

P2.12 - Cloning SLG and SRK genes as candidates for self-incompatibility in olive (*Olea europaea* L.): Domains organization and expression studies

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Olea europaea L. is one of the oldest agriculture tree crops and, in spite of its great cultural and economic importance, a few studies have been carried out on the reproductive barriers in this species, the main one being the self-sterility of most cultivars. The aim of this research was that of studying the self-incompatibility system in olive from cyto-histological and bio-molecular standpoints. Self-incompatibility is one of the most important systems adopted by many flowering plants to prevent inbreeding, maintaining so diversity within the species. A deep comprehension of this reproductive constrain is crucial because it may help to implement breeding strategies useful to obtain a higher yield of fruits. The available literature on the topic reports that olive trees adopt a Gametophytic Self-Incompatibility (GSI) system. According to this knowledge, a preliminary research approach was started to search genes responsible for GSI, such as S-RNase (S-locus ribonuclease) and SLF (S-locus F-box containing protein). At the same time, cyto-histological analyses by means of stain-clearing and aniline blue staining of pollinated and non-pollinated pistils, were also conducted in putative self-compatible and self-incompatible cultivars (*i.e.* Leccino and Frantoio, respectively). Both cyto-histological observations and bio-molecular results led us to suppose a Sporophytic Self-Incompatibility (SSI) system occurring in olive. Consequently, the main genes known to play a crucial role in SSI were searched, like SLG (S-locus Glycoprotein), SRK (S-locus Receptor Kinase), and SCR (S-locus Cysteine Rich protein). In order to obtain messengers encoded by these genes, either degenerated and non-degenerated primers were designed and tested on consensus sequences, belonging to SSI-related species (*e.g.* *Brassica* spp.), obtained by multiple alignments of records retrieved from the NCBI database. Different approaches based on the use of both cDNA and genomic DNA as templates allowed us to recover the full-length of an SLG-like gene and four sequences putatively encoding for SRK-like proteins. A differential expression of these genes among different olive tissues and organs (*i.e.* flowers of self-compatible and self-incompatible cultivars at different developmental stages, and samples deriving from buds, leaves, branches, fruits and roots) was then tested by means of Real-Time PCR analysis using different subdomain-specific primer combinations.

P2.13 - GreenPhyl: Phylogenomic resources for comparative and functional genomics

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With the increasing number of plant genomes being sequenced, a major objective is to transfer accurate annotation from characterized sequences to uncharacterized sequences. GreenPhyl (Conte et al., 2008, Nucleic Acid Research, 36: D991-8) is a tool for plant comparative genomics that predicts the function of genes based on their evolutionary relationship with genes of known function. The database (version 2) comprises protein sequences of 16 plant species fully sequenced including socio-economically important crops like rice, sorghum and maize that were grouped into gene families using similarity-based methods. GreenPhyl contains approximately 13,000 gene families being annotated, computational analyzes and external cross-references (InterPro, KEGG, Swiss-Prot, Pubmed) related to all gene members. Once manually annotated (*i.e.* properly named and classified), gene families are finally processed by phylogenetic analyses to distinguish orthologous and paralogous gene. Orthologous genes descend from the last common ancestor through speciation and most probably encode proteins with a similar function in different species. In addition, the website offers a range of user-friendly tools to query the data. These resources will be particularly helpful to molecular biologist for gene discovery and gene function inference. We believe that a better understanding of genome evolution will contribute to elucidate the genetic basis of important agronomic traits and therefore facilitate ongoing plant breeding efforts.