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MINISTERSTVO ŠKOLSTVÍ,
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OP Vzdělávání
pro konkurenceschopnost

INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

**Botanický ústav AV ČR, v.v.i. spolu s projektovými partnery
Ústavem biologie obratlovců AV ČR, v.v.i. a Ústavem
experimentální botaniky AV ČR, v.v.i. si Vás dovoluje pozvat na
6. oborovou konferenci na téma:**

Invaze a paraziti (téma 1)

Velikost genomu a polyploidizace (téma 2)

Program konference:

8:30 – 8:55 Příjezd účastníků

8:55 – 9:00 Úvodní slovo

Téma 1:

9:00 – 9:15 L. Hemrová: **Effect of intraspecific plant-soil feedback on species dynamics**

9:15 – 9:30 O. Mudrák: **Interaction of hemiparasitic species with clonal plants**

9:30 – 9:45 R. Rouchet: **Host-parasite coevolution**

9:45 – 10:00 J. Winternitz: **Examining the evidence for MHC-dependent mate selection**

10:00 – 10:15 Break

10:15-10:35 P. Vít: **Development of phylogenetic markers for closely related *Chenopodium* species**

10:35 – 10:55 J. Stone: **Which comes first, the edit or the splice? Using RNA-seq to study the order of mitochondrial RNA maturation events**

10:55 – 11:10 K. Oberlander: **The contrasting fates of polyploidy and plastid capture in an African plant radiation**

11:10 – 11:25 M. Krüger: **Bioinformatic tools and differential gene expression of arbuscular mycorrhizal fungi within roots of *Medicago truncatula***

11:25 – 11:40 R. Schmickl: **Phylogenetic marker development for target enrichment from transcriptome and genome skim data**

11:40 – 11:55 I. Hiiesalu: **Transgenerational plasticity**

11:55 |Závěrečná diskuze a ukončení

Místo konání: Průhonice

Datum konání: 16. 09. 2015

Bližší informace: Zuzana Münzbergová (zuzmun@natur.cuni.cz)

6. oborová konference probíhá v rámci realizace projektu: "Integrace experimentální a populační biologie pomocí nových metod v mezioborové problematice - cesta k excelenci s mladými vědci",



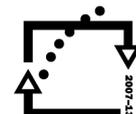
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reg.č.: CZ.1.07/2.3.00/30.0048, který je financován z ESF a státního rozpočtu ČR, prostřednictvím operačního programu Vzdělávání pro konkurenceschopnost (OPVK).

Téma 1

Lucie Hemrova: Effect of intraspecific plant-soil feedback on species dynamics

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. We found that distribution and local abundances of some of the species were partly driven by habitat conditions at the sites, however, the local dominants tend to performed worse at their home sites than at any other sites. The results indicate that intraspecific negative plant soil feedback may be a key factor determining performance of the dominants.

Ondřej Mudrák: Interaction of hemiparasitic species with clonal plants.

Hemiparasites are increasingly recognized as an important functional group with strong effect on other species. Typically it reduces their biomass and fitness. Recent studies found that species with high capacity for clonal growth are particularly vulnerable to parasitism. We conducted the pot experiment in which we tested the effect of hemiparasitic species *Rhinanthus alectorolophus* on clonal grass *Calamagrostis epigejos*. In the pots we planted two ramets of *C. epigejos*, which were either clonally connected or not connected. *R. alectorolophus* was sown or not sown next to one of the *C. epigejos* ramet. Though we did not find any significant differences in biomass of *C. epigejos*, we found that *R. alectorolophus* profit (have higher biomass) whet it infected the clonally interconnected ramets of *C. epigejos*.

Rouchet Romain: Host-parasite coevolution

Host-parasite coevolution can lead to the reciprocal local adaptation of both partners. Existence of local adaptation in such systems is an indirect evidence for coevolution of interacting species. It can be measured by cross-infection experiments comparing parasite preference between sympatric and allopatric host populations. We tested the host preference of two populations of a parasitic fish, the rosy bitterling, *Rhodeus ocellatus*, using two species of freshwater mussels that are both widely used as hosts of the bitterling eggs and embryos. We found no direct evidence for local adaptation but both bitterling populations exhibited preference toward hosts naïve to this bitterling species. We also found differences in host resistance depending on host species and population.

