

Machine Learning-Guided Transcription Factor Discovery for Increased Seed Lipid Content in Arabidopsis

Machine learning pinpoints organ-specific transcription factors to overexpress, raising Arabidopsis seed lipid content and accelerating regulator discovery.

Researchers at Purdue developed a method to increase seed lipid content through controlled over-expression of transcriptional regulators of *Arabidopsis thaliana*. Using machine-learning, this technology can target an organ and pinpoint key transcription factors and associated biological processes. Using this technology as a framework to better understand the seed lipid biosynthesis pathway, Purdue researchers identified both known transcriptional factor regulators of seed lipid content and predicted unknown ones. This technology helps researchers to better understand the role transcriptional factor regulators play in the expression of genes.

Technology Validation: Organ-specific datasets were created for the leaf, root, shoot, flower, seed, seedling, silique, and stem of model plant *Arabidopsis thaliana*, and then validated against known transcription factors regulators in the seed lipid biosynthesis pathway.

Advantages:

- Optimize transcriptional hypotheses test
- Improve understanding of gene regulatory networks

Applications:

- Increased seed lipid content
- Discovery of new transcription factors

TRL: 4

Intellectual Property:

Technology ID

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Category

Agriculture, Nutrition, &
AgTech/Crop Genetics &
Breeding
Biotechnology & Life
Sciences/Synthetic Biology &
Genetic Engineering
Biotechnology & Life
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