

POLYPLOIDY AND BIODIVERSITY

Rennes 11-12 October 2021

Abstracts

Oral presentations

Life with more than one genome

Yves Van De Peer*¹

¹Department of Plant Systems Biology – Belgium

Abstract

Thousands of species are currently polyploid, and contain multiple copies of their genome. On the other hand, the long-term establishment of organisms that have undergone ancient whole genome duplications (WGDs) has been exceedingly rare. The apparent paucity of ancient genome duplications and the existence of so many species that are currently polyploid provides a fascinating paradox. Interestingly, many ancient WGDs seem to have been established at very specific times in evolution, for instance during major ecological upheavals and periods of extinction. Our work has shown that WGDs observed for many different plant lineages seem to have coincided with the most recent major mass extinction, i.e. the K/Pg extinction, 66 million years ago. I will put forward different hypotheses of why polyploids, compared to their diploid progenitors, might have had some selective advantage that might explain their survival at times of extinction or environmental turmoil. On the other hand, the duplication of entire genomes also greatly increases the genomic (and physical) complexity of gene regulatory and interaction networks. It is currently unclear how the increased complexity, modularity and redundancy of duplicated gene regulatory networks might affect polyploids. Preliminary studies seem to suggest that more complex – e.g. more densely connected - duplicated networks might allow bigger and/or faster jumps in the fitness landscape, which might be advantageous in highly disturbed environments or during periods of environmental turmoil, while being disadvantageous in stable environments, where bigger ‘moves’ in the fitness landscape might be maladaptive or detrimental.

*Speaker

Autopolyploid speciation and expansion of *Biscutella laevigata*

Sandra Grünig*¹, Theofania-Sotiria Patsiou¹, and Christian Parisod¹

¹University of Fribourg – Switzerland

Abstract

The *Biscutella laevigata* species complex encompasses diploid and tetraploid lineages. The distribution of diploids in never-glaciated lowlands suggests that they were pushed out of the Alps during the Pleistocene, whereas tetraploids found at high-elevation in previously-glaciated areas were formed at this time and recolonized the whole Alps after the last glacial maximum (LGM). However, areas where the different lineages survived the LGM remain unclear, as is the role of hybridization between distinct diploids or the single vs multiple origin of tetraploids. We extensively sampled 17 diploid populations from all around the Alps and 19 tetraploid populations across the central Alps. Using ddRAD-seq we genotyped 370 individuals at 4444 high confidence SNPs. These data support divergent diploid lineages and a genetically coherent tetraploid group, suggesting their single origin followed by considerable expansion. Genetic admixture indicates unidirectional gene flow from diploid populations into expanding tetraploids. Although niche modelling suggests that tetraploids occupy a wider environmental space than diploids, there are a few alpine diploid populations and genetic data shows that tetraploids likely originated from such preadapted diploids. Integrating ecological modelling with spatially-explicit demographic inferences through time, we aim at better understanding how diploids and tetraploids diverged and expanded towards their current distribution.

*Speaker

Autopolyploid duckweed, the effects of WGD on duckweed morphology, physiology and phenotypic plasticity

Quinten Bafort^{*1}, Tian Wu¹, Annelore Natran¹, and Yves Van De Peer¹

¹vib-ugent center for plant systems biology – Belgium

Abstract

The evolutionary importance of autopolyploidy is a point of controversy amongst scholars of polyploidy that goes back at least 70 years. Historically autopolyploidy was thought to be extremely rare as a consequence of the fitness reduction due to the multivalent formation. Over time thought on this matter has changed considerably but there is still no real consensus on the relative importance of autopolyploids in evolution and the factors that contribute to their success. Nevertheless there is increasing evidence that the fate of neopolyploids depends strongly on the environment. There seems for example a link between polyploidy and stressful environments. It is however unclear whether this supposed link between polyploids and altered environments can be attributed to (1) the period of polyploid establishment where initial differences in morphology, life history traits and /or physiology could help to overcome initial competition with the diploids progenitors or (2) to differences in adaptive potential in the longer run or (3) a combination of both. Here I present how we use neopolyploid strains of the greater duckweed *Spirodela polyrhizha* to investigate (1) the relationship between the direct effects of WGD and fitness over a range of environmental conditions (2) and their long term adaptive potential using a combination of mutation accumulation and experimental evolution.

^{*}Speaker

Valued ecosystem engineer or tracked invasive species? The multifaceted consequences of recurrent hybridization and polyploidy in the saltmarsh grass genus *Spartina*.

Malika Ainouche*¹, Armel Salmon , Oscar Lima , Armand Cave-Radet , Abdelhak El-Amrani , Delphine Giraud , H el ene Rousseau , Mathieu Rousseau-Gueutin , Julien Boutte , Julie Ferreira De Carvalho , Olivier Coriton , and Virginie Huteau

¹UMR CNRS 6553 ECOBIO - Universit e de Rennes 1 – CNRS : UMR6553 – France

Abstract

The last two decades have tremendously increased our understanding of polyploid evolution, its importance and impact in biology, ecology, agronomy, and population management. Particularly, the awareness that modern angiosperm genomes range in complexity from those that have experienced few genomic duplication events to others that exhibit evidences of several tens of genomic multiples with various degree of diploidization, raised new questions regarding the nature and temporality of the associated evolutionary processes. In the last 20 years, we have been using the polyploid grass genus *Spartina*, (which encompasses several ecosystem engineer species on salt marshes), as a model system to explore the consequences of whole genome duplication in the contexts of neo- and meso-polyploidy at the tetraploid, hexaploid, heptaploid and dodecaploid levels, which allowed to revisit some paradigms of polyploid evolution. Challenges associated with the analysis of highly duplicated genomes in non-model species (*e.g.* reconstructing the reticulate history of mesoploid lineages, detecting homeologs with no diploid references) and consequences of polyploidy on ecologically relevant functions, stress tolerance and biological invasions, as well as their implication on the management of invasive populations will be presented.

