Myocilin Variants in Indian Patients With Open-angle Glaucoma

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Objective: To identify and evaluate MYOC variant alleles among patients with primary open-angle glaucoma (POAG) and age-matched control subjects in an Indian population.

Methods: Three hundred fifteen patients with POAG and 100 unrelated control subjects from the same ethnic background were enrolled in the study. The coding sequence of MYOC was amplified by polymerase chain reaction using genomic DNA, followed by sequencing of the polymerase chain reaction products. Four single nucleotide polymorphisms were genotyped in different Indian subpopulations comprising 1466 individuals using SEQUENOM’s homogeneous MassEXTEND assay.

Results: One novel mutation (Gly399Asp), 6 reported mutations (Gln48His, Thr256Met, Thr353Ile, Gln368Stop, Pro370Leu, and Ala427Thr), and 6 single nucleotide polymorphisms were identified in MYOC. Ala427Thr was identified in a patient with POAG and Parkinson disease. Four single nucleotide polymorphisms genotyped in control subjects were highly heterozygous and displayed a similar pattern of linkage disequilibrium among all linguistic groups.

Conclusions: MYOC mutations account for 2.2% of POAG cases. The Gln368Stop mutation (common among persons of the white race) found in 2 families does not seem to be of white race origin. Identification of a MYOC mutation (Ala427Thr) in a patient with POAG and Parkinson disease is interesting with respect to reported interaction of myocilin with synucleins.

Clinical Relevance: Studying the genetics of POAG is helpful for preclinical identification and for better disease management.
From that perspective, the role of the p53 codon 72 polymorphism and the apolipoprotein E ε allele in APOE have been examined for their association with POAG. In the Indian population, we examined genomic variation in MYOC, which could be tested for its association with POAG and could serve as markers to examine cosegregation of MYOC alleles with POAG in familial cases. The Indian population comprises 4693 communities, with several thousand endogamous groups, 325 functioning languages, and 25 scripts. Some geographical regions of India practice consanguinity. Few populations outside of Africa have the degree of genetic diversity found in the Indian subcontinent. The study subjects consisted of 4 major linguistic groups that define genetic variation in the population based on studies conducted on mitochondrial and autosomal genes.

**METHODS**

**SELECTION OF STUDY SUBJECTS**

Indian patients with POAG inhabiting West Bengal (eastern India), speaking Bengali, and belonging to the Indo-European linguistic group, regardless of any family history of POAG, were recruited from the Regional Institute of Ophthalmology, Kolkata, and from the Dristipradi Eye Clinic, Kolkata. Diagnoses were obtained from clinical oculic and systemic examinations. Ocular examinations included measurement of intraocular pressure using applanation tonometry (Goldmann tonometer) or noncontact air-puff tonometry. A Goldmann 3-mirror gonioscope was used to assess the angles of the anterior chamber and the optic disc. The optic disc was also evaluated using a +78-diopter lens in some patients. Automated threshold field analysis was performed using a Humphrey (Carl Zeiss Meditec Inc, Dublin, Calif) or Medmont (Medmont Internation Pvt Ltd, Victoria, Australia) version 6 field analyzer. The retinal nerve fiber layer was investigated by scanning laser polarimetry with the GDx Vcc (Carl Zeiss Meditec Inc).

For this study, the inclusion criteria were (1) optic disc cupping or visual field changes in patients with an intraocular pressure of greater than 20 mm Hg and (2) optic disc cupping and visual field changes in patients with an intraocular pressure of less than 21 mm Hg. Patients with a history of ocular inflammation, ocular trauma, or angle closure in any quadrant were excluded. Control subjects were subjected to routine eye examination and were chosen to match the age, race/ethnicity, geographic region, and linguistic background of the patients. Individuals were subjected to routine eye examinations, followed by retinal nerve fiber layer analysis using scanning laser polarimetry.

To study single nucleotide polymorphisms (SNPs) in the Indian population, 36 ethnic subgroups, classified on the basis of the 4 major linguistic groups and comprising 1466 individuals, were included in this study. The linguistic groups are Indo-European, Austro-Asiatic, Tibeto-Burman, and Dravidian. These individuals did not undergo any eye examination as part of this study.

