Late-Onset Macular Degeneration and Long Anterior Lens Zonules Result from a CTRP5 Gene Mutation

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PURPOSE. To identify the gene responsible for a complex ocular phenotype of late-onset macular degeneration, long anterior zonules (LAZ), and elevated intraocular pressure (IOP) and to study its expression.

METHODS. Ocular examination, visual field, fluorescein angiography, and electrophysiology testing were performed. One affected individual was treated with vitamin A. DNA from 55 family members (UM:H389) was used for linkage, mapping, and mutation analysis. Linkage analysis of macular degeneration and LAZ phenotypes was performed independently. Mutations in candidate genes were screened by sequencing. mRNA expression of CTRP5 and MFRP, which are bicistronic genes, was studied by semiquantitative RT-PCR (qRT-PCR) in various human tissues. CTRP5 expression was also evaluated by in situ hybridization.

RESULTS. Affected members had LAZ detectable by the third decade and/or macular degeneration by the fourth to fifth decade. A six-month treatment with vitamin A shortened dark adaptation considerably in one affected member. Both conditions mapped independently with zero recombination to 11q23, with maximum lod scores of 3.31 for macular degeneration and 5.41 for LAZ. The same CTRP5 missense mutation was identified in all affected individuals. Retinal pigment epithelium (RPE) and ciliary epithelium (CE) showed highest CTRP5 transcript expression, which was also true for MFRP. CTRP5 tissue expression was confirmed by in situ hybridization.

CONCLUSIONS. A single locus at 11q23 is implicated in a complex ocular phenotype involving RPE and CE, tissues of neuroectodermal origin. All individuals with either LAZ and/or macular degeneration carry the same CTRP5 S163R mutation, which is transmitted in autosomal dominant manner. (Invest Ophthal-mol Vis Sci. 2005;46:3363–3371) DOI:10.1167/iovs.05-0159

Clinical forms of macular degeneration have a broad phenotypic and genotypic spectrum. The disease is characterized by drusen, which subsequently can be associated with local tissue atrophy or with neovascularization of the choroid and lead to loss of central vision and blindness.1 To date, at least 10 genes associated with various forms of macular degeneration have been identified. Seven additional loci have been mapped, but the genes are yet to be cloned.2-5

We have studied a large pedigree (UM:H389) with progressive macular degeneration that manifests primarily by the fifth decade of life.6 Most of the older affected family members showed abnormally long anterior zonules (LAZ) on the anterior capsule of the crystalline lens and had a reduced zonule-free zone. Several younger family members who have not yet manifested macular degeneration have LAZ. Macular degeneration and LAZ both appear to segregate as autosomal dominant traits. Several older members with LAZ had ocular hypertension or glaucoma.

We have published the clinical characteristics of the macular degeneration and LAZ in this family.6-7 The macular findings have phenotypic overlap with Sorsby fundus dystrophy,8 late-onset macular degeneration associated with RDS peripherin gene mutations,9 age-related macular degeneration (AMD),10 and late-onset retinal degeneration (L-ORD).11 Co-occurrence of LAZ with macular degeneration has not been reported previously for any of these conditions, although several individuals in families with Sorsby fundus dystrophy are reported to have glaucoma.8,12-14

We conducted a genomewide search for linkage and found that both traits of macular degeneration and LAZ map to the same region (q23) of chromosome 11 and that both traits can be accounted for by an S163R missense mutation in the complement-C1q tumor necrosis factor-related protein gene, CTRP5. In the process, we definitively excluded most of the previously known macular degeneration loci and approximately 90% of the genome. In addition to this genetic analysis, tissue expression of CTRP5 and its bicistronic partner membrane-type frizzled-related protein (MFRP), was found to be highest in the retinal pigment epithelium (RPE) and in the ciliary epithelium (CE), tissues of neuroectodermal origin, and are implicated in the disease observed in family UM:H389.

