Abstract

Introduction:

Hypertrophic cardiomyopathy (HCM) is characterised by marked heterogeneity both in phenotype and genotype. One of the main objectives in medical care is early HCM diagnosis and prevention of cardiovascular events including sudden cardiac death (SCD). In a large number of patients, we do not detect any pathogenic or likely pathogenic (P/LP) variant within molecular genetic analysis. Since the genomic testing is time consuming, expensive and difficult to interpret, the patients should be carefully selected. A proper selection of patients helps to prevent SCD in asymptomatic high-risk patients and reduce the unnecessary preventive steps in low-risk individuals.

Hypothesis:

There are clinical and morphologic HCM characteristics associated with positive genotype.

Objectives:

1) Perform genomic testing in a large cohort of Czech HCM patients
2) Identify clinical and morphologic HCM characteristics associated with positive result of genomic testing (finding P/LP variant)
3) Utilize the clinical and morphologic HCM characteristics to predict the result of genomic testing
4) Facilitate cascade family genetic screening by genotyping HCM probands for early prevention of cardiovascular events before clinically overt HCM
5) Investigate the genotype and outcome of HCM patients treated with ASA

Methods:

Patients with clinical diagnosis of HCM were included in our study. Personal and family history was obtained. Clinical and imaging testing was performed. Blood sample was taken for genomic analysis.

Results:

A total of 336 HCM patients underwent genomic testing. We identified 72 P/LP variants in 70 (21 %) HCM patients, with the dominant role of MYBPC3. Patients with P/LP variants are younger, has more frequently family history of HCM and less likely arterial hypertension. The higher Mayo Score implies increased yield of genomic testing. Cascade genetic screening was demonstrated as case report of one family, with complete molecular genetic diagnosis and preventive effects on its members. Short- and long-term outcomes of HCM patients after ASA is favourable both in genotype positive and negative patients.

Conclusion:

We have found clinical and morphologic HCM characteristics associated with positive genotype. Predictive scoring system, which includes those characteristics, was tested on Czech HCM patient's cohort and effectively predicts the diagnostic yield of genomic testing. ASA is safe and effective treatment in HCM patients irrespective of their genetic background.

Keywords: Myocardial disease, Hypertrophic cardiomyopathy, Genetic testing