Keratan sulfate (KS) is an extracellular matrix (ECM) glycosaminoglycan (GAG) present in a host of tissues in many organisms spanning the animal kingdom. Its exact structure varies depending on the organism and tissue in which it is found (see Funderburgh 2002 for comprehensive review). The highest abundance of KS in the body is found in the cornea, where KS-GAGs covalently associate to core proteins, lumican, keratocan, or mimecan via an O-linkage to serine (Ser) or threonine (Thr) residues.

The linkage region of corneal KS-GAGs is comprised of two N-acetylgalactosamine (GlcNAc) residues, the innermost of which is fucosylated at its sixth carbon (C6). 1-3 Three mannose residues divide the molecule into its bi-antennary structure, from which its short and long arms extend (shown in Fig. 1). Both short and long arms contain GlcNAc and galactose residues linked in -3Galβ1-4GlcNAcβ1- conformation, also known as poly-N-acetyllactosamine. 7 The long arm of KS contains three regions of repeating disaccharides, distinguished by their degree of sulfation. The unsulfated region does not contain sulfate modification on GlcNAc or galactose and is one to two disaccharides long. The monosulfated region, however, is 10 to 12 disaccharides in length and carries sulfate groups at the C6 of GlcNAc residues. Sulfate moieties bind GlcNAc and, less frequently, galactose within the disulfated region of corneal KS-GAGs. The disulfated region varies in length and often terminates with a sialic acid capping structure. 2,4 The short arm of KS-GAGs lacks the mono- and disulfated regions described in KS-GAGs. The disulfated region varies in length and often terminates with a sialic acid capping structure.
above and instead terminates with sialic acid following one to two unsulfated disaccharide repeats. The frequent substitution of sulfate groups along their carbohydrate backbones confers upon KS-GAGs their dense negative charge, and, in turn, their hydrophilicity.

Importantly, the sulfation status of KS can impact on tissue function; a prime example is where a disturbed KS sulfation pathway leads to progressive loss of vision as in the inherited disease macular corneal dystrophy. The causative gene is CHST6, which encodes corneal GlcNAc 6-O-sulfotransferase (CGn6ST). Consequences of the abnormally sulfated PG population include altered collagen architecture within the cornea and stromal opacifications, which can only be treated by a corneal graft. Structural matrix changes mimicking those seen in human corneas with macular corneal dystrophy have also been documented in mouse corneas lacking Chst5, which is the murine orthologue of the human CGn6ST-encoding gene.

The apparent importance for properly formed KS has sparked recent interest in elucidating the biosynthetic mechanism that elongates and sulfates KS-GAGs. It is thought that at least four enzymes, including two glycosyltransferases and two sulfotransferases, are required for KS biosynthesis. A number of studies have posited that highly sulfated KS-GAGs are formed by addition of GlcNAc via β-1,3-N-acetylgalactosaminyltransferase 7 (β3GnT7), encoded by B3gnt7) to the nonreducing terminus of the growing KS chain. It is thought that CGn6ST (described above) subsequently sulfates the 6-O position of GlcNAc prior to galactosylation by β-1,4-galactosyltransferase 4 (β4GalT4, encoded by B4galnt4). It is hypothesized that these three steps repeat, forming a chain of disaccharides singly sulfated on GlcNAc residues. It has been suggested that galactose sulfation is achieved in a separate step, since the terminal, galactose residues. Our results suggest that without the ability to elongate KS chains via addition of GlcNAc residues at their non-reducing termini, the normal corneal stromal KS-PG phenotype is abolished.

