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Pathogen interactions in *B.pseudomallei* infection

J Wiersinga

The genome of *B. pseudomallei* is composed of two chromosomes of which the largest part represents the *B. pseudomallei* core genome, whereas the remaining accessory genome has been associated with bacterial virulence. Virulence factors, most notably quorum sensing, type III secretion system, lipopolysaccharide and other surface polysaccharides, flagella and various factors essential for the intracellular life cycle of *B. pseudomallei*, have been further characterized.

The neutrophils play a critical in host defense, which is initiated by the Toll-like receptors. The proinflammatory immune response – including the activation of coagulation – and its regulation have been further dissected.

In summary, severe melioidosis can probably be seen as the clinical manifestation of a pathogen recognition receptor mediated dysregulation of the immune response to invading *B. pseudomallei*. *B. pseudomallei* employs numerous tactics to evade the immune response. Studies on host–pathogen interactions in melioidosis have identified a whole range of potential new treatment targets.

Division of Infectious Diseases, Academic Medical Center, University of Amsterdam, The Netherlands

Address for correspondence: Prof JoostWiersinga, Division of Infectious Diseases, Academic Medical Center, University of Amsterdam, The Netherlands, +31(0)641375729 Email: w.j.wiersinga@amc.uva.nl
https://orcid.org/ 0000-0003-2277-1343