Polyploid evolutionary genomics: challenges and opportunities

Summer school, 10 to 20 July 2023

University of Fribourg, Switzerland

UNIVERSITÉ DE FRIBOURG
UNIVERSITÄT FREIBURG

Sunday 9 July: Welcome participants to Saint-Justin and Beauséjour

Symposium: Genome duplication at the intersection of biodiversity and crop sciences

PER 21 – A.230

Monday 10 July

9:30 - Welcome and general information

9:40 - Andrew L. Leitch “Genome downsizing after polyploidy: mechanisms, rates and selection pressures”

10:30 - Manuel Poretti “Chromosome rearrangements and evolutionary diversification of duplicated genomes”

10:50 - Coffee break

11 :30 - Kirsten Bomblies “How to tango with four - adaptation to tetraploidy, and how we can use genome scans to understand polyploid adaptation”

12:20 – Aled Evans “Determining the donor of the *Arabidopsis arenosa* sub-genome to *Arabidopsis suecica*”

12.40 – Lunch

14:00 - Boulos Chalhoub “Unraveling basis of success or polyploidy in cultivated crops: examples from wheat and oilseed rape”

14:50 – Pooja Garg “Development and morpho-genetic characterization of resynthesized allotetraploid *Brassica juncea* lines”

15:10 – Nam Hoang Van “Insights into whole-genome duplications and the evolution of C4 photosynthesis in Cleomaceae”

15:30 – Coffee break

16:00 –Kentaro Shimizu “Robustness of polyploid species: evolutionary genomic studies using *Arabidopsis kamchatica* and wheat”

16:50 – Jacobs Mac Kenzie ”Environmental effects on the genomics and epigenomics of subgenome dominance”

17:10 – Moeko Okada “Effects of allopolyploidization on homoeologous gene expression in synthetic hexaploids”

17:30 – Linda Schlatter “Insight into the Swiss breeding of induced-polyploid fodder plants by Agroscope”

18:00 – Symposium Reception (PER 21 ground floor)

Tuesday 11 July

9:30 - Christian Parisod “Adaptive radiation of diploids vs autotetraploids across ecological gradients”

10:20 – Teresa Zeni “Role of genome duplication in changing mountain landscapes: a preliminary report”

10:40 – Coffee Break

11:10 – Laura Steinmann “The role of the environment in the origin and evolution of *Arabidopsis* polyploids”

11:40 – Anna Glushkevich “Adaptive introgression provides adaptation to polyploidy in Siberian *Arabidopsis lyrata*”

12:00 – Loïc Pittet “Phylogeographical comparison of species of the *Salix retusa* polyploid complex in the European mountain system”

12:20 – Lunch

13:30 - Martin Lascoux “A ‘fast’ method to infer polyploid origin and introgression — With application to birch”

14:20 – Hannah Assour “Neopolyploidy in the great duckweed (Spirodela polyrhiza) alters the outcome of herbivory”

14:40 –Nikita Tikhomirov “Genomics of adaptation in mixed-ploidy aquatic plants *Potamogeton*”

15:00 – Coffee break

15:30 - Malika Ainouche “Hybridization, polyploidy and biological invasion”

16:20 - closing remarks and group photo

17:00 End

Module A: From sample to data

PER21- D.230

Wednesday July 12

8:30 Self-presentation by each participant

Prof. Parisod “General introduction to polyploidy”

Prof. Ainouche “Historical and new questions in polyploidy research”

13:30 Prof. Parisod, Prof. Ainouche, Prof. Leitch “Null hypotheses in polyploid research”

Participants will break out in small groups to discuss and manipulate main concepts related to the putative genomic, cytological and ecological consequences of polyploidy, and highlight hypotheses to be tested through empirical and experimental approaches. Participants will design the sampling of a mixed-ploid hybrid zone as to enable spatially-explicit analyses.

