Fruit Crispness Maintenance of Honeycrisp and its Progeny

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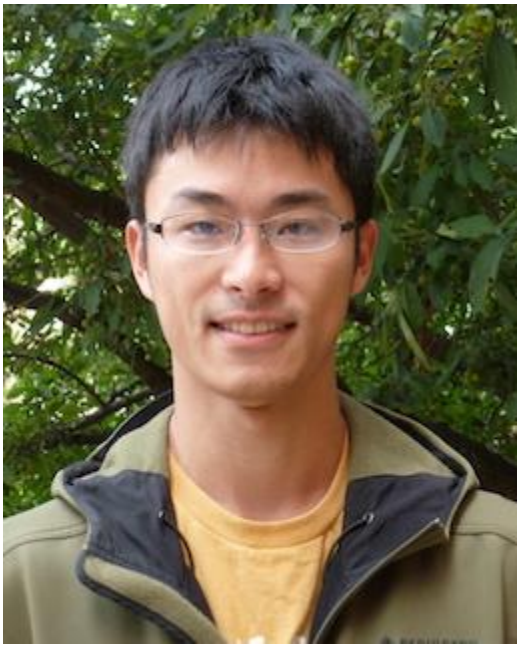

Fruit softening is a major postharvest problem of the apple industry, as consumers tend to prefer crisp rather than soft apples. Also, soft fruits are more susceptible to fungal infections, resulting in apple production losses. Honeycrisp (Malus × domestica Borkh.) is an apple cultivar with fruit that do not soften, and is known for exceptional crispness and excellent storage life. With adequate temperature and moisture storage conditions, the fruit is able to maintain its sensory firmness and crispness for over 6 months of storage. This non-softening trait of Honeycrisp is rare in other apple cultivars, therefore, Honeycrisp provides a valuable genetic resource for breeding new, high-quality cultivars with the ability to maintain firmness and crispness. Understanding genes associated with crispness maintenance can facilitate breeding processes via marker-assisted selection.

A full-sib breeding population from a cross between Honeycrisp and MN1764 (a softening apple variety) is the plant material in this study. Honeycrisp x MN1764 is the largest breeding population in Horticulture Research Center comprised of 174 genotypes, and both crispness maintenance and softening traits were observed among the progeny. Therefore, genes related to crispness maintenance can be identified by comparing the differentially expressed genes between fruit from different genotypes that retain or lose crispness over time.

Because softening is one of the ripening processes of apple fruit, and crispness is related to the integrity of cell wall, three hypotheses were proposed to explain crispness maintenance of Honeycrisp: (1) the low ethylene production of Honeycrisp fruit contributes to its “unripe” characteristics, including crispness maintenance; (2) critical cell wall-modifying enzymes causing softening might not be up-regulated during the storage period of Honeycrisp; (3) Honeycrisp fruit may continue cell wall synthesis during storage and thus retain crispness. To test these hypotheses, genes associated with these functions will be the main focus.

To narrow down the candidate genes involved in crispness maintenance, RNA-seq data of fresh and stored Honeycrisp and MN1764 have been generated. Several cell wall related genes that showed

different expression patterns between Honeycrisp and MN1764 were identified according to the RNA-seq results. Finally, real-time reverse transcription PCR (qRT-PCR) will be used to validate the RNA-seq results and the expression patterns of selected genes in fruit of the MN1764 x Honeycrisp progeny to crispness maintenance of Honeycrisp. By using the ful-sib progeny and RNA-seq technique, the genetic mechanisms under crispness maintenance of Honeycrisp fruit can be more clearly understood.

References

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