**COLLECTION OF BLOOD SAMPLES AND GENOMIC DNA PREPARATION**

Ten milliliters of peripheral blood was collected with EDTA from the patients with POAG and from controls with their written consent. The internal review committee on research approved the project per regulations of the Indian Council of Medical Research. For evaluation of the intragenic SNPs in MYOC in different linguistic groups of the Indian subcontinent, identification of populations and collection of samples were carried out with the help of trained anthropologists, social workers, and community health workers. Endogamy of the populations was established by taking extensive information about the marriage patterns, gathered through pedigrees and interviews with family members of the donor and through review of the published literature. It was ensured that individuals were unrelated at least to the first-cousin level, and attempts were made to collect blood samples from male and female subjects in equal numbers.

Genomic DNA was prepared from fresh whole blood using the conventional phenol-chloroform method, followed by ethanol precipitation. DNA was then dissolved in 10mM Tris-hydrochloride and 0.1mM EDTA (pH 8.0).

**POLYMERASE CHAIN REACTION, DNA SEQUENCING, RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS, AND GENOTYPING**

Polymerase chain reaction was carried out in a total volume of 25 µL containing 50 to 100 ng of genomic DNA to amplify MYOC exons and adjoining splice junctions as described previously. The polymerase chain reaction products, free of contaminating bands because of nonspecific amplification, were subjected to bidirectional sequencing using a DNA sequencer with dye termination chemistry (ABI 3130XL; Applied Biosystems, Foster City, Calif) to identify any alteration of sequence from the normal variant.

For detection of Gln368Stop in the family members of the proband, restriction fragment length polymorphism analysis using TaqI was performed as previously described. An Aval restriction fragment length polymorphism assay was used to detect the −83G>A polymorphism in the MYOC promoter, as described by Lam et al.

Probands and affected family members were genotyped using 2 short tandem repeat polymorphic markers (D1S2815 and D1S2790) that closely flank MYOC. The frequencies of the selected SNPs in different linguistic groups of the Indian population were identified using the homogeneous MassEXTEND assay, an effective genotyping method run on the MassARRAY system performed using the SEQUENOM (SEQUENOM Inc, San Diego, Calif) platform at the Center for Genomic Application (New Delhi, India). Commercially available software (As say Design 2.0; SEQUENOM Inc) was used to design the polymerase chain reaction and homogeneous MassEXTEND primers for each SNP to be investigated.

**BIOINFORMATIC ANALYSIS OF EXPERIMENTAL DATA**

Novel changes were evaluated for their potential effect on the protein product using the SIFT (sorting intolerant from tolerant) score (http://blocks.fhcrc.org/sift/SIFT.html). The SIFT software predicts the potential of a substituted amino acid to be deleterious in a protein sequence. A score less than 0.05 is the benchmark of deleterious change.

Evaluation of nucleotide changes for alteration in splicing was performed using Web-based software (ESEfinder [http://rulai.cshl.edu/tools/ESE] and RESCUE-ESE [relative enhancer and silencer classification by unanimous enrichment; http://genes.mit.edu/burgelab/rescue-ese/]). Determination of linkage disequilibrium among SNPs in MYOC was performed using Haploview 3.2 software (http://www.hapmap.org/cgi-perl /gbrowse/hapmap/).
RESULTS

The patient pool (probands) consisted of subjects with juvenile-onset POAG (57 individuals aged 10-35 years) and subjects with adult-onset POAG (258 individuals). The age at diagnosis ranged from 10 to 84 years, with a mean±SD age of 55.69±16.78 years. The patients were not known to have any other eye disorder. The mean±SD age of the 100 unrelated control subjects enrolled in the study was 53.86±8.92 years (age range, 40-80 years).

The nucleotide changes identified in the patients are given in Table 1 and Table 2 with the genotype of the patients, evaluation of the variant alleles, and potential downstream effect on the protein. Clinical information regarding the patients harboring MYOC mutations is given in Table 3.

