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# Molecular epidemiology of *B. pseudomallei* in Sri Lanka

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*B. pseudomallei* isolates obtained from melioidosis cases in Sri Lanka from 2006 to 2016 were subjected to MLST. From 108 isolates 46 sequence types were obtained. Using this typing scheme the Sri Lanka melioidosis population is most closely related to isolates from South-Central Asia.

Drawing together soil type, rainfall and elevation data it was found that most cases are associated with haplic arisol soils and tend to occur at low altitudes in regions with moderate amounts of variation between the wet and dry season.

We previously described a new eBURST group of predominantly Sri Lankan isolates. While the cluster still exists the majority of the newer isolates cluster elsewhere in the eBURST tree. However, all but one appears in the section of the tree dominated by isolates from Australia. Maximum likelihood trees group the isolates into 7 clusters. Of these, groups 1 and 3 to 5 have fairly limited geographic distributions but groups 2 and 6, the most diverse, have broad geographic distributions.

In contrast to the possibility of particular STs being more common due to differential virulence we explored the idea that some STs may have been introduced in a more recent, non-geological timeframe. To explore this we placed the data in a historical context by colouring cases/isolates in the maximum likelihood tree according to the historical territory where they occurred. Examining three historical periods (Early Kingdoms, Transitional and Dutch colonial) we observe very little correlation with the Early Kingdoms period but increasing correlation with the latter two periods. We believe that group 6 isolates and possibly group 2 likely represent predominantly indigenous or regional strains of *B. pseudomallei* while isolates from the other groups may have originated from sea trade at regularly interspersed sea ports on the west and south coasts of Sri Lanka that were used at the time.

Addition of new clinical and environmental isolates and the transition to whole genome sequencing will allow this and other hypotheses to be fully tested

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