

Studying the role of the strawberry Fra protein family in the flavonoid metabolism during fruit ripening

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Strawberry fruits are highly valued due to their flavor, aroma and benefits for human health. Much of these properties are due to their content in secondary metabolites, of which flavonoids are especially abundant. Flavonoids biosynthetic pathways are uncovered, yet little is known about the regulation.

The strawberry Fra proteins comprise a family of homologs of the major birch pollen allergen Bet v 1. Phenotypic analyses suggest that Fras are involved in color development in strawberries [1], a process that depends on the production of certain flavonoids. RNAseq analysis has identified at least 10 Fra members in strawberry, all with unique expression patterns suggesting functional specialization. Fras are structural homologs of the PYR/PYL/RCAR ABA receptor, and are able to bind flavonoids [2].

With these antecedents, our hypothesis is that Fras are involved in the regulation of the flavonoids pathway and, as the ABA receptor, would bind a protein interactor and a ligand to regulate a signaling route and/or act as molecular carriers.

To identify the interacting partners of Fras we are doing Y2H screens against strawberry fruit cDNA libraries and validating the interactions found by CoIP. These interactions will shed light on the functional diversity within the Fra family. In addition, stable transgenic lines that silence and overexpress different Fra members have been developed and their study will contribute to gain knowledge on how the flavonoid pathway, and hence, the fruit ripening, is regulated in strawberry; an economically important crop but for which basic research is still very limited.

References:

[1]Muñoz, C, et al. (2010). Mol Plant, 3(1): 113–24.

[2]Casañal, A, et al (2013).. J. Biol. Chem., 288(49): 35322–32.