A Nonsense Mutation in FAM161A Is a Recurrent Founder Allele in Dutch and Belgian Individuals With Autosomal Recessive Retinitis Pigmentosa

Kristof Van Schil,1 B. Jeroen Klevering,2,3 Bart P. Leroy,1,4,5 Jan Willem R. Pott,6 Dikla Bandah-Rozenfeld,7 Marijke N. Zonneveld-Vrieling,8 Dror Sharon,7 Anneke I. den Hollander,2,8,9 Frans P. M. Cremers,8,9 Elfride De Baere,1 Rob W. J. Collin,8,9 and L. Ingeboagh van den Born10

1Center for Medical Genetics, Ghent University and Ghent University Hospital, Ghent, Belgium
2Department of Ophthalmology, Radboud University Medical Center, Nijmegen, The Netherlands
3Division of Ophthalmology, Children’s Hospital of Philadelphia, Philadelphia, Pennsylvania, United States
4Department of Ophthalmology, University of Groningen, University Medical Centre Groningen, Groningen, The Netherlands
5Division of Ophthalmology, Hadassah-Hebrew University Medical Center, Jerusalem, Israel
6Department of Ophthalmology, University of Groningen, University Medical Centre Groningen, Groningen, The Netherlands
7Department of Ophthalmology, Hadassah-Hebrew University Medical Center, Jerusalem, Israel
8Department of Human Genetics, Radboud University Medical Center, Nijmegen, The Netherlands
9Radboud Institute for Molecular Life Sciences, Radboud University Medical Center, Nijmegen, The Netherlands
10The Rotterdam Eye Hospital, Rotterdam, The Netherlands

Correspondence: Rob W. J. Collin, Department of Human Genetics, Radboud University Medical Center, Geert Grooteplein Zuid 10, 6525 GA Nijmegen. The Netherlands; rob.collin@radboudumc.nl.

KVS and BJK contributed equally to the work presented here and should therefore be regarded as equivalent authors. RWJC and LIvdB contributed equally to the work presented here and should therefore be regarded as equivalent authors. Submitted: August 10, 2015 Accepted: September 30, 2015

Citation: Van Schil K, Klevering BJ, Leroy BP et al. A nonsense mutation in FAM161A is a recurrent founder allele in Dutch and Belgian individuals with autosomal recessive retinitis pigmentosa. Invest Ophthalmol Vis Sci. 2015;56:7418-7426. DOI:10.1167/iovs.15-17920

Purpose. To identify mutations in FAM161A underlying autosomal recessive retinitis pigmentosa (arRP) in the Dutch and Belgian populations and to investigate whether common FAM161A-associated phenotypic features could be identified.

Methods. Homozygosity mapping, amplification-refractory mutation system (ARMS) analysis, and Sanger sequencing were performed to identify mutations in FAM161A. Microsatellite and SNP markers were genotyped for haplotype analysis. Patients with biallelic mutations underwent detailed ophthalmologic examinations, including measuring best-corrected visual acuity, extensive fundus photography with reflectance and autofluorescence imaging, and optical coherence tomography.

Results. Homozygosity mapping in 230 Dutch individuals with suspected arRP yielded five individuals with a homozygous region harboring FAM161A. Sanger sequencing revealed a homozygous nonsense mutation (c.1309A>T; p.[Arg437*]) in one individual. Subsequent ARMS analysis and Sanger sequencing in Dutch and Belgian arRP patients resulted in the identification of seven additional individuals carrying the p.(Arg437*) mutation, either homozygously or compound heterozygously with another mutation. Haplotype analysis identified a shared haplotype block of 409 kb surrounding the p.(Arg437*) mutation in all patients, suggesting a founder effect. Although the age of onset was variable among patients, all eight developed pronounced outer retinal loss with severe visual field defects and a bull’s eye–like maculopathy, followed by loss of central vision within 2 decades after the initial diagnosis in five subjects.

