Persons with Age-Related Maculopathy Risk Genotypes and Clinically Normal Eyes Have Reduced Mesopic Vision

Beatrix Feigl, Dingcai Cao, Charles P. Morris, and Andrew J. Zele

PURPOSE. To determine whether participants with normal visual acuity, no ophthalmoscopically signs of age-related maculopathy (ARM) in both eyes, and who are carriers of the CFH, LOC387715, and HRTA1 high-risk genotypes (gene-positive) have impaired rod- and cone-mediated mesopic visual function compared with persons who do not carry the risk genotypes (gene-negative).

METHODS. Fifty-three Caucasian study participants (mean 55.8 ± 6.1) were genotyped for CFH, LOC387715/ARMS2, and HRTA1 polymorphisms. Single-nucleotide polymorphisms were genotyped in the CFH (rs380390), LOC387715/ARMS2 (rs10490924), and HRTA1 (rs11200638) genes using optimized gene-expression assays. The critical fusion frequency (CFF) mediated by cones alone (long, middle-, and short-wavelength sensitive cones, LMS) and by the combined activities of cones and rods (LMSR) were determined. The stimuli were generated using a four-primary photostimulator that provides independent control of the photoreceptor excitation under mesopic light levels. Visual function was further assessed using standard clinical tests, flicker perimetry, and microperimetry.

RESULTS. The mesopic CFF mediated by rods and cones (LMSR) was significantly reduced in gene-positive compared to gene-negative participants after correction for age (P = 0.05). Cone-mediated CFF (LMS) was not significantly different between gene-positive and gene-negative participants. There were no significant associations between flicker perimetry and microperimetry and genotype.

CONCLUSIONS. This is the first study to relate ARM risk genotypes with mesopic visual function in clinically normal persons. These preliminary results could become of clinical importance because mesopic vision may be used as a biomarker to document subclinical retinal changes in persons with risk genotypes and to determine whether those persons progress into manifest disease. (Invest Ophthalmol Vis Sci. 2011;52:1145-1150) DOI:10.1167/iovs.10-5967

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Corresponding author: Beatrix Feigl, Medical Retina Laboratory, Institute of Health and Biomedical Innovation, Queensland University of Technology, 60 Musk Avenue, Brisbane 4059, Queensland, Australia; b.feigl@qut.edu.au.
mittee and the tenets of the Declaration of Helsinki. Fifty-three healthy volunteers (28 female and 25 male) were enrolled through advertisement in university and community newspapers. Participants (mean age, 55.8 ± 6.1 years; range, 46–68 years) had no history of ocular or systemic disease and underwent a complete eye examination by an ophthalmologist (BF) according to the inclusion and exclusion criteria (Table 1). Participants had visual acuity ≥ 20/20, normal color and contrast vision, and no retinal anatomic abnormalities as measured with optical coherence tomography (OCT) and ophthalmoscopy. Crystalline lens and fundus grading was performed according to the Age-Related Eye Disease Study (AREDS) templates, and participants were excluded with any posterior subcapsular cataract, cortical, or nuclear opacities higher than grade 1 or signs of early ARM (level 1).15,16

Perimetry and mesopic vision testing was performed with the right eyes, and practice trials were conducted to familiarize participants with the protocols.

**Genotyping**

Saliva samples were collected (OraGene DNA Self-Collection kit; DNA Genotek Inc, Kanata, Ontario, Canada), and DNA was manually extracted from the participants’ sample using this protocol and genotyped for selected polymorphisms using optimized gene-expression assays (TaqMan Gene Expression Assay; Applied Biosystems, Inc., Foster City, CA) on a real-time thermal cycler (ABI 7500; Applied Biosystems, Inc.).17 DNA was screened for the SNPs in the complement factor H gene on 1q32, gene (CFH), and strong linkage disequilibrium has been demonstrated across this region. Ten participants were excluded from mesopic vision and performance trials after ophthalmological examination revealed a cataract > AREDS grade 1 (n = 1), early ARM (n = 5), congenital disc disorder (n = 1), protanopia (n = 1), macular glios (n = 1), and intraocular lens extraction after cataract (n = 1). Of the remaining 45 participants, 28 carried one or more of the risk genotypes (gene-positive), and 15 had no gene variants (gene-negative). Genotyping confirmed the strong linkage disequilibrium across the 1q26 by showing complete disequilibrium between the LOC387715 and HTRA1 genes. The investigator (BF) was masked to the genetic results as genotyping the complement factor H gene on 1q32, gene (CFH), and strong linkage disequilibrium has been demonstrated across this region.18,19, we therefore genotyped both SNPs in the ARMS2 and HTRA1 genes.

