

INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Botanický ústav AV ČR, v. v. i.
Ústav biologie obratlovců AV ČR, v.v.i.
Ústav experimentální botaniky AV ČR, v.v.i.

si Vás dovoluje pozvat na akci:

Závěrečný seminář projektu

Téma: Invaze a paraziti a velikost genomu a polyploidizace.

Název projektu: Integrace experimentální a populační biologie pomocí nových metod v mezioborové problematice - cesta k excelenci s mladými vědci

Datum a čas konání akce: 13.5. - 14.05.2015, 10:00 - 17:00 (10:00 - 15:00 pro 14.05.2015)

Místo konání akce: Ústav biologie obratlovců AV ČR, v.v.i., Květná 8, Brno, přednášková místnost, 1. patro.

Program - 13.05.2015 / Velikost genomu a polyploidizace

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| 10:00 - 11:00 | Petr Vít: The study of polyploidization as a dynamic process affecting plant variation. |
| 11:00 - 12:00 | Manuela Krüger: The study of plant genome and transcriptome as dynamic processes affecting plant variation. |
| 12:00 - 13:00 | Přestávka na oběd |
| 13:00 - 14:00 | James D. Stone: The application of next gen sequencing to the study of complex plant genomes. |
| 14:00 - 15:00 | Roswitha Schmickl: The role of whole-genome processes in invasion success of introduced plants. |
| 15:00 - 16:00 | Kenneth Oberlander: The role of whole-genome processes in adaptive radiation of plants. |
| 16:00 - 17:00 | Inga Hiiesalu: Transgenerational plasticity in clonal plants. |

Program - 14.05.2015. / Invaze a paraziti

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| 10:00 - 11:00 | Romain Rouchet: The impact of biological invasions on reciprocal relationships in biological communities. |
| 11:00 - 12:00 | Jamie Winternitz: Host-parasite interaction in ecological and evolutionary context: a comparative approach. |
| 12:00 - 13:00 | Přestávka na oběd |
| 13:00 - 14:00 | Ondřej Mudrák: Plant hemiparasites – functional and evolutionary relationships. |
| 14:00 - 15:00 | Lucie Hemrová: General patterns in local and regional dynamics of plant populations. |

Prezentace budou obsahovat představení dosažených výsledků vědecké činnosti postdoktoranda a jeho týmu, zhodnocení mezioborových přesahů do ostatních témat, zhodnocení a návrh další spolupráce. Více informací u organizátora: doc. Mgr. Jiří Doležal, PhD., Botanický ústav AV ČR, v.v.i., email: jiri.dolezal@ibot.cas.cz.

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Program - 13.05.2015 / Velikost genomu a polyploidizace

- 10:00 - 11:00 **Petr Vít:** The study of polyploidization as a dynamic process affecting plant variation.
- Polyploidization is one of the major evolutionary mechanisms in family Chenopodiaceae. It significantly affects evolutionary success of particular species in the term of reproduction success, ecological adaptability and population dynamics. We adopted multidisciplinary approach to reveal microevolutionary processes leading towards successful *Chenopodium* polyploids. Developed phytochrome markers (based on transcriptomes of related species and genera) together with knowledge of ploidy level and genome size variation will shed light on the evolution of *Chenopodium* species. Moreover, it will enable to reconstruct the phylogenetic relationships among closely related species in weedy *C. album* agg.
- 11:00 - 12:00 **Manuela Krüger:** The study of plant genome and transcriptome as dynamic processes affecting plant variation.
- How to bioinformatically separate RNA-Seq data of a mixed sample (plant and fungus), genome-guided Assembly with Trinity and subsequent gene annotation.
- 12:00 - 13:00 Přestávka na oběd
- 13.00 - 14.00 **James D. Stone:** The application of next gen sequencing to the study of complex plant genomes.
- Over the course of this project, our research has had two primary foci: (1) Mitochondrial (mt) transcription and the (2) expression of mt-targeted nuclear-encoded regulatory proteins. On the mt transcription front, we refined RNA-seq methods, improving their accuracy and sensitivity for mt transcripts (Stone and Štorchová 2015) as well as globally quantifying mt transcription and RNA editing in male sterile and male fertile plants (Stone et al. in prep.). On the second front, we optimized de novo transcriptome assembly procedures to maximize accuracy and completeness of pentatricopeptide repeat protein (PPR) reconstruction. This enormous, complex family of proteins is involved in numerous aspects of mt gene regulation, including those responsible for male sterility. Coordinating PPR transcription with their effects on mt gene expression promises a valuable contribution to our understanding of cytonuclear interactions (Stone et al., ongoing). Both of these research topics help us to understand plant male sterility, but are more broadly relevant to understanding mt genome evolution and cytonuclear coevolution.
- 14.00 - 15.00 **Roswitha Schmickl:** The role of whole-genome processes in invasion success of introduced plants.
- The introduction of high-throughput sequencing (HTS) technologies to plant systematics has the potential to greatly increase the amount of phylogenetically informative signal. Difficulties in phylogenetic reconstructions such as polytomies and low support values are expected to be at least partly overcome, as they are often the result of using only a small fraction of the genome. When HTS was introduced to plant phylogenetics, sequencing of the plastid genome was its first focus. Later approaches of genome skimming, the sequencing of the high-copy fractions of the nuclear, plastid and mitochondrial genome, resulted in the assembly of the rDNA cistron and nearly the complete plastid and mitochondrial genome. Currently, target enrichment of low-copy, orthologous nuclear exons is becoming increasingly popular, but up to now these loci have only rarely been used for plant phylogenetics (e.g., genus *Asclepias* (Apocynaceae), Asteraceae). For a phylogeny of southern African *Oxalis* target enrichment of low-copy nuclear genes was combined with genome skimming (Hyb-Seq), and the target enrichment probes were designed based on a combination of transcriptome and genome skim data. The results demonstrate that Hyb-Seq has a very promising future in phylogenomics, especially if one considers that there will be increasing accessibility to reference transcriptomes/genomes, increasing capacity of HTS platforms and steadily improving multiplex options. In the *Oxalis* case study in particular Hyb-Seq will contribute to

