

Enhancing Lipid Production in Plant Cells through Automated High-throughput Genome Editing and Phenotyping

Background/Objective

Plant bioengineering is a time-consuming and labor-intensive process with no guarantee of achieving desired traits. To overcome this limitation, we sought to integrate an automated biofoundry with single-cell metabolomics to expedite the engineering of plant genomes and characterization of cellular effects, which has never been done before. Here, we present a fast, automated, scalable, high-throughput pipeline for plant bioengineering (FAST-PB) in model systems.

Approach

This pipeline seamlessly integrates the iBioFAB biofoundry for automated synthetic biology with matrix-assisted laser desorption/ionization Fourier transform ion cyclotron resonance mass spectrometry (MALDI FT-ICR MS) for high-throughput single-cell lipid identification.

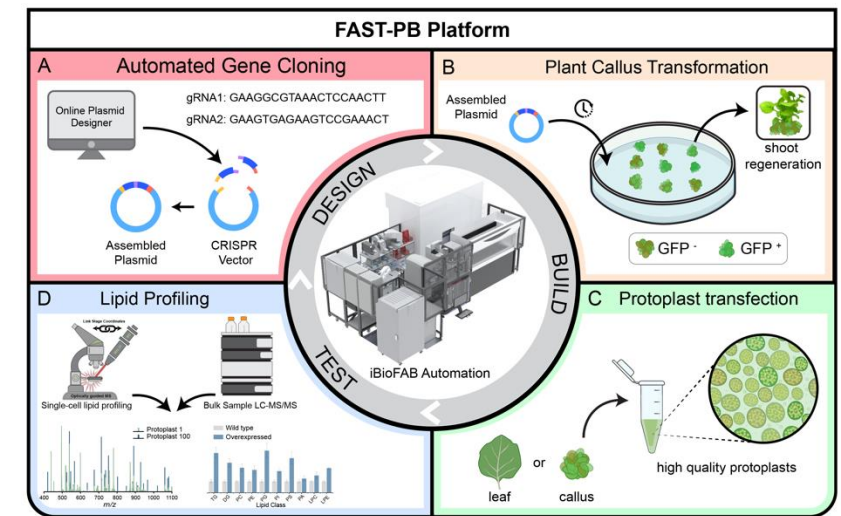
Results

Using FAST-PB in protoplasts, we found that 49 PEG2050 increased transfection efficiency by over 45%. For proof-of-concept, we established a reporter-gene-free method for CRISPR editing and phenotyping via mutation of *high chlorophyll fluorescence 136*. Diverse lipids were enhanced up to sixfold using CRISPR activation of lipid controlling genes. Lastly, FAST-PB enabled high-throughput single-cell lipid profiling by integrating MALDI-MS with the biofoundry, differentiating engineered and unengineered protoplast and callus cells using single-cell lipidomics.

Significance/Impacts

These innovations massively increase the throughput of synthetic biology, genome editing, and metabolic engineering and may change what is possible using single-cell metabolomics in plants, such as C_4 grasses. This workflow streamlines discovery, characterization, and fine-tuning of traits in highly scalable small cell cultures, leading to the regeneration of full plants after the desired phenotypes have been optimized.

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Overview of the FAST-PB for high-throughput genome editing and lipid 872 engineering in protoplast and callus cell systems.