Association of Variants in TMEM45A With Keratoglobus

Chen Weiner, MSc; Idan Hecht, MD; Alina Kotlyar, BSc; Nadav Shoshany, MD; David Zadok, MD; Uri Elbaz, MD; Fani Segev, MD; Anat Maytal, MD; Yafit Hachmo, PhD; Carine Michiels, PhD; Olivier De Backer, PhD; Noam Shomron, PhD; Adi Einan-Lifshitz, MD; Eran Pras, MD

Aim Keratoglobus is a rare corneal thinning disorder characterized by generalized thinning and globular protrusion of the cornea. Affected individuals typically have significantly decreased vision and are at risk of corneal perforation. The genetic basis and inheritance pattern of isolated congenital keratoglobus are currently unknown.

Objective To identify the genetic basis of isolated congenital keratoglobus.

Method Design This case series and molecular analysis studied 3 unrelated nonconsanguineous families with keratoglobus at a medical center in Israel. Data were collected from June 2019 to March 2021 and analyzed during the same period.

Main Findings Whole-exome sequencing and direct Sanger sequencing, expression analysis by real-time polymerase chain reaction, splice-site variant analysis, immunohistochemical staining, and histological evaluation of a knockout mouse model.

Results Four pediatric patients (3 male individuals) from 3 families had clinical findings consistent with keratoglobus. These included globular protrusion, corneal thinning more prominent at the periphery, and high astigmatism. Truncating and splice site variants were identified in the TMEM45A gene, which fully segregate with the disorder. All affected individuals were homozygous or compound heterozygous for variants in the TMEM45A gene, while unaffected family members were heterozygous carriers. Expression analysis in healthy controls showed that TMEM45A was expressed 23 times higher in the human cornea compared with peripheral blood. Immunohistochemical staining of the TMEM45A protein in normal cornea confirmed its expression in the corneal stroma and epithelium. A TMEM45A knockout mouse model showed structural features consistent with keratoglobus.

Conclusions and Relevance Expression of TMEM45A has been previously shown to result in upregulation of extracellular matrix components and fibrosis. These results suggest that isolated congenital keratoglobus is an autosomal recessively inherited disorder associated with variants in the TMEM45A gene.

Implication Keratoglobus is considered a congenital disorder; however, there have been reports of acquired forms. Congenital keratoglobus can be isolated or associated with systemic connective tissue disorders such as Ehlers-Danlos syndrome, Marfan syndrome, Rubinstein-Taybi syndrome, and brittle corneal syndrome. For isolated keratoglobus, an autosomal recessive pattern of inheritance has been suggested, yet the exact genetic basis of the condition remains unknown. Management of keratoglobus consists of protective eyewear, and early reports indicate that corneal cross-linking may also be effective. Identifying the genetic basis of keratoglobus could allow earlier screening, diagnosis, and treatment, in addition to providing insights into genetic counseling and a basis for future therapeutic approaches.
Methods

The study and informed consent procedures were approved by the institutional review board at Shamir Medical Center and followed the tenets of the Declaration of Helsinki. Informed written consent was obtained from all the participants involved in the study. Participants were not offered any compensation or incentives to participate. The approval of the local ethic committee of the University of Namur, Belgium, was obtained for all the experiments involving mice in this study, which were performed according to the European legislation. Data were collected from June 2019 to March 2021 and analyzed during the same period.

Clinical evaluation included slitlamp biomicroscopy (Haag Streit International) and intraocular pressure measurement (Goldmann applanation tonometry; Haag Streit International). Conorneal topographic and pachymetric maps were obtained using the TMS-5 (Tomey Corporation) and the Oculus Pentacam (Oculus). Biometric measurements were obtained using the Zeiss IOL Master 700 (Carl Zeiss Meditec) and anterior segment optical coherence tomography with the Spectralis OCT (Heidelberg Engineering).

