Genetic Association of the PARL-ABCC5-HTR3D-HTR3C Locus With Primary Angle-Closure Glaucoma in Chinese

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Purpose: This study evaluates the associations of haplotype-tagging single nucleotide polymorphisms (SNPs) in the PARL-ABCC5-HTR3D-HTR3C region with primary angle closure glaucoma (PACG), with a view to identify the responsible SNP in this region.

Methods: Thirty SNPs from the PARL-ABCC5-HTR3D-HTR3C region were genotyped in a Hong Kong Chinese cohort of 422 PACG patients and 400 control subjects, using TaqMan SNP genotyping assays. Single marker and haplotype-based association analyses were performed.

Results: Two synonymous ABCC5 SNPs, namely rs939336 (p.Cys594=; P = 0.013; odds ratio [OR] = 1.46; 95% confidence interval [CI], 1.08 to 1.97) and rs1132776 (p.Ala395=; P = 0.009; OR = 1.47; 95% CI: 1.10 to 1.95), were associated with PACG. Mild associations were found for two non-synonymous SNPs, rs12493550 (p.Ala295Glu; P = 0.035; OR = 1.47; 95% CI: 1.10 to 1.95) and rs12493550 (p.Ala295Glu; P = 0.035; OR = 1.47; 95% CI: 1.10 to 1.95), which were also associated with PACG. Single marker and haplotype-based association analyses were performed.

Conclusions: These findings enrich the allelic spectrum of ABCC5 in PACG. We identified no tagging SNP responsible for the association of the whole region. Further deep sequencing analysis of this region should be warranted to uncover whether there is still disease-associated variant in this region.

Keywords: PARL-ABCC5-HTR3D-HTR3C, genetic association, primary angle-closure glaucoma, glaucoma genetics
Methods

Study Subjects

A total of 422 PACG patients and 400 control subjects were recruited from the eye clinics at the Hong Kong Eye Hospital and the Prince of Wales Hospital, Hong Kong. All participants are Han Chinese and newly recruited. They received complete ocular examinations and investigations, including visual acuity assessment, IOP measurement by Goldmann applanation tonometry, anterior segment examination and gonioscopy with slit-lamp biomicroscope, fundal examination, visual field testing by standard automated perimetry, and retinal nerve fiber layer thickness measurement by optical coherence tomography (OCT). The recruited PACG patients fulfilled the diagnostic criteria from the International Society of Geographical and Epidemiological Ophthalmology (ISGEO). A visual field defect was defined as glaucoma hemifield test outside normal limits, and pattern SD with P < 0.05, or a cluster of more than three points with P < 0.05 in the superior or inferior hemifield of the pattern deviation plot, one of which with P < 0.01. The history of acute angle closure (AAC) attack of each PACG patient was collected according to the published criteria.12 Patients who had AAC without any secondary causes were defined as acute primary angle closure (APAC). Otherwise, those without any record or history indicating an acute attack were subcategorized as non-APAC. Any patients with angle closure or ocular hypertension from the following causes were excluded: uveitis, neovascularization of iris/angle, iris/ciliary body cysts, posterior segment hemorrhage or tumor, Marfan syndrome, Axenfeld-Rieger syndrome, trauma, steroid, and/or iatrogenic.

Control subjects were recruited from patients attending the eye clinics for unrelated eye conditions. They were Han Chinese aged 60 years or above. Older control subjects were intentionally recruited, with the objective of excluding late-onset glaucoma. They underwent complete ocular assessment and had no history of any ocular diseases, except for mild cataract or refractive error. Also, all control subjects had open anterior chamber angle (Shaffer grade 3 or 4 open anterior chamber angle on gonioscopy) and IOP lower than 21 mm Hg without IOP-lowering medications. Any individuals with a family history of glaucoma were excluded.

The study protocol was approved by the Ethics Committee for Human Research, the Chinese University of Hong Kong. Informed consent was obtained from each participant. The study was conducted in accordance with the tenets of the Declaration of Helsinki.

SNP Selection and Genotyping

Haplotype-tagging SNPs within the PARL-ABCC5-HTR3D-HTR3C region were selected from the CHB population, using the HapMap Genome Browser release #27 data set (http://hapmap.ncbi.nlm.nih.gov/cgi-perl/gbrowse/hapmap27_B36/). A total of 29 haplotype-tagging SNPs were picked up based on the criteria of an r^2 cutoff of 0.8 between SNPs and a minor allele frequency (MAF) cutoff of 0.05. Moreover, a synonymous exonic SNP, rs939336, which was in complete LD with the reported SNP rs1401999, was also selected. Thus, a total of 30 SNPs were included.

