GENETIC DIVERSITY OF RHIZOBIA ASSOCIATED WITH PEANUT AND COMMON BEAN FROM BRAZILIAN AGRICULTURAL FIELDS

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Abstract:

Peanut (Arachis hipogaea L.) and common bean (Phaseolus vulgaris L) are important legumes grown in tropical, subtropical and temperate regions. These crops can obtain the nitrogen through the symbiosis with diazotrophic bacteria belonging mainly to the Bradyrhizobium and Rhizobium genera, respectively. The objective of our study was to investigate the diversity of the symbionts of peanut and common bean isolated from field experiments, without history of inoculation with rhizobia. The isolates received proper identifications and are deposited at the "Coleção de Microrganismos de Interesse do Agronegócio do Laboratório de Microbiologia do Solo" at IAPAR. For the diversity study, 30 strains trapped by peanut and 44 by common bean were selected for genetic characterization. Three strains recommended for the commercial production of inoculants for the bean crop (SEMIA 4077, SEMIA, 4080 and SEMIA 4088) and one for the peanut crop (SEMIA 6144) were included as comparison. For the genetic characterization, genomic DNA was extracted and subject to BOX-PCR (Polymerase Chain Reaction) with BOX-A1R primer. The genetic similarity between the strains was determined by the PCR fingerprints cluster analysis, analyzed with the Bionumerics 6.0 software, using the Jaccard coefficient and the UPGMA (Unweighted Pair-Group Method with Arithmetic mean) algorithm. To determine the diversity of all 78 strains symbionts of peanut and common bean, the program Past (PAlaeontological STatistics) was used, considering the cluster analysis with 70% of similarity. Although these strains have been isolated from only two host plants all strains were distributed in 40 groups, with a high Shannon (H') index, of 3.5, and only seven strains from peanut were grouped with 100% of genetic similarity. The Shannon (H') indices from cluster analyses of two rhizobial populations were of 2.94 with the strains isolated from peanut and of 2.81 with the strains from common bean, with no statistical difference (t-test, p=0.05) between the populations. Therefore, this study shows the importance of the culture collections for the knowledge and maintenance of bacteria representing soil microbial diversity.

Key words: Shannon Diversity Index, BOX-PCR, Biological Nitrogen Fixation, Symbiosis