

Molecular epidemiology of *B.pseudomallei* in South Asia.

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Burkholderiapseudomallei, the etiological agent of melioidosis, is gaining recognition as an important cause for community-acquired bacteraemia and pneumonia worldwide. While the disease is known to be highly endemic in Thailand and Northern Australia, there is mounting evidence from the published literature suggesting the possibility of melioidosis being endemic in South Asian countries such as India, Sri Lanka and Bangladesh. Nevertheless, protean clinical manifestations and the lack of awareness among microbiologists and clinicians restrict our understanding regarding the real burden of this disease in the South Asian countries.

Molecular epidemiology of *B. pseudomallei* in South Asia remains far from well-elucidated. Among the various molecular epidemiological tools available for studying the genetic relatedness/diversity among bacterial species, multi locus sequence typing (MLST) is a reliable, reproducible and cost-effective tool. Till date, MLST results of 223 isolates reported from South Asia countries (comprising 109, 78, 33 and 4 isolates each from Sri Lanka, India, Bangladesh and Pakistan respectively) are available on the MLST database <https://pubmlst.org/bpseudomallei/>.

Genetic diversity, both at inter- and intra-national levels are high among the *B. pseudomallei* isolates in this region. STs 1137 and 1368 are the predominant genotypes reported from Sri Lanka and India respectively.

In our attempts to further elucidate the molecular epidemiology of melioidosis in India, we used MLST of clinical and environmental *B. pseudomallei* isolates obtained from distant geographical locations in southern part of the sub-continent and compared their genetic diversity with the isolates from rest of the world. Indian *B. pseudomallei* STs were genetically diverse from those of Australasian and South East Asian STs. There was no significant association between the isolated ST and the site of infection, clinical manifestations and/or the outcomes. Further, O-lipopolysaccharide diversity was studied among the Indian isolates (n=213) and LPS-B (71%) was the most predominant form observed. Among the virulence determinants, presence of Bim ABp was observed in more than 90% of the isolates.

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