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Coinheritance of *OLFM2* and *SIX6* variants in a Chinese family with juvenile-onset primary open-angle glaucoma: A case report

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Abstract

BACKGROUND

Juvenile-onset primary open-angle glaucoma (JOAG), characterized by severe elevation of intraocular pressure and optic neuropathy prior to the age of 40, is a rare subtype of primary open-angle glaucoma. Several genetic mutations have been associated with JOAG.

CASE SUMMARY

The proband patient was a young male, diagnosed with primary open-angle glaucoma at the age of 27. The patient and his unaffected parents who have been excluded from classic genetic mutations for primary open-angle glaucoma were included to explore for other possible genetic variants through whole genome sequencing and bioinformatics analysis. In this trio, we found two heterozygous variants inherited from the parents in the proband: c.281G>A, p.Arg94His in *OLFM2* and c.177C>G, p.Ile59Met in *SIX6*. Both genetic mutations are predicted through bioinformatics analysis to replace evolutionary conserved amino acids, therefore rendering a pathogenic effect on proteins. In contrast, very low frequencies for these genetic mutations were recorded in most common control databases.

CONCLUSION

This is the first report on coinherited mutations of *OLFM2* and *SIX6* in a JOAG family, which shows the complexity of JOAG inheritance. Large-scale clinical screening and molecular functional investigations on these coinherited mutations are imperative to improve our understanding of the development of JOAG.

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Core Tip: This report describes a case of juvenile-onset primary open-angle glaucoma (JOAG) with a coinheritance of *OLFM2* and *SIX6* variants, which might contribute to the onset of JOAG. This finding may enrich the genetic spectrum of JOAG and prompt us to further investigate the functional effects of the two variants on JOAG.

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INTRODUCTION

Primary open-angle glaucoma (POAG) is a group of polygenic heterogeneous diseases, with characteristic glaucomatous optic neuropathy and visual-field defects. POAG is the second most common cause of irreversible blindness worldwide^[1]. Juvenile-onset primary open-angle glaucoma (JOAG) is a unique subtype of POAG, characterized by an early disease onset prior to 40-years-old, usually a significantly elevated intraocular pressure (IOP) and severe glaucomatous optic neuropathy^[2]. JOAG progresses more rapidly in comparison with classic adult-onset POAG^[3].

POAG is essentially a neurodegenerative disease in the elderly population^[4], whose onset is determined by interactions between various environmental and genetic factors. JOAG, due to its early onset, is likely subsequent to a genetic mutation. Currently, several genes, including *MYOC*, *OPTN*, *CYP11B1*, *OAS3*, *PITX2* and *LTBP2* have been reported to be associated with JOAG^[5-7] through traditional Mendel genetic analysis. However, clinically there are still many JOAG cases that cannot be attributed to these reported genetic mutations. Therefore, a strategy using whole genome sequencing (WGS) and *de novo* mutation trio analysis^[8] can be used to explore novel genetic variants.

In this current study, we performed WGS on a trio (the proband and his unaffected parents) at Zhongshan Ophthalmic Center to identify potential disease-causing mutations. After excluding classic glaucoma-associated gene mutations, we surprisingly found two heterozygous gene variants that were predicted to be potentially pathogenic *via* bioinformatics analysis in the proband. To our knowledge, this is the first report on a JOAG family that has been associated with a coinheritance of *OLFM2* (c.281G>A, p.Arg94His) and *SIX6* (c.177C>G, p.Ile59Met) variants.

CASE PRESENTATION

Chief complaints

A 27-year-old male was admitted to our hospital due to elevated IOP of both eyes for nearly 3 months.

History of present illness

There was no relevant ocular or medical history.

History of past illness

The patient was previously diagnosed with myopia, and he was allergic to cefradine. No history of systemic hypertension, diabetes mellitus, coronary heart disease, stroke, smoking or obesity was reported.



Personal and family history

There was no remarkable personal and family history.

Physical examination

His myopic refractive error at -3.00 diopter of both eyes was detected. The IOPs without prescription medications at the initial visit in Zhongshan Ophthalmic Center were 28.7 mmHg in the right eye and 31.4 mmHg in the left eye, which was recorded as the peak IOP. Best corrected visual acuity was 1.0 in each eye measured by the standard Snellen chart.

Laboratory examinations

Routine blood examination, liver and kidney function and electrolyte test indicators were normal.