Conclusions. A founder mutation in FAM161A p.(Arg437*) underlies approximately 2% of arRP cases in the Dutch and Belgian populations. The age of onset of the retinal dystrophy appears variable, but progression can be steep, with almost complete loss of central vision later in life.

Keywords: FAM161A, retinitis pigmentosa, founder mutation, bull’s eye-like maculopathy

Retinitis pigmentosa (RP; MIM[268000]) is a set of hereditary retinal dystrophies affecting more than 1 million people worldwide. It is a progressive disease that typically presents with degeneration of the rod photoreceptors, followed by loss of cone photoreceptor function. Most patients experience night blindness as the initial symptom. Subsequently, a gradual constriction of the peripheral visual fields occurs, followed by loss of central vision. The clinical presentation of RP is highly variable and is matched by an impressive genetic heterogeneity: currently, mutations in 55 genes have been implicated in the pathogenesis of autosomal recessive RP (arRP).1,2 Genes that are mutated in RP encode proteins with diverse functions in multiple cellular processes, including the phototransduction cascade, the visual cycle, cytoskeletal dynamics, regulation of gene transcription, and ciliary function.2

In 2010, two back-to-back studies revealed null-mutations in FAM161A as a cause of arRP in the Israeli and German population, respectively.3,4 FAM161A encodes a 716aa protein that localizes to the connecting cilium, the basal body region, and the adjacent centriole in photoreceptor cells.5,6 The
connecting cilium is a key structure in mediating the high-throughput transport of essential proteins and lipids from the inner segment (IS) to the outer segment (OS). The photoreceptor OS is in fact considered a specialized and modified cilium that is not self-sustaining and relies on the IS for the synthesis of the essential proteins and lipids. \( \text{FAM161A} \) is a microtubule-associated cilium protein presumably involved in maintaining microtubule stability. The interaction with other ciliary and centrosomal proteins known to be implicated in retinal dystrophies, like SDCCAG8, CEP290, lebercilin, and POC1B, points to a possible role for \( \text{FAM161A} \) in transport processes between the IS and OS. \( \text{FAM161A} \) is also expressed in the retina, where it is found in the photoreceptor OS, which is essential for the transport of essential proteins and lipids. The interaction with other ciliary and centrosomal proteins known to be implicated in maintaining microtubule stability. The interaction with other ciliary and centrosomal proteins known to be implicated in retinal dystrophies, like SDCCAG8, CEP290, lebercilin, and POC1B, points to a possible role for \( \text{FAM161A} \) in transport processes between the IS and OS. \( \text{FAM161A} \) is also expressed in the retina, where it is found in the photoreceptor OS, which is essential for the transport of essential proteins and lipids.
## Table. Clinical Overview

