

TITLE: MOLECULAR CHARACTERIZATION OF THE ANTIMICROBIAL SUBSTANCE PRODUCERS *BACILLUS SAFENSIS* T052-76 AND *BACILLUS VELEZENSIS* T149-19 ISOLATED FROM SWEET POTATO (*IPOMOEA BATATAS*)

AUTHORS: MATEUS, J.R.¹; DAL'RIO, I.¹; MOTA, F.F.²; DIAS, B.C.¹; SELDIN, L.¹

INSTITUTIONS: ¹UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, INSTITUTO DE MICROBIOLOGIA PAULO DE GÓES, RIO DE JANEIRO, RJ (AVENIDA CARLOS CHAGAS FILHO, 373, CIDADE UNIVERSITÁRIA, CEP 21941-902, RIO DE JANEIRO – RJ, BRAZIL);

² FUNDAÇÃO OSWALDO CRUZ, INSTITUTO OSWALDO CRUZ (IOC), RIO DE JANEIRO, RJ (AVENIDA BRASIL 4365, MANGUINHOS, CEP 21045900, RIO DE JANEIRO – RJ, BRASIL)

ABSTRACT:

Sweet potato plants (*Ipomoea batatas* L.) present a complex root system composed by fibrous roots - specialized in nutrient absorption - and tuberous roots - specialized in nutrient storage. The tuberous roots are used for human consumption, for animal feed and for the development of industrial products. In Brazil, sweet potato is considered a subsistence crop, with great social importance for family-based agriculture. However, the crop is usually affected by the sweet potato foot-rot disease, which is caused by the phytopathogen *Plenodomus destruens*, resulting in the total loss of crop production. In a previous study of our group, two strains (*B. safensis* T052-76 and *B. velezensis* T149-19) were able to inhibit the fungus *P. destruens* *in vitro* and to remain in the rhizosphere of sweet potato during 180 days of growth protecting the plants in the field. Based on these promising results, we performed the complete sequencing of the genome of both *Bacillus* strains. We aimed not only to annotate the CDS using RAST software and identify the antimicrobial substance (AMS) coding regions, using antiSMASH, in genomes but also to compare the gene sequences of the metabolic pathways of the AMS and determine the synteny and genomic context among other close related *Bacillus* genomes from GenBank. Preliminary results showed that genome of the strain *B. velezensis* T149-19 presented 4,140 CDS while *B. safensis* T052-76 3,888 CDS. Their GC contents were 46.5% and 41.7%, respectively. Various potential genes coding for antimicrobial substances were observed in their genomes. Genome mining of *B. velezensis* T149-19 revealed 19 gene clusters hypothetically related to the synthesis of secondary metabolites, such: mycosubtilin, bacilaene, macrolactin, bacilibactin and bacilysin, all those with 100% similarity with clusters for AMS already established in literature. *B. safensis* T052-76 genome showed 10 clusters hypothetically related to secondary metabolites, but some of them showed low similarities to previously described genes. Two regions showed 85% similarity with bacilysin and sporulation killing factor skfA. We believe that genomic analysis of T149-19 and T052-76 strains could facilitate exploitation of their genetic resources in order to produce secondary metabolites for agricultural biotechnology and biomedical purposes.

Keywords: *Bacillus velezensis*, *Bacillus safensis*, sweet potato, *Plenodomus destruens*, antimicrobial substances

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