Fuchs’ Endothelial Corneal Dystrophy and RNA Foci in Patients With Myotonic Dystrophy

V. Vinod Mootha,1,2 Brock Hansen,1 Ziye Rong,1 Pradeep P. Mammen,3 Zhengyang Zhou,2 Chao Xing,2,4,5 and Xin Gong1

1Department of Ophthalmology, University of Texas Southwestern Medical Center, Dallas, Texas, United States
2McDermott Center for Human Growth and Development, University of Texas Southwestern Medical Center, Dallas, Texas, United States
3Department of Internal Medicine, University of Texas Southwestern Medical Center, Dallas, Texas, United States
4Department of Bioinformatics, University of Texas Southwestern Medical Center, Dallas, Texas, United States
5Department of Clinical Sciences, University of Texas Southwestern Medical Center, Dallas, Texas, United States

Correspondence: V. Vinod Mootha, University of Texas Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas, TX 75390, USA; Vinod.Mootha@UTSouthwestern.edu.
Submitted: June 5, 2017
Accepted: August 15, 2017

Fuchs’ endothelial corneal dystrophy (FECD, Mendelian Inheritance in Man [MIM] 136800) is an age-related degenerative disorder of the endothelium resulting in corneal edema and loss of vision. FECD affects 4% of whites over the age of 40 in the United States1 and is the leading indication for corneal transplantation.2 The corneal endothelium, the inner postmitotic hexagonal monolayer of cells responsible for maintenance of stromal dehydration, is prone to oxidative damage, apoptosis, and premature senescence in FECD.3–9 The basement membrane of the endothelium, Descemet’s membrane, becomes diffusely thickened and develops focal excrescences termed guttatae that are visible with slit-lamp and specular microscopy. Progression loss of central endothelial cell density results in corneal edema, scarring, and loss of vision. FECD can be inherited as an autosomal dominant trait with genetic heterogeneity.11 Rare heterozygous mutations in collagen, type VIII, alpha 2 gene (COL8A2, MIM 120252) cause an early-onset corneal endothelial dystrophy.12 Other genes including solute carrier family 4, sodium borate transporter, member 11 (SLC4A11, MIM 610206), transcription factor 8 (TCF8, MIM 189909), lipoxygenase homology domains 1 (LOXHD1, MIM 613267), and ATP/GTP binding protein-like 1 (AGBL1, MIM 615523) collectively account for a small fraction of adult-onset FECD cases.13–20 Genome-wide association studies of adult-onset FECD have implicated transcription factor 4 (TCF4, MIM 602272) and more recently KN motif–ankyrin repeat domain-containing protein 4 (KANK4, MIM 614612), laminin gamma-1 (LAMC1, MIM 150290), and Na+, K+ transporting ATPase, beta-1 polypeptide (ATPB1, MIM 182350), with the TCF4 locus noted to have a predominant effect.21,22

CTG triplet repeat expansions in the third intron of TCF4 (CTG18.1 locus) are the most common genetic cause of adult-onset FECD cases in the United States23,24 TCF4 is a conserved class I basic helix-loop-helix (bHLH) transcription factor that binds to the canonical Ebox promoter sequences of target

PURPOSE. The most common cause of Fuchs’ endothelial corneal dystrophy (FECD) is an intronic CTG repeat expansion in TCF4. Expanded CUG repeat RNA colocalize with splicing factor, muscleblind-like 1 (MBNL1), in nuclear foci in endothelium as a molecular hallmark. Myotonic dystrophy type 1 (DM1) is a neuromuscular disorder caused by a CTG repeat expansion in the 3′-untranslated region (UTR) of DMPK. In this study, we examine for RNA-MBNL1 foci in endothelial cells of FECD subjects with DM1, test the hypothesis that DM1 patients are at risk for FECD, and determine prevalence of TCF4 and DMPK expansions in a FECD cohort.

