

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 *Cyanoderma 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.

Biosynthetic genes coding for bioactive anthraquinones in *Hypericum* plants and *Hypericum*-borne endophytic microorganisms – „a possible crosstalk“

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study form: full time

Annotation: Endophytic fungi belong to the most important producers of bioactive anthraquinones. Their occurrence in plants is scarce, however, there is one exception represented by some species of the genus *Hypericum* which are the only producers of bioactive anthraquinones, especially hypericin with enormous pharmacodynamics potential in the plant kingdom. The aim of this work is to ascertain whether biosynthetic genes of the polyketide pathway leading to production of anthraquinones are present in both, *Hypericum* plants and *Hypericum*-borne endophytic isolates and how their products communicate in the course of biosynthesis.

Bioprocess optimisation for biomass production of fungal endophytes grown in bioreactor for pharmaceutical purposes

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study form: full time

Annotation: Some *Hypericum*-borne endophytic isolates are producers of important bioactive anthraquinones but their growth under *in vitro* conditions is slow. Insufficient biomass increase limits genetic and metabolomics studies and their perspective use for biotechnological production. The aim of this thesis is focused on optimisation of bioprocesses for biomass production of some *Hypericum*-borne endophytic microorganisms with biosynthetic potential for production of bioactive anthraquinones in a small-scale bioreactor.

Biotechnological platforms for production of bioactive phloroglucinols

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study form: full time

Annotation: Polycyclic polyprenylated acylphloroglucinols (PPAPs) belong to the profiling secondary metabolites in the genus *Hypericum*. There are approximately 600 PPAPs but only several were identified in the genus *Hypericum*. This project is aimed at phytochemical screening of PPAPs in rare *Hypericum* spp. and elaboration of experimental systems for their prospective biotechnological production. As a short-term objective the root cultures of the PPAPs producers taking into account positive correlation between biomass production and PPAPs content will be established followed by optimization of the conditions for continuous PPAPs production in small-scale laboratory bioreactor.

Comparative genomics of *Acinetobacter* spp. isolates from extreme environments

supervisor: doc. RNDr. Peter Pristaš, CSc. (peter.pristas@upjs.sk)

study form: full time

Annotation: Bacteria belonging to the genus *Acinetobacter* have recently emerged as important nosocomial pathogens. However, very similar isolates are frequently found in natural environments, especially in environments contaminated by heavy metals or organic pollutants. The extreme ecological versatility and adaptability of *Acinetobacter* spp. is due to its genome plasticity. *Acinetobacter* spp. pan-genome is very dynamic mainly due to large number of mobile genetic elements, mainly plasmids. The acquisition of new genetic traits and determinants by horizontal gene transfer allowed *Acinetobacter* spp. to colonize wide spectrum of extreme environments, contributing thus to the development of a multi-resistant strains. The aim of the project is a genomic analysis of selected *Acinetobacter* spp. isolates from extreme environments, obtaining complete genome sequences of several *Acinetobacter* spp. plasmids and subsequent comparative genomic analysis with aim of better understanding of mechanisms allowing plasmids to become effective vectors of gene exchange.

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.