UPLC-MSE : a fast and convenient method for profiling phytoplankton metabolites : application to the identification of pigments and structural analysis of metabolites in Porphyridium purpureum.

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Résumé

A fast and high-resolution UPLC-MSE analysis was used to identify phytoplankton pigments in an ethanol extract of Porphyridium purpureum (Pp) devoid of phycobiliproteins. In a first step, 22 standard pigments were analyzed by UPLC-MSE to build a database including retention time and accurate masses of parent and fragment ions. Using this database, seven pigments or derivatives previously reported in Pp were unequivocally identified: β,β-carotene, chlorophyll a, zeaxanthin, chlorophyllide a, pheophorbide a, pheophytin a, and cryptoxanthin. Minor amounts of Divinyl chlorophyll a, a chemotaxonomic pigment marker for prochlorophytes, were also unequivocally identified using the database. Additional analysis of ionization and fragmentation patterns indicated the presence of ions that could correspond to hydroxylated derivatives of chlorophyll a and pheophytin a, produced during the ethanolic extraction, as well as previously described galactosyldiacylglycerols, the thylakoid coenzyme plastoquinone, and gracilamide B, a molecule previously reported in the red seaweed Gracillaria asiatica. These data point to UPLC-MSE as an efficient technique to identify phytoplankton pigments for which standards are available, and demonstrate its major interest as a complementary method for the structural elucidation of ionizable marine molecules.

Mots-Clés: carotenoid, chlorophyll, dereplication, divinyl chlorophyll a, galactosyldiacylglycerol, gracilamide, mass spectrometry, MSE, phytoplankton, pigment, Porphyridium purpureum, UPLC

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