

## **GENERATION AND ANALYSIS OF EXPRESSED SEQUENCE TAGS FROM CAROB (*CERATONIA SILIQUA* L.) FLOWERS**

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Carob is a trioecious cesalpinoid legume tree which is mainly used for production of gelling agents (from endosperm) in food industry, for agroforestry and soil preservation in marginal dry areas, and as ornamental. This species is highly plastic in sexuality and is considered an anomalous cesalpinoid, having unusual flower features (missing floral organs, absence of petals, variability in organ number per whorl).

With the main aims of identifying flower-expressed genes and of developing specific markers, 1056 clones from a cDNA library of carob flowers at different developmental stages were bidirectionally sequenced. A total of 1376 high quality ESTs clustered into 1095 unigenes, consisting of 213 contigs and 882 singletons. Carob ESTs were subjected to BLAST search against the GenBank nr database, and GO annotation tool from the TAIR website (<http://www.arabidopsis.org/tools/bulk/go/index.jsp>) was used for the functional classification of the unigenes. Several homologs of genes involved in flower development and sexual reproduction (MADS-box genes, AP2, YABBY, etc.) were identified. Furthermore, using Msatfinder (<http://www.genomics.ceh.ac.uk/msatfinder/>) we identified thirty-eight di, tri and tetranucleotide EST-SSR, which could be potentially useful markers. A preliminary test of some carob genic microsatellites on Italian and Spanish carob accessions suggests their usefulness for genotyping and genetic diversity analysis.