

TITLE: FUNGI COMMUNITY PROFILE IN COFFEE FRUITS

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ABSTRACT:

The presence of microorganisms in coffee fruits has been studied due to the fermentation process they are involved to. The metabolites produced during the post-harvest period can diffuse in the grains and influence the final quality of the beverage. Environmental factors, such as temperature and altitude can influence this process, as well as the local microbial community. We evaluated the fungi community profile present in *Coffea arabica* L. fruits, collected in eight farms located in different altitude (735 to 1,078m height). In each farm, samples were collected in three sites. At each site three coffee plants were selected and ten fruits per plant were collected, 30 fruits forming a composite sample. The total DNA was extracted using the Nucleo Spin Soil Kit, according to the manufacturer's recommendations. Nested PCR-DGGE technique was used. For that, the first PCR reaction was performed with the NS1 and EF3 primers and then a Nested PCR reaction with the FF390 and FR1-GC primers. From the product of the second reaction, 20 µL was applied on an 8% (w/v) acrylamide gel with a denaturing gradient from 35% to 55% (where 100% corresponds to 7 mol L⁻¹ urea and 40% formamide) to obtain the community profile. The gel was subjected to vertical electrophoresis at 60 V for 12 h at 60 °C, then stained for 40 min with *Sybr Gold* (1x) (Molecular Probes, Leiden, The Netherlands); the gel was then photographed under UV light on a Molecular Imaging System (Loccus Biotechnologic L-Pix Chemi). The DGGE profiles were analysed and compared using BioNumerics software (Version 5.1, Applied Maths NV). Dendrogram showed two groups highly similar within them (84% and 88%). The first group (farms DB, WT and FS) involves those located in altitude ranging from 907 to 1,052 m and the second (farms FA, LP, FC and ST), from 735 to 1,078 m. One sample LD (in 969 m height) was distinct from the others (62% of similarity). The altitude factor exhibited no influence on the species richness and on the fungal community profile, suggesting that other factors might influence the local microbial community, such as soil, moisture, temperature, coffee variety and soil microbial community.

KEYWORDS: microorganism, DGGE, species richness, *Coffea arabica*

DEVELOPMENT AGENCY: FAPES, FAPEMIG, CAPES and CNPq.