# Analysis of the taxonomic profile of the bacteriome in *Coffea canephora* fruits

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Plants are holobiont organisms that maintain a constant symbiotic relationship with various microorganisms. These, in turn, plays a fundamental role in plant development as well as in plant survival. In coffee, studies have been demonstrating that certain species of bacteria, in addition to performing vital functions for the growth and development of the crop, influence the quality of the beans and may be responsible for changing the sensory profile of coffee. However, information regarding the natural diversity of bacteria inhabiting conilon (*Coffea canephora*) coffee cherries is limited. Therefore, this study aimed to characterize the bacteriome of *C. canephora* fruits. Three composite samples of coffee cherries were collected in the field and subjected to maceration in liquid nitrogen for DNA extraction. To assess the bacteriome profile, polymerase chain reactions (PCR) were conducted to amplify the V3-V4 regions of the 16S rDNA. The sequencing of the 16S libraries was carried out using the Illumina NovaSeq 6000 platform, and the sequencing reads were processed through 16S amplicon sequencing. A total of 7,706 sequences from the 16S region were obtained after removing low-quality sequences and contaminants. Taxonomic analysis revealed that the most abundant bacterial phylum was Proteobacteria, which represents one of the largest groups within the Bacteria domain. This phylum is significant for hosting species with a relevant role in promoting plant growth and they can participate in metabolic processes that affect coffee quality. At the genus level, the most abundant was *Methylobacterium-Methylorobrum*, followed by *Pantoea*. Bacteria from these genera form endophytic and epiphytic associations, providing nutrients to plants and acting as biological control agents. However, studies that relate these genera to coffee beverage quality are still scarce. Understanding the bacterial diversity present in conilon coffee cherries can be useful for advancing fermentation technologies, aiming to obtain higher quality beans.

**Key words**: Conilon coffee; Microorganisms; Bacteria.

**Análise do perfil taxonômico do bacterioma em frutos de *Coffea canephora***

No café, algumas espécies de bactérias, além de desempenharem funções vitais para o crescimento e desenvolvimento da cultura, influenciam na qualidade dos frutos. O objetivo do estudo foi caracterizar o bacterioma dos frutos de *Coffea canephora*. Após a extração de DNA, reações em cadeia da polimerase (PCR) foram realizadas para amplificarem as regiões V3-V4 do 16S rDNA. O sequenciamento foi efetuado utilizando a plataforma Illumina NovaSeq 6000. Um total de 7.706 sequências da região 16S foram obtidas. A análise taxonômica mostrou que o filo bacteriano mais abundante foi Proteobacteria. Em nível de gênero, o mais abundante foi *Methylobacterium-Methylorobrum*.

**Palavras-chave**: Café conilon; Microrganismos; Bactérias.