In total, 53 participants were genotyped and examined ophthalmologically. Ten participants were excluded from mesopic vision testing and perimetry testing after ophthalmological examination revealed a cataract > AREDS grade 1 (n = 1), early ARM (n = 5), congenital disc disorder (n = 1), protanopia (n = 1), macular glios (n = 1), and intraocular lens extraction after cataract (n = 1). Of the remaining 45 participants, 28 carried one or more of the risk genotypes (gene-positive), and 15 had no gene variants (gene-negative). Genotyping confirmed the strong linkage disequilibrium across the 1q26 by showing complete disequilibrium between the LOC387715 and HTRA1 genes. The investigator (BF) was masked to the genetic results as genotyping was performed after the vision testing.

**Clinical Testing**

We assessed flicker perimetry (Medmont Perimeter M700; Medmont International, Vermont, Australia)20 using the standard M700 flicker protocol. The flicker stimuli (800 ms duration) are equivalent to a Goldman size III (0.43°). Landers et al.22 describe formulas to convert between M700 and Humphrey visual field indices.

Standard automated perimetry was evaluated (MP-1 Microperimeter, Nidek Co., Ltd, Gamagori, Aichi, Japan) using the a program for equivalence to the standard Humphrey field test (MP-1 Humphrey 10-2 program). The microperimeter allows visualization of the retinal localisation of the threshold measurement.23 and an autotracking system corrects the stimulus projection every 40 ms to compensate for eye movements. Standard perimetric indices (mean sensitivity and pattern defect) were used for statistical analysis of all visual field data.

Optical coherence tomography (OCT) (Stratus III; Carl Zeiss Pty Ltd, OberKochen, Germany) imaging was performed in both eyes using six diagonal fast, low-density 6 mm scans (128 A-scans/diagonal) and six diagonal slow, high-density 6 mm scans (512 A-scans/diagonal) at 30° angles. Visual acuity (Bailey-Lovie charts), contrast vision (Pelli-Robson), and color vision (Lanthony desaturated) were assessed in both eyes in accordance with standard procedures.

**Mesopic Vision Testing with the Four-Primary Photostimulator**

The photostimulator is a two-channel, Maxwellian view optical system with four narrow bandwidth primary lights for each channel derived from light emitting diode–interference filter combinations with dominant wavelengths of 459 nm (blue), 516 nm (greenish-yellow), 561 nm (green), and 658 nm (red). The design and control of the photostimulator is described in detail elsewhere.24–26 Independent control of the excitation of the four photoreceptor types in the human eye is achieved using the method of silent substitution.26

To evaluate long-, middle- and short-wavelength-sensitive cone (L-, M- S-cone) and rod (R) activity under mesopic light levels, we investigated two types of luminance stimuli, one mediated by cones alone (LMS) and the other mediated by the combined activities of rod and cones (LMSR). The LMS stimulus modulates cone luminance signals to the postreceptor magnocellular (MC) pathway, and rod excitations remain steady. Because S-cones do not contribute to luminance, modulating cone luminance (L+M) requires a proportional change in S-cone excitation to prevent a change in chromaticity.27–28 The LMSR stimuli measured combined LMS-cone and rod inputs to the postreceptor MC pathway.

The stimulus was a 2° circular field set within a 15° surround and positioned at 7.5° temporal eccentricity, the approximate locus of equal rod and cone density.29 Any difference in sensitivity to the two stimulus types reflects local rod and cone interactions (within the stimulus area) in the inferred MC pathway.27 This configuration is important for studying persons at risk of ARM because we can evaluate both rod and cone function in the same retinal area; the first photoreceptor losses occur parafoveally in ARM.30 The time-averaged retinal illumination was 33 photopic Troland with a chromaticity metamer to the equal-energy-spectrum \[L/(L+M) = 0.667, S/(L+M) = 1.0\]. Participants were dark adapted for 10 minutes because pilot studies indicate this was sufficient to study mesopic vision under our experimental conditions. Testing was performed with natural pupils through a 2 mm artificial pupil; refractive correction was placed on the instrument side of the artificial pupil if required. The critical fusion frequency (CFF) was measured for the two postreceptor stimulus types modulated at 15% Michelson contrast (LMS and LMSR) using a paradigm developed by the coauthors.27 The stimulus was presented in a 1 second raised cosine envelope and alternated with a 1 second steady field. On each trial, the initial frequency was randomly set between 5 and 30 Hz, and the observer altered the stimulus frequency using a method of adjustment to determine the CFF, that is, the transitional frequency between seeing flicker and no-flicker (steady). Six repeats were performed for each stimulus type.