**Methods**

**Knockout Mouse Production**

Knockout vector for B3gnt7 was prepared by recombineering technique. Bacterial artificial chromosome (BAC) clones (RP24-231G17 and RP24_144F16), which included B3gnt7, were obtained from BACpac resources (Children’s Hospital Oakland Research Institute, Oakland, CA, USA). Because most of the protein coding sequence is encoded on exon 2 of the gene, the loxP sequence was inserted before and after exon 2. A neo cassette, which consists of flippase recombinase target (FRT)-phosphoglycerate kinase promoter (PGK)-neomycin resistant gene (neo)-FRT was also inserted downstream of exon 2. The DNA fragment containing modified B3gnt7 was retrieved to pBSII-DTA vector and used as a knockout vector. This vector was introduced into RENKA mouse embryonic stem (ES) cells, which were derived from C57BL/6 strain by electroproporation. Resultant homologous recombinant clones were isolated after G418 selection. Homologous recombination occurred on the ES clones and was confirmed by Southern blot analysis. The confirmed ES cells were then used to create chimeric mice carrying ES-derived germ cells. The chimeric mice were mated with C57BL/6j mice to obtain B3gnt7 heterozygous mice, and the heterozygote mice were intercrossed to produce wild-type (WT; B3gnt7“+/-”), heterozygous (“+/-”), and null (“-/-”) mice. B3gnt7 heterozygous mice were also mated to C57BL/6j mice to maintain the strain. All procedures were approved by the Committee for Animal Experiments at Kansai Medical University, conducted according to the Guideline for Animal Experimentation at Kansai Medical University, and treated in accordance with the ARVO Statement for the Use of Animals in Ophthalmic and Vision Research.

**Corneal Thickness Assay**

Excised eyes of 32 mice (12- to 16-week-old mice of both sexes, 5 WT, 10 htz, and 17 null) were embedded in Tissue-Tek OCT compound (Sakura Finetek, Tokyo, Japan) and immediately frozen by dry ice. Axial whole eye sections (4 μm) were taken using Kawamoto’s film method. It was inferred that the sections were central and suitable for analysis when pupil...
diameter was at its maximum and the optic nerve was present in the section. Unstained central corneal sections were then directly observed using phase-contrast mode of an All-in-One Microscope BZ-9000 (Keyence, Osaka, Japan). Thickness of the central cornea, stroma, and epithelium was analyzed using a measurement module of the microscope, which quantifies distance between two parallel lines. A mean value of each section was calculated from three measurements per section. Statistical analysis of thicknesses was performed by 1-way ANOVA with Dunnett’s post hoc test. P < 0.03 compared with WT was considered significant.

Western Blot
Protein Extraction. Ten corneas from each group were minced manually using a scalpel and placed in extraction solution containing 4 M guanidine hydrochloride (Gu-HCl); 50 mM Trisydrochloride (Tris/HCl), pH 8.0; 10 mM EDTA; 1 mM PMSF; and 1× protease inhibitor cocktail (Nacalai Tesque, Kyoto, Japan). The protease inhibitor cocktail was diluted from a 100× stock, comprised of 50 mmol/L 4-(2-aminophethyl) benzenesulfonyl fluoride hydrochloride (AEBSF), 15 μmol/L aprotinin, 100 μmol/L E-64, and 100 μmol/L leupeptin hemisulfate monohydrate. Corneal tissue was physically pulverized using a benchtop homogenizer (Polytron 1600 E with PT-DA 1605 blade; Kinematica AG, Luzern, Switzerland) and then incubated 48 hours with rotation at 4°C in extraction solution (above). Following extraction, samples were centrifuged to separate debris in the pellet from extracted protein in the supernatant solution; the supernatant was then dialyzed in 1 L 6 M urea with 50 mM Tris/HCl (pH 8.0). The dialysis solution was refreshed at 4 hours of incubation, after which dialysis was continued overnight at 4°C with agitation. Resultant protein solutions were again centrifuged to remove debris and then concentrated by centrifugation in centrifugal filter units (Amicon Ultra-4, pore size: 30 kDa; Merck Millipore, Cork, Ireland) at 4°C and 2330g. Protein concentration of each extract was determined using the Pierce BCA Protein Assay kit (Pierce Biotechnology, Rockford, IL, USA) after dilution of the extract was determined using the Pierce BCA Protein Assay kit before PNGase-F digestion. PNGase-F treatment was performed by following the protocol of the company (New England Biolabs, Ipswich, MA, USA). In brief, a volume equaling 5 μg resuspended protein was denatured at 100°C for 10 minutes in manufacturer-provided glycoprotein denaturing buffer. Manufacturer-provided reaction buffer and NP-40 solution, which allows PNGase F activity in the presence of SDS, were added to denatured samples. Digestion was achieved by addition of 1 μL PNGase F (100 U/μg protein) at 37°C overnight. Digested samples were directly analyzed using SDS-PAGE and Western blot.

