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Metagenomic study of diverse ingredients and seasoning material used in table olive elaboration

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Table olive has been reported as splendid carrier of beneficial microorganisms to the human body. However, scarce information is available about different ingredients used in the processing and packaging, such as salt and seasoning material. In this sense, we used an optimized Illumina 16S rRNA gene-based analysis protocol to decipher the bacterial profiles of different ingredients used during table olive elaboration (garlic, pepper, fennel, thyme and salt) and analysis of the ITS region for the yeast profile. Metagenomics data were analyzed by QIIME pipeline. The analysis of 16SrRNA gene showed that in salt the predominant genus of bacteria was *Salinibacter* (42.44%) from *Rhodothermaceae* family, followed by other genus included in the Archaea family *Halobacteriaceae* (21.06%). It is also remarkable that the presence of *Enterobacteriaceae*, highly represented in fennel (71.23%), pepper (60.93%) and garlic (24.26%) samples, meanwhile the most representative genus in garlic was *Pediococcus* (31.58%) from *Lactobacillae* family. The analysis of ITS region showed predominance of *Pichia* genus, being in pepper (68.66%), salt (35.25%), garlic (30.53%) and to a lesser extent in fennel (2.55%). It is also noteworthy the presence of the genera *Candida* in fennel (69.56%). The use of this methodology open a new door to the knowledge of the microbiota associated to table olive processing, limited until the moment by the lack of specific culture media in mostly cases.

Biography

Antonio Benítez Cabello has obtained a degree in Biology from Seville University. Currently, he is pursuing his Doctoral degree with the thesis which focuses on the search for microorganisms with technological and probiotic properties. He has attended various national and international congresses and has published 2 papers in reputed journals. Recently, he has received a mobility grant from the Spanish government for learning assembly techniques, genomes and microbial diversity studies by massive sequencing techniques.

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