

FAD2 GENE SEQUENCING IN SOME OLIVE CULTIVARS FROM QOM REGION

Maisa Asheri^{1*}, Mohammad Mehdi Sharifani¹, Ahad Yamchi¹, Seyed Mehdi Hosseini Mazinani²

¹Faculty of Plant Production, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran

²National Institute of Genetic Engineering and Biotechnology, Tehran, Iran

*Corresponding Author's E-mail Address: maisaasheri@yahoo.com

INTRODUCTION

Fatty acid desaturases are enzymes capable of modifying carbon-carbon bonds within fatty acids. All higher plants contain one or more oleic acid desaturases that catalyze insertion of a double bond between carbons 12 and 13 of oleic acid to produce linoleic acid, an unsaturated fatty acid. Fatty Acid Desaturase 2 (FAD2) genes' encoding enzymes convert oleic acid to linoleic acid. The higher the amount of oleic acid, the better the olive oil quality as long as it falls within the permitted range by IOC. In this study, five olive cultivars according to their fatty acid profiles with different range of oleic acid were chosen (Mari, Shengeh, Arbequina, Beledy, and Koroneiki). The aim of this study is to identify differences in FAD2-2 gene sequences of local and imported varieties.

MATERIALS AND METHODS

Forward and Reverse primers were designed for FAD2-2 gene using OLIGO ver 5.0 software. Extracting DNA was carried out with CTAB method and a PCR approach was performed to amplify FAD2-2 gene. After sequencing the PCR products, these sequences were aligned together, and then alignment of each of these with the NCBI reference accession, using Multalin software, was conducted.

RESULTS AND DISCUSSION

Alignment of the four olive cultivar sequences with the Koroneiki sequence as the cultivar with a proven good quality oil showed that cultivars shared different percentages of identity. Mari shows 95%, Arbequina 96%, Beledy 93% and Shengeh 91% identity with the Koroneiki sequence. Furthermore, alignment of Arbequina, Koroneiki, Shengeh, Mari and Beledy sequences with FAD2 cDNA clone from olive cultivar Picual (Accession No. AY733077) registered in NCBI shows 92, 90, 87, 85, and 84% identity, respectively. Relatively low percentages of shared identity could possibly be the result of comparing the sequences directly from PCR products with cDNA clone without exon parts in NCBI. Results of aligning FAD2 gene sequences implied that there are considerable differences in sequences of FAD2 genes among studied cultivars.

Key words: FAD2, gene sequencing, olive oil, oleic acid

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