Multimodular type I polyketide synthases in algae evolve by module duplications and displacement of AT domains in trans

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Abstract

BACKGROUND: Polyketide synthase (PKS) catalyzes the biosynthesis of polyketides, which are structurally and functionally diverse natural products in microorganisms and plants. Here, we have analyzed available full genome sequences of microscopic and macroscopic algae for the presence of type I PKS genes. RESULTS: Type I PKS genes are present in 15 of 32 analyzed algal species. In chlorophytes, large proteins in the MDa range are predicted in most sequenced species, and PKSs with free-standing acyltransferase domains (trans-AT PKSs) predominate. In a phylogenetic tree, PKS sequences from different algal phyla form clades that are distinct from PKSs from other organisms such as non-photosynthetic protists or cyanobacteria. However, intermixing is observed in some cases, for example polyunsaturated fatty acid (PUFA) and glycolipid synthases of various origins. Close relationships between type I PKS modules from different species or between

modules within the same multimodular enzyme were identified, suggesting module duplications during evolution of algal PKSs. In contrast to type I PKSs, nonribosomal peptide synthetases (NRPSs) are relatively rare in algae (occurrence in 7 of 32 species). CONCLUSIONS: Our phylogenetic analysis of type I PKSs in algae supports an evolutionary scenario whereby integrated AT domains were displaced to yield trans-AT PKSs. Together with module duplications, the displacement of AT domains may constitute a major mechanism of PKS evolution in algae. This study advances our understanding of the diversity of eukaryotic PKSs and their evolutionary trajectories.

Beteiligte Forschungseinheiten

Microbiome Dynamics Gianni Panagiotou Mehr erfahren

Leibniz-HKI-Autor*innen

Ekaterina Shelest

Details

Themenfelder

Vorhersage genregulatorischer Elemente und Gencluster in Pilzen

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