METHODS
Clinical Studies
Informed consent was obtained from all participating individuals, according to protocols approved by institutional review boards at the University of Michigan, The Johns Hopkins University, and the National Eye Institute. The protocol is in accord with the tenets of the Declaration of Helsinki. Clinical examinations were performed on 42 members of family UM:H389, including all living individuals older than 48 years. The macular degeneration was described earlier in some these...
The family is of French and English extraction and immigrated in the 1800s.

The ocular examination included biomicroscopy, gonioscopy, intraocular pressure (IOP), and retinal funduscopy. Psychophysical testing included standard visual field measurement by Humphrey and/or Goldmann perimetry. In patient V:32, the time course of recovery of cone and rod sensitivity was evaluated in the central 10° after a 5-minute exposure to a 2700 cd/m² white bleaching light. A version of the same instrument, modified to perform von Bekesy tracking, was used to measure changes in threshold as a function of time.

For linkage analysis the two phenotypes, LAZ and macular degeneration, were treated as independent traits in this family, using the MLINK program of the LINKAGE package (http://linkage.rockefeller.edu/soft/ linkage/; provided in the public domain by the Rockefeller University, New York, NY) and an affected-only model.19,20 The disease was coded as an autosomal dominant trait with 0.0001 gene frequency for the affected allele. Marker allele frequencies were taken from the genome database. Lod scores for markers near the L-ORD locus at 11q23 were also calculated in an age-dependent penetrance model, with individuals older than age 48 and without macular changes coded as unaffected.

### Vitamin A Supplementation

One subject (V:32), with extensive drusen accumulation in the temporal perifovea of both eyes, was symptomatic family members, had preservation of central vision that was determined, the subject was given oral 15,000 IU vitamin A palmitate daily, and visual function at night and in dim light. After baseline visual function was determined, the subject was given oral 15,000 IU vitamin A palmitate daily, and visual function was evaluated again from 2 to 6 months later. This subject was selected for these measurements because the subject was considerably symptomatic but, unlike other such symptomatic family members, had preservation of central vision that allowed the performance of psychophysical tests with ease. All visual function tests were performed with natural pupils.

### Genotyping

Genotyping was performed by using microsatellite markers on leukocyte DNA collected from 48 family members and seven spouses. DNA from two subjects from the Centre d’Etude du Polymorphisme Humain (CEPH) were analyzed concurrently as the control. A linkage-mapping program (MD-10, ver. 2.0; Applied Biosystems, Inc. [ABI], Foster City, CA) was used for genome scans. Allele sizes were estimated with a commercial standard (ROX50 standard; ABI). Genotypes were then analyzed on computer (Genescan and Genotyper software; ABI). Allele frequencies were obtained from the CEPH database.

### Linkage Analysis

For linkage analysis the two phenotypes, LAZ and macular degeneration, were treated as independent traits in this family, using the MLINK program of the LINKAGE package (http://linkage.rockefeller.edu/soft/linkage/; provided in the public domain by the Rockefeller University, New York, NY) and an affected-only model.19,20 The disease was coded as an autosomal dominant trait with 0.0001 gene frequency for the affected allele. Marker allele frequencies were taken from the genome database. Lod scores for markers near the L-ORD locus at 11q23 were also calculated in an age-dependent penetrance model, with individuals older than age 48 and without macular changes coded as unaffected.

### Mutation Analysis

The sequences containing exons and exonic-intron boundaries of the MFRP and CTRP5 genes were amplified using primers reported earlier.13 Mutation analysis was performed by sequencing the PCR-amplified products, as previously described (3100 Sequencer; ABI).21

### RNA Isolation

Tissues were dissected from human donor eyes obtained within 16 to 20 hours of death through the Midwest Eye Bank and Transplantation Center in Ann Arbor, MI. Retina, RPE, optic nerve (ON), and cornea were collected from a 69-year-old donor eye; iris and ciliary body (CB) were collected from a 75-year-old donor eye; and CE was dissected from a 53-year-old donor eye. After they were harvested, these tissues were stored in RNA extraction reagent (TRIZol; Invitrogen, Carlsbad, CA) at −80°C. Cultured RPE, orbital fibroblasts (OF), sclera, and Tenon’s capsule (TC) were harvested and stored in the same reagent (TRIZol; Invitrogen). Similarly, cell lines derived from nonpigmented epithelium (NPE), smooth muscle (SM), trabecular meshwork (TM), lens epithelium (LE), and RPE were also harvested in the extraction reagent (TRIZol; Invitrogen) for use in this study. RNA was isolated with the reagent, according to the manufacturer’s protocol.