*Speaker

Genomic relationships among diploid and polyploid species of the genus *Ludwigia* sp section *Jussiaea* using genomic in situ hybridization

Dominique Barloy*^{1,2}, Luis Portillo - Lemus^{3,4}, Virginie Huteau⁵, and Olivier Coriton⁵

¹Ecology and Ecosystem Health, INRA, Agrocampus Ouest – INRA, Agrocampus Ouest – France

²Institut Agro - Agrocampus Ouest – Agrocampus Ouest – France

³Ecology and Ecosystem Health, INRA, Agrocampus Ouest – Agrocampus Ouest – France

⁴Agrocampus Ouest – Agrocampus Ouest – France

⁵UMR IGEPP – INRAE – France

Abstract

Polyloidization has been considered as a major driving force of plant speciation and evolution. The advantage of polyploidy is reported in invasive plants as an important determinant of invasiveness in plant. The genus *Ludwigia* sp section *Jussiaea*, which contains at least three invasive species, represents a polyploid complex with 2x, 4x, 6x and 10x ploidy levels suggesting a possible hybrid origin for the polyploid species. The aim of the present study is to understand the genomic relationships among diploid and polyploid species of section *Jussiaea* species. Morphological and cytogenetic observations, Genomic in situ hybridization (GISH) and flow cytometry were used to characterize the genomic composition and distribution of these species and their ploidy levels. Genome sizes obtained were in agreement with the diploid, tetraploid, hexaploid and decaploid ploidy levels. Results of GISH showed that progenitors of *Ludwigia stolonifera* (4x) were *Ludwigia peploides* subsp. *montevidensis* (2x) and *Ludwigia helminthorrhiza* (2x), this latter also participated for one part (2x) to *Ludwigia ascendens* genome (4x). *Ludwigia grandiflora* subsp. *hexapetala* (10x) resulted of hybridization between *L. stolonifera* (4x) and *Ludwigia grandiflora* subsp. *grandiflora* (6x). One progenitor of *L. grandiflorasubsp. grandiflora* was identified as *L. peploides* (2x). Our results suggested the existence of several processes of hybridization and polyploidy, probably allopolyploid events, in section *Jussiaea* which explain the diversity of ploidy levels. The success of GISH opens up the potential for future studies to identify the other missing progenitors.

*Speaker

Environmental cues are relevant for duplicate gene retention

Marc Beringer^{*1,2}, Rimjhim Roy Choudhury³, and Christian Parisod^{1,2}

¹University of Fribourg – Switzerland

²University of Bern – Switzerland

³University of Zurich – Switzerland

Abstract

Whole genome duplication (WGD) events have occurred in most plant lineages, followed by long-term genome re-organization known as genome fractionation or diploidization. Gene duplicates from a WGD event are expected to degenerate unless selection pressures support their long-term retention. Therefore, functions of retained duplicates highlight traits that were important during the history of diploidization.

The *Biscutella laevigata* (Brassicaceae) species complex has undergone a WGD event after divergence from *Arabidopsis*, leading to current diploid species with a wide distribution across environmental gradients. Their partially fragmented genomes, enriched in stress-responding duplicates, offer an excellent system to study the influence of environmental cues on genome fractionation.

We produced the first diploid genome assembly of *B. laevigata* subsp. *austriaca* and found that almost half of all investigated loci belong to pairs of retained duplicated genes. Signals of selection revealed increased purifying selection on duplicates as compared to singletons, showing that selection counteracts pseudogenization of specific duplicated loci. Subjecting clones of the genome-sequenced individual to cold, heat, drought and herbivory stresses revealed the expression of retained duplicates and singletons. We found a considerable fraction of retained pairs with parallel expression changes of both duplicates in response to the same environmental stress, indicating retention related to dosage increase. Additionally, we found pairs showing expression changes of duplicates in response to different stresses, as expected under retention through sub-functionalization related to environmental cues.

Retained duplicates related to dosage increase present evidence of purifying selection similar to duplicates related to sub-functionalization. These stress induced duplicates further share strength of purifying selection with all other non-induced retained duplicates. This suggests that other cues of equivalent importance as environmental stresses resulted in the retention of non-induced duplicate pairs and indicates that external factors are relevant in duplicate gene retention.

*Speaker

Separating the effects of polyploidization and hybridization with resynthesized *Capsella* polyploids

Tianlin Duan^{*1}, Martin Lascoux¹, Adrien Sicard², Sylvain Glémin³, and Marion Orsucci²

¹Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Norbyvägen, Uppsala, 18D 75326, Sweden – Sweden

²Department of Plant Biology The Swedish University of Agricultural Sciences (SLU), PO Box 7080, SE-750 07 Uppsala, Sweden – Sweden

³CNRS, ECOBIO (Ecosystèmes, biodiversité, évolution), University of Rennes 1, UMR 6553, Rennes, France – UMR CNRS ECOBIO-UNIVERSITE RENNES1 – France

Abstract

Allopolyploidy consists of two distinct processes: polyploidization and hybridization, both of which could bring massive genomic changes, yet allopolyploidy occurred frequently during plant evolution. Results from studies on allopolyploid species have been mixed: some showed mild chromosomal, epigenetic or transcriptomic changes while others reported more dramatic alterations. In most cases, the timescale of these changes and the relative contributions from polyploidization and hybridization to them remain unclear.