METHODS. Using FISH, we examined for nuclear RNA-MBNL1 foci in endothelial cells from FECD subjects with DM1. We examined 13 consecutive unrelated DM1 patients for FECD using slit-lamp and specular microscopy. We genotyped TCF4 and DMPK repeat polymorphisms in a FECD cohort of 317 probands using short-tandem repeat and triplet repeat-primed PCR assays.

RESULTS. We detected abundant nuclear RNA foci colocalizing with MBNL1 in endothelial cells of FECD subjects with DM1. Six of thirteen DM1 patients (46%) had slit-lamp and specular microscopic findings of FECD, compared to 4% disease prevalence (P = 5.5 × 10−6). As expected, 222 out of 317 (70%) FECD probands harbored TCF4 expansion, while one subject harbored DMPK expansion without prior diagnosis of DM1.

CONCLUSIONS. Our work suggests that DM1 patients are at risk for FECD. DMPK mutations contribute to the genetic burden of FECD but are uncommon. We establish a connection between two repeat expansion disorders converging upon RNA-MBNL1 foci and FECD.

Keywords: Fuchs’ endothelial corneal dystrophy, myotonic dystrophy, triplet repeat expansion, DMPK, nuclear RNA foci
genes.\textsuperscript{25,26} The CTG18.1 locus was discovered in 1997 by the repeat expansion detection assay, with expanded alleles of greater than 57 CTG repeats found to be unstable and present in 3% of subjects in Caucasian pedigrees.\textsuperscript{27} TCF4 expansions of greater than 40 CTG repeats confer a significant risk for the development of FECD with an odds ratio (OR) of 32.3 in whites.\textsuperscript{24} The expanded allele was shown to cosegregate with complete penetrance in 52% of 29 white FECD families and with incomplete penetrance in an additional 10% of these families.\textsuperscript{24} Transethnic studies have been performed in Singapore-Chinese, Indian, and Japanese documenting the association of the triplet repeat expansion with FECD in nonwhite populations.\textsuperscript{26–30}

Myotonic dystrophy type 1 (DM1) is a paradigm for genetic disorders caused by CTG expansions. In DM1, the expansion is within the 3' untranslated region (UTR) of the dystrophin myotonia protein kinase gene.\textsuperscript{31,32} The expanded DM1 repeat RNA associates with the splicing factor muscleblind-like 1 (MBNL1) in nuclear foci that can be visualized by fluorescent in situ hybridization (FISH) and that are a molecular hallmark for \( \text{MBNL1} \) in nuclear foci which is a molecular hallmark for disease.\textsuperscript{33}\textsuperscript{34} Association of MBNL1 with mutant RNA associates with the splicing factor muscleblind-like 1 (MBNL1) in nuclear foci that can be visualized by fluorescent in situ hybridization (FISH) and that are a molecular hallmark for disease. Accumulation of expanded CUG repeat RNA nuclear foci\textsuperscript{33} with colocalization with MBNL1 and missplicing of target genes\textsuperscript{36} has been recently reported in endothelial cells of FECD subjects with the TCF4 repeat expansion.

Gatley et al.\textsuperscript{37} reported FECD in four DM1 subjects including a mother–daughter pair. No molecular studies were performed and because these are both common disorders, it can be concluded that additional studies were warranted. In this study, we explored the association between DM1 and FECD. We detected the presence of nuclear RNA-MBNL1 foci in endothelial cells from an organ donor whose corneas were found to be unsuitable for transplantation for the findings of FECD. Surprised that the donor did not harbor a TCF4 expansion, we hypothesized correctly that the subject harbored a CTG repeat expansion in the 3' UTR of the \( \text{DMPK} \) gene and subsequently confirmed a clinical diagnosis of DM1. Additionally, we tested the hypothesis that DM1 patients are at risk for FECD and determined prevalence of TCF4 and DMPK triplet repeat expansions in a University of Texas Southwestern (UTSW) FECD cohort.

