Mutational spectrum of the ZEB1 gene in corneal dystrophies supports a genotype-phenotype correlation


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The corneal dystrophies represent a group of inherited corneal disorders that are genetically and phenotypically heterogeneous, and have been classified by phenotypic description, pathologic examination, and genetic analysis.1 Posterior polymorphous corneal dystrophy (PPCD) is a rare autosomal dominant disorder of the corneal endothelium1 that shows highly variable expressivity in age of presentation and clinical severity.2–4 Clinically, PPCD is characterized by the presence of vesicles, bands, and geographic opacities involving the endothelium and Descemet’s membrane.2,3 The inter- and intrafamilial phenotypic spectrum of PPCD is wide, with some patients remaining asymptomatic with a nonprogressive course, while others show severe progressive disease developing visual impairment due to corneal edema and requiring corneal transplantation.2,4–6

PPCD has been mapped to three different genetic loci.5,7,8 and there is evidence of further genetic heterogeneity.9–11 PPCD1 (MIM #609141) was mapped to chromosome 20p11.2-q11.2, and mutations were reported in visual system homeobox gene 1 (VSX1; MIM #609140) in PPCD and keratoconus (KTCN1; MIM 148300).12 PPCD2 (MIM #605020) was mapped to chromosome 20p11.2-q11.2, and mutations were reported in visual system homeobox gene 1 (VSX1; MIM #605020) in PPCD and keratoconus (KTCN1; MIM 148300).12 PPCD2 (MIM #605020) was mapped to chromosome 20p11.2-q11.2, and mutations were reported in visual system homeobox gene 1 (VSX1; MIM #605020) in PPCD and keratoconus (KTCN1; MIM 148300).12 PPCD3 (MIM #613270) results from mutations in ZEB1 (MIM #120252), located on chromosome 1p34.3-p32.38. Mutations in ZEB1 support a genotype–phenotype correlation in PPCD. A recent study demonstrated a frameshift mutation (c.1578_1579insG) and a novel nonsense mutation (c.2249C>T; p.Gln640His) of ZEB1 in PPCD patients harboring a missense ZEB1 mutation (p.Gln640His). Real-time quantitative PCR (RT-qPCR) performed on cultured corneal keratocytes harboring the missense ZEB1 mutation (p.Gln640His) demonstrated that COL4A1 and COL4A2 were markedly downregulated, and COL4A3, COL4A4, and COL8A2 were moderately downregulated.

Conclusions. Our data combined with the previously reported mutational spectrum of ZEB1 support a genotype–phenotype correlation: missense substitutions in the ZEB1 protein are associated with keratoconus, whereas protein truncating ZEB1 mutations result in PPCD. The dysregulation of α-type IV collagens represents a common link between ZEB1 mutation and the clinical phenotypes (PPCD3, FEDC, and keratoconus).

Keywords: keratoconus, posterior polymorphous corneal dystrophy, Fuchs’ endothelial dystrophy, ZEB1, corneal dystrophies, hereditary
corneal dystrophy (FEDC1; MIM 136800).\textsuperscript{13} PPCD3 (MIM 609141) was mapped to chromosome 10p11.2 and mutations were detected in zinc finger E box-binding homeobox 1 (ZEB1; MIM 189909) which also is known as transcription factor 8 (TCF8) by some investigators.\textsuperscript{5,11} Mutations in ZEB1 account for 
approximately 30\% of PPCD patients.\textsuperscript{5,9–11} and all
the reported ZEB1 mutations responsible for PPCD3 are truncating.\textsuperscript{5,9–11} Missense mutations in ZEB1 have also been reported in Fuchs' endothelial corneal dystrophy (FEDC6, MIM 613270).\textsuperscript{14,15}

Although PPCD, Fuchs' endothelial dystrophy, and keratoconus are clinically and pathologically distinct, keratoconus has been associated with PPCD\textsuperscript{12,16–20} and Fuchs' endothelial dystrophy,\textsuperscript{10} suggesting a common link.\textsuperscript{12,17–21} Here, we report the results of ZEB1 sequencing in a cohort of patients with keratoconus and PPCD. Our data combined with the previously reported mutational spectrum of ZEB1 supports a genotype-phenotype correlation, in which protein truncating ZEB1 mutations result in PPCD, and missense substitutions in the ZEB1 protein are associated with keratoconus and Fuchs' endothelial dystrophy.