Molecular analysis was performed at the Matlow’s Ophthalmico-Genetic Laboratory, Shamir Medical Center in Be’er Ya’akov, Israel. Genomic DNA and RNA were extracted from whole blood using standard protocols. The disorder was assumed to have an autosomal recessive mode of inheritance, associated with rare variants (minor allelic frequency <0.01). Whole-exome sequencing was performed on DNA samples of 2 affected siblings and their mother from family 1 and on 10 additional siblings from family 2. Sequencing was performed using the NovaSeq platform, version 6 (Agilent SureSelect) (mean coverage was about 149 reads). The Genomic Intelligence platform was used for bioinformatic analysis and prioritization of variants. Filtration process of identified variants took into consideration the association of the gene with disorders of the cornea and/or connective tissue diseases, predicted pathogenicity, and rarity and concordance with autosomal recessive inheritance mode. For direct Sanger sequencing of the candidate gene TMEM45A, primers were designed using Primer 3, version 4.1.0 to cover the gene (ENST00000403410) coding region (CCDS87113), and sequencing was carried out at a commercial sequencing service (Macrogen Europe) using the ABI BigDye Terminator version 3.1 Cycle sequencing kit (Applied Biosystems) in a Mastercycler pro 384 sequencer (Eppendorf). A primer list is provided in the eTable in the Supplement. Human corneal tissue was obtained from human cadaver donors that did not meet the criteria for clinical use. Corneal tissue was harvested in Shamir Medical Center, preserved in Optisol, and kept in a temperature of 4 to 8 °C until processing up to 2 weeks later. Complementary DNA was synthesized using a high-capacity complementary DNA reverse-transcription kit (Applied Biosystems) for gene expression analysis on quantitative polymerase chain reaction (PCR) and for gel electrophoresis analysis of abnormal splicing in the presence of the c.637-1G>T variant.

Key Points

**Question** What is the genetic basis of isolated congenital keratoglobus?

**Findings** In this case series, among 3 unrelated families, variants in the TMEM45A gene were found to fully segregate with the disease. Expression analysis of TMEM45A indicated high expression in the human cornea, and histologic staining of the TMEM45A protein confirmed its expression in the corneal stroma and epithelium. TMEM45A knockout mice exhibited structural features consistent with keratoglobus.

**Meaning** Isolated congenital keratoglobus is an autosomal recessively inherited disorder associated with variants in the TMEM45A gene; these results may contribute to earlier screening and diagnosis, genetic counseling, and could provide a basis for future therapeutic approaches.

The cornea was preserved in Optisol until horizontally sectioned 2 to 3 μm thick and embedded in paraffin or stained in hematoxylin-eosin. Following standard processing, primary antibody specifically binding human TMEM45A (NB2-49355, 1:50; Novus Biologicals) was applied and incubated overnight. Specific antibodies for Vimentin (347M-16, 1:50; Dako) were also applied and incubated. Secondary antibody Alexa Fluor 647 (A-21245, 1:50) was conjugated against TMEM45A, and Alexa Fluor 488 (ab150117, 1:100) was conjugated against vimentin. A TMEM45A knockout mouse model was used to evaluate the consequences of TMEM45A deficiency on corneal development. Generation of TMEM45A knockout mice was described elsewhere. Briefly, the International Mouse Phenotyping Consortium (TMEM45A<sup>tm1a(KOMP)Mbp</sup>) knockout first allele was introduced into the mouse genome by recombination in 14Tg2a ES cells. Mice carrying this allele were crossed with PGK-Cre transgenic mice to obtain animals with deleted TMEM45A exons 3 and 4 (alleles TMEM45A<sup>tm1a(KOMP)Mbp</sup>). Homozygous, heterozygous, and wild-type mice were obtained by intercrossing TMEM45A<sup>tm1a(KOMP)Mbp</sup> heterozygous animals. All mice used in this work have a mixed 129/Ola and C57BL/6 genetic background.

These mice develop normally and display no obvious phenotype; however, no analysis of a possible ocular phenotype was performed. Human and mouse TMEM45A orthologs show a 65% of amino acid identity. Ten TMEM45A knockout mice (study group), 8 wild-type mice, and 3 heterozygous mice (control group) were bred and examined at age 1 to 2 months. Genotyping of the animals was performed by PCR using DNA extracted from ear punch biopsies. Tissue was sent by express delivery from Namur, Belgium, to Matlow’s Ophthalmogenic Laboratory in Israel using a dedicated delivery service. The samples were transported in a temperature kept between 15 and 25 °C, after which they were kept in 4 to 8 °C until processing. Clinical examination of the cornea and histological analysis (using hematoxylin-eosin and Periodic acid–Schiff stains) was done for both groups. Clinical evaluation included high-resolution and high-magnification imagery of the
eyes of the living mice. Images were sent blinded (i.e., unla-
beled by group) and evaluated independently by 3 experi-
enced ophthalmologists including 1 corneal specialist (E.P.,
N.S., and A.E.L.) for clinical signs consistent with keratoglo-
bus including globular protrusion, overall shape, corneal scar-
ing and opacities, and depth of the anterior chamber.

