

TITLE: PHYSIOLOGICAL AND MOLECULAR STUDIES OF *RUMMELIIBACILLUS STABEKISII* PP9 ISOLATED FROM ANTARCTIC SOIL

AUTHORS: LANDIM, C. F. A. L.; VOLLÚ, R. E.; J. DIOGO.; SELDIN, L

INSTITUTION: UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, RIO DE JANEIRO, RJ (AV. CARLOS CHAGAS FILHO, 373, BLOCO I, SALA I1-060)

ABSTRACT

The genus *Rummeliibacillus* is constituted of aerobic or facultative, Gram-positive, rod-shaped, round-spore-forming bacteria. There are three species already described to belong to this genus: *Rummeliibacillus stabekisii*, *R. pycnus* and *R. suwonensis*. However, very little is known about the general metabolism and the biotechnological potential of *Rummeliibacillus*. In this study, we characterized the whole-genome of *Rummeliibacillus stabekisii* strain PP9 available in literature (GOLD ID: Gp0150242) to gain a better understanding of this poorly studied species. This strain has previously been isolated from an Antarctic soil. The PP9 genome was re-annotated using RAST (Rapid Annotation using Subsystem Technology), and PHAST (PHAge Search Tool) was used to identify and annotate prophage sequences within PP9 genome. All Protein *coding* sequences (CDS) were re-classified according to the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (NC-IUBMB). Based on RAST annotation, 3078 CDS were obtained and grouped in 11 sub-categories: metabolism (995), cell wall and capsule (101), stress response (95), transport (83), motility and chemotaxis (80), virulence and defense (58), cell division, cell cycle and respiration (51), transposable elements (46), regulation and cell signaling (44) and dormancy and sporulation (40). Genome analyses revealed the PP9 potential for arsenic reduction (*ars* operon: genes *arsR*, *arsB* and *arsC*) and for phenylacetic acid degradation (*paa* genes). PHAST results detected the presence of four sequences related to unclassified phages in PP9 genome. From the 1018 CDS related to enzymatic activity, 232 were classified as hydrolases (including lipase, protease, amidase, amylase, pullulanase, carboxylesterase and collagenase). However, enzymatic assays in laboratory conditions showed very low activity of protease, lipase, amidase, amylase, and cellulase. Further experiments are necessary to better characterize the enzymatic activity in *R. stabekisii* strain PP9.

Keyword: *Rummeliibacillus*, genome, biotechnology, hydrolase

Development Agency: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior

