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Freshwater macrophyte metabolomics: Progress and prospects

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Abstract

The history of the study of allelopathy in aquatic ecosystems goes back over 100 years. However, the importance of this phenomenon for understanding the structural and functional organization of aquatic ecosystems is beginning to become clear only now. The known information on the low molecular weight metabolome (LMWM) of various macrophytes demonstrates that over 1500 different LMWOCs (low molecular weight organic compounds) can be found in its composition. Moreover, the number of LMWOCs in certain plant species growing in certain habitats can exceed 200 compounds. It is shown that there are patterns of formation and changes in LMWM macrophytes, both depending on the geographical place of plant growth, and the impact of various biotic and abiotic factors. Particular attention is drawn to the issues related to the study of the allelopathy of macrophytes in freshwater ecosystems. For macrophytes of various ecological groups, their inhibiting allelochemicals are described, as well as ecological targets - algae, and cyanobacteria. The direction of studying the potential biological activities of major LMWOCs of aquatic macrophytes using the QSAR method is of great importance. The questions of the chemical protection of aquatic plants against consumers, pests, and pathogens are of theoretical and practical importance. It is shown that it is realistic to create new generation algicides based on natural allelochemicals to prevent and suppress the "bloom" of water bodies. The allelopathy (as a natural phenomenon) can be used for the development of a nature-like convergent technology to control the “bloom” in aquatic ecosystems. Metabolomics is the scientific study of chemical processes involving metabolites, the small molecule substrates, intermediates and products of cell metabolism. The metabolome represents the complete set of metabolites in a biological cell, tissue, organ or organism, which are the end products of cellular processes. Messenger RNA (mRNA), gene expression data and proteomic analyses reveal the set of gene products being produced in the cell, data that represents one aspect of cellular function.

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