062; Thermo Fisher Scientific) and with or without 44 units/mL IFN-γ (485-MI; R&D Systems). Culture at 33°C with IFN-γ is defined as permissive growth condition, whereas culture at 37°C without IFN-γ is defined as nonpermissive growth condition.

**Light Microscopy**

Cell morphology images were acquired with an Infinity 1 camera (Lumenera Corp., Ottawa, ON, Canada) attached to an inverted phase-contrast microscope.

**Growth Curve and Doubling Time**

MCEC cells were seeded at 5 × 103 or 1 × 104 cells/well (total 2500 cells/well or 5000 cells/well) in 24-well plates. Cells in four wells of 24-well plates were trypsinized to suspension and counted with a Cellometer Auto T4 (Nexcelom Bioscience, Lawrence, MA, USA). Doubling time was calculated using GraphPad Prism 6.1c (GraphPad Software, Inc., La Jolla, CA, USA).

**Western Blot of SV40 Large T Antigen**

MCECs were seeded at 5 × 104/mL (total 1 × 105 cells/well) in six 35-mm dishes and cultured with IFN-γ at 33°C to subconfluence. While one dish was subject to protein extraction as the sample for the permissive condition, the remaining five dishes were switched to 37°C without IFN-γ for the subsequent nonpermissive culture. In the following 5 days, one dish was subjected to protein extraction on each day (24, 48, 72, 96, and 120 hours) in the nonpermissive condition. Cells in each dish were washed two times with ice-cold PBS and suspended in 100 µL RIPA buffer (50 mM Tris base, 150 mM NaCl, 0.5% deoxycholic acid-sodium salt, 2% SDS, and 1% NP40, pH 7.5) with Complete Protease Inhibitor Cocktail
TABLE 1. Composition of Extracellular Solutions, mM

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<tr>
<th>mM</th>
<th>Base</th>
<th>BR Lac</th>
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<td>Glucose</td>
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(#4693159001; Roche Diagnostics, Indianapolis, IN, USA). Then the sample was sonicated and centrifuged for 20 minutes at 12000g at 4°C. Cell lysate samples (15 μL) were mixed with Protein Loading Buffer Blue (2X) (EC-886, National Diagnostics, Atlanta, GA, USA) and a total volume of 30 μL was resolved on 1.5-mm-thick 10% SDS-polyacrylamide gels and wet-transferred to polyvinylidene difluoride membranes (Bio-Rad, Hercules, CA, USA). Membranes were blocked with 5% nonfat milk in TBST (25 mM Tris base, 137 mM NaCl, 0.1% Tween20) and probed with primary antibodies in the same buffer overnight at 4°C. The following primary antibodies were used: rabbit anti-SV40 T Ag 1:5000 (sc-20800; Santa Cruz Biotechnology, Dallas, TX, USA); and anti-glyceraldehyde 3-phosphate dehydrogenase antibody 1:1000 (sc-52233; Santa Cruz Biotechnology). Next, membranes were probed with secondary antibody (goat anti-rabbit IgG peroxidase-conjugated antibody, #A0545, or goat anti-mouse IgG peroxidase-conjugated antibody, #A924; Sigma-Aldrich Corp.) for an hour at room temperature. Bound secondary antibodies were detected using an enhanced chemiluminescence assay (Supersignal West Pico, #34080; Thermo Fisher Scientific). Band densities with an enhanced chemiluminescence assay (Supersignal West Pico, #34080; Thermo Fisher Scientific) were quantified using ImageJ (http://imagej.nih.gov/ij/; provided in the public domain by the National Institutes of Health, Bethesda, MD, USA).

TABLE 2. Murine Gene Primers

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<th>Sequence (5' – 3')</th>
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<td>Phosphate-dependent glutaminase 1 (Gls1, kidney)</td>
<td>AGACTGTCGACACAGAAATCTTCAGACGAGATGAGCCAGTGCTG</td>
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<td>mGls2 NM_001033264.3</td>
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<td>AATAGGACACCAAGAGCTTGCAGTG</td>
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<td>Glutamate dehydrogenase (Gdh)</td>
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<tr>
<td>mACTB NM_007393.3</td>
<td>Beta-actin (Actb)</td>
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<td>SLC9A6; NHE1, Sodium Hydrogen Exchanger 1</td>
<td>CTTGTGATGACCCAGCTCCAGAG</td>
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<td>Na-K-adenosine triphosphatase</td>
<td>CATTGACAGAGATGCATTCAGCAGTCC</td>
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Intracellular pH (pHᵢ) Measurement