<table>
<thead>
<tr>
<th>Patient ID/ Sex/ Age at Diagnosis/ Origin</th>
<th>FAM161A Mutations</th>
<th>Diagnosis/ Recent Exam</th>
<th>History</th>
<th>VA Snellen, LogMAR</th>
<th>Refraction</th>
<th>Lens</th>
<th>Ophthalmoscopy</th>
<th>Goldmanmann Perimetry</th>
<th>Optical Coherence Tomography</th>
<th>Fundus Autofluorescence</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1/M/Dutch c.1309A&gt;T p.(Arg437*)</td>
<td>c.1309A&gt;T p.(Arg437*)</td>
<td>20/4</td>
<td>Night blindness and visual field loss noted in third decade</td>
<td>0.12 (0.9)</td>
<td>0.3 (0.5)*</td>
<td>RE</td>
<td>LE</td>
<td>0.625 to 1.50 × 25°</td>
<td>0.625 to 1.50 × 25°</td>
<td>PSC cataract</td>
</tr>
<tr>
<td>P2/M/Dutch</td>
<td>c.1309A&gt;T p.(Arg437*)</td>
<td>11/65</td>
<td>Night blindness since age 15 y; fast decrease of VA since age 20 y; visual field loss since age 30 y</td>
<td>LP (2.7)</td>
<td>IP (2.7)</td>
<td>6.00 to 5.00</td>
<td>5.5 to 2.00</td>
<td>95° × 125°</td>
<td>PSC cataract (visually disturbing)</td>
<td>Constricted up to 5° (RE) and 10° (LE) at age 31 y</td>
</tr>
<tr>
<td>P3/F/Dutch</td>
<td>c.1309A&gt;T p.(Arg437*)</td>
<td>25/67</td>
<td>Night blindness and visual field loss since age 25 y; subsequent loss of VA</td>
<td>LP (2.7)</td>
<td>IP (2.7)</td>
<td>2.50</td>
<td>2.50</td>
<td>PSC cataract</td>
<td>Bitemporal optic disc; severely attenuated vessels; preserved doughnut-shaped area of retina surrounding the atrophic macula; severe chorioretinal atrophy with intraretinal bone-spicule pigmentsations in periphery</td>
<td></td>
</tr>
<tr>
<td>P4/F/Dutch</td>
<td>c.1309A&gt;T p.(Arg437*)</td>
<td>41/57</td>
<td>Night blindness and visual field loss noted in third decade</td>
<td>0.7 (0.8)</td>
<td>0.6 (0.2)</td>
<td>RE</td>
<td>LE</td>
<td>-0.75 to -0.75</td>
<td>-0.75 to -0.75</td>
<td>PSC cataract (visually disturbing)</td>
</tr>
<tr>
<td>P5/F/Dutch</td>
<td>c.1309A&gt;T p.(Arg437*)</td>
<td>31/52</td>
<td>Night blindness and visual field loss noted in second decade</td>
<td>0.05 (1.3)</td>
<td>0.5 (0.3)</td>
<td>RE</td>
<td>LE</td>
<td>-0.75 to 2.25</td>
<td>-0.75 to 2.25</td>
<td>PSC cataract (visually disturbing)</td>
</tr>
<tr>
<td>P6/M/Dutch</td>
<td>c.1504delG p.(Arg501Valfs*6)</td>
<td>19/25</td>
<td>Night blindness and visual field loss noted in second decade</td>
<td>0.9 (0.04)</td>
<td>0.9 (0.04)</td>
<td>RE</td>
<td>LE</td>
<td>0.75 to 0.75</td>
<td>0.75 to 0.75</td>
<td>PSC cataract (mild)</td>
</tr>
<tr>
<td>P7/F/Belgian c.1507C&gt;T p.(Arg523*)</td>
<td>c.1507C&gt;T p.(Arg523*)</td>
<td>52/43</td>
<td>Night blindness since age 7 y; visual field loss since age 23 y; marked loss of VA since age 40 y</td>
<td>LP (2.7)</td>
<td>IP (2.7)</td>
<td>-2.50 to -3.00</td>
<td>-2.50 to -2.90</td>
<td>95° × 145°</td>
<td>Waxy optic disc with temporal pallor, severely attenuated retinal vessels; RPE atrophy more pronounced in confluent mound flecks around vascular arcades and interlobes, peripheral mixed mammillary and bone-spicule pigmentsations</td>
<td>General perception of object/ central vision in RE. NR in LE</td>
</tr>
<tr>
<td>P8/F/Belgian c.1851-1G&gt;T p.(G&gt;T)</td>
<td>c.1851-1G&gt;T p.(G&gt;T)</td>
<td>25/62</td>
<td>Night blindness since age 6 y; visual field loss since age 10 y; marked loss of VA since age 38 y</td>
<td>0.05 (1.3)</td>
<td>0.2 (0.7)</td>
<td>RE</td>
<td>LE</td>
<td>-0.80 to 2.00</td>
<td>-0.80 to 2.00</td>
<td>Pseudophakia</td>
</tr>
</tbody>
</table>

