

**Title: GENETIC DIVERSITY OF BACTERIA ASSOCIATED WITH DEGRADED PASTURES**

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**Abstract:**

Livestock production in Brazil is mostly dependent on pastures, being most used grasses due to its adaptability to various soil types. For instance, *Brachiaria* spp., have highlighted, due to their resistance to various types of biotic and abiotic stress. The inadequately managed used in most pastures has caused high rates of degradation, compromising the soil and its microorganisms. Knowing such a community is useful to explore the mechanisms that involving the bacteria-plant interactions. Among the microorganisms that allow better plant development, in those conditions, diazotrophic bacteria gain evidence. In this context, this paper has as objective to evaluate the genetic diversity of bacteria associated with *Brachiaria decumbens*, grown in soils with different times of fertilization and degrees of degradation. Were analyzed 60 bacterial isolates of pastures with different periods without nitrogen fertilization and different degradation stages. These belonging to the niches, rhizosphere and endophytes root (20 isolated by grassland, 10 of each niche). The pastures were classified as degraded (with 30 years without fertilization); in intermediate degradation (with six years without fertilizer) and not degraded; (with three years without fertilization). Genetic diversity was evaluated by the BOX-PCR technique, for visualization of the profiles bands by agarose gel electrophoresis 1.2%. Band profiles observed were transformed into binary spreadsheet to obtain a dendrogram of similarity, calculated by the Jaccard coefficient, in the PAST® software. The generated dendrogram allowed the visualization of similarity between the samples analyzed. The isolates belonging to the rhizosphere, of degraded pastures, has a higher genetic similarity when compared with the rhizosphere isolates from others treatments. Endophytic bacteria, obtained high degree of variability, regardless of the level of degradation on the pastures, although they form some groups according to the niche and of the time that the pastures were fertilized, was observed two isolates with 100% similarity, belonging to the pasture with intermediate degradation. The obtained results, demonstrate that, independent of the degradation level and colonization niche, high dissimilarity was observed among isolates. The greater genetic diversity can provide improvements in the development of plants that constitute these pastures.

**Keywords:** degradation of pastures, genetic variability, grass *Brachiaria*, promotion of plant growth.

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