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MOLECULAR IDENTIFICATION OF YEASTS FROM TRADITIONAL TURKISH CHEESES FOR SELECTION OF STRAINS POSSESSING FLAVOUR PRODUCTION POTENTIAL

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The aim of the research was to apply the molecular techniques for identification of wild yeasts isolated from traditional Turkish cheese samples. The yeast isolation from cheese samples was performed by spreading plate method, using YEPD (yeast extract–peptone–dextrose) agar medium at 28℃ for 2–6 days, after that the selected yeast strains, which had different colony morphology, were purified on YEPD medium. The species level identification of the stains was performed by amplification and restriction analysis of ITS1-5.8S rDNA-ITS2 region directly from yeast colony. Primer pairs used to amplify the ITS region were ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3'). PCR products were digested without further purification with different restriction enzymes such as *Hae* III and *Hinf* I. The identification of the isolates was performed through a comparison of the restriction profile of each isolate with the reference yeast strains. In this research, 39 yeast strains were analyzed. These yeasts were isolated from 34 traditional Turkish cheese samples, such as Tulum cheese, Turkish white cheese, Kasseri cheese, Mihalic cheese, Sepet cheese, Kelle cheese, etc. According to microscopic morphology, colony morphology and restriction analysis of ITS1-5.8S rDNA-ITS2 region, the 39 yeast strains were identified as *Saccharomyces cerevisiae*, *Torulaspora delbrueckii*, *Kluyveromyces marxianus*, *Kluyveromyces lactis*, *Debaryomyces hansenii*, *Candida bechii*, *Pichia guilliermondii* and *Yarrowia lipolytica*. *Debaryomyces hansenii* was found as the most widespread species in the analyzed cheese samples. In further studies, the yeast strains will be submitted to technological characterization, such as proteolytic and lipolytic activities, and bioflavour production potential.
Keywords: Traditional Turkish cheeses, yeast, molecular identification

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