Jamie Winternitz: Examining the evidence for MHC-dependent mate selection in humans and non-human primates

Compounds of the Major Histocompatibility Complex (MHC) are integral for effective vertebrate adaptive immune response, and are also implicated as cues for sexual selection. The evidence for



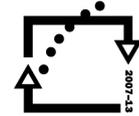
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this is supportive of MHC-based preference for diverse and dissimilar mating partners, in a range of vertebrates from fish to non-human primates. However, the evidence for a similar role of these genes and the evolutionary benefits of their diversity in human mate choice has been more controversial. Using meta-regression techniques, we examined the moderators of effects sizes of 34 primary studies on MHC-mediated mate choice in humans and non-human primates and show that diversity is more influential than dissimilarity for mate choice. Additionally, our results identify intriguing new patterns, such as the contrast in effects of MHC class I (for more similar mates) vs class II, and also provide valuable methodological guidance for how to set the research agenda over the coming years, such as favoring large-scale studies (given low effect sizes) and designs involving multiple loci (and, if possible, information on genome-wide diversity, too), as well as contrasting (rather than pooling) effects of MHC class I and II.

Téma 2:

Petr Vít: Development of phylogenetic markers for closely related *Chenopodium* species

Traditional phylogenetic markers have a restricted use for phylogeny reconstruction of closely related *Chenopodium* species. We have developed new phylogenetic markers based on coding sequences of phytochrome genes. They were developed from published transcriptomes of related species (e.g. *Beta*, *Sponacia*, *Atriplex*) and our transcriptome of *Chenopodium ficifolium*. Markers had a detail resolution and enabled us to reconstruct *Chenopodium* phylogeny. We were also able to resolve relationships of closely related species. Results will be used for analyses of genome size evolution, correlation with ecology, involvement in evolutionary constraints etc.

Manuela Krüger: Bioinformatic tools and differential gene expression of arbuscular mycorrhizal fungi within roots of *Medicago truncatula*

Arbuscular mycorrhizal (AM) fungi are key drivers in ecosystems as about 80% of all land plants form AM. There is large progress ongoing to obtain the complete genome of the model fungus in AM research, *Rhizophagus irregularis* DAOM197198 (Tisserant et al. 2012, 2013; Lin et al. 2014). In our study we used the combined genome data sets for *R. irregularis* as reference for genome-guided and de novo assembly with the RNA-Seq assembler Trinity for analyses of differential expressed genes within roots of *Medicago truncatula* either inoculated with *R. irregularis* DAOM197198 (former *Glomus* group Ab) or *Claroideoglomus claroideum* (former *Glomus* group B) or both AM fungi. *Medicago truncatula* (barrel medic) was inoculated either with a single inoculum, consisting of *Rhizophagus irregularis* DAOM197198 or *Claroideoglomus claroideum*, or a mixed inoculum composed of both AM fungal species. RNA of the symbiotic roots was extracted and sent for NextSeq500 sequencing on one lane (~400 M, 75 cycles, PE) and bioinformatically analysed with Trinity either in de novo or genome-guided mode (Grabherr et al. 2011).

James Stone: Which comes first, the edit or the splice? Using RNA-seq to study the order of mitochondrial RNA maturation events.



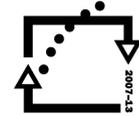
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RNA editing and splicing are two essential steps for producing mature mRNAs from primary mt transcripts. Previous research using sanger sequencing and a limited set of cDNAs suggested that splicing precedes RNA editing. We expand on this approach using RNA-seq data to examine the entire mt transcriptome. By parsing millions of aligned reads, we can compare editing extent in spliced and unspliced transcripts more comprehensively than previously possible. We find cases where editing obligately precedes splicing, others where it follows, and the majority where splicing and editing appear to happen independently. Splice-altered cis motifs targeted by trans editing factors seem to explain cases where editing happens sequentially. Similar approaches can be used to study sequential editing across transcripts, providing a mechanistically rich picture of organellar transcription.

