# A mitochondrial carrier protein from *Chlamydomonas* alter the root architecture in Camelina.

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## Project goals:

Our research aims to sustainably increase oilseed yield in the non-food oil seed crop plants, *Camelina sativa*, thereby making it a commercially viable alternative for biofuels and bioproducts production. Camelina has been has shown considerable promise as a dedicated industrial oilseed crop because it requires low agronomic inputs, is naturally more resistant to both biotic and abiotic stress than other oilseed crops, and Camelina oil-based blends have been tested and approved as liquid transportation fuels[1,2]. The limitation in commercial adoption of camelina as an oilseed crop is its modest oil yield than its relative *Brassica napus*. The overall goal of this project is to boost the seed oil production of Camelina while retaining its low-input and stress resistance advantage. In this project, we seek to identify, optimize and combine traits that contributes to the flow of carbon from source to sink. Here we describe the impact of expression of LIP36 gene ( Low $CO_2$ induced protein) on roots, which are the main sink organs during early stages of plant development.

## Abstract:

The expression of *LIP36* (Low $CO_2$ induced protein) gene, a mitochondrial carrier protein from *Chlamydomonas reinhardtii* carbon concentrating mechanism, under constitutive promoter (35S) in Camelina has resulted in 40-70% increase in seed oil yield per hectare relative to control plants in field trials. *LIP36* is proposed to act as dicarboxylate transporter in mitochondria thereby promoting the cellular redox balance, photorespiratory flux and anapleurotic metabolism. This increases the flux through metabolic pathways that facilitates the fixation of $CO_2$ released during respiration and photorespiration. The expression of this gene promotes the non-cyclic TCA pathway and provides the carbon skeleton for N-fixation. One of the project goals was to

identify the positive traits that can result in better seedling establishment thereby contributing towards plant productivity. In the current work we further characterize the phenotype of the *LIP36* expressing Camelina plants. During early stages of development, the transgenic camelina plants has longer root length and higher rate of root elongation as compared to that of WT plants. The metabolite analysis on roots showed that the overexpressing lines has lower sucrose levels and alteration in mitochondrial metabolism. Genes related energy metabolism such as those involved in TCA cycle, oxidative phosphorylation and glucose metabolism are differentially regulated suggesting that the energy requirements in the root mitochondria have been altered. Thus, during early stages of the plant growth, the roots may be the active sink organs in the plants expressing LIP36 gene.

## References


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