

YEAST DIVERSITY IN SOIL UNDER DIFFERENT TYPES OF VEGETATION REVEALED IN DGGE

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Abstract:

Yeast are unicellular fungi that participate in important ecological processes, such as the cycle of nutrients in the soil. The diversity and the role of communities of yeast present in soils is still little explored because of difficulties of cultivation, since the culture media used do not cover the nutritional needs of all species, thus underestimating the diversity of this group. The advent of molecular techniques such as PCR-DGGE has provided advances in microbial diversity studies as they allow the detection of viable but not yet culturable species that can occur in soils, generating information on the diversity of yeasts that grow in soils and the answer these front communities to environmental changes, such as the type of vegetation present. In this context, this study aimed to evaluate the diversity of yeasts in soil samples under different types of vegetation by PCR-DGGE. 16 soil samples were used, with 4 samples for each of the types of vegetation, as follows: Capim, Canga, Eucalipto and Mata. Genomic DNA was extracted from all samples with commercial kit and amplified by nested PCR with primer to the 26S ribosomal RNA gene, generating a 250bp fragment which was separated in polyacrylamide gel 8% with denaturing gradient of 30 to 60% at 70V for 16 hours. The gel was revealed and the captured image was analyzed by BioNumerics. The dominant bands in the gel were excised and sequenced subsequently, compared with sequences from GenBank and the phylogenetic relationships obtained by MEGA 6 program. The pattern of diversity of communities was different for each area evaluated, and the areas with the greatest diversity according to the band's profile generated were Mata and Eucalipto, and lower diversity for Capim and Canga. The standard yeast community has been revealed by the formation of two clusters, one with Mata and Eucalipto, and other with Capim and Canga, probably due to greater similarity between vegetation this areas. Sequencing of the dominant bands in the areas of Mata, Eucalipto and Canga reveal the presence of *Cryptococcus podzolicus* (7 sequences), a type of yeast commonly isolated from soil, and some species of unculturable fungi (4 sequences).

Keywords: *Cryptococcus podzolicus*, DGGE, Independent cultivation, sequencing, 26S rDNA.

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