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Analysis of up-regulated gene families during Langra mango (*Mangifera indica L.*) fruit development

Zainab Khanum, Atta-ur-Rahman, M Iqbal Choudhary and M Kamran Azim
University of Karachi, Pakistan

Langra mango fruit is the export quality variety of Pakistan. This variety is well known for its taste and aroma. Much of the transcriptomics work has been conducted on the ripening physiology of the mango fruit but there has been less focus on the mango organogenesis. To better understand the temporal and spatial dynamics during the mango fruit's development, the plant's developmental genetics approach was followed. This approach involved mRNA sequencing by using the SOLiD 5500™ Genetic Analyzer platform. De novo transcriptome assembly and de novo transcript quantification was carried out for eight different developmental stages of a Langra mango fruit by using SATRAP assembler pipeline and RSEM, respectively. BLASTx program for NCBI nr-database, KAAS and BlastKOALA tools were used for gene functional annotation and metabolic pathways identification. Simple sequence repeats in transcripts were identified by GMATA software. This revealed a repertoire of up-regulated gene families during development with no prior literature support. Around ten gene families are enriched during the Langra mango fruit's development. Up-regulated genes involved in plant's development, embryogenesis and immune response were classified, especially the GIGANTEA (GI) nuclear protein gene. GI gene is climate and photoperiod regulated and is a key player in plant's circadian clock control, flowering time regulation, drought tolerance and salt tolerance. Up-regulated gene products were also classified which are responsible for ROS control and have nutraceutical properties including defense against cancers and human pathogens. The Langra mango fruit's developmental transcriptome was also compared with the mango transcriptomes from Pakistan, China and Mexico.

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Biography

Zainab Khanum has her expertise in transcriptomics. Her research interests include developmental genetics and human cancers related functional genomics. She is a Biotechnology graduate from University of Karachi, Pakistan. She is currently enrolled in PhD program at International Center for Chemical and Biological Sciences, University of Karachi, Pakistan. She has expertise in manual extraction of high quality total RNA, next generation mRNA sequencing and bioinformatics. She looks forward to conduct her future research on projects that will benefit the health sector, agriculture sector and economy of her country.

zainab12khanum@gmail.com

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