**TITLE:** BACTERIAL COMMUNITY ASSOCIATED WITH SWEET POTATO PLANTS (*IPOMOEA BATATAS*) SLIGHTLY RESPOND TO THE INTRODUCTION OF ANTIMICROBIAL SUBSTANCE-PRODUCING *BACILLUS* STRAINS IN A GREENHOUSE EXPERIMENT

**AUTHORS:** DE LACERDA, J.R.M.<sup>1</sup>; MARQUES, J.M.<sup>2</sup>; LOPES, I.D.N.<sup>1</sup>; VOLLÚ, R.E.<sup>1</sup>; COELHO, M.R.R.<sup>3</sup>; GOULART, F.R.V.<sup>1</sup>; ALVIANO, C.S.<sup>1</sup>; SELDIN, L.<sup>1</sup>

**INSTITUTION:** 1. UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, RIO DE JANEIRO - RJ (CENTRO DE CIÊNCIAS DA SAÚDE, AVENIDA CARLOS CHAGAS FILHO, 373, CIDADE UNIVERSITÁRIA, ILHA DO FUNDÃO, CEP 21941-902) - BRASIL; 2. UNIVERSIDADE FEDERAL DO PARÁ, BELÉM – PA (INSTITUTO DE CIÊNCIAS BIOLÓGICAS, RUA AUGUSTO CORRÊA, 01, GUAMÁ, CEP 66075-970) - BRASIL; 3. EMPRESA BRASILEIRA DE PESQUISA AGROPECUÁRIA - EMBRAPA AGROBIOLOGIA, SEROPÉDICA - RJ (RODOVIA BR 456, KM 7, CEP 23890-000) - BRASIL.

ABSTRACT: Sweet potato (Ipomoea batatas (L.) Lam.) is a subsistence crop with great social importance in Brazil. In the Northeast region of the country, this crop is often committed by sweet potato foot-rot disease, which is caused by the phytopathogen *Plenodomus destruens*, resulting in great economy losses. In a previous study, two endophytic strains (T149-19 and T052-76) identified as Bacillus sp. and able to produce antimicrobial substances (SAMs) against Plenodomus destruens were isolated from sweet potato roots. However, their ability to persist *in situ* in close contact to sweet potato roots has never been tested so far. Therefore, in this study a 180 days-greenhouse experiment was carried out using the two strains and sweet potato seedlings. The effect of the introduction in separate of the two strains on the root-associated microbial community (rhizosphere; rhizosphere/rhizoplane and endosphere) and the persistence of the bacterial inoculants were evaluated using molecular approaches (Polymerase Chain Reaction-Denaturing Gradient Gel Electrophoresis - PCR-DGGE) based on the rrs gene (16S rRNA coding gene for bacteria) and the ITS region (internal transcribed spacer for fungi) and statistical analysis (Permutation test, P<0.05). A band corresponding to each of the inoculated bacteria was observed in the different DGGE until the end of the experiment. DGGE fingerprints showed that strain T052-76 influenced the bacterial community present in the rhizosphere and rhizosphere/rhizoplane samples up to 90 days of experiment. Statistical analysis showed a significant difference (41% of dissimilarity) between the inoculated samples and the controls (without T052-76 inoculum). Oppositely, no significant statistical difference (1% of dissimilarity) was observed when strain T149-19 was used. When the fungal communities were considered, they varied throughout the experiment period but no significant influence was observed with the inoculation of either T149-19 or T052-76. The results presented here demonstrate the stability of both Bacillus strains in the sweet potato rhizosphere and also their low influence in the microbial community associated with the plant. These characteristics make Bacillus sp. T149-19 and T052-76 of great interest for agriculture.

Keywords: Antimicrobial substance, Bacillus sp., Plenodomus destruens, Rhizosphere, Sweet potato

Development Agency: CAPES, CNPq, FAPERJ