

## Lipid species profiling of yeast mutants defective for putative glycerolipid acyltransferases by mass spectrometry

Ayciriex S.<sup>1</sup>, Ejsing C.S.<sup>2</sup>, Le Guedard M.<sup>1</sup>, Bessoule J.J.<sup>1</sup>, Lessire R.<sup>1</sup>, Shevchenko A.<sup>2</sup>, Schmitter J.M.<sup>3</sup> and Testet E.<sup>1</sup>

<sup>1</sup> Membrane Biogenesis Laboratory, University of Bordeaux UMR5200/CNRS, France;

<sup>2</sup> Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany;

<sup>3</sup> Biological Mass spectrometry Laboratory, Institut Européen de Chimie et Biologie, CBMN-UMR5248, University of Bordeaux, France

In addition to their structural properties as main constituents of biological membranes, lipids play a multitude of roles such as in cell signalling, energy storage, and protein transport. Their biological importance has led to an increasing focus on analytical methods for the characterisation of their individual molecular species. Improvements in mass spectrometric technology has provided a great advantage for the characterisation and quantification of molecular lipid species in total lipid extracts (Han and Gross, 2005; Murphy *et al.*, 2001). For instance, phospholipid molecular species can be identified on the basis of a characteristic fragment of the lipid class, the nature of the acyl chains and their positions on the glycerol backbone.

A method allowing the quantitative profiling of the yeast lipidome was developed in a recent study using automated shotgun infusion strategy (Ejsing *et al.*, 2009). We applied this method to characterise several lysophospholipid acyltransferase yeast mutants produced using reverse-genetics. These enzymes are involved in essential biological processes like *de novo* synthesis or remodelling of the phospholipid membrane component (Testet *et al.*, 2005; Le Guedard *et al.*, submitted). The comparative analysis of phospholipid molecular species from the wild-type strain and the corresponding deletion mutants has allowed us to identify lipid compositional changes, and has given us significant indications about the *in vivo* function of the encoded lysophospholipid acyltransferases.

### References:

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