

3rd International Conference and Exhibition on Metabolomics & Systems Biology

March 24-26, 2014 Hilton San Antonio Airport, San Antonio, USA

Assessing original biomarkers of nitrogen stressed cultured microalgae using metabolomics approach: An application to biodiesel dedicated photobioreactor monitoring

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Microalgae appear to be one of the most promising sustainable resources as alternative crops for the production of renewable transport fuel. The exploitation of this bioresource requires, however, a fine monitoring of the culture conditions, for example by using more relevant control variables than usual macroscopic indicators (biomass or pigment estimation). In this proof of principle study, we propose to search potential biomarkers of progressive nitrogen regime culture conditions using an untargeted metabolomic approach based on LC-HRMS combined to a non-invasive analysis based on FTIR spectroscopy. One microalgae model was investigated i.e. *Chlamydomonas reinhardtii* to characterize the effect of progressive nitrogen regime in batch culture conditions on its metabolome. FTIR allowed assessing the intracellular macrometabolic perturbations, highlighting the over-accumulation of carbohydrates. LC-HRMS complemented the macromolecular information by revealing the dependence of microalgae metabolotypes on nitrogen regime conditions tested for cells culture. Patterns of significantly modulated metabolites were detected during those slight contrasted nitrogen regimes and interesting features were structurally elucidated. This included metabolites belonging to the pantothenate, branched chain and aromatic amino acids pathways. In the last step of this study, amino acid targets proposed by metabolomics investigations were assessed on nitrogen-limited continuous culture on photobioreactors, in order to test validity of proposed targets in real small-scale industrial production conditions. Results were very encouraging and suggested the possibility of using potentially relevant metabolites as intracellular biomarkers only (tryptophan) or as both intra and extracellular biomarkers (e.g. 2-methylbutyric acid and ketoleucine).

Biography

Olivier Goncalves has completed his Ph.D. at the age of 28 years from Nantes University and postdoctoral studies from EMBL. He firstly developed skills in transcriptomics as assistant Prof. in Clermont-Ferrand University (France) in the LMGE laboratory (UMR CNRS 6023), and is actually assistant Prof. at Nantes University in the GEPEA laboratory (UMR CNRS 6144) developing skills in metabolomics and fluxomics. He is author or co-author of 43 act of communications (18 written + 25 oral).

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