



## An Intraocular Pressure Polygenic Risk Score Stratifies Multiple Primary Open-Angle Glaucoma Parameters Including Treatment Intensity

Qassim, A., Souzeau, E., Siggs, O. M., Hassall, M. M., Han, X., Griffiths, H. L., Frost, N. A., Vallabh, N. A., Kirwan, J. F., Menon, G., Cree, A. J., Galanopoulos, A., Agar, A., Healey, P. R., Graham, S. L., Landers, J., Casson, R. J., Gharahkhani, P., Willoughby, C., ... Craig, J. E. (2020). An Intraocular Pressure Polygenic Risk Score Stratifies Multiple Primary Open-Angle Glaucoma Parameters Including Treatment Intensity. *Ophthalmology*, 127(7), 901-907. <https://doi.org/10.1016/j.ophtha.2019.12.025>

[Link to publication record in Ulster University Research Portal](#)

**Published in:**  
Ophthalmology

**Publication Status:**  
Published (in print/issue): 01/07/2020

**DOI:**  
[10.1016/j.ophtha.2019.12.025](https://doi.org/10.1016/j.ophtha.2019.12.025)

**Document Version**  
Author Accepted version

**General rights**  
Copyright for the publications made accessible via Ulster University's Research Portal is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

**Take down policy**  
The Research Portal is Ulster University's institutional repository that provides access to Ulster's research outputs. Every effort has been made to ensure that content in the Research Portal does not infringe any person's rights, or applicable UK laws. If you discover content in the Research Portal that you believe breaches copyright or violates any law, please contact [pure-support@ulster.ac.uk](mailto:pure-support@ulster.ac.uk).

## **An intraocular pressure polygenic risk score stratifies multiple primary open angle glaucoma parameters including treatment intensity**

Ayub Qassim MBBS<sup>[†]</sup>,<sup>1</sup> Emmanuelle Souzeau PhD,<sup>1</sup> Owen M Siggs MD DPhil,<sup>1</sup> Mark M Hassall MBBS DPhil,<sup>1</sup> Xikun Han MSc,<sup>2</sup> Helen L Griffiths,<sup>3</sup> Andrew J Frost FRCOphth PhD,<sup>4</sup> Neeru A Vallabh MBBS,<sup>5</sup> James F Kirwan FRCOphth,<sup>6</sup> Geeta Menon MBBS FRCOphth,<sup>7</sup> Angela J Cree MSc,<sup>3</sup> Anna Galanopoulos MBBS,<sup>8</sup> Ashish Agar MBBS PhD,<sup>9</sup> Paul R Healey MMed PhD,<sup>10</sup> Stuart L Graham MBBS PhD,<sup>11</sup> John Landers MBBS PhD,<sup>1</sup> Robert J Casson MBBS DPhil,<sup>12</sup> Puya Gharahkhani PhD,<sup>2</sup> Colin E Willoughby MBChB MD,<sup>13,14</sup> Alex W Hewitt MBBS PhD,<sup>15</sup> Andrew J Lotery MD FRCOphth\*,<sup>3</sup> Stuart MacGregor PhD\*,<sup>2</sup> Jamie E Craig MBBS DPhil\*<sup>1</sup>

### **Affiliations:**

1. Department of Ophthalmology, Flinders University, Flinders Medical Centre, Bedford Park, Australia.
2. QIMR Berghofer Medical Research Institute, Brisbane, Australia.
3. Clinical and Experimental Sciences, Faculty of Medicine, University of Southampton, Southampton, SO16 6YD, UK
4. Department of Ophthalmology, Torbay Hospital, Torquay, Devon, TQ2 7AA UK
5. Department of Eye and Vision Science, Institute of Ageing and Chronic Disease, University of Liverpool, Liverpool, UK
6. Department of Ophthalmology, Portsmouth Hospitals, Portsmouth, UK
7. Department of Ophthalmology, Frimley Park Hospital NHS Foundation Trust, Frimley GU16 7UJ, UK
8. South Australian Institute of Ophthalmology, Royal Adelaide Hospital, Adelaide, Australia
9. Department of Ophthalmology, Prince of Wales Hospital, Randwick, Australia
10. Centre for Vision Research, Westmead Institute for Medical Research, University of Sydney, Australia
11. Faculty of Medicine and Health Sciences, Macquarie University, Australia
12. South Australian Institute of Ophthalmology, University of Adelaide, Adelaide, Australia
13. Biomedical Sciences Research Institute, Ulster University, Coleraine, BT52 1SA, Northern Ireland, UK
14. Royal Victoria Hospital, Belfast Health and Social Care Trust, BT12 6BA, Belfast, Northern Ireland, UK
15. Menzies Institute for Medical Research, University of Tasmania, Australia.