Thursday July 13

8:00 Dr. Felber et al. “Field excursion: Sampling a mixed-ploidy hybrid zone”

Participants will implement the sampling of a hybrid zone between diploids and autotetraploids of Anthoxanthum alpinum. Participants will learn about polyploid systems in the flora of the Alps.

Supporting literature: Felber et al. 1996. Habitat differentiation in a narrow hybrid zone between diploid and tetraploid *Anthoxanthum alpinum*. New Phytol 133:531–540. https://doi.org/10.1111/j.1469-8137.1996.tb01921.x

Meeting point: 8h00 in front of the Natural History Museum.

Pic-Nic and water provided. Bring good shoes (hike from 1250 to 2000 m asl) and adapted clothes.

Friday July 14

8:30 Prof. Leitch et al. “Flow cytometry”

Participants will learn to estimate the genome size and ploidy level of plants, and will practice on samples collected during the field excursion to assess the distribution of cytotypes and compare results with the situation twenty years ago.

Module B: Polyploid genomes

PER21- D.230

13:30 Dr Bafort, Dr Li “Assembly of polyploid genomes and subgenome evolution”

Participants will learn about the extra complexities of (the assembly of) polyploid genomes that consist of (very) similar or identical subgenomes. Participants will learn about how to look for evidence of subgenome dominance, and ongoing rediploidization.

Saturday July 15

8:30 Dr Bafort, Dr Li. “Ks age distribution and genomic dot plots”

The construction of Ks age distributions and genomic dot plots are two of the most widely used and important ways to find evidence for ancient polyploidy. Where the construction of Ks distributions is not based on structural information and can be even based on extensive transcriptome information, the construction of genomic dot plots requires structural information and a well-assembled genome.

13:30 Dr Li, Dr Bafort, Dr. Simion “Gene trees – species tree reconciliation”

Gene tree reconciliation enables to look for evidence for (very) ancient polyploidy, where this is often not possible with Ks age distributions, because of saturation of synonymous mutations for large evolutionary distances. Participants will learn to work with software to construct Ks age distributions, to make genomic dot plots, and to perform gene tree – species tree reconciliation.

Sunday July 16 - Free day

Monday July 17

8:30 Prof. Shimizu, Dr Hatakeyama “RNA-seq analysis using subgenome classification methods”

For high quality RNA-seq analysis of allopolyploid species, bioinformatic workflows called subgenome classification methods were developed. We will introduce bioinformatic workflow for subgenome classification methods (HomeoRoq, EAGLE-RC) combined with RNA-seq mapping and quantification tools. We also focus on significant changes in homeolog expression ratio.

13:30 Prof. Shimizu, Dr Hatakeyama “Robustness of polyploid species”

Recent studies using several allopolyploid species showed that allopolyploid species inherited and combined the gene expression patterns of progenitor species. We suggest that they contributed to the environmental robustness of allopolyploid species.

Module C: Polyploid populations

PER21- D.230

Tuesday July 18

8:30 Prof. Parisod, Dr Salmon, Dr Choudhury “Genotyping polyploids”

Genotyping polyploids is challenging. Participants will learn about avoidable pitfalls when calling for single nucleotide polymorphisms as well as structural variants among polyploid samples and about strategies to accurately assess (fixed or partial) heterozygotes.

13:30 Prof. Parisod, Dr Grünig “Autopolyploid populations”

Participants will learn how to assess tetrasomic inheritance and to compare the linkage and structure of genomic variation within and among populations of diploid-autotetraploid systems.

Wednesday July 19

8:30 Prof. Lascoux, Dr Tiret “Allopolyploid populations”

Participants will learn how to deal with genomic variation in allopolyploid systems that include whole-genome duplication and hybridization, with the latter that seems to matter more than the former, at least for expression.

13:30 Prof. Lascoux, Dr Tiret “Demography and selection in polyploids”

Participants will learn that parental legacy plays an important role and seems to have a rather long-lasting effect. So to understand an allopolyploid we need to understand its parental species. Although allopolyploid subgenomes have been in the same individuals for a long time and therefore have had the same demography they still differ significantly.