**METHODS**

**Subjects**

The study was approved by the UTSW Institutional Review Board (IRB) and conducted in adherence to the tenets of the Declaration of Helsinki.

We obtained corneas from a 54-year-old white male organ donor with “muscular dystrophy” who had succumbed to a cardiac arrest from the eye bank at UT Transplant Services. Certified eye bank technicians had examined the corneas using Cellchek EB-10 specular microscopy (Konica Medical, Irvine, CA, USA) and detected FECD findings of confluent endothelial guttae and decreased endothelial cell density, and therefore found them to be unsuitable for transplantation. Additional control tissues were also obtained from the eye bank.

To test the hypothesis that patients with DM1 are at risk for FECD, we examined 13 consecutive unrelated patients with an established diagnosis of DM1 over the age of 40 (mean = 54.8, standard deviation [SD] = 10.3) from the UTSW Neuromuscular Cardiomyopathy Clinic (Table 1). Clinical genetic testing results for DM1 were obtained where available. All DM1 subjects were white. All subjects underwent an eye examination including slit-lamp microscopy by a cornea fellowship-trained ophthalmologist (VVM). Inclusion criterion for FECD was the presence of slit-lamp examination findings of grade 2 or higher on the modified Krachmer FECD grading scale: grade 0: no central guttae; grade 1: up to 12 scattered central guttae; grade 2: 12–50 scattered central guttae; grade 3: 1–2 mm confluent central guttae; grade 4: 2–5 mm of confluent central guttae; grade 5: >5-mm confluent central guttae without stromal edema; grade 6: >5-mm confluent central guttae with stromal edema.\textsuperscript{13} Specular microscopy of the corneal endothelium was performed by certified ophthalmic technicians using a Konan SL Specular Microscope (Konica Medical). The endothelial cell density and morphology parameters were calculated by the center method using the microscope's automated software: We obtained central corneal thickness.
performing the FISH assay, we stained the cells with anti-

[continued text]

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>FECD</th>
<th>Non-FECD</th>
<th>P Value‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex, No. (%)</td>
<td>M</td>
<td>1 (16.7)</td>
<td>6 (85.7)</td>
</tr>
<tr>
<td></td>
<td>F</td>
<td>5 (83.3)</td>
<td>1 (14.3)</td>
</tr>
<tr>
<td>Age, mean (SD), y</td>
<td>57.4 (10.0)</td>
<td>52.1 (10.0)</td>
<td>3.7 × 10⁻¹</td>
</tr>
<tr>
<td>Krachmer grade, mean (SD)</td>
<td>5.1 (1.0)</td>
<td>0.7 (0.5)</td>
<td>1.7 × 10⁻⁶</td>
</tr>
<tr>
<td>CCT, mean (SD), μm</td>
<td>586.1 (17.7)</td>
<td>589.6 (27.3)</td>
<td>7.0 × 10⁻¹</td>
</tr>
<tr>
<td>Cell density, mean (SD), cells/mm²</td>
<td>2066.5 (273.4)</td>
<td>3059.6 (478.6)</td>
<td>7.8 × 10⁻¹</td>
</tr>
<tr>
<td>CV, mean (SD)</td>
<td>347.2 (2.7)</td>
<td>321.5 (2.5)</td>
<td>1.3 × 10⁻¹</td>
</tr>
<tr>
<td>Hexagonal cells % (SD)</td>
<td>55.5 (8.1)</td>
<td>62.4 (6.6)</td>
<td>3.9 × 10⁻²</td>
</tr>
</tbody>
</table>

* Both eyes of each subject were used for comparison.
‡ Ultrasound pachymetry and specular microscopy were not performed on subject VVM085.

