

Analysis of Novel Bioproduct Pathways in Populations of Arthrospira platensis at Microorganism Resolution

OVERVIEW

Arthrospira platensis (Spirulina) is a filamentous cyanobacterium that has received much attention thanks to its potential as a renewable source of fuels and bioproducts, and current commercial-scale cultivation. Recent progress in metabolic engineering of Spirulina allows for the rapid and directed tailoring of both growth improvements and synthesis of novel bioproducts. Identifying which pathways are responsible for lipid production under stressed and mixed population conditions presents a unique analytical challenge. Here we demonstrate that ultrahighresolution imaging mass spectrometry (IMS) is suitable for global lipidome profiling in single microorganisms. MALDI imaging

coupled with Fourier transform ion cyclotron mass spectrometry was applied for the analysis of population heterogeneity to bioproduct yield and investigation of lipid rearrangements within wax ester producing strains.



RELEVANCE / BACKGROUND

- A high-throughput monitoring strategy that recognizes lipid fluctuations due to stress or lipid speciation events without sample preprocessing could provide timely information on e.g. population heterogeneity and physiological adaptation to environmental stressors
- Variability in single filaments can skew results and give falsely high (or low) values to a particular cell type during culture evaluations
- Matrix assisted laser desorption ionization, imaging mass spectrometry (MALDI-IMS) is powerful technique that is useful for characterization of lipids
- We report, for the first-time, high-resolution MALDI-IMS for unambiguous visualization and identification of lipids associated with a single-algae-filament.
- Lipidomic investigation is used to direct trait engineering and model the conversion of biomass to high value products.

SUMMARY

 Spirulina samples were immobilized on plasma-cleaned glass microscope slides. A key innovation of this method was the removal of salt prior to immobilization and subsequent sublimation without the delocalization of filaments. DHB and super-DHB matrices were evaluated for lipidomic coverage. A Bruker Solarix 7 T FT-ICR MS was used for data collection, and SCiLS Lab software was used to process and analyze data. High resolution and mass accuracy were utilized to determine elemental formula assignments for lipids, and assignments were confirmed with a custom database matching algorithm. Statistical population analysis was utilized to understand the diversity of lipid production between and within algae populations. Sample extracts were collected for compositional analysis, lipid quantitation, and lipid assignment validation by MS/MS..



ACCOMPLISHMENTS AND PROGRESS

High Spatial Resolution Imaging



Figure 1. 10 μ m spatial resolved MS images of single filaments.

This work was authored by the National Renewable Energy Laboratory, operated by Alliance for Sustainable Energy, LLC, for the U.S. Department of Energy (DOE) under Contract No. DE-AC36-08GO28308. Funding provided by the Bioenergy Technologies Office (BETO) at the US. Department of Energy Energy Efficiency and Renewable Energy office.. The views expressed in the article do not necessarily represent the views of the DOE or the U.S. Government. The U.S. Government retains and the publisher, by accepting the article for publication, acknowledges that the U.S. Government retains a nonexclusive, paid-up, irrevocable, worldwide license to publish or reproduce the published form of this work, or allow others to do so, for U.S. Government purposes. We acknowledge help from Hannah Alt, Kylie Smith, Nicholas Sweeney, and this work was carried out in close collaboration on engineered A. platensis strains created by Lumen Bioscience, Seattle, WA, and in particular by Damian Carrieri and Rachelle Lim.

High throughput Screening of Dense Cultures



Figure 2. MALDI FTICR imaging analysis of replicate filaments from algae cultures demonstrating population heterogeneity at 10 µm resolution. Mutant strains selectively express wax esters. Ion images of assigned lipids, MGDG, DGDG and wax ester expressed uniquely in genetically engineered and wildtype strains of A. platensis.



Peter V. Shanta, Steven M. Rowland, Lieve M. L. Laurens

ASMS 2020

CONCLUSIONS

- An optimized method for sample immobilization and matrix deposition enabled ion imaging of algae filaments at 10 µm resolution.
- A high-throughput monitoring strategy that recognizes lipid fluctuations due to stress or lipid speciation events without sample preprocessing could provide timely information on e.g. population heterogeneity.
- The novel approach we are developing here combines the use of a custom lipidomics database as a training tool for robust full lipidomics profiling of uncharacterized microbial species
- Metabolic engineering of A. platensis to produce novel lipids can be detected by high-throughput lipidomics and by MALDI – imaging mass spectrometry (MALDI-IMS)
- This approach has many potentially useful applications, including early signs of genetic drift within a cell population, metabolic engineering optimization and general culture health monitoring where univariate and multivariate analytical approaches can be applied to MALDI-imaging data

Single Filament Separation and Interrogation for Discriminate Analysis of Population Heterogeneity



Figure 3. Single filaments were immobilized for IMS analysis Three ion images showing lipid heterogeneity within population.

Figure 4. Discriminate PCA investigation of single filaments. Results show that transgenic algae express several spatially resolved phenotypic traits, including lipid rearrangements in acyl chain length, loss/gain of lipid classes, and effects on algae growth.