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

Hysi PG(1), Cheng CY(2), Springelkamp H(3), Macgregor S(4), Bailey JN(5), Wojciechowski R(6), Vitart V(7), Nag A(8), Hewitt AW(9), Höhn R(10), Venturini C(11), Mirshahi A(10), Ramdas WD(12), Thorleifsson G(13), Vithana E(14), Khor CC(15), Stefansson AB(16), Liao J(17), Haines JL(18), Amin N(19), Wang YX(20), Wild PS(21), Ozel AB(22), Li JZ(22), Fleck BW(23), Zeller T(24), Staffieri SE(9), Teo YY(25), Cuellar-Partida G(26), Luo X(27), Allingham RR(28), Richards JE(29), Senft A(30), Karssen LC(19), Zheng Y(31), Bellenguez C(32), Xu L(20), Iglesias AL(19), Wilson JF(33), Kang JH(34), van Leeuwen EM(19), Jonsson V(35), Thorsteinsdottir U(13), Despriet DD(29), Ennis S(36), Moroi SE(37), Martin NG(38), Jansonius NM(39), Yazar S(40), Tai ES(41), Amouyel P(42), Kirwan J(43), van Koolwijk LM(19), Hauser MA(44), Jonasson F(45), Leo P(46), Loomis SJ(47), Fogarty R(48), Rivadeneira F(49), Kearns L(9), Lackner KJ(50), de Jong PT(51), Simpson CL(52), Pennell CE(53), Oostra BA(54), Uitterlinden AG(49), Saw SM(55), Lottery AJ(56), Bailey-Wilson JE(52), Hofman A(57), Vingerling JR(12), Maubaret C(58), Pfeiffer N(10), Wolfs RC(29), Lemij HG(59), Young TL(27), Pasquale LR(60), Delcourt C5(8), Spector TD(8), Klaver CC(12), Small KS(8), Burdon KP(48), Stefansson K(13), Wong TY(61), BMES GWAS Group; NEIGHBORHOOD Consortium; Wellcome Trust Case Control Consortium (2), Viswanathan A(62), Mackey DA(63), Craig JE(64), Wiggs JL(65), van Duijn CM(66), Hammond CJ(1), Aung T(67)

1 1] Department of Twin Research and Genetic Epidemiology, King's College London, London, UK. 
2] Department of Ophthalmology, National University of Singapore and National University Health System, Singapore. 
3] Saw Swee Hock School of Public Health, National University of Singapore and National University Health System, Singapore. 
4] Duke-National University of Singapore Graduate Medical School, Singapore.

3 1] Department of Ophthalmology, Erasmus Medical Center, Rotterdam, the Netherlands. 
2] Department of Epidemiology, Erasmus Medical Center, Rotterdam, the Netherlands.

4 1] Statistical Genetics, QIMR Berghofer Medical Research Institute Royal Brisbane Hospital, Brisbane, Queensland, Australia.

5 1] Department of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland, Ohio, USA.

6 1] Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA. 
2] National Human Genome Research Institute, US National Institutes of Health, Baltimore, Maryland, USA.

7 Medical Research Council (MRC) Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, UK.

8 Department of Twin Research and Genetic Epidemiology, King's College London, London, UK.

9 Centre for Eye Research Australia, University of Melbourne, Royal Victorian Eye and Ear Hospital, Melbourne, Victoria, Australia.

10 Department of Ophthalmology, University Medical Center Mainz, Mainz, Germany.

11 1] Department of Twin Research and Genetic Epidemiology, King's College London, London, UK. 

12 1] Department of Ophthalmology, Erasmus Medical Center, Rotterdam, the Netherlands.
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 × 10^(-8) for rs6445055), two on chromosome 9 (P = 2.80 × 10^-11 for rs2472493 near ABCA1 and P = 6.39 × 10^-11 for rs8176693 within ABO) and one on chromosome 11p11.2 (best P = 1.04 × 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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