

## Phylogenetic distribution of extracellular guanyl-preferring ribonucleases renews taxonomic status of two bacillus strains

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### Abstract

© 2016 Applied Microbiology, Molecular and Cellular Biosciences Research Foundation. The potential of microbial ribonucleases as promising antitumor and antiviral agents, determines today's directions of their study. One direction is connected with biodiversity of RNases. We have analyzed completed and drafted *Bacillus* genomes deposited in GenBank for the presence of coding regions similar to the gene of an extracellular guanyl-preferring RNase of *Bacillus amyloliquefaciens* (barnase). Orthologues of the barnase gene were detected in 9 species out of 83. All of these belong to "B. subtilis" group within the genus. *B. subtilis* itself, as well as some other species within this group, lack such types of RNases. RNases similar to barnase were also found in species of "B. cereus" group as a part of plasmid-encoded S-layer toxins. It was also found that taxonomic states of culture collection strains, which were initially described based on a limited set of phenotypic characteristics, can be misleading and need to be confirmed. Using several approaches such as matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS), sequencing of genes for 16S ribosomal RNA and RNA polymerase subunit beta followed by reconstruction of phylogenetic trees, we have re-identified two RNase-secreting *Bacillus* strains: *B. thuringiensis* B-388 which should be assigned as *B. altitudinis* B388 and *B. intermedius* 7P which should be renamed as *B. pumilus* 7P. Therefore, small secreted guanyl-preferring RNases are the feature of "B. subtilis" group only, which is characterized by distinctive lifestyle and adaptation strategies to environment.

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### Keywords

16S rRNA gene, *Bacillus altitudinis*, *Bacillus pumilus*, Barnase, Extracellular ribonuclease, Phylogeny, RpoB, Taxonomy revision