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Heart Failure and Cardiomyopathies

IMPACT OF SCN10A GENE POLYMORPHISM FOR CARDIAC CONDUCTION ABNORMALITY IN PATIENTS WITH HYPERTROPHIC CARDIOMYOPATHY

Poster Contributions
Hall C
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Session Title: Heart Failure and Cardiomyopathies: Diagnostic, Prognostic and Therapeutic Strategies in Cardiomyopathies
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Background: Arrhythmias are associated with reduced quality of life and poor prognosis in patients with hypertrophic cardiomyopathy (HCM). Recently, a nonsynonymous single nucleotide polymorphism, rs6795970, in SCN10A gene is reported to be associated with PR interval, a marker of cardiac atrioventricular conduction. In addition, this polymorphism is reported to be strongly associated with cardiac arrhythmias. We examined whether this PR prolonging allele (A allele) in the SCN10A gene may be associated with cardiac conduction abnormality in patients with HCM.

Methods and Results: We genotyped this polymorphism in 149 patients with HCM. The conduction abnormality was defined as first-degree heart block, bundle-branch block, bifascicular heart block, and atrial fibrillation. Patients were divided into two groups: group A of 92 patients without conduction abnormality and group B of 57 patients with conduction abnormality. Distribution of the SCN10A genotypes (G/G, G/A, and A/A) among the patients with HCM was 71%, 26%, and 3%, respectively. The abnormality of cardiac conduction was documented in 29% with G/G, 61% with G/A or A/A. In addition, there was a significant difference in the distribution of genotypes between the two groups (p=0.0018). Prolongation of the P wave and QRS durations were significantly associated with the A allele.

Conclusion: The SCN10A gene polymorphism is associated with abnormality of heart conduction in patients with HCM.

Association of the *SCN10A* Genotypes (rs6795970) and Conduction Abnormality

	G/G (n=77)	G/A (n=26)	A/A (n=3)	G/A+A/A (n=29)
P wave duration (ms)	107±12	109±11	126±15 *	112±12
PR interval (ms)	184±31	197±31	197±45	197±31
QRS duration (ms)	101±21	113±25	111±10	112±24 **
QTc interval (ms)	427±47	415±55	414±38	416±53

Values are expressed as mean ± SD.
*P<0.05 among the groups
**P<0.05 vs G/G patients