Poster

Improvement of olive oil quality: Metabolic, biochemical and molecular analysis of squalene biosynthesis in olive

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Keywords: Olive oil; Squalene synthase; Gene expression

ABSTRACT

The virgin olive oil (VOO) is a natural olive juice of special importance in Mediterranean diet due to both its beneficial effects on human health [1] and its exceptional organoleptic properties. These characteristics are due to the presence of the major components, which are the triacylglycerols, and certain groups of compounds encompassed under the term of minor components. Among the minor compounds of VOO, squalene is a polyunsaturated triterpene which is an intermediate metabolite in the synthesis of steroids and terpenoids [2]. In recent years, special attention has been paid to squalene because of the benefits that its ingestion contributes to health. Squalene is considered a natural antioxidant and has been frequently used as an additive to lipid emulsions and as drug carrier in pharmaceutical and vaccine applications. In addition, clinical studies indicate that as a component of olive oil it also has a preventive effect on breast cancer, possesses tumor-protective and a cardio-protective properties [3]. The richest source of squalene is shark liver oil (60% fresh weight), but because of the care protection of marine species concerns, the production of squalene from shark liver oil has been questioned. For this reason, the extraction of squalene from plant species would be of great interest to have a sustainable source of squalene.

In this study, the identification of olive genes with a high degree of similarity with the squalene synthase (SQS) genes of the model plant Arabidopsis was carried out from the olive transcriptome and also through the olive genome, both deposited in GenBank [4, 5]. From the identified sequences, a pair of specific oligonucleotides for each sequence were designed and used to obtain the full-length cDNA clones encoding for olive SQS. In addition, we are analyzing the olive SQS genes expression levels in mesocarp and seed during the olive fruit development and ripening by QPCR. Finally, in order to confirm the functional identity of olive SQS cloned genes, we are going to carry out their functional expression in the bacteria E. coli followed by the biochemical characterization of the corresponding recombinants enzymes.

Therefore, the general objetive of this study is to improve the VOO nutritional and technological quality by increasing the squalene content of olive fruit. To achieve this, we focus on the isolation and characterization of the main genes involved in squalene synthesis in olive mesocarp.

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