Thursday July 20

8:30 Prof. Lascoux, Dr Tiret “Signatures of selection”

Participants will learn to analyze patterns of selection and highlight selective sweeps in allopolyploids.

13:30 Prof. Lascoux, Prof. Parisod “Interpretations and conclusions”

Participants will revisit hypotheses formulated at the beginning of the summer school in light of the approaches they have been practicing and highlight perspectives for polyploidy research at the population level.

Thursday July 20

Check out from housing in between 9 am and 11 am.

Abstracts

Andrew L. Leitch
Queen Mary University of London, United Kingdom

“Genome downsizing after polyploidy: mechanisms, rates and selection pressures”

Manuel Poretti
University of Fribourg, Switzerland

“Chromosome rearrangements and evolutionary diversification of duplicated genomes”

Chromosome rearrangements (CRs) are known to promote the reduction of genome size and chromosome numbers (i.e. diploidization) in plants undergoing recurrent whole-genome duplications. Such phenomenon appears decisive for the evolutionary diversification of plants, however the genomic basis of chromosomal restructuring remains underexplored.

In our study, we combine cutting-edge sequencing technologies (Oxford Nanopore, PacBio Iso-Seq and Hi-C) to build, annotate, and compare chromosome-scale genome assemblies of closely related Biscutella species. These plant species diversified independently following a whole genome duplication event and colonized different environmental niches, making the Biscutella genus a unique system for understanding the impact of diploidization on plant adaptation in natural populations.

The availability of chromosome-scale genome assemblies is crucial for investigating structural variation. Although the complexity of large and repetitive plant genomes often hinders such analyses, we provide guidelines for the assembly and annotation of high-quality genomes and shed light on the molecular mechanisms underlying CRs (with a special focus on transposable elements). Through comparative genomics, we quantify the impact of different restructuring events on genome divergence and assess molecular processes that alter genome size and content, determining to what extent different types of restructuring events affect the gene space vs the repetitive fraction during diploidization and species diversification.

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Kirsten Bomblies
ETH-Zurich, Switzerland

“How to tango with four - adaptation to tetraploidy, and how we can use genome scans to understand polyploid adaptation”

Aled Evans
Aberystwyth University, United Kingdom

“Determining the donor of the *Arabidopsis arenosa* sub-genome to *Arabidopsis suecica*”

Boulos Chalhoub
Agroscope Changins, Switzerland

“Unraveling basis of success or polyploidy in cultivated crops: examples from wheat and oilseed rape”

Pooja Garg
ICAR-NIPB, India

“Development and morpho-genetic characterization of resynthesized allotetraploid *Brassica juncea* lines”

"In India, rapeseed-mustard is used widely as an oilseed crop after soybean and Brassica juncea (Indian mustard) (AABB; 2n=36) contribute more than 95% of total oilseed brassica. It has a low genetic diversity owing to its emergence from diploid species i.e., Brassica rapa (AA; 2n=20) and Brassica nigra (BB; 2n=16), making it more prone to many biotic and abiotic stresses. It highlights the need for genetic improvement to widen genetic diversity to enhance adaptability and yield potential. In light of enhancing the diversity of B. juncea, resynthesis is a promising approach, utilizing multiple accessions of B. rapa and B. nigra, potentially leading to development of new gene combinations.

