Twenty four novel odd-carbon glycerophospholipid species have been formulated in conjunction with the LIPID MAPS Project for use as LC/MS internal standards. To bracket the entire range of biologically relevant phospholipids, four lipids per diradyl class (ranging from small saturated to large polyunsaturated species) were prepared. Odd-carbon standards were chosen for this project due to the fact that they do not occur naturally in most mammalian systems. Due to varying ionization efficiencies across a lipid class, multiple standards within a class with varying degrees of unsaturation and carbon chain length are required for the production of standard curves for all possible biologically relevant species.

Standards from six diradyl and two lyso lipid classes have been incorporated into LIPID MAPS LC/MS protocols for normalization and quantitation of data. As an aid to the lipid community, fully annotated MS/MS fragmentation data for all of the standards is now available on the LIPID MAPS public website.

continued overleaf
Recognition of the importance of lipid signaling in cellular function has led to rapid progress in the technology of lipid analysis. Measurements of lipid species changes are central to defining the networks of cell signaling (e.g., receptor activation by hormones or drugs) and lipids are involved in many biochemical and pathological processes. During the last several years our laboratory has focused on developing efficient methods for extraction of glycerophospholipids from biological systems and their detection and identification by mass spectrometry. We analyze phospholipid changes in mammalian cells as a result of a defined ligand stimulation strategy that supports the research questions of the consortium. The improvement of mass spectrometry techniques for phospholipid analysis combined with sophisticated computational methods developed in our group has facilitated simultaneous analysis of hundreds of phospholipid species in mammalian cells. This information is presented as Lipid Arrays (or more precisely as virtual arrays) and allows identification of temporal changes in membrane phospholipid species between two contrasting biological conditions (e.g., unstimulated basal vs. stimulated or as a contrast between normal and disease stages). Using the lipidomics approach, we are able to identify approximately 450 phospholipid species from total membrane extracts and qualitatively measure pattern response changes initiated by cell surface receptors. As such, this approach facilitates the elucidation of the metabolic changes induced by a perturbation in the cell and recognition of patterns of signaling.


For information about procedures and guidance in the application of these Lipid Standards visit: www.lipidmaps.org/downloads/2007_methods_chapters.pdf

Glycerophospholipid standards
A total of 24 phospholipid standards have been formulated in methanol.
Single use, 1 mL ampoules are sufficient for over 50 samples (based on cell extracts from 10 million cells).

Cardiolipin Standards also available.

Phospholipid stability graphs for GPCho (A), GPEtn (B), and GPGro (C) odd-carbon standards stored at -20°. Ampoules are monitored bi-monthly by LC/MS/MS analysis

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