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a better understanding of the origin of invasiveness within the genus.

15:00 - 16:00

Kenneth Oberlander: The role of whole-genome processes in adaptive radiation of plants.

Ployploidy, or whole-genome duplication, has had a substantial impact on the evolution of land plants and has been the subject of intense recent scientific scrutiny. Major macro-evolutionary explanations for the prevalence of polyploids among land plants have included increased diversification rates among polyploids (supported by paleopolyploidisation events underlying speciose clades such as seed plants and angiosperms), or adaptive advantages of polyploids in highly disturbed systems (supported by a global latitudinal gradient in polyploid prevalence, clusters of polyploidisation events associated with the Cretaceous-Paleogene mass extinction, and an over-representation of polyploids amongst humanities most pernicious weeds). Here we seek to clarify the relative contributions of these two hypotheses against the context of the spectacular Cape Flora of South Africa, a hotspot of angiosperm diversity and endemism with a history of climatic and geological stability. Contrary to expectations of a polyploid-enriched flora predicted by the polyploidy-linked-to-diversification scenario, the Cape Flora is significantly polyploid-depauperate compared to global values and may be one of the most polyploid-poor floras on the planet. This is consistent with the hypothesis of polyploidy linked to disturbance. We explore this in more detail in a speciose Cape lineage known to undergo substantial polyploidisation: *Oxalis*. Flow cytometric analyses show that at least 50 % of sampled Cape *Oxalis* (180 of approximately 220 spp.) are or contain polyploids. More interestingly, virtually all well-sampled species contain both diploids and polyploids, suggesting that polyploids originate rapidly and independently across multiple lineages. Explicit chromosomal reconstructions on *Oxalis* phylogenies reveal an overwhelmingly diploid past; almost all nodes are reconstructed as unambiguously diploid. Character-dependent diversification rate analyses support a substantially lower diversification rate among polyploid *Oxalis* lineages than among diploids. Thus, even in a Cape lineage with extremely high rates of whole genome duplication, polyploids are suppressed to the point of having played a minimal long-term evolutionary role. Taken as a whole, these data are more consistent with the idea that polyploids thrive in disturbed environments, and show that diploidy and diversity can be strongly associated in a stable world.

16:00 - 17:00

Inga Hiiesalu: Transgenerational plasticity in clonal plants.

Plants are known to be plastic in their responses to changing environmental condition, such as light, nutrients and water availability. Plants can adapt to these changes by regulating the growth of their shoots, roots, flowers or physiology. During the past three decades it has been repeatedly shown that the phenotype expressed by a parent plant in response to stressful environmental conditions can be passed on to the offspring. This phenomenon is called transgenerational plasticity. Maternal effects present an important form of transgenerational plasticity and in this case the offspring's phenotype is particularly affected by the mother environment. Processes governing maternal effects are not yet clearly understood, however they could be mediated by epigenetic inheritance. Epigenetic processes determine how a genotype is translated into a phenotype. Our first aim was to study if maternal effect is adaptive in an a clonal species *Taraxacum brevicorniculatum*. Our second aim was to test if there exists a link between offspring phenotype determined by mother environment and epigenetic variation.

