

Phylogenetic diversity of *Burkholderia pseudomallei* isolated from veterinary cases and the environments in Peninsular Malaysia

ABSTRACT

This study was designed to determine the genotype and the phylogeny of *Burkholderia pseudomallei* isolated from veterinary cases and from the animal environments in Peninsular Malaysia. The Malaysian *B. pseudomallei* population were then compared to those found elsewhere. A total of 113 isolates from veterinary cases (35) and the environment (56 from soil and 22 from water) were characterized using multilocus sequence typing (MLST). Two novel alleles, allele 97 and 69 of the gene locus *ace* and *lepA* respectively were recovered. Isolates were resolved into 12 distinct sequence types (STs) out of which five were novel, namely ST1130, ST1131, ST1338, ST1339 and ST1367. The isolates from veterinary cases co-clustered with those from the environment. *B. pseudomallei* isolates in this study were highly clonal and have descended from a common ancestor clonal complex (CC) 48 found in Southeast Asia. This study shows that veterinary case isolates are often caused by similar STs, with similar populations found in the direct animal environment and those previously reported to cause human infections in Malaysia and elsewhere. Isolates of *B. pseudomallei* from human infections have been given more attention, with a comparatively lower focus on isolates from animals and the farm environment. This study highlighted the genotype and phylogeny of *B. pseudomallei* isolated from animals and the environment and their relations to the isolates from human cases reported in Malaysia and elsewhere. Most STs reported in this study, from veterinary cases and animal environment are similar to those previously reported as causing human infections in Malaysia and elsewhere. Therefore, even though direct zoonosis is uncommon, monitoring melioidosis occurrences in animals can provide insights on the bacterial strains infecting humans.

Keyword: *Burkholderia pseudomallei*; Phylogeny; Veterinary; Environmental; Sequence types