

GENETICS

Gene clusters in biosynthesis of skyrin in lower eukaryotes

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study form: full time

Annotation: Endophytic microorganisms infect plant tissues and very often are able of mutualistic coexistence. Endophytic fungi are the most common endophytes colonizing plants. Some of them synthesize host-specific secondary metabolites or their intermediates which rank them among candidates not only for the study of gene function but also for prospective biotechnological production. Several endophytic fungi including those which were isolated from some representatives of the genus *Hypericum* produce wide spectrum of anthraquinones. One of them is bioactive bisanthraquinone skyrin, a putative intermediate in biosynthesis of anti-tumour drug hypericin synthesized by some representatives of the genus *Hypericum*. Gene cluster consisting of five genes of polyketide biosynthesis leading to skyrin was recently identified in endophytic fungus *Cyanodermella asteris*. Preliminary *in silico* analysis confirmed the presence of this gene cluster also in other endophytes with sequenced genome which colonize some of *Hypericum* species. The aim of this thesis is to identify the genes of this gene cluster in endophytic fungi isolated from the genus *Hypericum* as well as in the host plants which are producers of hypericin and its intermediate skyrin and to earn new findings about regulation of hypericin biosynthesis and crosstalk between endophytic fungi and their hosts in secondary metabolism.

Phylogenomics and phyloproteomics of extreme environments microbiomes

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study form: full time

Annotation: Recently, there is a growing interest in the extreme environments study. The driving force of this interest is a better understanding of conditions for the existence of life on the Earth and in the Space, understanding of genetic adaptations to life in extreme environments and practical applications of information obtained in modern biotechnologies as well. Extreme environments are a rich source of undiscovered biodiversity, and multiple biologically active compounds. Most of anthropogenic and natural extreme environments are inhabited by microorganisms, mainly bacteria. The aim of the project is an analysis of genetic diversity of selected extreme environments microbiomes using modern phylogenomic and phyloproteomic approaches, characterization of new species of bacteria, identification of genetic adaptations to the life in extreme environments and the characterization of parvome, small biologically active biomolecules produced by microbiomes of extreme environments.