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Functional analysis of differentially expressed genes associated with glaucoma from DNA microarray data

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ABSTRACT. Microarray data of astrocytes extracted from the optic nerves of donors with and without glaucoma were analyzed to screen for differentially expressed genes (DEGs). Functional exploration with bioinformatic tools was then used to understand the roles of the identified DEGs in glaucoma. Microarray data were downloaded from the Gene Expression Omnibus (GEO) database, which contains 13 astrocyte samples, 6 from healthy subjects and 7 from patients suffering from glaucoma. Data were pre-processed, and DEGs were screened out using *R* software packages. Interactions between DEGs were identified, and networks were built using Search Tool for the Retrieval of Interacting Genes/Proteins (STRING). GENECODIS was utilized for the functional analysis of the DEGs, and GOTM was used for module division, for which functional annotation was conducted with the Database for Annotation, Visualization, and Integrated Discovery (DAVID). A total of 371 DEGs were identified between glaucoma-associated samples and normal samples. Three modules included in the PPID database were generated with 11, 12, and 2 significant functional annotations, including immune system processes, inflammatory responses, and synaptic

vesicle endocytosis, respectively. We found that the most significantly enriched functions for each module were associated with immune function. Several genes that play interesting roles in the development of glaucoma are described; these genes may be potential biomarkers for glaucoma diagnosis or treatment.

Key words: Astrocytes; Optic nerve; Differentially expressed genes; Module analysis; Functional analysis