### Real-Time Semiquantitative RT-PCR

Total RNA was treated with RNase-free DNase and purified (RNasefree DNase; Promega, Madison, WI) and used for first-strand cDNA synthesis (SuperScript First-Strand Synthesis System for RT-PCR; Invitrogen). Primers for qRT-PCR were designed from regions of gene sequences that expand over at least one intron, by using commercial software (Beacon Designer 2.0 software program; Bio-Rad, Hercules, CA; Table 1). Three sets of control primers were derived from the GAPDH, HPRT, and -b-actin genes were used to normalize and validate the CTRP5 and MFRP gene expression.11,22 A supermix (iQ SYBR Green Supermix; Bio-Rad) and a thermocycler (iTeycycler; Bio-Rad) were used to perform quantitative PCR and a melt-curve analysis. The relative quantity of expression of CTRP5 and MFRP in different samples was calculated by the comparative threshold cycle (Ct) method.22 Expression data were calculated from three independent qRT-PCR reactions performed for each RNA sample. These were normalized to the expression levels of three control housekeeping genes, and the mean results are presented on an arbitrary scale, to represent the relative levels of expression.

### In Situ Hybridization

Probes were generated from cDNA clone IMAGE:5278184, which contains the full-length (1.5 kb) coding sequence of human CTRP5. The CTRP5 cDNA fragment was amplified with T3 and T7 primers, and T3 and T7 RNA polymerases were used to generate digoxigenin-labeled sense and antisense riboprobes, respectively (DIG-RNA label-

Individuals with LAZ; (●) individuals with late-onset macular degeneration; (◇) individuals with macular degeneration and LAZ; (◆) unaffected. Slashed symbols: deceased. a, anterior capsule is absent for ascertainment of LAZ; b, not available for clinical examination; c, status of LAZ is unknown; d, status of macular degeneration is unknown. Filled bars: haplotype associated with the disease. Individual identification numbers are shown in roman numerals. The individual identification numbers shown for family members are the same as the identification numbers shown in our previously published pedigree of the family. Haplotypes of individuals III:4, III:3, III:11, III:12, IV:1, and IV:2 are derived from the data of their offspring and shown in parentheses. Ages of some members are shown in arabic numerals below the identification number. The sex of the family members is not shown, to maintain the privacy of individuals at risk of development of macular degeneration later in life.
According to previously published protocols. Maintenance and segments of human eyes, and also from the eyes of albino mice, ular pressure and glaucoma subsequently developed. With late-onset macular degeneration and LAZ elevated intraoc-
secutive generations (Fig. 1). In several older family members
deviation that became symptomatic in the fourth to fifth
cade. Ten individuals in UM:H389 were affected with macular
degeneration identified marker D11S4127 as the proximal boundary for macular degeneration. One died subsequent to initial retinal examina-
tion (IV:29), two were not available for evaluation of the
definitive signs of macular degeneration. The lens and zonules
could not be evaluated in four older members with macular
degeneration distal to this marker. A recombination in IV:17
with macular degeneration and LAZ phenotype, we
excluded the loci for pigmentary dispersion syndrome, Marfan
syndrome, pseudoxfoliation syndrome, and previously
mapped glaucoma loci. Further, more than 90% of the
genome was excluded before identifying positive lod scores,
indicating linkage on the long arm of chromosome 11 for both
LAZ and macular degeneration.

Recombination events in individuals V:23 and V:9 with LAZ iden-
tified the same locus for both LAZ and macular degeneration.

Two of three individuals affected with both macular degen-
eration and LAZ had elevated IOP (IV:8 and IV:11), and in one
(IV:13), glaucoma developed and was treated with topical
medication. No other systemic abnormalities were noted in the
medical history of members of this family. From the clinical
data, it could not be determined whether macular degenera-
tion and LAZ were associated with a single locus or were two
independent traits cosegregating in this family.

