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

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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. FAM161A is a microtubule-associated cilary protein presumably involved in maintaining microtubule stability. The interaction with other cilary and centrosomal proteins known to be implicated in retinal dystrophies, like SDCCAG8, CEP290, lebercilin, and POCI1B, points to a possible role for FAM161A in transport processes between the IS and OS.\textsuperscript{5,6,8} In addition to its ciliary function, a recent study presenting the FAM161A interactome also suggests a role for FAM161A in more general cellular processes, in the Golgi apparatus, centrosome, and/or the microtubule network.\textsuperscript{9}

In this study, we aimed to explore the contribution of \textit{FAM161A} mutations to the genetic spectrum of arRP in the Dutch and Belgian populations. A previously described nonsense mutation p.(Arg437*)\textsuperscript{3,10–12} was identified in eight individuals, five times in a homozygous state and three times in compound heterozygous state with another protein-truncating mutation. Detailed clinical examinations revealed some common phenotypic features related to \textit{FAM161A}-associated arRP.

**Methods**

**Subjects**

This study was approved by the medical ethics committees of the participating centers, and adhered to the tenets of the Declaration of Helsinki. Before this study, patients and their relatives consented to participate in this study, to retrieve the medical records, and to analyze their DNA.

**Genetic Evaluation**

To identify conspicuous homozygous regions potentially harboring the genetic defects underlying arRP in the Dutch population, we previously performed genome-wide homozygosity mapping in 230 affected individuals from 186 unrelated, mainly nonconsanguineous families using the Affymetrix GeneChip Genome-Wide Human SNP Array 5.0 platform. Homozygous regions were identified using Partek genomic suite software (Partek, St. Louis, MO, USA), as described previously.\textsuperscript{13} In patients with homozygous regions encompassing \textit{FAM161A} (NM_001201543.1), all exons and intron-exon boundaries of this gene were analyzed with Sanger sequencing as reported previously.\textsuperscript{14} Following the identification of the c.1309A>T; p.(Arg437*) mutation, the presence of this variant was assessed in 100 Belgian and 184 Dutch unrelated individuals affected with suspected autosomal recessive or isolated RP using amplification-refractory mutation system (ARMS) analysis. For this, three different primers were designed: a wild-type (wt) forward primer (F_wt), a mutated forward primer containing the c.1309A>T mutation at the 3' end (F_mut) and a wt reverse primer (R_wt). This mutation was confirmed by Sanger sequencing in all mutation-positive patients. All heterozygous carriers were screened for a second mutation by amplifying all coding regions of \textit{FAM161A}, followed by Sanger sequencing (BigDye Terminator v3.1 Cycle Sequencing Kit on an ABI 3730XL genetic Analyzer; Applied Biosystems, Foster City, CA, USA). A single heterozygous patient, for whom no second mutated allele was found, was screened for mutations in two \textit{FAM161A}-associated CRX-bound regions (CBRs).\textsuperscript{3,14} Furthermore, quantitative PCR (qPCR) analysis on genomic DNA was performed to determine the presence of any coding copy number alterations, as previously described.\textsuperscript{15} qBasePlus software (Biogazelle, Zwijnaarde, Belgium) was used for data-analysis\textsuperscript{16} and two reference genes were used for normalization of the relative quantities. Two positive controls with known copy number were used as a reference to calculate the copy numbers.\textsuperscript{15} Conventional PCR primers were designed using Primer3Plus,\textsuperscript{17} qPCR primers using PrimerXL (http://www.primersx.org/, in the public domain). All primer sequences can be found in Supplementary Table S1. Patient numbering is used throughout the text only for patients having a homozygous (P1-P5) or compound heterozygous \textit{FAM161A} mutation (P6-P8). The patient with only one heterozygous mutation is referred to as P9.

**Haplotype Analysis**

In total, 19 markers were genotyped (see Supplementary Table S2), 18 of which were single nucleotide polymorphisms (SNPs), and one flanking microsatellite. Five of the 18 SNPs were included because of their presence in the haplotypes of the German patients described by Langmann et al.\textsuperscript{3} Thirteen additional tagging SNPs were selected using the QuickSNP software.\textsuperscript{18} All primer sequences can be found in Supplementary Table S1.

**Clinical Evaluation**

We collected the available clinical data from the medical files of all eight patients with two \textit{FAM161A} mutations, and retrospective data on visual acuity were converted into logMAR scores. Some patients were reevaluated after the identification of the causative \textit{FAM161A} mutations. Ophthalmic examination included measurement of best-corrected visual acuity (BCVA) (Early Treatment Diabetic Retinopathy Study charts; Precision Vision, Inc., La Salle, IL, USA), biomicroscopy, ophthalmoscopy, and fundus photography. Additional tests were Goldmann kinetic perimetry and ERG according to the standards of the International Society for Clinical Electrophysiology of Vision (ISCEV).\textsuperscript{19} Spectral-domain optical coherence tomography (SD-OCT) and blue-light (488 nm) autofluorescence imaging (BAF; Heidelberg Spectralis HRA+OCT; Heidelberg Engineering, Heidelberg, Germany) was carried out as described previously.\textsuperscript{20} As \textit{FAM161A}-related arRP is a ciliopathy and ciliopathies can be quite diverse and involve other organ systems, we used a questionnaire to identify extraoocural features, such as nephropathy, polydactyly, intellectual disability, and obesity. \textit{FAM161A} is not included in the clinical overview given in the Table, due to the lack of clinical information.