**Results**

**Clinical Findings**

We identified 4 patients from 3 families with isolated congeni-
tal keratoglobus (Table). Family 1 has a nonconsanguineous
Ashkenazi Jewish pedigree (Figure 1). Two siblings (patients
II-1 and II-2 from family 1) have been diagnosed with congeni-
tal keratoglobus. Patient II-2 from family 1, a teenager, with
normal development, no dysmorphic features, or easy bruising,
was first diagnosed before age 5 years. Their ocular
examination demonstrated hypermetropia with high astig-
matism in both eyes, thin corneas, and irregular corneal
opacifications. Visual acuity was 20/80 OD and 20/100 OS.
Corneal topographic and pachymetric maps (eFigure 1 in the
Supplement) of both eyes revealed the classic finding of dif-
fuse thinning, more marked in the peripheral cornea with
maximal steepening in the nasal corneas (corneal curvature
of more than 51 diopters in the anterior sagittal curvature
map). At the thinnest point, the corneal thickness was 244
μm and 286 μm in the right and left eyes, respectively. Dur-
ing follow-up, they experienced spontaneous hydrops in the
right eye. The rest of the ocular examination, including intraocular
pressure and endothelial cell counts, was normal. Tympa-
nometry and audiometry tests as well as echocardiography results were normal. Patient II-1 from family 1, a younger sibling, also had keratoglobus. They had similar corneal thinning and opacifications in the absence of any systemic findings, dysmorphic features, or developmental delays. Neither parent had ocular or systemic illness. The older sibling (patient II-3 from family 1) had alopecia areata but was otherwise healthy without evidence of ocular abnormalities.

Independently, we identified a second nonconsanguine-
ous family (family 2) of Ashkenazi descent. Both parents were

<table>
<thead>
<tr>
<th>Family</th>
<th>Patient No./age (decade)</th>
<th>Relation to proband</th>
<th>Variant</th>
<th>Zygosity*</th>
<th>Affected</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>I-1/sixth Parent</td>
<td>c.154C&gt;T</td>
<td>1/2</td>
<td>Not affected</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>I-2/sixth Parent</td>
<td>c.154C&gt;T</td>
<td>1/2</td>
<td>Not affected</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>II-1/first Sibling</td>
<td>c.154C&gt;T</td>
<td>2/2</td>
<td>Affected</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>II-2/second Proband</td>
<td>c.154C&gt;T</td>
<td>2/2</td>
<td>Affected</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>II-3/second Sibling</td>
<td>c.154C&gt;T</td>
<td>1/2</td>
<td>Not affected</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>I-1/fifth Parent</td>
<td>NA</td>
<td>NA</td>
<td>Not affected</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>I-2/fifth Parent</td>
<td>NA</td>
<td>NA</td>
<td>Not affected</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>II-1/first Proband</td>
<td>c.154C&gt;T</td>
<td>2/2</td>
<td>Affected</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>I-1/fifth Parent</td>
<td>c.154C&gt;T</td>
<td>1/2</td>
<td>Not affected</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>I-2/fourth Parent</td>
<td>c.637-1G&gt;T</td>
<td>1/2</td>
<td>Not affected</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>II-1/second Proband</td>
<td>c.154C&gt;T + c.637-1G&gt;T</td>
<td>2/2</td>
<td>Affected</td>
<td></td>
</tr>
</tbody>
</table>

* Zygosity 1, wild type; zygosity 2, variant.

c.154C>T indicates TMEM45A gene variant c.154C>T, p.Arg52* rs201699180.
c.637-1G>T indicates TMEM45A gene variant c.637-1G>T rs766210908. HTZ indicates heterozygous; HMZ, homozygous; NA, not available.

