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Plan Statistical analysis

Project title: Genetic and risk factors in exfoliation glaucoma (Glaugene)

NCT: N.A.

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All statistical analyses will be performed using SPSS version 28.0.1.0 (IBM, 1 New Orchard Road Armonk, NY 10504, USA) software. Clinical characteristics of the cohort will be compared in relation to progression/no progression of glaucoma based on guided progression analysis (GPA). Categorical variables will be compared with Fisher's exact test while continuous variables with Student's t-test. The single nucleotide polymorphism (SNP) allele distribution between no progression and progression cases based on GPA will be compared using Fisher's exact test. The distribution of the haplotypes between no progression and progression cases based on GPA will be compared using Chi2 analyses within the Haploview 4.1 software. The relation between the SNPs and progression/no progression in glaucoma will be tested using regression analyses (logistic or linear). In these analyses, mean deviation (MD) and visual field index (VFI), in addition to GPA, will be used as outcome variables measuring progression/no progression of glaucoma. Potential covariates will be first tested for association with the outcome variable (i.e., GPA, MD, and VFI) using univariate linear or logistic regression (depending on the character of the outcome variable). Associated variables will then be included as covariates in multivariate regression analyses. Finally, a regression analysis will be performed, including the genotypes of the two SNPs as predictors (both SNPs within the same model) and GPA/MD/VFI as outcome variables.

A power analysis based on Fisher's exact test will be performed using the Power and Sample Size Calculations software (http://biostat.mc.vanderbilt.edu/PowerSampleSize). Each SNP will be analysed separately. In all cases, the type I error (α error) will be set to 0.05.