METHODS

Clinical Assessment

Patients affected with either keratoconus or posterior polymorphous corneal dystrophy were recruited as part of ongoing studies from Belfast (Belfast Health and Social Care Trust, Belfast, UK), Bristol (Bristol Eye Hospital, Bristol, UK), and Toronto (Department of Ophthalmology and Vision Sciences, The Hospital for Sick Children, University of Toronto, Toronto, Ontario, Canada). A total of 96 unrelated individuals (192 chromosomes) without ocular disease (aged 60 and over) was used as normal controls. All studies adhered to the tenets of the Declaration of Helsinki, and were approved by the relevant institutions with all participants giving written informed consent. In subjects with pathogenic sequence variants a medical history was taken to identify nonocular features previously associated with ZEB1: inguinal hernias, hydropses, Dupuytren's contractures, bony lumps, spinal disease, otosclerosis, and Osgood-Schlatter disease.\textsuperscript{5,11}

Patients were diagnosed with PPCD if they exhibited the characteristic endothelial changes in both eyes (vesicles, bands, or geographic opacities in the endothelium) on slit-lamp biomicroscopy. The diagnosis of keratoconus was based on well-established clinical signs on slit-lamp biomicroscopy and cycloplegic retinoscopy, and a confirmatory videokeratographic map.\textsuperscript{22,23} Videokeratographic evaluation was performed on each eye using the Topographic Modelling System-1 (Computed Anatomy, Inc., New York, NY), Orbscan II (Bausch & Lomb, Salt Lake City, UT), or the Pentacam (Oculus, Wetzlar, Germany). When determining the familial segregation of ZEB1 sequence variants, all available family members underwent clinical and topographic examination to determine their clinical status and were screened molecularly.

DNA Extraction and Sequencing

Genomic DNA was extracted from peripheral blood leukocytes using a Wizard Genomic DNA Purification Kit (Promega, Southampton, UK) according to the manufacturer's instructions. PCR primers for amplification and sequencing of the exons, flanking intron sequences, and 5' and 3' untranslated regions (UTR) of ZEB1 were identical to those described by Krafchak et al.\textsuperscript{2} with adapted conditions, except for two additional primers for sequencing that were designed using Primer3 (v. 0.4.0) software (available in the public domain at http://frodo.wi.mit.edu/primer3/)\textsuperscript{24} and are listed in Supplementary Table S1. Bidirectional cycle sequencing was performed using BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems, Warrington, UK) and electrophoresed on an ABI PRISM 3730 DNA sequencer (Applied Biosystems, Warrington, UK). Sequencing results were analyzed manually using the sequence analysis software SeqScape 2.1.1 (Applied Biosystems). Identified sequence variants were described according to the guidelines published by the Human Genome Variation Society. Variants were annotated in accordance with NCBI NM_030751.5. (Build GRCh37/hg19).

Deleterious structural effects of amino acid substitutions on protein function were assessed using the PolyPhen-2 (Polyorphism Phenotyping v2; available in the public domain at http://genetics.bwh.harvard.edu/pph2/),\textsuperscript{25} Sorting Intolerant from Tolerant (SIFT; available in the public domain at http://sift.jcvi.org/),\textsuperscript{26} and Pathological Mutations (PMut; available in the public domain at http://mmb2.pcb.ub.es:8080/PMut/)\textsuperscript{27} algorithms. The conservation of the affected amino acid across species was analyzed using Homologene (available in the public domain at http://www.ncbi.nlm.nih.gov/homologene/) and multiple sequence alignment using the UCSC Genome Browser (available in the public domain at http://genome.ucsc.edu/). ZEB1 sequence variants that were absent from controls were assessed to determine potential effects on splicing using Human Splicing Finder Version 2.4.1 (available in the public domain at http://www.umd.be/HSF/).\textsuperscript{28}