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10:00 - 11:00

Romain Rouchet: The impact of biological invasions on reciprocal relationships in biological communities.

This project aimed to study the impact of biological invasions on reciprocal relationships in biological communities, and more specifically the reciprocal relationship between bitterlings and their freshwater mussel hosts. I started this project by studying the potential of *Rhodeus ocellatus*, an bitterling originating from Asia, to become invasive in Europe, by benefiting from the recent

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invasion of an Asian mussel, and more importantly its potential effects on the European bitterling-freshwater mussel system. This work involved a large scale garden experiment to measure those potential effects at a demographic level over eight months, as well as a high number of behavioural tests under controlled conditions (behavioural interactions, host preference).

A second conducted project aimed at understanding the coevolutionary patterns between different populations of bitterling and freshwater mussels in China, involving field work and behavioural tests in the laboratory.

11:00 - 12:00

Jamie Winternitz: Host-parasite interaction in ecological and evolutionary context: a comparative approach.

Large-scale comparative analyses across ecological gradients can illuminate the evolutionary forces shaping adaptive genetic variability in wild populations, a fundamental concern of evolutionary biology with significance for conservation genetics. In particular, comparisons of genetic diversity at immunity genes, like those of the Major Histocompatibility Complex (MHC) are important to identify processes of selection that may impact the disease susceptibility of endangered species and of potential zoonotic reservoirs. Next-generation sequencing (NGS) has revolutionized the field of molecular ecology and provides researchers with the ability to record genetic polymorphism across previously unattainable numbers of individuals and nonmodelspecies. However, NGS is prone to a number of sources of error that may have consequences for intra- and interspecies genetic inferences, and these have received only limited attention in terms of the estimation and reporting of genotyping error rates. Here we use simulated Illumina NGS data to quantify genotyping error and optimize de novo assembly parameters with Stepwise Threshold Clustering, by minimizing error and maximizing the retrieval of true alleles. As an empirical example, we use targeted NGS sequencing of MHC Class II loci from three species of African rodents with individual sample replicates, under the expectation of identical genotypes, to test the efficacy of the genotyping program. Accurate genotyping is the first step in this large-scale comparative study across 50 African rodent species. The ultimate goal is to broaden our understanding of the evolutionary forces shaping immune gene variability in a taxonomic group that is frequently the reservoir of numerous infectious diseases impacting humans and wildlife.

12:00 - 13:00

Přestávka na oběd

13.00 - 14.00

Ondřej Mudrák: Plant hemiparasites – functional and evolutionary relationships.

Hemiparasites are increasingly recognized as key stone species with important effect on the ecosystem. We studied different aspects of the hemiparasites' ecology in different habitats. We found that hemiparasites significantly differ in functional traits from the co-occurring species and that they affect functional trait composition of host community. Generally, the species promoted by hemiparasites were those with low competitive ability. They had low plant height, a low capacity for clonal growth, a tap root during the whole lifecycle, were monocyclic (with annual shoots) and had low leaf dry matter contents. Hemiparasites also increased functional diversity for clonality, which indicated a better coexistence of species with various capacities for clonal growth. We conclude that functional traits highlight the processes by which hemiparasites affects vegetation structure and species coexistence.

14.00 - 15.00

Lucie Hemrová: General patterns in local and regional dynamics of plant populations.

Due to human-induced changes in climate and land-use the question about determinants of species dynamics and distribution for predicting future species prospect have been more urgent. During project we focused on assessing determinants of dynamics and distribution of dry grassland species in the Czech Republic. Within set of eighty-six dry grassland species we identified those of which current distribution in landscape was a result of higher dispersal rates in past and those of which current distribution suggest equilibrium dynamics in landscape. We also identified life-history traits responsible for different patterns of species dynamics. For smaller set of 18 species we then modeled hypothetical potential to spread in landscape using detailed information on their



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population dynamics and dispersal and examined to what extent spread potential resulted from population vs. dispersal characteristics of the species and how it could be predicted by species life-history traits. Finally, we focused on determinants of species dominance in dry grasslands to understand species dynamics and coexistence in dry grassland communities. On the example of four grassland species and using extensive field and garden experiments we identified determinants of dominance for each of the four species.