Association of Pattern Dystrophy With an HTRA1 Single-Nucleotide Polymorphism

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Objective: To evaluate if adult-onset foveomacular vitelliform dystrophy (AOFVD) and butterfly-shaped pigment dystrophy (BSPD) are associated with risk single-nucleotide polymorphisms (SNPs) for age-related macular degeneration (AMD).

Methods: This was a tertiary referral center–based cross-sectional study including 35 consecutive patients with BSPD and AOFVD, 317 patients with AMD, and 159 unaffected individuals. Demographics, clinical information, and ophthalmic imaging studies were collected. Sequencing was performed for the peripherin/RDS and BEST1 genes, and genotyping was performed for SNPs in the genes for complement factor H (CFH) (rs1061170), HTRA1 (rs11200638), and complement component 3 (C3) (rs2231099).

Results: Adult-onset foveomacular vitelliform dystrophy and BSPD were diagnosed in 24 (68.6%) and 11 (31.4%) of the 35 patients, respectively. The mean (SD) age of patients with pattern dystrophy (PD) was 75.3 (10) years and median visual acuity was 0.7. Pattern dystrophy was associated with the HTRA1 risk allele compared with unaffected individuals (odds ratio, 1.72; 95% CI, 1.11-2.66; P = .03). The HTRA1 SNP showed similar prevalence in patients with AMD and PD. The CFH risk allele was significantly less common in patients with PD compared with patients with AMD (odds ratio, 0.47; 95% CI, 0.28-0.76; P = .002). No mutations in peripherin/RDS or BEST1 were detected.

Conclusions: The AOFVD and BSPD phenotypes are associated with an HTRA1 risk SNP. These phenotypes often present in elderly individuals who do not carry peripherin/RDS gene mutations and are associated with retinal pigment epithelium alterations and increased risk for choroidal neovascularization. Further research is required to evaluate if AOFVD and BSPD phenotypes in aged individuals are associated with AMD.

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Pattern dystrophy (PD) of the retinal pigment epithelium (RPE) is a common form of macular degeneration. In ophthalmoscopy, PD is characterized by the accumulation of a yellowish-brown material at the level of the RPE and by RPE alterations in the macular area.

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This process can lead to a wide variety of clinical presentations and patterns that were classified by Gass into 5 major forms including adult-onset foveomacular vitelliform dystrophy (AOFVD), butterfly-shaped pigment dystrophy (BSPD), reticular dystrophy, multifocal dystrophy, and fundus pulvulentis (coarse mottling). Yet, Gass and others also noted that additional forms of PD are observed and that eyes of the same patient may manifest different forms of PD.1,3 While patients with PD often retain better than 20/40 acuity, as the disease progress, patients may encounter visual loss secondary to RPE atrophy or due to the development of choroidal neovascularization.4

Autosomal dominant inheritance mode was reported in PD, and several mutations in the peripherin/RDS gene were associated with the PD phenotype.3,9 Infrequently, patients showing a PD-like phenotype carry a BEST1 gene mutation.10,11 Yet, many patients with the clinical diagnosis of PD carry neither a peripherin/RDS nor a BEST1 gene mutation.8 Vitelliform macular lesion may also be associated with cuticular drusen. Cuticular drusen phenotype by itself was associated with the Tyr402His variant of the complement factor H (CFH) gene, an established risk single-nucleotide polymorphism for age-related macular degeneration (AMD). This CFH variant was not detected in patients manifesting the combination of vitelliform lesion and cuticular drusen.13,15
Although PD phenotypes such as AOFVD and BSPD may be distinct from typical non-neovascular AMD, both conditions have variable appearances that have some common features including RPE alterations and yellowish subretinal deposits that appear as vitelliform lesions in PD and as pseudodrusen in association with AMD. Another characteristic common for both diseases is presentation in elderly individuals who often have a positive family history. This study aims to further evaluate the genetic basis of AOFVD and BSPD and to assess its genetic similarity with AMD. To that end, we have studied patients with the clinical diagnosis of AOFVD and BSPD. All patients had a negative family history for maculopathy. Genotyping was performed for the major risk single nucleotide polymorphisms (SNPs) for AMD in the genes for CFH (rs1061170, Y402H variant), HTRA1 (rs12200638, +504G>A), and complement component 3 (C3) (rs2231099, R102G). These SNPs were previously associated with AMD in several populations including the Israeli population. The peripherin/RDS and BEST1 genes were also genotyped to exclude mutations in these genes as a cause for the PD phenotype.