Endo-β-Galactosidase Digestion. To gain insight into the KS structure of htz and null corneas, endo-β-galase was used. Five micrometers corneal extract was precipitated from the extraction solution (see Protein Extraction section) with methanol/chloroform as described in the PNGase F Digestion section and resuspended in 1% SDS. Resuspended solution was diluted and adjusted to 100 μL 50 mM sodium acetate, pH 6.5, 0.1% Triton X-100, and 1× protease inhibitor cocktail. Then, 0.5 milliliters of endo-β-galase was added (0.1 mL/μg protein) and allowed to incubate overnight at 37°C with rotation. The protein samples were subsequently precipitated with methanol/chloroform as described above and were resuspended in electrophoresis sample buffer, described in the next section.

Electrophoresis. Five micrograms protein was prepared for Western blotting from untreated, PNGase F- and endo-β-galase-digested samples. Samples were adjusted to 60 μL containing 1× NuPAGE LDS sample buffer and 1× reducing agent (Thermo Fisher Scientific, Rockford, IL, USA) and were denatured by boiling and then loaded into a 4% to 12% Bis-Tris polyacrylamide gel (Thermo Fisher Scientific). Constant voltage (200 V) was applied for 45 minutes or until samples reached the bottom of the gel. Immediately after electrophoresis, protein samples within the acrylamide gel were transferred to a PVDF membrane by electroblotting at 30 V for 1 hour. Blocking the protein-laden membrane was achieved at room temperature using 5% skimmed milk for 1.5 hours. Goat polyclonal anti-lumican primary antibody (R&D Systems, Minneapolis, MN, USA) was diluted 1:1000 in 5% skimmed milk and applied to the membrane for 1 hour. PBS with 0.1% Tween-20 (PBS-T) was used to rinse excess antibody from the membrane (3×, 5 minutes each). Horseradish peroxidase-conjugated secondary antibody (Santa Cruz Biotechnology, Santa Cruz, CA, USA), which recognized goat IgG, was diluted 1:2000 in 5% skimmed milk and applied to the membrane surface for 1 hour. To develop the membranes, Chemi-Lumi One chemiluminescence substrate (Nacalai Tesque) was applied to the membrane for 2 minutes. Chemiluminescent images were captured using LAS 3000 Mini camera and software (Fuji Photo Film, Tokyo, Japan) using 1 to 10 minutes of exposure, depending on the amount of signal produced by the membrane.

Electron Microscopy
Whole corneas from WT, htz, and null mice were excised and immediately prefixed in 4% paraformaldehyde in 0.1 M Sorensen phosphate buffer (pH: 7.4) for 10 minutes. After initial fixation, excess prefixative was rinsed with 1× Tris-acetate buffer, and whole corneas were further dissected into quarters. “Untreated” (i.e., not subjected to chondroitinase ABC or buffer reaction conditions) corneal quarters were immediately placed into 2.5% (w/v) glutaraldehyde (Agar Scientific Ltd., Stansted, United Kingdom) in 25 mM sodium acetate buffer (pH 5.7) with 0.05% cupromeronic blue (w/v) (Sigma, St. Louis, MO, USA) and magnesium chloride (MgCl2) at critical electrolyte concentration, 0.1 M—a concentration measured again using the Pierce BCA Protein Assay Kit before PNGase-F digestion. PNGase-F treatment was performed by following the protocol of the company (New England Biolabs, Ipswich, MA, USA). In brief, a volume equaling 5 μg resuspended protein was denatured at 100°C for 10 minutes in manufacturer-provided glycoprotein denaturing buffer. Manufacturer-provided reaction buffer and NP-40 solution, which allows PNGase F activity in the presence of SDS, were added to denatured samples. Digestion was achieved by addition of 1 μL PNGase F (100 U/μg protein) at 37°C overnight. Digested samples were directly analyzed using SDS-PAGE and Western blot.
known to enhance PG staining. To allow for KS visualization, remaining corneal quarters from each genotype were digested with chondroitinase ABC for 4 hours at 37°C in the following reaction mixture: 1 µg/mL chondroitinase ABC was added to 1X Tris-acetate buffer + bovine serum albumin (pH 8), including 10 µg/mL general protease inhibitor. Samples were subjected to constant agitation for the duration of the reaction. Following incubation, specimens were rinsed in 25 mM sodium acetate buffer containing 0.1 M MgCl₂ and further fixed/stained overnight at room temperature on a rotator in the cupromeronic blue solution described above. One corneal quarter from each group was also processed in buffer solution lacking chondroitinase ABC as a control. Fixed and stained specimens (untreated, chondroitinase ABC digested, and buffer treated) were washed three times (10 min/wash) in 0.5% (w/v) sodium tungstate (Sigma) and then dehydrated using an ascending series of ethanol solutions (70% to 100%) for 15 minutes each. Propylene oxide (Agar Scientific Ltd.) was used as a transition solvent between ethanol and resin steps by washing dehydrated samples twice in 100% propylene oxide (15 min/wash), followed by incubation in a 1:1 mixture of propylene oxide and resin for 1 hour. Six changes, approximately 3 hours each, of Araldite resin (CY212 monomer; Taab Laboratories, Aldermaston, United Kingdom) containing dodecylsuccinic anhydride (DDSA) hardener (Agar Scientific Ltd.) and benzyl di-methyl amine (BDMA) accelerator (Agar Scientific Ltd.) ensured total removal of residual propylene oxide and complete infiltration of resin into each specimen block. Samples were then transferred to molds and polymerized for a minimum of 24 hours at 60°C. Ultrathin sections (~90 nm) were cut using a Leica UC6 ultramicrotome (Leica Microsystems (UK) Ltd., Milton Keynes, United Kingdom) equipped with a diamond knife. Sections were collected on copper grids (3.05 mm) and stained for 30 minutes with a saturated uranyl acetate solution for added contrast, followed by three rinses in 0.2-µm filtered distilled water (5 min/rinse). Sections were allowed to dry and examined using a JEOL 1010 transmission electron microscope (Jeol (UK) Ltd., Welwyn Garden City, United Kingdom) operating at 80 kV.

