Microcyclamide biosynthesis in two strains of Microcystis aeruginosa: from structure to genes and vice versa.

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Abstract

Comparative analysis of related biosynthetic gene clusters can provide new insights into the versatility of these pathways and allow the discovery of new natural products. The freshwater cyanobacterium Microcystis aeruginosa NIES298 produces the cytotoxic peptide microcyclamide. Here, we provide evidence that the cyclic hexapeptide is formed by a ribosomal pathway through the activity of a set of processing enzymes closely resembling those recently shown to be involved in patellamide biosynthesis in cyanobacterial symbionts of ascidians. Besides two subtilisin-type proteases and a heterocyclization enzyme, the gene cluster discovered in strain NIES298 encodes six further open reading frames, two of them without similarity to enzymes encoded by the patellamide gene cluster. Analyses of genomic data of a second cyanobacterial strain, M. aeruginosa PCC 7806, guided the discovery and structural elucidation of two novel peptides of the microcyclamide family. The identification of the microcyclamide biosynthetic genes provided an avenue by which to study the regulation of peptide synthesis at the transcriptional level. The precursor genes were strongly and constitutively expressed throughout the growth phase,

excluding the autoinduction of these peptides, as has been observed for several peptide pheromone families in bacteria.

Beteiligte Forschungseinheiten

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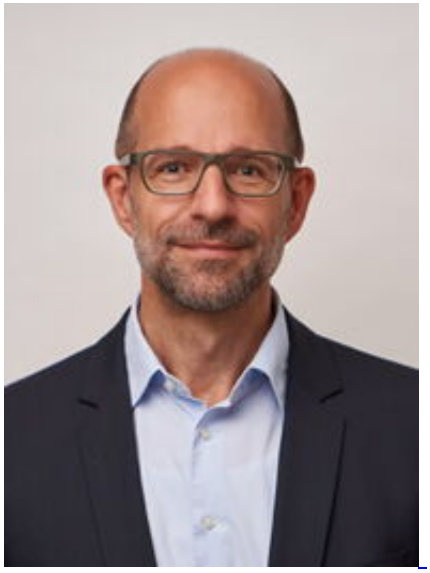

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