In an attempt to broaden the diversity of B. juncea, we have developed 90 resynthesized B. juncea lines (RBJ) using different accessions of B. rapa and B. nigra as parents. These lines are in S8 generation and show a high degree of diversity for yield-contributing traits alongwith tolerance to different biotic and abiotic stresses (heat tolerance, white rust, powdery mildew). These synthetic allotetraploid lines were subjected to genotype-by-sequencing (GBS) and data is being analyzed for intergenomic interactions, recombination, and evolutionary pattern of allotetraploid brassica species. The proposed work will lead to understanding the evolution and stability of amphidiploid Brassica species from its diploid progenitor, revealing the genetic mechanism of polyploidization in crops and developing a robust method to comprehend the convoluting evolutionary process. These characterized lines will be further utilized in the mustard improvement program for oilseed security in India"

Nam Hoang Van
Wageningen University & Research, Nederland

“Insights into whole-genome duplications and the evolution of C4 photosynthesis in *Cleomaceae*”

The Cleomaceae is the sister family to the Brassicaceae (including the model species Arabidopsis and Brassica crops). The Cleomaceae contains species with different photosynthesis types, including C3, C4 and C3-C4 intermediate plants. As the Brassicaceae does not have a true C4 species, the Cleomaceae serves as a valuable model system for photosynthesis research that aim to improve crops. The Cleomaceae also includes several economically important leafy, medicinal and ornamental plants. Despite its scientific and economical importance, there is still a lack of research efforts to develop genetic and genomic resources for the Cleomaceae. We generated a reference genome for the C4 species G. gynandra which facilitates comparative genomics with its C3 relative, Tarenaya hassleriana, to elucidate the polyploidy history of the Cleomaceae family after its divergence from the Brassicaceae and identify the factors contributed to the evolution of C4 photosynthesis in the Cleomaceae. Our result found that these species evolved through step-wise ancient polyploidy events, in which a whole-genome duplication event (Gg-α) occurred first, followed by an addition of a third genome (Th-α, +1x) to T. hassleriana but not to G. gynandra. The evolution of C4 photosynthesis in the Cleomaceae resulted from a series of processes, including differential duplication, retention, recruitment and expression modification of C4-related genes. This led to the preferential expression of these genes in leaf mesophyll or bundle-sheath cells depending on their functions. Collectively, this study enhances our understanding of the polyploidy history and its impact on the evolution of C4 photosynthesis in the Cleomaceae.

Kentaro Shimizu
University of Zurich, Switzerland

“Robustness of polyploid species: evolutionary genomic studies using *Arabidopsis kamchatica* and wheat”

Jacobs Mac Kenzie
Michigan State University, USA

”Environmental effects on the genomics and epigenomics of subgenome dominance”

Allopolyploidization, whole-genome duplication coupled with interspecific hybridization, can disrupt genetic and epigenetic processes resulting in altered DNA methylation patterns, changes in gene expression, and transposable element reactivation, commonly referred to as genomic shock. Homoeologous genes may be expressed at non-equal levels in allopolyploids, with genome-wide expression abundance patterns being highly skewed towards one subgenome deemed the “dominant” subgenome. The dominant subgenome in naturally established allopolyploids has also been shown to exhibit dominance in resynthesized hybrids and allopolyploids. Furthermore, subgenome dominance has been shown to be established in the initial F1 hybrids. It is consistently biased towards the same subgenome among all resynthesized lines and with an increased magnitude over subsequent generations. This raises the question if subgenome dominance is predetermined based on certain genomic features (e.g., the density of nearby transposable elements) or an external stimulus. However, the mechanisms leading to subgenome dominance remain poorly understood. It remains to be determined whether or not subgenome dominance is the result of genomic and/or epigenomic factors in one subgenome and/or if environmental factors contribute to the observed dominance patterns. In addition, I am passionate in instilling excitement for polyploidy in the undergraduate classroom. I will present progress I have made in developing problem based learning exercises that lead undergraduate students through the entire process of investigating the origin of polyploids and the evolution of subgenomes.

Moeko Okada
University of Zurich, Switzerland

“Effects of allopolyploidization on homoeologous gene expression in synthetic hexaploids”

Polyploidization is a common phenomenon in many plants and animals and is considered an important driving force of evolution. However, how polyploidization contributes to evolution and environmental adaptation is still under discussion. In this study, we investigated the relationship between allopolyploidization and environmental response. Using cold response as an example, we conducted homoeologous expression analysis of two synthetic hexaploid wheat obtained from interspecific crosses between tetraploid wheat cultivar Langdon and two lines of Aegilops tauschii Coss.