**Table 1. Eligibility and Ineligibility Criteria**

<table>
<thead>
<tr>
<th>Eligibility Criteria</th>
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<tr>
<td>Age between 45 and 68 years</td>
<td>Aphakia or pseudophakia</td>
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<tr>
<td>Visual acuity ≥ 20/20 in both eyes</td>
<td>Cataract &gt; grade 1 (AREDS)</td>
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<tr>
<td>Normal color vision in both eyes (Lanthony)</td>
<td>Glaucoma and/or IOP &gt; 22 mmHg</td>
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<tr>
<td>Normal contrast vision (Pelli-Robson)</td>
<td>Diabetes and diabetic retinopathy</td>
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<tr>
<td>No ARM in both eyes (according to AREDS)</td>
<td>No retinal vein or artery occlusion</td>
</tr>
<tr>
<td>Normal OCT in both eyes</td>
<td>Uncontrolled hypertension</td>
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<tr>
<td>Normal peripheral fundus</td>
<td>Recent myocardial infarct or stroke</td>
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<tr>
<td></td>
<td>Uncontrolled hypertension</td>
</tr>
<tr>
<td></td>
<td>Uncontrolled hypertension</td>
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<td>Major illness with chronic medication</td>
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**Statistical Analysis**

We first examined the distributions of the variables that did not show major deviations from normality. Therefore, we used parametric tests...
that allowed for controlling age, an important factor for studying age-related maculopathy. We performed Pearson’s correlation to determine the relationship between mesopic CFF, mean sensitivity (MS) and pattern defect (PD) (microperimetry and flicker perimeter), retinal thickness (OCT), and age. ANOVA was performed to evaluate the difference between the CFF measurements, flicker perimeter, microperimetry, and the odds ratio (OR) of the three SNPs, with age controlled. The following odds ratios were assigned to each genotype according to previously published values: CFH rs380390, 1.85, TT OR = 7.4, CC + GG OR = 1; LOC387715/ARMS2 rs10490920, 3.69, TT OR = 6.09, GT OR = 1.35, GG OR = 1; HTRA1 rs11200638, 2.21, AA OR = 6.56, AG OR = 1.85, GG OR = 1.

### RESULTS

The genotype frequencies of all tested SNPs were in Hardy-Weinberg (HWE) equilibrium as assessed using the HWE correction step was used to set CFF. The outliers were removed from subsequent statistical analysis. Of the remaining 36 participants, 11 were classified as normal (low-risk homozygous, gene-negative) and 25 gene-positive (hetero- or homozygous carriers of either one or more than one gene variant tested). Table 2 shows the individual gene variant distributions (e.g., all persons who were heterozygous for the LOC gene variant and not accounting for other coexisting gene variations in these persons). The mean values (±SD) of the CFF for LMSR and LMS for each genotype are given in Tables 3 and 4. Note that LOC and HTRA1 CFF values are the same because of the linkage disequilibrium. Data demonstrate that LMSR CFF decreases in gene-positive compared to gene-negative participants, with the exception of the high-risk homoygote CFH.

Mean sensitivities and pattern defects were determined for microperimetry and flicker perimeter with four and five exclusions, respectively, because of increased false positive responses. The MS and PD ± SD for the microperimeter (n = 32) were 17.8 dB (±0.93 SD) and −1.6 dB (±0.96 SD), respectively. The mean MS and PD for flicker perimeter (n = 31) were 25.08 dB (±0.7) and 0.9 dB (±0.6), respectively. The values for both flicker and microperimetry were within normal ranges. Mean central retinal thickness as measured with the OCT (228.6 μm ± 19.6) was within normal limits in all participants. Microperimetry mean sensitivity and pattern defect were significantly correlated with age (r = −0.39, P ≤ 0.05) and LMSR (r = 0.42, P < 0.02; Fig. 1). Figure 1 shows that lower LMSR CFF was associated with lower MS on the microperimeter. A significant correlation between central retinal thickness (OCT) and age (r = −0.4, P = 0.02) was found as demonstrated previously.

ANOVA demonstrates a significant reduction of LMSR CFF in gene-positive compared with gene-negative participants without correction for age (F1,35 = 4.16, P = 0.05) and after correction for age (F1,35 = 5.18, P = 0.03; Fig. 2). There was no significant difference between gene-positive and gene-negative participants in the other clinical tests (flicker perimeter, microperimetry) as well as in mean retinal thickness (OCT).

