

Abstract

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Project Title: Molecular epidemiology of the non-HIV associated cryptococcal genotype, VNlc/M5/ST5, in Thailand

Investigator: Popchai Ngamskulrungroj

E-mail Address: popchai.nga@mahidol.ac.th

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Abstract:

Despite a strong association between *C. neoformans* and HIV status of the patients globally, most of cryptococcosis in Far East Asia occurs in non-HIV individuals. Further molecular epidemiological studies, using MLST, revealed more than 95% of the cryptococcal strains belonged to a specific sub-type of the molecular type VNlc/ST5 genotype. Such association of this genotype has never been specifically explored in other part of Asia. Therefore, this study aims to investigate the VNlc/ST5 genotype distribution among cryptococcosis patients in Thailand, a South East Asian country.

Fifty-one of *C. neoformans* isolates were collected from clinical samples in Siriraj Hospital, Bangkok, Thailand. The strains were mostly isolated from HIV positive (88.57%) and all were molecular type VNI MAT α . Multilocus Sequence Typing (MLST) analysis identified five sequence types (ST) in Siriraj Hospital. ST4 (45.10%) and ST6 (35.29%) were found to be the two most common. The other less common were ST5 (15.69%), ST32 (1.96%) and ST93 (1.96%). The ST5 was, unlike what reported in the Far East Asia, mostly (83.3%) found in HIV patient ($p = 0.657$) and there was no significant change in ST5 prevalence over the past 10 years ($p = 0.548$). Further analysis of co-morbidities showed higher morbidity and delays in cryptococcal diagnosis in a group with TB co-infection or with non-HIV status.

Our study suggested that, though Thai is genetically closely-related to the Far East Asian, ST5 in Thailand is not associated with non-HIV status. Thus, such association might not relate to the host genetic. However, the definite mechanism remains a mystery.

Keywords: Cryptococcus, HIV, AIDS, molecular epidemiology