

Unravelling the Genetic Diversity of *Burkholderia pseudomallei* in Sri Lanka using Multilocus Sequence Typing

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Burkholderia pseudomallei is the causative agent of a potentially fatal infectious disease, melioidosis. Sri Lanka has been recently confirmed as endemic to melioidosis, and the case fatality rate is 24%. A small number of clinical strains has been characterized and therefore, little is known about genomic epidemiology of *B. pseudomallei* in the country. The main aim of the present study is to determine genetic diversity among 87 clinical isolates using multilocus sequence typing (MLST). MLST analysis resulted in 43 STs, of which 22 were novel: ST 1880-85, 1887-95, 1898, 1900, 1928-30, 1933-34. A total of 196 isolate records with 72 STs reported from Sri Lanka (including those submitted previously) was used for the e-BURST (based upon sequence typing) analysis which showed a considerable genetic diversity among clinical isolates with 72 STs in just 196 isolates comprising multiple sub-groups within a clonal complex. Seventeen singletons (ST 308, 338, 944, 1314, 1133, 202, 1141, 1142, 1144, 132, 1887, 1890, 1883, 1895, 1881, 1930, 421) were found. The ST1132 was the ancestral genotype in Sri Lanka while ST1137 was the commonest ST with 35 isolates. Two distinct alleles *ace* 55, and *ndh* 124 were unique to Sri Lanka. Shared STs observed were 202, 594 (Australia, Thailand), 912 (Cambodia), 501 (India, Thailand), 912 (Cambodia and India), 1692, 293, 1143, 1152 (India), ST13, ST655, ST308 (Thailand), 132 (Australia) and 421 (Belgium). Sri Lankan *B. pseudomallei* population is intermediate between Southeast Asia and Oceania, possibly due to multiple introductions through anthropogenic sources, especially including travel and trade routes.

Keywords: multilocus sequence typing, *Burkholderia pseudomallei*, Sri Lanka, clinical isolates