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P766 : Functional Analysis

Using Genome Information To Identify The Regulation Of Fruit Texture In Apple

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In apple, texture is an important factor determining consumer acceptance. Apple texture is complex, caused by a combination of cell wall properties, cell morphology and turgor. In a collaborative programme with IASMA, PFR is utilising genomic information to understand the genetic control of texture in apples. In a mapping population of 600 seedlings of ‘Royal Gala’ x ‘Braeburn’, we have identified combinations of soft and firm texture apples at harvest that demonstrate both softening and non-softening phenotypes after storage. The SNP-plex approach has allowed construction of a high density genetic map for QTL mapping of texture. Using transgenics, we have shown a strong ethylene control of fruit softening, and the contribution of the ethylene-related cell wall enzyme POLYGALACTURONASE (PG), in determining texture. As the levels of the cell wall enzymes PG and B-GALACTOSIDASE protein vary across different commercial apple varieties with a range of textures, we have targeted these candidates for further analysis. Using a microarray and genome screening approach, we have identified a number of ethylene-related genes and transcription factors that are up regulated with ethylene. Using the whole genome sequence, we have isolated the promoters of the PG and BGAL genes and screened them in a transient assay against a transcription factor library to assess the transcriptional regulation of these genes. We anticipate that this integrated approach, involving phenotypic analysis, QTL mapping, transgenics, transcriptomics and information from the apple whole genome sequence will enable us to identify key regulation points controlling fruit texture in apple.