To distinguish the short- and long-term effects of allopolyploidy and compare the effects of polyploidization and interspecific hybridization in the same system, we created a series of diploid hybrids, autotetraploids and resynthesized allotetraploids with the two diploid parental species of the allotetraploid *Capsella bursa-pastoris*, *C. orientalis* and *C. grandiflora*. These lines were then grown together with natural accessions of *C. bursa-pastoris* and phenotypes and RNA-sequencing data of both inflorescences and leaves were compared among the groups.

Preliminary analyses showed that: a) compared to interspecific hybridization, polyploidization has much less distorting effects on the pattern of gene expression and may restore the fertility of hybrids; b) the natural allotetraploid plants differ from the resynthesized allotetraploids in floral morphology, pollen viability, homeolog expression bias, transgressive expression and expression level dominance, indicating the contribution of long-term evolution; c) the order of polyploidization and hybridization has moderate effects on phenotypes, but no obvious effects was found on overall expression pattern.

^{*}Speaker

Transposons and genome evolution in natural polyploid plants

Christian Parisod*¹

¹University of Fribourg – Switzerland

Abstract

Transposons are selfish jumping genes commonly activated by gene flow such as at the origin of allopolyploid species. Transposons however have an elusive impact on adaptive processes in their host plant populations. Our work in large-genome species such as Mediterranean wild wheats (*Aegilops* spp) supports an overall accumulation of transposons along with nearly-neutral diversification. In these cases, allopolyploidy indeed promoted the accumulation of incompatible transposons and genome-wide reproductive isolation despite limited ecological differentiation among species. In populations from alpine environments exposed to contrasted environments over short distances, we reported that transposons interact with the gene space and interfere with adaptive processes along chromosomes of the diploid Alpine rock-cress (*Arabis alpina*). We now use Buckler mustards (*Biscutella laevigata*) to investigate how transposons interact with autopolyploidy and adaptation under environmental heterogeneity. The role of transposons as ballast or powerhouse of diversification and adaptation must be further quantified to shed light on what makes the bulk of genomic DNA.

*Speaker

Interspecific hybridizations and dynamics of transposable elements in the wheat genome

Nathan Papon^{*1}, Romain De Oliveira¹, H el ene Rimbart¹, Etienne Paux¹, and Fr ed eric Choulet¹

¹G en etique Diversit e et Ecophysiologie des C er eales - Clermont Auvergne – Universit e Clermont Auvergne : UMR1095, Institut National de Recherche pour l’Agriculture, l’Alimentation et l’Environnement : UMR1095 – Campus des C ezeaux / 63000 Clermont-Ferrand - INRAE / 5 chemin de Beaulieu / 63039 Clermont-Ferrand Cedex 2, France

Abstract

Besides being one of the most important crops worldwide, bread wheat (*Triticum aestivum* L.) is also one of the most complex plant species. Indeed, it arose from two hybridization events resulting in a large (~16 Gb), allohexaploid (AABBDD), and highly repetitive (85 % of transposable elements, TEs) genome. Because they are the main constituents of the wheat genome, TEs have long been considered as key drivers of its structure and evolution. Particularly, it has been suggested that interspecific hybridizations led to massive TE amplifications. To investigate whether polyploidization events resulted in major TE bursts in the wheat genome, we develop a dedicated strategy to cope with the complexity of wheat genome based on the collinearity of orthologous genes. We analyzed the size and TE content of orthologous intergenic regions in five *Triticeae* species representing the three subgenomes at different ploidy levels: *T. aestivum* (AABBDD), *T. durum* (AABB), *T. dicoccoides* (AABB), *T. urartu* (AA) and *Aegilops tauschii* (DD). The comparison of TE content between all shared homologous subgenomes revealed that species-specific sequences represent 8 to 34% of the genomes. While recent transposition events were detected involving almost half of the TE families (47%, 238 TE families), deletion appeared to be the main driver of genomic variability. Moreover, the transpositional activity detected result from the same TE families regardless of the ploidy levels showing no reactivation of TE after hybridization. Our results provide new insights into the genomes evolution of *Triticeae* especially on the TE variability and suggest that despite of the identification of TE families still active, hybridization events did not trigger massive transpositional bursts during the wheat genome evolution.

^{*}Speaker

Genome downsizing after polyploidy: mechanisms, rates and selection pressures

Xiaotong(elaine) Wang^{*1,2}, Joe Morton^{1,2}, Jaume Pellicer^{1,3}, Ilia Leitch¹, and Andrew Leitch²

¹Royal Botanic Gardens, Kew, Surrey TW9 3AB, UK – United Kingdom

²Queen Mary University of London, Mile End Road, London E1 4NS, UK – United Kingdom

³Institut Botànic de Barcelona (IBB, CSIC-Ajuntament de Barcelona), Passeig del Migdia sn, 08038, Barcelona, Spain – Spain

Abstract

An analysis of over 10,000 plant genome sizes (GS) indicate that most species have smaller genomes than expected given the incidence of polyploidy in their ancestries, suggesting selection for genome downsizing. However, comparing ancestral GS with the incidence of ancestral polyploidy suggests that the rate of DNA loss following polyploidy is likely to have been very small (4-70 Mb/million years, 4-482 bp/generation). This poses a problem, how might such small DNA losses be visible to selection, overcome the power of genetic drift, and drive genome downsizing? We explore that problem, focusing on the role that double-strand break (DSB) repair pathways (non-homologous end joining (NHEJ) and homologous recombination (HR)) may have played. We also explore two hypotheses that could explain how selection might favour genome downsizing following polyploidy, to reduce: (1) nitrogen (N) and phosphate (P) costs associated with synthesising nucleic acids in the nucleus and the transcriptome, and; (2) the impact of scaling effects of GS on cell size, which influences carbon dioxide uptake and water loss. We explore the hypothesis that losses of DNA must be fastest in early polyploid generations. Alternatively, if DNA loss is a more continuous process over evolutionary time, then we propose it is a byproduct of selection elsewhere, such as limiting the damaging activity of repetitive DNA. If so then the impact of GS on photosynthesis, water use efficiency and/or nutrient costs at the nucleus level, may be emergent properties, which have advantages, but not ones that could have been selected for over generational timescales.

