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USE OF FOURIER TRANSFORM INFRARED SPECTROSCOPY FOR THE CHARACTERIZATION OF ALGAL COMPOSITION AND THE SELECTION OF STRAINS FOR PRODUCTIVE PROCESSES

PALMUCCI M., GIORDANO M.

Dipartimento di Scienze del Mare, Università Politecnica delle Marche, Via Brecce Bianche, 60131 Ancona (Italy)

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The characterization of biomass is typically a rather lengthy, complex, costly and time consuming endeavor. Because of this, screening of species and growth condition for commercial applications is often limited to few organisms and growth treatments or based solely on literature information. Conversely, Fourier Transform Infrared (FTIR) spectroscopy allows a reliable, fast, and inexpensive assessment of the quality of biomass, without the need for extractive procedures and distinct analytical methods for the different pools. Furthermore, the use of FTIR spectroscopy minimizes sample size, because few cells are needed for each measurement.

Our work was performed on 11 microalgal species belonging to a wide range of taxa. Each of these species was subjected to three growth regimes that differed for the availability of nitrogen (provided as nitrate). We chose this cultural system because an imbalance in the external C:N ratio may appreciably affect C allocation thus allowing the generation of biomass with a variety of stoichiometries.

We developed a new computational method for the semi-quantification of macromolecular pools; this made it possible to partially overcome the difficulties associated with a quantitative use of whole cell FTIR spectroscopy. No obvious relationship was observed between the taxonomy and the C allocation patterns of the 11 algal species. Most species responded to a lower N availability by accumulating lipids or carbohydrates. *Dunaliella parva* and *Thalassiosira pseudonana*, however, were homeostatic with respect to their organic cell composition. The cell lipid content showed a a hyperbolic relationship with cell volume. The FTIR data were selectively validated by comparison with commonly used methods.

Our results confirmed that FTIR spectroscopy is a powerful tool for the assessment of biomass quality and for the rapid screening of large number of species and growth conditions. Since this methodology allows the simultaneous determination of all main macromolecular pools, it can be applied regardless of what end product is targeted.