Bypassing the requirement for fatty acyl elongation, a suppressing story

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Very long chain fatty acids (VLCFA) 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].

Fatty acyl elongation is essential for both yeast and plants and thus provide an efficient genetic system to identify new genes involved in VLCFA biosynthesis or function. We first carried out a plant suppressor screen using a fertile *pas2* allele that identifies three independent Suppressor of PAS2 Function (SOP). The three genes turned out to be associated with in exosome function involved in RNA quality control. Then, we used a yeast multicopy suppressor screen with an *A. thaliana* cDNA library to suppress *phs1* defective growth. Loss of function of *PHS1*, the yeast *PAS2* ortholog, prevents growth and also induces cytokinesis defects. The screen identified the PTPLA as a new dehydratase gene in Arabidopsis involved in VLCFA elongation in both yeast and plant. Functional analysis of PTPLA in Arabidopsis demonstrated the existence of a fatty acid elongase complex activity independent of PAS2-based complex but also uncovered unsuspected regulatory interactions between the two complexes.

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