Program

Wednesday 11th May 2016

17:00-20:00  Registration and poster set-up (Hotel Lone, Conference centre)
20:00-22:00  Welcome reception (Hotel Lone)

Thursday 12th May 2016

From 8:00  Registration (Conference centre)
8:30-9:00  Welcome addresses and organizational information

Session 1: Polyploidy in deep time (long-term consequences of polyploidy)
Chairperson: Aleš Kovarik

9:00-9:30  Jonathan F. Wendel: The wondrous yycles of polyploidy in plants
9:30-10:00 M. Eric Schranz: Ancient angiosperm MADS-Box transcription factor duplications revealed by Synteny-Network (SynNet) phylogenomic analysis

10:00-10:30 Coffee break

10:30-10:50 Dirk Albach: Is genome downsizing correlated with diversification of polyploid lineages?
10:50-11:10 Alexandre Pelé: The poor lonesome *Brassica napus* A subgenome may not survive without its mate
11:10-11:30 Hanna Weiss-Schneeweiss: More than meets the eye: contrasting evolutionary trajectories in polyploids of the *Prospero autumnale* complex (Hyacinthaceae)
11:30-11:50 Blaine Marchant: How polyploidy, transposable elements, and life history traits shape fern genome evolution
11:50-12:05 Itay Mayrose: PloiDB: a phylogenetic framework for investigating the evolutionary consequences of polyploidy
12:05-12:20 Armel Salmon: How to detect duplicated sequences within highly polyploid species without any reference? An introduction to the use of the Pyro- and Illu-haplotyper pipelines for *Spartina* genomics
12:20-12:35 Sarah Marburger: Causes of genome size expansion in neotropical catfish – unravelling the evolutionary history of the Corydoradinae

12:45-14:00 Lunch break

Session 1: Polyploidy in deep time (long-term consequences of polyploidy)
Session 2: Polyploidy at shallower time-scales (immediate responses to polyploidy)
Chairperson: Andrew Leitch

14:00-14:30 Pamela S. Soltis and Douglas E. Soltis: Polyploidy and evolutionary novelty across microevolutionary and macroevolutionary timescales
14:30-15:00 Malika Ainouche: Genome merger as evolutionary springboard: Insights from recurrent hybridization and polyploidy in *Spartina*

15:00-15:30 Coffee break
Session 1: Polyploidy in deep time (long-term consequences of polyploidy)
Session 2: Polyploidy at shallower time-scales (immediate responses to polyploidy)
Chairperson: Pamela Soltis

15:30-15:45 Yves Van de Peer: Of dups and dinos: evolution at the K/Pg boundary
15:45-16:05 Keith Adams: Reshaped patterns of alternative splicing after allopolyploidy in Brassica napus
16:05-16:25 Natasha Glover: Homoeologs: What are they? How to infer them? What are they useful for?
16:25-16:40 James J Clarkson: Diploidisation through time: comparing neopolyploids and established polyploids
16:40-16:55 Annalieise S. Mason: Multi-genome meiosis in synthetic Brassica hybrids and polyploids
16:55-17:10 Antoine Fort: Maternal parent hypermethylation overcomes inter-ploidy and inter-species F1 seed abortion blocks in Arabidopsis thaliana
17:10-17:25 Mischa A. Olson: Perturbations of meiotic recombination in neopolyploid maize

17:30-18:30 Poster sessions 1 and 2 (PS1-1/PS1-25; PS2-1/PS2-19)

Friday 13th May 2016

Session 1: Polyploidy in deep time (long-term consequences of polyploidy)
Session 2: Polyploidy at shallower time-scales (immediate responses to polyploidy)
Chairperson: Ovidiu Paun

9:00-9:25 Aleš Kovarik: Epigenetic impacts of recent allopolyploidy on ribosomal RNA genes in Tragopogon mirus and its interpopulation hybrids
9:25-9:45 Terezie Mandáková: Multiple patterns of genome evolution in the Brassicaceae: a lesson from the polyploid-rich genus Cardamine
9:45-10:00 Elvira Hörandl: The evolution of apomixis in angiosperms: a consequence of hybridity, polyploidy, or of environmental influence?
10:00-10:30 Coffee break

Session 1: Polyploidy in deep time (long-term consequences of polyploidy)
Session 2: Polyploidy at shallower time-scales (immediate responses to polyploidy)
Chairperson: Hanna Weiss-Schneeweiss

