



University of Tsukuba

Plant Transgenic Design Initiative

57th PTraD Research Seminar

T-PIRC Research Seminar

Date and Time: 2020/9/17 (Thu) 16:00-17:00

Place: Online sessions (TBA)

Transcriptome analysis in agricultural crops

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Transcriptome study provides an essential platform to analyze the association between genotype and phenotype, which gives a better understanding of the underlying pathways and mechanisms controlling development and for improving the quality traits of an agricultural crop.

The development of non-pollinated highbush blueberry seedless fruit differs from other crops because late dropped after anthesis. Therefore, the mechanism during development of non-pollinated highbush blueberry was investigated. To provide insights into blueberry parthenocarpic cultivar during fruit development, the transcriptomic profiles of middle-parthenocarpic ('Echota') and non-parthenocarpic ('Elliott') after four weeks of anthesis were analyzed using RNA-sequencing technology. From KEGG analysis, proteins related with carbohydrate metabolism, energy metabolism, and biosynthesis of secondary metabolites were upregulated during blueberry development.

In addition, lotus root (*Nelumbo nucifera*) is an edible rhizome that is widely cultivated in Japan. The consumption/production of fresh-cut lotus root has continuously increased as more consumers demand convenient and ready-to-eat foods. However, the processing, storage, and transportation of fresh-cut fruits and vegetables promotes physiological deterioration, such as browning, which leads to a reduction in the value of the product. This study aimed to reduce the browning of lotus root pericarps during long-term storage and long-distance transport, and to clarify the functions of unigenes and browning-associated metabolic pathways using RNA-sequencing techniques. We found that the secondary metabolism, lipid metabolism, and redox state were significantly upregulated in the un-packaging and pack with distilled water when compared with after harvest sample.

Furthermore, russetting is an important surface disorder of many fruit crop species and compromises both fruit appearance and postharvest performance. Russetting is a disorder developed by apple fruits that consists of cuticle cracking followed by the replacement of the epidermis by a corky layer that protects the fruit surface from water loss and pathogens. This study, apple (*Malus × domestica*) fruit of 'Fuji' and 'Goldfarm' cultivar was obtained from 1, 2, 3, 4, 5 weeks after full flowering. For transcriptome analysis, 4 weeks after full flowering was investigated. The result found that the highest number of DEPs was related with lipid metabolism, secondary metabolite, and membrane metabolism, especially Goldfarm cultivar.

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