Imaging examinations

Fundus examination with color photos was accomplished with particular attention paid to make sure that image focus was exactly on the optic disk margins. The result showed vertical cup disc ratio of his right eye was 0.7 and his left eye was 0.8 with localized cupping in both eyes. A localized retinal nerve fiber layer thinning corresponding to the optic disc cupping was detected by Heidelberg Spectralis optical coherence tomography (Heidelberg Engineering, Heidelberg, Germany) in each eye, with an average retinal nerve fiber layer thickness significantly reduced at 69 μ m oculus dexter and 67 μ m oculus sinister. Visual field defects were detected by Humphrey Visual Field Analyzer (Zeiss Meditech, Jena, Germany) in both eyes with the visual field mean deviation of -6.75 dB oculus dexter and -5.30 dB oculus sinister (Figure 1).

Further diagnostic work-up

WGS: WGS followed the same protocol as previously reported^[9]. The sequencing depth among participants ranged from 54.23X to 60.27X, with the percentage of coverage more than 10X at 91.53% to 92.20%. Mutations identified were analyzed using an autosomal recessive model as well as *de novo* dominant model. We have excluded mutations with a minor allele frequency more than 0.1% in either the Genome Aggregation Database or the Exome Aggregation Consortium. According to the data from the Human Phenotype Ontology, the names of the reference genes screened are listed in the Supplementary Table 1. The screening criteria for deleterious mutations were based on the American College of Medical Genetics guidelines^[10]. In trio-based WGS, the single nucleotide polymorphism in some of the major gene loci (Supplementary Table 2) that were previously reported to affect JOAG phenotype, such as MYOC and LTBP2^[6,7] as well as *de novo* dominant mutations were not detected. Importantly, it was found that the proband (II1) had coinherited mutations. The proband has a c.281G>A, p.Arg94His in OLFM2 (NM_058164.3) inherited from his father (I1) and a c.177C>G, p.Ile59Met in SIX6 (NM_007374.2) inherited from his mother (I2), which cosegregates with the phenotype in a recessive pattern (Figure 2). Interestingly, the OLFM2 mutation from the father is also transmitted to another sibling (II2), who is exempt from any glaucoma phenotypes. The OLFM2 mutation (c.281G>A, p.Arg94His) had a minor allele frequency of 0.005% in the Exome Aggregation Consortium and 0.004% in the Genome Aggregation Database, while the specific mutation was classified as deleterious in MutationTaster, mCAP and CADD. The SIX6 mutation (c.177C>G, p.Ile59Met) was absent in the Exome Aggregation Consortium and had a minor allele frequency of 0.0004% in the Genome Aggregation Database, which was classified as deleterious in MutationTaster, Fathmm and mCAP. Importantly, these mutations were found to be highly conserved across various species (Figure 3).

Sanger sequencing: Amplification using PCR followed by Sanger sequencing was used to confirm the identified mutations of OLFM2 and SIX6 in each family member. Sequencing was performed on an ABI 3730xl DNA analyzer (Applied Biosystems, Foster City, CA, United States). The reference genes were obtained from the Ensembl genome browser (in the public domain, <http://www.ensembl.org>). The primers used for PCR amplification are listed in Table 1.

Table 1 Primer sequences used for Sanger sequencing

Gene	Sequence, 5'-3'	Product size in bp
<i>OLFM2</i>	F: CGTCGGTGTGGTGTGTGTAC	372
	R: TGTGGCTCATATTGGACCCCT	
<i>SIX6</i>	F: AATCCGCCTCATCAACAAGC	825
	R: CAGAACGCAGGGCTCTTAAC	

F: Forward; R: Reverse.

FINAL DIAGNOSIS

JOAG in both eyes.

TREATMENT

Since the diagnosis of glaucoma, the patient has been routinely treated with medication (brimonidine tartrate eye drops, three times a day; travatan, *quaque nocte*; azopt, twice a day) to control IOP for more than 3 months. At the age of 28, the patient received an express implant (Glaucoma Filtration Device Version P-200) in the right eye. One month later, his left eye was also treated with an express implant (Glaucoma Filtration Device Version P-200). Antibiotic eye drops (compound neomycin sulfate) and eye ointment (tobramycin dexamethasone) were used for anti-inflammation postoperatively.

OUTCOME AND FOLLOW-UP

The IOPs were well controlled at middle 10 s in both eyes postoperatively and during regular follow-up.

