

Clustering gene expression changes reveals pathways toward glaucoma prevention

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Glaucoma is the second-most common cause of blindness in the US, and occurs due to loss of retinal ganglion cells and degeneration of the [optic nerve](#). Although it is known that high levels of pressure within the eye predispose individuals to the development of glaucoma, the [molecular mechanisms](#) involved are poorly defined.

In new research from The Jackson Laboratory in Bar Harbor, Maine, Simon John and colleagues analyzed gene expression patterns in the [retina](#) and optic nerves of mice that develop age-related glaucoma. Using a method that involved the clustering of samples that showed similarity in expression profiles, the researchers were able to identify molecular signatures of early events in glaucoma progression- events that were detectable before there was morphological evidence of damage.

Activation of part of the [innate immune system](#) called the complement cascade, and upregulation of endothelin 2- a protein that can increase blood pressure- were among these early changes. Notably, the researchers found that genetically and pharmacologically interfering with these changes protected mice from developing glaucoma.

The researchers believe that they have identified pathways that might be targeted in the development of new [glaucoma](#) therapeutics, and hope that their method of clustered gene expression analysis will be useful in uncovering the early molecular events that underlie other diseases.

Provided by Jackson Laboratory

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