\* Joint senior authors

† Corresponding author

Dr Ayub Qassim, Department of Ophthalmology, Flinders University, Bedford Park, Australia.

E-mail: [ayub.qassim@flinders.edu.au](mailto:ayub.qassim@flinders.edu.au)

Level 2 Car Park Tenancies, 1 Flinders Drive, Bedford Park, SA, 5042, Australia

**Financial support:** This work was supported by grants from the National Health and Medical Research Council (NHMRC) of Australia (#1107098; 1116360, 1116495, 1023911), the Ophthalmic Research Institute of Australia, the BrightFocus Foundation, International Glaucoma Association, UK and Eire Glaucoma Society and the Mason Medical Research Foundation. SM, JEC and AWH are supported by NHMRC Fellowships. The funding organization had no role in the design or conduct of this research.

**Conflict of Interest:** no conflicting relationship exists for any author.

**Running head:** POAG phenotype stratified by an IOP polygenic risk score

**Abbreviations/Acronyms:**

IOP: intraocular pressure; POAG: primary open angle glaucoma; PRS: polygenic risk score; ANZRAG: Australian and New Zealand Registry of Advanced Glaucoma; SD: standard deviation; MYOC: myocilin; OPTN: optineurin; TBK1: TANK-binding kinase 1; CI: confidence interval; GWAS: genome wide association study; SNP: single nucleotide polymorphism; OR: odds ratio; MD: mean deviation; VCDR: vertical cup-to-disc ratio; PROGRESSA: Progression Risk Of Glaucoma; RElevant SNPs with Significant Association; SLT: selective laser trabeculoplasty; IGGC: International Glaucoma Genetics Consortium.

## **Abstract**

**Objective:** To examine the combined effects of common genetic variants associated with intraocular pressure (IOP) on primary open angle glaucoma (POAG) phenotype using a polygenic risk score (PRS) stratification.

**Design:** Cross-sectional study.

**Participants:** For the primary analysis, we examined the glaucoma phenotype of 2,154 POAG patients enrolled in the Australian and New Zealand Registry of Advanced Glaucoma (ANZRAG) including cases recruited from the UK. For replication, we examined an independent cohort of 624 early POAG patients.

**Methods:** Using IOP genome-wide association study summary statistics, we developed a PRS derived solely from IOP associated variants and stratified POAG patients into three risk tiers. The lowest and highest quintiles of the score were set as the low and high risk groups respectively and the other quintiles as the intermediate risk group.

**Main Outcome Measures:** Clinical glaucoma phenotype including maximum recorded IOP, age of diagnosis, number of family members affected by glaucoma, cup-to-disc ratio, visual field mean deviation, and treatment intensity.

**Results:** There was a dose-response relationship between the IOP PRS and the maximum recorded IOP, with the high genetic risk group having a higher maximum IOP by 1.7 (SD 0.62) mmHg than the low genetic risk group ( $P = 0.006$ ). Compared to the low genetic risk group, the high genetic risk group had a younger age of diagnosis by 3.7 (1.0) years ( $P < 0.001$ ), more family members affected by 0.46 (0.11) members ( $P < 0.001$ ), and higher rates of incisional surgery (odds ratio 1.5; 95% confidence interval 1.1 - 2.0;  $P = 0.007$ ). There was no statistically significant difference in mean deviation. We further replicated the maximum IOP, number of family members affected by glaucoma and treatment intensity (number of medications) results in the early POAG cohort ( $P \leq 0.01$ ).

**Conclusions:** The IOP polygenic risk score was positively correlated with maximum IOP, disease severity, need for surgery and number of family members. Genes acting via IOP

mediated pathways, when considered in aggregate have clinically important and reproducible implications for glaucoma patients and their close family members.

