

International Conference on
BIOINFORMATICS & SYSTEM BIOLOGY
&
3rd International Conference on
SURGERY & ANAESTHESIA

March 20-21, 2019 | Singapore City, Singapore

Insilco studies of mango genome cultivars and development of analysis tool

Rabia Faizan, Tayyaba Qamar, Muhammad Ahmed and Uzma Mahmood
Sir Syed University of Engineering & Technology Karachi, Pakistan

Mango is one of the famous and fifth most important subtropical/tropical fruit crop worldwide with the production centred in India and South-East Asia. Mango breeding is still mostly the selection of trees with superior fruit traits rather than hybrid production and evaluation due to the difficulty of specific pollination. Recently, there has been a worldwide interest in mango genomic to produce tools for Market Assisted Selection and trait association. There are five transcriptomes produced respectively in Israel, India, Mexico, Pakistan and the US. Our project "Mango Genome Database" is constructed upon the completion of the Pakistan leaf transcriptome and chloroplast genome of *Mangifera Indica* L. specie sequencing with the aim of providing the scientific community with an accurate data and annotation of the mango genome sequence. The project

is consisting of a website which contains the information of predicted genes of the whole genome of Mango and the unigenes annotated in other species, GO (Gene Ontology) terms providing a glimpse of the pathways and traits in which they are involved. The annotated and analysed sequence data then can be browsed through Gene search page or queried using various categories in the search sites. The whole genome sequences and genetic results can also be accessed and downloaded through different modules present in a website including (Blast, Data Downloads and BI Tools). The online analysis tools involve the Blast server for the Mango datasets, a sequence gene retrieval module, Phylogeny, plotting and other alignment tools.

rabiatabassumkhi@gmail.com