METHODS

PATIENTS

A sequential group of 35 patients who were diagnosed with AOFVD or BSPD by retina specialists (E.A., I.C., and E.B.) was included in the study. To limit the bias that might be introduced by incorporating variable phenotypes of PD that potentially overlap with the phenotype of AMD, we limited this study to typical AOFVD and BSPD phenotypes. Diagnosis was based on ophthalmoscopy according to the classification of Gass and was assisted by optical coherence tomography (OCT) to identify the vitelliform lesions. All patients were referred for evaluation of maculopathy in the retina service of the Hadassah–Hebrew University Medical Center between July 2010 and September 2011. Data including demographics, family history for maculopathy, and ophthalmic findings were collected. Ophthalmic imaging including OCT images (Spectralis [Heidelberg Engineering] or Stratus [Carl Zeiss Meditec]), autofluorescence (HRA), and fluorescein angiography, when available, were analyzed.

Blood samples were collected from each patient and DNA was extracted for genetic analysis. The study was approved by the institutional ethics committee, and each patient signed an informed consent form. Genotyping for the major risk SNPs for AMD in CFH, C3, and HTRA1 was compared with data from a group of 159 unaffected controls and 317 patients with AMD whose data were sequentially collected from the same retina clinic. Inclusion criteria for the control group included age older than 60 years, clear media that enabled ophthalmoscopy, and absence of intermediate-size drusen, multiple small drusen, or retinal pigment epithelial abnormalities (Age-Related Eye Disease Study category I). Age-related macular degeneration was diagnosed according to the Age-Related Eye Disease Study criteria.

GENETIC TESTING

DNA was extracted from whole blood using the FlexiGene DNA Kit (QIAGEN); DNA was then used as a template for polymerase chain reaction (PCR) amplification and sequencing for the peripherin/RDS and BEST1 genes. All 3 encoding exons of the peripherin/RDS gene were sequenced. Because of the exons’ length and composition, exon 1 was divided into 2 overlapping fragments and exon 3 was divided into 2 fragments of which only the first fragment, composed of 647 base pairs, was studied. The remaining region of the exon is noncoding and, thus, was not sequenced. The encoding exons of the BEST1 gene were sequenced, and exon 10 was divided into 2 overlapping fragments (eTable, http://www.archophthalmol.com). Exon boundaries were included in the analysis.

Polymerase chain reaction was performed for the fragments containing the SNPs in the CFH (rs1061170), HTRA1 (rs12200638), and C3 (rs2231099) genes using specific pre-designed primers (eTable) and ReadyMix PCR reaction mixture (Sigma-Aldrich), for a total volume of 25 µL. The PCR reactions were performed with an annealing temperature of 58°C to 60°C, elongation temperature of 72°C, and melting temperature of 94°C (eTable). The PCR products were evaluated on a 1.5% agarose gel to confirm the success of the PCR reaction, followed by automatic sequencing (Macrogen), where a preprovided primer (eTable) was used to extend the PCR product with fluorescent nucleotides to provide the sequence of the targeted area.

STATISTICAL ANALYSIS

Statistical analysis was performed using SPSS (IBM SPSS) and Instat software (GraphPad), as we have previously described. Briefly, logistic regression, Fisher exact, and χ² tests were applied to assess odds ratios, confidence intervals, and significance.