**Results**

**Identification of \textit{FAM161A} Mutations**

Following genome-wide homozygosity mapping in a large cohort of Dutch RP patients,\textsuperscript{15} five patients with homozygous regions of at least 2 Mb encompassing \textit{FAM161A} were analyzed for mutations in this gene. In one individual (P1), a homozygous nonsense mutation was identified, c.1309A>T; p.(Arg437*) (Fig. 1A). This mutation had previously been identified in three German families segregating arRP.\textsuperscript{3} To further explore the prevalence of this mutation in the Dutch and Belgian populations, ARMS analysis was performed for this mutation (Fig. 1A). Of 284 patients, 2 additional patients carried the p.(Arg437*) mutation in a homozygous state (P2 and P3), whereas 4 individuals were heterozygous carriers of this mutation. Screening of the coding region revealed a second heterozygous mutation in three of them, that is, P6...
Diffuse scleral reflectance with a hypo-autofluorescent ring around the macula

Constricted up to 5–8

Severely atrophic retina with

age 31 y

Founder Mutation in FAM161A

Clinical Overview

T c.1309A

LP (2.7) LP (2.7)

6.00 to 1.50

LP (2.7) LP (2.7)

5.5 to 2.00

LP (2.7) LP (2.7)

4.00 to 2.00

LP (2.7) LP (2.7)

4.00 Pseudophakia

Marked hypo-autofluorescence of area around optic disc & vascular arcades, with hyper-autofluorescent spots in the midperiphery

Medullated optic discs, severely attenuated vessels; preserved RPE atrophy periphery with bone-spicule pigmentation

Constricted up to 10° RE and 5–10° LE (at age 55 y)

Preserved RPE and photoreceptors in the macular region

Marked hypo-autofluorescence of area around optic disc & vascular arcades, with hyper-autofluorescent spots in the posterior pole and midperiphery

Medullated optic discs, severely attenuated vessels; preserved RPE atrophy periphery with bone-spicule pigmentation

Constricted up to 15–20° BE

Preserved RPE and photoreceptors in the macular region

Hyper-autofluorescence ring around the fovea, with hyper-autofluorescent spots in the midperiphery

Medullated optic discs, severely attenuated vessels; preserved RPE atrophy periphery with bone-spicule pigmentation

Constricted up to 5° with small temporal island BE

Preserved RPE and photoreceptors in the macular region

Diffuse scleral reflectance with a hypo-autofluorescent ring around the macula

Isolated inferior or temporal hypopigmented area of retina

Constricted up to 5° (RE) and 10° (LE) at age 31 y

Severely atrophic retina with a relatively preserved retina with a RPE/choroid band in the area corresponding with the ring that surrounds the macula

PSE, posterior subcapsular; VE, visual field.

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.[Cyss501Valfs*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 Phet. 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.11+5G>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 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 2 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 and 58 years, respectively.

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: 61,669,931–62,579,956 [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: 61,825,142–62,234,345 [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.](http://iovs.arvojournals.org/pdfaccess.ashx?url=/data/journals/iovs/934655/ on 05/08/2017)
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.

Electoretinogram 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 \textit{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 \textit{FAM161A}, but only one of these carried a homozygous \textit{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.\textsuperscript{13} The relatively small size of the common haplotype block identified in all mutation carriers, including the previously described German patients,\textsuperscript{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.

Despite a number of recent studies, the exact function of \textit{FAM161A} is not completely understood. In gene trapped \textit{Fam161a} mice, it was shown that Fam161a is located in the cilia of rod and cone photoreceptors and that this protein is vital for the integrity of the connecting cilium. The structural abnormalities in these \textit{Fam161a}\textsuperscript{+/-} mice implicate a crucial role for this protein in the structural composition, maintenance, and function of the connecting cilium; the latter was also demonstrated by the misrouting of the cargo proteins opsin and rds/peripherin.\textsuperscript{21} In our study, as well as in previously published work, the vast majority of \textit{FAM161A} alleles are protein-truncating mutations that are predicted to completely abolish the function of the \textit{FAM161A} protein, whereas only two missense mutations have been reported so far.\textsuperscript{10,22} Hence, impaired transport of proteins essential for phototransduction in the OS of photoreceptor cells is the most likely molecular mechanism underlying \textit{FAM161A}-associated arRP.

From a clinical point-of-view, the limited number of previous studies dealing with \textit{FAM161A} mutations has shown a wide range of disease severity,\textsuperscript{3,4,12,23,24} although only two reports focus on the phenotype.\textsuperscript{12,24} As in other studies, the age of onset of \textit{FAM161A}-associated RP in our patient cohort was variable, ranging from the first to the third decade of life. Most patients with \textit{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.\textsuperscript{4,23} However, it is not a finding limited to RP caused by mutations in \textit{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 \textit{FAM161A}-RP patients in other studies.\textsuperscript{3,12,24} One of the patients in the report by Bandah-Rozenfeld et al.\textsuperscript{4} shows a

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure4}
\caption{Evolution of VA in patients with \textit{FAM161A} mutations. Graph showing the evolution of BCVAs expressed in logMAR (y-axis) over time (age, x-axis) for six patients (P1–P6) carrying mutations in the \textit{FAM161A} gene. For P7 and P8, no extensive follow-up data were available, only showing the VA at two and one time points, respectively. Snellen VA was transformed into logMAR for visualization purposes. A logMAR value of 1.9 was assigned to counting fingers (CF), 2.3 to hand movements (HM), and 2.7 to LP. When the VA differed in both eyes, the eye with the best VA at onset was used. When the VA at onset was identical, the recordings of the RE were taken.}
\end{figure}
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.,12 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.,3 but in a recent report by Duncan et al.24 VA appeared remarkably well preserved, even in older patients. The notion in the earlier 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 extracocular 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 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.

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