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Transcriptional Adaptation of *Burkholderia pseudomallei* Within Macrophage Cells

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Burkholderia pseudomallei is the causative agent of melioidosis, a disease endemic to Southeast Asia and Northern Australia. It has been established that *B. pseudomallei* maintains the ability to exist as a facultative intracellular pathogen within phagocytic and non-phagocytic cells. Understanding the interaction between the bacterium and host macrophage cells is crucial to appreciate the strategies used by this bacterium to survive and progress onto disease manifestation. In this study, we applied high density bacterial specific microarrays to unravel the pathogen's expression profile over a 6 hour period of infection in human monocyte-like U937 cells. Microarray analysis of intracellular bacteria isolated from infected macrophage cells identified approximately 22.4% *B. pseudomallei* genes as differentially regulated throughout the 6-hour infection period. Most of these genes were down-regulated and involved in metabolism, cell envelope and motility, replication, transport and regulatory functions. Similar patterns of regulation were previously observed in *Salmonella sp.*, *Shigella sp.* and *Escherichia coli*, indicating a common theme during bacterial infection of human cells. *B. pseudomallei* genes that were consistently up-regulated included the tss-5 type VI secretion system as well as genes involved in anaerobic metabolism and ABC transport systems. The up-regulation of the type VI secretion system suggests a possible role in virulence. We conclude that *B. pseudomallei* is able to ensure survival in host cells by adopting strategies that allow adaptation to hostile environments, avoidance of immune responses and regulation of novel virulent determinants.

Keywords: *Burkholderia pseudomallei*, Macrophage, Microarray, Strategies of adaptation