**Linkage and Haplotype Analysis**

On the basis of significantly negative lod scores, we excluded
all the previously mapped macular degeneration loci, including
the RDS/peripherin, Stargardt macular degeneration, Stargart-
dyno honeycomb retinal dystro-
phy, Best or vitelliform macular degeneration, North Carolina
macular degeneration (MCDR1), MCDR2, MCDR3, and
ARMDI loci. Similarly, for the LAZ phenotype, we
excluded the loci for pigmentary dispersion syndrome, Marfan
syndrome, pseudoxfoliation syndrome, and previously
mapped glaucoma loci. Further, more than 90% of the
genome was excluded before identifying positive lod scores,
indicating linkage on the long arm of chromosome 11 for both
LAZ and macular degeneration.

**RESULTS**

**Clinical Studies**

In the UM:H389 family, 55 family members were examined.
Several family members affected with macular degeneration
were examined on multiple occasions over more than a de-
cade. Ten individuals in UM:H389 were affected with macular
degeneration that became symptomatic in the fourth to fifth
decade. The macular degeneration phenotype in this family
followed an autosomal dominant inheritance across four con-
secutive generations (Fig. 1). In several older family members
with late-onset macular degeneration and LAZ elevated intraoc-
ular pressure and glaucoma subsequently developed.

The LAZ phenotype was observed in 18 individuals be-
tween 24 to 80 years of age. All six individuals with LAZ over
the age of 48 years also showed the macular degeneration
phenotype. The remaining 12 with LAZ were between 24 to 47
years of age and were presumed to be too young to show
definitive signs of macular degeneration. The lens and zonules
could not be evaluated in four older members with macular
degeneration. One died subsequent to initial retinal examina-
tion (IV:29), two were not available for evaluation of the
anterior segment (IV:17 and IV:20), and one was aphakic after
cataract surgery (V:4). However, all children of V:4 had LAZ,
indicating linkage on the long arm of chromosome 11 for both
LAZ and macular degeneration.

Further analysis of markers D11S908, D11S4127, D11S925,
D11S4167, and D11S4151 at 11q23 gave positive lod scores
for both the macular degeneration and the LAZ phenotype
(Table 2). All individuals affected with both macular degener-
ation and LAZ carried the identical haplotype at 11q23, implic-
ating the same locus for both traits.

Recombinations observed in family members with macular
degeneration localized this phenotype to a 6-cM interval
between the markers D11S4127 and D11S925. A recombina-
tion was observed in three affected siblings (IV:8, IV:11, and
IV:13) at the marker D11S4127, placing the gene for macular
degeneration distal to this marker. A recombination in IV:17
with macular degeneration identified marker D11S925 as the
distal boundary.

Similar information was developed for the trait of LAZ. Individuals IV:8, IV:11, and IV:13, who determined the proximal
boundary for the macular degeneration locus, also had
LAZ, which identifies D11S4127 as the proximal boundary for
LAZ. Unfortunately, individuals IV:17 and V:44 who defined
the distal boundary for the macular degeneration locus, were
not available for anterior segment examination. However, re-
combination events in individuals V:23 and V:9 with LAZ iden-
tified D11S4151 as the distal boundary for the LAZ locus.
Individual IV:24 was clinically negative for LAZ at age 44, but
inherited the haplotype associated with LAZ distal to D11S925,
thereby identifying this marker as the distal boundary for the
LAZ locus. These observations localized the loci for both the
macular degeneration and the LAZ to the 6-cM interval at
11q23 between markers D11S4127 and D11S925. Haplotype
analysis by incorporating single-nucleotide polymorphisms
(SNPs) in the region further narrowed the critical interval to a
1.35-Mb region between markers rs3181261 (V:24) and
rs715849 (V:44; Fig. 2). The recombination observed in the

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**Table 2. Two-point lod Scores of Markers on Chromosome 11 Versus Macular Degeneration and Anterior Lens Zonules Loci**