pHᵢ measurements were performed as described previously.² Briefly, MCECs were cultured on poly-L-lysine and fibronectin precoated 25-mm diameter glass coverslips (GG-25-pd; Neuvitro Corporation, Vancouver, WA, USA) for 2 to 3 days in semipermissive condition. Before each experiment, cells were incubated with 10 μM of pH-sensitive fluorescent dye BCEOFC-AM (2'7'-bis(carboxyethyl)-5(6)-carboxylfluorescein-acetoxy-methyl ester, B1170; Thermo Fisher Scientific) in Ringer’s solution for 30 minutes at room temperature, and washed in dye-free Ringer’s solution for another 30 minutes. The Ringer’s solution constitution is listed in Table 1. All of the experimental solutions were equilibrated with air (or 5% CO₂ for bicarbonate-rich [BR] solutions) and adjusted to pH 7.5 with 1N NaOH at 37°C. Osmolarity of all solutions was adjusted to 295 to 300 mOsm with mannitol. Coverslips with subconfluent cells were mounted into a perfusion chamber, and the chamber was then placed on a stage warmer (37°C) of an inverted microscope (Eclipse TE200; Nikon, Tokyo, Japan). Solutions were kept at 37°C in a warming box, and the flow of the perfusate (~0.5 mL/min) was achieved by gravity. Cells were imaged with an oil-immersion objective (×40; Nikon). BCECF fluorescence was excited alternately at 495 ± 10 nm and 440 ± 10 nm, and the emitted light was collected through a bandpass filter (520–550 nm). Fluorescence ratios (495/440) were obtained at 1 Hz, and converted into pHᵢ using the high K⁺/nigericin calibration approach.³³

RNA Extraction, RT-PCR, and Real-Time Quantitative PCR

Total RNA from the MCEC cell lines (cultured in 33°C, IFN-γ [+]) was extracted and purified using the RNeasy mini kit (#74104; Qiagen) with DNase digestion (#79254; Qiagen). Complementary DNA was generated with a High Capacity RNA-to-cDNA Kit (Applied Biosystems, Foster City, CA, USA) at 10 ng RNA/μL reverse transcription reaction concentration. Real-time quantitative PCR reactions were set up in triplicate using PowerUp SYBR Green Master Mix (A25741; Thermo Fisher Scientific). Reactions were performed with murine gene primers listed in Table 2. A 2⁻ΔΔCt experimental design was used for relative quantification and normalized to mouse ACTB (β-actin) for differential expression levels of target genes.
Metabolites Extraction and Gas Chromatography Mass Spectrometry (GC-MS) Measurements

Slc4a11+/+ and Slc4a11−/− MCEC in 8% FBS OptiMEM-I in T75 flasks seeded at 5×10^4/mL (total 2.5×10^5 cells) were grown to confluence for 4 days at 33°C with IFN-γ then switched to serum-free OptiMEM-I supplemented with 200 mg/L CaCl2 and 0.08% chondroitin sulfate for 12 hours. Then the cells were incubated with serum-free Dulbecco’s modified Eagle’s medium (DMEM) conditional medium with 2.5 g/L U^{13}C_{6}-D-glucose (CLM-1396-0; Cambridge Isotope Laboratories, Tewksbury, MA, USA) + 4 mM L-glutamine and incubated for 12 hours. Serum-free DMEM conditional medium was made using DMEM (glucose-free, glutamine-free, pyruvate-free, Gibco #A1443001; Thermo Fisher Scientific) supplemented with CaCl2 200 mg/L, 0.08% chondroitin sulfate (Sigma-Aldrich Corp.), and the isotope-labeled glucose and nonlabeled glutamine (Sigma-Aldrich Corp.). After 12-hour incubation, isotope-labeled cells were washed three times with ice-cold 0.9% NaCl, quenched with 2 mL ice-cold 100% methanol, scraped off the plate and removed together with 2 mL quenching methanol into centrifuge tubes, vortexed thoroughly, and centrifuged at 8000g for 2 minutes. Supernatants were collected and the cell pellet was resuspended with 900 μL 90% methanol twice following vortex and centrifugation. Total supernatant was kept stationary at −20°C for 1 hour, then centrifuged at 15,000g for 5 minutes at 4°C. The supernatant was collected to new tubes and dried in a centrifugal evaporator at room temperature overnight. The level of each metabolite isotopologue was measured using GC-MS as reported previously.34 The fraction of each isotopologue and the contribution of ^13C to the total carbon pool of each metabolite was calculated as previously reported.35 Briefly, the isotopologue distributions were corrected based on the natural abundance of elements, and the fraction is the contribution of each isotopologue to the total abundance of all the isotopologues. The contribution of ^13C to the total carbon pool of each metabolite is the weighted average of all the labeled isotopologues according to the fraction distribution.

