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著者	Horie Minoru
journal or publication title	Journal of Arrhythmia
volume	32
number	5
page range	313-314
year	2016-10
URL	http://hdl.handle.net/10422/00012330

doi: 10.1016/j.joa.2016.07.001

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Journal of Arrhythmia 32 (2016) 313–314

Contents lists available at ScienceDirect

Journal of Arrhythmia

journal homepage: www.elsevier.com/locate/joa

Editorial

Molecular genetics have opened a new era for arrhythmia research, but also Pandora's box?

Our so-called fate is largely ordained by our ancestors, not by the stars.

…Pandora regretted opening her box.

In “The Island” by Victoria Hislop (British novelist).

The Japanese Heart Rhythm Society and the Asia Pacific Heart Rhythm Society have jointly produced a series of review and original articles on up-to-date themes in heart rhythm research. This special issue will focus on “genes and arrhythmias”, which are currently in the spotlight as a novel field of cardiovascular medicine. Scientific progress in genetics prompted the discovery of new genes responsible for heart diseases and elucidated their specific molecular mechanisms of pathogenicity. For example, variants of genes encoding a variety of ion channels or their associated proteins were found to cause inherited arrhythmias, such as long QT syndrome, Brugada syndrome, catecholaminergic polymorphic ventricular tachycardia, progressive cardiac conduction defect, and short QT syndrome. Thanks to functional analysis by using electrophysiological methods, the precise mechanisms underlying their respective pathogenicity have been fully proven, even by employing cardiomyocytes differentiated from patient-specific iPS cells. Rapid adoption and spread of genetic tests for these diseases have offered us a unique approach, not only for diagnosis, but also for risk assessment and therapeutic decisions, and eventually for personalized medicine. Notably because the list of inherited arrhythmias is still expanding.

According to our rapidly developing knowledge on these inherited arrhythmias, several key guidelines are now available in regard to genetic testing, diagnosis, and treatment [1–5]. Though these publications cover important recommendations, we still need some details for the diagnosis and therapy of this new disease category, especially after the advent of high-output sequencing techniques using next generation sequencers, because we would identify too many variants from both patients and healthy individuals. It is of extreme clinical importance to distinguish between pathogenic variants and those of uncertain significance (i.e., VUSs). Additionally, these variants include a number of single nucleotide polymorphisms (SNPs), and the distribution of SNPs

http://dx.doi.org/10.1016/j.joa.2016.07.001
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differs considerably depending on ethnic group. Therefore, ethnicity-specific SNP databases are required to make a decision whether a variant detected in a patient family is significant or not. Now that we have opened a door to modern molecular genetics (or Pandora's box) as a new technology, it is definitely up to us to manage it in an appropriate way (excluding VUSs). The importance of making an accurate diagnosis prior to genetic testing is now more necessary than before. Therefore, this issue of Journal of Arrhythmia highlights the articles from the invited experts in this field, especially from the Asia Pacific region, to describe and review their most specialized research themes regarding “genes and arrhythmias”. The editors believe that this state-of-art coverage will be useful for understanding the new era in genes and arrhythmias.

Conflict of interest

The author declares no conflict of interest related to this study.

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