<table>
<thead>
<tr>
<th>Markers</th>
<th>Distance* (cM)</th>
<th>0</th>
<th>0.001</th>
<th>0.05</th>
<th>0.1</th>
<th>0.2</th>
<th>0.3</th>
<th>0.4</th>
<th>Zmax</th>
<th>Theta</th>
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<td></td>
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<td></td>
</tr>
<tr>
<td>D11S908</td>
<td></td>
<td>-2.125</td>
<td>-0.1083</td>
<td>0.535</td>
<td>0.73</td>
<td>0.712</td>
<td>0.486</td>
<td>0.192</td>
<td>0.73</td>
<td>0.1</td>
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<tr>
<td>D11S4127</td>
<td>5</td>
<td>-1.285</td>
<td>-0.2483</td>
<td>1.19</td>
<td>1.256</td>
<td>1.054</td>
<td>0.686</td>
<td>0.262</td>
<td>1.256</td>
<td>0.1</td>
</tr>
<tr>
<td>S163R</td>
<td>1.6</td>
<td>3.311</td>
<td>3.305</td>
<td>3.021</td>
<td>2.716</td>
<td>2.058</td>
<td>1.33</td>
<td>0.549</td>
<td>3.311</td>
<td>0</td>
</tr>
<tr>
<td>D11S924</td>
<td>0.2</td>
<td>0.901</td>
<td>0.898</td>
<td>0.733</td>
<td>0.579</td>
<td>0.524</td>
<td>0.144</td>
<td>0.055</td>
<td>0.901</td>
<td>0</td>
</tr>
<tr>
<td>D11S925</td>
<td>3</td>
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<td>-0.301</td>
<td>1.162</td>
<td>1.213</td>
<td>0.993</td>
<td>0.629</td>
<td>0.256</td>
<td>1.213</td>
<td>0.1</td>
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<td>-0.477</td>
<td>0.979</td>
<td>1.027</td>
<td>0.804</td>
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<td>0.136</td>
<td>1.027</td>
<td>0.1</td>
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<td>-3.901</td>
<td>-0.675</td>
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<td>0.064</td>
<td>0.023</td>
<td>0.064</td>
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<tr>
<td>D11S908</td>
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<td>0.206</td>
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<td>3.846</td>
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<td>4.609</td>
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<td>3.705</td>
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<td>D11S925</td>
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<td>2.999</td>
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<td>1.081</td>
<td>0.395</td>
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<tr>
<td>D11S4151</td>
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<td>-4.08</td>
<td>-0.848</td>
<td>-0.349</td>
<td>-0.079</td>
<td>-0.011</td>
<td>-0.006</td>
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</table>

* Distance to the next distal marker.
ward et al. have reported a point mutation in the \( \beta \)-amyloid precursor protein (APP) gene in a family with autosomal dominant \( \beta \)-amyloid deposition in the eye (LAZ). No mutations were found after gene sequencing in family UM:H389 with late-onset macular degeneration (AMD) in families with L-ORD. We performed mutation analysis on both genes, which are fully sequenced. In contrast, we found a serine163arginine change in the \( \beta \)-amyloid protein (APP) gene in 100 normal control subjects. The same mutation was observed in all 100 normal control subjects. The change was found to be absent in 1000 normal control subjects. The change was found to be absent in 1000 normal control subjects.

### Mutation Analysis of Candidate Genes

Several candidate genes were identified in the 1.35-Mb critical interval by consulting the National Center for Biotechnology Information database (www.ncbi.nlm.nih.gov/ provided in the public domain by the National Institutes of Health, Bethesda, MD). The \( MFRP \) gene, previously shown to carry mutations in the mouse retinal degeneration 6 (rd6), and the \( CTRP5 \) gene, located in the 3'-untranslated sequence of the \( MFRP \) gene, were identified as candidate genes, due to their location in the critical interval.

While these studies were in progress, Hayward et al. have reported a point mutation in \( CTRP5 \) in families with L-ORD by Hayward et al. In addition, the change was found to be absent in 1000 normal control subjects analyzed by Hayward et al.