Statistical Analysis

Statistical analysis was carried out using GraphPad Prime 6.0c (GraphPad Software, Inc., La Jolla, CA, USA). Student’s t-test or paired t-test were used for two-group comparison. Two-way ANOVA was used for metabolite data.

RESULTS

Conditional Immortal Slc4a11+/+ MCEC and Slc4a11−/− MCEC Growth Characteristics

The genotypes of both the mice used for cell expansion (Fig. 1A, left panel) and of the derived MCECs (Fig. 1A, right panel). Slc4a11+/+ MCECs, and Slc4a11−/− MCECs, were determined by PCR analysis of mouse or cell line genomic DNA. For the mice used, Slc4a11 wild-type alleles are present in Slc4a11+/+ mice (left two lanes) and in Slc4a11−/− mice (right two lanes), whereas Slc4a11 knockout alleles are present in Slc4a11−/− mice (middle two lanes) and in Slc4a11+/+ mice. For Immorto (tsTag) gene, all of the mice we used carry only one allele of the gene, and the other allele is detected as a null allele. We selected Slc4a11+/+ Immorto+/+ mice and Slc4a11−/− Immorto−/− mice for cell expansion. Genotypes of derived cell lines were confirmed by PCR of the cell line genomic DNA for Slc4a11 and Immorto (tsTag) genes (Fig. 1A, right panel). Verification of Slc4a11 mRNA expression in the cell lines was carried out by RT-PCR showing only Slc4a11+/+ but not Slc4a11−/− MCEC expresses Slc4a11 mRNA (Fig. 1B).

Next, we examined the cell morphology and growth doubling time of Slc4a11+/+ MCECs and Slc4a11−/− MCECs. The two cell lines remained proliferative to passage 49 and are still propagating. We noticed a fibroblastic-like cell morphology in Slc4a11+/+ MCECs cultured under permissive conditions (IFN-γ +, 33°C), in which the cells are elongated and lacking contact inhibition at high density. However, Slc4a11−/− MCECs had a more hexagonal shape closely resembling corneal endothelial primary culture and form a monolayer when confluent in the same IFN-γ (+) medium (Fig. 1C). We asked if IFN-γ stimulated SV40 large T antigen (tsTag) expression changes the MCEC morphology, so IFN-γ was removed, but the cells were kept at 33°C to see if the morphology was affected in Slc4a11−/− MCECs. We define this 33°C IFN-γ (−) culture condition as “semipermissive.” Indeed, in the semipermissive condition, Slc4a11−/− MCECs presented with a more hexagonal shape and cell monolayer was formed once confluent (Fig. 1C). In contrast, Slc4a11−/− MCEC morphology in semiper-
Disrupted Glutaminolysis in Slc4a11−/− Mice

SLC9A6; NHE1, Sodium Hydrogen Exchanger 1), Na+/HCO3− cotransporter (SLC4A4; NBCe1, Sodium Bicarbonate Cotransporter electrogenic), H+/Lactate− cotransporters (SLC16A1; MCT1, Mono-Carboxylate Transporter 1; and SLC16A3; MCT4, Mono-Carboxylate Transporter 4) (Fig. 3A). Similarly, BCEF-based continuous pH monitoring of apparent proton fluxes indicate the activity of bicarbonate transporters (Fig. 3B), Na+/H+ exchangers (Fig. 3C), and lactate transporters (Fig. 3D) are present and comparable between the Slc4a11−/− and Scl4a11+/+ MCECs (see below).

Sodium Bicarbonate Cotransporter: In Figure 3B left panel, cells were initially perfused with bicarbonate-free (BF) Ringer’s and then changed to BR ([HCO3−] 28.5 mM) Ringer’s. Due to simple diffusion of dissolved CO2 inward across the plasma membrane, the cell rapidly acidifies as CO2 reacts with intracellular H2O to form H2CO3 and further release one H+.
as a weak acid. Then pH slowly rises, which indicates the Na-/HCO₃⁻ cotransporters are moving weak base HCO₃⁻ inward using Na⁺ inward transmembrane electrochemical gradient. We determined the initial slope of this pH rise as an indirect measure of the apparent Na⁺/HCO₃⁻ cotransport activity. This assay revealed no significant difference between Slc4a11⁻/⁻ and Slc4a11⁺/⁺ MCECs in apparent bicarbonate transporter activity (Fig. 3B, Student’s t-test, P = 0.48, n = 3 in each group). The overshoot after CO₂/HCO₃⁻ removal is an additional indication that there was HCO₃⁻ accumulation inside the cell during BR perfusion.