We conducted a subanalysis of the individual gene variant combinations and divided those into five groups according to each persons’ genetic combination; group 1 included all gene-negative participants (n = 11), group 2 consisted of all participants who were only heterozygous for LOC/HTRA1 (n = 13), group 3 consisted of participants with only the CFH homo- or heterozygous variant and heterozygous for LOC/HTRA1 (n = 6), group 4 included all participants with only the homo- or heterozygous CFH variant (n = 4), and group 5 consisted of persons only homozygous for the LOC/HTRA1 variant (n = 2; Table 5). Table 5 demonstrates the CFF results for both LMS and LMSR for each group and shows a trend of lower LMSR values in all groups with the risk genes compared with the gene-negative group. A two-sample t-test with equal variances revealed a significant difference for group 2 with lower LMSR CFF in participants heterozygous for the LOC/HTRA1 compared with group 1 (gene-negative) (P = 0.01). Groups 3 to 5 in particular homozygotes were not significantly different compared with group 1, most likely because of small sample sizes in these remaining subgroups.

### DISCUSSION

This is the first demonstration that in a randomly chosen sample with normal visual acuity and central visual fields and no clinical signs of ARM in both eyes, persons with ARM risk genotypes have on average lower mesopic visual function after correction for age compared with those who do not carry the risk genotype (gene-negative). The reduction in rod- and cone-mediated (LMSR) and not cone-mediated only (LMS) mesopic vision is consistent with rod dysfunction or selective rod loss as demonstrated histologically, psychophysically, and electrophysiologically in early ARM and ageing. Previous studies demonstrate reduced rod-mediated neuroretinal function in early ARM sufferers that exceeds those changes associated with normal aging. Delayed dark adaptation as well as reduced scotopic sensitivity are evident in early ARM. Foveal crit-

### Table 2. The Distribution of Genotypes

<table>
<thead>
<tr>
<th>Gene Variant</th>
<th>Low-Risk Homozygotes (n)</th>
<th>Heterozygotes (n)</th>
<th>High-Risk Homozygotes (n)</th>
</tr>
</thead>
<tbody>
<tr>
<td>LOC rs10490924</td>
<td>15 (GG)</td>
<td>19 (GT)</td>
<td>2 (TT)</td>
</tr>
<tr>
<td>HTRA1 rs1120038</td>
<td>15 (GG)</td>
<td>19 (AG)</td>
<td>2 (AA)</td>
</tr>
<tr>
<td>CFH rs380390</td>
<td>5 (GG)</td>
<td>21 (CG)</td>
<td>10 (CC)</td>
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### Table 3. Mean (±SD) LMSR CFF for Each of the Gene Variants

<table>
<thead>
<tr>
<th>Gene Variant</th>
<th>Low-Risk Homozygotes</th>
<th>Heterozygotes</th>
<th>High-Risk Homozygotes</th>
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<tbody>
<tr>
<td>LOC rs10490924</td>
<td>15.3 (±1.25)</td>
<td>14.4 (±0.96)</td>
<td>14.9 (±0.95)</td>
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<tr>
<td>HTRA1 rs1120038</td>
<td>15.3 (±1.25)</td>
<td>14.4 (±0.96)</td>
<td>14.9 (±0.95)</td>
</tr>
<tr>
<td>CFH rs380390</td>
<td>14.8 (±1.19)</td>
<td>14.9 (±1.08)</td>
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</tbody>
</table>

### Table 4. Mean (±SD) LMS CFF for Each of the Gene Variants

<table>
<thead>
<tr>
<th>Gene Variant</th>
<th>Low-Risk Homozygotes</th>
<th>Heterozygotes</th>
<th>High-Risk Homozygotes</th>
</tr>
</thead>
<tbody>
<tr>
<td>LOC rs10490924</td>
<td>19.8 (±1.07)</td>
<td>19.4 (±1.43)</td>
<td>19.7 (±1.27)</td>
</tr>
<tr>
<td>HTRA1 rs1120038</td>
<td>19.8 (±1.07)</td>
<td>19.4 (±1.43)</td>
<td>19.7 (±1.27)</td>
</tr>
<tr>
<td>CFH rs380390</td>
<td>19.4 (±1.17)</td>
<td>20.1 (±1.45)</td>
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</table>
Critical fusion frequency is reduced under photopic light levels in advanced ARM but is not sensitive as a diagnostic tool, consistent with our observation that there were no differences in thecone-mediated (LMS) CFF in gene-positive and -negative participants. These preliminary results in persons with no signs of ARM signify rod-mediated mesopic visual function testing as important for the evaluation of older persons with ARM risk genotypes, and that it may become a functional biomarker for disease.