RESULTS

Abundant discrete, punctate nuclear RNA foci were identified in 85% of the endothelial cells examined from the subject (16-1348) with FECD and muscular dystrophy (Fig. 1A). Nuclear RNA foci were detected in 61% of the endothelial cells from the subject (16-3407) with FECD and TCF4 triplet repeat expansion included as a positive control (Fig. 1A). Additionally, we demonstrated colocalization of the splicing factor MBNL1 with the nuclear RNA foci (Fig. 1B) in the subject (16-1348) with FECD and muscular dystrophy. Genotyping results indicated that the subject (16-1348) did not have a TCF4 triplet expansion but rather had homozygous alleles with 12 CTG repeats at the CTG18.1 locus (Supplementary Fig. S1). Then, we hypothesized that the subject (16-1348) harbored a DMPK triplet repeat expansion. STR analysis detected an expansion at the second allele (Supplementary Table 1).

TABLE 2. A Comparison* of FECD and Non-FECD Subjects Among DM1 Patients†

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Without TCF4 Expansion</th>
<th>With TCF4 Expansion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex, No. (%)</td>
<td>n = 95*</td>
<td>n = 222*</td>
</tr>
<tr>
<td>M</td>
<td>20 (21.1)</td>
<td>80 (36.0)</td>
</tr>
<tr>
<td>F</td>
<td>75 (78.9)</td>
<td>139 (62.6)</td>
</tr>
<tr>
<td>Ethnicity, No. (%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caucasian</td>
<td>71 (75.3)</td>
<td>204 (95.8)</td>
</tr>
<tr>
<td>Other†</td>
<td>3 (3.2)</td>
<td>3 (1.4)</td>
</tr>
<tr>
<td>Age, mean (SD), y</td>
<td>67.9 (9.6)</td>
<td>69.6 (10.1)</td>
</tr>
<tr>
<td>Hexagonal grade, mean (SD)</td>
<td>5.1 (1.2)</td>
<td>5.8 (0.6)</td>
</tr>
</tbody>
</table>

* There are a few missing values in some variables.
‡ Fisher's exact test was performed when comparing other variables.
*R* Including Asian, Hispanic, and mixed ancestry.

FISH

Corneal endothelial cells from an organ donor with FECD were examined for the presence of expanded CUG repeat RNA foci. FISH with chemically synthesized (CAG)₆CA-₅ Texas red-labeled 2-0-methyl RNA 20-mers probe (8 µL at 20 ng/µL) (Integrated DNA Technologies, Coralville, IA, USA) and staining with 4′,6-diamidino-2-phenylindole, H-1500 DAPI (Vector Labs, Burlingame, CA, USA) of endothelial cells from this subject and controls were performed as we previously reported. Cells were imaged at ×60 magnification using a Widefield Delovi-

[continued text]
difference between the two groups in terms of age and CCT (Table 2). Specular microscopy confirmed the presence of guttae in all FECD subjects diagnosed by slit-lamp examination (Fig. 2). Based on specular microscopy, the eyes of FECD subjects had a lower endothelial cell density ($P$ value = $7.8 \times 10^{-3}$) and lower percentage of hexagonal cells ($P$ value = $3.9 \times 10^{-2}$) compared to the eyes of non-FECD subjects, which is compatible with the increased cellular senescence seen in FECD.

Next, we examined prevalence of the TCF4 and DMPK triplet repeat polymorphisms in the UTSW FECD cohort and found that 222 of 317 (70%) probands harbored TCF4 expansions. As we had previously reported, the subjects with the TCF4 triplet repeat expansion had a greater clinical severity of disease in comparison to their counterparts without the expansion (Table 3). 40 Out of 95 FECD subjects who did not harbor an expansion in TCF4, only 1 subject was identified with a DMPK triplet repeat expansion with alleles of 15 and 71 CTG repeats (Supplementary Fig. S2). She had undergone cataract surgery and corneal transplantation in both eyes for Krachmer grade 6 severity of FECD. Review of her past medical history revealed no prior clinical diagnosis of myotonic dystrophy. 43

Our observations confirm that TCF4 triplet repeat expansions are the predominant cause of FECD. DMPK1 triplet repeat expansions, however, can also contribute to the overall genetic burden of this disease and provide a different molecular and clinical perspective on the pathogenesis of Fuchs' Dystrophy in Myotonic Dystrophy Patients

**DISCUSSION**

Ocular findings frequently associated with DM1 include ptosis, cataracts, reticular macular dystrophy, and peripheral pigmen-

tary retinopathy. 41 Our results indicate that FECD may also be a common ocular finding, with 46% of our DM1 patients affected by FECD. A previous clinical study of DM1 subjects with a mean age of 38 (SD = 13.3) years found no abnormalities in corneal endothelial cell density or morphology using specular morphology. 42 We intentionally screened DM1 subjects over the age of 40 years because FECD is a disease of middle age. Additional studies on larger DM1 cohorts are warranted to validate our findings on the penetrance of the FECD trait with expansions in the DMPK triplet repeat polymorphism and to determine any sex bias. Further studies are also warranted to assess FECD clinical severity and any positive correlation to CTG repeat number as previously reported with TCF4 triplet repeat expansions. 40 Nearly all DM1 subjects develop a cataract. 41 Patients with comorbid FECD should be counseled that they are at increased risk of corneal edema that may require corneal transplantation at the time of or after their cataract surgery.

We found a subject in our UTSW FECD cohort with a DMPK expansion without a prior clinical diagnosis of DM1. Individuals with small DMPK expansions have a mild DM1 phenotype. They may be asymptomatic except for cataracts and lead active lives with normal life spans. 45

Our observations confirm that TCF4 triplet repeat expansions are the predominant cause of FECD. DMPK1 triplet repeat expansions, however, can also contribute to the overall genetic burden of this disease and provide a different molecular and clinical perspective on the pathogenesis of
FECD. Several genetic diseases are caused by CTG expansions, and the link between molecular mechanism and disease is best characterized for DM1. As a result, DM1 offers insights that may prove valuable for FECD, where we are in the early stages of understanding mechanism and therapeutic development.

DM1 and FECD, however, are not identical diseases even though they both originate from noncoding CTG expansions. The DMPK expansion in DM1 results in a multiorgan disease that involves various tissues in the eye including lens, retina, and corneal endothelium. In contrast, the TCF4 repeat expansion appears to affect the corneal endothelium without any clinically apparent sequela to other ocular tissues or bodily organs. We speculate that differences in triplet repeat length and/or tissue specific factors define the phenotypic spectrum of these two triplet repeat expansions.

We report here that mutant expansions in DMPK and TCF4 share important similarities, including (1) nuclear foci that contain expanded CUG repeats, (2) association of foci with MBNL1 protein, and (3) an ability to cause FECD. These results suggest that the triplet expansions in both DMPK and TCF4 may cause the same corneal endothelial tissue phenotype of FECD through shared molecular mechanisms that are triggered by toxic gain-of-function RNA. These findings provide a new window on the molecular pathogenesis of FECD and suggest that the DM1 paradigm can be used to facilitate therapeutic development.

Acknowledgments

The authors thank the patients for their participation in this study and also thank Aimee Tilley and Bryan Gallerson for study coordination efforts. We thank eye bank technician Christina Megedyuk and eye bank director Donna Drury at Transplant Services at the University of Texas Southwestern for their efforts. We thank the collaborating corneal specialists Wayne R. Bowman, James P. McCulley, Steven Verity, Sandhya Iyer, Brad Bowman, and Walter Beebe. We thank David R. Corey, PhD, for helpful discussions on the project and manuscript.

Supported by National Institutes of Health Grants R01EY022161 (VVM) and P30EY020799, and an unrestricted grant from Research to Prevent Blindness, New York, New York, USA. Support also came from National Institutes of Health Grants U54AR068791 (PPM) and UL1TR001105 (CX).

Disclosure: V.V. Mootha, None; B. Hansen, None; Z. Rong, None; P.P. Mammen, None; Z. Zhou, None; C. Xing, None; X. Gong, None

References


