

Publication

A hypomorphic variant in EYS detected by genome-wide association study contributes toward retinitis pigmentosa

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The genetic basis of Japanese autosomal recessive retinitis pigmentosa (ARRP) remains largely unknown. Herein, we applied a 2-step genome-wide association study (GWAS) in 640 Japanese patients. Meta-GWAS identified three independent peaks at $P < 5.0 \times 10^{-8}$, all within the major ARRP gene EYS. Two of the three were each in linkage disequilibrium with a different low frequency variant (allele frequency A, p.G843E) of unknown significance. mRNA harboring c.2528 G > A failed to restore rhodopsin mislocalization induced by morpholino-mediated knockdown of eys in zebrafish, consistent with the variant being pathogenic. c.2528 G > A solved an additional 7.0% of Japanese ARRP cases. The third peak was in linkage disequilibrium with a common non-synonymous variant (c.7666 A > T, p.S2556C), possibly representing an unreported disease-susceptibility signal. GWAS successfully unraveled genetic causes of a rare monogenic disorder and identified a high frequency variant potentially linked to development of local genome therapeutics.

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