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## Use of Comparative Genomics To Resolve an Unusual Case of Aminoglycoside Susceptibility in the Melioidosis Pathogen *Burkholderia pseudomallei* in Bangladesh

Mirjam Kaestli, Saika Farook, Md. Shariful Alam Jilani, Shaheda Anwar, Tanvir Ahmed Siddiqui, Mark Mayo, Yuwana Podin, Jessica R. Webb, David A. B. Dance, and Bart J. Currie

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### ABSTRACT.

Melioidosis is an emerging tropical infectious disease with a rising global burden caused by the environmental bacterium *Burkholderia pseudomallei*. It is endemic in Southeast and South Asia, including Bangladesh. A rare aminoglycoside-susceptible *B. pseudomallei* isolate (Y2019) has recently been reported from a melioidosis patient in Dhaka, Bangladesh. To understand the geographical origins of Y2019, we subjected it and 10 other isolates from Bangladesh to whole-genome sequencing. In a phylogenetic tree with a global set of *B. pseudomallei* genomes, most Bangladeshi genomes clustered tightly within the Asian clade. In contrast, Y2019 was closely related to ST881 isolates from Sarawak, Malaysian Borneo, a gentamicin-sensitive sequence type, suggesting infection in Borneo. Y2019 also contained the same gentamicin sensitivity conferring nonsynonymous mutation in the drug efflux pump encoding the *amrB* gene. In the absence of a full travel history, whole-genome sequencing and bioinformatics tools have revealed the likely origin of this rare isolate.

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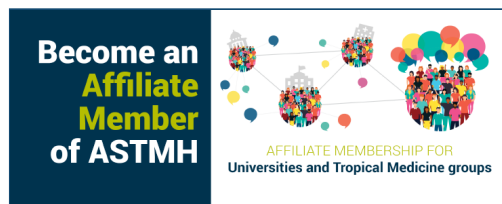
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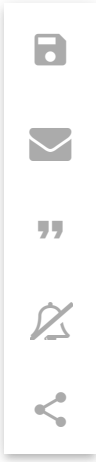
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 241 18th Street South, Suite 501  
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[journal@ajtmh.org](mailto:journal@ajtmh.org)

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