Genomic DNA was extracted from peripheral blood using the Qiagen QIAamp DNA kit (Qiagen, Hilden, Germany) according to the manufacturer’s protocol. All SNPs were genotyped in the PACG and control samples using TaqMan SNP genotyping assays (Applied Biosystems, Foster City, CA, USA) with a Roche LightCycler 480 Real-Time PCR system (Roche Diagnostics; Basel, Switzerland) according to the manufacturer’s instructions.

Statistical Analysis

The PLINK software package (version 1.07; http://pngu.mgh.harvard.edu/~purcell/plink/) was used for statistical analysis.13 Hardy-Weinberg equilibrium (HWE) of each SNP in the control group was analyzed using the χ^2 test. Allelic and genotypic associations of each SNP with PACG were analyzed using the χ^2 or Fisher’s exact test. Odds ratios (OR) and 95% confidence intervals (CIs) were estimated with the major allele as reference. Because the 30 selected SNPs are located in a continuous region with strong LD, the association was corrected for multiple testing using the SNPSpD program (http://gump.qimr.edu.au/general/daleN/SNPSpD/), which takes the correlations between SNPs into account.14 After correction, an experiment-wide significance threshold of 0.0028 was required to keep the type I error rate at 0.05 level in these 30 SNPs. Logistic regression analyses were performed to adjust for age and sex. Furthermore, if multiple SNPs were found to be significant, logistic regression analyses were performed to adjust the association of individual SNP for the other SNPs to determine whether this SNP could explain the association of the other SNPs. If a SNP maintained the significance after adjustment, it is likely the responsible SNP in this region.

LD and haplotype-based association were assessed using the Haploview software.15 The global haplotype associations of SNPs of interest (e.g., those in the same LD block) were assessed by omnibus test, followed by haplotype-specific association analysis. Correction for multiple testing in haplotype association analysis was performed by using the permutation test (number of iterations = 10,000).

Statistical Power Analysis

For the 30 SNPs for fine mapping, their MAFs ranged from 0.089 to 0.488. Therefore, assuming an allelic OR of 1.64 (derived from the PACG GWAS study),16 our sample size provides 70.3% to 94.2% of statistical power to detect a significant association at α level of 0.05.

Results

Supplementary Table S1 showed the characteristics of the PACG patients and controls. There was no significant difference in sex between the PACG and control groups. Among the PACG patients, 93 had a history of AAC attack and 329 participants developed PACG without an acute attack history.

All of the SNPs conformed to HWE (P > 0.05) in the control group and were included for further analysis. The call rate of each SNP was >98%. In single SNP association analysis, one SNP (rs3749446) in PARL, two in ABCC5 (rs959356 and rs1132776), and one in HTR3D (rs12493550) were associated with PACG (Supplementary Table S2). Logistic regression analysis revealed that three SNPs in ABCC5 (rs959356: P = 0.013, OR = 1.46, 95% CI: 1.08 to 1.97; rs1132776: P = 0.009, OR = 1.47, 95% CI: 1.10 to 1.95; rs9838667: P = 0.024, OR = 1.27, 95% CI: 1.03 to 1.57; Table 1) and one in HTR3D (rs12493550 in HTR3D (P = 0.035, OR = 1.71, 95% CI: 1.04 to 2.82; Table 1) were nominally associated with PACG after adjusted for age and sex. However, conditional analysis revealed that no SNPs remained significant when adjusting each other (Supplementary Table S3). Haplotype associations of the four SNPs were not independent. Notably, none of the associations could withstand the correction for multiple testing (P > 0.0028).
In this study, we identified two synonymous ABCC5 SNPs, namely rs939336 (p.Cys594=) and rs1132776 (p.Ala395=), and one intronic ABCC5 SNP, rs9838667, to be associated with PACG in the Chinese population. Also, LD analysis revealed that the LD block defined by rs939336 and rs1132776 had the strongest association with PACG. Apart from the three ABCC5 SNPs, mild associations were also detected for the SNP in HTR3D (rs12493550), whereas no SNP in PARL and HTR3C was associated with PACG. Conditional analysis revealed that none of the four SNPs in ABCC5 and HTR3D achieved significance in PACG after adjusting for other factors, suggesting that none of these four SNPs can fully explain the association detected in this region, and thus the responsible SNP remains to be identified. In subgroup analysis, only SNP rs10937152 in PARL was found to be associated with PACG, whereas rs3811725 in PARL, rs9838667, rs1016752, and rs939336, and rs1132776 in ABCC5 and rs12493550 in HTR3D were associated with non-PACAP.