Family 1

II-1

HMZ c.154C>T

II-2

HTZ c.154C>T

I-1

HTZ c.154C>T

I-2

NA

Family 2

II-1

HMZ c.154C>T

II-2

HTZ c.154C>T

III-1

IV-1

Compound HTZ c.154C>T and c.637-1G>T

I-2

NA

I-1

NA

Family 3

II-1

HMZ c.154C>T

II-2

HTZ c.637-1G>T

I-1

HTZ c.154C>T

c.154C>T indicates TMEM45A gene variant c.154C>T, p.Arg52* rs201699180.
c.637-1G>T indicates TMEM45A gene variant c.637-1G>T rs766210908. HTZ indicates heterozygous; HMZ, homozygous; NA, not available.
Figure 2. Clinical and OCT Images of Patient II-2 From Family 1 and Patient II-1 From Family 3

A) Protruding cornea and deep anterior chamber in patient II-2 from family 1. B) Protruding cornea and deep anterior chamber in patient II-1 from family 3. C) Corneal OCT of the left eye of patient II-1 from family 3. Notice significant thinning at the peripheral nasal aspect of the cornea.

Clinical photographs of patient II-2 from family 1 (A) and patient II-1 from family 3 (B). Visible in both is a protruding cornea and deep anterior chamber. C) Corneal optical coherence tomographic (OCT) image of the left eye of patient II-1 from family 3. Notice significant thinning at the peripheral nasal aspect of the cornea.

Molecular Findings

To investigate the molecular characteristics of the disease in family 1, we conducted whole-exome sequencing of samples from the mother (patient I-2) and one affected sibling (patients II-1 and II-2) from family 1 and both affected siblings (patients II-1 and II-2 from family 1). Whole-exome sequencing yielded 16,102 point variants, none of which appeared in genes with previous association with corneal or connective tissue diseases. Considering concordance with the presumed mode of inheritance, minor allele frequency less than 0.01, and expected deleteriousness of the variant, narrowed down the count to only 1 variant. Using Sanger sequencing, we confirmed segregation for a TMEM45A variant in all members of family 1 (including the father [patient I-1 from family 1] and the unaffected sibling [patient II-2 from family 1]).

These results confirmed that both parents were heterozygous carriers of a truncating variant c.154C>T (NM_001363876; c.154C>T; p.Arg52* rs201699180) in the TMEM45A gene. Affected siblings in family 1 (II-1 and II-2) were homozygous to the same variant and the unaffected sibling in family 1 (II-3) was a heterozygous carrier (Figure 1). This rare variant (minor allele frequency range, 0.00025-0.00008) is predicted to cause a premature stop codon at amino acid 52 (of 291 in the wild-type protein). Pathogenic variants in other genes previously associated with keratoglobus, including brittle cornea syndrome (ZNF469, MIM 612078; PRDM5, MIM 614161), Ehlers-Danlos syndrome (COL5A1, MIM 130000; COL5A2, MIM 130010), Rubinstein-Taybi syndrome (CREBBP, MIM 180849; EP300, MIM 613684), and Marfan syndrome (FBN1, MIM 154700), were ruled out.

Following identification of the variant in family 1, direct sequencing of the TMEM45A gene was carried out in the other families (families 2 and 3). The affected individual in family 2 (patient II-1) was found homozygous to the same truncating variant (c.154C>T, rs201699180). Samples from the parents were unavailable for analysis. In family 3, affected individual II-1 was found heterozygous for the same truncating variant (c.154C>T, rs201699180), alongside a single base exchange at position c.637-1G>T (NM_001363876, rs766210908, both not reported in ClinVar) at intron 5 acceptor site. This rare change (minor allele frequency range, 0.000004-0.000008) is located within the canonical splice acceptor site and is predicted to result in loss of function. The influence of this variant on the predicted protein structure is illustrated in eFigure 2 in the Supplement.19,20