All individuals are unrelated, except P4 and P5, who are sisters. All full field ERG was nonrecordable except for P4, for whom it was not performed. BE, both eyes; CE, counting fingers; F, female; M, male; NP, not performed; NR, nonrecordable; PSC, posterior subcapsular; VE, visual field. *Amblyopia.
carried a 1-bp deletion leading to a frameshift and the incorporation of a premature stop codon (c.1501del, p.[Cys501Valfs*4]), P7 carried a second nonsense mutation (c.1567C>T, p.[Arg523*]), and P8 carried a mutation abolishing the 5' splice site of the first intron (c.183+1G>T). No second exonic mutation was detected in the fourth heterozygous carrier. Copy number variations of the coding region of FAM161A as a potential second mutation were excluded by genomic qPCR analysis. Since the expression of FAM161A is known to be strictly regulated by the retinal transcription factor CRX, reflected by the association of the gene with two evolutionarily conserved upstream and intronic CBRs respectively (Supplementary Fig. S1), we hypothesized that disruption of the binding sequence for CRX could alter the regulation of this gene.14 Hence, both CBRs were sequenced for this individual but no sequence variation was identified. Interestingly, Phet had two nieces with RP, whose DNA was not present in the initial cohort. Sanger sequencing subsequently revealed the p.(Arg437*) mutation to be present in homozygous state in these two sisters (P4 and P5). Of note, both sisters also carry a heterozygous mutation in RPE65 (c.1115G>A) that is recurrently present in the village where they live. In total, eight individuals were identified with biallelic mutations in FAM161A, with the p.(Arg437*) representing at least one of the two alleles in all cases. All FAM161A mutations identified in this study are depicted in Figure 1B.

The p.(Arg437*) Mutation in FAM161A Is a Founder Mutation

Given the high prevalence of the p.(Arg437*) mutation in the Dutch and Belgian cohorts, on top of the fact that this mutation had also been described in the German population,3 we hypothesized that this allele may represent a founder mutation. To assess this, haplotype analysis was performed in all patients carrying this mutation by genotyping the 5 SNPs reported by Langmann et al.3 and extended by 13 additional SNPs. The haplotype was compared with the previously reported haplotype of the German patients. All individuals homozygous for the p.(Arg437*) mutation (P1 to P5), were also homozygous for the following SNPs: c.1309A>T, c.1567C>T, c.1791C>T, c.1832C>G, c.1839A>T, and c.1908G>A. In addition, Phet was found to be homozygous for the following SNPs: c.1166A>G, c.1167A>G, c.1567C>T, c.1791C>T, c.1832C>G, c.1839A>T, c.1908G>A, and c.1914G>A. All of these SNPs are located within the coding region of FAM161A and are present in high frequency in the German population. Therefore, Phet was excluded from further analysis. In conclusion, the high prevalence of the p.(Arg437*) mutation in the Dutch and Belgian cohorts is consistent with it being a founder mutation.

