

MicroRNA Analysis of Tomato Fruits Cultivated under a High-Salt Condition

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Summary

Tomato is one of the most popular vegetable in the world. Recently, many tomato cultivars have been developed to improve tomato-specific flavor for increased palatability as well as nutritional quality. Comprehensive gene expression analysis revealed that fatty acid and amino acid synthesis-related genes were up-regulated under a low-water condition. In case the plants are exposed to an environmental stress, they change their own metabolism to eliminate the stress. Abscisic acid is increased under drought, which should in turn affects human lipid metabolism after ingestion. Some dietary miRNAs may also be involved in human physiology. The aim of this study is to find out whether miRNA in tomato influences human metabolism.

Micro-Tom was cultivated under a low-water condition after flowering, prior to harvesting mature fruits. miRNA expression analysis was performed using miRNA GeneChip 4.0. A total of 4 miRNA species were obtained with 2-times higher expression; these were, has-miR-3163-3p, has-miR-4481, has-miR-4468-5p, has-miR-548ac and has-miR-4701-3p. In addition, HBII-85, as a small RNA in nucleolus, was found. The target genes for these miRNAs were extracted from miRDB with the target score of more than 90. When the canonical pathway containing putative target genes were explored in Ingenuity Pathway Analysis (IPA), 28 pathways were extracted as significantly up- or down- regulated pathways and they were classified into the 6 categories: immune system, nervous system, MAPK family, cardiac hypertrophy, cancer and others.

Also, tomato miRNAs with more than 2-times increased expressions were sly-miR399 and sly-miR395, although such expressions in leaves and fruits have been already reported, but the target genes are still unknown. In particular, sly-miR395 decreased by 10 times less than expected under a normal condition. This result suggests that sly-miR395 is essentially involved in salt-stress response.