Human Corneal Keratocyte Cell Culture

Human corneal kerocytes were cultured directly from residual normal donor corneoscleral rims (n = 4) and from corneal tissue obtained from a patient harboring a missense mutation in ZEB1 (c.1920G > T; p.Gln640His) undergoing corneal transplantation. Corneal stromal tissue was dissected, fragmented, and plated on 60 mm Petri dishes. The cells were maintained separately in Dulbecco's modified Eagle's medium/nutrient Ham's F-12 (1:1) medium (Gibco; Invitrogen Ltd., Paisley, UK) supplemented with 10% fetal calf serum (FCS) and penicillin/streptomycin mix (1:1) (Sigma-Aldrich Company Ltd., Dorset, UK), at 37°C in a 5% CO2 incubator (MiniGalaxy A C&M Scientific; Scientific Laboratory Supplies Ltd., Notting- ham, UK). The phenotype of the cells was assessed on the basis of the distinctive morphology of human corneal keratocytes and positive vimentin (DAKO Denmark A/S, Glostrup, Denmark), and CD34 (Santa Cruz Biotechnology, Inc., Santa Cruz, CA) immunofluorescence staining. The cultured cells also were negative for cytokeratin 3 (Millipore, Billerica, MA) immunofluorescence indicating an absence of corneal epithelial cell contamination. Cells were cultured until 90% confluence (10–14 days) and total RNA was extracted using the TRI Reagent (Sigma-Aldrich Company, Ltd.) and quantified on the Nanodrop-1000 (Nanodrop Technologies, Wilmington, DE). RNA quality was determined with the Bioanalyzer (Agilent Technologies UK Limited, Cheshire, UK).

Real-Time Quantitative PCR (RT-qPCR)

Total RNA (1 µg) isolated from human corneal kerocytes was reverse transcribed into cDNA using the Quantitect Reverse Transcription Kit (Qiagen, West Sussex, UK) according to manufacturer's protocol. RT-qPCR was performed by using a real-time PCR system (LightCycler 480; Roche Diagnostics, Basel, Switzerland). Primer sequences were obtained from PrimerBank (available in the public domain at http://pga.mgh.harvard.edu/primerbank/)\textsuperscript{29} for COL4A1, COL4A2, COL4A3, COL4A4, COL4A5, COL4A6, COL8A2, and ZEB1. Real-time PCR reactions were performed in 10 µL final volume
containing 10 ng of cDNA, gene-specific primers, and fluorescent dye SYBR green I (Permenetas UK Ltd., Cambridge, UK; conditions available on request). All PCR reactions were performed in technical triplicates. All mRNA levels were measured as CT threshold levels and were normalized with five reference genes\(^\text{30}\): glyceraldehyde-3-phosphate dehydrogenase (\textit{GAPDH}), peptidylprolyl isomerase A (\textit{PPIA}), ubiquitin C (\textit{UBC}), hypoxanthine quinine phosphoribosyl transferase 1 (\textit{HPRT1}), and ribosomal protein L5 (\textit{RPL5}) CT values. Values were expressed as fold increase over the corresponding values for control by the 2\(^ {-\Delta \Delta Ct} \) method. The ACI validation experiments showed similar amplification efficiency for all templates used (difference between linear slopes for all templates less than 0.1). Three independent experiments were performed and the average (±SEM) results were calculated using GraphPad software (GraphPad Software, San Diego, CA). Data were expressed as the mean values ± SEM and analyzed using Student’s \( t \)-test. Statistical differences in the mean were considered statistically significant at \( P < 0.05 \).

**RESULTS**

Sanger sequencing of the entire coding region of \textit{ZEB1} (exons 1–9) was performed on 70 unrelated patients with keratoconus (27 familial and 43 sporadic cases) and 18 unrelated patients with PPCD (7 familial and 11 sporadic cases). Pathogenicity of identified sequence variants was determined by filtering using the in-house sequencing data from 96 control subjects, data from dbSNP (Build 137), the May 2012 release of the 1000 Genomes (1 KG) Project (available in the public domain at http://browser.1000genomes.org/index.html), and the Exome Variant Server (EVS), NHLBI Exome Sequencing Project (ESP; Seattle, WA, available in the public domain at http://evs.gs.washington.edu/EVS/), segregation in familial cases, residue conservation, splicing analysis, and structural modeling.