**Immunofluorescence**

WT and null whole mouse eyes were harvested fresh, embedded in OCT compound, frozen on dry ice, and stored at −80°C. Whole-eye cryosections 10 µm thick were collected on poly-lysine–coated glass slides (Fisher Scientific, Loughborough, United Kingdom), using a Bright OTF5000 cryostat (Bright Instruments Ltd., Luton, United Kingdom). Sectioning was performed along the eye globe’s sagittal plane, and sections were only kept for analysis if the iris was disconnect ed, indicating corneal tissue was centrally located over the pupil. To prevent nonspecific background labeling between anti-mouse secondary antibody and IgG native to mouse corneal tissue, primary and secondary antibodies were incubated overnight at 4°C with constant rotation in the following reaction mixture: primary and secondary antibodies were diluted 1:10 and 1:50, respectively, in 1X PBS with 0.1% Tween-20 and 2% BSA (PBS-T+BSA). This preincubation facilitated the interaction between secondary antibodies and the Fc region of primary antibodies, minimizing erroneous localization of secondary to murine corneal sections. For 30 minutes prior to tissue application, heat-deactivated normal mouse serum was added to antibody and control mixtures at a concentration of 5 µL/µg secondary antibody to bind potentially free secondary antibody (further reducing background labeling). Rehydration of sections was achieved by applying PBS-T for 5 minutes. Sections were immersed for 30 minutes in 1% Triton X-100 in PBS to further reduce background fluorescence. Sections were briefly rinsed in PBS-T prior to blocking or, in some cases, application of the keratanase or chondroitinase ABC enzymes. When applied, both keratanase and chondroitinase ABC were prepared at a 0.4 U/mL concentration in either 10 mM Tris-HCl (keratanase) or 50 mM Tris and 60 mM sodium acetate with 0.02% BSA (chondroitinase ABC); digestion occurred for 2 hours at 37°C in both cases. Sections were rinsed with PBS-T following enzyme incubation (where applicable) and blocked for 30 minutes with 10% (v/v) normal goat serum in PBS-T+BSA. Finally, tissue sections were covered in a generous volume of the antibody mixture for 4 hours at room temperature in a humid atmosphere. Following application of primary-secondary complexed antibody solutions, sections were thoroughly washed with PBS-T and mounted with Vectashield dual mountant and 4',6-diamidino-2-phenylindole (DAPI) stain. Control solutions were prepared as described above, except PBS-T+BSA buffer replaced the volume of the primary antibody. Slides were stored at 4°C for no more than 24 hours before imaging as described below. Images were collected with an Olympus BX40 fluorescence microscope equipped with an SIS F-View black and white digital camera (Olympus Keymed Ltd., Southend-on-Sea, United Kingdom). Olympus Cell*P imaging software (Olympus Keymed Ltd., Southend-on-Sea, United Kingdom) was used to capture images in TIFF format.

