In silico protein prediction of the 16S ribosomal RNA gene from novel rhizobacterium Bacillus cereus UPMLH24

ABSTRACT

In this study, computational methods were used to predict information hidden in the small subunit 16S rRNA gene from newly isolated plant growth-promoting rhizobacteria B. cereus strain UPMLH24. In the present study, the computational methods employed revealed that the small subunit 16S rRNA gene sequence from B. cereus strain UPMLH24 contained a number of small open reading frames that encoded several functional proteins. Computational predictions classified seven phyla of organisms associated with small open reading frames of novel B. cereus strain UPMLH24. The data generated from computational predictions in the present study could form the basis for further research to advance new hypotheses in the microbiology of rhizobacteria.