Glaucoma refers to a group of progressive optic neuropathies with a characteristic pattern of retinal ganglion cell death and visual field loss.<sup>1</sup> Intraocular pressure (IOP) is currently the only proven modifiable risk factor for primary open angle glaucoma (POAG), in which the iridocorneal angle is open and there is no secondary cause of IOP elevation.<sup>2</sup> Despite this, elevated IOP is not essential for the diagnosis of POAG, nor is it effective for screening for glaucoma.<sup>1,3</sup> The current methods of IOP assessment are limited to the time of measurement and are a poor measure of an individual's IOP profile, maximum and fluctuations. Additional IOP measurements are more informative for glaucoma management as both diurnal and long-term IOP fluctuations have been reportedly associated with glaucoma progression.<sup>4,5</sup>

Glaucoma is highly heritable and several genes with a Mendelian pattern of inheritance have been associated with POAG.<sup>6</sup> Monogenic variants causing glaucoma are relatively rare but carry a high risk of developing the disease. Family-based genetic linkage analysis has identified three genes associated with Mendelian glaucoma; myocilin (*MYOC*), optineurin (*OPTN*) and TANK-binding kinase 1 (*TBK1*) genes.<sup>7-10</sup> Pathogenic variants in the *MYOC* gene account for 2-4% of adult-onset POAG.<sup>10</sup> The most common pathogenic variant in the *MYOC* gene in individuals of European ancestry (p.Gln368Ter) has a minor allele frequency of 0.13%, yet carries a significant risk of glaucoma with high IOP in those who carry it (in a population based setting odds ratio [OR] = 6.76 with 95% confidence interval [CI] of 4.05-11.29).<sup>11</sup> In family-based studies, the penetrance of p.Gln368Ter to manifest POAG is reported at approximately 80% by the seventh decade of life.<sup>11</sup>

IOP in the normal population is a polygenic trait, with recent large genome-wide association studies (GWAS) discovering more than one hundred common loci associated with IOP, accounting for 40% of the heritability.<sup>12-14</sup> Khawaja *et al.* reported that these single nucleotide polymorphisms (SNPs) explained 17% of IOP variance in an independent clinical study, and 9% in the UK biobank study which likely reflects the difference in IOP measurement methods.<sup>14</sup> In contrast to the aforementioned monogenic variants, each SNP contributes a very small

effect size. For instance, variants in or near the genes *TMCO1* and *CAV2*, two of the most strongly associated loci with IOP and glaucoma, are present in 10-15% of the population but account for a modest risk of glaucoma individually (OR 1.1 - 1.4).<sup>12-14</sup> However, the combined effects of these common SNPs significantly affect the observed clinical phenotype.<sup>12</sup>

To understand the impact of these common variants, we consider the total number of variants an individual is carrying multiplied by their effect size, to generate a weighted polygenic risk score (PRS).<sup>15</sup> A genetic risk stratification may then be done by calculating an aggregate score of all the SNPs an individual has associated with a trait. For instance, a person with the majority of the discovered IOP variants (a high IOP PRS) is hypothesised to have a higher IOP than someone who has only a few. The PRS model of risk prediction has been used to stratify individualised disease risk in several medical conditions such as coronary artery disease, atrial fibrillation and breast cancer.<sup>16-18</sup> Recently, a PRS derived from the known IOP variants has been reported to account for a higher risk of developing glaucoma;<sup>12</sup> however, the influence of the IOP PRS on a wider range of glaucoma-related phenotypes has not been described. In this study, we aimed to characterise the clinical features of glaucoma patients with a high burden of IOP associated variants in a large national Australian glaucoma registry along with ethnically similar cases from the UK.

## **Methods**

### **Study participants**

The study adhered to the tenets of the Declaration of Helsinki and followed the National Health and Medical Research Council statement of ethical conduct in research involving humans. Informed consent was obtained from all participants, and the study was approved by the Southern Adelaide Clinical Human Research Ethics Committee.

The study participants were enrolled in the Australian and New Zealand Registry of Advanced Glaucoma (ANZRAG).<sup>19</sup> The study includes both advanced and non-advanced glaucoma cases. Advanced glaucoma was defined by a Humphrey 24-2 visual field mean deviation (MD) < -15 dB in the worse eye, or loss of at least two of the central visual field points on the pattern deviation map.<sup>19</sup> Non-advanced glaucoma was defined by optic nerve head changes with corresponding visual field defects consistent with glaucoma, but not fitting the aforementioned criteria. The study sample included additional ethnically matched advanced glaucoma cases recruited from the UK.<sup>20</sup> Only patients of European ancestry with POAG were included to utilise the currently published IOP SNPs. Patients with variants in the known POAG genes (*MYOC*, *OPTN* and *TBK1*) were excluded. The highest IOP measurement recorded with Goldmann applanation tonometry by the referring ophthalmologist before treatment of either eye for each participant was recorded. High tension glaucoma was defined as a maximum recorded IOP > 21 mmHg. Other data recorded at the time of recruitment included age at diagnosis, vertical cup-to-disc ratio (VCDR), and glaucoma surgery. Family history was self-reported and recorded for affected relatives up to the fourth degree by the referring clinician. Where applicable, the family tree of affected individuals was recorded and reviewed by the registry staff before recording the number of family members affected by glaucoma in the registry.