### \( CTRP5 \) and \( MFRP \) Expression in Human Ocular Tissues and Cell Lines

Quantitative expression profiles of both \( CTRP5 \) and \( MFRP \) were determined in the human ocular tissues by qRT-PCR. The highest level of \( CTRP5 \) mRNA expression was observed in the RPE. Lower levels were present in the CB (Fig. 3). Cultured RPE cells also showed a significant and almost equal level of \( CTRP5 \) expression as did native RPE. Low levels of expression were detected in the ON, sclera, and retina. Cultured human cells derived from LE showed a significant level of \( CTRP5 \) expression. An RPE cell line also showed expression of \( CTRP5 \), but the amount was much lower than that in the primary RPE tissue. Low levels of \( CTRP5 \) expression were detected in the cell lines derived from ciliary SM and TM (Fig. 3). Similar to the pattern of expression of the \( CTRP5 \) transcript, the highest levels of \( MFRP \) expression were detected in the RPE and CB. No significant expression was detected in the retina, cornea, ON, and sclera. Low levels of expression were detected in CE and cultured RPE but not in other tissues and cell lines tested (Fig. 4).

### Cellular Localization of the \( CTRP5 \) Gene in Human Ocular Tissue

\( CTRP5 \) expression was detected in the sections of human eye by in situ hybridization using labeled riboprobes (Figs. 5A–D). Corresponding to the expression detected by qRT-PCR, the \( CTRP5 \) gene was detected in the RPE layer in the human retinal sections by in situ hybridization (Figs. 5B, 5C). Expression was also observed in the retinal ganglion cell layer and in a few cells of the nuclear layer, perhaps representing a subset of amacrine cells (Fig. 5B). The expression of \( CTRP5 \) in the CB and iris could not be resolved by in situ hybridization because of interference from the pigmented cells. \( CTRP5 \) expression in the remaining parts of the anterior segment of the human eye was not significant.

In situ hybridization of tissue sections from albino mice localized \( CTRP5 \) expression to the RPE and CE, consistent with our observations on the expression of \( CTRP5 \) in human ocular tissue by in situ hybridization and q-RT PCR (Figs. 5C, 5D).

### Improvement of Rod Psychophysical Function after Vitamin A Supplementation

Individual V:32, who was the 48-year-old offspring of IV:11, reported sensitivity to daylight glare and reduced visual function at night. The subject had LAZ and extensive accumulation of drusen in a region 15° temporal from the fovea (Fig. 6), but the macula otherwise appeared clinically normal, and visual acuity was better than 20/20 in each eye. Other aspects of retinal function were also normal, including visual fields and electroretinogram responses. Although dark-adaptation testing gave normal absolute rod thresholds centrally, a 1-log-unit elevation of this threshold was measured in the area with...
drusen (15° nasal to fixation). The recovery of rod sensitivity from adaptation to a bleaching light was markedly delayed, as judged by the cone–rod break time of 18 minutes, which is prolonged far beyond the upper limit of the normal range seen in our control subjects (6.9 minutes; Fig. 7).

After this evaluation, the subject was started on a daily intake of 15,000 IU vitamin A palmitate and returned at 2, 4, and 6 months for reevaluation. After 2 months, this individual’s dark-adaptation function had improved considerably, and the cone–rod break was 14 minutes. After 4 months, the cone–rod break was not further shortened, but the slope of the rod limb became steeper. These improved results were maintained after 6 months. This also suggests that the improved dark-adaptation function was reproducible and similar to that established for control subjects. Absolute threshold remained normal and unchanged throughout the study. Concomitantly, the subject volunteered that the visual function in dim light had improved appreciably and previous sensitivity to glare was reduced.