**RESULTS**

*B3gnt7*-Null Mouse Phenotype

Intercross of *B3gnt7* heterozygotes produced WT, htz, and null mice at normal Mendelian frequency. *B3gnt7*-null mice were born without any detectable abnormalities and were indistinguishable from WT and *B3gnt7*-htz littersmates during development from neonate to adult stages, indicating neither abnormalities nor major visible phenotypes arise from *B3gnt7*-null mutation. A 1-year follow-up study showed that *B3gnt7*-null mutations were nonlethal, and mice maintained normal development, lacking any overt abnormalities. Intercross of null mice produced litters of comparable size to those of intercrossed WT mice, indicating that the mutant mice have normal reproductive potential.

**Corneal Thickness**

Thickness measurements of the whole cornea, the collagen-rich corneal stroma, and the corneal epithelium in WT, *B3gnt7*-htz, and *B3gnt7*-null eyes were collected (Fig. 2). Dimensions of the cornea were comparable in WT and htz tissue, with the epithelium measuring 34 ± 1 vs. 33 ± 1 µm, the whole cornea measuring 109 ± 2 vs. 108 ± 3 µm, and the stroma measuring 75 ± 2 vs. 75 ± 3 µm (all comparisons WT versus htz). None of these small differences were statistically significant. Corneal epithelial thickness in the *B3gnt7*-null mouse, at 32 ± 1 µm, also showed no statistical differences (P = 0.4702 and P = 0.8898, respectively) to the epithelial thickness measurements of the WT or htz corneas. In contrast, a noteworthy decrease in corneal stromal thickness in *B3gnt7*-null mouse eyes, measured at 60 ± 2 µm, was noted. This measurement was less than the corresponding values for the WT and htz corneal stromas (75 ± 2 and 75 ± 3 µm, respectively; P = 0.0024 and P = 0.0002). Given that the epithelial thicknesses in each of the three genotypes was unaltered, the reduction in stromal thickness was reflected in the whole cornea thickness measurements. The *B3gnt7*-null whole cornea was thinner than WT and htz corneas (93 ± 2 vs. 109 ± 2 and 108 ± 3 µm, respectively; P = 0.0011 and P = 0.0002).
Keratan Sulfate in B3gnt7 KO Cornea

**KS Chain Length, Lumican Production, and Galactose Sulfation**

KS-chain length, lumican expression, and galactose sulfation patterns in WT, htz, and null tissues were investigated using extracted corneal protein for Western blot analyses. Three samples were prepared for each genotype: untreated, PNGase F digested, and endo-β-galactosidase digested. The untreated samples, prepared to determine intact KS-GAG chain length as a function of the rate at which lumican migrated through the electrophoretic gel, revealed that WT and htz produced similar high-to-low molecular weight smear patterns, ranging from ~160 to 45 kDa (Fig. 3, lanes 1 and 2, respectively). In contrast, B3gnt7-null corneal extracts showed a more condensed band from ~65 to 45 kDa (Fig. 3, lane 3), suggesting that lumican from B3gnt7-null extracts may be substituted with lower-molecular-weight (i.e., shorter) KS-GAGs compared with WT or htz samples. To confirm that this finding was a consequence of KS-GAG chain length, PNGase F was used to cleave KS side chains from their lumican core proteins. After PNGase F predigestion, all three samples showed identical narrow bands at ~40 kDa (Fig. 3, lanes 4–6), which corresponds to the known molecular weight of lumican, ~36 to 40 kDa. 29 Endo-β-galactosidase (endo-β-gal-ase) treatment was used to probe for aberrant galactose sulfation of KS-GAGs, as its cleavage site is the β-1,4 glycosidic linkage between unsulfated galactose and GlcNac (sulfated or unsulfated). 30 It should be noted that endo-β-gal-ase will cleave at each unsulfated galactose along KS-GAGs, leaving lumican core proteins bound to the KS linkage region and GAG stub proximal to the innermost unsulfated galactose. Therefore, because WT, htz, and null samples that were digested with this enzyme produced bands of comparable molecular weight and density at ~47 kDa (Fig. 3, lanes 7–9), it was inferred that the innermost unsulfated galactose was not atypically oversulfated in B3gnt7-HTZ and -null mutants. Whether or not galactose residues in the non-reducing terminal region of KS are affected by the B3gnt7 mutation remains unknown.

