

Dual fatty acid elongase complex interactions in Arabidopsis

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Very long chain fatty acids (VLCFAs) are required for the synthesis of triacylglycerols, waxes, phospholipids and sphingolipids. Fatty acyl chain length is essential for plant development in particular for membrane trafficking during cell division and cell differentiation [1–3]. VLCFAs are elongated by the sequential addition of two carbons through four successive enzymatic reactions gathered in the endoplasmic reticulum within a protein complex named the elongase. The acyl-CoA dehydratase PASTICCINO2 (PAS2) is involved in the third step of elongation [3]. The *pas2* mutants show strong defects such as lost of cellular adherence, defects in division plate formation and vesicular dynamic[3,4].

In order to identify new factors associated with the biosynthesis of VLCFAs, a yeast multicopy suppressor screen with an *A. thaliana* cDNA library was carried out in *phs1* strain. Loss of function of *PHS1*, the yeast *PAS2* ortholog, prevents growth and induces cytokinesis defects. The screen identified the *PTPLA* as a dehydratase-like gene involved in VLCFA elongation in both yeast and plant. Functional analysis of *PTPLA* in Arabidopsis demonstrated the existence of a new fatty acid elongase complex activity independent of *PAS2*-based complex but also uncovered unsuspected regulatory interactions between the two complexes.

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