Na⁺/H⁺ exchanger: In Figure 3C left panel, cells were initially perfused with BF Ringer’s and then switched to BF Ringer’s containing 28.5 mM Na-Aacetate. Once dissolved in solution, a small fraction of Na-Aacetate becomes noncharged acetic acid that readily diffuses across the membrane and rapidly acidifies the cell cytosol. Then pH recuperates due to the activity of Na⁺/H⁺ exchangers and Slc4a11 proton permeability.\(^2^{5}\) Here, we measured the initial slope of this pH recovery as an indirect measure of the apparent Na⁺/H⁺ exchanger activity, revealing that there is a borderline significant difference between Slc4a11⁺/⁺ and Slc4a11⁻/⁻ MCECs (Fig. 3C, paired t-test, 2-tailed P = 0.10, 1-tailed P = 0.05, n = 5 in each group) that can be attributed to Slc4a11 proton permeability.\(^2^{5}\)

H⁺-lactate cotransporter: Because we recently demonstrated that lactate transport is a significant component of the corneal endothelial pump,\(^3^{6}\) we next examined the lactate-dependent H⁺ fluxes in MCECs. Cells were initially perfused with BR Ringer’s, and where indicated (horizontal bars), 20 mM lactate (dissolved in BR Ringer’s, pH 7.4) was applied twice for 60 seconds (Fig. 3D, upper panel). The cells were then switched to perfusion with BF Ringer’s and again 20 mM lactate (dissolved in BR Ringer’s, pH 7.4) was applied twice for 60 seconds. Lactate exposure (pH 7.4) induces intracellular acidification due to the activity of H⁺-lactate cotransporters (Mono-Carboxylate Transporters, MCTs),\(^3^{7}\) in which the lactate transmembrane inward gradient favors the inward movement of lactate and H⁺ together causing intracellular H⁺ accumulation. The acidification is less prominent in BR than in BF Ringer’s because HCO₃⁻/CO₂⁻ offers extra H⁺ buffering power. We measured the initial slope of the induced acidification on lactate perfusion as an indirect measure of the apparent H⁺-lactate cotransporter activity. Figure 3D lower panel shows there was no significant difference between Slc4a11⁺/⁺ and Slc4a11⁻/⁻ MCECs in both BR and BF Ringer’s (t-test, in BR P = 0.25, in BF P = 0.35, n = 5 in each group).