DISCUSSION

JOAG is a rare subtype of POAG that is closely associated with genetic mutations. In the present study, we have for the first time, reported a coinheritance of mutations in *OLFM2* (c.281G>A, p.Arg94His) and *SIX6* (c.177C>G, p.Ile59Met) in a patient with JOAG through WGS and bioinformatics analysis. The potentially pathogenic mutations in *OLFM2* and *SIX6*, inherited from the father and the mother, respectively, might be responsible for the onset of JOAG in this proband. Digenic inheritance is the simplest form for genetically complex diseases. By contrast with the thousands of reports that mutations in single genes cause human diseases, there are many human disease phenotypes with evidence for digenic inheritance in some pedigrees. Therefore, whether the inherited pattern of the proband is consistent with digenic inheritance needs to be further verified through functional research. Our report of coinherited *OLFM2* and *SIX6* variants in a JOAG family indicates the complexity of JOAG inheritance and enriches our understanding of the mutation spectrum in JOAG.

OLFM2 encodes a secreted glycoprotein in the Noelin family of olfactomedin domain-containing proteins that regulate the timing of neuronal differentiation during development^[11]. The olfactomedin domain-containing protein that has been studied most comprehensively is myocilin encoded by the *MYOC* gene. Through phylogenetic analysis in humans, it was suggested that *MYOC* may have evolved from *OLFM2* through gene duplication followed by exon fusion, which may partially explain a 31% homology between *MYOC* and *OLFM2*^[12]. *MYOC* is the first candidate gene mapped for POAG. Mutations in *MYOC* account for 4%-35% of adult-onset POAG and for more than 10% in JOAG^[12-14]. Therefore, it is reasonable to speculate that certain mutations in *OLFM2* may also have detrimental effects in the development of JOAG. Funayama *et al*^[15] reported that the Arg144Gln (exon 4) mutation in *OLFM2* might result in POAG in Japanese patients. They also found that the combination of single