**Electron Microscopy: Tissue Architecture**

Corneal tissue was examined by electron microscopy at high magnification such that aligned collagen fibrils were oriented in longitudinal section. Visualization of polyaminic PG structures was achieved via the inclusion of cupromeronic blue in the primary fixative. 25,31 Because cupromeronic blue binds the two major families of PGs native to the corneal stroma—CS/DS-PGs and KS-PGs—chondroitinase ABC was required to distinguish CS/DS from KS in electron micrographs. Tissue from all three groups was either left intact (Fig. 4, left column) or subjected to chondroitinase ABC (Fig. 4, right column), an enzyme that hydrolyzes glycosidic linkages within the core structure of CS/DS-GAGs 32,33 without affecting KS-PGs. It should be noted that heparan sulfate, a third class of PGs, is also present in corneal tissue, albeit at much lower levels in the stroma than either KS- or CS/DS-PGs. 34 Chondroitinase ABC preincubation was therefore sufficient for distinction between the two major classes of stromal PGs.

Non–enzyme-treated WT corneas showed many electron dense structures extending perpendicularly from collagen fibril axes, which sometimes appeared to associate with collagen at consistent distances (Fig. 4a, white asterisks). Occasionally, longer filaments traversing through or aligning with collagen fibrils were identifiable (Fig. 4a, black arrows). Very fine, short strands of low contrast were also observed projecting outward from collagen fibril axes (Fig. 4a, black arrowhead) throughout the untreated WT stroma. Non–enzyme-treated B3gnt7-HTZ tissue (Fig. 4c) presented phenotypically similar to the WT tissue, with numerous electron dense structures associating with collagen in parallel and perpendicular fashions (Fig. 4c,
black arrows). Polyanionic structures observed in untreated B3gnt7-null tissue appeared several-fold longer than those in WT or htz samples and contained many filamentous offshoots extending perpendicularly from their axes (Fig. 4e, white arrowheads). Critical measurements for accurate comparison of PG length were not possible without three-dimensional imaging, owing to the tortuous course of these structures, which ramified in and out of the plane of the ultrathin section. Additionally, whereas most of the PGs found in WT specimens in this study associated orthogonally to collagen fibrils, the structures prevalent in the null specimen mainly aligned parallel to fibril axes.

Compared with their untreated counterparts shown in the left column of Figure 4, overall GAG content visibly decreased in all specimens following chondroitinase ABC digestion (Fig. 4, right column). Black arrowheads in Figures 4b and 4d identify residual short strands, thought to be KS-PGs owing to their chondroitinase ABC resistance, found throughout the stroma in WT and htz samples (Figs. 4b, 4d, black arrowheads). Interestingly, B3gnt7-null corneal specimens did not feature polyanionic structures following chondroitinase ABC digestion, suggesting an atypical absence of KS in circumstances where both alleles of B3gnt7 were mutated. Additionally, the irregular PGs found throughout the untreated null sample were totally eliminated from the null corneal stroma upon chondroitinase ABC preincubation, suggesting the anomalous PGs were elongated electron-dense CS/DS-PG filaments.

The cupromeronic blue-enhanced PG phenotypes discussed here were similar at anterior, middle, and posterior stromal depths, as was collagen fibril diameter. No aberrantly thick or thin collagen fibrils were observed in any of the genotypes or stromal regions studied (data not shown). Finally, corneal tissue that was incubated in buffer-maintained morphology and proteoglycan content comparable to non–enzyme-treated tissue, confirming that diminished PG content was dependent on active chondroitinase enzyme.

