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Improving Bacillus Altitudinis B-388 Genome Scaffolding Using Mate-Pair Next-Generation Sequencing

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Abstract

© 2016, Springer Science+Business Media New York.Bacillus species, generally regarded as soil microorganisms, are present in human gastrointestinal tract (GIT) in quantities, which cannot be explained by their entrance with food only. They are capable of growing in GIT and interacting with intestinal microbiota and host organism by excretion of enzymes and low-molecular weight compounds, which exert digestion-facilitating, antagonistic, immunomodulating, antiviral, anticancer properties or mediate cell communication. For better understanding of its probiotic potential, we have sequenced genome of Bacillus altitudinis B-388 using mate-pair technology. It allowed us to improve quality of the genome sequence. The number of contigs decreased from 59 to 8. N50 contig length increased by four times. The number of identified genes raised from 3730 to 3774 (3645 proteins and 73 RNAs) with the reduction of frameshifted genes. The calculated size of B. altitudinis B-388 genome is 3,743,699 bp, with a G + C content of 41.17 mol%. Additional incomplete prophage sequence in genome of B. altitudinis B-388 was revealed. It was found that cryptic plasmid encodes SoxR, an oxidative stress response regulator. To date, the reported sequence is the most thorough presentation of B. altitudinis genome among four whole-genome sequences of this species deposited in GenBank.

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Keywords

Antagonism, Bacillus altitudinis, Intestinal microbiota, Mate-pair next-generation sequencing, UV resistance

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