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

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Submitted: June 5, 2017
Accepted: August 15, 2017
Citation: Mootha VV, Hansen B, Rong Z, et al. Fuchs' endothelial corneal dystrophy (FECD) and RNA foci in patients with myotonic dystrophy. Invest Ophthalmol Vis Sci. 2017;58:4579–4585. DOI:10.1167/iovs.17-22350

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-MBN1 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 x 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-MBN1 foci and FECD.

Keywords: Fuchs’ endothelial corneal dystrophy, myotonic dystrophy, triplet repeat expansion, DMPK, nuclear RNA foci

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 States4 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 guttae that are visible with slit-lamp and specular biomicroscopy.10 FECD is a clinical diagnosis based on the presence of confluent central guttae on slit-lamp microscopy. Progressive 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 and ankyrin repeat domain-containing protein 4 (KANK4, MIM 614612), laminin gamma-1 (LAMC1, MIM150290), 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...
genes.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.27 TCF4 expansions of greater than 40 CTG repeats confer significant risk for the development of FED with an odds ratio (OR) of 32.3 in greater than 40 CTG repeats confer significant risk for the disease.33,34 Association of MBNL1 with mutant RNA affects situ hybridization (FISH) and that are a molecular hallmark for (MBNL1) in nuclear foci that can be visualized by fluorescent in situ hybridization (FISH) and that are a molecular hallmark for disease.33,34 Association of MBNL1 with mutant RNA affects some MBNL1 target genes in affected brain, muscle, and heart tissues.34 Accumulation of expanded CUG repeat RNA nuclear foci33 with colocalization with MBNL1 and missplicing of target genes36 has been recently reported in endothelial cells of FED subjects with the TCF4 repeat expansion.

Gattey et al.37 reported FEDC 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 FEDC. 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 FEDC. 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 DMPK gene and subsequently confirmed a clinical diagnosis of DM1. Additionally, we tested the hypothesis that DM1 patients are at risk for FEDC and determined prevalence of TCF4 and DMPK triplet repeat expansions in a University of Texas Southwestern (UTSW) FEDC 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 (Koran Medical, Irvine, CA, USA) and detected FEDC 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 FEDC, we examined 13 consecutive unrelated patients with an established diagnosis of DM1 over the age of 40 (mean = 54.8, standard deviation [SD] = 10.5) 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 FEDC is Krachmer grade of 2 or greater in the more severely affected eye by slit-lamp microscopy.

**Table 1.** Demographic Information and Microscopy Results of DM1 Patients

<table>
<thead>
<tr>
<th>Subject</th>
<th>Age</th>
<th>Sex</th>
<th>OD Grade</th>
<th>OS Grade</th>
<th>OD CCT, μm</th>
<th>OS CCT, μm</th>
<th>OD Cell Density, Cells/mm²</th>
<th>OS Cell Density, Cells/mm²</th>
<th>OD CV</th>
<th>OS CV</th>
<th>TCF4 Alleles</th>
<th>DMPK Alleles</th>
<th>FEDC Status</th>
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<tbody>
<tr>
<td>VVM681†</td>
<td>52</td>
<td>F</td>
<td>2</td>
<td>1</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
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<td>573</td>
<td>2857</td>
<td>2588</td>
<td>31</td>
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<tr>
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<td>3</td>
<td>3</td>
<td>571</td>
<td>557</td>
<td>2857</td>
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<td>3</td>
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<td>600</td>
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<td>2551</td>
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<td>56, 62</td>
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<td>2817</td>
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<td>35</td>
<td>38</td>
<td>56, 54</td>
<td>16, 39</td>
<td>5, &gt;100</td>
</tr>
</tbody>
</table>

CCT, central corneal thickness based on ultrasound pachymetry; CV, coefficient of variation of endothelial cell size; F, female; M, male; NA, not available; N, no; Y, yes.

* Inclusion criterion for FEDC is Krachmer grade of 2 or greater in the more severely affected eye by slit-lamp microscopy.
† This subject harbored both DMPK and TCF4 triplet repeat expansions. Southern blot analysis of expanded DMPK alleles presented where available.
‡ This subject harbored both DMPK and TCF4 triplet repeat expansions. Southern blot analysis of expanded DMPK alleles presented where available.
MBNL1 antibody as previously described. 22 Analyzed to derive percentage of cells with RNA foci. After IL, USA). Images were processed using ImageJ software.

3 were imaged at 60 magnification using a Widefield DeltaVision pDV fluorescence microscope (GE Healthcare, Chicago, IL at 20 ng/l). Texas red-labeled 2-O-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, Texas). Then, we hypothesized that the subject (16-1348) harbored a triplet expansion but rather had homozygous alleles with 12 CTG18.1 triplet repeat polymorphism using a combination of STR analysis and TP-PCR assay.

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)6CA5 Texas red-labeled 2-O-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.23 Cells were imaged at ×60 magnification using a Widefield Delavision pDV fluorescence microscope (GE Healthcare, Chicago, IL, USA). Images were processed using ImageJ software (https://imagej.nih.gov/ij/). Fifteen representative images were analyzed to derive percentage of cells with RNA foci. After performing the FISH assay, we stained the cells with anti-MBNL1 antibody as previously described.22

Genotyping of DMPK and TCF4 Triplet Repeat Polymorphisms

DNA from the organ donor corneal tissue was extracted with Trizol reagent (Life Technologies, Carlsbad, CA, USA) per the manufacturer’s protocol. Genomic DNA was extracted from leukocytes of peripheral blood samples from each study subject using Autogen Flexigene (Qiagen, Valencia, CA, USA).