**FIGURE 1.** FAM161A mutations identified in this study. (A) Identification of FAM161A founder mutation. Results of the ARMS reaction and subsequent Sanger sequencing analysis in patients homozygous for the c.1309A>T mutation, P (hom), heterozygous patients, P (het) and controls with two wild-type (wt) alleles, C (wt). The ARMS analysis consisted of two PCR reactions for every patient, one with a forward primer matching the wt allele (WT lane), the other one with a primer matching the mutated allele (MUT lane). P (hom) will only have amplification in the MUT lane. P (het) in both lanes and C (wt) only in the WT lane. Every mutation detected with the ARMS reaction was confirmed by Sanger sequencing. (B) Overview of FAM161A mutations identified in this study. The p.(Arg437*) founder mutation (red) is located in the third and largest exon of FAM161A. Presence of this mutation has been demonstrated in a total of nine Dutch and Belgian patients, of which five were homozygous for this mutation. In three heterozygous patients, a second mutation has been identified (black): c.183+1G>T, disrupting the 5' splice site of the first intron; p.[Cys501Valfs*4], a frameshift mutation leading to the incorporation of a premature stop codon; p.(Arg523*), a second nonsense mutation further downstream in the third exon. In one patient (P5) no second mutation was identified.
for a number of investigated SNPs surrounding the mutation, allowing construction of the haplotype carrying the nonsense mutation. The three individuals who carried compound heterozygous mutations (P6 to P8) also carried one of these haplotypes, together with a different haplotype harboring the second mutation. In addition, the disease haplotype identified in this study corresponded to the haplotype of the German patients who were homozygous for the p.(Arg437*) mutation (Fig. 2). The 17 SNPs (rs7609513–rs7574631) that together define the shared haplotype block are spread out over a region of 409 kb, delimited by recombination events at flanking SNP rs1406002 and flanking microsatellite D2S337, pointing to a maximal length of 910 kb for the common haplotype and further emphasizing that the p.(Arg437*) mutation represents a founder allele. Not taking into account the initial patient P1 included in the homozygosity study, Phet and her two nieces P4 and P5 identified the founder mutation in 5 out of 284 patients, corresponding to a prevalence of approximately 2% in the Dutch and Belgian populations.

Clinical Evaluation

Eight affected individuals from seven families were included in the study and an overview of the mutations and the clinical data is presented in the Table and Figure 3. The p.(Arg437*) mutation was found in a homozygous state in five patients of four families, albeit that there was no reported parental consanguinity but for P8, whereas P4 and P5 originate from a genetic isolate.

The initial symptom was night blindness in all eight affected individuals, but the age at which it was noted varied from 6 to 25 years. In patient P2, the diagnosis was established during a routine ophthalmic checkup at the age of 11 years; it took another 4 years before this patient became aware of night blindness. Subjects P7 and P8 experienced night blindness from the age of 7 and 6, but were only diagnosed with RP at the age of 32 and 25, respectively, indicating that the night blindness did not have an impact on their daily life and was not a reason to consult an ophthalmologist at an earlier age.

The nyctalopia was followed by progressive concentric constriction of the peripheral visual fields in all patients, and deterioration of central vision. Of six patients, follow-up data on BCVA were available and are displayed in Figure 4. These data show a loss of central vision after the age of 25 and legal blindness (visual acuity [VA] < 20/400, logMAR 1.3) in the sixth decade in P2 and P3. The other four individuals retained good central vision (≥20/40, logMAR 0.3) even within the sixth decade (P4 and P5) but with small visual fields. No extensive follow-up data were available on P7 and P8, but BCVAs in the better eye were light perception (LP) with localization and decimal BCVA of 0.05 (logMAR 1.3) at ages 43 and 63 years, respectively, with self-reported rapid deterioration of central vision at ages 30 and 36, respectively.

All patients displayed a mild to moderate myopia; anisometropia was the cause of amblyopia in patient P1. Posterior subcapsular cataracts were present in all eight patients. These typical cataracts developed from the third decade; patient P8 underwent cataract extractions at the ages of 57 left eye (LE) and 58 right eye (RE).

Ophthalmoscopy revealed the classic symptoms of RP consisting of waxy pallor of the optic discs and in advanced cases pale-white discs, attenuated retinal vessels, and atrophy of the RPE and choriocapillaris in the midperiphery with intraretinal spicular pigmentation in all eight, combined with

