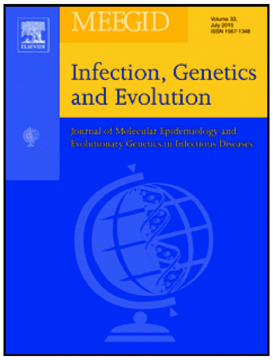

Genes under positive selection in the core genome of pathogenic Bacillus cereus group members

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Genes under positive selection in the core genome of pathogenic *Bacillus cereus* group members

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Abstract

In this comparative genomics study our aim was to unravel genes under positive selection in the core genome of the *Bacillus cereus* group. Indeed, the members of this group share close genetic relationships but display a rather large phenotypic and ecological diversity, providing a unique opportunity for studying how genomic changes reflect ecological adaptation during the divergence of a bacterial group. For this purpose, we screened ten completely sequenced genomes of four pathogenic *Bacillus* species, finding that 254 out of 3,093 genes have codon sites with d_N/d_S (ω) values above one.