Analysis of the Splice Site Variant c.637-1G>T rs766210908

To analyze the consequence of the variant c.637-1G>T (rs766210908) at the canonical acceptor site, we amplified a segment of TMEM45A complementary DNA by PCR using primers located in exon 3 (forward) and exon 7 (reverse) (primer set 1, eTable in the Supplement and Figure 3). Gel electrophoresis of the PCR products showed that in addition to the expected 1057 base-pairs product, a smaller fragment estimated at 907 base pairs was seen in patient I-2 from family 3, alongside the full 1057 base-pair sequence found in the healthy control (Figure 3D). Sequencing the gene coding region, we found that the alteration in the acceptor site introduces abnormal splicing from a potential donor site located in exon 4, resulting in a shorter transcript by 150 base pairs (from 213 base pairs in the reference allele to 63 base pairs in the alternative allele; Figure 3). This alteration reduces the overall TMEM45A protein length by 17% (from 291 amino acids to 241) and is predicted to affect transmembrane and small extracellular and cytoplasmatic sections of the protein, presumably leading to its loss of function. The influence of this variant on the predicted protein structure is illustrated in eFigure 2 in the Supplement.19,20
**Association of Variants in TMEM45A With Keratoglobus**

**Figure 3. Analysis of the Splice Site Variant c.637-1G>T**

**A** Genomic sequence, **TMEM45A** exons 4-6

<table>
<thead>
<tr>
<th>Schematic</th>
<th>Exon 4</th>
<th>Intron</th>
<th>Exon 5</th>
<th>Intron</th>
<th>Exon 6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild-type</td>
<td>213 bp</td>
<td>1.4k bp</td>
<td>185 bp</td>
<td>10k bp</td>
<td>146 bp</td>
</tr>
</tbody>
</table>

**B** cDNA sequence, **TMEM45A** exons 4-6, reference allele

<table>
<thead>
<tr>
<th>Schematic</th>
<th>Exon 4</th>
<th>Intron</th>
<th>Exon 5</th>
<th>Intron</th>
<th>Exon 6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reference allele</td>
<td>213 bp</td>
<td>1.4k bp</td>
<td>185 bp</td>
<td>10k bp</td>
<td>146 bp</td>
</tr>
</tbody>
</table>

**C** cDNA sequence, **TMEM45A** exons 4-6, alternative allele

<table>
<thead>
<tr>
<th>Schematic</th>
<th>Exon 4</th>
<th>Intron</th>
<th>Exon 5</th>
<th>Intron</th>
<th>Exon 6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alternative allele</td>
<td>63 bp</td>
<td>185 bp</td>
<td>146 bp</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**D** Gel electrophoresis of cDNA fragments obtained by PCR

<table>
<thead>
<tr>
<th>Product</th>
<th>1500 bp</th>
<th>1000 bp</th>
<th>500 bp</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td>1057 bp</td>
<td>907 bp</td>
<td></td>
</tr>
</tbody>
</table>

**TMEM45A Expression Analysis in the Human Cornea**

Given that this gene has not been previously described to be expressed in the eye or associated with any ocular diseases, we proceeded to evaluate its expression within the cornea. As corneal tissue from affected individuals was unavailable, we analyzed the expression of **TMEM45A** in healthy human cadaver corneas. Using quantitative PCR, we confirmed that **TMEM45A** is expressed in the human cornea, with messenger RNA levels 23 times higher compared with peripheral blood (eFigure 3 in the Supplement).

**Immunohistochemical Staining of TMEM45A Protein in the Human Cornea**

We hypothesized, based on the pathophysiology of keratoglobus, which is thought to involve the corneal stroma, that the **TMEM45A** gene is also involved with corneal stromal integrity. Immunohistochemical staining of **TMEM45A** protein in normal human corneas showed expression in corneal epithelium and stroma, localized to the cytoplasm (Figure 4). Interestingly, protein expression was evident in the stroma, with staining in a small percentage of stromal keratocytes, also located cytoplasmically (Figure 4).

**TMEM45A Knockout Mouse Model Analysis**

A model of mice deficient for **TMEM45A** has been previously described.6 These mice develop normally, are fertile, and do not display any obvious abnormal phenotype. We investigated the corneal phenotype of these mice. Gross appearance of the eye was similar in wild-type and **TMEM45A** knockout mice. However, histological examination showed a consistently thinner stroma in **TMEM45A** knockout mice (eFigure 3 in the Supplement). Stromal thickness was 40 to 50 μm in the central cornea of the **TMEM45A** knockout mice compared with 80 to 90 μm in the wild type. No stromal disruption was observed in the anterior stroma and the epithelial and endothelial layers of the cornea appeared normal (eFigure 4 in the Supplement).