We genotyped the TCF4 CTG18.1 triplet repeat polymorphism using a combination of STR analysis and TP-PCR assay and examined the amplicons with the ABI 3730XL DNA analyzer (Applied Biosystems, Foster City, CA, USA) as previously reported.24 We genotyped the CTG triplet repeat locus at the 3’ UTR of DMPK with STR analysis and TP-PCR using locus-specific primers (Supplementary Table 1).

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 homoyzogous 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 one allele at the DMPK locus with 10 CTG repeats, and the TP-PCR assay detected an expansion at the second allele (Supplementary Fig. S1). A certified eye bank technician contacted the family of the organ donor for additional past medical history and learned that a clinical diagnosis of DM1 for the subject (16-1348) had been made 12 years prior at the age of 42. The subject’s medical diagnosis had been confirmed with clinical genetic testing which showed evidence of a trinucleotide repeat expansion in the myotonic dystrophy alleles using Southern blot analysis. The CTG repeat numbers of the two DMPK alleles were 10 and approximately 300, respectively.

Then, we examined 13 consecutive unrelated patients with an established diagnosis of DM1 for findings of FECD. Our genotyping results confirmed that all DM1 patients had DMPK triplet repeat expansions; one DM1 subject harbored both DMPK and TCF4 triplet repeat expansions (Table 1). We observed that 6 out of 13 (46%) of the DM1 subjects had slit-lamp examination findings of grade 2 or higher on the modified Krachmer FECD grading scale, which is significantly higher than the 4% prevalence of FECD in the US population over the age 40 (P value = 5.5 × 10−6). The female DM1 subjects were more likely to be affected with FECD than their male counterparts (P value = 2.9 × 10−2; Table 2), compatible with the known female bias for FECD.38,39 There was no significant

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

<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></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M</td>
<td>1 (16.7)</td>
<td>6 (85.7)</td>
<td>2.9 × 10−2</td>
</tr>
<tr>
<td>F</td>
<td>5 (83.3)</td>
<td>1 (14.3)</td>
<td></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>2066.3 (27.4)</td>
<td>5095.6 (478.6)</td>
<td>7.8 × 10−3</td>
</tr>
<tr>
<td>CV, mean (SD)</td>
<td>34.7 (2.7)</td>
<td>32.1 (5.2)</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 VVM683.

**Table 3.** Demographic Information of FECD Cohort

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Without TCF4 Expansion n = 95*</th>
<th>With TCF4 Expansion n = 222‡</th>
<th>P Value‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex, No. (%)</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>M</td>
<td>20 (21.1)</td>
<td>80 (36.0)</td>
<td>8.2 × 10−3</td>
</tr>
<tr>
<td>F</td>
<td>75 (78.9)</td>
<td>139 (62.6)</td>
<td></td>
</tr>
<tr>
<td>Ethnicity, No. (%)</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Caucasian</td>
<td>71 (75.3)</td>
<td>204 (95.8)</td>
<td>2.5 × 10−7</td>
</tr>
<tr>
<td>African</td>
<td>20 (21.3)</td>
<td>6 (2.8)</td>
<td></td>
</tr>
<tr>
<td>Other‡</td>
<td>3 (3.2)</td>
<td>3 (1.4)</td>
<td></td>
</tr>
<tr>
<td>Age, mean (SD), y</td>
<td>67.9 (9.6)</td>
<td>69.6 (10.1)</td>
<td>1.5 × 10−1</td>
</tr>
<tr>
<td>Krachmer grade, mean (SD)</td>
<td>5.1 (1.2)</td>
<td>5.8 (0.6)</td>
<td>4.3 × 10−7</td>
</tr>
</tbody>
</table>

* There are a few missing values in some variables.
‡ Fisher’s exact test was performed when comparing sex and ethnicity distribution, and 2-sample t-test was performed when comparing other variables.
§ Including Asian, Hispanic, and mixed ancestry.

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The 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 \((P = 7.8 \times 10^{-3})\) and lower percentage of hexagonal cells \((P = 3.9 \times 10^{-2})\) 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.

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 \(DMPK\) triplet repeat expansion 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. 43 Our observations confirm that \(TCF4\) triplet repeat expansion are the predominant cause of FECD. \(DMPK\) 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 retinopathy. 44

**FIGURE 1.** Nuclear RNA foci accumulate and colocalize with MBNL1 in corneal endothelial cells with triplet repeat expansion in \(DMPK\) gene. (A) FISH with a \((CAG)_{6}CA-5\) Texas red-labeled 2-O-methyl RNA 20-mers probe (Integrated DNA Technologies) on endothelial cells of FECD/DM1 subject (16-1348) with an expanded \(DMPK\) allele with 300 CTG repeats revealed punctate, nuclear RNA foci (red). RNA foci were present in endothelial cells from a FECD subject (16-3407) with an expanded \(TCF4\) allele with 71 CTG repeats and absent in cells from unaffected subject (16-0729) without the \(DMPK\) and \(TCF4\) repeat expansions. DNA was stained with DAPI (blue). The scale bar represents 25 μm. (B) Colocalization of MBNL1 with the expanded CUG repeat nuclear foci. After hybridization with RNA probe (red), cells were stained with anti-MBNL1 antibody (green) and DAPI (blue). The scale bar represents 10 μm.
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 Drurry 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

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