**Mutational Analysis of ZEB1 in Keratoconus**

In patients with keratoconus, we identified 7 heterozygous sequence variants; 3 nonsynonymous and 4 synonymous (Table 2). Three of these were known SNPs (rs80191451, rs7918614, and rs55238902) and one was a novel SNP (c.5177T > A; p.Pro1059Pro) seen in 5/96 (5%) of controls, although absent from the 1KG and EVS datasets. There were 3 novel heterozygous sequence variants (c.1574G > A; p.Gly525-Glu, c.1920G > T; p.Gln640His, and c.2673G > C; p.Pro891-Pro), which were absent from controls (192 chromosomes), and the 1KG and ESP datasets.

The novel heterozygous sequence variant exon 7, c.1574G > A (p.Gly525Glu), was identified in a patient with sporadic keratoconus. This sequence variant results in a nonconservative substitution of a nonpolar neutral amino acid (glycine) with a polar negatively charged hydrophilic residue (glutamic acid). The glycine at position 525 is well conserved in primates, although in the chicken and shrew the residue is a glutamic acid. PMut predicted that the variant was pathologic with a score of 0.8 and high reliability, whereas PolyPhen-2 and SIFT predicted this substitution was benign and tolerated, respectively. Given this evidence, we proposed that p.Gly525Glu is classified as potentially pathogenic. As the novel synonymous change c.2673G > C (p.Pro891Pro) was absent from controls, and the 1KG and ESP datasets, we sought to determine whether there was an impact on splicing due to the impact of the nucleotide substitution on exonic splicing enhancers (ESE) and silencers (ESS).\(^\text{31}\) On ESE analysis the nucleotide change c.2673G > C alters the predicted ESE binding site, but we were unable to obtain RNA from the patient to assess whether this nucleotide change results in aberrant \textit{ZEB1} splicing.

The novel heterozygous pathogenic mutation in exon 7, c.1920G > T (p.Gln640His), was identified in two siblings with keratoconus (Fig. 2B). The nucleotide change causes the conserved polar amino acid glutamine to be substituted by the positively charged, basic amino acid histidine. The glutamine at position 640 is the last amino acid of the homeodomain, and is well conserved across primates and other vertebrates as demonstrated in Figure 2C. SIFT analysis predicted that the variant was damaging, whereas PolyPhen-2 and PMut predicted this substitution was benign and neutral, respectively.

**Table 1. \textit{ZEB1} Sequence Variants Identified in the Posterior Polymorphous Corneal Dystrophy Patient Cohort**

<table>
<thead>
<tr>
<th>Nucleotide Position</th>
<th>Amino Acid Change</th>
<th>Exon/Intron</th>
<th>Cases</th>
<th>Controls</th>
<th>dbsNP rs #</th>
<th>1KG (MAF %)</th>
<th>ESP (MAF %)</th>
<th>Classification</th>
</tr>
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<tbody>
<tr>
<td>c.192C &gt; T</td>
<td>p.Asp64Asp</td>
<td>Exon 2</td>
<td>2/18</td>
<td>0/96</td>
<td>rs7918614</td>
<td>Yes (6.7)</td>
<td>Yes (6.4)</td>
<td>Polymorphism</td>
</tr>
<tr>
<td>c.260-136T</td>
<td>NA</td>
<td>Intron 2</td>
<td>1/18</td>
<td>1/96</td>
<td>rs2839663</td>
<td>Yes (1.0)</td>
<td>No</td>
<td>Polymorphism</td>
</tr>
<tr>
<td>c.1578_1579insG</td>
<td>p.Val526X2</td>
<td>Exon 7</td>
<td>2/18</td>
<td>0/96</td>
<td>rs34846414</td>
<td>Yes (1.9)</td>
<td>Yes (1.94)</td>
<td>Polymorphism</td>
</tr>
<tr>
<td>c.2061A &gt; C</td>
<td>p.Pro687Pro</td>
<td>Exon 7</td>
<td>2/18</td>
<td>0/96</td>
<td>NA</td>
<td>No</td>
<td>No</td>
<td>Pathogenic mutation</td>
</tr>
<tr>
<td>c.2249C &gt; A</td>
<td>p.Ser750X</td>
<td>Exon 7</td>
<td>2/18</td>
<td>0/96</td>
<td>NA</td>
<td>No</td>
<td>No</td>
<td>Pathogenic mutation</td>
</tr>
</tbody>
</table>