Total RNA was extracted from leaves in control and cold condition. The RNA-seq reads were mapped against the A, B, and D subgenomes of the wheat genome (CS RefSeq v1.1, IWGSC 2018), respectively. Homoeolog triads, the set of homoeologous genes on A-, B-, and D-subgenome, were identified by homology search. Then, the origin of the reads was defined using EAGLE-RC (Kuo et al. 2020) to evaluate the expression level of each homoeolog.

The expression level of each homoeologous genes (A, B, and D) were similar among parental accessions and synthetics, respectively. Based on these expression level of each homoeologous genes, the expression ratios of the AB and D genomes (A + B : D) were calculated. Only 1% of homoeolog triads showed a significant difference in response to cold between subgenomes. This suggests that there is no drastic change, so-called “genome shock”, at least for gene expression regulation before and after polyploidization.

Linda Schlatter
Agroscope Zurich

“Insight into the Swiss breeding of induced-polyploid fodder plants by Agroscope”

Tetraploid ryegrass, fescues and Kentucky bluegrass are important components of Swiss grasslands due to their larger leaves, better digestibility and higher disease resistance compared to their diploid counterpart. Agroscope has been doubling ploidy levels of its most promising variety candidates for more than 50 years now by applying colchicine to freshly germinated seeds. Ploidy of colchicine treated plants was assessed based on leaf width, habitus and thousand grain weight, which are indicative of ploidy level. However, this method proved to be not very accurate and even in later generations, after investing considerable amount of work and field space, these populations were often found to be diploid and were eliminated. In order to determine the ploidy level earlier in the breeding process, flow cytometer analyses have been implemented in the breeding process two years ago. By staining the nuclear DNA with propidium iodide, the freshly colchicinated plants are now tested for ploidy shortly after germination. Only completely or mostly tetraploid plants are transplanted into the field and open-pollinated one year later. The progeny is then tested again for ploidy and only completely tetraploid plants are integrated into the regular breeding process. In the last two years, it has been possible for the first time to record how efficiently colchicine works in different species and how species behave when different ploidies are crossed. In the course of these measurements, many new questions have arisen, which hopefully can be answered in the future and thereby further improving the breeding process of polyploid varieties.

Christian Parisod
University of Fribourg, Switzerland

“Adaptive radiation of diploids vs autotetraploids across ecological gradients”

Teresa Zeni
University of Innsbruck, Austria

"Role of genome duplication in changing mountain landscapes: a preliminary report"

Polyploidy is a key feature of plant biodiversity. A recent comprehensive analysis of global chromosome count data has shown that the frequency of polyploids increases with latitude. Much less is known about ploidy variation and distribution in mountain areas. In temperate mountain ranges the frequency of polyploids may rise towards high-elevation habitats (due to, for instance, their higher stress tolerance) and with increasing distance from glacial refugia (due to better colonizing abilities). Employing flow cytometry, we aim to establish ploidy levels of a flora-wide sampling of several ten thousand individuals of angiosperms from 100 elevational transects in the Eastern Alps and spanning from 550 m below timberline to 550 m above it. Generalized linear mixed effects models will be used to analyse whether there is a generic pattern of increasing polyploid frequency with increasing elevation and /or distance from the closest Pleistocene refugium. We will test if climatic niches differ among cytotypes of the same species, fitting species distribution models separately at the species and the cytotype level. Using predictive modelling, we will further investigate if risk from climate change is biased towards low or high ploidy levels and estimate the extent of future cryptic biodiversity loss under climate change scenarios. This project represents an unprecedentedly broad empirical test at the landscape level of the long-standing hypothesis of a positive association between genome duplication and spatio-temporal environmental variation. We will present the project and some preliminary results concerning the distribution of polyploids along the altitudinal gradient.