An independent cohort of early glaucoma patients enrolled in the Progression Risk Of Glaucoma; RElevant SNPs with Significant Association (PROGRESSA) study were then used for replication. Only participants with established perimetric glaucoma, defined by two consecutive reliable visual field examinations with Glaucoma Hemifield Test "Outside Normal Limits", pattern standard deviation <5%, or a cluster of 3 contiguous points depressed <5% in the pattern standard deviation map, at least one of which is <1%, were included. Data recorded included self-reported family history of glaucoma, maximum IOP recorded at any visit, VCDR and visual field at the last visit, number of topical glaucoma medications and previous selective laser trabeculoplasty (SLT). The number of topical medications and SLT are routinely updated at each visit for this cohort. A small proportion (2.4%) have had an



incisional surgery for the management of their glaucoma which would significantly alter their medical management. Thus for the medical treatment analysis, we have used the highest number of drops at any one appointment for each patient.

### **Polygenic risk score**

The IOP derived PRS was comprised of 146 statistically independent genome-wide-significant SNPs (P value threshold at  $5 \times 10^{-8}$  and LD-clumping at  $r^2 = 0.1$ ) as reported previously (Supplementary Table 1).<sup>12</sup> Briefly, SNPs influencing IOP were discovered by a GWAS of cornea-compensated IOP measured by Ocular Response Analyzer in participants of the UK Biobank study (N = 103,914).<sup>12,21</sup> This was meta-analysed with GWAS results from the International Glaucoma Genetics Consortium (IGGC, N = 29,578) using the inverse variance weighted method (METAL software).<sup>22</sup> A weighted PRS was then derived for each individual in the ANZRAG study cohort using PLINK (version 1.90 beta),<sup>23</sup> taking into account the effect size of each SNP using the UK Biobank GWAS summary statistics. None of the study participants in ANZRAG or PROGRESSA were part of the discovery cohort. A percentile score was then derived within the ANZRAG and the PROGRESSA cohorts. We classified patients into three risk groups; the top 20% of the genetic risk score were classified as the high risk group; the middle 60% as the intermediate risk group; and the bottom 20% as the low risk group. Additionally, we calculated the recently published 12-SNP unweighted POAG PRS by Fan et al. for our primary cohort for comparison.<sup>24</sup> A detailed comparison between these scores is presented summarised in Supplementary Table 2. Genotyping was done in several phases on either Illumina Omni1M, OmniExpress or HumanCoreExome arrays (Illumina, San Diego, CA, USA) as described previously.<sup>12</sup>

### **Statistical analysis**

The Shapiro-Wilk test was used to assess for normality. Analysis of variance of continuous variables by PRS groups was done using Kruskal–Wallis test. Count and categorical variables were compared using Pearson's chi-squared test. For two-group comparisons, the Mann-

Whitney U test was used. Logistic regression models were fitted for binary outcomes and negative binomial regression was used for count data (number of family members affected). Linear regression using the continuous numerical PRS as the explanatory variable was used to compare the aforementioned two scores. All analysis was done using R (version 3.5.1, RCore Team, Austria).<sup>25</sup> The significance level (alpha) was set at 0.05.

## Results

A total of 2,154 eligible POAG patients from ANZRAG with mean age at recruitment of 77.4 (SD 13.2) years were included. The majority of the study cohort (N = 1,664; 77%) had advanced glaucoma as defined above. This included 381 cases recruited from the UK (N = 290 from Southampton and N = 91 Liverpool) who were ethnically matched to the rest of the cohort. A summary of the glaucoma phenotype across the three genetic risk groups is summarised in Table 1.

