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Poster Abstract - C.53

ESTree db: AN ENGINE FOR PEACH EST RELATED INFORMATION RETRIEVAL

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The ESTree db (http://www.itb.cnr.it/estree/) is a collection of *Prunus persica* expressed sequenced tags (ESTs). At the moment, it encompasses more than 20,000 peach EST sequences, representing ten different cDNA libraries.

The ESTree db core structure is a MySQL relational database where all the results of the sequence analysis pipeline are stored. This analysis pipeline is a fully automatic procedure that starting from raw EST sequences fills up all the tables in the database. A php-based web interface allows querying the db and creates user-friendly graphical displays on-the-fly. The result is a web site where users can access data on sequence annotation (both versus the GenBank nr db and versus the Gene Ontology viridiplantae db), view the complete BLAST outputs, retrieve links to the best blast hits, to the NiceZyme (Expasy) db and to the KEGG Biochemical Pathways db. All the sequences of the db have been assembled with CAP3 and contig alignments and graphical displays are available. Putative SNP detection has been performed with the AutoSNP program and SNP data are also displayed. The db has been furnished with a text search utility and a local BLAST utility. Downloads of sequences, contig consensus sequences and AutoSNP SNP reports have been prepared in various formats. Statistics on the db status and on matching ontologies are provided. The ESTree db is continuously growing and new features are added, including data derived from peach microarray analysis.

The ESTree db is the first web resource reporting data on putative SNP sites in peach, and will be the main repository of data obtained by the ESTree Interuniversitary Centre units, allowing the creation of a platform for easy data integration and retrieval, with the aim to provide a tool to improve knowledge on peach genomics and functional genomics.