*Speaker

Genetic architecture of glucosinolate diversity in *Brassica napus* and progenitor species for chemical ecology and breeding

Julie Ferreira De Carvalho*¹, Anani Amegan Missinou¹, Nathalie Marnet², Oumayma Hamzaoui¹, David Abdel Sayed¹, Yann Guitton³, Lionel Lebreton¹, Christophe Langrume¹, Christophe Mougel¹, Anne-Marie Chèvre¹, Maria Manzanara-Dauleux¹, Alain Bouchereau^{1,2}, Regine Delourme¹, Anne Laperche¹, and Antoine Gravot^{1,2}

¹Institut de Génétique, Environnement et Protection des Plantes – Université de Rennes, Agrocampus Ouest : UMR1349, Institut National de Recherche pour l’Agriculture, l’Alimentation et l’Environnement : UMR1349 – France

²P2M2 – Platform P2M2, Profiling Platform of Metabolic and Metabolomic, UMR1349 IGEPP, INRAE, Le Rheu, France – France

³Oniris, Laboratoire d’Etude des Résidus et Contaminants dans les Aliments (LABERCA), – Université Nantes Angers Le Mans – Nantes, F-44307, France

Abstract

Glucosinolate compounds represent an important group of secondary metabolites, specific to the Brassicales order, implicated in plant defense against microbial pathogens and insect herbivores. Although previously described in Brassicaceae, the underlying genetic and phytochemical diversity of glucosinolates has scarcely been approached in the context of the Brassica complex and oilseed rape recent breeding history.

Thus, to investigate the impact of low glucosinolate breeding, we performed mass-spectrometry on a panel of 270 *B. napus*, 10 *B. oleracea* and 11 *B. rapa* representing different cultigroups. We quantified and annotated 36 glucosinolate compounds in leaf and root tissue, as well as 34 phenolics in leaf tissue. In addition, genotyping was achieved to perform Genome-Wide Association (GWA) mapping on the *B. napus* panel and identify genomic regions associated with the different metabolites.

While we revealed in *Brassica sp* contrasted quantitative ratios of the main categories of glucosinolates and predominance of aromatics and indolics in roots compared to leaves, we also described wider quantitative range of aliphatic methionine-derived compounds in the leaves of both progenitors compared to *B. napus* panel. This is due to the extreme accumulation of a few glucosinolate molecules (mostly C3 and C4) in progenitors. Using multivariate analyses and clustering, several chemotypes of *B. napus* were described and specific glucosinolate and phenolic compounds were pinpointed. These particular molecules were further investigated in GWA mapping, and underlying genes were unravelled in *B. napus*.

Results on specific molecules and underlying metabolic pathways discriminating *B. napus* and its progenitors will be investigated further in plant-insect/microbe experiments in order to understand the molecular bases of these interactions and improve oilseed rape breeding.

*Speaker

Cryptic diversity of diploid progenitors for improvement of an allopolyploid, *Brassica napus*

Cyril Falentin¹, Franz Boideau¹, Loeiz Maillet¹, Julien Boutte¹, Julie Ferreira De Carvalho¹, Gwenaelle Deniot¹, Pascal Glory¹, Maryse Lode-Taburel¹, Gwenn Trotoux¹, Virginie Huteau¹, Marie Gilet¹, Jérôme Morice¹, Olivier Coriton¹, Mathieu Rousseau-Gueutin¹, and Anne-Marie Chèvre^{*1}

¹Institut de Génétique, Environnement et Protection des Plantes, UMR1349 – INRAE, Université de Rennes I, Agrocampus Ouest – France

Abstract

The genetic diversity of allopolyploid crops is often limited due to their origin and impact of selective pressure. Conversely, their diploid parental species, especially the wild forms, may be a reservoir of diversity that are often poorly explored for breeding. This is particularly true for the allotetraploid *Brassica napus* (AACC, $2n=4x=38$), which derives from the diploid species *B. rapa* (AA, $2n=2x=20$) and *B. oleracea* (CC, $2n=2x=18$). We took the unique opportunity that these two species are growing under a large climatic gradient, from North of Europe to South of North Africa (center of origin) to collect ~100 populations of wild forms or local landraces of each species. This extensive sampling was performed in the framework of H2020 Prima BrasExplor project (2020-2023) involving 11 partners from 6 countries. All this unique material will be sequenced using Illumina to identify through Genomic-Environmental-Association and physiological approaches the genetic determinants involved in climatic adaptation including resistance to biotic and abiotic stresses. As the recent genome assembly of various *Brassica* individuals using new sequencing technologies revealed the presence of important intraspecific structural variations (SVs), it will be crucial to consider these SVs as they may hamper the introgression of traits of interest from the diploid to the allotetraploid oilseed rape. Fortunately, the important genetic shuffling caused by the modified control of the recombination process in allotriploid hybrids will enable to rapidly and efficiently increase *B. napus* diversity.