We further report a novel relationship between microperimetry and the four-primary photostimulator where lower MS and PD are significantly correlated with lower LMS CFF. Although the microperimeter background light level is in the upper mesopic range and the achromatic test stimuli estimate visual sensitivity mediated by rods and cones in different states of relative sensitivity, its inbuilt fixation tracking system may improve the detection of functional vision changes over that of other conventional ophthalmic tests we performed under photopic illuminations (e.g., color vision, flicker perimetry). Although microperimetry results were not significantly reduced in gene-positive compared with gene-negative participants in this cohort, future studies in a larger cohort of older gene-positive participants may have increased statistical power to detect subclinical deficits.

The SNPs identified in this study have been all related to neovascular AMD. Ischemia due to underlying cardiovascular conditions has been suggested as a major factor in the development of ARM and in neovascular AMD. Moreover, a recent study has identified three other gene variants on chromosomes 15, 16, and 22 with an increased risk of AMD that are related to the cholesterol metabolism and thus cardiovascular risk factors. A person with these gene variants may be predisposed to functional deficits because of ischemic insults. Thus a test that increases the oxygen demand by both increased photoreceptor activity (during mesopic conditions) and increased blood flow (during flicker stimulation) as used in our experiment may facilitate the early detection of the first functional deficits.

The demonstrated relationship between a risk genotype and impaired mesopic visual function in persons with clinically normal eyes is important because visual function may be responsive to appropriate environmental manipulation such as changing diet and lifestyle. Persons with ARM risk genotypes who smoke or have a poor diet have an approximate doubling of the risk of ARM progression, compared with those who are gene positive but do not have such environmental exposures. Moreover, late stages of ARM may be preventable because recent studies indicate that a healthy lifestyle including a healthy diet, physical activity, adequate vitamin D intake, and not smoking can decrease the risk for developing intermediate age-related macular degeneration by about twofold. These findings support our approach that the application of sensitive tests as biomarkers for the early detection and appropriate monitoring of disease is vital because risk is modifiable. Monitoring visual function with a quantitative test will further enable the evaluation of the effect of lifestyle changes on a person’s health (such as change in a person’s environmental exposures) and reduce the economic costs associated with the most common cause of blindness in the western world. The study findings may have future applications in the verification of subclinical ARM without genetic assessment.

Assessing mesopic vision as a biomarker of subclinical ARM may have potential significant implications in determining the pathomechanisms of the subtypes of neovascular ARM such as occult, classic, polypoidal choroidal vasculopathy, or retinal angiomatosus proliferations that are poorly understood. It has been demonstrated that different gene variants promote subtypes of ARM. Further longitudinal clinical investigation is required to study persons with significantly reduced mesopic vision and gene-positive carrier status to determine whether visual function deteriorates faster than those in the low-risk (gene-negative) group and to understand the relationship between genotype and phenotype by quantitatively measuring visual function related to genotypes to determine progression to ARM.

**FIGURE 1.** Rod- and cone-mediated (LMSR) critical fusion frequency (CFF) as a function of microperimetry (MP-1) mean sensitivity (MS). There is a significant correlation between LMSR CFF and MS.

**FIGURE 2.** Mean LMSR CFF values for participants who were heterozygous and homozygous for high-risk CFH, LOC, and HRTA1 SNPs are significantly lower compared with the gene-negative participants (*P* = 0.01 compared with gene-negative participants (group 1)).

**TABLE 5.** The LMSR and LMS CFF for Each of the Gene Combinations

<table>
<thead>
<tr>
<th>Gene Combinations (n = 36)</th>
<th>LMSR CFF</th>
<th>LMS CFF</th>
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<tbody>
<tr>
<td>Group 1 (gene-negative) (n = 11)</td>
<td>15.4 (±1.38)</td>
<td>19.8 (±1.13)</td>
</tr>
<tr>
<td>Group 2 (LOC/HTRA1 heterozygous) (n = 15)</td>
<td>14.22 (±0.78)*</td>
<td>19.1 (±1.19)</td>
</tr>
<tr>
<td>Group 3 (CFH, LOC/HTRA1 heterozygous) (n = 6)</td>
<td>14.85 (±1.25)</td>
<td>20.1 (±1.78)</td>
</tr>
<tr>
<td>Group 4 (CFH only) (n = 4)</td>
<td>15.1 (±0.92)</td>
<td>20.2 (±0.96)</td>
</tr>
<tr>
<td>Group 5 (LOC/HTRA1 homozygous) (n = 2)</td>
<td>14.9 (±0.95)</td>
<td>19.7 (±1.27)</td>
</tr>
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</table>

* *P* = 0.01 compared with gene-negative participants (group 1).
Acknowledgments

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