IX International Strawberry Symposium

Symposium nr 690, abstract nr 144 (oral presentation)

High-throughput mapping of cell wall glycans to unveil cell wall disassembly, a key process determining strawberry fruit softening

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Abstract

The short shelf life of strawberry fruit is a major limitation that produces important economic losses related to postharvest spoiling. Fruit texture of fleshy fruits is a complex trait but mainly rely on mechanical properties of parenchyma cell walls. Several studies support the relevance of cell wall modifying enzymes on cell wall deconstruction, decreasing cell wall strength and cell to cell adhesion, and ultimately producing the softening of the fruit at macroscopic level. Previous studies on our group showed that transgenic silencing of ripening-specific genes encoding some of these enzymes reduced softening and increased postharvest shelf life in strawberry (*Fragaria* × *ananassa*, cv. 'Chandler') fruits. In this research, to further investigate the cell wall remodelling process associated to strawberry softening a high-throughput analysis of cell wall composition based on monoclonal antibodies against different polysaccharide epitopes has been performed. To this purpose, cell walls were isolated from non-transgenic fruits at different developmental stages as well as from ripe fruits of selected transgenic lines with genes involved in metabolism of pectins (pectate lyase, polygalacturonase, β-galactosidase, pectin acetil esterase), hemicellulose/cellulose (endo-β-glucanase) or lignin (cinnamyl alcohol dehydrogenase) down-regulated. These transgenic lines showed a large variability in fruit firmness at ripening. Cell walls were fractionated and subjected to a carbohydrate microarray. The results obtained unveiled a common pattern of cell wall composition on those transgenic lines with firmer phenotypes, specially defined by the higher content of pectins on those cell wall fractions more imbricated in the matrix, which can be interpreted as a less degraded cell wall structure.

Acknowledgements: This research was supported by FEDER EU Funds and the Ministerio de Economía y Competitividad of Spain (grant reference AGL2017-86531-C2-1-R). Universidad de Málaga. Campus de Excelencia Internacional Andalucía Tech.

Keywords: Fruit softening; cell wall; pectins; cell wall modifying enzymes; carbohydrate microarray