DISCUSSION

Family UM:H389 segregated two ocular phenotypes—macular degeneration and LAZ—both in an autosomal dominant fashion. Although several family members showed both conditions, incomplete clinical data precluded determining that the two conditions cosegregate. After our initial description of this family, we uncovered an additional branch of the pedigree and obtained further clinical information to initiate a genome-wide linkage study. Both conditions mapped to a 1.35-Mb interval on 11q23 that includes CTRP5, a gene implicated in L-ORD. Sequencing revealed an S163R mutation in CTRP5 in all family members who had either macular degeneration or LAZ. Complete concordance of LAZ and the disease haplotype was observed in family members aged 24 to 80 years. The youngest individual with macular degeneration in this family was 48 years old at diagnosis. LAZ were present in individuals as young as 24 years.

Based on the expression of CTRP5 in the RPE and the CE, the next goal is to understand the role of this gene in the two tissues involved in the UM:H389 family phenotype. The CTRP5 gene encodes a secretory protein with homology to short-chain collagens and is predicted to be a member of extracellular matrix. The retina from a CTRP5 Ser163Arg–bearing patient with L-ORD showed retinal degeneration and a thick layer of extracellular deposits between RPE and Bruch’s membrane. The Ser163Arg mutation appears to cause an age-
related accumulation of substances between Bruch's membrane and RPE. Similar sub-RPE deposits have also been observed in retinas from patients with mutations in the TIMP3, HEMICENTIN-1, and EFEMP1 genes and in mouse retina lacking collagen 18A. These genes, TIMP3, EFEMP1, and HEMICENTIN-1, encode for extracellular matrix proteins, and mutations in these genes result in macular dystrophy with subretinal deposits similar to our family UM:H389 with a mutation in CTRP5. These observations suggest that the extracellular matrix proteins encoded by these genes are important in normal RPE function.

Based on the LAZ in UM:H389, it appears that CTRP5 also has a role in the CE. Although the same S163R CTRP5 mutation was found to be associated with L-ORD, anterior segment anomalies have not been reported in patients with L-ORD. It is critical to screen for anterior segment changes in existing pedigrees carrying the S163R mutation in CTRP5. The clinical finding of LAZ has been described in both black and white populations, with and without elevated IOP and/or glaucoma. Other reports on zonules relate to known abnormalities associated with pseudoexfoliation, Marfan syndrome, homocystinuria, and ectopia lentis. It appears that the LAZ are structurally robust, because cataract complications, spontaneous crystalline lens subluxation, or zonular dehiscence have not been reported in cases of LAZ. Understanding the role of CTRP5 in the CE and normal zonule anatomy is of interest for the study of the mechanism underlying LAZ phenotype.

Our study in one patient with macular degeneration with the CTRP5 mutation may provide clues to the course of degeneration. It has been reported that delayed dark-adaptation is an early retinal phenotypic marker of L-ORD, which manifests up to a decade before macular degeneration. A 1-month, high-dose vitamin A (50,000 IU per day) supplementation improved dark adaptation kinetics in three patients with L-ORD. Several members of our UM:H389 family reported impaired visual function at night and in dim lighting, before onset of macular degeneration. Rod absolute-threshold sensitivity was elevated in four of five affected individuals tested, albeit after structural tissue damage had already occurred in the macula. A 48-year-old (V:32) family member, who had macular drusen, but otherwise structurally normal features on clinical examination, reported impaired vision under scotopic conditions, which was confirmed by prolonged dark adaptation. After the patient had taken 15,000 IU daily of vitamin A palmitate for 6 months, the time course of rod dark adaptation improved in this subject, implying that there is a metabolic deficiency compromising the function of these photoreceptors. The functional improvement does not mean, however, that structural degeneration of macular tissue would benefit from a strategy of vitamin A supplementation. Reversal of night blindness by vitamin A supplementation in patients with Sorsby fundus dystrophy has also been reported.

A slowed time course of dark adaptation and/or elevated rod dark-adapted absolute threshold sensitivity has also been found with Sorsby macular degeneration. Malattia Leven-
subretinal deposition of lipofuscin material and/or thickening, degeneration. It is not surprising that L-ORD and LAZ phenotypes in UM:H389 cosegregate. Understanding the pathophysiology of disease manifested in both the anterior and posterior segments in patients with CTRP5 mutations and other related extracellular matrix genes will help in unraveling the process of late-onset macular degeneration.

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References