RESULTS

CLINICAL CHARACTERISTICS

Thirty-five patients (70 eyes) were evaluated (20 women; 15 men); the mean (SD) age at presentation was 75.3 (10) years (range, 46–93 years), and this was similar to the mean (SD) age of patients with AMD (78.1 [7.6]; P = .22). Both patients with AMD and PD were older than the controls (mean [SD] age, 70.8 [8.2]; P < .05). None of the patients with PD had a positive family history for maculopathy. Mean visual acuity was 0.7 (range, counting fingers from 10 cm to 1.25 decimals). Patients showed BSPD (11 of 35 [31.4%]) or AOFVD (24 of 35 [68.6%]) (Figure 1 and Figure 2) phenotypes. Autofluorescence imaging (n = 15 patients) showed either central foci or multifocal linear hyperfluorescent patterns in the macular area (Figure 2). Optical coherence tomography (n = 20 patients) showed subretinal dome-shaped deposits (18 patients) and RPE atrophic changes (4 patients, 2 of them had both subretinal deposits and atrophic changes) in both AOFVD and BSPD (Figure 1 and Figure 2). Choroidal neovascularization was diagnosed in 8 eyes (5 with AOFVD, 3 with BSPD) of 8 patients (22.8%) based on clinical, fluorescein angiogram, and OCT findings (Figure 1).

GENOTYPING

No known or novel mutations in the peripherin/RDS or the BEST1 genes were detected in this group of patients. Several SNPs that were previously reported in unaffected individuals from other populations were also found in the Israeli patients with PD. The prevalence of these SNPs was similar to that reported in other unaffected populations (data not shown).
Risk-associated SNPs in CFH, C3, and HTRA1 were identified in 42.8%, 39.4%, and 52.4% of patients with PD, respectively (Table). The AMD risk alleles in CFH and C3 were not associated with PD, and their prevalence was similar in the patients with PD and controls. In fact, the CFH risk allele was significantly less common in patients with PD compared with patients with AMD (odds ratio, 0.47; 95% CI, 0.28-0.76; \( P = .002 \)). The risk allele in HTRA1 was associated with patients with PD compared with unaffected individuals (odds ratio, 1.72; 95% CI, 1.11-2.66; \( P = .03 \)) and showed similar prevalence in patients with AMD and PD (odds ratio, 0.84; 95% CI, 0.52-1.34; \( P = .54 \)). There was no significant difference in the distribution of the C3 SNP between patients with PD and AMD and between patients with PD and unaffected individuals. Analysis according to genotypes showed similar results to allele-based analysis (Table).

GENOTYPE-PHENOTYPE CORRELATION

Mean (SD) age at presentation of patients with PD who were positive (\( n = 18 \)) or negative (\( n = 17 \)) for the HTRA1 SNP was 74.7 (10.8) and 75.9 (11.4) years, respectively (\( P = .74 \)). While the HTRA1 SNP was associated with PD, the phenotype of carriers (either homozygotes or heterozygotes) of the HTRA1 risk SNP was similar to HTRA1-negative patients with PD (Figure 1 and Figure 2). There was no difference in the prevalence of HTRA1 and CFH alleles between the AOFVD and BSPD phenotypes, respectively (data not shown). There was also no association between the development of choroidal neovascularization and the SNPs that were evaluated.

**COMMENT**

We have characterized the genotype of patients with AOFVD or BSPD who had a negative family history for maculopathy. None of the cases showed a peripherin/RDS or BEST1 gene mutation. Yet, these phenotypes of PD were associated with an HTRA1 SNP. This SNP was associated with AMD in several populations including in Israel.\(^{20-22,26} \) Since the HTRA1 SNP is in complete linkage disequilibrium with an ARMS2 SNP, it is not possible to determine which of the 2 genes, HTRA1 or ARMS2, has a functional role in PD.\(^{21,26} \) In this group of patients, there was no association between PD phenotypes that we evaluated and the major risk SNPs for AMD in the CFH and C3 genes. In fact, the CFH SNP was less common in PD compared with AMD and its prevalence was similar in patients with PD and unaffected individuals.
Associated with disease duration. Francis and colleagues found the development of choroidal neovascularization was represented in PD phenotypes that may be associated with variable visual outcome and age at onset in association with AMD, but it is associated with an SNP. Further research is required to evaluate if such PD phenotypes have variable visual outcome and age at onset in association with AMD.