IDENTIFICATION OF MUTATIONS IN MYOC

Five mutations (Gln48His, Thr353Ile, Gln368Stop, Pro370Leu, and Ala427Thr) were detected in the heterozygous state in MYOC in patients with POAG (Table 1 and Table 2). Among these, Gln48His (c.144G/H11022 T), located in exon 1 of MYOC and identified in 3 patients with juvenile-onset POAG, has been reported previously by our laboratory. The Thr353Ile (c.1058C/H11022 T) mutation was identified in a patient with sporadic juvenile-onset POAG. Pro370Leu (c.1109C/H11022 T), associated with a severe glaucoma phenotype worldwide, was detected in 18-year-old woman. The mutant allele was found to segregate within the family in all 3 members affected with POAG but was not detected in any family member without POAG. Ala427Thr (c.1279G/H11022 A) was identified in 2 patients with sporadic POAG. One of the patients with the mutation also has Parkinson disease. The other patient with the mutation was diagnosed as having POAG at age 46 years. Vision in the left eye was greatly reduced at that time and was reported as finger counting.

Thr256Met was detected in the heterozygous state in a 49-year-old man with no family history of glaucoma. The patient was diagnosed as having the disease at age 46 years, when his visual field analysis showed minimum enlargement of a blind spot in both eyes. Gly399Asp was detected in a patient with sporadic juvenile-onset POAG in the homozygous state (Table 3). Both residues were found to be conserved based on MYOC sequences in human, mouse, rat, and pig, and the changes were absent in controls. The Thr256Met change has been previously reported in 1 patient from a study of normal-tension glaucoma. This study did not provide a detailed clinical description of that patient and characterized the variant as a polymorphism. However, the substitution of a polar (uncharged) hydrophilic residue by a nonpolar residue suggests this variant may be disease causing.

Table 1. Mutations in MYOC in Eastern Indian Patients With Primary Open-angle Glaucoma

<table>
<thead>
<tr>
<th>Nucleotide Change</th>
<th>Exon</th>
<th>Amino Acid Change</th>
<th>Genotype</th>
<th>SIFT Score</th>
<th>No. of Changes</th>
<th>Patients (n = 315)</th>
<th>Control Subjects (n = 100)</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.144G&gt;T</td>
<td>1</td>
<td>Gln48His†</td>
<td>Heterozygous</td>
<td>0.09</td>
<td>3</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.767C&gt;T</td>
<td>3</td>
<td>Thr256Met*</td>
<td>Heterozygous</td>
<td>0.15</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.1058C&gt;T</td>
<td>3</td>
<td>Thr353Ile*</td>
<td>Heterozygous</td>
<td>0.01</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.1102C&gt;T</td>
<td>3</td>
<td>Gln368Stop</td>
<td>Heterozygous</td>
<td>. . .</td>
<td>2</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.1109C&gt;T</td>
<td>3</td>
<td>Pro370Leu*†</td>
<td>Heterozygous</td>
<td>0.03</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.1196G&gt;A</td>
<td>3</td>
<td>Gly399Asp*‡</td>
<td>Homozygous</td>
<td>0.00</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.1279G&gt;A</td>
<td>3</td>
<td>Ala427Thr‡</td>
<td>Heterozygous</td>
<td>0.02</td>
<td>2</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

Abbreviation: SIFT, sorting intolerant from tolerant.† Already published.‡ Novel change.

Table 2. Single Nucleotide Polymorphisms in MYOC in Eastern Indian Patients With Primary Open-angle Glaucoma

<table>
<thead>
<tr>
<th>Nucleotide Change</th>
<th>Location</th>
<th>Amino Acid Change</th>
<th>Source</th>
<th>No. of Changes</th>
<th>Patients (n = 315)</th>
<th>Control Subjects (n = 100)</th>
</tr>
</thead>
<tbody>
<tr>
<td>−83G&gt;A</td>
<td>Promoter</td>
<td>Not applicable</td>
<td>Alward et al,17 1998</td>
<td>220</td>
<td>69</td>
<td></td>
</tr>
<tr>
<td>c.227G&gt;A</td>
<td>Exon 1</td>
<td>Arg76Lys*</td>
<td>Alward et al,17 1998</td>
<td>220</td>
<td>69</td>
<td></td>
</tr>
<tr>
<td>c.855G&gt;T</td>
<td>Exon 3</td>
<td>Thr285Thr†</td>
<td>. . .</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.952C&gt;T</td>
<td>Exon 3</td>
<td>Leu318Leu†</td>
<td>. . .</td>
<td>2</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.1041T&gt;C</td>
<td>Exon 3</td>
<td>Tyr347Tyr</td>
<td>Fingert et al,3 1999</td>
<td>8</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>c.1182C&gt;T</td>
<td>Exon 3</td>
<td>Thr394Thr†</td>
<td>. . .</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

