GENETIC ANALYSIS OF SAFFOLD VIRUS-PENANG IN RELATION TO OTHER NEWLY DISCOVERED SAFFOLD VIRUSES

Kenny Voon¹, Qi Mei Ng², Meng Yu³, Lin-Fa Wang³ and Kaw Bing Chua²

¹International Medical University, Kuala Lumpur, Malaysia; ²Temasek Life Science Laboratory, Temasek, Singapore; ³CSIRO Livestock Industries, Australian Animal Health Laboratory, Geelong, Victoria, Australia

Abstract. Viruses in the family Picornaviridae are classified into nine genera. Within the family Picornaviridae, two species: *Encephalomyocarditis virus* and *Thei-lovirus*, are listed under the genus *Cardiovirus*. A novel *Theilovirus*, Saffold virus (SAFV), was first reported in 2007. Since then, numerous SAFV isolates have been detected around the world and genetic recombinations have been reported among them. In 2009, SAFV-Penang was isolated from a febrile child with influenza-like illness in Malaysia. SAFV-Penang is a genotype 3 SAFV. In this study we investigated the genome features of SAFV-Penang to exclude the possibility it is a recombinant variant. SAFV-Penang was found not to be a recombinant variant but to have three unique non-synonymous substitutions, alanine [A⁶⁸⁹], lysine [K⁷⁰⁸] and isoleucine [I⁷²⁴] in the VP1 protein.

Keywords: Saffold virus, SAFV-Penang, genetic analysis

Correspondence: Kenny Voon, International Medical University, Jalan Jalil Perkasa 19, Bukit Jalil, 57000, Kuala Lumpur, Malaysia. Tel: +603 27317245; Fax: +603 86567229 E-mail: kenny_voon@imu.edu.my