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\( ^{c} \) No. 5
Figure 1. (A) Segregation analysis of the c.2249C > A, p.Ser750X ZEB1 mutation in a UK family affected by PPCD. (B) Slit-lamp examination of individual II:2 showed corneal endothelial vesicles seen typically in PPCD. (C) Sequence chromatogram showing the heterozygous c.2249C > A, p.Ser750X mutation in exon 7 of ZEB1 identified in the family affected by PPCD. FP, forward primer; RP, reverse primer. (D) Pentacam corneal topography images of right (OD) and left (OS) eyes of the proband (individual II:2). The upper maps show corneal steepening with regular astigmatism, but no signs of keratoconus. The lower maps show a general increase in corneal thickness (central corneal thickness 651 μm associated with PPCD).
TABLE 2. *ZEB1* Sequence Variants Identified in the Keratoconus Patient Cohort

<table>
<thead>
<tr>
<th>Nucleotide Position</th>
<th>Amino Acid Change</th>
<th>Exon/Intron</th>
<th>Cases</th>
<th>Controls</th>
<th>dbSNP rs#</th>
<th>1KG (MAF %)</th>
<th>EVS (MAF %)</th>
<th>Classification</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.192C&gt;T</td>
<td>p.Asp64Asp</td>
<td>Exon 2</td>
<td>1/70</td>
<td>0/96</td>
<td>rs7918614</td>
<td>Yes (6.7)</td>
<td>Yes (6.45)</td>
<td>Polymorphism</td>
</tr>
<tr>
<td>c.235A&gt;C</td>
<td>p.Asn78Thr</td>
<td>Exon 2</td>
<td>2/70*</td>
<td>0/96</td>
<td>rs80194531</td>
<td>Yes (1.2)</td>
<td>Yes (1.68)</td>
<td>Polymorphism</td>
</tr>
<tr>
<td>c.1257G&gt;A</td>
<td>p.Ala191Ala</td>
<td>Exon 7</td>
<td>1/70</td>
<td>0/96</td>
<td>rs3528902</td>
<td>Yes (1.2)</td>
<td>Yes (1.95)</td>
<td>Polymorphism</td>
</tr>
<tr>
<td>c.1574G&gt;A</td>
<td>p.Gly525Glu</td>
<td>Exon 7</td>
<td>1/70</td>
<td>0/96</td>
<td>NA</td>
<td>No</td>
<td>No</td>
<td>Potentially pathogenic</td>
</tr>
<tr>
<td>c.1920G&gt;T</td>
<td>p.Gln640His</td>
<td>Familial keratoconus and FECD</td>
<td>0/96</td>
<td>NA</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>Pathogenic mutation</td>
</tr>
<tr>
<td>c.2673G&gt;C</td>
<td>p.Pro891Pro</td>
<td>Exon 8</td>
<td>1/70</td>
<td>0/96</td>
<td>NA</td>
<td>No</td>
<td>No</td>
<td>Potentially pathogenic</td>
</tr>
<tr>
<td>c.3177A&gt;T</td>
<td>p.Pro1059Pro</td>
<td>Exon 9</td>
<td>3/70</td>
<td>5/96</td>
<td>NA</td>
<td>No</td>
<td>No</td>
<td>Polymorphism</td>
</tr>
</tbody>
</table>

* Patients were African American and sequencing of *ZEB1* in ethnically matched controls detected this variant in 3/23 controls.

FIGURE 2. (A) Segregation analysis of the c.1920G>T, p.Gln640His *ZEB1* mutation in the family affected by keratoconus (siblings) and Fuchs’ endothelial corneal dystrophy (mother). (B) Sequence chromatogram showing the heterozygous c.1920G>T, p.Gln640His mutation in exon 7 of *ZEB1*. (C) Multiple sequence alignment showing highly conserved glutamine at position 640 in exon 7 of *ZEB1*. 

Downloaded From: http://iovs.arvojournals.org/pdfaccess.ashx?url=/data/journals/iovs/933469/ on 06/09/2017
A. Individual II:1

(B) Pentacam corneal topography images of right (OD) and left (OS) eyes of the proband (individual II:1; Fig. 2). The upper maps show inferior corneal steepening with a maximal corneal power of 56.6 D (OD) and 59.1 D (OS) associated with corneal thinning (bottom maps) confirming keratoconus. (B) Pentacam corneal topography corneal thickness maps of the mother of the proband (individual I:2; Fig. 2). The maps show a general increase in corneal thickness especially in the right eye (OD) associated with corneal endothelial pump failure and corneal hydration associated with FECD.

