

Genetics

Phylogenomics and phyloproteomics of extreme environments microbiomes

supervisor: doc. RNDr. Peter Pristaš, CSc.

consultant: prof. RNDr. Jana Kaduková, PhD.

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.

Correlation analysis of metabolome and miRNA of some *Hypericum* spp.

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study form: full time

Annotation: The representatives of the genus *Hypericum* are important sources of pharmacodynamically effective bioactive substances. The phytocomplex *Herba Hyperici* consists along with unique photodynamic pigments – naphthodianthrone (hypericin and its derivatives) also of other phenolic compounds like hyperforin and adhyperforin and related phloroglucinols, flavonoids (rutin, quercetin, isoquercetin, quercitrin, hyperosid, biflavones – kaempferol, amentoflavone), chlorogenic acid i.e. Naphthodianthrone and phloroglucinols belong to polyketide group but regulation of their biosynthesis is still far from being understood. Despite there are several candidate biosynthetic genes identified from transcriptomic data their function has not been experimentally verified yet. Although the function of miRNA in regulation of secondary metabolism is known, information on their role in regulation of the profiling secondary metabolites in the genus *Hypericum* is missing. The aim of this thesis is to create miRNA profile for selected species/tissues of the genus *Hypericum* possessing different biosynthetic potential and, based on correlations with the metabolome to identify and verify specific miRNA with regulation role.

Endophytes from *Hypericum* spp., their characterization, identification and study of interactions with host plant

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study form: full time

Annotation: Endophytes, organisms colonizing the living internal tissues without causing any symptoms of disease in the host cells, are important components of plant micro-ecosystems. There is very little information about the relationship between endophytes and their host plants. One of the benefits of interaction between host plants and endophytes is possibility of production of important secondary metabolites (e.g. taxol, camptothecin, podophyllotoxin ...) originally produced by plant.

Only one endophytic fungus *Thielavia subthermophila* isolated from *Hypericum perforatum*, in which hypericin and its proposed precursor emodin were detected, has been identified so far. The search for more endophytes from *Hypericum* spp. capable of producing important plant secondary metabolites requires a screening of many endophytes, which includes morphological, enzymatic, metabolomic characterization and genetic identification. An important part of the work will be transcriptomic and/or genomic analysis of selected endophytes with the aim of clarifying and validating candidate genes with a supposed role in the biosynthesis of bioactive metabolites in *Hypericum* spp.

Metabolome of the genus *Hypericum* aimed at identification of metabolic intermediates involved in biosynthesis of hypericin

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study form: full time

Annotation: The genus *Hypericum* comprises about 500 plant species distributed worldwide. The most known and the best studied representative of the genus is called *Hypericum perforatum* L. (St. John's Wort). The extracts of *H. perforatum*, as well as from some other species of the genus *Hypericum*, contain important bioactive compounds such as naphthodianthrone (hypericins), phloroglucinols (hyperforins) and flavonoids (quercetin, rutin, hyperoside). The effects of photo-activated hypericin, acting in photodynamic therapy of tumors, and anti-depressive, anti-inflammatory or anti-mycotic effects of above-mentioned compounds are eminent. The studies focused to reveal the presence, amount and localization of secondary metabolites in tissues of *Hypericum* spp. should contribute to elucidation of biosynthesis pathway of hypericin and its precursors. Up today, the arguments considering emodin and (or) emodin-anthrone to be the precursors of hypericins are not sufficiently acknowledged. The bis-anthraquinone skyrin, which was previously proclaimed to be a potential precursor of protohypericin in study of Hölzl and Petersen (2003) is also of interest. The aim of the dissertation thesis is to study the presence of these bioactive compounds in different representatives of the genus *Hypericum* to clarify the role of emodin, emodin-anthrone, and skyrin in biosynthesis of hypericin, and also to analyze the candidate genes. In order to enrich the knowledge about metabolome of the genus *Hypericum*, the analysis of the presence of another medically important compounds like melatonin will be investigated in selected *Hypericum* species.