

MLST analysis of *Burkholderiapseudomallei* isolates from Sri Lanka

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Introduction

Burkholderiapseudomallei is a Gram-negative bacterium found in soil and water in tropical and subtropical regions worldwide. It causes melioidosis, a severe disease with a broad spectrum of clinical presentations that may include joint pain, cough, skin infections, lung nodules and pneumonia. It is hyperendemic to Southeast Asia and northern Australia. The endemic area includes Sri Lanka. A project to screen undifferentiated fever cases to identify potential melioidosis cases resulted in a dramatic rise in the number of culture confirmed cases with over 50 cases being reported each year in recent years. Although the majority of strains are YLF, around 15% of strains belong to the Australian BTFC cluster and a dominant exclusive Australian ST was found to be present in Sri Lanka.

Methods

B. pseudomallei clinical isolates from patients in Sri Lanka were characterized using a molecular genotyping method, multilocus sequence typing (MLST). Sequence types (ST) and clinical data were submitted to the international *B. pseudomallei* database (<http://pubmlst.org/bpseudomallei>). The database was used to aid in understanding ST abundance.

Results

A total of 108 strains, clinical isolates from 2006 to 2015, were genotyped. A further 70 strains are in the process of being submitted to the public database. The preliminary results of analysis of twelve samples have shown a high genotypic variation. Out of these, five strains were found to be novel. Of the remaining seven, two were of Indian and Thai origin. As of August 2017, Sri Lanka has the largest representation of all the South Asian countries in the international *B. pseudomallei* database with a total of 109 isolates accounting for around 2.27% of the entire database.

Discussion and Conclusion


A higher resolution genotyping approach (i.e. whole genome sequencing) is needed for a comprehensive comparison between these strains and to understand the presence of the Australian BTFC cluster plus the dominant exclusive Australian ST in Sri Lanka.

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