**FIGURE 2.** Haplotype analysis of FAM161A locus in Dutch, Belgian, and German patients. Eighteen SNPs and one microsatellite marker spread over a region of 910 kb (chr2: 61,669,931 [D2S337]–62,579,956 [rs1406002] [hg19]) were used to perform haplotype analysis in the eight individuals carrying the putative p.(Arg437*) founder mutation. An identical (orange) haplotype block of 409 kb (chr2: 61,825,142 [rs7574631]–62,234,345 [rs7609513] [hg19]) linked to disease could be identified in each of the patients. As expected, the five homozygous patients (P1–P5) described in this study and the three homozygous German patients described by Langmann et al.3 carried two copies of this disease haplotype block, whereas the three heterozygous patients had only one copy. Remarkably, P8 and Phet appear to share the same haplotype combination, while the splice site mutation identified in P8 was absent in Phet.
deep intraretinal nummular pigmentations in two (P7 and P8). In four subjects (P1, P4, P5, and P6), a bull’s eye–like maculopathy consisting of mild RPE alterations surrounding the fovea was documented at some stage of the disease. In patient P6, this lesion became apparent at age 24. In the three older patients (P2, P3, and P8), a narrow ring of recognizable retinal tissue that surrounds the completely atrophic macular center (Fig. 3) was observed, respectively at age 62, 65, and 67. The retinal tissue peripheral to this ring is also severely atrophic with disseminated, irregular pigmentary deposits. In patients P2 and P3, central ring-like depigmentation or bull’s eye–like macular lesions were seen at ages 44 and 53, respectively. Patient P7 displayed a relatively preserved fovea but without function.

Electroretinogram responses could not be elicited in any of the patients, not even at the early stages.

The BAF images on recent examination revealed a hyperautofluorescent ring around the fovea (Fig. 3) in patients P1, P4, P5, and P6. In patients P2 and P8, hyperautofluorescence in accordance with the doughnut-shaped preservation of the RPE was seen. In patients P1, P4, P5, and P6 IS and OS junctions were intact on OCT at the macular region, whereas they were absent in the other three patients tested.

Although one of the patients (P1) was treated for hypertension and diabetes, we did not detect any extraocular features that were suggestive for syndromic RP.

**DISCUSSION**

Genetic evaluation of *FAM161A* in a Dutch and Belgian cohort of genetically unsolved arRP patients, revealed eight individuals with biallelic *FAM161A* mutations. All individuals carried at least one c.1309A>T, p.(Arg437*) nonsense mutation; five were homozygous, whereas three were compound heterozygous in conjunction with a second protein-truncating allele. In addition, in one affected heterozygous individual related to two affected homozygous individuals, no second *FAM161A* mutation could be found despite copy number screening and evaluation of retina-specific CBRs. However, mutations in
noncoding regions of FAM161A such as deep intronic mutations, or involvement of mutations in a different retinal dystrophy gene cannot be excluded. Haplotype analysis revealed that the p.(Arg437*) mutation represents a founder allele present in the Dutch, Belgian, and German population.

Following homozygosity mapping, five patients from our cohort showed a significant homozygous region encompassing FAM161A, but only one of these carried a homozygous FAM161A mutation p.(Arg437*). Yet, this mutation was detected homozygously in four other patients from our cohort. As it appeared, these patients were either not analyzed by homozygosity mapping (P4 and P5) or the homozygous region surrounding the p.(Arg437*) mutation was below the threshold of 250 consecutive homozygous SNPs that was used to identify significant homozygous regions.13 The relatively small size of the common haplotype block identified in all mutation carriers, including the previously described German patients,3 supports the hypothesis that this mutation is an ancestral allele that has spread over northwest Europe, explaining the relatively high prevalence of this mutation in our arRP cohorts.

From a clinical point-of-view, the limited number of previous studies dealing with FAM161A mutations has shown a wide range of disease severity,3,4,12,23,24 although only two reports focus on the phenotype.12,24 As in other studies, the age of onset of FAM161A-associated RP in our patient cohort was variable, ranging from the first to the third decade of life. Most patients with FAM161A-associated RP display lens opacities and a mild to moderate myopia. This applies to the Dutch/Belgian patients in this study, but was also mentioned by others.4,23 However, it is not a finding limited to RP caused by mutations in FAM161A.