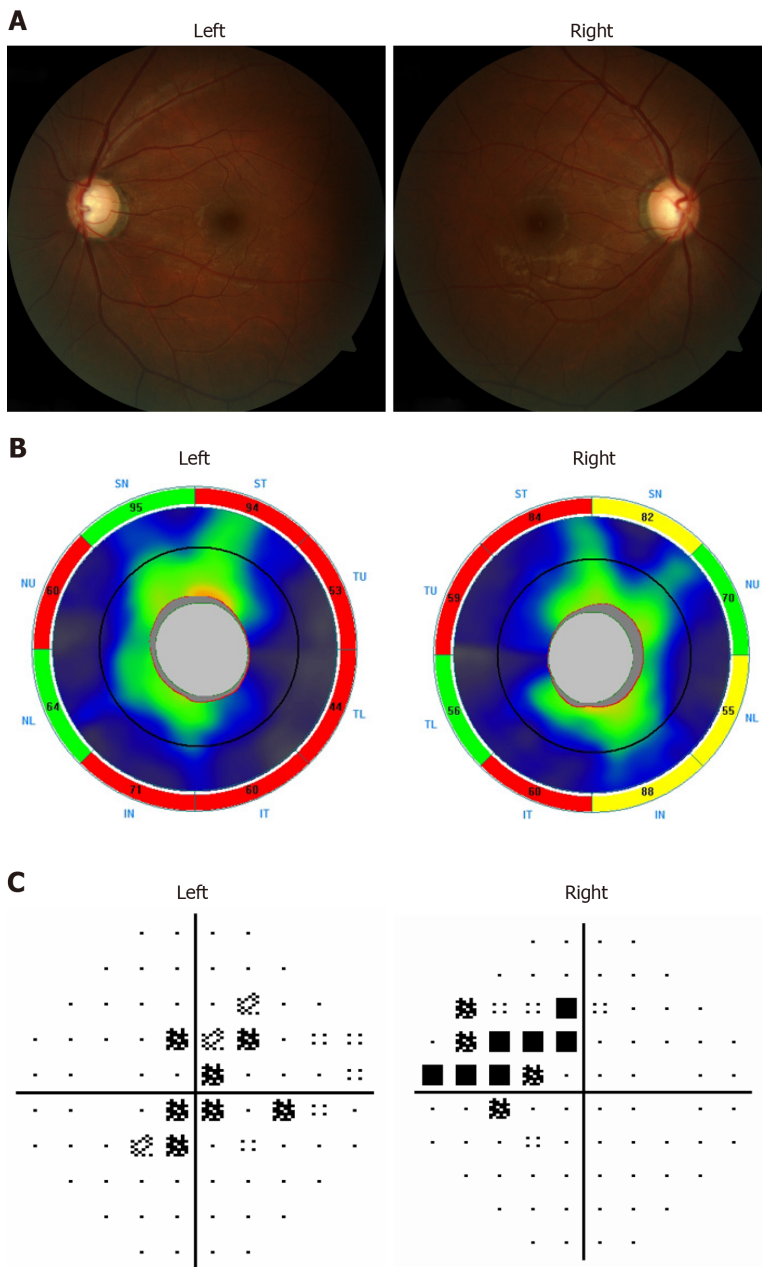


Figure 1 Ocular assessments of the proband. A: Fundus photo of the right and left eye; B: Ocular coherence tomography-retinal nerve fiber layer of both eyes (Key: S: Superior; T: Temporal; N: Nasal; I: Inferior); C: Right and left nasal step visual field defects consistent with glaucomatous damage.

nucleotide polymorphisms in *OLFM2*/317G and *OPTN*/603A was significantly associated with IOP elevation. However, their data were derived from sporadic case analysis, and there was no genetic information based on family inheritance. The origin of disease-causing mutations was unknown.

Loss of retinal ganglion cells (RGCs) and their axons are the primary diagnostic pathology in glaucoma. We have long known that the retina and optic nerve are embryonically and structurally part of the brain. Numerous studies have attempted to establish connections between glaucoma and neurodegeneration in the brain^[16,17]. Previously, it was reported that *OLFM2* was mainly expressed in the olfactory bulb, cortex, piriform cortex, olfactory trabeculae and inferior and superior colliculus in the brain. Functional investigation using *Olfn2*-KO^{LacZ} mice demonstrated that the loss of *Olfn2* caused a reduction of synaptic proteins in the brain and the retina^[18]. Although not systemically investigated, the impairment of synaptic connections between neurons within the retina and the brain can potentially affect structural and functional integrity of RGCs and their axons. Interestingly, it was shown that genetic mutant *Olfn2* in mouse was associated with abnormal psychological phenotypes such as anxiety and reduced levels of exploratory and locomotor activities^[18], while ours and various other studies have shown that psychological conditions such as anxiety are

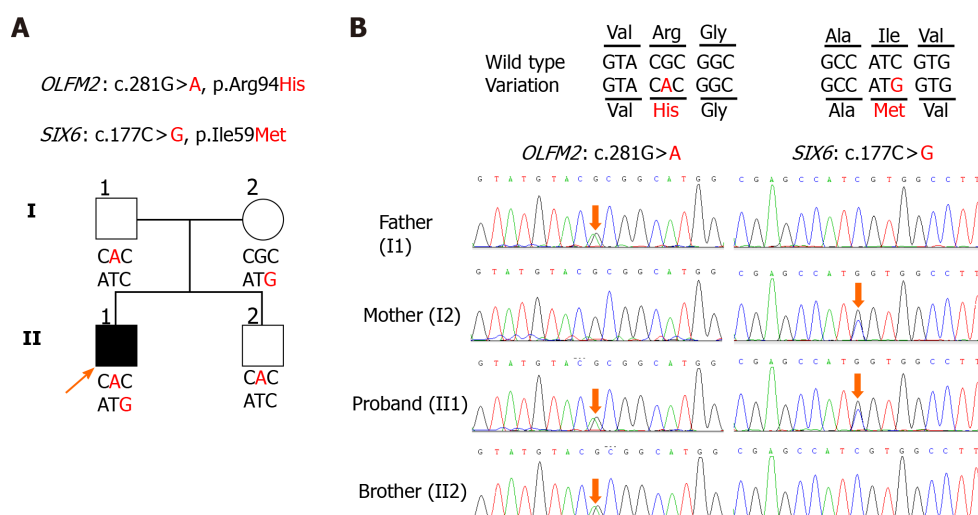


Figure 2 Coinheritance of *OLFM2* and *SIX6* variants might be associated with juvenile-onset primary open-angle glaucoma. A: The proband coinherited *OLFM2* and *SIX6* variants, indicated with a black arrow. The square represents male, circle represents female, and affected individual was shown by a filled symbol; B: The Sanger sequencing DNA chromatograms of *OLFM2* and *SIX6* for the proband and unaffected family members. The mutated nucleotides are marked with red arrows.

strongly connected with the incidence of POAG^[19-21] likely through reduced retrograde axonal transport of neurotrophic factors, such as brain-derived neurotrophic factor. Taken together, *OLFM2* is likely a candidate gene for POAG/JOAG.

