



THE PREVALENCE OF OPTINEURIN MUTATIONS IN A LARGE SERIES OF GLAUCOMA PATIENTS

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Background/Purpose: In 2002 Rezaie and colleagues described a new gene for glaucoma, optineurin. This gene was found in the GLC1E linkage interval, a region found by studying a large family with autosomal dominant normal tension glaucoma (NTG). Rezaie found optineurin mutations in 16.7% of 52 NTG families. One mutation, Glu50Lys, was present in 13.5% of families. The Arg545Gln mutation and a premature stop mutation were each found in one family. The Met98Lys variation was found both in affected individuals and control subjects, but was more prevalent among affected individuals (13.6%) than among control subjects (2.1%). We have screened a large number of open angle glaucoma patients for the four optineurin sequence variations described by Rezaie.

Design: Multi-center, multi-national genetic screening study

Participants/Testing: 1048 glaucoma patients and 251 control subjects were molecularly screened using SSCP. The glaucoma patients were from the USA, Japan, and Australia. They had a wide variety of open-angle glaucoma sub-types and included 353 NTG patients.

Results: Only one patient was found to have the Glu50Lys mutation. This patient's DNA had been obtained because of a strong family history of NTG. The overall prevalence of the Glu50Lys mutation was 0.10% of all glaucoma patients. The premature stop mutation was not found. Both the Arg545Gln and Met98Lys variations were ethnically skewed polymorphisms, being common among Japanese patients and controls and uncommon among Caucasians.

Conclusions: The Glu50Lys optineurin mutation can cause familial NTG, a very rare disease. Optineurin mutations do not play a major role in non-familial NTG or other types of glaucoma.