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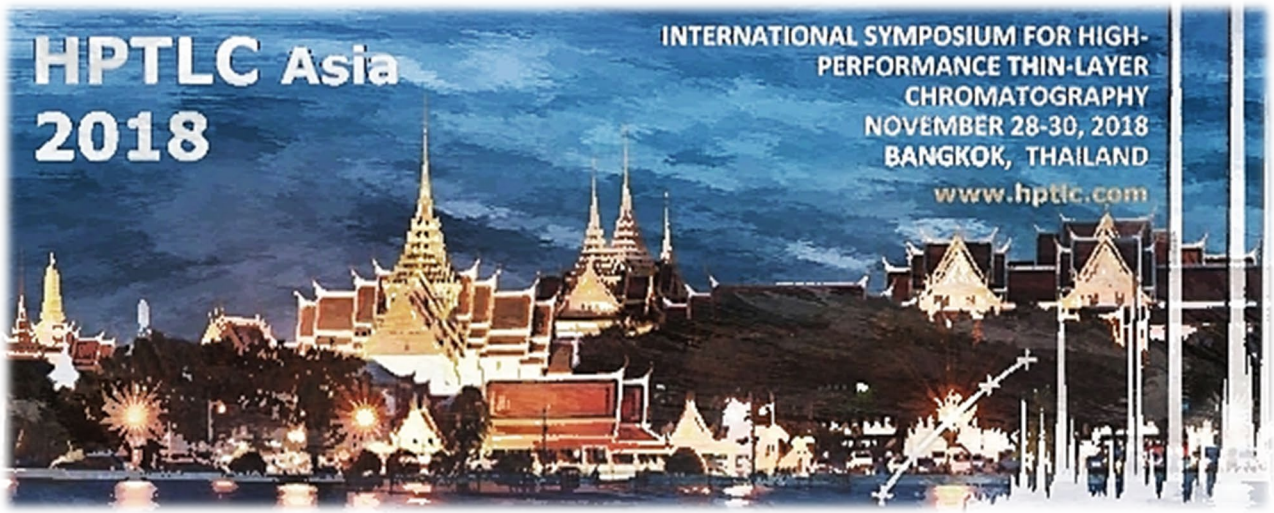

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HPTLC of lipid-based mixtures in different matrices: Combination of densitometry and mass spectrometry for obtaining qualitative and quantitative sample information

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In complex samples, such as derived from food or lipidomics (LC), hundreds of analytes can be present. A substantial part of these compounds has not yet been identified. As the quantification is still based on the availability of target compounds as calibration standards, it becomes too costly or directly impossible to obtain standards for all possible unknown compounds. In this context, while performance of modern analytical instruments progressively increases, semi-quantitative approaches make sense. As it has been recognized in LC, there is no self-sufficient technique for lipid analysis. Despite the high separation efficiency of column LC using reversed phase, quantification by LC–mass spectrometry (MS) is complicated due to the high dependence of response factors on ionization conditions, even for structurally similar lipids eluted at different retention times. High-performance thin-layer chromatography (HPTLC) has been very popular in lipid analysis. Unlike LC, most of the separation of lipid samples are performed on silica gel plates, which allow to group lipids in classes according to their polar head, each class including different lipid fatty acid chain lengths. A strong point of HPTLC is multiple detections. Coupling of ultraviolet/focal length scanning densitometry with MS opens the door to obtain representative profiles and deep identifications of lipid molecular species in complex samples, with the possibility of selectively detecting a desired zone of plate. All these aspects, as well as some strategies for obtaining reliable semi-quantitative information, will be discussed in the light of recent literature concerning glycerophospholipids, (glyco)sphingolipids, fatty acids, glycerolipids, and other lipids found in different matrices of interest.

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