The high IOP genetic risk group had a significantly higher maximum IOP by 1.3 mmHg (95%CI: 0.32 - 2.7 mmHg;  $P = 5.5 \times 10^{-3}$ ) compared to the intermediate and low genetic risk groups. The maximum IOP was not statistically significantly different in the intermediate group relative to the low risk group (mean difference of 0.54 mmHg, 95% CI -1.5 - 0.47 mmHg;  $P = 0.08$ ). Similarly, the high genetic risk group was more likely to present as high tension glaucoma, defined by a maximum IOP above 21 mmHg (OR = 1.9; 95% CI 1.3 - 2.8;  $P = 7.9 \times 10^{-4}$  relative to the low-risk group). Further analysis by decile groups of the IOP PRS shows a continuous variant dose-response relationship between higher IOP PRS and maximum IOP, signifying the cumulative effects of the common IOP variants (Figure 1A).

The mean age of glaucoma diagnosis was significantly different across the genetic risk groups ( $P = 1.3 \times 10^{-4}$ ). The high genetic risk group were diagnosed with glaucoma on average 2.2 (SD 0.80) years earlier than the intermediate group ( $P = 5.5 \times 10^{-3}$ ) and 3.7 (SD 1.0) years than the

low genetic risk group ( $2.4 \times 10^{-4}$ ). The high risk group were more likely to have family members affected by glaucoma relative to the low risk group (OR = 1.6, 95% CI 1.2 - 2.1,  $P = 1.1 \times 10^{-3}$ ). The number of self-reported family members affected by glaucoma was also higher in the high IOP PRS group compared to the intermediate (mean 0.29, SD 0.1,  $P = 5.2 \times 10^{-3}$ ) and low risk groups (mean 0.46, SD 0.11,  $P = 1.8 \times 10^{-4}$ ). Furthermore, there was a linear relationship between the IOP PRS and the number of family members affected by glaucoma which highlights the importance of these variants and their impact on the development of glaucoma (Figure 1B).

There was no significant difference between the Humphrey visual field mean deviation between the IOP PRS groups ( $P = 0.18$ ). However, the high genetic risk group were more likely to require an incisional surgery for the management of their glaucoma relative to the intermediate and low risk groups (OR = 1.3, 95% CI = 1.0 - 1.6;  $P = 0.049$  and OR = 1.5; 95% CI = 1.1 - 2.0;  $P = 7.9 \times 10^{-3}$  respectively). Further, the high IOP PRS group were more likely to require bilateral incisional surgeries than the intermediate and low risk groups (OR = 1.4, 95% CI = 1.0 - 1.8;  $P = 0.02$ ).

For replication, we stratified an independent cohort of early perimetric POAG patients ( $N = 624$ ), with an average age of 69.5 (10) years, into three risk groups based on the same absolute numerical IOP PRS cut-off used above. There was a similar association of increasing maximum IOP, number of family members affected, and treatment intensity (Table 2 and Figure 2). The high risk group had more than twice as many family members affected as the low risk group, and were more likely to require more intensive medical therapy to control their disease ( $P \leq 0.01$ ). There was no significant association between the PRS and the length of follow-up ( $P = 0.65$ ).

A recently reported PRS associated with POAG in European white populations was associated with a younger age of glaucoma diagnosis.<sup>24</sup> For comparison, we calculated this PRS in our

primary cohort (ANZRAG, n = 2,154; Supplementary Table 2). The IOP PRS presented in this study was more strongly associated with the age of glaucoma diagnosis ( $P = 2.0 \times 10^{-5}$ ) than the 12-SNP PRS reported by Fan *et al.* ( $P = 2.6 \times 10^{-4}$ ) and explained a greater variance of this outcome ( $R^2$  of linear regression 0.89% vs 0.65% respectively; Supplementary Table 3). The 12-SNP PRS was not associated with the maximum IOP recorded ( $P = 0.45$ ), and explained less variance in the need for incisional surgery outcome compared to the IOP PRS ( $R^2$  of linear regression 0.53% vs 0.79% respectively; Supplementary Table 3). Due to the inclusion of two VCDR-associated POAG risk variants near *CDKN2B-AS1* and *SIX6*, the 12-SNP PRS was associated with a higher VCDR but not the IOP PRS (Supplementary Table 3).

