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**BIOCHEMICAL AND MOLECULAR CLASSIFICATION OF YEASTS FROM TRÁS-OS-MONTES HONEY**

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Honey is composed essentially by sugars, which represent 95-99% of the product dry matter. The contaminant flora of food with high level of sugars is constituted almost exclusively by moulds and osmotolerant yeasts. Fermentation led by these microorganisms is an irreversible phenomenon that occurs in honey generally stored after granulation. In this case, honey presents a "wine" odour, acid flavour and gas, becoming improper for consumption. The first goal of this work consisted in the isolation of yeast strains present in Trás-os-Montes honey. The second goal was to compare different methodologies for identification of yeasts and to establish the most efficient method for routine analyses. In this direction, two commercial methods of identification based in phenotypic characteristics (Galleries API 20C AUX and RapID Yeast Plus system) and sequencing of two genomic regions (5.8S-ITS and D1/D2 domains of 26S rRNA gene) were used. PCR amplicons were sequenced and analyzed using appropriate software. With BLAST application, available in European Molecular Biology Laboratory (EMBL) or National Center for Biotechnology Information (NCBI) databases a comparison was performed, obtaining homology percentages that allowed the identification of yeast isolates. The described molecular biology methods seem very adequate, however DNA sequencing nowadays requires considerable costs for application in routine analyses. The most common yeast species found were *Zygosaccharomyces rouxii*, *Zygosaccharomyces mellis*, *Pichia membranifaciens* and *Candida magnoliae*.