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Biodiversity

BD P01. CULTURABLE ORGANOTROFIC BACTERIA FROM HIGH-ALTITUDE ANDEAN LAKES

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The Andean Altiplano is a sedimentary volcanic plateau at about 4.000 m. Several lakes in the Altiplano are formed over evaporitic endorheic basins. These aquatic ecosystems present extreme conditions (high solar irradiance, arid conditions, low nutrient concentrations, heavy metals, large temperature fluctuations) and are a source of microorganisms with potential biotechnological applications.

Lately, many studies have reported that the assessment of bacterial diversity by cultivation-independent methods is the most appropriate for studying diversity, owing to the existence of a host of unculturable. However, cultivation remains the preferred method for the acquisition of an accurate picture of the physiology and complex ecological interactions in which microorganisms engage.

In this study, we attempted to determine the culturable bacterial diversity and extend the culture collections of Andean lakes in Argentina. Bacteria were isolated from Socompa and Diamante lakes in the Argentinean Puna. They were grown in different broth: LB, MGM, PY and 6WS. The pure and cellular morphology were determined by phase contrast microscopy and Gram stain. Bacterial diversity among the isolated was evaluated by PCR-amplified 16S rDNAs followed by phylogenetic analysis of 16S rDNA sequences. Twenty six strains were found. A neighbor-joining tree of the partial 16S rDNA sequences resulted in the division of the 18 strains of Socompa into two major groups, 14 strains of (γ)Proteobacteria (77.7%) and 4 strains of Firmicutes (22.3%). Eigth strains of Diamante resulted in the division into 6 strains of Firmicutes (75%) and 2 strains Actinobacteria (25%). The (γ)Proteobacteria was group more diversity, including several genus: Salinivibrio, Shewanella, Pseudomona, Halomona, Aeromona, Idiomarina and Chromohalobacter. Additionally, seven new species candidates were found in Socompa, based on similarities of the 16S rDNA sequences to those of previously reported species.

BD P02. GENOTYPIC DIFFERENCES BETWEEN PEANUT RHIZOBIA POPULATIONS OBTAINED FROM DIFFERENT CROPPING AREAS OF CÓRDOBA PROVINCE IN ARGENTINA

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Peanut (Arachis hypogaea) is one of the most important crop of Córdoba province in central region of Argentina. Peanut establish a symbiotic relationship with rhizobial strains which constitute stable populations in soils of typical peanut cropping area. Degree of genetic diversity of peanut nodulating populations has not been fully addressed. Aim of present work was to carry out a genetic characterization of rhizobia isolated from peanut nodules growing on soils with previous peanut cropping history (Río Cuarto and Cabrera) and soils with no previous peanut cropping history (La Aguada and Chaján) and compare them. Ten different 16S rRNA RFLP genotypes were obtained as result of combination of restriction patterns obtained with four endonucleases. Cluster analysis of genotypes showed at 80 % similarity the formation of two main groups. Group Ib clustered majority of strains from unrelated origins Río Cuarto and Chaján, whereas group IIc clustered majority of strains from unrelated origins Cabrera and La Aguada, suggesting genetic relationship between peanut nodulating populations isolated from different peanut cropping system. Diversity indexes showed that populations obtained from soils with strong previous history were less diverse compared to soils with no previous history, suggesting that the presence of the legume selects particular taxa of rhizobia. Sequence analysis of 16S rRNA gene demonstrated the identity of isolates with strains of Bradyrhizobium sp., Bradyrhizobium japonicum or Bradyrhizobium elkanii genus and the phylogenetic association between rhizobia populations from sites with different peanut cropping history. Higher polymorphism and diversity was reached in the analysis of ERIC-PCR. Peanut strains clustered at very low levels of similarity (55 %). Populations of different origins, such as Cabrera and La Aguada, clustered together although at elevated genetic distance. ERIC results indicate the presence of very different rhizobia populations in soils of Córdoba province. In spite of the presence of certain linkage between non related rhizobial populations according their origin, global analysis of genotypic properties showed that peanut nodulating populations have high diversity independently of their geographical origin and that the presence of a legume crop affects soil biology through influencing rhizobia nodulating populations. We speculate that knowledge of such properties can contribute to improve the global development of peanut crop.