FIGURE 3. (A) Pentacam corneal topography images of right (OD) and left (OS) eyes of the proband (individual II:1; Fig. 2). The upper maps show inferior corneal steepening with a maximal corneal power of 56.6 D (OD) and 59.1 D (OS) associated with corneal thinning (bottom maps) confirming keratoconus. (B) Pentacam corneal topography corneal thickness maps of the mother of the proband (individual I:2; Fig. 2). The maps show a general increase in corneal thickness especially in the right eye (OD) associated with corneal endothelial pump failure and corneal hydration associated with FECD.
RT-qPCR of Mutant ZEB1 (p.Gln640His) Cultured Corneal Keratocytes

The expression of COL8A2 and the basement collagen genes (COL4A1, COL4A2, COL4A3, COL4A4, COL4A5, and COL4A6) was evaluated by RT-qPCR in cultured corneal keratocytes obtained from a patient harboring a missense mutation in ZEB1 (c.1920G>T, p.Gln640His, Table 3). COL4A1 and COL4A2 were markedly downregulated, and COL4A3, COL4A4, and COL8A2 were moderately downregulated. The expression level of ZEB1 was unchanged in the corneal keratocytes harboring the ZEB1 mutation.

DISCUSSION

ZEB1 encodes the two-handed zinc-finger homeodomain transcription factor, which can act as either a transcriptional enhancer or repressor.32 Mutations in ZEB1 have been reported in posterior polymorphous corneal dystrophy (PPCD3; MIM #609141) and Fuchs’ endothelial corneal dystrophy (FECD6; MIM #613270), and herein we report a missense mutation in ZEB1 associated with keratoconus and highlight a genotype-phenotype correlation. Missense substitutions in the ZEB1 protein are associated with FECD6 and keratoconus, whereas protein truncating mutations result in PPCD3 (Fig. 4, Supplementary Table S5). Genotype-phenotype correlations also exist in TGFB1 (MIM *601692) associated corneal dystrophies where specific missense mutations associated with arginine at codon 124 and 555 result in different phenotypic manifestations.33,34

The largest published series reported ZEB1 mutations in 25% of patients with PPCD (8/32 probands)11 and the prevalence of mutations in ZEB1 in PPCD has varied from 9.1% to 45.4%.5,9–11 In our study ZEB1 mutations were detected in 11.1% (2/18 probands) with PPCD. The majority of mutations were reported in exon 7, which most likely represents the relative size of this exon consisting of 1811 bps or 54% of the total ZEB1 transcript (3575 bps). All reported ZEB1 mutations have been unique, although the methionine at codon 1 mutation results from two different nucleotide substitutions; c.1A>G (p.Met1Val)10 and c.2T>G (p.Met1Arg).11 Although p.Met1Val and p.Met1Arg mutations are missense, it is predicted that they would result in a truncation of the ZEB1 protein as the initiation of translation is disrupted.10 All ZEB1 mutations reported in PPCD3 are nonsense, frameshift, and missense, which result in protein truncation.5,6,9–11 The proposed pathogenic mechanisms are haploinsufficiency either due to nonsense mediated decay or analysis identified the variant in both affected (keratoconus) siblings and the affected (FECD) mother, while it was absent in the unaffected father as shown in Figure 2A.
loss of functional domains due to truncations in the ZEB1 protein, or dominant-negative effects from the truncated mutant ZEB1 protein.5

Liskova et al. failed to detect an association of keratoconus and ZEB1 mutations in their PPCD3 cohort.4 Three PPCD5 patients harboring keratometry readings representing central steepening and increased corneal refractive power (corneal power > 49 D), and no corneal thinning or other signs of keratoconus.4 In our study, the keratoconus patients harboring a pathogenic missense ZEB1 mutation did not have evidence of PPCD3 and had characteristic features of keratoconus, including typical corneal topography. Missense mutations in ZEB1 have been reported in Fuchs’ endothelial dystrophy (FECD).14,15 although only identified in 2% (7/384) of cases in the largest published series.14 Genetic variation in the transcription factor 4 gene (TCF4; MIM602272) has been associated with the development of FECD, in a potential mechanism involving altered ZEB1 expression.5