10:30-10:50 Mario Vallejo-Marín: Interfertility and phenotype of independently originated populations of the neo-allopolyploid Mimulus peregrinus (Phrymaceae)
10:50-11:05 Thomas Wolfe: The impact of allopolyploidy on gene expression in Dactylorhiza
11:05-11:20 Clayton J. Visger: Using synthetic spike-in RNAs to quantify expression level divergence following autopolyploidy
11:20-11:35 Ovidiu Paun: Molecular basis of adaptive diffusion after recurrent allopolyploidization in Dactylorhiza
11:35-11:50 Boulos Chalhoub: Deciphering the post-neolithic Brassica napus oilseed genome reveals the fascinating diversifying force of polyploidy
11:50-12:05 David Kopecký: Unexpected gene expression changes in newly developed Festuca × Lolium hybrids
12:05-12:20 Jasna Puizina: Triparental origin of triploid onion Allium × cornutum (Clementi ex Visiani, 1842) (2n = 3x = 24)
12:20-12:35 Juraj Paule: Polyploidy and range expansion in the South American genus Fosterella (Bromeliaceae)
12:45-14:00  Lunch break

Session 1: Polyploidy in deep time (long-term consequences of polyploidy)
Session 2: Polyploidy at shallower time-scales (immediate responses to polyploidy)
Chairperson: Maurine Neiman

14:00-14:30  Rob Denton: Polyploid Ambystoma salamanders at the interface of environment, genomics, and ecology
14:30-15:00  Michael S. Barker: Multiple whole genome duplications during the evolution of hexapods
15:00-15:30  Anna Selmecki: Polyploidy can drive rapid adaptation in yeast
16:00  Bus departure to Bale (Histria aromatica - autochthonous aromatic herb plantation) and Svetvinčenat (conference dinner)

Saturday 14th May 2016

Session 2: Polyploidy at shallower time-scales (immediate responses to polyploidy)
Session 3. Polyploidy in light of ecological genetics
Chairperson: Malika Ainouche

9:00-9:25  Andrew R. Leitch: Genome size and chromosomal ploidal level influence angiosperm species biomass under nitrogen and phosphorus limitation
9:25-9:45  Kirsten Bomblies: Adaptive evolution of meiosis in response to whole genome duplication and habitat
9:45-10:00  Kentaro Shimizu: Advantages and tradeoffs of “general purpose genotype”: zinc accumulation, cold response and genome-wide homeolog expression in the self-compatible allopolyploid Arabidopsis kamchatlica
10:00-10:30 Coffee break

Session 3. Polyploidy in light of ecological genetics
Chairperson: Jonathan Wendel

10:30-10:50  Petr Šmarda: The worldwide distribution of polyploid plants
10:50-11:05  Magdalena Holcová: Adaptive evolution of meiosis in diploid and polyploid Arabidopsis arenosa across its native range
11:05-11:20  Julie Ferreira de Carvalho: Dead-end trajectory of young triploid apomicts: Can transposable elements improve their adaptive potential?
11:20-11:35  Thomas Dejaco: Diploidization without reduction of genome size in an Alpine jumping bristletail
11:35-11:50  Peter Schönswetter: Evolutionary patterns, contact zones and ecological segregation in an alpine autopolyploid complex
11:50-12:05  Jun Sese: Genome-wide statistical detection of hyper-biased homeologs in allopolyploid and their changes after hybridization
12:05-12:20  Warren Albertin: Hybridization in yeast is associated with phenotypic novelty for life-history, metabolic and proteomic traits
12:20-12:35  Jeannette Whitton: Disentangling the causes of differences in distribution of diploid sexual and autopolyploid apomictic Easter daisies (Townsendia hookeri: Asteraceae)
12:45-14:00 Lunch break
Session 2: Polyploidy at shallower time-scales (immediate responses to polyploidy)
Session 3. Polyploidy in light of ecological genetics
Chairperson: Jasna Puizina

14:00-14:30   **Maurine Neiman**: Sex, phosphorus & polyploidy: Can nutrient costs of nucleic acids contribute to ploidy and sex polymorphism in nature?
14:30-15:00   **Levi Yant**: Borrowed alleles and convergence: serpentine adaptation in the face of inter- and intraspecific gene flow

15:00-15:30   Coffee break

15:30-15:45   **Laura Bankers**: Influences of ploidy level and reproductive mode on patterns of adaptive molecular evolution in a New Zealand freshwater snail
15:45-16:00   **Kyle McElroy**: Evaluating the dynamics of transposable element evolution in non-hybrid polyploids
16:00-16:15   **Veit Herklotz**: The fate of ribosomal RNA genes in spontaneous dogrose hybrids (*Rosa* L. sect. *Caninae* (DC.))
16:15-16:30   **Helene Rousseau**: Polyploidy and phenotypic novelty: Phylogenetic context of DMSP (dimethylsulfiniopropionate) biosynthesis in *Spartina* (Poaceae, Chloridoideae)
16:30-16:45   **Leen Leus**: Are tetraploid roses better resistant to stress compared to diploids?

17:00-18:00   **Poster session 3** (PS3-1/PS3-35)

18:00   Poster awards and closing ceremony