GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

KCNE1 112G>A polymorphism and atrial fibrillation risk: a meta-analysis

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Genet. Mol. Res. 13 (4): 8367-8377 (2014)
Received August 7, 2013
Accepted March 18, 2014
Published October 20, 2014
DOI http://dx.doi.org/10.4238/2014.October.20.12

ABSTRACT. KCNE1, a membrane protein that spans the membrane once is responsible for modulating potassium channel functions and plays an important role in the etiology of arrhythmia. Emerging evidence indicates that a common polymorphism (112G>A; rs1805127 G>A) in the *KCNE1* gene contributes to atrial fibrillation (AF) risk; however, these studies showed inconclusive results. In this meta-analysis, we derived a more precise estimation of the association between the *KCNE1* 112G>A polymorphism and AF risk. The following databases were searched: Web of Science (1945-2013), the Cochrane Library Database (Issue 12, 2013), PubMed (1966-2013), EMBASE (1980-2013), CINAHL (1982-2013), and the Chinese Biomedical Database (1982-2013). The crude odds ratios with their 95% confidence intervals were calculated. Nine case-control studies were included, with a total of 1792 AF patients and 1924 healthy controls. The meta-analysis results indicated that the *KCNE1* 112G variant is associated with an increased risk of AF. Further subgroup analysis based on ethnicity revealed significant associations between the *KCNE1* 112G variant and an increased risk of AF among both Asians and Caucasians. No publication bias was detected in this meta-analysis. In conclusion, our results indicate that the *KCNE1* 112G polymorphism may be a risk factor for AF. *KCNE1* 112G>A may be

useful as a biomarker for predicting the development of AF.

Key words: Atrial fibrillation; KCNE1; Meta-analysis; Polymorphism; Susceptibility