## Discussion

Common genetic variants associated with both glaucoma and IOP have been identified via genome-wide association studies. Genetic risk score stratification can be used to estimate the combined effect size of these variants on the patient. In this study, glaucoma patients in the high IOP genetic risk group had a higher maximum (pre-treatment) IOP, younger age of glaucoma diagnosis, and were more likely to require incisional surgery to control their disease than those in the intermediate or low IOP genetic risk groups. We have further replicated these results in an independent cohort of early glaucoma patients and observed a similar association with the higher genetic risk group requiring more intensive medical therapy for glaucoma management.

Interestingly, despite the clinically modest difference in the maximum IOP between the high and low IOP genetic risk groups (between 1-2 mmHg in two independent cohorts), we observed a stronger relationship in treatment intensity. In the ANZRAG cohort, the incisional surgery rate was 50% in the high genetic risk group compared to 38% in the low risk group. Similarly, in the early glaucoma cohort, 38% of the high genetic risk group required 2 or more medications or SLT for glaucoma management compared to 23% in the low genetic risk group.

Thus, IOP genetic risk variants and stratification may offer further insight into an individual's chronic exposure to higher IOP than sporadic clinic measurements. Further, these risk variants confer increased risk of developing POAG in carriers,<sup>12</sup> thus patients with higher polygenic risk scores had significantly more family members affected by glaucoma.

*TMCO1* was one of the earliest reported genes to be associated with POAG in common variant studies, and remains one of the most strongly associated variants with IOP and POAG.<sup>12,14,26</sup> A variant in *TMCO1* gene is reportedly associated with conversion from ocular hypertension to glaucoma in non-Hispanic whites<sup>27</sup> In another study, individuals homozygous for a variant near *TMCO1* were reported to have a younger age of POAG onset.<sup>28</sup> However, the clinical utility of genetic risk scores is expanding due to the accelerated discovery of disease-associated loci as larger genome-wide association studies are conducted. While early studies on using genetic risk scores for POAG were limited,<sup>29,30</sup> Macgregor *et al.* have recently reported an IOP based genetic risk score accounting for a significant risk of developing glaucoma (OR = 5.6 in the highest decile of the score relative to the lowest).<sup>12</sup> Fan *et al.* reported a PRS inclusive of 12-SNPs associated with POAG to be associated with a younger age of glaucoma diagnosis.<sup>24</sup> This PRS was inclusive of two variants near *CDKN2B-AS1* and *SIX6* associated with POAG and VCDR but not IOP,<sup>7,24,26</sup> which in addition to the low number of variants used in the score, may account for why this PRS was not associated with the maximum IOP phenotype in our study cohort. This supports the fact that inclusion of additional low impact variants leads to better PRS models for complex traits.<sup>31</sup> Further research is needed on a more comprehensive PRS inclusive of variants associated with POAG and its endophenotypes.

Conversely, the effects of Mendelian variants on glaucoma phenotype have been well described. Pathogenic variants in the *MYOC* gene are most commonly associated with high IOP and more advanced disease.<sup>32</sup> In contrast, duplications and triplications involving *TBK1* and missense variants in *OPTN* cause familial normal tension glaucoma, and are typically not

found in high tension glaucoma.<sup>7-9</sup> While these genes are important in familial glaucoma and highly predictive of disease risk, they are a relatively rare cause of POAG in the general population. Thus, genetic risk stratification using common variants of IOP is more widely applicable to most POAG patients. Our results show that the cumulative effect of IOP-associated genetic variants may predict an individual's lifetime IOP exposure, and support the utility of genetic risk scores in POAG monitoring. Further, PRS risk stratification can be done before the clinical presentation of the disease, and therefore may be useful for identifying high-risk individuals for screening. To our knowledge, this is the first study to detail the clinical glaucoma phenotype based on the combined effect of common IOP variants.

This study has several strengths. We utilised the large UK Biobank cohort to derive a genetic risk score of corneal compensated IOP. Using this score inclusive of variants at a strict genome-wide threshold, we characterised the clinical glaucoma phenotype that is attributable to the genetic biomarkers of IOP and its associated pathways. Inclusion of additional POAG risk and other endophenotype variants may yield a better glaucoma risk profiling. Our study cohort was also independent allowing validation of the discovered variants. We have further replicated our findings in another independent POAG cohort with mild glaucoma allowing further generalisability across the glaucoma severity spectrum. Our study has also some limitations. There may be inter-clinician variability in the rate of incisional surgeries as this was not done per protocol. A mixed-effects model with the referring clinician as a random-effect intercept yielded similar results in the estimated effect size of the IOP PRS on incisional surgery risk. Patient-reported family members affected has not been validated in a glaucoma setting and may lack sensitivity and specificity. While our replication of this finding in an independent sample suggests plausible correlation, the effect size may be under or overestimated due to recall and survival biases and community under-diagnosis of glaucoma. Genetic risk scores are limited by the genetic pool of the discovery cohort. Our results are limited to the ethnicities of the European ancestry individuals of the UK Biobank study which matched our prediction target cohort. Validation is needed in other ethnicities. We have only