* Already published.† Novel change.
Table 3. Clinical Features of Patients With Primary Open-angle Glaucoma (POAG) Carrying MYOC Mutations

<table>
<thead>
<tr>
<th>Patient</th>
<th>Age at Diagnosis, y</th>
<th>Mutation</th>
<th>POAG Subtype</th>
<th>RE, LE Intraocular Pressure, mm Hg</th>
<th>RE:LE Cup/Disk Ratio</th>
<th>Visual Field Changes</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>GL14*</td>
<td>20</td>
<td>Gln48His</td>
<td>Sporadic juvenile</td>
<td>20, 14 PO</td>
<td>0.9:1</td>
<td>Glaucomatous field changes</td>
<td>...</td>
</tr>
<tr>
<td>GL41*</td>
<td>70</td>
<td>Gln48His</td>
<td>Familial</td>
<td>24, 36</td>
<td>0.9:0.5</td>
<td>Diffused depression with scotoma in superotemporal quadrant</td>
<td>Early cataract in LE, trabeculectomy in LE</td>
</tr>
<tr>
<td>GL92*</td>
<td>32</td>
<td>Gln48His</td>
<td>Sporadic juvenile</td>
<td>28, 38</td>
<td>0.5:0.7</td>
<td>Glaucomatous field changes</td>
<td>...</td>
</tr>
<tr>
<td>GL452</td>
<td>46</td>
<td>Thr256Met</td>
<td>Sporadic juvenile</td>
<td>27, 30</td>
<td>0.5:0.5</td>
<td>Minimum enlargement of blind spot in BE</td>
<td>Spondylosis</td>
</tr>
<tr>
<td>GL178</td>
<td>32</td>
<td>Thr353Ile</td>
<td>Sporadic</td>
<td>16, 12</td>
<td>0.9:0.5</td>
<td>Superior and inferior arcuate scotoma in RE, isolated paracentral scotoma in LE</td>
<td>...</td>
</tr>
<tr>
<td>GL34*</td>
<td>18</td>
<td>Pro370Leu</td>
<td>Familial juvenile</td>
<td>18, 24 PO</td>
<td>0.8:0.7</td>
<td>Superior and inferior arcuate scotoma in RE, scotomatosus defect in supranasal quadrant in LE</td>
<td>...</td>
</tr>
<tr>
<td>GL145*</td>
<td>55</td>
<td>Gln368Stop</td>
<td>Familial</td>
<td>21 BE, PO</td>
<td>0.9:0.8</td>
<td>Superior arcuate defect</td>
<td>Left eye has myopic chorioretinopathy and squint, cataract in BE</td>
</tr>
<tr>
<td>GL429</td>
<td>62</td>
<td>Gln368Stop</td>
<td>Familial</td>
<td>18, 14</td>
<td>0.7:0.8</td>
<td>Vision loss in RE, superior arcuate defect with gross constriction in LE</td>
<td>Retina detachment occurred in RE</td>
</tr>
<tr>
<td>GL52</td>
<td>20</td>
<td>Gly399Asp</td>
<td>Familial juvenile</td>
<td>30, 27</td>
<td>0.9:0.8</td>
<td>Superior and inferior arcuate scotoma in BE</td>
<td>...</td>
</tr>
<tr>
<td>GL211</td>
<td>46</td>
<td>Ala427Thr</td>
<td>Sporadic</td>
<td>30, Not measured†</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>GL437</td>
<td>76</td>
<td>Ala427Thr</td>
<td>Sporadic</td>
<td>14, 14</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
</tbody>
</table>

Abbreviations: BE, both eyes; LE, left eye; PO, postoperative; RE, right eye.
*Already published.†Not visible because of dense cataract.

