

1. 25%

Fatty acids are synthesized in the stroma of plant and algal chloroplasts by the fatty acid synthase complex. Newly synthesized fatty acids are then used to generate plastidial lipids that are essential for chloroplast structure and function. Here, we show that inhibition of fatty acid synthesis in the model alga *Chlamydomonas reinhardtii* activates autophagy, a highly conserved catabolic process by which cells degrade intracellular material under adverse conditions to maintain cell homeostasis. Treatment of *Chlamydomonas* cells with cerulenin, a specific fatty acid synthase inhibitor, stimulated lipidation of the autophagosome protein ATG8 and enhanced autophagic flux. We found that inhibition of fatty acid synthesis decreased monogalactosyldiacylglycerol abundance, increased lutein content, down-regulated photosynthesis, and increased the production of reactive oxygen species. Electron microscopy revealed a high degree of thylakoid membrane stacking in cerulenin-treated cells. Moreover, global transcriptomic analysis of these cells showed an up-regulation of genes encoding chloroplast proteins involved in protein folding and oxidative stress and the induction of major catabolic processes, including autophagy and proteasome pathways. Thus, our results uncovered a link between lipid metabolism, chloroplast integrity, and autophagy through a mechanism that involves the activation of a chloroplast quality control system. (Plant Physiology (2018) 178, 1112-1129)

1)給此研究下一個英文標題?(英文)

2)以下除了專有名詞外，需用中文敘述

a)這篇摘要敘述此研究在研究什麼樣的問題?

b)此研究用了哪些研究方法，這些研究得到什麼樣的結論?

c)此研究最主要的結論是什麼?

2. 25%

Transcription factors regulate multiple networks, mediating the responses of organisms to stresses, including drought. Here, we investigated the role of the wheat transcription factor TaSHN1 in crop growth and drought tolerance. TaSHN1, isolated from bread wheat, was characterized for molecular interactions and functionality. The overexpression of *TaSHN1* in wheat was followed by the evaluation of T₂ and T₃ transgenic lines for drought tolerance, growth, and yield components. Leaf surface changes were analysed by light microscopy, SEM, TEM, and GC-MS/GC-FID. TaSHN1 behaves as a transcriptional activator in a yeast transactivation assay and binds stress-related DNA *cis*-elements, determinants of which were revealed using 3D molecular modelling. The overexpression of TaSHN1 in transgenic wheat did not result in a yield penalty under the controlled plant growth conditions of a glasshouse. Transgenic lines had significantly lower stomatal density and leaf water loss and exhibited improved recovery after severe drought, compared with control plants. The comparative analysis of cuticular waxes revealed an increased accumulation of alkanes in leaves of transgenic lines. Our data demonstrate that TaSHN1 may operate as a positive modulator of drought stress tolerance. Positive attributes could be mediated through an enhanced accumulation of alkanes and reduced stomatal density. (Plant, Cell and Environment (2018) 41, 2549-2566)

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見背面

3. 25%

Plant starch is the main energy contributor to the human diet. Its biosynthesis is catalyzed and regulated by co-ordinated actions of several enzymes. Recently, a factor termed Protein Targeting to Starch 1 (PTST1) was identified as being required for correct granule-bound starch synthase (GBSS) localization and demonstrated to be crucial for amylose synthesis in Arabidopsis. However, the function of its homologous protein in storage tissues (e.g. endosperm) is unknown. We identified a PTST1 homolog in barley and it was found to contain a crucial coiled-coil domain and carbohydrate-binding module. We demonstrated the interaction between PTST1 and GBSS1 by fluorescence resonance energy transfer (FRET) in barley endosperm. By tagging PTST1 with the fluorophore mCherry, we observed that it is localized in the stroma of barley endosperm amyloplasts. PTST1 overexpression in endosperm increased endogenous *gbss1a* gene expression and amylose content. *Gbss1a* and *ptst1* mutants were generated using clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-related protein 9 (Cas9)-based targeted mutagenesis. Homozygous *gbss1a* mutants showed a waxy phenotype. Grains of *ptst1* mutants did not accumulate any starch. These grains dried out during the desiccation stage and were unable to germinate, suggesting that PTST1 is essential for development of starchy endosperm and viable grains. (Journal of Experimental Botany (2019) 70, 485-496)

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4. 25%

Despite well-established roles of microRNAs in plant development, little has been addressed to understand their effects in seeds especially on lipid metabolism. In this study, we showed that overexpressing microRNA167A (miR167OE) in camelina (*Camelina sativa*) under a seed-specific promoter changed fatty acid composition and increased seed size. Specifically, the miR167OE seeds had a lower α -linolenic acid with a concomitantly higher linoleic acid content than the wild type. This decreased level of fatty acid desaturation corresponded to a decreased transcriptional expression of the camelina fatty acid desaturase3 (*CsFAD3*) in developing seeds. MiR167 targeted the transcription factor auxin response factor (*CsARF8*) in camelina, as had been reported previously in Arabidopsis. Chromatin immunoprecipitation experiments combined with transcriptome analysis indicated that *CsARF8* bound to promoters of camelina *bZIP67* and *ABI3* genes. These transcription factors directly or through the *ABI3*-*bZIP12* pathway regulate *CsFAD3* expression and affect the α -linolenic acid accumulation. In addition to decipher the miR167A-*CsARF8* mediated transcriptional cascade for *CsFAD3* suppression, transcriptome analysis was conducted to implicate mechanisms that regulate seed size in camelina. Expression levels of many genes were altered in miR167OE, including orthologs that have previously been identified to affect seed size in other plants. Most notably, genes for seed coat development such as suberin and lignin biosynthesis were down-regulated. This study provides valuable insights on regulatory mechanism of fatty acid metabolism and seed size determination, and suggests possible approaches to improve these important traits in camelina. (The plant Journal (2019) <https://doi.org/10.1111/tpj.14223>)

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