ACC.17™

717
JACC March 21, 2017
Volume 69, Issue 11

Heart Failure and Cardiomyopathies

WHOLE GENOME SEQUENCING IN FOUR HYPERTROPHIC CARDIOMYOPATHY FAMILIES WITH SUDDEN CARDIAC DEATH

Poster Contributions
Poster Hall, Hall C
Friday, March 17, 2017, 10:00 a.m.-10:45 a.m.

Session Title: Population Specific Cardiomyopathies: From Exomes to Databases
Abstract Category: 12. Heart Failure and Cardiomyopathies: Basic
Presentation Number: 1122-259

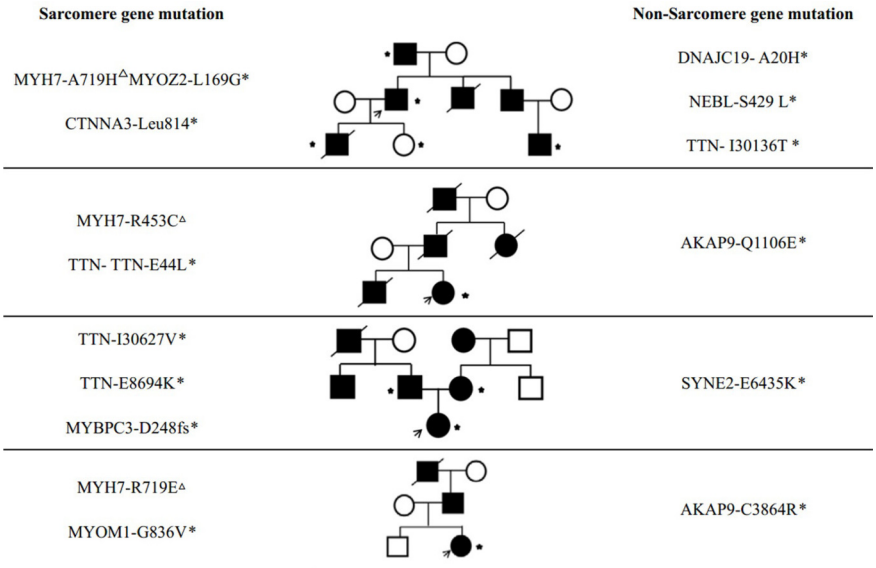
Authors: *Xiying Guo, Chaomei Fan, Chi Cai, Yinjian Yang, Fujian Duan, Lei Tian, Yishi Li, Key Laboratory of Clinical Trial Research in Cardiovascular Drugs, Ministry of Health, Fuwai Hospita, Beijing, People's Republic of China*

Background: Hypertrophic cardiomyopathy (HCM) is the most common reason for sudden cardiac death (SCD) in adolescents. The genetic background of HCM related SCD remains unclear. The aim of this study was to investigate the genetic features of SCD in families with HCM.

Methods: Four HCM families with SCD were selected from Fuwai Hospital. Information for SCD was confirmed by at least two family members and reconfirmed by hospital records. Whole genome sequencing (WGS) was performed on patients with SCD attacks and their immediate HCM family members. If samples of SCD cases were not available, their immediate family members with HCM would be sequenced. Sanger sequence was used to verify the mutations detected by WGS in families and 200 unrelated healthy controls.

Results: Ten HCM patients from 4 families were sequenced. Mutations of reported sarcomere gene MYH7 were identified with 3 families. Co-segregation analysis in the family exposed MYBPC3-D248fs in the 3 rd family, which runs great risk to be a new pathologic mutation. Multiple sarcomere gene mutations related to HCM were found in all 4 families. Moreover, mutations associated with dilated or arrhythmogenic right ventricular cardiomyopathy and ion channel disease were also detected in all 4 families. The genetic mutations were shown in the Figure.

Conclusions: Multiple mutations of sarcomere gene and other cardiomyopathy or ion channel disease gene was common in HCM families with SCD. Multiple gene mutations might be a potential risk factor for SCD in HCM.



Footnote: △, known pathologic mutation; *, novel mutation; ⬟patients underwent the whole genome sequencing.