*Speaker

Combining synteny and sequence-based approaches to investigate genome evolution after polyploidization

Elise Parey¹, Alexandra Louis², Lada Isakova², Jérôme Montfort³, Yann Guiguen³,
Hugues Roest Crollius*⁴, and Camille Berthelot⁵

¹Institut de Biologie de l'École Normale Supérieure (IBENS) – École Normale Supérieure de Paris - ENS Paris, CNRS : UMR8197, Institut National de la Santé et de la Recherche Médicale - INSERM : U1024 – 46 rue d'Ulm, Paris F-75005, France

²Institut de biologie de l'ENS Paris – École normale supérieure - Paris, Université Paris sciences et lettres, Centre National de la Recherche Scientifique, Institut National de la Santé et de la Recherche Médicale : U1024, Centre National de la Recherche Scientifique : UMR8197 – France

³LPGP – UR1037 Fish Physiology and Genomics, INRA, Rennes – France

⁴Institut de biologie de l'ENS Paris – École normale supérieure - Paris, Institut National de la Santé et de la Recherche Médicale : U1024, Centre National de la Recherche Scientifique : UMR8197 – France

⁵Institut de biologie de l'ENS Paris – École normale supérieure - Paris, Université Paris sciences et lettres, Centre National de la Recherche Scientifique, Institut National de la Santé et de la Recherche Médicale : U1024, Centre National de la Recherche Scientifique : UMR8197 – France

Abstract

Whole-genome duplications (WGDs), or polyploidizations, are major evolutionary events contributing extensively to species diversification processes. However, accurately tracing genes and genome evolution after WGD is challenging as these events are followed by massive gene losses, gene conversions and widespread evolutionary divergence. To address this, we developed a novel gene tree correction method, named SCORPiOs (Synteny-guided CORrection of Paralogies and Orthologies). SCORPiOs integrates information from the genomic organization of genes, or synteny, to complement classical sequence-based gene tree construction methods. We apply SCORPiOs to a large set of gene phylogenies containing 101 vertebrates, including 74 teleost species sharing a common 320 million years old WGD event. By combining these refined gene trees together with a state-of-the-art ancestral teleost karyotype reconstruction, we establish a genomic atlas of WGD-duplicated regions across teleosts. We reveal that gene losses after the WGD have unequally affected duplicated chromosomes, with some genomic regions displaying pronounced retention biases on one of the homeologues. Analyzing strong disagreements between sequence and synteny predictions for gene family evolution, we uncover WGD-duplicated regions likely subjected to homeologous recombination for an extended period of time following polyploidization. We also applied SCORPiOs to Faboideae, a sub-family of the flower plants Leguminosae that were subject to a WGD. Corrected Faboideae gene trees show markedly different evolutionary patterns compared to their uncorrected versions. Altogether, our results show that improving the reconstruction of gene phylogenies sheds light on the contribution of WGDs to the evolution of vertebrate and plant genomes.

*Speaker

Three founding ancestral genomes involved in the origin of sugarcane

Simon Rio*¹, Nicolas Pompidor¹, Carine Charron¹, Catherine Hervouet¹, Stéphanie Bocs¹, Gaëtan Droc¹, Ronan Rivallan¹, Aurore Manez¹, Therese Mitros², Kankshita Swaminathan³, Jean-Christophe Glaszmann¹, Olivier Garsmeur¹, and Angélique D'hont¹

¹CIRAD -UMR AGAP – Centre de coopération internationale en recherche agronomique pour le développement [CIRAD] – France

²Department of Molecular Cell Biology [Berkeley] – United States

³Department of Crop Sciences, University of Illinois – United States

Abstract

Modern sugarcane cultivars (*Saccharum* spp.) are high polyploids, aneuploids ($2n \sim 12x \sim 120$) derived from interspecific hybridizations between the domesticated sweet species *Saccharum officinarum* and the wild species *S. spontaneum*. To analyse the architecture and origin of such a complex genome, we analysed the sequences of all 12 homologous haplotypes (BAC clones) from two distinct genomic regions of a typical modern cultivar, as well as the corresponding sequence in *Miscanthus sinense* and *Sorghum bicolor*, and monitored their distribution among representatives of the *Saccharum* genus. The diversity observed among haplotypes suggested the existence of three founding genomes (A, B, C) in modern cultivars, which diverged between 0.8 and 1.3 Mya. Two genomes (A, B) were contributed by *S. officinarum*; these were also found in its wild presumed ancestor *S. robustum*, and one genome (C) was contributed by *S. spontaneum*. These results suggest that *S. officinarum* and *S. robustum* are derived from interspecific hybridization between two unknown ancestors (A and B genomes). The A genome contributed most haplotypes (nine or ten) while the B and C genomes contributed one or two haplotypes in the regions analysed of this typical modern cultivar. Interspecific hybridizations likely involved accessions or gametes with distinct ploidy levels and/or were followed by a series of backcrosses with the A genome. The three founding genomes were found in all *S. barberi*, *S. sinense* and modern cultivars analysed. None of the analysed accessions contained only the A genome or the B genome, suggesting that representatives of these founding genomes remain to be discovered. This evolutionary model, which combines interspecificity and high polyploidy, can explain the variable chromosome pairing affinity observed in *Saccharum*. It represents a major revision of the understanding of *Saccharum* diversity.

