A novel variant of KCNQ1 gene and pathogenicity prediction in a family with long QT syndrome type 1

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Abstract

We report a novel heterozygous missense variant of *KCNQ1* in a family exhibiting LQTS with complete penetrance and predict its pathogenicity through multiple prediction software programs and 3D model analysis. Whole-exome sequencing (WES) was performed in a family with symptoms of LQTS. The pathogenicity of the identified variant was predicted for its effect on a 3D model of KCNQ1, and in-depth functional analysis was performed for mechanistic speculation. A novel heterozygous variation c.716T>G in *KCNQ1* with autosomal dominant inheritance was identified. We demonstrated that this variant, which is located in the conserved hot spot domain, was evaluated as likely pathogenic. *In silico* prediction indicated that the variation was involved in the process of channel closing/opening. This study reports a novel variation in *KCNQ1*, provides supportive evidence for pathogenicity prediction and enhances variant interpretation for patients with LQTS.

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