**Slc4a11 NH₃/H⁺ Flux Is Intact in Slc4a11⁻/⁻ MCECs But Impaired in Slc4a11⁺/⁺ MCECs.** We recently reported that human SLC4A11 mediates electrogentic transmembrane NH₃/H⁺ fluxes,\(^2^{7}\) and this result has been verified by two other independent groups.\(^2^{5,2^{6}}\) Furthermore, a recent report from a third group shows murine Slc4a11 mediates similar electrogenic transmembrane NH₃/H⁺ fluxes.\(^2^{4}\) So we next set out to determine if the Slc4a11-mediated NH₃/H⁺ flux is impaired in Slc4a11⁻/⁻ MCECs (Fig. 4A). Cells were initially incubated with BF Ringer’s, pulsed with 10 mM NH₃Cl in BF Ringer’s, and then switched back to BF Ringer’s. Once dissolved in solution, a small fraction of NH₃Cl forms NH₃, a small noncharged molecule that is readily membrane diffusible. On entry, NH₃ instantaneously reacts with intracellular H₂O to form NH₄⁺ and releases OH⁻. The latter rapidly alkalizes the cell, causing the initial rapid alkalining phase (100–120 seconds) on NH₃Cl application. Eventually the cell will reach an equilibrium where intracellular [NH₃] equals extracellular [NH₃]. Then a slow acidification occurs in the midphase (120–400 seconds) of the NH₃Cl pulse, indicating there is an additional weak acid NH₄⁺ (or NH₃H⁺ equivalently) flux entering the cell.\(^3^{8}\) In this case, Slc4a11 activity brings more NH₄⁺ into the cell. Figure 4B shows that the rate of this slow acidification is significantly faster in Slc4a11⁺/⁺ MCECs compared with Slc4a11⁻/⁻ MCECs, consistent with the additional NH₄⁺ influx provided by Slc4a11. Then, when the NH₃Cl was washed away by BF Ringer’s, there is a pronounced and rapid acidification on NH₃Cl removal (400–440 seconds) (Fig. 4B). This is due to the rapid exit of NH₃ gas and the conversion of accumulated NH₄⁺ to NH₃ + H⁺. The rapid acid loading immediately after NH₃Cl removal is a reflection of the amount of weak acid (NH₄⁺ or NH₃H⁺) that has entered the cell during the NH₃Cl pulse.\(^3^{8}\) And even though NH₃Cl was removed in this phase on the outside, there is NH₄⁺ temporarily trapped intracellularly.\(^3^{8}\) The amount of NH₄⁺ trapped is directly correlated with the extent of the acidification according to the Henderson-Hasselbalch equation.\(^3^{8}\) Figure 4A shows that the depth of this acid load is much greater in Slc4a11⁻/⁻ MCECs. The pH recovery (440–520 seconds) from this acid load is a phenomenon of the collective effect from Slc4a11-mediated NH₃/H⁺ efflux and Na⁺/H⁺ exchanger-mediated H⁺ extrusion. We measured the initial rate of pH recovery as a measure of apparent NH₄⁺/H⁺ efflux, which is significantly slower in Slc4a11⁻/⁻ MCECs (Fig. 4B). To more accurately represent the Slc4a11-mediated NH₃/H⁺ efflux, we performed further analysis by subtracting the Na⁺/H⁺ exchanger-mediated apparent pH recovery (Fig. 5C), to obtain the adjusted NH₃/H⁺ efflux. The average of apparent Na⁺/H⁺ exchanger activity (0.0041/s) between Slc4a11⁺/⁺ and Slc4a11⁻/⁻ MCECs was used given there was no statistical significance between the two cell lines. Figure 4C shows that the adjusted NH₃/H⁺ efflux is 0.0041 ± 0.0015/s (n = 5) in Slc4a11⁻/⁻ MCECs, and significantly smaller 0.0005 ± 0.0003/s (n = 5, P = 0.0547) in Slc4a11⁺/⁺ MCECs.
Impaired Glutaminolysis Is Present in Slc4a11<sup>−/−</sup> MCECs as Seen in Slc4a11<sup>−/−</sup> CHED Mouse Model

Many of the enzymes involved in glutamine metabolism exhibit an aberrant expression pattern in Slc4a11<sup>−/−</sup> mouse corneal endothelium, although the kidney-type glutaminase 1 (Gls1) is upregulated 3-fold in Slc4a11<sup>−/−</sup> mouse corneal endothelium, the liver-type glutaminase 2 (Gls2) can no longer be detected in these cells. Therefore, we set out to determine if the Slc4a11<sup>−/−</sup> MCEC recapitulates this expression difference and manifests as functional differences in glutamine metabolism. Consistent with the observation in mouse corneal endothelial tissue in vivo, we observed an upregulation of Gls1, and a downregulation of Gls2 mRNA expression in Slc4a11<sup>−/−</sup> MCECs (Fig. 5A). These changes in gene expression were also evident at the level of metabolic flux. Our previous studies demonstrated that glutamine supplies approximately 50% of TCA cycle carbon chains in human corneal endothelium. Consistent with this earlier observation, we find that 50% of citrate and approximately 35% of a-ketoglutarate (a-KG), fumarate, and malate carbon chains were labeled with U-<sup>13</sup>C-glucose-sourced carbon in Slc4a11<sup>+/+</sup> MCECs in the presence of unlabeled glutamine (Fig. 5C). Figure 5B shows the schematic of TCA cycle intermediates analyzed, where <sup>13</sup>C isotope-labeled green in the setting where cells were cultured with U-<sup>13</sup>C-glucose and unlabeled glutamine. In contrast to wild type, Slc4a11<sup>−/−</sup> MCECs exhibit a significantly increase in the percentage of TCA cycle intermediates that contain carbons derived from U-<sup>13</sup>C-glucose, with approximately 75% of citrate and approximately 50% of a-KG, fumarate, and malate carbon chains being labeled with U-<sup>13</sup>C-glucose-sourced carbon. These results indicate that the contribution of glutamine to the TCA cycle is decreased in Slc4a11<sup>−/−</sup> MCECs relative to Slc4a11<sup>+/+</sup> MCECs and support our previous observation that SLC4a11 is essential for facilitating glutaminolysis.

