

The relationship between bacterial sources and genotype to the antimicrobial resistance pattern of *Burkholderia pseudomallei*

ABSTRACT

Background: Melioidosis is a fatal emerging infectious disease of both man and animal caused by bacteria *Burkholderia pseudomallei*. Variations were suggested to have existed among the different *B. pseudomallei* clinical strains/genotypes which may implicate bacterial susceptibility and resistance toward antibiotics. **Aim:** This study was designed to determine whether the phenotypic antibiotic resistance pattern of *B. pseudomallei* is associated with the source of isolates and the genotype. **Materials and Methods:** A collection of 111 *B. pseudomallei* isolates from veterinary cases of melioidosis and the environments (soil and water) were obtained from stock cultures of previous studies and were phylogenetically characterized by multilocus sequence typing (ST). The susceptibility to five antibiotics, namely meropenem (MEM), imipenem, ceftazidime (CAZ), cotrimoxazole (SXT), and co-amoxiclav (AMC), recommended in both acute and eradication phases of melioidosis treatment were tested using minimum inhibitory concentration antibiotics susceptibility test. **Results:** Majority of isolates were susceptible to all antibiotics tested while few resistant strains to MEM, SXT, CAZ, and AMC were observed. Statistically significant association was found between resistance to MEM and the veterinary clinical isolates ($p < 0.05$). The likelihood of resistance to MEM was significantly higher among the novel ST 1130 isolates found in veterinary cases as compared to others. **Conclusion:** The resistance to MEM and SXT appeared to be higher among veterinary isolates, and the novel ST 1130 was more likely to be resistant to MEM as compared to others.

Keyword: Animals; Antimicrobial; *Burkholderia pseudomallei*; Environmental; Resistance; sequence types; Veterinary isolates.