ventricular tachycardia. We hypothesised that this SNP act a role in ventricular tachycardia.

Methods 220 patients diagnosed as ventricular tachycardia and 1000 healthy subjects were included in the present study. All patients were genotyped for SNPs using a Rotor-Gene TM 6000 High Resolution Melt system. A case-control analysis were performed by accurate statistical analysis adjusting for potential confounding factors.

Results The association of SNP rs11970286 and QT was significant (p=0.018). We also found significant association between SNP rs11970286 and idiopathic ventricular tachycardia, as well as ventricular tachycardia after acute myocardial infarction (p=0.001, OR=2.226; p=0.005, OR=4.010 respectively).

Conclusions Our findings suggest that SNP rs11970286 might be risk factors for ventricular tachycardia in Chinese population. And QT interval may confer an intermediate phenotype. The identification of causal genes and mechanisms at the loci remains a major task.

GW23-e1713 **ASSOCIATION OF SNP RS11970286 AND VENTRICULAR TACHYCARDIA IN CHINESE HAN POPULATION**

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Objectives Ventricular tachycardia is a kind of serious arrhythmia. Some recent Genome-wide association studies identified susceptibility locus, among which SNP rs11970286 has a documented role in the regulation of QT interval. However, few researchs foucs on the relevance of common variants and