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Safina Abdul Razzak, J Mol Genet Med 2018, Volume 12
DOI: 10.4172/1747-0862-C1-025

Joint Meeting on
4th World Congress on
HUMAN GENETICS & GENETIC DISEASES
and
3rd International Conference on
MOLECULAR MEDICINE & DIAGNOSTICS
April 19-20, 2018 Dubai, UAE

Comparative transcriptomics of mango (*Mangifera indica* L.) cultivars provide insights of biochemical pathways involved in flavor and color

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Mango is an economically important fruit crop of many tropical and subtropical countries. Recently, leaf and fruit transcriptomes of mango cultivars grown in different geographical regions have characterized. Here, we presented comparative transcriptome analysis of four mango cultivars i.e. cv. Langra, cv. Zill, cv. Shelly and cv. Kent from Pakistan, China, Israel and Mexico respectively. De novo sequence assembly generated 30,953-85,036 unigenes from RNA-Seq datasets of mango cultivars. KEGG pathway mapping of mango uni-genes identified terpenoids, flavonoids and carotenoids biosynthetic pathways involved in flavor and color. The analysis revealed linalool as major mono-terpenoid found in all cultivars studied whereas, monoterpene α-terpineol was specifically found in cv. Shelly. Ditepene gibberellin biosynthesis pathway was found in all cultivars whereas, homoterpene synthase involved in biosynthesis of 4,8,12-trimethyltrideca-1,3,7,11-tetraene (TMTT; an insect induced diterpene) was found in cv. Kent. Among sesquiterpenes and triterpenes, biosynthetic pathway of Germacrene-D, an anti-bacterial and anti-insecticidal metabolite was found in cv. Zill and cv. Shelly. Two bioactive triterpenes, lupeol and β-amyrin were found in cv. Langra and cv. Zill. Uni-genes involved in biosynthesis of carotenoids, β-carotene and lycopene, were found in cultivars studied. Many uni-genes involved in flavonoid biosynthesis were also found. Comparative transcriptomics revealed naringenin (an anti-inflammatory and antioxidant metabolite) as central flavanone responsible for biosynthesis of an array of flavonoids. The present study provided insights on genetic resources responsible for flavor and color of mango fruit.

Biography

Safina Abdul Razzak is currently an MS (Bioinformatics) candidate at Mohammad Ali Jinnah University, Pakistan. She has completed her Bachelor's degree in Bioinformatics from Baqai Medical University in 2013. She has 4 years of experience in genomics field from International Center for Clinical and Biological Sciences. Currently, she is appointed as a Bioinformatician in Mohammad Ali Jinnah University along with her studies. She is involved in research on plant and human genomics, transcriptomics and exomics research projects.

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