SIX6 is also known as *OPTX2*, which belongs to the *SIX*/Sine oculis homeobox family that covers 1 homeobox DNA-binding domain. Various reports on pathogenic mutations in *SIX6* have been connected to POAG. The connection between single nucleotide polymorphisms (rs33912345, rs10483727 and rs12436579) in *SIX6* and POAG was established by genome-wide association studies^[22,23]. Another study including POAG patients with missense variant in *SIX6* (rs33912345) showed that a smaller optic disc rim area, larger vertical cup-disc ratio and significantly decreased average nerve fiber layer thickness are detected in patients with homozygous mutations in contrast to those with the nonrisk allele^[24,25]. It was found in another study that clinical features in POAG patients appear to be dependent on the *SIX6* genotype^[26].

In our study, we found two missense mutations in *OLFM2* (c.281G>A, p.Arg94His) and *SIX6* (c.177C>G, p.Ile59Met) by WGS in a trio. Interestingly, the proband with JOAG coinherited one mutation from each parent. Furthermore, we included another nine trios with a JOAG proband and unaffected parents to verify the deleterious mutations. However, we did not find any duplicate cases due to an insufficient number of trios. Nevertheless, combined with various functional studies on *OLFM2* and *SIX6* mutations, we still suspected the coinherited variants might contribute to occurrence of JOAG. Based on data from the FANTOM5 dataset^[27,28], *OLFM2* and *SIX6* are both expressed in the human retina. In mice, *OLFM2* is mainly detected in RGC^[18]. In an *in vitro* disease model using the *SIX6* risk allele (rs33912345; C>A; His141Asn) carrying glaucoma patient-specific induced pluripotent stem cells for functional RGC regeneration, it was demonstrated that the number of RGCs generated was decreased and the expression of RGC regulatory genes were suppressed by altered *SIX6* function^[29]. In *Olfm2*-KO^{LacZ} mice, the primary wave at the visual cortex in visual evoked potential was found to be significantly reduced when compared with those in wild-type littermates. A slight reduction in the number of RGCs and their axons was also observed in the *Olfm2*-KO^{LacZ} mice. In zebrafish, it was found that *Olfm2*-KO retarded nervous system development^[30]. Additionally, loss of *SIX6* in early development may cause small eye phenotype, under-development of the lens and reduced neural fiber layer around the optic nerve head^[26]. There are clinical studies in which patients with anophthalmia and microphthalmia were found to have *SIX6* mutations^[31]. Significantly, mutations in *OLFM2* can also result in anophthalmia, microphthalmia and coloboma^[32], which altogether indicate that *OLFM2* and *SIX6* may have interactions working together in shaping eye development. We hypothesize that *OLFM2* and *SIX6* genes and their protein products may interact to regulate a critical pathway in ocular development, which if disturbed may lead to the pathogenesis of JOAG/POAG.

