

Desaturase gene expression in specific fatty acid desaturase mutants from *Arabidopsis thaliana*: evidence of compensatory pathways

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Synthesis of glycerolipids in plants takes place almost exclusively in plastids and in the endoplasmic reticulum (ER) through two pathways, the “prokaryotic pathway” and the “eukaryotic pathway”. In the prokaryotic pathway, glycerolipids are synthesized entirely in plastids. On the other hand, in the eukaryotic pathway, phospholipids are synthesized in the ER while MGD, DGD and SL are synthesized in plastids from PC produced in the ER. In both glycerolipid synthetic pathways, fatty acid desaturases are key enzymes that introduce double bounds in fatty acid chains. They produce polyunsaturated fatty acids (PUFAs) which are important in maintaining membrane fluidity and function [1]. PUFAs also serve as precursors of plant hormones like jasmonates [2] that are involved in defence signalling against pathogen attack, wound response, plant development and adaptation to environmental stress. The relative amount of glycerolipid synthesized and desaturated by the two pathways may vary in different tissues and in different plant species. *Arabidopsis thaliana* is an example of 16:3 plants, in which both pathways are almost equally involved in total glycerolipid synthesis [3]. On the other hand, in 18:3 plants (such as *Glycine max*) the leading pathway is the eukaryotic one. Although several lines of evidence indicate the existence of regulatory mechanisms that coordinate the activity of both pathways for glycerolipid synthesis in plants, molecular and biochemical components of this regulatory mechanism as well as how this coordination takes place are still unknown.

As a first step to understand how the communication between the chloroplast and the reticulum takes place, we have studied the changes in gene expression profiles of fatty acid desaturases in response to specific mutations in the desaturase pathway from *Arabidopsis thaliana*. We have analysed five different mutants, *fad2*; *fad5*; *fad6*; *act1* and the triple mutant *fad3/fad7/fad8*. These mutations affected to desaturases operating in both glycerolipid synthetic pathways. The analysis of the effect of each mutation in the expression profiles of the rest of the desaturase genes has allowed us to observe transcriptional responses associated to the existence of compensatory pathways between the chloroplast and the reticulum to minimize the effects of the mutation. It has also helped us to identify the key role of the palmitoyl desaturase, *fad5*, in controlling the flux through the prokaryotic pathway.

[1] Wallis & Browse (2002) Prog. in Lipid Res. **41**: 254-278

[2] Weber *et al.* (1997) Proc. Natl. Acad. Sci. **94**: 10473-10478

[3] Browse *et al.* (1986) Biochem. J. **235**: 25-31

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