

A SEARCHABLE EST COLLECTION FROM SAFFRON STIGMAS

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Saffron (*Crocus sativus* L.) is a triploid, sterile plant, probably derived from a species found in Eastern Greece, *Crocus cartwrightianus*. It was known to the Sumerians, 5.000 years ago. Its stigmas constitute the most expensive (by weight) spice on Earth. They contain the pigment crocin, the flavour picro- (from the Greek bitter) -crocin, and the aroma safranal. All three substances are derivatives of the carotenoid metabolism. Approximately 150.000 flowers (or 2.000 m² field area) are needed for one kilogram of dried saffron. Today, the greatest saffron producing countries are Greece, Spain, Turkey, Iran, India, and Morocco. The largest saffron importers are Germany, Italy, U.S.A., Switzerland, United Kingdom, and France.

We sequenced 9769 ESTs from a saffron stigma cDNA library. After trimming of low quality sequences and vector removal, the collection was reduced to 6603 high quality sequences. These sequences were clustered and assembled to detect sequence redundancy. Sequences with >85% identity over a region longer than 60 nucleotides were clustered, yielding 519 tentative consensus sequences (contigs) and 1699 singletons. Contigs and singletons were automatically annotated, using BLASTX similarity searches against the UniProt database. EST sequences and their electropherograms, as well as clusters and contigs, preliminary annotation with references to the publicly available databases (UniProt, Gene Ontology, KEGG) are collected in a MySQL database and are accessible via a PHP-based interface through user-friendly graphical views. The web site will be made publicly accessible.