Novel allelic profile of the clinical strains of burkholderia pseudomallei on multi locus sequence typing from India

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Background: Melioidosis is an emerging infectious disease caused by soil inhabitant gram negative bacterium Burkholderia pseudomallei. The disease which is endemic in Thailand and Northern Australia has shown an increasing trend in India in past few years. Epidemiological study of clinical isolates and their genetic relatedness to strains from neighboring south Asian countries remains undefined. The aim of the study was to analyze the molecular diversity of clinical B. pseudomallei isolates from southern India.

Methods & Materials: A total of 28 clinical strains of B. pseudomallei isolated from patients diagnosed with melioidosis at a tertiary care teaching hospital in southern India were included in the study. All isolates were subjected to Multi locus sequence typing (MLST) by amplification and sequencing of seven housekeeping genes. Sequences obtained from each locus were compared with the mlst database available on http://mlst.net. Further, sequence types (ST) were assigned for each isolate and their genetic relatedness using e-burst analysis to the STs of isolates reported from neighboring countries of south Asia.

Results: Of the 28 isolates tested, 26 isolates had novel allelic profiles and 2 isolates matched with previously reported allelic profiles. Among the 26 isolates with novel allelic profiles, 15(53.6%) isolates were assigned as a new ST 1368 and the other 10(38.4%) isolates were assigned STs 1369, 1370 (2), 1371(2), 1372, 1375(2), 1379 and 1380. One isolate had a novel allele in the gltB region. Two isolates which matched in their STs with previously reported isolates on the MLST database belonged to a single patient who presented initially with a systemic illness followed by a localized form of re-infection. Upon eburst analysis, we observed distinct molecular epidemiology of our isolates in comparison with STs reported from the neighboring countries of south Asia.

Conclusion: Predominance of a novel ST 1368 among our patients, which does not demonstrate genetic relatedness with other STs from neighboring countries of South Asia as well as from Australia was observed in the study. Further, our study findings underscore the high level of genetic diversity among clinical isolates of B. pseudomallei from coastal parts of south western India.

http://dx.doi.org/10.1016/j.ijid.2016.02.441