

## **‘Omics’ of *B. pseudomallei***

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*Burkholderiapseudomallei*, the cause of melioidosis, has been subjected to intense scrutiny across a range of ‘Omics’ systems from genome, to transcriptome, proteome and metabolomics analysis. The combination of two or more of these methods into a multi-layered approach is known as integrated systems biology. *B. pseudomallei* has been subject to extensive whole genome sequencing, its core genome extensively annotated and corresponding transcriptome explored. The rich pool of openly accessible *B. pseudomallei* genome data has clarified the molecular epidemiology, phylogenetic proximity of near-neighbour species and organisation of key operons.

Proteomic analysis with MALDI-TOF is now in use to assist laboratory identification of *B. pseudomallei* isolates from clinical samples, and has been used as an early warning in an outbreak investigation. The large genome of *B. pseudomallei* corresponds to an extensive repertoire of metabolic functions that enable bacterial adaptation to and survival in a wide range of environmental niches. The volatile organic compounds generated by active *B. pseudomallei* include sulphur compounds that explain the earthy, truffle-like odour of mature laboratory cultures. Single cell cytomic analysis of viable *B. pseudomallei* is at an early stage, but promises to set more mature genomic and other molecular analyses in a cellular context. The combination of these emerging analytical methods is expected to improve our understanding of disease pathogenesis, and open up new route to diagnosis, treatment and prevention.

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