Assessment of genetic biodiversity of indigenous *Rhizobium* species using ERIC-PCR and REP-PCR techniques

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Ecophysiological tools and approaches will provide a conceptual framework for characterizing the plant-rhizobia-environment status using selected plant species and genotypes in each reference production area. The mechanisms and underlying genes that influence the host-rhizobia-environment interaction are being rapidly elucidated in model legume species.

Soil bacteria of the genus *Rhizobium*, have the capacity to infect the plants roots, induce the root nodule development and colonize nodule cortical cells. Within these nodules, the bacteria fix atmospheric nitrogen providing the nitrogen requirements for plant development.

We have studied the diversity in *Rhizobium* strains isolated from nodules of *Lotus corniculatus*, that grown in both contaminated and uncontaminated soils, with the aim to determine the divergence between strains.

The molecular polymorphism analysis is useful to evaluate the relation between soil contamination levels and the presence of heavy-metal resistance genes *Rhizobium* isolates.

The strains diversity was assessed using DNA primers corresponding to Repetitive Extragenic Palindromic – PCR (REP-PCR) and primers for Enterobacterial Repetitive Intergenic Consensus- PCR (ERIC-PCR).

Cluster analysis revealed that the pressure of abiotic factors such as contamination by heavy-metals, in rhizosphere, could be the cause of the reduction of the Rhizobia diversity isolated from the nodules of *Lotus corniculatus.*