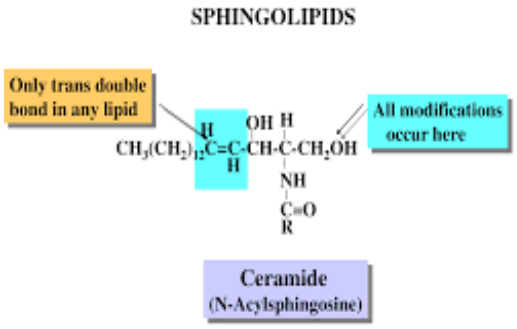
Quantitation of sphingolipids in mammalian cell lines by Liquid Chromatography-Mass Spectrometry in analysis of membrane lipids

In this chapter, scientists at DBT's Regional Centre for Biotechnology (RCB), Faridabad presented a simple, sensitive, and robust method to simultaneously quantitate sphingolipids of the early steps of the metabolic pathway by a liquid chromatography–mass spectrometry-based method using mammalian cells as model system.



Sphingolipids are a major class of bioactive structural lipids that also play diverse roles in signalling events in different disease conditions like cancer. They form a dynamic metabolic network, and alterations in their metabolism are known to contribute to progression of the disease. Therefore, quantitation of such metabolites from mammalian cells as a disease model system can provide us a vivid picture of the regulatory nodes in the pathway that can be targeted to identify sphingolipids-based biomarkers or targets for future therapies.

Link: https://link.springer.com/protocol/10.1007/978-1-0716-0631-5_7