*Speaker

Analyses of allelic diversity at the self-incompatibility locus in tetraploid populations of *Arabidopsis arenosa* reveal an absence of a major bottleneck associated with autopolyploidy

Xavier Vekemans*¹, Vincent Castric, and Céline Poux

¹UMR 8198 Evo-Eco-Paleo – CNRS, Université de Lille – France

Abstract

Plant self-incompatibility (SI) is a genetic system that prevents selfing and enforces outcrossing. Because of strong balancing selection, the genes encoding SI are predicted to maintain extraordinarily high levels of polymorphism, both in terms of the number of functionally distinct S-alleles that segregate in SI species and in terms of their nucleotide sequence divergence. Thanks to this property, patterns of variation in SI allelic diversity are good markers to reveal strong genetic bottlenecks in the distant past, for instance bottlenecks associated with speciation or polyploidy events. However, documenting polymorphism of these genes also presents important methodological challenges that have so far largely prevented the comprehensive analysis of complete allelic series in natural populations. We have developed a powerful methodological approach based on a computationally optimized comparison of short Illumina sequencing reads from genomic DNA to a database of known nucleotide sequences of the extracellular domain of SRK (eSRK). By examining mapping patterns along the reference sequences, we obtained highly reliable predictions of S-genotypes from individuals collected from natural populations of *Arabidopsis arenosa* (diploid or tetraploid populations). We observed that allelic diversity was similar in diploid and tetraploid populations, suggesting absence of major bottleneck events associated with polyploidy. However, gene diversity at the S-locus was substantially lower in tetraploids as compared to diploids, in contrast to the neutral expectation of higher diversity in tetraploids. Numerical simulations showed that this observation is the consequence of interference between balancing selection and dominance interactions among S-alleles, which are enhanced in tetraploids. This dominance effect was more important than the effect of an increase in effective population size in the tetraploids, thereby causing a reduction rather than an increase in gene diversity.

*Speaker

Genomic and transcriptomic evolution of a recent allopolyploid species

Martin Lascoux
Department of Ecology and Genetics
Uppsala University
Uppsala, Sweden

The shepherd's purse (*Capsella bursa-pastoris*) is a young allopolyploid weed with a worldwide distribution. It originates from a hybrid between *C. grandiflora*, an outcrosser with a high genetic diversity and *C. orientalis*, a self-fertilizing species with low diversity. As *C. bursa-pastoris* originated recently one could expect the genetic polymorphism of the two subgenomes to follow similar trajectories and their transcriptomes to start functioning together. To test this hypothesis we sequenced the genomes and the transcriptomes (three tissues) of *C. bursa-pastoris* and its parental species. Both at genomic and transcriptomic levels we observed a strong parental legacy. At the genomic level, the *C. orientalis* subgenome accumulated more deleterious changes than the *C. grandiflora* one. Comparison of the divergence in expression between subgenomes, on the one hand, and divergence in expression between the parental species, on the other hand, indicated a strong parental legacy with a majority of genes exhibiting a conserved pattern and cis-regulation. However, a large proportion of the genes that were differentially expressed between the two subgenomes, were also under trans-regulation reflecting the establishment of a new regulatory pattern. Parental dominance varied among tissues: expression in flowers was closer to that of *C. orientalis* and expression in root and leaf to that of *C. grandiflora*. Since deleterious mutations accumulated preferentially on the *C. orientalis* subgenome, the bias in expression towards *C. orientalis* observed in flowers indicates that expression changes could be adaptive and related to the selfing syndrome, while biases in the roots and leaves towards the *C. grandiflora* subgenome may be reflective of the differential genetic load.

Chromosomal flip-flop disturbs the meiosis maestro in *Brassica napus*

Franz Boideau^{*1}, Gautier Richard¹, Olivier Coriton¹, Virginie Huteau¹, Caroline Belser²,
Gwenaëlle Deniot¹, Frédérique Eber¹, Cyril Falentin¹, Julie Ferreira De Carvalho¹,
Marie Gilet¹, Maryse Lode-Taburel¹, Loeiz Maillet¹, Jérôme Morice¹, Gwenn Trotoux¹,
Jean-Marc Aury², Anne-Marie Chèvre¹, and Mathieu Rousseau-Gueutin¹

¹Institut de Génétique, Environnement et Protection des Plantes, UMR1349 – INRAE, Université de
Rennes I, Agrocampus Ouest – France

²Génomique Métabolique, Genoscope, Institut François Jacob, CEA, CNRS, Univ Evry, Université
Paris-Saclay – Génomique Métabolique, Genoscope, Institut François Jacob, CEA, CNRS, Univ Evry,
Université Paris-Saclay – France

Abstract

Recombination is the main mechanism generating new genetic diversity through the reshuffling of parental alleles at each generation. It is also the main tool used by breeders in order to generate new varieties able to face the challenging climate change and the reduction of phytosanitary input. However, meiotic recombination is highly regulated: firstly, in frequency with one obligate crossover and rarely more than three (independently of the chromosome length); and secondly, in distribution at the chromosome scale, with most crossovers being restrained in euchromatic regions and being deprived in the close centromeric regions. By comparing a cultivated and a semi-resynthesized *Brassica napus* ($2n = 4x = 38$) genetic maps sharing one common parent, we were able to respectively retrieve four and six large regions ($> 1\text{Mb}$) deprived of recombination in normally recombining region. In *Arabidopsis* or other species, it was shown that methylation and/or structural variations within euchromatic region locally negatively affects recombination. To determine if such factors may explain the lack of recombination in our hybrids, we performed whole genome bisulfite sequencing and observed that three of these non-recombining regions presented a much higher DNA methylation level than the neighboring recombining region. We also compared the whole genome assemblies of the parental lines and identified that two regions lacking recombination were inverted. Using oligo-FISH painting or optical mapping, we validated the presence of these latter paracentric inversions. Finally, we performed pairwise comparisons of the high-quality genome assemblies of nine *B. napus* varieties in order to establish the frequency of such chromosomal inversions between varieties and discuss their putative impact on evolution and classic breeding programs.

^{*}Speaker

Variation in the pathways and rates of inter-ploidy gene flow across multiple plant systems: Putting the diploid – polyploid reproductive barrier to a test

Martin Certner^{*1,2}

¹University of Fribourg – Switzerland

²Institute of Botany of the Czech Academy of Sciences – Czech Republic

Abstract

Ploidy-level differences are traditionally considered very efficient reproductive barriers. Indeed, the process of whole genome duplication directly provides first-generation polyploid mutants with postzygotic reproductive isolation from their diploid progenitors, known as the "triploid block". However, it has been long suspected that the intensity of triploid block may substantially differ among plant species.