In conclusion, our data show that the AOFVD and BSBD phenotypes with a negative family history for the disease are a relatively common clinical diagnosis in the retina clinic. It is often diagnosed in elderly individuals and it is associated with an HTRA1 SNP. Further research is required to evaluate if such PD phenotypes have variable visual outcome and age at onset in association with AMD mutation status, as well as to test the association of these phenotypes with AMD.

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Despite the lack of peripherin/RDS or BEST1 mutations in our patients, their ophthalmoscopy, OCT, and fluorescein angiography findings were indistinguishable from previous reports of autosomal dominant PD associated with peripherin/RDS mutations.\(^1\)\(^-\)\(^6\) On the other hand, patients included in the current study presented to the retina clinic at an older age compared with previous reports in the literature for PD.\(^2\)\(^7\) This finding may stem from several factors, among them lack of timely diagnosis of these cases while the visual acuity was not yet affected and variable genetic backgrounds for similar PD phenotypes that may be associated with variable age at onset.

Substantial visual loss due to RPE atrophy or the development of choroidal neovascularization was reported to be common in PD and is thought to be associated with disease duration. Francis and colleagues\(^4\) found visual acuity of 20/200 or less in both eyes in 44% of 16 patients with PD carrying the peripherin/RDS mutation who were 70 years or older. In comparison, none of the patients in our study had such poor visual acuity in both eyes, including none of our 16 patients who were older than 70 years. Further research is required to compare visual consequences of patients with PD with and without peripherin/RDS mutations and to correlate it with age at onset.

The peripherin/RDS gene has a structural role in photoreceptor outer segment discs and is known to interact with rod outer segment membrane protein 1 (ROM1) and to be associated with several types of retinal degenerations.\(^6\)\(^,\)\(^1\)\(^1\)\(^-\)\(^2\)\(^,\)\(^2\)\(^6\)\(^,\)\(^2\)\(^7\) The retinal function of the HTRA1 and ARMS2 genes is poorly understood, and neither of these genes is known to interact with the peripherin/RDS or BEST1 gene products. Recently, the ARMS2 gene was suggested to be a component of the extracellular matrix. Such function, if validated, may potentially underlie the association of HTRA1/ARMS2 with both drusen and vitelliform lesion formation.\(^2\)\(^0\)

Several weaknesses of this research should be acknowledged. First, while none of the patients included in the study had mutations in the peripherin/RDS gene and none had a positive family history for the disease, it is still possible that other family members of our patients had PD. Conceivably, relatives of patients with PD who also carry the HTRA1 risk SNP have increased risk for the disease. Second, while the $C3$ SNP is less common in patients with PD compared with patients with AMD, we cannot exclude a low-magnitude association between the $C3$ or $C3$ SNPs and PD phenotypes. Yet, our data show that such an association, even if present, is of low magnitude compared with the association of typical AMD with these SNPs.

In conclusion, our data show that the AOFVD and BSBD phenotypes with a negative family history for the disease are a relatively common clinical diagnosis in the retina clinic. It is often diagnosed in elderly individuals and it is associated with an HTRA1 SNP. Further research is required to evaluate if such PD phenotypes have variable visual outcome and age at onset in association with AMD mutation status, as well as to test the association of these phenotypes with AMD.

Abbreviations: AMD, age-related macular degeneration; C3, complement component 3; CFH, complement factor H; Het, heterozygote; PD, pattern dystrophy; OR, odds ratio.