Despite clinical variability in disease severity, age of onset, and progression, a specific finding in the current study was the very distinct “ring” or “doughnut” of relatively preserved retinal tissue surrounding the macula. This phenomenon was present in three older patients in their seventh decade. The fact that two of these patients had documented bull’s eye-like lesions in their fourth and fifth decades, as well as the presence of bull’s eye-like maculopathy in two younger patients (P1 and P6) seems to suggest that these phenotypes may be sequential. Although the clinical description is often limited, bull’s eye-like patterns can be observed in the fundus photographs of some FAM161A-RP patients in other studies.3,12,24 One of the patients in the report by Bandah-Rozenfeld et al.4 shows a
fundus autofluorescence image that may even be indicative of a ring of preserved retinal tissue around the macular center. It would be interesting to investigate whether the presence of a bull’s eye–like maculopathy precedes atrophy of the posterior pole, and would thereby act as a negative prognostic factor for VA in FAM161A-related RP. Or, as suggested by Rose et al., it that there might be two different phenotypes as observed by fundus autofluorescence pattern.

Progression of the FAM161A RP phenotype results in legal blindness in our older patients. This bleak prognosis for VA later in life was also observed by Langmann et al., but in a recent report by Duncan et al. VA appeared remarkably well preserved, even in older patients. The notion in the latter study that foveal cones are preserved until the late stages of disease progression was therefore not corroborated by our study, adding to the evidence that this phenotype is indeed highly variable. FAM161A-related arRP is a ciliopathy and the phenotypes of this group of disorders can be quite diverse and known to involve other organ systems. We used a questionnaire to identify extraocular features, but except for one patient known with diabetes and hypertension, none of the patients show such associations. Obviously, this does not allow us to entirely and reliably exclude the presence of syndromal abnormalities that can only be brought to light with additional investigations, for instance blood tests or renal ultrasonography in case of renal developmental abnormalities.

In conclusion, we have identified a founder mutation in FAM161A underlying visual impairment in approximately 2% of Dutch and Belgian arRP patients. The phenotype of the Dutch/Belgian FAM161A-related retinal dystrophy is characterized by a severe chorioretinal atrophy that involves the posterior pole in the later stages, resulting in a very low BCVA. A null allele of FAM161A that is often limited to LP. A bull’s eye pattern was present in most of the patients in the early to midphase of the disease. This maculopathy may well progress to complete central chorioretinal atrophy with the exception of a thin “ring” or “doughnut” shape of relatively preserved retinal tissue surrounding the posterior pole.

Acknowledgments
We gratefully acknowledge Saskia van der Velde-Visser, Willy Verhoef-Thuis, Marlie Jacobs-Camps, and Lonneke Duijkers for technical assistance. We thank our German colleagues Thomas Langmann, Heidi Stöhr, Bernhard Weber, and Andreas Gal for kindly sharing the DNA samples of the German patients previously reported by Langmann et al. Finally, we thank Ramon van Hiet for providing visual acuity data of the patients from Nijmegen. Supported by the Netherlands Organization for Scientific Research (TOP-Grant 91200047), the Algemene Nederlandse Vereniging ter Voorkoming van Blindheid, the Gelderse Blinden Stichting, the Landelijke Stichting voor Blinden en Slechtzienden, the Macula Degeneratie Fonds, the Rotterdamse Stichting Blindenbelangen, and the Stichting Blinden-Penning (FPMC and AidH); the SWOO Flieringa Foundation (LJvdB); and grants from Belspo (IAP Project P7/43), Belgian Medical Genomics Initiative (EDB), and Funds for Research in Ophthalmology (KVS). KVS is doctoral fellow from the Institute for Innovation by Science and Technology. EDB and BPL are senior clinical investigators of the Research Foundation-Flanders (FWO).

Disclosure: K. Van Schil, None; B.J. Klevering, None; B.P. Leroy, None; J.W.R. Pott, None; D. Bandah-Rosenfeld, None; M.N. Zonneveld-Vrieling, None; D. Sharon, None; A.J. den Hollander, None; F.P.M. Cremers, None; E. De Baere, None; R.W.J. Collin, None; L.L. van den Born, None.

References


