

Modification of Gene Expression in Ripening Fruit

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Abstract

Fruit ripening is a coordinated series of biochemical changes that renders the fruit attractive to eat. The fruit may soften, develop colour, change starch or acid into sugar, become flavoursome, produce more ethylene, increase in sensitivity to ethylene, and respire more rapidly.

This syndrome is under contemporary genetic control as illustrated by mutants with fruit that develop normally but lack the ability to ripen, or are deficient or modified in an aspect of ripening. Molecular analysis has revealed changes in gene expression in ripening avocado, tomato, pear and apple fruits. Genes encoding β -1, 4-glucanase (avocado), polygalacturonase (tomato) and trypsin inhibitor (tomato) are among those whose expression increases through ripening.

To modify the softening of tomato fruits, antisense constructs with constitutive promoters have been used to reduce the apparent expression of the polygalacturonase gene. The experiments confirmed a role for polygalacturonase in fruit softening but a need for other inputs was also indicated. In experiments using chimaeric genes, the coding sequence of polygalacturonase linked to a fruit-specific and ethylene-sensitive promoter was introduced into the *rin* tomato genome. *Rin* plants have fruit which do not ripen or accumulate polygalacturonase. The transformed *rin* fruit accumulated polygalacturonase but did not ripen or soften. This experiment confirms conclusions drawn from the use of antisense constructs that polygalacturonase action is not the sole determinant of texture changes in ripening tomatoes.

Ethylene has a key role throughout ripening. The molecular biology of ethylene production and perception is gradually unfolding. A cDNA for ACC synthase for zucchini, a small gene family whose expression correlated with Ethylene Forming Enzyme (EFE) activity, and a consensus sequence in promoters that are ethylene sensitive have all been described. There is accumulating evidence that some of these sequences and the polygalacturonase sequence are conserved between species, and this will be useful in extending the presently available information.