Laura Steinmann
Max Planck Institute, Germany

"The role of the environment in the origin and evolution of *Arabidopsis* polyploids"

All flowering plants are ancient polyploids. Moreover ~30% of flowering plant species have recently duplicated again. On an evolutionary time scale whole-genome duplication (WGDs) events are not randomly distributed and seem to accumulate at the times of extreme climate change. Contemporary polyploids show a strong latitudinal pattern with polyploid frequency increasing toward the poles suggesting an adaptive advantage of polyploids. These distribution patterns of polyploids seem to be largely shaped by climatic factors, mainly temperature. Two main hypotheses could explain the pattern: (1) a climate-related induction of unreduced gametes increasing the rates of polyploid formation or (2) an adaptive advantage of polyploids under certain challenging climatic conditions. We aim to study these questions using Arabidopsis lyrata as a model with at least three independent origins of tetraploids. We investigate the predisposition to polyploidy by exploring the variation of unreduced gametes formation in different genetic and environmental contexts and using a combination of common garden experiments and population genetic approaches like GWAS and QTL mapping to study the underlying genetics. We explore the genetics of adaption in polyploids vs. diploids using environmental association analysis like LFMM taking advantage of the wide geographical spread of the model A. lyrata system.

Anna Glushkevich
Max Planck Institute, Germany

“Adaptive introgression provides adaptation to polyploidy in Siberian *Arabidopsis lyrata*”

Both animal and plant polyploid species were shown to have enhanced gene flow. Such introgression can be a source of local adaptations as well as adaptations to the whole genome duplication itself. Adaptive introgression of miotic genes was previously found between tetraploid European Arabidopsis lyrata and tetraploid Arabidopsis arenosa. However, while A. arenosa is distributed across Europe, A. lyrata has a wider geographic range. Moreover, A. lyrata tetraploids were found in several areas of Siberia. Adaptations to polyploidy and the origin of these populations have not been studied yet.
We generated short-read resequencing data of 26 tetraploid and 52 diploid A. lyrata plants from Siberia and used Twisst to find introgression hotspots in Siberian A. lyrata populations.
Overall topology weighting statistics suggest independent origins of two tetraploid lineages in Siberia: around the Polar part of the Urals and in the Eastern part of Siberia around the Lena river. Several genome regions showed a distinctly common origin in both tetraploid lineages, suggesting they were introgressed. These regions had an overrepresentation of genes involved in the cell cycle and chromosome segregation - both processes were shown to play a crucial part in adaptation to polyploidy in A. arenosa and European A. lyrata. Some genes, for example, ASY3, showed gene flow signatures in European populations. Other genes, such as synaptonemal complex protein ZYP1, are likely introgressed only in Siberia. These findings suggest the vital importance of these genes for adaptation to polyploidy and the large impact of gene flow on polyploid formation.

Loïc Pittet
University of Göttingen, Germany

“Phylogeographical comparison of species of the *Salix retusa* polyploid complex in the European mountain system”

Species distribution is a dynamic process that evolves through space and time and entails that the current range is a snapshot of a long-term process. In the European mountains, climatic oscillations and glaciations during the Pleistocene caused range fluctuations of species. Polyploid plants are thought to perform better in colder climates and as re-colonizers of previously glaciated areas.
In Europe, the genus Salix comprises about 65 species exhibiting different growth forms, habitats, and ploidy levels. Both the high polyploid species Salix retusa and the diploid species Salix serpillifolia are prostrate willow species. Salix retusa occurs in most of the European Mountains while S. serpillifolia is restricted to extremer, high alpine conditions in the Alps. Flow Cytometry and next generation RAD (Restriction site Associated DNA) sequencing allow us to address questions about the effects of ploidy level on the dynamic of distribution and characterize the species genetic structures across their whole European distribution area.
For Salix retusa, each of the three ploidy level created its own genetic cluster and probably survived the LGM in one of the major hypothetical glacial refugia in the Iberian, Apennine, and Balkan Peninsulas. For Salix serpillifolia, the results indicate two genetic clusters representing the eastern and southwestern part of the Alps and admixture in central Alps. Both recolonization from marginal refugial areas and nunatak

survival is possible. Polyploids are more successful than diploids to occupy a large distribution area, but are not superior in the coldest, high alpine zones.

