

GWAS identifies two common loci associated with pigment dispersion syndrome/pigmentary glaucoma and implicate myopia in its development

Mark J Simcoe (1) , Ameet Shah (2) , Baojian Fan (3) , H el ene Choquet (4) , Nicole Weisschuh (5) , Naushin H Waseem (6) , Chen Jiang (4) , Ronald B Melles (7) , Robert Ritch (8) , Omar A Mahroo (1) , Bernd Wissinger (5) , Eric Jorgenson (4) , Janey L Wiggs (3) , David F Garway-Heath (9) , Pirro G Hysi (10) , Christopher J Hammond (10)

1 Department of Ophthalmology, Kings College London, London, UK, SE1 7EH; Department of Twins Research and Genetic Epidemiology, Kings College London, London, UK, SE1 7EH; Institute of Ophthalmology, University College London, London, United Kingdom, EC1V 9EL.

2 Department of Ophthalmology, Royal Free Hospital NHS Foundation Trust, Pond Street, London, United Kingdom.

3 Massachusetts Eye and Ear Infirmary, Harvard Medical School, Boston, Massachusetts, USA.

4 Division of Research, Kaiser Permanente Northern California (KPNC) , Oakland, CA, 94612, USA.

5 Institute for Ophthalmic Research, Centre for Ophthalmology, University of T ubingen, T ubingen, Germany.

6 Institute of Ophthalmology, University College London, London, United Kingdom, EC1V 9EL.

7 KPNC, Department of Ophthalmology, Redwood City, CA 94063, USA.

8 Einhorn Clinical Research Center, New York Eye and Ear Infirmary of Mount Sinai, New York, NY.

9 National Institute for Health Research Biomedical Research Centre at Moorfields Eye Hospital NHS Foundation Trust and UCL Institute of Ophthalmology, London, UK.

10 Department of Ophthalmology, Kings College London, London, UK, SE1 7EH; Department of Twins Research and Genetic Epidemiology, Kings College London, London, UK, SE1 7EH.

PURPOSE: To identify genetic variants associated with pigment dispersion syndrome and pigmentary glaucoma in unrelated patients, and to further understand the genetic and potentially causal relationships between pigment dispersion syndrome and associated risk factors.

DESIGN: A two-stage genome-wide association meta-analysis with replication and subsequent in-silico analyses including Mendelian randomisation.

SUBJECTS: A total of 574 cases with pigmentary glaucoma and/or pigment dispersion syndrome and 52,627 controls of European descent.

METHODS: Genome-wide association analyses were performed in four cohorts and meta-analysed in three stages: first a discovery meta-analysis of three cohorts, secondly replication was performed in the fourth cohort, thirdly all four cohorts were meta-analysed to increase statistical power. Two-sample Mendelian randomisation was utilised to determine whether refractive error and intraocular pressure exert causal effects over pigment dispersion syndrome.

RESULTS: Significant association was present at two novel loci for pigment dispersion syndrome/pigmentary glaucoma. These loci and follow up analyses implicate the genes GSAP (lead SNP: rs9641220, $p=6.0\times 10^{-10}$) and GRM5/TYR (lead SNP: rs661177, $p=3.9\times 10^{-9}$) as important factors in disease risk. Mendelian randomisation showed significant evidence that negative refractive error (myopia) exerts a direct causal

effect over pigment dispersion syndrome ($p=8.9 \times 10^{-7}$) .

MAIN OUTCOME MEASURES: A) The association of genetic variants with pigment dispersion syndrome and, B) whether myopia exerts causal effects over pigment dispersion syndrome.

CONCLUSIONS: Common SNPs relating to the GSAP and GRM5/TYR genes are associated risk factors for the development of pigment dispersion syndrome and pigmentary glaucoma. Although myopia is a known risk factor, this study is the first to use genetic data to demonstrate that myopia is, in part, a cause of pigment dispersion syndrome and pigmentary glaucoma.

Copyright © 2022. Published by Elsevier Inc.

Ophthalmology. 2022 Jan 11;S0161-6420(22) 00022-7. doi: 10.1016/j.ophtha.2022.01.005. Online ahead of print.

PMID: 35031440 DOI: 10.1016/j.ophtha.2022.01.005