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Correlation of Variable Virulence Genes with Variable Clinical Presentations of *Burkholderia pseudomallei*: A Way Forward

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Raj and colleagues[1] had shown greater genetic diversity among clinical isolates of *Burkholderia pseudomallei* and $BimA_{Bm}$ were significantly associated with sepsis and mortality. Their study had also given a clue about the divergence of Indian variants of *B. Pseudomallei's* behavior and virulence.

Their study showed the odds of sepsis associated with $BimA_{Bm}$ were 6.46-fold higher than those with $BimA_{Bp}$ but with a wide confidence interval of 1 to 32. Therefore, this does not provide a precise representation of the mean study population. Many other factors other than the known risk factors, like intrahost adaptive changes, cause intracellular replication, and cell-to-cell fusion, or mutation capabilities in a patient with an infection may modify the clinical manifestation of melioidosis.

Most of the descriptions of melioidosis cases in the medical literature are full of acute severe and septicemic cases of melioidosis. However, occasionally nonsevere cases of asymptomatic latent melioidosis are detected. From a series of 17 consecutive respiratory cases so far, we have come across 3 who had chronic courses with nonsevere presentation who were incidentally detected and came with respiratory symptoms. These cases support the possibility of a correlation between indolent cases and variable virulence genes shown by variable clinical presentations among isolates from India. All the cases are hospital-based, highly selective cases. Clinically nonsevere cases must be underreported. Therefore, population-based data can be different from hospital statistics.

The presence of various virulence factors plays a pivotal role in each stage of intracellular infection, enabling the infection to advance swiftly.[2] Once *B. pseudomallei* invades or gets engulfed by the host cells, it endeavors to evade the host cell's killing mechanisms within the phagosome and makes use of the type III secretion system to facilitate its escape. Additionally, numerous unknown virulence factors modify the host cell, while the bacteria endure a change in molecular metabolism, resulting in a remarkable increase in intracellular replication. *B. pseudomallei* uses the polymerization of host cell actin, forming "actin tails" that drive the bacterium toward host cell membranes. Through the type VI secretion system, this process of fusion of host cells into giant cells facilitates efficient cell-to-cell propagation.[3]

The speciation has become essential to determine virulence, a better understanding of the epidemiology, and pathogenicity. Studying the variable genomic traits of *Burkholderia* offers a valuable point of reference for monitoring antimicrobial resistance and virulence, which ultimately may lead to a decrease in the prevalence of pathogenic strains through improved epidemiological understanding.

The bacterial transcriptome analysis revealed the presence of virulence factors and regulatory proteins associated with the T6SS during infection. Utilizing a library of transposon mutant and isogenic mutants demonstrated deletion of the bicA gene of *B. pseudomallei*, which encodes a putative T3SS/T6SS regulator, significantly impacts the bacteria's survival and virulence in acute and chronic gastrointestinal infections.[4]

The cluster 1 type VI secretion gene, BPSS1504, is known to enhance the intracellular virulence of *B. pseudomallei*.[5] Our understanding of the virulence due to the regulation of such molecules is of utmost importance in comprehending how this adaptable pathogen modulates its lifestyle.

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Conflict of Interest
None declared.

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