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Determination of Metabolite and Lipid Turnover Rates in Live Microalgae by Pulse-Chase Analysis and Laser Ablation Electrospray Ionization Mass Spectrometry Tarek R. Mansour,^a Sylwia A. Stopka,^a Bindesh Shrestha,^a Éric Maréchal,^b Denis Falconet,^b and Akos Vertes^a

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INTRODUCTION

- The model organism, Chlamydomonas reinhardtii has been explored to further understand important biological processes, such as photosynthesis and lipid production, for its relevance as a biofuel source.¹
- Laser ablation electrospray ionization (LAESI) coupled with ion mobility separation (IMS) for mass spectrometry (MS) has been applied in the profiling of metabolites, lipids, and peptides from cell populations and tissue sections.²
- Stable isotope pulse-chase analysis followed by MS allows time course profiling of labeled metabolites, enabling the determination of molecular turnover rates under varied stress conditions.
- In this study, pulse-chase analysis followed by LAESI-IMS-MS (Figure 1) was used to monitor the ¹⁵N ¹⁴N isotope exchange and to determine the turnover rates of nitrogen containing compounds in small cell populations of *C*. reinhardtii.



Figure 1. Schematic of pulse-chase analysis. In the pulse phase, C reinhordtii cells are inoculated in an ¹⁵Nlabeled TAP medium. Within the chase phase, an excess of ¹⁴N medium is introduced. Over time, nitrogen containing compounds undergo and ¹⁵N to ¹⁴N isotope exchange that is analyzed using LASSI-MS-MS.

METHODS

- Wild type C. reinhardtii was cultured in tris-acetate phosphate (TAP) medium at a constant temperature (27 °C) in an orbital shaker (80 RPM) incubator under a 12 h light (100 µmol·m²sec⁻¹) - 12 h dark cycle.
- In the pulse phase, cells were cultured in ¹⁵N-labeled TAP medium for 96 h. The chase phase was initiated by replacing the ¹⁵N-labeled medium with an excess of ¹⁴N-TAP medium.
- During the chase phase, sampling was performed at various time points by mid-IR laser ablation (2.94 µm wavelength and 5 ns pulse length) of the cell pellets. The generated plume was ionized by an electrospray, and a time-of-flight MS equipped with traveling-wave IMS analyzed the m/z and drift times (DT) of individual ions, respectively.
- Following the time course of exchanging the ¹⁵N-labeled metabolites and lipids in the sample by their ¹⁴N counterparts provided insight into the turnover rates of these molecules.

PULSE-CHASE ANALYSIS

- Both ¹⁵N-labeled and ¹⁴N media provided similar growth results for the *C. reinhardtii* cells. The mass spectra of cells cultured in ¹⁵N-labeled and ¹⁴N media, obtained by LAESI-MS, show similar ion distributions in both environments (Figure 2a).
- The number of nitrogen atoms present in the compound were determined by the shift in m/z upon isotope substitution. For example, the incorporation of a single ¹⁵N was found in highly abundant nitrogen containing lipids, diacylg/veryl-N,N-trimethylhomoserines (DGTS), in *C reinhardtii* cells and was verified by tandem MS (see Figure 2b).



Figure 2. (a) Representative LASS mass spectra of *C. reinhardtii* cells cultured in ¹⁵N (top) and ¹⁴N (bottom) media. (b) MS/MS spectra of DGTS [18:3/16:3) [ipid species cultured in ¹⁵N-TAP (top) and ¹⁴N-TAP (bottom) media show successful incorporationed a single ¹⁵N into the head group of DGTS [18:3/16:3) (into 1 a 1 anu shift in the *m*/z value.

To visualize differences between the labeled and unlabeled compounds, HDMS Compare was employed. Ions with the same DT but with m/z differing by a small integer revealed the number of replaceable N atoms in the molecule. For example, ¹⁴N and ¹⁵N chlorophyll *a* ions exhibited the same DT, but the m/z value was shifted by 4 units due to the presence of 4 N atoms in the molecule (Figure 3).

LIPID AND PEPTIDE KINETICS

- Time course profiles were obtained by LAESI-MS analysis for the exchange from ¹⁵N to ¹⁴N in N-containing compounds. Turnover rates and half-lives were then calculated, e.g., for two DGTS lipids that were detected in *C. reinhardtii* cells (Figure 4).
- Signal enhancement of low abundance peptides was observed by LAESI-IMS-MS. A 2.8 kDa peptide was only detected after IMS separation. The pulse-chase analysis revealed the incorporation of 36 nitrogen atoms into this molecule (Figure 5).

RESULTS AND DISCUSSION



Figure 3. (a) Due to the similarity in the mobility of loss from L relational time like and the like of the loss of the los



Figure 4. (a) LASS1465 speech; af C. anisheddi cells during pain Lines (b) (b) Lass (b) Lass



Figure 5. (a) LAESI-IMS-MS spectra of the 4+ charge state of a 2.8 kDa peptide followed in *C*-reinhardtri during pulse-chase analysis over a 72 h time period. Corresponding DT window for the selected peptide ion (4+) for each time point is shown at the right. (b) Kinetics of the peptide turnover for the two charge states with corresponding turnover rates and half-lives.

CONCLUSIONS

- Pulse-chase method followed by LAESI-IMS-MS can add insight into metabolic network dynamics and molecular turnover rates in live biological systems.
- For the detection of ¹⁵N to ¹⁴N kinetics, IMS was a valuable tool by reducing iosbaric interferences and aiding in the detection of low abunadance species.

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