**Discussion**

We showed that homozygous and compound heterozygous truncating and splice variants in the **TMEM45A** gene (MIM 616928) fully segregate with isolated congenital keratoglobus among 3 unrelated nonconsanguineous families. Expression analysis of **TMEM45A** revealed high expression in the human cornea, and histologic staining of the **TMEM45A** protein in normal corneas showed its presence in the corneal epithelium and stroma. **TMEM45A** knockout mice showed corneal thinning consistent with keratoglobus. Taken together, these results confirm that isolated congenital keratoglobus may be a heritable recessive defect resulting from loss of function variants in **TMEM45A**.

The **TMEM45A** gene (also called DERP7, DNAPTP4, or FLJ10134) has been primarily studied as an upregulated marker in various cancers and as an actor of keratinization. It belongs to the TMEM family, encoding uncharacterized predicted transmembrane proteins. Their subcellular localiza-
tion and functions remain mostly unknown, with most available information coming from transcriptomic studies or bioinformatic predictive tools. Animal models show that expression of TMEM45A results in upregulation of extracellular matrix components and fibrosis. This protein is also overexpressed in many cancers. Taken as a whole, it seems that TMEM45A is involved with extracellular structural and fibrotic processes as well as in keratinization. In keratoglobus, several aspects suggest a pathophysiologic association with extracellular matrix components in the corneal stroma. These include the characteristic ectatic clinical nature of thinning and protrusion, the association of keratoglobus with connective tissue disorders, and the typical histopathologic findings, which include stromal thinning and disruption of the collagen-rich Bowman layer, the anterior part of the corneal stroma. Taken together, the preliminary evidence on the functions of TMEM45A appear to coincide with the current evidence on keratoglobus pathophysiology.

We observed that the corneal stroma of TMEM45A knockout mice was about 2 times thinner than that of wild-type mice. It should be noted that several elements must be taken into account when using mouse models in the context of keratoglobus. First is that human and mouse TMEM45A orthologs encode proteins sharing only 65% of amino acids identity. Second, there is a significant difference between the anterior stroma in humans and mice. Finally, we looked at mice that were only 1 to 2 months old. Although congenital keratoglobus in humans can be evident at an early age, progression with age is often seen, a course that might also occur in mice, limiting signs of the disease to those evident at an early age.

The TMEM45A-containing chromosomal locus (3p14-q13) has previously been associated with another related corneal ectatic disorder, autosomal dominant keratoconus. A 2004 report on a large Italian pedigree with autosomal dominant keratoconus mapped the locus to the one containing TMEM45A (3p14-q13). Several genes within this locus were examined and did not show pathogenic variants; however, TMEM45A was not one of them. None of the other loci and genes associated with keratoconus are in proximity with TMEM45A, apart from this locus. It would be interesting to look for variants in TMEM45A in sporadic or familial cases of keratoconus.

Limitations
This study has several limitations. First, only 4 individuals with keratoglobus from 3 unrelated families were available for testing owing to the rare nature of the disorder. Second, corneal tissue of affected individuals was unavailable. Third, topographic and pachymetric maps of mice corneas were unavailable. Finally, 2 healthy individuals from family 2 were not available for genetic analysis and their molecular details could not be determined.

Conclusions
To conclude, keratoglobus is a rare corneal ectatic disorder whose genetic basis and inheritance pattern were previously unknown. We identified variants of the gene TMEM45A that fully segregate with isolated congenital keratoglobus. These results may contribute to earlier screening and diagnosis in genetic counseling and could provide a basis for future therapeutic approaches.
Association of Variants in TMEM45A With Keratoglobus


Conflict of Interest Disclosures: None reported.

Additional Contributions: We thank the parents of patients II-2 from family 1 and II-1 from family 3 for granting permission to publish this information. We also thank Lucie Moniquet (University of Namur, Namur, Belgium) for mouse breeding, genotyping, and sample collection. Compensation was received.

Additional Information: This work was performed in partial fulfillment of the requirements for a PhD degree by Chen Weiner at the Sackler Faculty of Medicine, Tel Aviv University, Israel.

REFERENCES