

GENETICS

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.

Biodiversity of wood-destroying fungi as a source of new biologically active substances with potential use in antimicrobial therapy

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Annotation: The unprecedented rise in antibiotic resistance is a serious medical problem today, and recent analysis suggests that infections due to antibiotic-resistant bacteria will become the leading cause of death in developed countries in the near future. Despite advances in synthetic chemistry, substances of natural origin are used for antibacterial treatments. Although the first widely used antibiotic came from fungi, with the progress in chemistry, in Europe, we lost knowledge on the possible therapeutic or preventive use of biologically active substances produced by fungi. The aim of the thesis is to explore yet unrecognized biodiversity of wood-destroying fungi as a source of new biologically active substances with potential use in antimicrobial therapy. Within the project, the genetic diversity of selected species of wood-destroying fungi will be studied and methods for their in vitro cultivation will be developed. The biological activity of fungi will be analysed and active substances produced by the fungi will be purified, and the chemical structure and antimicrobial activity will be investigated.

Endophytic microorganisms as a model for study of biosynthetic genes

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Annotation: Endophytic microorganisms are integral part of a plant lifecycle. Their mutual relation and communication channels attract many scientists. There is a strong evidence that endophytic microorganisms produce several metabolites that are typical for their hosts but it is not clear whether they synthesize the products on a complementary base or independently, and what are the differences in genetic determination and epigenetic regulation. Naphthodianthrone hypericin and the

proposed precursor skyrin belong to the profiling secondary metabolites found only in some *Hypericum* spp. Biosynthesis of hypericin which is not completely uncovered is accompanied with production of several anthraquinone intermediates which are, along with the final products, present also in *Hypericum*-borne endophytes. It is anticipated that hypericin biosynthesis in endophytes is regulated by simultaneous expression of biosynthetic gene clusters. *In silico* approach of the host plants revealed several tens of gene candidates. The aim of this work is to contribute to the knowledge of hypericin biosynthesis based on proposed analogy of the key biosynthetic genes in the hosts and their symbiotic microorganisms. Candidate genes will be selected based on published and acquired genomic data of endophytes and transcriptomic and genomic data of their plant hosts. For functional validation purposes the transformation system of selected endophytes or heterologous eukaryotic system will be adopted.

Comparative study of hypericin biosynthetic genes

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Annotation: Hypericin, a bioactive naphthodianthrone with substantial diagnostic and therapeutical potential in oncology is synthesized in plant kingdom only by some representatives of the genus *Hypericum*. However, wide spectrum of anthraquinone derivatives including hypericin and its proposed precursors is present in some lower eukaryotic organisms including endophytic fungi which were also identified in some *Hypericum* hosts. Taking into account that the hypericin biosynthetic pathway in plant producers is not fully understood, the role of the candidate genes could not be experimentally validated yet. The aim of this work is to perform genome-wide comparative study using the publicly accessible and *de novo* acquired transcriptomic and genomic data from fungal endophytes and their *Hypericum* hosts. The to-date data indicate that in the fungal genomes the biosynthetic genes of the polyketide pathway leading to anthraquinones are concentrated in the biosynthetic gene clusters while the information on their organization and distribution in the genomes of plant hosts are not available so far. Comparative study of fungal and plant candidate genes would bring new knowledge on genetic determination and regulation of hypericin biosynthesis in its natural producers.