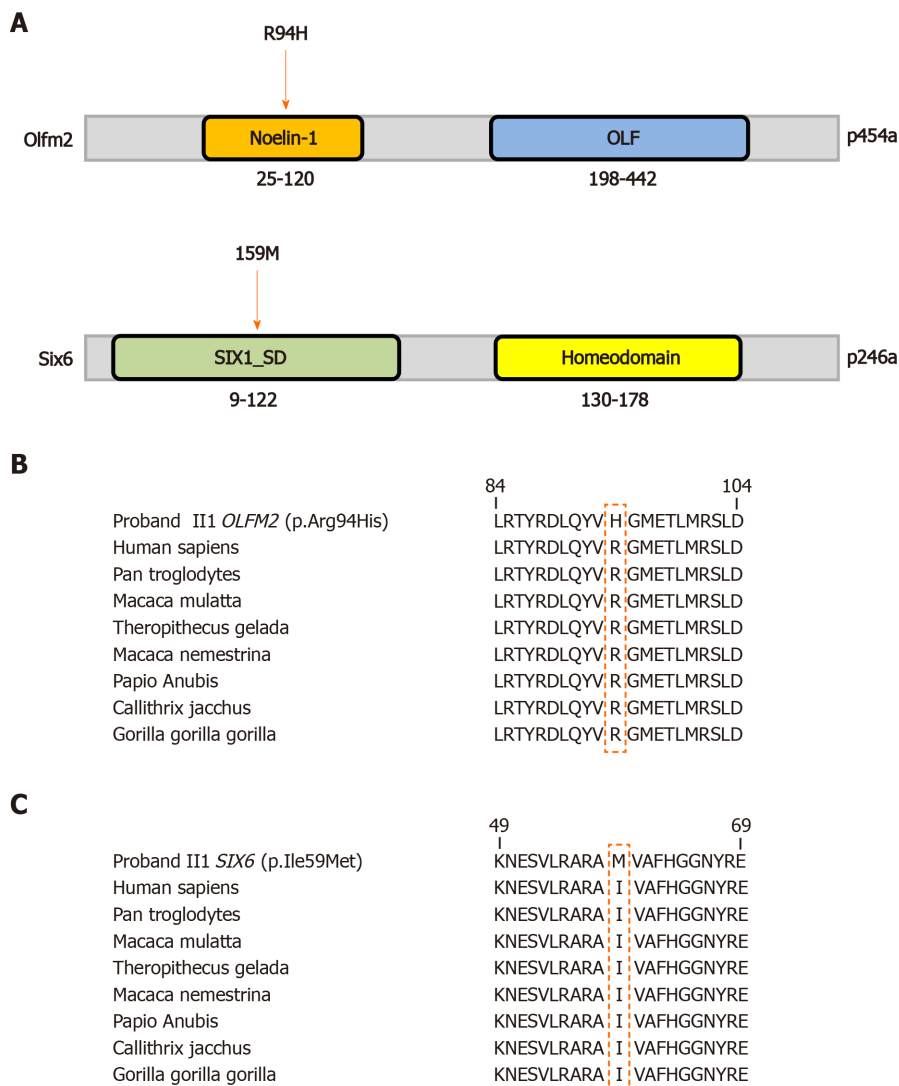


Figure 3 Evolutionary conservation of amino acids for the p.(Arg94His) and p.(Ile59Met) mutations. A: Schematics of the functional domains of the *Olfm2* and *Six6* proteins and locations of the corresponding mutations; B and C: The mutation and wild type residues for *OLFM2* p.Arg94 (B) and *SIX6* p.Ile59 (C) were highlighted with a red box. Noelin-1: Neurogenesis glycoprotein domain; OLF: Olfactomedin-like domain; SIX1_SD: Transcriptional regulator, SIX1, N-terminal SD domain; homeodomain: DNA binding domain, involved in the transcriptional regulation of key eukaryotic developmental processes.

To date, there are only two reports on glaucoma that have shown clear evidence for digenic inheritance^[33,34]. In primary congenital glaucoma, *LTBP2* p.R299X homozygous mutation plus *CYP11B1* p.E387K heterozygous mutation resulted in a severe clinical phenotype and poor prognosis^[33]. Carriers of both the *MYOC* and *CYP11B1* mutations lead to POAG at an earlier age (27-years-old) compared with carriers of only the *MYOC* mutation (51-years-old)^[34]. These data indicate that coinherited mutations may play an important role in determining the age of disease onset. Under this situation, one genetic mutation may work as a “dominator” while the other functions as a “regulator”. Therefore, a conservative approach to counselling may be warranted, under the assumption that some *SIX6* mutations may render susceptibility but are not sufficient to cause glaucoma. The existence of another genetic mutation, for example, *OLFM2*, may facilitate a pathogenic effect of *SIX6* mutations. To investigate our hypothesis, functional work on the association between *OLFM2* and *SIX6* should be carried out in the future.

CONCLUSION

In summary, we identified a coinheritance of *OLFM2* and *SIX6* variants in a core family of JOAG through WGS, Sanger sequencing and bioinformatics analysis. This specific inheritance would not have been identified through traditional Mendelian

inheritance studies or analysis with a gene chip-based test. WGS covering a great number of annotated exons was the best option for finding novel mutations. It should be emphasized that a WGS strategy on trios is crucial for further genetic studies in JOAG/POAG. Additionally, previous families investigated by Mendelian inheritance should be further explored with a WGS approach. JOAG/POAG is a group of polygenic heterogeneous diseases in which a single genetic mutation may not be sufficient to cause a clinical phenotype. Genetic mutations from digenic or polygenic inheritance may result in pathogenesis changes that are beyond physiological compensation. Large-scale clinical screening and molecular functional investigations into the association of this coinherited *OLFM2* and *SIX6* variants are imperative to enrich our understanding on the pathogenesis of JOAG/POAG.

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