used SNPs that reached genome-wide significance in the GWAS to calculate the PRS. While the inclusion of additional SNPs would include further low-impact susceptibility SNPs, it would also introduce further 'noise' to the PRS and may not improve risk stratification.<sup>33</sup>

In conclusion, our IOP PRS correlates with the maximum recorded IOP and glaucoma severity of POAG patients in a national glaucoma registry. Our result supports the clinical utility of PRS in POAG risk stratification.

### **Acknowledgments:**

This work was conducted using the UK Biobank Resource (application number 25331) and publicly available data from the International Glaucoma Genetics Consortium.

### **Figure legends:**

**Figure 1.** A continuous variant dose-response relationship between IOP PRS and (A) the maximum recorded IOP in the ANZRAG cohort ( $P = 1.9 \times 10^{-3}$  for linear model trend); (B) the mean number of family members affected by glaucoma ( $P = 1.3 \times 10^{-5}$  for negative binomial generalised linear model trend). The squares represent the mean values for each PRS decile group, and the error bars represent the 95% confidence interval of the mean. The grey line is the line of best fit with the 95% confidence interval lightly shaded around the line.

IOP: intraocular pressure; PRS: polygenic risk score.

**Figure 2.** Replication of the (A) maximum IOP recorded ( $P = 5.0 \times 10^{-4}$  for one-way analysis of variance) and (B) the number of family members affected by glaucoma ( $P = 1.0 \times 10^{-3}$  for one-way analysis of variance) in an independent cohort of early POAG patients ( $N = 624$ ). The squares represent the mean values for each PRS group, and the error bars represent the 95% confidence interval of the mean.

IOP: intraocular pressure; PRS: polygenic risk score; POAG: primary open angle glaucoma.



## References

1. Casson RJ, Chidlow G, Wood JP, et al. Definition of glaucoma: clinical and experimental concepts. *Clinical & Experimental Ophthalmology* 2012;40:341–349.
2. Conlon R, Saheb H, Ahmed IIK. Glaucoma treatment trends: a review. *Canadian Journal of Ophthalmology* 2017;52:114–124.
3. Tielsch JM, Katz J, Singh K, et al. A Population-based Evaluation of Glaucoma Screening: The Baltimore Eye Survey. *American Journal of Epidemiology* 1991;134:1102–1110.
4. Caprioli J, Coleman AL. Intraocular pressure fluctuation a risk factor for visual field progression at low intraocular pressures in the advanced glaucoma intervention study. *Ophthalmology* 2008;115:1123-1129.e3.
5. Asrani S, Zeimer R, Wilensky J, et al. Large diurnal fluctuations in intraocular pressure are an independent risk factor in patients with glaucoma. *J Glaucoma* 2000;9:134–142.
6. Wang K, Gaitsch H, Poon H, et al. Classification of common human diseases derived from shared genetic and environmental determinants. *Nat Genet* 2017;49:1319–1325.
7. Wiggs JL, Pasquale LR. Genetics of glaucoma. *Hum Mol Genet* 2017;26:R21–R27.
8. Aung T, Rezaie T, Okada K, et al. Clinical features and course of patients with glaucoma with the E50K mutation in the optineurin gene. *Invest Ophthalmol Vis Sci* 2005;46:2816–2822.
9. Awadalla MS, Fingert JH, Roos BE, et al. Copy number variations of TBK1 in Australian patients with primary open-angle glaucoma. *Am J Ophthalmol* 2015;159:124-130.e1.
10. Fingert JH, Héon E, Liebmann JM, et al. Analysis of Myocilin Mutations in 1703 Glaucoma Patients From Five Different Populations. *Hum Mol Genet* 1999;8:899–905.
11. Han X, Souzeau E, Ong J-S, et al. Myocilin Gene Gln368Ter Variant Penetrance and Association With Glaucoma in Population-Based and Registry-Based Studies. *JAMA Ophthalmol* 2018.
12. MacGregor S, Ong J-S, An J, et al. Genome-wide association study of intraocular pressure uncovers new pathways to glaucoma. *Nature Genetics* 2018;50:1067.
13. Gao XR, Huang H, Nannini DR, et al. Genome-wide association analyses identify new loci

influencing intraocular pressure. *Hum Mol Genet* 2018;27:2205–2213.