Martin Lascoux
Uppsala University, Sweden

“A ‘fast’ method to infer polyploid origin and introgression — With application to birch”

Hannah Assour
University of Pittsburgh, USA

“Neopolyploidy in the great duckweed (*Spirodela polyrhiza*) alters the outcome of herbivory”

Polyploidy is a dramatic mechanism of differentiation and speciation in plants that can shape the evolutionary dynamics of species interactions. Yet, knowledge of whether ploidy-induced variation has effects on plant-herbivore dynamics is scarce. Here, we test whether aphid herbivores exhibit preference for a diploid or polyploid host cytotype and whether ploidy impacts plant resistance and tolerance to aphids, measured as aphid and plant performance respectively. To answer these questions, we evaluated aphid choice and compared the effects of the water-lily aphid (Rhopalosiphum nymphaeae) herbivore on multiple independently synthesized lines of neopolyploid greater duckweed (Spirodela polyrhiza) and their immediate diploid progenitors in growth chamber experiments. Both aphids and duckweeds are fast-growing organisms, producing multiple asexual generations within several weeks, providing a unique opportunity to evaluate population growth rates of both partners during their interaction. We found that when plants were size matched, aphids did not show a preference for one cytotype over another. We also found that polyploid plants performed as well or worse under aphid herbivory compared to their diploid progenitors. Similarly, aphid growth rates were either the same or higher on polyploid plants. Thus, polyploid plants exhibited lower tolerance and resistance than their diploid progenitors. However, these results varied by genotype, indicating that the effect of polyploidy depends on the plant’s genetic origin. Consequently, it is possible that plant polyploidy may not confer any higher tolerance or resistance to herbivory. Instead, plant polyploidy may contribute to herbivore success and host range expansion, eventually promoting evolutionary diversification of the herbivore.

Nikita Tikhomirov
Max Planck Institute, Germany

“Genomics of adaptation in mixed-ploidy aquatic plants *Potamogeton*”

In the course of adaptation to polyploidy, the multiplied gene set is optimized and pairwise segregation of meiotic chromosomes is restored in a process known as (re-)diploidization. As the number of sequenced polyploid genomes grows, it becomes clear that there is no universal scenario for this process neither in plants nor in animals, and the mechanisms behind diploidization remain poorly understood. Differently pronounced subgenome- and lineage-specific biases individualize the evolution of polyploid groups and affect their environmental adaptation and diversification.

A model system of an established and diverse polyploid lineage occupying a wide range of environments must promote studies of factors driving polyploid evolution. In this project, we propose such a system chosen among aquatic angiosperms: the cosmopolitan aquatic plant genus Potamogeton comprises ca. 80 species, roughly half of which are tetraploid.

Using genus-wide whole-genome resequencing data mapped to our draft reference assembly for the diploid Potamogeton acutifolius, we got evidence supporting the single origin of tetraploidy in Potamogeton and its emergence due to genome hybridization rather than duplication. This setting permits studies of lineage-specific diploidization patterns, which will be facilitated by the pan-genome resource for Potamogeton that we are currently creating. In addition, we set out to inspect diploidization and environmental adaptation of polyploids at a finer scale in a range-wide resequencing dataset for a cosmopolitan tetraploid P. perfoliatus, where we found a few genetic lineages with marked geographic preferences despite the effective dispersal of aquatic plants with waterfowl.

Malika Ainouche
University of Rennes, France

“Hybridization, polyploidy and biological invasion”

Participants List

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Symposium only

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