**Immunofluorescence: Confirming the KS and CS/DS Phenotypes**

The mouse monoclonal antibody 1B4, which is specific for low sulfated KS, was applied to cryosections of WT and null corneas to localize KS-GAGs. Traditionally, detection of highly sulfated KS is achieved with 5D4, a mouse monoclonal antibody with specificity for KS hexasaccharides with a minimum of five sulfate moieties. However, previous work has demonstrated the 5D4 epitope is not present in mouse corneal tissue at a concentration sufficient for immunofluorescent labeling. As such, we instead probed samples with 1B4 to visualize low sulfated KS. Figure 5a shows the WT corneal stroma was diffusely fluorescent when probed for sulfated KS-GAGs. Additionally, brightly punctate fluorescence was discernible at various stromal depths (Fig. 5a, white arrows). These results contrasted with null tissue, which showed only faint epithelial staining juxtaposed to a dark stroma (Fig. 5e).
Figures 5b and 5d represent tissue sections that were subjected to keratanase digestion before immuno-labeling for KS. Because stromal fluorescence in the WT was abolished following keratanase predigestion, it was inferred that the signal observed in the undigested WT tissue was indeed due to specific labeling of KS-GAGs.

Immunofluorescence was also used to detect possible changes in CS/DS content of the null corneal stroma compared with WT tissue. To this end, 2B6 antibody, which requires chondroitinase ABC predigestion to reveal the chondroitin-sulfate and DS epitopes, was applied to corneal sections. Both WT (Fig. 5c) and null (Fig. 5g) specimens produced fluorescent signal through the depth of the cornea. The null specimen displayed slightly stronger signal compared with the WT, perhaps reflecting the appearance of the distinctively elongated family of electron dense PG filaments observed in untreated tissue.

**Figure 4.** Electron micrographs of untreated (a, c, e) and chondroitinase ABC-digested (b, d, f) WT, htz, and null corneal stromal tissue. All images show striated collagen fibrils running in longitudinal section. Putative CS/DS-PGs (black arrows, a, c) were observed throughout the stroma of untreated WT (a) and htz (c) corneal tissue and sometimes associated with collagen fibrils at regular intervals (white asterisks, a). KS-PGs appeared shorter and projected outward to the next nearest collagen fibril in untreated WT tissue (black arrowhead, a). Untreated null specimens (e) possessed markedly elongated, branched PG filaments (white arrows) that were not seen in WT or htz samples. In all three groups, overall PG content decreased on chondroitinase ABC preincubation, although only the WT and htz (b, d, respectively) specimens contained residual short chain KS-PGs (black arrowheads). The lack of any discernible PGs following enzymatic digestion in the null (f) samples suggested an abnormal KS-PG phenotype, arising from defunct β3GnT7. All images were taken at 20,000× magnification. **Scale bar** denotes 100 nm.
electron micrographs. The 2B6 antibody was also applied to sections without revealing the epitope via chondroitinase ABC predigestion as a form of negative control. As expected, neither WT nor null (Figs. 5d, 5h, respectively) corneas exhibited positive fluorescence under these conditions.

**DISCUSSION**

The work presented here revealed for the first time a relationship between β3GnT7 and the KS-PG phenotype in murine corneal tissue. Our findings, discussed below, demonstrated that an abnormally attenuated β3GnT7-null mouse corneal stroma lacked histochemically detectable KS-PGs. The concurrent appearance of elongated, branched electron dense PG filaments in this knockout mouse, which were susceptible to chondroitinase ABC, perhaps complementing their endogenously expressed 3GnT7, and KS-PG synthesis in absence of typical KS-PGs.

Because in vitro work by Kitayama et al. identified β3GnT7 as a key enzyme in KS-GAG elongation, we hypothesized that KS-PGs would be altered in the B3gnt7-null tissue, thereby affecting overall corneal architecture. Lumican from B3gnt7-null cornea appeared to be modified with shorter carbohydrate chains than those from WT and B3gnt7-null cornea (Fig. 3), indicating that β3GnT7 is a major enzyme contributing to corneal KS-GAG synthesis. This is consistent with previously published in vitro observations. Endo-β-gal-N-acetylgalactosaminidase digestion of keratanase KSase incubation, implied a lack of sulfated KS-GAGs throughout the depth of the corneal stroma. A brighter stromal fluorescent signal from the null specimen, relative to the WT control, was sensitive to keratanase (KSase) digestion (b). The lack of fluorescent signal in the null corneal stroma, without (e) or with (f) KSase incubation, implied a lack of sulfated KS-GAGs in the mutated corneal stroma. Chondroitinase ABC-liberated CS/DS-GAG fragments fluoresced at all stromal depths and featured occasional bright punctae (white arrows).