Gln368Stop (c.1102C>T), a common mutation among persons of white race with variable penetrance,19 was detected in 2 familial cases of POAG. The change was identified in family 1 (Figure 1A) and is the first report of this mutation among Asians.20 In addition to the proband, the mutation was present in III:8, III:9, IV:1, and IV:4. However, none of the mutation carriers in the family showed any sign of disease onset, which indicates possible incomplete penetrance in the family. On screening other candidate genes (OPTN, CYP1B1, and OPTC) for a potential digenic form of the disease in the proband, no suspected variant allele was detected. The mutation was also detected in the heterozygous state in 3 of 4 individuals in family 2 (Figure 1B). Field analysis of the proband, diagnosed at the age of 62 years, showed complete diminution of vision in the right eye and a superior arcuate defect with gross field constriction in the left eye. Trabeculectomy was performed in both eyes. Two of her daughters (II:2 and II:5) were heterozygous for the mutation and were found to be glaucomatous by retinal nerve fiber layer analysis, while the genotypically normal son (II:3) had no aberration on retinal nerve fiber layer analysis. Haplotype analysis based on 2 short tandem repeat polymorphic markers (D1S2815 and D1S2790) and an SNP marker (−83G>A) suggested that the mutant chromosome in the 2 families does not share a common origin (Figure 1). Allele sizes for the short tandem repeat polymorphic markers in the patients with POAG of white race (241 base pair [bp], 245 bp for D1S2790 and 220 bp, 233 bp for D1S2815) were different from those of 2 Indian patients (250 bp, 244 bp for D1S2790 and 222 bp, 224 bp for D1S2815), suggesting the absence of any founder mutation.

**MYOC SNPs IN THE INDIAN POPULATION**

We detected 6 nucleotide variants, 4 of which were coding SNPs (c.855G>T, c.952C>T, c.1041T>C, and c.1182C>T); these nucleotide variants represented silent changes and rare variants and were identified only among patients (Table 1 and Table 2). Among these, the silent change (Thr394Thr [c.1182C>T]) was predicted to affect splicing of the gene by in silico analysis but needs to be validated experimentally. Two variants (−83G>A and c.227G>A) were detected in patients and controls in similar frequencies. Based on the distribution of the alleles and the genotypes between the patients and the controls, neither of the polymorphisms was found to be associated with the POAG.

We had intended to evaluate linkage disequilibrium among heterozygous SNPs and haplotype diversity in the MYOC locus using healthy individuals. This information might be useful to evaluate MYOC variant alleles (using suspect SNPs) for their association with POAG in nonfamilial cases (case-control studies). In this context, it is noteworthy that the HapMap project (http://www.hapmap.org/cgi-perl/gbrowse/gbrowse/hapmap) does not include the Indian subcontinental population, representing one sixth of the world’s population. Therefore, we selected 4 SNPs—c.227G>A (rs2234926), intron 1 C>A (rs171002),...
tron 2 A>G (rs235873), and intron 2 G>T (rs235869)—in MYOC to determine the heterozygosity and pairwise linkage disequilibrium between these markers in the Indian population, as part of the effort undertaken by the Indian Genome Variation consortium. The 4 SNPs were found to have a heterozygosity value of 0.3 or higher in all linguistic groups except the Tibeto-Burman one (Figure 2A). Only 2 SNPs (rs171002 and rs235869) of the 4 SNPs examined were included in the HapMap project and were observed to have similar heterozygosity among 4 world populations (Figure 2B). Estimation of pairwise linkage disequilibrium (r²) between the markers indicated the presence of the following 3 groups: (1) markers 1 (reference sequence [rs] 235869), 3 (rs171002), (2) marker 4 (rs2234926), and (3) marker 2 (rs235873) as shown in Figure 2. The pattern was mostly similar in the 4 linguistic groups of India, as shown in Figure 2B. An estimation of haplotype diversity among these linguistic groups indicates 4 common predominant haplotypes in addition to a few rare ones found in low frequencies.

