

Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma

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Elevated intraocular pressure (IOP) is an important risk factor in developing glaucoma, and variability in IOP might herald glaucomatous development or progression. We report the results of a genome-wide association study meta-analysis of 18 population cohorts from the International Glaucoma Genetics Consortium (IGGC), comprising 35,296 multi-ancestry participants for IOP. We confirm genetic association of known loci for IOP and primary open-angle glaucoma (POAG) and identify four new IOP-associated loci located on chromosome 3q25.31 within the FNDC3B gene ($P = 4.19 \times 10^{-8}$ for rs6445055), two on chromosome 9 ($P = 2.80 \times 10^{-11}$ for rs2472493 near ABCA1 and $P = 6.39 \times 10^{-11}$ for rs8176693 within ABO) and one on chromosome 11p11.2 (best $P = 1.04 \times 10^{-11}$ for rs747782). Separate meta-analyses of 4 independent POAG cohorts, totaling 4,284 cases and 95,560 controls, showed that 3 of these loci for IOP were also associated with POAG.

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