<table>
<thead>
<tr>
<th></th>
<th>No. (%)</th>
<th>PD</th>
<th>AMD</th>
<th>OR (95% CI)</th>
<th>P Value</th>
<th>Control, No. (%)</th>
<th>OR (95% CI)</th>
<th>P Value</th>
</tr>
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<tbody>
<tr>
<td><strong>CFH</strong></td>
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<td></td>
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<td></td>
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<tr>
<td>Wild (TT)</td>
<td>20 (57.1)</td>
<td>73 (23)</td>
<td></td>
<td>0.19 (0.08-0.40)</td>
<td>&lt;.001</td>
<td>79 (49.7)</td>
<td>0.56 (0.24-1.32)</td>
<td>.22</td>
</tr>
<tr>
<td>Het (T/C)</td>
<td>9 (25.7)</td>
<td>172 (54.3)</td>
<td>83 (29.6)</td>
<td>17 (10.7)</td>
<td>1.39 (0.49-4.00)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Risk (CC)</td>
<td>6 (17.1)</td>
<td>72 (22.7)</td>
<td>0.3 (0.12-0.80)</td>
<td>.46</td>
<td>100 (62.9)</td>
<td>3.15 (1.35-7.27)</td>
<td>.008</td>
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<tr>
<td>Risk/wild alleles</td>
<td>21/49 (30/70)</td>
<td>316/318 (49.8/50.2)</td>
<td>0.47 (0.28-0.76)</td>
<td>.002</td>
<td>97/221 (30.5/69.5)</td>
<td>0.98 (0.62-1.56)</td>
<td>.95</td>
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<td><strong>HTRA</strong></td>
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<tr>
<td>Wild (GG)</td>
<td>17 (48.6)</td>
<td>139 (43.8)</td>
<td>35 (20.6)</td>
<td>101 (63.5)</td>
<td>.02</td>
<td></td>
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<tr>
<td>Het (G/A)</td>
<td>13 (37.1)</td>
<td>119 (37.5)</td>
<td>0.89 (0.42-1.92)</td>
<td>53 (33.3)</td>
<td>1.46 (0.66-2.33)</td>
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<tr>
<td>Risk (AA)</td>
<td>5 (14.3)</td>
<td>59 (18.6)</td>
<td>0.69 (0.24-1.96)</td>
<td>5 (3.1)</td>
<td>5.95 (1.55-22.73)</td>
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<tr>
<td>Risk/wild alleles</td>
<td>23/47 (32/67.1)</td>
<td>237/397 (37.4/62.6)</td>
<td>0.84 (0.52-1.34)</td>
<td>.54</td>
<td>63/255 (19.8/80.2)</td>
<td>1.72 (1.11-2.66)</td>
<td>.03</td>
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<td><strong>C3</strong></td>
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<td></td>
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<tr>
<td>Wild (CC)</td>
<td>20 (60.6)</td>
<td>175 (55.2)</td>
<td>53 (31.4)</td>
<td>100 (62.9)</td>
<td>.37</td>
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<td>Het (G/G)</td>
<td>13 (39.4)</td>
<td>123 (38.8)</td>
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<td>50 (31.4)</td>
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<tr>
<td>Risk (GG)</td>
<td>0 (0)</td>
<td>19 (6)</td>
<td>.79</td>
<td>9 (5.7)</td>
<td></td>
<td>68/250 (27.4/72.6)</td>
<td>0.92 (0.53-1.60)</td>
<td>.89</td>
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<td>Risk/wild alleles</td>
<td>13/53 (19/78.0)</td>
<td>161/473 (25.4/74.6)</td>
<td>0.74 (0.42-1.33)</td>
<td>.39</td>
<td>159/250 (63.6/36.4)</td>
<td>0.85 (0.47-1.57)</td>
<td>.64</td>
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</table>
REFERENCES

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