We aimed at assessing the strength of inter-ploidy reproductive barriers in three European plant species with well documented contact zones of cytotypes allowing population-level ploidy coexistence (i.e., *Arabidopsis arenosa*, Brassicaceae; *Tripleurospermum inodorum*, Asteraceae; *Butomus umbellatus*, Butomaceae). The main research approaches included manipulated inter- and intra-ploidy crosses, F1-hybrid phenotyping, intensive flow cytometric screening of both natural and experimental progeny arrays, and plant genotyping using microsatellite markers.

A strong triploid block was detected in *Arabidopsis*, which mainly manifested during the endosperm development but also translated into lower seed germination and survival of inter-ploidy hybrids. Interestingly, the contact zone with the least genetic differentiation of cytotypes showed lowest signs of triploid block. The situation was different in both other species, where triploids were readily formed in mixed-ploidy populations or even stabilized by clonal reproduction as dominant cytotypes and did not exhibit lower vitality. Reproductive interactions involving triploid individuals always resulted in profound variation in nuclear DNA content of the progeny. However, the occasional formation of euploids could be the key to facilitating inter-ploidy gene flow. Though the inter-ploidy gene flow never seemed to compromise integrity of the coexisting diploid and polyploid lineages, it might serve as a source of adaptive genetic variation. In *Tripleurospermum*, even aneuploid F2 hybrids could participate in inter-ploidy crosses and signs of bidirectional gene flow between 2x and 4x were detected in natural populations. Genetic structure of *Butomus* populations suggested both occasional genetic recombination between locally coexisting cytotypes and recurrent origins of triploids.

*Speaker

Power and weakness of repetition – evaluating the phylogenetic signal from repeatomes in the family Rosaceae with two case studies from genera prone to polyploidy and hybridization (Rosa and Fragaria)

Ales Kovarik^{*1}, Veit Herklotz , Volker Wissemann , Jana Lunerova , Radka Vozarova , Sebastian Buschmann , Klaus Olbricht , Marco Groth , Sonia Garcia , and Christiane Ritz

¹Institute of Biophysics, Czech Academy of Science – Czech Republic

Abstract

Plant genomes consist to a considerable extent of non-coding repetitive DNA. Several studies showed that phylogenetic signals can be extracted from such repeatome data by using among-species dissimilarities from the RepeatExplorer2 pipeline as distance measures. Here, we advanced this approach by adjusting the read input for comparative clustering indirectly proportional to genome size and by summarizing all clusters into a main distance matrix subjected to Neighbor Joining algorithms and Principal Coordinate Analyses. Thus, our multivariate statistical method works as a "repeatomic fingerprint" and we proved its power and limitations by exemplarily applying it to the family *Rosaceae* at intrafamilial and, in the genera *Fragaria* and *Rosa* at intrageneric level. We also demonstrate the utility of 5S rDNA cluster graphs for identification of interspecific hybrids and allopolyploids. Since repeatomes can be technically easy and comparably inexpensively retrieved even from samples of rather poor DNA quality, our phylogenomic method serves as a valuable alternative when high quality genomes are unavailable, for example in the case of old museum specimens.

^{*}Speaker

GenAPoPop1.0: Computing population genetic indices and inferring reproductive modes from genotype diversity in polyploid populations

Solenn Stoeckel^{*1}, Ekaterina Bocharova^{2,3}, and Dominique Barloy⁴

¹Institut de Génétique, Environnement et Protection des Plantes – Université de Rennes 1 : UMR1349, Université de Rennes, Agrocampus Ouest : UMR1349, Institut national d'enseignement supérieur pour l'agriculture, l'alimentation et l'environnement, Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement : UMR1349, Institut national d'enseignement supérieur pour l'agriculture, l'alimentation et l'environnement, Institut national d'enseignement supérieur pour l'agriculture, l'alimentation et l'environnement – France

²Koltzov Institute of Developmental Biology RAS, Moscow – Russia

³Molecular Genetics Laboratory, Russian Federal Research Institute of Fisheries and Oceanography, Moscow – Russia

⁴Écologie et santé des écosystèmes – Agrocampus Ouest, Institut national d'enseignement supérieur pour l'agriculture, l'alimentation et l'environnement, Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement : UMR985, Institut national d'enseignement supérieur pour l'agriculture, l'alimentation et l'environnement – France

Abstract

Abstract:

Understanding the ecological and evolutionary impacts of polyploidy, especially on reproductive modes, implies to be able to easily compute population genetic indices and to quantitatively infer the respective rates of clonality, selfing and outcrossing producing current descendants.

We developed a user-friendly software to analyze genotypes of spatio-temporally-sampled individuals, with a special focus on analyzing and interpreting reproductive modes in polyploid populations. This software, part of the project ANR Clonix2D, named GenAPoPop (for *Genetic Analyses of Polyploid Populations*), was written using Qt, python and fortran, works on Gnu/Linux, MacOS and Windows, and run locally with no internet connection. It allows computing major population genetic indices for polyploids (F-statistics, linkage disequilibrium, probability of identity, spatial and temporal Fst, genotypic and genetic diversities, etc.) only using a graphical interface and a new method to obtain posterior probabilities of reproductive modes in polyploid populations using temporal genotypings. It aims to ease and broaden the computation of genetic indices in research projects and facilitate polyploid population studies in population genetic courses and student trainings.

*Speaker

We will present the software interface, and provide some results obtained on a tetraploid sea anemone and one a decaploid invasive plant species.

