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Paper Poster Session

More microbiology and infectious diseases

### Multilocus sequence typing of two strains of *Burkholderia pseudomallei* from melioidosis patients in the Philippines

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**Background:** Melioidosis, an infection caused by *Burkholderia pseudomallei* (Bp), is common in Thailand and Northern Australia. However, the prevalence in Philippines is still unknown. One of the widely used methods to establish *B. pseudomallei* endemicity is through a genotyping technique called multilocus sequence typing (MLST). MLST harnesses the discriminating power of multiple housekeeping genes or markers to differentiate bacterial isolates. Currently, there are no reports that attempts to do *B. pseudomallei* typing in the Philippines.

**Material/methods:** Two isolates from two melioidosis patients were studied. The first isolate came from psoas abscess of 74-year-old Filipino male. Second isolate came from blood of 57-year-old Filipino female presented as pneumonia. Both isolates underwent gram staining and culture cultivation on blood agar and MacConkey agar. Identification was made by VITEK 2, an automated instrument for identification of microorganism, and growth on Ashdown's Agar. They were subjected thru DNA extraction, *B. pseudomallei*-specific polymerase chain reaction (PCR) real-time assay, and MLST.

**Results:** Both isolates showed gram negative bacilli and grew white and light pink colonies on blood agar and MacConkey Agar respectively. *B. pseudomallei* were identified by VITEK 2 and growth of wrinkled purple colonies on Ashdown's agar. First isolate was susceptible to ceftazidime, levofloxacin, meropenem and trimethoprim-sulfamethoxazole while second isolate was only susceptible to levofloxacin. Extracted genomic DNA samples of the isolates were tested with real-time PCR assay and confirmed to be *B. pseudomallei*. Each isolate was assigned a name: UMASS strain (first isolate) and St. Luke's strain (second isolate). eBurst analysis was used to group all strains (ST) in the database by relatedness (Figure 1). MLST showed UMASS strain, identified as ST58, was clustered with Group 1 Bp ST. This group includes hundreds of STs with the founder located in Thailand. ST 58 is related to the founder ST and was clustered with other environmental and clinical strains from China and Thailand. St. Luke's strain was found to have an unreported ST, assigned as ST1366, and was clustered with Group 3 Bp STs. This group represents a potential source for domestic and exported melioidosis as well as animal and human cases in the islands of the Pacific and far South East Asia.

**Conclusions:** This MLST showed that UMASS strain is a part of an already established group of Bp ST. In contrast, St. Luke's strain is a new Bp ST that is a part of a rather interesting group of Bp ST, which has a relatively diverse host interaction and seems to share a common region of origin. Although this reports typing of only two Bp strains, the findings here suggest that more MLST should be done on more clinical samples to establish further the distribution and epidemiology of melioidosis in the Philippines.



