

Editorial

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Multicenter Cohort Analysis Unveil Inherited Arrhythmia in Korea

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 See the article "Clinical and Genetic Features of Korean Inherited Arrhythmia Probands" in volume 53 on page 693.

Inherited arrhythmias (IAs) without identifiable structural heart diseases are mainly associated with mutations in genes encoding iso channels or their regulatory proteins.¹⁾ The main IAs are Brugada syndrome (BrS), long QT syndrome (LQTS), idiopathic ventricular fibrillation (IVF), short QT syndrome, early repolarization syndrome, catecholaminergic polymorphic ventricular tachycardia. IAs are responsible for the 10% of sudden death.²⁻⁴⁾

Individuals with IAs are usually asymptomatic until the first symptoms or events (dizziness, syncope, or cardiac arrest) occur, and the timing of onset varies with the diseases. Diagnosis is made through characteristic electrocardiographic characteristics, clinical features, and genetic analysis. Genetic testing is also recommended for family members to assess their risk of developing the disease.

Although the main IAs, such as J wave syndrome,⁵⁾ BrS,⁶⁾ and acquired LQTS,⁷⁾ are common in Asian populations, little is known about its clinical characteristics and genetic background in Asian populations. This study⁸⁾ is a retrospective, multicenter cohort study in Korean, which investigated the clinical characteristics of Korean IA probands and further analyze the genetic findings via next-generation sequencing (NGS). It showed that the most common disease entity was IVF (36.2%), followed by BrS (35.8%) and LOTS (20.4%) in Korean IA cohort. In BrS and IVF, males were predominant (92.6% and 82.3%, respectively) and in LQTS, females were predominant (77.8%). Family history of SCD was more common in BrS and rare in IVF (26.3% and 7.3%, respectively). There was significant difference of left ventricular ejection fraction between positive and negative genotype probands (54.7% and 59.3%, p=0.005). The genetic testing yield was highest in IVF (54.0% for positive genotype and 13.5% for pathogenic or likely pathogenic variant), and relatively low in BrS (19.5% for positive genotype) and LQTS (23.8% for positive genotype). Among probands with pathogenic of likely pathogenic variants, 90% were detected with cardiomyopathy-related variants that encode sarcomere proteins (hypertrophic cardiomyopathy-related; MYBPC3, MYH7, TNNI3) and desmosome protein (arrhythmogenic right ventricle dysplasia-related; DSG2, DSP, JUP).

In Korea, genetic testing had not been covered by the National Health Insurance Service (NHIS) for a long time, and it has not been widely used in real-world practice, except for LQTS, which has a high diagnostic and therapeutic value. However, it has recently been

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covered by the NHIS and is being used for various diseases as the rate of reimbursement increases. In the field of IA, genetic testing is also widely used in terms of diagnosis, prognosis, and treatment, and it is expected that more help will be provided as these data accumulate. In this study, genetic variants in cardiomyopathy-related genes were observed at a high rate in genetic testing of patients who had been classified for IVF. Considering this, genetic testing will be of significant help in making a more accurate clinical diagnosis in IAs of unknown cause.

The genetic analysis via NGS reported by Jeong et al.⁸⁾ show clinical characteristics and genetic findings of Korean IA probands. From the data presented, it was possible to understand characteristics of the three common IAs of Koreans such as IVF, BrS, and LQTS. However, we are still at an early stage in the interpretation of genetic tests, and it will take years before we deeply appreciate the role of these genetic factors in IA fields. More studies are needed in Korean IA probands to improve our understanding of the genetic mechanism.

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