In a previous study, an intronic SNP rs1401999 in ABCC5 was found to be associated with ACD and PACG (OR = 1.3).5 In this study, we identified two synonymous coding variants rs939336 (p.Cys594=; OR = 1.46) and rs1132776 (p.Ala395=; OR = 1.47) to be associated with PACG. Of note, the SNP rs939336 is in complete LD with rs1401999 in Chinese, suggesting the associations of the two coding SNPs with PACG
are genuine. Although these two SNPs do not result in an alteration of amino acid, they can probably influence the processes of translation and expression, although their exact biological mechanism awaits further investigation.

**ABCC5**, also known as multidrug resistance protein 5 (MRP5), participates in transmembrane transportation of various molecules and mediation of cellular export of cyclic nucleotides including a second messenger cyclic guanosine monophosphate (cGMP), which plays a role in cell prolifera-

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**Table 2.** Two-SNP Sliding Window Analysis Across the PARL-ABCC5-HTR3D-HTR3C Region in PACG

<table>
<thead>
<tr>
<th>Locus ($P_{	ext{cand}}$)</th>
<th>SNPs</th>
<th>Haplotype</th>
<th>PACG</th>
<th>Control</th>
<th>$P$</th>
<th>OR (95% CI)</th>
<th>$P_{	ext{perm}}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Window 6 (0.041)</td>
<td>rs953419-rs3749446</td>
<td>TG</td>
<td>0.138</td>
<td>0.179</td>
<td>0.026</td>
<td>0.73 (0.50–1.07)</td>
<td>0.105</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CA</td>
<td>0.464</td>
<td>0.469</td>
<td>0.85</td>
<td>0.98 (0.75–1.29)</td>
<td>0.158</td>
</tr>
<tr>
<td></td>
<td></td>
<td>TA</td>
<td>0.398</td>
<td>0.353</td>
<td>0.062</td>
<td>1.21 (0.91–1.61)</td>
<td>0.968</td>
</tr>
<tr>
<td>Window 7 (0.043)</td>
<td>rs3749446-rs4148594</td>
<td>AG</td>
<td>0.149</td>
<td>0.168</td>
<td>0.301</td>
<td>0.87 (0.60–1.26)</td>
<td>0.554</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GA</td>
<td>0.139</td>
<td>0.175</td>
<td>0.04</td>
<td>0.76 (0.52–1.11)</td>
<td>0.11</td>
</tr>
<tr>
<td></td>
<td></td>
<td>AA</td>
<td>0.712</td>
<td>0.657</td>
<td>0.016</td>
<td>1.29 (0.96–1.73)</td>
<td>0.041</td>
</tr>
<tr>
<td>Window 13 (0.014)</td>
<td>rs3792584-rs939336</td>
<td>AT</td>
<td>0.151</td>
<td>0.11</td>
<td>0.014</td>
<td>1.44 (0.95–2.17)</td>
<td>0.03</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GC</td>
<td>0.059</td>
<td>0.069</td>
<td>0.454</td>
<td>0.85 (0.48–1.48)</td>
<td>0.718</td>
</tr>
<tr>
<td></td>
<td></td>
<td>AC</td>
<td>0.79</td>
<td>0.821</td>
<td>0.108</td>
<td>0.82 (0.58–1.16)</td>
<td>0.205</td>
</tr>
<tr>
<td>Window 14 (0.003)</td>
<td>rs939336-rs1312776</td>
<td>TT</td>
<td>0.151</td>
<td>0.11</td>
<td>0.014</td>
<td>1.44 (0.95–2.17)</td>
<td>0.026</td>
</tr>
<tr>
<td></td>
<td></td>
<td>TC</td>
<td>0</td>
<td>0</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CC</td>
<td>0.849</td>
<td>0.89</td>
<td>0.014</td>
<td>0.70 (0.46–1.05)</td>
<td>0.005</td>
</tr>
<tr>
<td>Window 15 (0.037)</td>
<td>rs1132776-rs7636910</td>
<td>GC</td>
<td>0.383</td>
<td>0.415</td>
<td>0.209</td>
<td>0.88 (0.66–1.18)</td>
<td>0.702</td>
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<tr>
<td></td>
<td></td>
<td>TA</td>
<td>0.162</td>
<td>0.116</td>
<td>0.011</td>
<td>1.47 (0.99–2.20)</td>
<td>0.022</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CA</td>
<td>0.455</td>
<td>0.469</td>
<td>0.589</td>
<td>0.95 (0.72–1.24)</td>
<td>0.529</td>
</tr>
<tr>
<td>Window 22 (0.038)</td>
<td>rs4912518-rs12493550</td>
<td>CA</td>
<td>0.057</td>
<td>0.035</td>
<td>0.037</td>
<td>1.67 (0.85–3.27)</td>
<td>0.089</td>
</tr>
<tr>
<td></td>
<td></td>
<td>TG</td>
<td>0.076</td>
<td>0.059</td>
<td>0.176</td>
<td>1.31 (0.78–2.27)</td>
<td>0.381</td>
</tr>
<tr>
<td></td>
<td></td>
<td>CG</td>
<td>0.867</td>
<td>0.906</td>
<td>0.014</td>
<td>0.68 (0.44–1.05)</td>
<td>0.035</td>
</tr>
<tr>
<td>Window 23 (0.050)</td>
<td>rs12493550-rs7622660</td>
<td>GC</td>
<td>0.085</td>
<td>0.071</td>
<td>0.503</td>
<td>1.22 (0.73–2.03)</td>
<td>0.526</td>
</tr>
<tr>
<td></td>
<td></td>
<td>AT</td>
<td>0.058</td>
<td>0.035</td>
<td>0.0531</td>
<td>1.70 (0.87–3.32)</td>
<td>0.089</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GT</td>
<td>0.857</td>
<td>0.894</td>
<td>0.027</td>
<td>0.71 (0.47–1.08)</td>
<td>0.068</td>
</tr>
</tbody>
</table>
The expression of ABCC5 was detected in multiple human tissues, including the structures of the anterior segment of the eye, such as iris, ciliary body, lens, and cornea. Interestingly, the association of ABCC5 with PACG argues favorably for a role in eye development through the regulation of GMP, which potentially influences anterior chamber depth. A significant reduction of body length and ocular size occurred after activity of endogenous ABCC5 in zebrafish was inhibited. The ABCC5 gene was first identified to influence ACD, which is a key anatomical risk factor of PACG. ABCC5 also provides resistance of anticancer drugs. It interacts with the mitochondrial integral membrane protein PARL, a mitochondrial function suggesting the potential involvement of mitochondrial dysfunction in the pathogenesis of PACG. PARL encodes a mitochondrial integral membrane protein and has a key role in the regulation of mitochondrial function. Expression of an ortholog of human PARL, Rhomboid-7 (rho-7), was shown to cause neurodegeneration in Drosophila. Recently, mitochondrial abnormalities have been linked with psychiatric neurodegenerative disorders, such as schizophrenia and Parkinson's disease. In addition, PARL was also associated with ocular diseases, such as Leber's hereditary optic neuropathy (LHON) and peristalsis and secretory reflexes and transmits information to the central nervous system. PARL-ABCC5-HTR3D-HTR3C Locus and PACG analysis. ABCC5 was associated with vomiting within 24 hours after chemotherapy. The central nervous system was found to be associated with vomiting within 24 hours after chemotheraphy. However, due to the very limited studies on this gene, the expression of HTR3D is to be detected in human tissues. In this study, we found an SNP rs12493550 in HTR3D that was associated with PACG, suggesting that the abnormality in signal transmission may have a role in the pathogenesis of PACG.