Although, if β3GnT2 participates in KS biosynthesis, its action is apparent insufficiency to fully elongate KS-GAGs in absence of β3GnT7. Future studies should determine whether these results are reflected in all KS-PG core proteins, including keratocan and micromucin, because we analyzed lumican KS-PGs as a representative carrier of KS-GAGs in the mouse cornea.

We believe the widespread disappearance of KS-PGs from EM and fluorescence images of the affected null cornea, but not in the WT, supports the idea that the biosynthetic mechanism underlying KS-PG synthesis was disrupted in cases where both alleles of B3gnt7 were deactivated (Fig. 6). These results confirmed predictions of in vitro work, despite the biosynthesis environment in vivo differing. Whereas in vitro studies were conducted with solubilized enzymes and synthetic oligosaccharide constructs, in vivo glycosyltransferases and sulfotransferases are membrane-bound enzymes within Golgi compartments. Indeed, it is as yet unconfirmed whether or not these glycosyl- and sulfotransferases are membrane-bound enzymes within Golgi compartments.

Architecture of the B3gnt7-null mouse cornea emulates stromal changes characteristic of human macular corneal dystrophy (MCD) and Cbsf5-null mouse, both of which lack properly sulfated KS throughout the corneal matrix. Corneal phenotypes in both human MCD and murine Cbsf5-null present with a ~20% reduced stromal thickness, and...
nance of interfibrillar spacing. The relatively thin corneal stroma of the B3gnt7-null specimen perhaps arises from a comparable change in collagen packing, although this hypothesis should be demonstrated empirically in future publications.

In addition to the anomalous KS-PG phenotype discovered in the B3gnt7-null cornea, a concomitant appearance of uniquely elongated, branched electron dense PG filaments was found when corneas were examined using electron microscopy. The susceptibility of these PGs to chondroitinase ABC digestion indicates the atypical PGs were CS/DS in nature. Similar CS/DS structures were previously observed by electron microscopy in Chst5-null corneas of mice lacking keratan sulfate sulfotransferase.\(^1\) Lateral aggregation or end-to-end aggregation of single GAGs were suggested as possible mechanisms generating these supernormal structures, and we speculate that similar processes may underlie their appearance in B3gnt7 mutants as well. However, future work is required on this knockout to reveal the nature of the highly electron dense structures revealed by electron microscopy. That said, an argument for upregulation of CS/DS-PGs in absence of KS-PGs could be rationalized. Considering that corneal transparency partially relies on repulsion between negatively charged KS- and CS/DS-PGs,\(^4\) it is unsurprising that upregulation of CS/DS-PGs may prevent the breakdown of collagen organization necessary for corneal clarity in the event of a charge deficit (i.e., in the absence of elongated, sulfated KS). Indeed, this compensation mechanism was posited before by Hayashida et al.,\(^1\) whose work revealed Chst5-null mice formed “caterpillar-like” structures susceptible to chondroitinase ABC digestion, similar—if not, identical—to those described in this study. The possibility of a compensatory mechanism is further supported by the work of Plaas et al.,\(^49,50\) which characterized the GAG content of normal human corneas versus those affected by MCD. Their work demonstrated that diseased tissue contained fewer sulfated KS-PGs, and CS/DS-PGs were significantly increased and were in an atypically oversulfated form.

The data within demonstrate that the GlcNAc-transferring ability of B3gnt7 is necessary for synthesis of corneal KS-GAGs and aid our understanding of the structure–function relationship between KS and corneal ultrastructural organization.

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**References**


**FIGURE 6.** Hypothesized KS biosynthetic pathway in the absence of functional B3gnt7. We hypothesize that without operative B3gnt7, GlcNAc cannot be added to its Gal substrate (shown by a red X over GlcNAc) to form the KS repeating disaccharide. Without a terminal GlcNAc residue, perhaps the catalytic addition of Gal, GlcNAc, and sulfate cannot repeat as normal (red X over arrowed loop), resulting in an atypically shortened KS structure.