14. Khawaja AP, Cooke JB, Wareham NJ, et al. Genome-wide analyses identify 68 new loci associated with intraocular pressure and improve risk prediction for primary open-angle glaucoma. *Nat Genet* 2018;50:778–782.

15. Torkamani A, Wineinger NE, Topol EJ. The personal and clinical utility of polygenic risk scores. *Nature Reviews Genetics* 2018:1.

16. Mavaddat N, Michailidou K, Dennis J, et al. Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *The American Journal of Human Genetics* 2019;104:21–34.

17. Inouye M, Abraham G, Nelson CP, et al. Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. *J Am Coll Cardiol* 2018;72:1883–1893.

18. Khera AV, Chaffin M, Aragam KG, et al. Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. *Nature Genetics* 2018;50:1219–1224.

19. Souzeau E, Goldberg I, Healey PR, et al. Australian and New Zealand Registry of Advanced Glaucoma: methodology and recruitment. *Clinical & Experimental Ophthalmology* 2012;40:569–575.

20. Ennis S, Gibson J, Griffiths H, et al. Prevalence of myocilin gene mutations in a novel UK cohort of POAG patients. *Eye* 2010;24:328–333.

21. Sudlow C, Gallacher J, Allen N, et al. UK Biobank: An Open Access Resource for Identifying the Causes of a Wide Range of Complex Diseases of Middle and Old Age. *PLOS Medicine* 2015;12:e1001779.

22. Loh P-R, Tucker G, Bulik-Sullivan BK, et al. Efficient Bayesian mixed-model analysis increases association power in large cohorts. *Nature Genetics* 2015;47:284–290.

23. Purcell S, Neale B, Todd-Brown K, et al. PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. *Am J Hum Genet* 2007;81:559–575.

24. Fan BJ, Bailey JC, Igo RP, et al. Association of a Primary Open-Angle Glaucoma Genetic Risk Score With Earlier Age at Diagnosis. *JAMA Ophthalmol* 2019.

25. R Core Team. R: A Language and Environment for Statistical Computing. Vienna, Austria: R Foundation for Statistical Computing; 2018. Available at: <https://www.R-project.org/>.
26. Burdon KP, Macgregor S, Hewitt AW, et al. Genome-wide association study identifies susceptibility loci for open angle glaucoma at *TMCO1* and *CDKN2B-AS1*. *Nature Genetics* 2011;43:574–578.
27. Scheetz TE, Faga B, Ortega L, et al. Glaucoma Risk Alleles in the Ocular Hypertension Treatment Study. *Ophthalmology* 2016;123:2527–2536.
28. Sharma S, Burdon KP, Chidlow G, et al. Association of genetic variants in the *TMCO1* gene with clinical parameters related to glaucoma and characterization of the protein in the eye. *Invest Ophthalmol Vis Sci* 2012;53:4917–4925.
29. Mabuchi F, Mabuchi N, Sakurada Y, et al. Additive effects of genetic variants associated with intraocular pressure in primary open-angle glaucoma. *PLoS One* 2017;12. Available at: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5568337/> [Accessed February 5, 2019].
30. Tham Y-C, Liao J, Vithana EN, et al. Aggregate Effects of Intraocular Pressure and Cup-to-Disc Ratio Genetic Variants on Glaucoma in a Multiethnic Asian Population. *Ophthalmology* 2015;122:1149–1157.
31. Boyle EA, Li YI, Pritchard JK. An expanded view of complex traits: from polygenic to omnigenic. *Cell* 2017;169:1177–1186.
32. Souzeau E, Tram KH, Witney M, et al. Myocilin Predictive Genetic Testing for Primary Open-Angle Glaucoma Leads to Early Identification of At-Risk Individuals. *Ophthalmology* 2017;124:303–309.
33. Chatterjee N, Shi J, García-Closas M. Developing and evaluating polygenic risk prediction models for stratified disease prevention. *Nat Rev Genet* 2016;17:392–406.