The present study carried out among 315 patients with POAG identified 7 mutations in 11 patients. Therefore, our study revealed MYOC mutations in 2.2% of POAG cases, which is consistent with the reported involvement of MYOC in 2% to 4% of patients with the disease. We, and other investigators,20 identified a single mutation in exon 1 (Gln48His), compared with 6 MYOC disease-causing variants identified in exon 3 among Indian patients with POAG. MYOC exon 3 codes for the olfactomedin domain, which is important with respect to the functionality of the protein.21

Of these novel variants identified, Gly399Asp was found in the proband in the homozygous state. The subject’s heterozygous parents (aged 48 and 40 years) did not manifest glaucoma. This suggests that this variant is not truly pathogenetic or that the likely disease mechanism for this particular mutation is unlike other exon 3 MYOC mutations.22,23 However, mutation of the same codon with Val instead of Asp has been reported to cause late-onset POAG (mean age at onset, 51 years) in a Guianese family and juvenile-onset POAG when the mutation is present with a CYP1B1 mutation (Arg368His).24 Therefore, it is likely that in the Indian family of the proband, the heterozygote parent might manifest POAG at a later age and that the homozygous genotype for the mutation resulted in juvenile-onset POAG in the proband. We are investigating defects in other candidate genes in the proband for a potential digenic form of the disease. Thr256Met and Gly399Asp, being nonconservative substitutions in the functional olfactomedin domain of MYOC, are expected to have deleterious effects on protein function.21

In the course of our study, we identified one mutation (Pro370Leu) associated worldwide with a severe glaucoma phenotype and another mutation (Gln48His) as a potential risk factor for glaucoma among patients of Indian origin.25 We also identified the Gln368Stop mutation, which has to date been predominantly found among persons of white race/ethnicity.

Figure 1. Pedigrees of eastern Indian families with a Q368X mutation in MYOC. Haplotypes are shown based on 2 microsatellite markers and an intragenic single nucleotide polymorphism marker (−83G>A) in the order of D1S2815 (1q24.4), −83G (intragenic), and D1S2790 (1q24.3). A, Family 1. B, Family 2. mt indicates mutant haplotype; squares, men; circles, women; filled symbols, individuals manifesting primary open-angle glaucoma; virgule, deceased; and arrow, proband.

Identification of the Ala427Thr mutation in MYOC in a patient with Parkinson disease represents an interesting case. Recently, it has been shown that γ-synuclein overexpression inhibits secretion of myocilin from cells to cultured media in the mouse HT22 hippocampal cell line.26 γ-Synuclein and α-synuclein are expressed in the human trabecular meshwork, and mutations in α-synuclein cause Parkinson disease and other neurodegenerative disorders.17,26 This information points toward a possible connection between α-synuclein and MYOC and invokes a putative involvement of α-synuclein with MYOC mutations in POAG. However, the observation may be coincidental and would require further evidence to substantiate the potential interaction between these 2 genes.

Analysis of 4 intragenic SNPs in the Indian population revealed 3 SNPs (SNP1 [rs235869], SNP2 [rs235873], and SNP4 [rs2234926] in Figure 2) that could serve as markers to examine cosegregation of MYOC alleles with POAG in familial cases. The lower pairwise linkage disequilibrium (r²) for SNP2, relative to the other 3 SNPs, suggests late arrival of SNP2 in the Indian population.
The identification of informative SNPs in the diverse population groups within India will provide greater opportunity to study cosegregation of MYOC alleles with juvenile-onset POAG in familial cases of the disease. In addition to direct mutation screening, linkage-based diagnosis of familial juvenile-onset POAG cases will assist clinicians in better management of the disease.

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Author Contributions: Dr Ray had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

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Reference:
12. Sambrook J, Fritsch EF, Maniatis T. Isolation of high-molecular-weight DNA from...


**From the Archives of the Archives**

The most essentially different forms are alcohol and tobacco amblyopia on the one hand, and quinine amaurosis on the other.

In the former group there is the clinical picture of a retrobulbar partial optic neuritis with a central scotoma and normal limits of the field. The anatomical changes are limited to the papillomacular bundle of fibers.

The second group is characterized by the existence of vascular changes, diminution of the caliber of the vessels, and necrosis in consequence of ischemia and of the toxic effect on the nerve elements. To this group belong quinine, salicylic acid, male fern, pomegranate root. There is excessive contraction of the visual field, but never multiple peripheral neuritis.