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Low prevalence of myocilin mutations in an African American population with primary open-angle glaucoma

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Purpose: Mutations in the myocilin gene (MYOC) are associated with primary open-angle glaucoma (POAG) in many different populations. This study represents the first large survey of MYOC mutations in an African American population.

Methods: We recruited 529 African American subjects with POAG and 270 African American control subjects in this study. A complete eye examination and blood collection was performed in all study subjects. Genomic DNA was extracted. The entire coding sequence of MYOC was amplified and sequenced using the Sanger method. Identified MYOC variants were compared with previously reported MYOC mutations.

Results: We identified a total of 29 MYOC variants including six potential MYOC mutations. Two mutations (Thr209Asn and Leu215Gln) are novel and are found only in cases and no controls. We also identified four previously reported MYOC mutations in cases and no controls (Tyr453MetfsX11, Gln368X, Thr377Met, and Ser393Arg). The overall frequency of glaucoma-causing MYOC mutations in our African American population with POAG was 1.4%.

Conclusions: We identified two novel probable glaucoma-causing MYOC mutations (Thr209Asn and Leu215Gln). This study indicates that, despite the high prevalence of POAG, MYOC mutations are rare in the African American population.


**METHODS**

*Study subjects:* The study adhered to the tenets of the Declaration of Helsinki. Informed consent was obtained from all study participants. The research was reviewed and approved by the Institutional Review Board from all participating institutions, including both Duke University Medical Center (Durham, NC) and the Massachusetts Eye and Ear Infirmary (Boston, MA). Study subjects were recruited from the Duke University Eye Center (Durham, NC) and the Massachusetts Eye and Ear Infirmary (Boston, MA) for a total of 529 African American subjects with POAG and 270 African American control subjects. Subjects with POAG were unrelated and met the following inclusion criteria: 1) age of onset greater than 18 years; 2) glaucomatous optic neuropathy in both eyes; and 3) visual field loss consistent with optic nerve damage in at least one eye. Glaucomatous optic neuropathy was defined as a cup-to-disc ratio greater than 0.7 or focal loss of the nerve fiber layer resulting in a notch, associated with a glaucanomatous visual field defect. Visual fields were performed using standard automated perimetry or frequency doubling test. An open anterior chamber angle has been found in all the POAG cases. IOP was not used as an inclusion criterion. The exclusion criteria for POAG subjects included the diagnosis of a secondary form of glaucoma or a history of ocular trauma. The control subjects were examined by a board-certified ophthalmologist. The control subjects were unrelated and met the following criteria: 1) no first-degree relative with glaucoma; 2) IOP less than 21 mmHg in both eyes without treatment; 3) no evidence of glaucomatous optic neuropathy in either eye; and 4) normal visual field in both eyes. The normal controls were recruited specifically for optic neuropathy in either eye; and 4) normal visual field in both eyes without treatment; 3) no evidence of glaucomatous optic neuropathy in either eye; and 4) normal visual field in both eyes. The normal controls were recruited specifically for this study and visual field was included in the eye exam.

*Genomic DNA sequencing:* Genomic DNA was extracted using standard methodology as previously described [36-38]. Briefly, genomic DNA was purified using a modified salting-out method. Primers flanking the entire coding sequence of *MYOC* were designed with Primer3 software [39]. Primer sequences are provided in Table 1. The amplified region covered at least 50 base pairs into each intron to screen for potential mutations affecting exon splicing. Platinum Taq DNA polymerase (Invitrogen, Carlsbad, CA) was used for all of the polymerase-chain reactions (PCR). The PCR amplifications were performed in ThermoHybaid MBS PCR machines (Thermo Scientific, Waltham, MA). Completed PCR reactions were purified and sequenced in the forward direction using BigDye chemistry (Applied Biosystems, Carlsbad, CA). Potential mutations were confirmed by additional sequencing in the reverse direction. All the sequences were analyzed using the Sequencher 4.9 software package (Gene Codes, Ann Arbor, MI). The Fisher’s exact test was used to test the association of all variants with POAG.

**RESULTS**

The study data set was composed of 529 African American subjects with POAG and 270 African American control subjects. The mean age of diagnosis in the subjects with POAG was 54.8 years and 42.5% of these subjects were female. In comparison, the mean age of the control subjects was 57.5 years (ranging from 40 to 85 years) and 53.3% of the control subjects were female.

