



Service Priorities and Programmes
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Submitting author: Dr Chloe MAK

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Genetic Basis of 28 Hong Kong Chinese Patients with Channelopathies and Cardiomyopathies: A 10-year Regional Laboratory Experience

Chloe Miu MAK¹, Sammy Pak-lam CHEN¹, Ngai-shing MOK², Wai-kwan SIU¹, Hencher Han-chih LEE¹, Chor-kwan CHING¹, Ping-tim TSUI², Nai-chun FONG³, Yuet-ping YUEN⁴, Wing-tat POON⁵, Chun-yiu LAW³, Yeow-kuan CHONG¹, Albert Yan-wo CHAN¹, Tak Cheung YUNG⁶, Katherin

1Kowloon West Cluster Laboratory Genetic Service, Genetic Pathology Laboratory, Department of Pathology, Princess Margaret Hospital, Hong Kong SAR, China

2Department of Medicine and Geriatrics, Princess Margaret Hospital, Hong Kong SAR, China

3Department

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Introduction

Hereditary channelopathies and cardiomyopathies are potentially lethal, clinically and genetically heterogeneous involving at least 90 genes. It is an important cause of sudden cardiac death and morbidities. Genetic testing can provide accurate diagnosis, guide the treatment and enable cascade screening.

Objectives

Molecular basis among Hong Kong Chinese is largely unknown. Here we described 28 unrelated patients with positive genetic findings detected from 2006 to 2015.

Methodology

Sanger sequencing was performed in 28 unrelated patients with clinical diagnosis of channelopathies and cardiomyopathies for KCNQ1, KCNE1, KCNE2, KCNH2 and SCN5A for long QT syndrome; SCN5A for Brugada syndrome; RYR2 for catecholaminergic polymorphic ventricular tachycardia; MYH7 and MYCBP3 for hypertrophic cardiomyopathy; LMNA for dilated cardiomyopathy and PKP2 and DSP for arrhythmogenic right ventricular dysplasia/cardiomyopathy.

Result

There were 17 males and 11 females. Mean age of presentation was 39 years (range 1 – 80 years). Major clinical presentations include syncope, palpitation and abnormal ECG findings. Family history was present in 13 of them (46.4%). There were 26 different heterozygous mutations detected, with 6 novel (2 in SCN5A (NM_198056.2:c.429del and c.2024-11T>A), 2 in MYBPC3

(NM_000256.3:c.906-22G>A and c.2105_2106del) and 2 in LMNA
(NM_170707.3:c.73C>A and c.1209_1213dup)).

We characterized the genetic heterogeneity in channelopathies and cardiomyopathies among Hong Kong Chinese with 10-year case series. Proper interpretation of the genetic findings is difficult and requires expertise and long experience. Caution regarding issues of non-penetrance, variable expressivity, phenotype-genotype correlation, susceptibility risk and digenic inheritance is necessary for genetic counselling and cascade screening.