We detected a pathogenic missense mutation in ZEB1 associated with keratoconus and FECD segregating in a family suggesting common pathophysiological mechanisms. The dysregulation of z-type IV collagen represents a common link between ZEB1 mutation and the clinical phenotypes (PPCD3, FECD, and keratoconus). Mutations in type IV collagens (COL4A3, COL4A4, and COL4A5) cause Alport syndrome, a triad of nephropathy, sensorineural deafness, and eye features that include anterior lenticonus, PPCD, and keratoconus.36 Ectopic COL4A3 protein has been demonstrated in the corneal endothelium of an individual with PPCD3 resulting from a truncating mutation in ZEB1, and the expression of COL4A3 is increased in the corneal endothelium of ZEB1-null mice.37 The COL4A3 promoter contains a complex promoter binding site,3 and there is functional evidence that ZEB1 interacts with these proximal and distal E2-box motifs to regulate COL4A5 expression.38 Altered ZEB1-mediated COL4A3 transcriptional repression resulting from truncating mutations is proposed to result in PPCD3.38 In the corneal endothelium of a patient with PPCD3 resulting from a ZEB1 truncating mutation, qPCR demonstrated ZEB1 expression was reduced whereas COL4A3 expression was 4- to 5-fold higher than in the normal corneal endothelium.58 However, the actual site of the truncating ZEB1 mutation and the impact on ZEB1 protein structure was not reported.58 In our study, a missense mutation (p.Gln640His) in the homeodomain of ZEB1 resulted in a downregulation in z-type IV collagens, whereas the expression of ZEB1 mRNA was unaltered.

ZEB1 core and secondary binding sites have been reported in the promoter sites of COL8A2 and the basement collagen genes (COL4A1, COL4A2, COL4A3, COL4A5, and COL4A6), with only the COL4A3 promoter containing a complex site consisting of the core and proximal downstream secondary sequence.7 Given these findings, and that alterations in z-type IV collagen have been implicated in PPCD5,57-58 and corneal disease,36,39,40 we assessed the gene expression of COL8A2 and the basement collagen genes (COL4A1, COL4A2, COL4A3, COL4A4, COL4A5, and COL4A6) by RT-qPCR in cultured corneal keratocytes obtained from a patient harboring a missense mutation in ZEB1 (c.1920G > T; p.Gln640His). COL4A1, COL4A2, and COL4A3 expression were markedly reduced in corneal keratocytes harboring a missense ZEB1 mutation (p.Gln640His).

Reduced expression of COL4A1 and COL4A3 has been reported in keratoconus.59,60 Sequencing COL4A3 and COL4A4 in 104 unrelated Slovenian patients with keratoconus did not detect mutations, although there were significant differences in the genotypes of seven previously reported polymorphisms in COL4A3 and COL4A4 between keratoconic patients and controls.53 COL4A1 mutations result in a variety of ocular defects, including abnormalities in the cornea and anterior segment.12,43 Mutational screening of COL4A1 in 15 Ecuadorian keratoconus families failed to detect pathogenic variants.44 Given the significant disruption in COL4A1 expression detected in our study and previously in keratoconus,59 further work is required to determine the role of COL4A1 in keratoconus. We detected a reduction in COL8A2 expression in corneal keratocytes harboring a missense ZEB1 mutation (p.Gln640His). Disruption of COL8A1 and COL8A2 in a knockout mouse model resulted in corneal thinning: kerato-globus.45 Missense mutations in COL8A2 result in PPCD and FECD8, although no pathologic variants have been reported in keratoconus.46

The findings reported herein and in the literature support the proposal that missense substitutions in the ZEB1 protein are associated with FECD6 and keratoconus, whereas protein truncating mutations result in PPCD3. We propose that the functional impact of the class of mutation on ZEB1 alters downstream gene expression and this forms the basis of the genotype–phenotype correlation. The identification and characterization of the molecular pathways regulated by ZEB1 in the cornea and the functional impact of mutations on these pathways is required to understand fully the observed genotype–phenotype correlations. Keratoconus and FECD result in significant ocular morbidity and are major indications for corneal transplantation.47 Dissecting the role of ZEB1 in the pathogenesis of inherited corneal dystrophies will provide important insights into maintenance of corneal shape and clarity.

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