DISCUSSION

Here we report the generation of the first immortalized MCECs. The use of H-2K<sup>b</sup>-tsA58 transgenic Immortomouse not only circumvents the limitations and uncertainties associated with in vitro transfection-based immortalization (e.g., initial requirement of large number of cells, different sites of gene integration, multiple copy numbers), but also allows for the production of genetically matched cell lines directly from a transgenic mouse model: Slc4a11<sup>+/−</sup> MCECs and Slc4a11<sup>−/−</sup> MCECs. The conditional immortalization approach provided another advantage that the expression of SV40 large T antigen can be eliminated by simple temperature maneuver and/or removal of IFN-γ. We found that the SV40 large T antigen declined and could be virtually eliminated (Fig. 2B) in the semipermissive condition (IFN-γ [+], 35°C). This condition was preferred because it allowed repeated expansion of MCECs, avoided large cell losses, yet retained endothelial morphology and transport function.

Analysis of ion transporter activity in the two lines of MCECs show that apparent bicarbonate transport, Na<sup>+</sup>/H<sup>+</sup> exchanger, and lactate transport activities were not significantly changed by Slc4a11 knockout (Fig. 3). As expected, Slc4a11<sup>+/−</sup> MCECs showed significantly less NH<sub>3</sub>/H<sub>2</sub>O flux relative to Slc4a11<sup>+/+</sup> MCECs (Fig. 4), consistent with the known NH<sub>3</sub>/H<sub>2</sub>O permeability provided by SLC4A11. The impaired ability to facilitate NH<sub>3</sub>/H<sub>2</sub>O transport in Slc4a11<sup>−/−</sup> MCECs is likely the cause of observed changes in glutamine metabolism. Ammonia was reported to inhibit both the N-ethylmaleimide-sensitive and -insensitive fraction of...
glutaminase.39,40 In Slc4a11−/− MCECs, expression changes of glutaminolysis enzymes is consistent with our observation in Slc4a11−/− CHED mouse corneal endothelium tissue.39 Further analysis of TCA cycle intermediates in Slc4a11−/− MCECs indicated that 50% of citrate and approximately 35% of other TCA cycle intermediates were derived from glucose, which is similar to what was found in an immortalized human corneal endothelial cell line.41 However, in Slc4a11−/− MCECs, we found a significantly increased fraction from glucose-sourced TCA cycle intermediates were derived from glucose, which is consistent with the finding that glutaminase enzyme expression via p53 phosphorylation, which is consistent with the finding that glutaminase GLS2 expression changes of Glis1 found in the Slc4a11−/− MCECs (Fig. 5A) may be a compensatory response to glutaminase inhibition.

Interestingly, both human SLC4A11 and murine Slc4a11 genes were reported to be a target of p53,33 a main cell metabolism regulator.34 Conversely, knock-down of Slc4a11 in bovine nucleus pulposus cells inhibits p53 activity by abolishing p53 phosphorylation.44 This suggests that the SLC4A11 transporter could indirectly regulate glutaminolysis enzyme expression via p53 phosphorylation, which is consistent with the finding that glutaminase GLS2 is a target of p53.44

Additionally, we observed fibroblast-like morphology changes only in Slc4a11−/− MCECs when tsTAg was induced by IFN-γ (Fig. 1C). Given the direct inhibition from tsTAg on Rb and p53 protein,45 it will be of interest to study if the Slc4a11 transporter plays a role in corneal endothelial cell proliferation, polarity formation, and EMT transformation.

In summary, we successfully established two genetically matched conditionally immortal MCECs: Slc4a11+/− MCECs and Slc4a11−/− MCECs. These cells remain proliferative with reasonable endothelial morphology after prolonged culture, and present key active ion transport activities as expected from corneal endothelial cells. Slc4a11+/− MCECs recapitulate glutaminolysis enzyme expression changes as seen in Slc4a11−/− mouse corneal endothelial tissue. These cell lines allowed us to carry out further investigations using cellular-based approaches requiring a significantly larger sample volume than mouse tissue can achieve. Further analysis of TCA cycle intermediates suggests functionally impaired glutaminolysis in Slc4a11−/− MCECs. These Slc4a11+/− MCEC and Slc4a11−/− MCEC cell lines provide an excellent tool for future cell-based experiments to study the pathophysiological changes resulting from loss of Slc4a11 function and for potential therapeutic pharmaceutical reagent screening.

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References


Disrupted Glutaminolysis in Slc4a11−/− Mice