In a subgroup analysis, one SNP had an association with PAC. In contrast, six SNPs showed a significant association with non-PAC. This discrepancy could be explained by the fact that ABCC5 could be a gene for chronic primary angle closure, whereas the difference between APAC and non-APAC could indicate that APAC requires other or additional triggering factors for acute onset. Near work, pupil dilation, and emotional factors, such as intense concentration, emotional stress, and excitement, are precipitating factors. Another explanation could be the relatively small sample size of the APAC group, which might provide insufficient statistical power to reveal the association of the SNPs with APAC. With 93 APAC cases, the statistical power was less than 40% to detect an association of the strongest SNPs (i.e., rs939336 and rs1152776) with PACG.

There are some other limitations in this study. First, the statistical significance of the nominally significant SNPs did not withstand correction for multiple testing, likely due to limited sample size. However, the ORs of the associated SNPs were consistent with that of the SNP rs1401999 in a previous study. Second, the classification of PACG in this study was based on whether the patients had a history of acute angle closure attack. Because all patients had glaucomatous changes, they were all PACG patients. Whether the SNPs detected in this study are also associated with primary angle closure suspect (PACS) and/or primary angle closure (PAC), which are earlier stages in the primary angle closure disease (PACD) spectrum, remains unknown. Elucidation of this may help to explain whether the genes at the PARL-ABCC5-HTR3D locus have a role in early pathogenesis of PACG.

In summary, this study has enriched the spectrum of associated SNPs at the PARL-ABCC5-HTR3D locus in PACG. Two coding variants in ABCC5 were associated with PACG. Although the responsible SNP had not been pinpointed, our data suggested it is more likely to locate in the region of ABCC5 and HTR3D. Furthermore, we identified discrepancies in the association profiles between APAC and non-APAC. These findings provide new clues for further genetic and biological investigations on PACG.

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References


