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Novel insight into transcriptional regulation of key genes of citrulline biosynthetic pathway mediated by rootstock

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Watermelon is considered to be a largest natural source of citrulline. Transcriptional regulation of citrulline biosynthetic pathway genes and quantification of citrulline at different developmental stages of fruit was studied in homografted, hetero grafted and non-grafted watermelon. Citrulline content continues to increase until ripe stage in grafted and no grafted plants with highest content was observed in heterografted followed by homografted and non-grafted watermelon. High transcript level for GAT, NAG and NAGK can be related to high citrulline amount in hetero grafted and among downstream stream genes, ASS gene

family interact synergistically while ASL gene family work antagonistically resulted in low degradation of citrulline in hetero grafted. Experiment was laid out according to Randomized Complete Block Design (RCBD) and three biological replicates were used for analysis. The significant differences between expression values were statistically evaluated by standard deviation. Two ways ANOVA for citrulline quantity was performed and tested for statistical significance using Statistics 8.1.

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