We identified a total of 29 sequence variants, including 28 coding variants. Of these 29 variants, we identified four known myocilin mutations (Table 2), including two nonsense mutations (Tyr453MetfsX11 and Gln368X) and two missense mutations (Thr377Met and Ser393Arg). These 4 mutations are all located in exon 3. Each mutation was found in 1 POAG patient and no controls. They have all been previously reported as glaucoma-causing mutations [17]. We also identified two novel missense mutations: Thr209Asn in one POAG patient and Leu215Gln in two POAG patients, but not in controls (Table 2). Both of these novel mutations are located in exon 2. Combining all the patients with myocilin mutations, we have identified six different myocilin mutations in 7 African American POAG patients and no controls, accounting for approximately 1.4% of all the POAG patients. These African American patients carrying myocilin mutations tend...
We also identified an additional twelve non-synonymous coding variants (Table 3), which appear to be neutral polymorphisms. Four of them (Arg76Lys, Val329Met, Glu352Lys, Lys398Arg) were previously reported as neutral polymorphisms [17]. All of the variants except for Val329Met were identified in both cases and controls. Val329Met was found in 2 cases but no control subjects. Two of the variants in exon 3, Thr353Ile and Lys500Arg, were previously reported with uncertain pathogenicity [17]. We identified Thr353Ile in only 1 control and the Lys500Arg variant in 4 cases and 2 controls. The remaining six variants were novel, including Ala108Gly, Arg126Gln, Arg226Gln, Gly244Ser, Ser333Cys, and Asp446Tyr [17]. Each of these novel variants was found in only 1 control subject, except for Ser333Cys, which was found in 1 case and 1 control.

In addition, we also identified 10 synonymous coding variants and one variant in the 5′-untranslated region (5′-UTR; Table 4). None of these silent variants were found to have a significant association with POAG. The 5′ UTR variant has not been previously reported and was only found in 1 control subject.

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Overall, the frequency of non-synonymous changes was not significantly different between cases and controls. Only one control subject was found to carry multiple non-synonymous variants of Asp446Tyr and Lys500Arg. The Asp446Tyr variant has not been previously reported and the Lys500Arg variant is considered to be of uncertain pathogenicity [17]. All other individuals had no more than 1 non-synonymous coding variant. Multiple synonymous variants did occur together frequently, more commonly in cases than in controls. These multiple synonymous variants were found in 10.8% of cases and 5.6% of controls, which was significantly different (Fisher’s exact test, p=0.02).

**DISCUSSION**

This study is the largest survey of myocilin mutations in African American subjects with and without POAG. We identified six myocilin mutations in seven POAG patients. The overall frequency of glaucoma-causing mutations in POAG subjects was 1.4%. Our finding is very similar with those in the Moroccan population [29], but is significantly
However, further studies are needed to replicate these findings. Although the frequency of several sequence variants differed between cases and controls, these differences were not statistically significant (Fisher’s exact test, p>0.05).

Comparing to the previous screen of myocilin mutations in African American POAG subjects and controls [30], our larger study not only corroborated their findings for three of the probable glaucoma-causing mutations (Gln368X, Ser393Arg, and Tyr453FS), but also identified one POAG subject with the Thr377Met mutation. This mutation is one of the most commonly found POAG-causing mutations and has been previously identified in populations from Australia, United States of America, Greece, the former Yugoslavian Republic of Macedonia, India, Finland, and Morocco [29,33,34,42-45]. Although the previous African American study found Glu352Lys variant in 2 POAG patients and no controls [30], we found this variant in 13 POAG patients and 5 controls that were heterozygous for the variant. The frequency in cases and controls was not statistically different by the Fisher’s Exact Test (p>0.05). Our data supported the reclassification of this variant as a polymorphism (dbSNP; rs61745146).

In summary, we have performed the largest screening of myocilin mutations in the African American population. The overall frequency of probable glaucoma-causing mutations in myocilin was lower in our data set of African American POAG subjects compared to prior reported frequencies of 2%–4% in many different populations [18]. This difference could be due to ascertainment bias due to recruitment of prevalent cases from glaucoma clinics compared with incident cases in a population-based study. Our study not only confirms the contribution of myocilin mutations in the African American population, but also suggests the greater genetic heterogeneity of POAG in this admixed population.

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