Inga Hiiesalu: Transgenerational plasticity

We studied transgenerational plasticity as maternal effects in plants which reproduce clonally. As one of the mechanisms that could govern transgenerational plasticity are various epigenetic processes, we aimed to link maternal effect with epigenetic variation. During the project three greenhouse experiments and extensive molecular analysis using *Taraxacum brevicorniculatum* and *Glechoma hederacea* as model organisms were carried out. On the base of the studies we can conclude that: Maternal effects are important in clonal plants such as apomictic *Taraxacum brevicorniculatum*, which could govern adaptation to various stress factors. We found adaptive reaction in shoot biomass and root length in response to drought stress. In other words, the offspring with previous maternal stress memory performed better in stress conditions compared to offspring without maternal stress memory. Transgenerational plasticity could provide important source of variation in plants which have low genetic variability – i.e. typically clonal plants. Our molecular analysis indicate that DNA methylation, as an important epigenetic regulatory mechanism could be related to processes of transgenerational plasticity.

R. Schmickl: Phylogenetic marker development for target enrichment from transcriptome and genome skim data

Phylogenetics benefits from using a large number of putatively independent nuclear loci and their combination with other sources of information, such as the plastid and mitochondrial genomes. To facilitate the selection of orthologous low-copy nuclear (LCN) loci for phylogenetics in non-model organisms, we created an automated and interactive script to select hundreds of LCN loci by a comparison between transcriptome and genome skim data. We used our script to obtain LCN genes for southern African *Oxalis* (Oxalidaceae), a speciose plant lineage in the Greater Cape Floristic Region. This resulted in 1,164 LCN genes greater than 600 bp. Using target enrichment combined with genome skimming (Hyb-Seq) we obtained on average 1,141 LCN loci, nearly the whole plastid genome and the nrDNA cistron from 23 southern African *Oxalis* species. Despite a wide range of gene trees, the phylogeny based on the LCN genes was very robust, as retrieved through various gene and species tree reconstruction methods as well as concatenation.



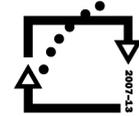
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K. Oberlander: The contrasting fates of polyploidy and plastid capture in an African plant radiation

Polyploidy or whole genome duplication (WGD) is thought to play an extensive role in angiosperm evolution, possibly even serving as a substantial causal mechanism for generating diversity. Other genome-level processes, such as chloroplast capture, are less well-known and could potentially also play a major evolutionary role. In the course of this post-doc we explored the possible role that WGD has taken in an angiosperm clade both species- and polyploid-rich: the African *Oxalis* radiation (> 230 spp.). Through flow cytometric analysis of > 3000 accessions, we established that African *Oxalis* is tremendously rich in polyploids: a minimum of 50 % of currently recognized species have or contain polyploids, with polyploid series very common. Curiously, almost all species have extant diploid representatives. Coupled with ancestral chromosome number reconstructions and modelling of differential rates of diversification between diploids and polyploids on single-locus phylogenies, this indicates that despite rampant WGD, polyploidy has played a surprisingly small role in the long-term evolution of the genus. We explored the possible signal that allopolyploidisation might have left on the African *Oxalis* phylogeny using new genomics techniques capable of capturing large numbers of low-copy nuclear loci as well as substantial fractions of the plastid genome. In support of a minimal role for allopolyploidy in *Oxalis* evolution, preliminary low-copy nuclear trees generally group species with multiple accessions and ploidy levels as monophyletic with strong support. In contrast, however, preliminary chloroplast trees are both strongly supported and radically different from nuclear trees. Explanations for this pattern could be high levels of incomplete lineage sorting and/or substantial amounts of between-species plastid introgression. Given the strong support for species-level monophyly and long branches subtending many of these species, this constitutes suggestive evidence for abundant chloroplast capture events, with very little nuclear introgression, rather than ILS. Ironically, given the paucity of evidence for allopolyploidisation, this implies that chloroplast capture has been primarily mediated through large numbers of *diploid* hybrids. This suggests that two genome-level processes occur in abundance in African *Oxalis*, but with very different evolutionary fates: high rates of WGD followed generally by extinction/lowered speciation of the polyploids, and high rates of inter-species chloroplast traffic amongst the diploids, with large chances of plastome fixation but little or fleeting nuclear introgression. This work highlights two major implications: 1) monoplod chloroplast capture could play a substantially larger role in evolutionary processes than previously thought and 2) the power of flow cytometric techniques, in combination with genomics-level data, to explore the impact of genome-level processes on species-rich radiations.