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Finding flavor genes

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Abstract

A key enzyme involved in flavor biogenesis in ripening strawberries has been discovered using customized cDNA microarrays.

Significance and context

Fruit development and maturation is a highly coordinated process. It is characterized by profound changes in color, aroma and weight, exemplified at the biochemical level by the accumulation of sugars and the synthesis of aromatic compounds responsible for the flavor and scent of the ripe fruit. In the strawberry, a few hundred different molecules belonging to several chemical classes have been implicated in the complex process of aroma biosynthesis. But information on the molecular events that control flavor formation is still lacking. One way to address the complex process of fruit maturation is to examine changes in gene expression at a global level, in the hope of finding transcripts whose expression coincides with the physiological modifications that occur during ripening. Aharoni *et al.* used cDNA microarray technology to look at 1,701 strawberry cDNA clones and measured expression profiles at various stages of fruit development. Using this approach, they identified a novel enzyme with an important role in fruit ripening.

Key results

Aharoni *et al.* randomly isolated 1,701 cDNA clones from a strawberry fruit cDNA library and 480 clones from petunia corolla (as control) and printed the PCR-amplified clones on chemically modified glass slides using a robotic device. They used these microarrays to monitor changes in gene expression at three fruit developmental stages (from green to red). Using a rigorous statistical analysis, the authors found that 401 clones were differentially expressed between all three stages, with 177 clones being upregulated between the green and red stages. Sequences of the latter group of genes revealed that more than 50% were related to primary and secondary metabolism. From the other sequences potentially involved in flavor formation, Aharoni *et al.* identified a novel gene (*SAAT*) for an alcohol acetyltransferase, an enzyme that catalyzes the final step in the synthesis of volatile esters. This gene shows 16-fold greater expression during the red stage than the green stage of fruit development. The authors expressed recombinant SAAT in *Escherichia coli* and confirmed that the enzyme has alcohol

acetyltransferase activity. Analysis of a series of potential substrates suggests that SAAT is responsible for formation of the predominant esters found in ripe strawberries.

Links

Access to *Arabidopsis* cDNA microarrays is provided by the [Arabidopsis Functional Genomics Consortium](#) (AFGC). Links to information on plant microarrays can also be found via the [Virtual library:plant-arrays](#).

Reporter's comments

Large-scale cDNA microarrays are now used with model systems to investigate global patterns of gene expression at the level of the whole organism. The utility of microarrays that cover a restricted portion of the genome, like that described in this paper, will become increasingly recognized, however. This paper is a first example of the use of customized plant cDNA microarrays from a non-model system. It provides a good example of how a small selected array can be used to study a particular developmental process. It also shows that the role of a novel gene (*SAAT*), whose function might have escaped rigorous database searches because of its relative lack of homology with other alcohol acetyltransferases, can be established. The isolation of acetyltransferases could be helpful in improving the flavor composition of commercial fruits.

Table of links

[Plant Cell](#)

[Arabidopsis Functional Genomics Consortium](#)

[Virtual library: plant-arrays](#)

References

1. Aharoni A, Keiser LCP, Bouwmeester HJ, Sun Z, Alvarez-Huerta M, Verhoeven HA, Blaas J, Houwelingen AMML van, Vos RCH De, Voet H van der, et al: Identification of the *SAAT* gene involved in strawberry flavor biogenesis by use of DNA microarrays. *Plant Cell*. 2000, 12: 647-662. 1040-4651