

Transcriptional Analysis of Two Oil Accumulating Tissues from Olive Fruit

M. Luisa Hernández¹, Antonio Muñoz-Mérida², M. Dolores Sicardo¹, Oswaldo Trelles²,
Victoriano Valpuesta³ and José M. Martínez-Rivas¹

¹Department of Physiology and Technology of Plant Products, Instituto de la Grasa (IG-CSIC), 41012 Sevilla, Spain. ²Integrated Bioinformatics, National Institute of Bioinformatics, University of Málaga, 29071 Málaga, Spain. ³Department of Molecular Biology and Biochemistry, Instituto de Hortofruticultura Subtropical y Mediterránea, University of Málaga (IHSM-UMA-CSIC), 29071 Málaga, Spain.

The development of new cultivars with increased oil content in the olive fruit mesocarp is one of the more important aims of the olive breeding programs. However, understanding of the molecular basis of this trait requires the generation of sequence information and genomic tools, which are still scarce in olive.

Within the project OLEAGEN, three non-normalized cDNA collections corresponding to seeds and mesocarp tissue at two different developmental stages from Picual cultivar have been synthesized and sequenced using 454 pyrosequencing technology. After ESTs assembly, the resulting contigs have been annotated and incorporated to the olive sequence database generated within the project. *In silico* expression analysis has been performed, with special emphasis in those unigenes that codify enzymes of the metabolic pathways for fatty acid biosynthesis, triacylglycerol assembly, biosynthesis of plastidial lipids and carbon supply for fatty acid and glycerolipid biosynthesis. Genes with differential expression between the studied tissues have been identified, and its involvement in the regulation of the mentioned metabolic pathways will be discussed.