Regulation Mechanism of Primary Metabolism in Tomato Fruit under Salt Stress

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Summary

Fruit composition largely affects fruit and consumers tastes. Salt stress improves the quality of tomato fruits with increased sugar and amino acid contents such fructose and GABA. However, regulation mechanisms how salt stress improves the fruit composition is not fully understood to date. In this study, to clarify the mechanism(s) underlying this phenomenon, we investigated metabolic alterations in transgenic tomato fruits with suppressed expression of ADP-glucose pyrophosphorylase genes under 160 mM of salt stress, focusing on sugar and starch. The transgenic tomato plants we submitted in the present study were generated by RNAi method in our previous research and designed $35S::AgpSI^{RNAi}$ and $35S::AgpLI^{RNAi}$. The plants were raised by hydroponic culture and treated with the 160 mM salt stress by adding NaCl to the hydroponic culture medium after flowering period. Fruits were sampled at 10 days after flowering (DAF) as immature-green stage and at 42 DAF as mature-red stage. Quantification of starch content in immature-green fruit revealed that starch accumulation was 5-times enhanced by the salt stress in wild type plants as observed in our previous research. However, no or largely-reduced starch accumulation were observed in the 35S::AgpS1^{RNAi} and the 35S::AgpS1^{RNAi} fruits, respectively. Accumulation of soluble sugars such glucose, fructose and sucrose in red-ripe fruits were also 2.4-times enhanced by the salt stress in wild-type plants. However, such a promotion effect of salt-stress on the fruit sugar contents was not observed in the 35S:: AgpS1^{RNAi} and the 35S:: AgpS1^{RNAi} fruits, indicating the increased sugars in the salt-stressed fruit is caused by the increased starch in immature-green stage. In this study, to explore a factor regulating AgpS1 and AgpL1 genes in immature-green fruits, we also analyzed the effect of various fruit components such proline, GABA, polyamine and ions derived from NaCl on the expression of the genes. Quantitative RT-PCR analyses revealed that the both genes were strongly induced by proline treatment at transcriptional level. Interestingly, AgpS1 only responded to GABA but not to polyamines. In contrast, AgpL1 only responded to polyamines but not to GABA. Those results indicated two genes, AgpS1 and AgpL1, are differentially regulated in immature-green fruits.