Analysis combining correlated glaucoma traits identifies five new risk loci for open-angle glaucoma

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Open-angle glaucoma (OAG) is a major cause of blindness worldwide. To identify new risk loci for OAG, we performed a genome-wide association study in 3,071 OAG cases and 6,750 unscreened controls, and meta-analysed the results with GWAS data for intraocular pressure (IOP) and optic disc parameters (the overall meta-analysis sample size varying between 32,000 to 48,000 participants) , which are

glaucoma-related traits. We identified and independently validated four novel genome-wide significant associations within or near MYOF and CYP26A1, LINC02052 and CRYGS, LMX1B, and LMO7 using single variant tests, one additional locus (C9) using gene-based tests, and two genetic pathways - "response to fluid shear stress" and "abnormal retina morphology" - in pathway-based tests.

Interestingly, some of the new risk loci contribute to risk of other genetically-correlated eye diseases including myopia and age-related macular degeneration. To our knowledge, this study is the first integrative study to combine genetic data from OAG and its correlated traits to identify new risk variants and genetic pathways, highlighting the future potential of combining genetic data from genetically-correlated eye traits for the purpose of gene discovery and mapping.

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