Keywords: population genetics, partial clonality, partial selfing, polyploidy

Teasing apart the effects of phylogeny and shift in mating system on gene expression in *Capsella*

Zebin Zhang^{*1}, Marion Orsucci², Dmitro Kryvokhyzha³, Pascal Milesi¹, and Martin Lascoux¹

¹Uppsala University – Sweden

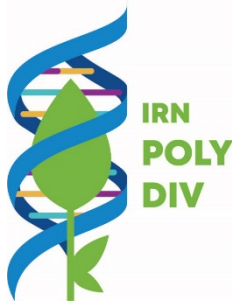
²Swedish University of Agricultural Sciences – Sweden

³Lund University – Sweden

Abstract

Mating system transition from outcrossing to selfing is common in seed plants and has a profound impact on genomic variation and population ecology, but transcriptomic consequences remain poorly understood. An excellent model for understanding gene expression pattern changes associated with transition to selfing is provided by *Capsella* genus which has 4 species in total but occurred such transition 3 times in history. In allotetraploid *Capsella bursa-pastoria*, the two subgenomes have been proved by expression unequally and overall bias towards that of selfing parent in flowers whilst opposite towards outcrossing one in other tissues. However, it is neither clear what factor drives these biases across tissues nor the general expression pattern changes associated with mating system transition. In this study, we compared the transcriptomic differences between outcrossers and selfers, diploids and tetraploids independently. Within diploid species, we observed both phylogeny and mating system transition affecting the gene expression differences between mating systems although primarily explained by phylogeny relationship. However, mating system transition had a major impact on global gene expression in flower but also in the other two tissues even less pronounced. To validate the roles observed in diploids whether work in tetraploid, we replaced *C. grandiflora* by *C. rubella* as a "parental" species to eliminate the mating system effect, on the one hand, and replace *C. orientalis* by *C. rubella* to reduce the phylogeny effect. We observed the phylogeny relationship drives the expression bias towards that of outcrosser parent whilst mating system transition drives the expression towards that of selfer parent. Overall we assume mating system transition is a complicated process that evolves many tissues and genes functioning together, and the three transitions to selfing in *Capsella* maybe underwent convergent evolution.

*Speaker



POLYPLOIDY AND BIODIVERSITY

Rennes 11-12 October 2021

Abstracts

POSTERS

Duplicated divergence in the Rosaceae family depending of duplication mechanism

Martin Leduc*¹, Nathalie Leduc¹, Tanguy Lallemand¹, Jérémy Clotault¹, and Claudine Landes¹

¹IRHS — Institut de Recherche en Horticulture et Semences – Univ Angers, Institut Agro, INRAE, IRHS, SFR QUASAV, F-49000 Angers, France – France

Abstract

Gene duplication is known to be an important factor of evolution. Different mechanisms for gene duplication have been discovered like whole genome duplication, segmental duplication, tandem duplication, transposon-mediated duplication and retroduplication. For each of these mechanisms, the resulting duplicated region have different characteristics. For instance, the promoting region is not always duplicated alongside the coding sequence. Hence, these differences might affect the retention rate and evolution of the duplicated gene. In this study, we try to investigate if the duplication mechanism influence the evolution of the duplicated gene with an emphasis on sequence divergence and selective pressure. We developed a pipeline which combines different tools to i) detects duplicated genes, ii) infer their duplication mechanism, iii) analyse sequence evolution and selective pressure. For now, only segmental and tandem duplication are inferred and every other duplicates are grouped in an "other" category. We tested this method on seven species from the *Rosaceae* family with high quality sequenced genomes comprised of 5 diploids, 1 diploid with recent WGD and 1 octoploid. We demonstrate how this pipeline succeed in detecting paralogs using a multi-species and orthogroups based approach, use genomic context to infer duplication mechanisms and finally how these mechanisms affect sequence divergence and selective pressure.

*Speaker

Transposable Element annotation in allotetraploid *Nicotiana tabacum* and its extant diploid progenitor genomes

Corinne Mhiri^{*1}, Veronique Jamilloux², Nathalie Choisne², and Marie-Angèle Grandbastien¹

¹Institut Jean-Pierre Bourgin – AgroParisTech, Université Paris-Saclay, Institut National de Recherche pour l’Agriculture, l’Alimentation et l’Environnement : UMR1318 – France

²Unité de Recherche Génomique Info – Institut National de Recherche pour l’Agriculture, l’Alimentation et l’Environnement : UR1164 – France

Abstract

Allopolyploidy is known to have a significant impact on plant evolution, frequently causing epigenetic, structural and functional genomic modifications. Due to their transpositional activity and repetitive nature, transposable elements (TEs) may play a key role in these genomic alterations. We focused our investigations on one of the most recent *Nicotiana* allopolyploids (formed ca 0.5 MYA), i.e. *N. tabacum* (tobacco), which arose from hybridization between progenitors of the extant diploid species *N. sylvestris* and *N. tomentosiformis*, and which contains well characterized active TEs. We conducted TE annotations by using pipelines of the REPET suite on publicly available genomes. REPET analysis reveals that TEs represent over 65% of the three *Nicotiana* genomes, with a major contribution of retrotransposons (over 40%). Around 1900 to 2230 TE consensus sequences were generated for each genome, and clustered by the MCL algorithm. We analyzed the distribution and genome coverage of different active endogenous retrotransposon families - including Tnt1-across tobacco and its parental genomes. Preliminary results show that the distribution of clusters matching these families over the 3 *Nicotiana* species fits well with what is known about these retrotransposon biology, abundance and diversity. As shown for Tnt1, complete copies display a higher copy number and genome coverage than incomplete ones, underlying the persistent activity of this retrotransposon in these *Nicotiana* species. Such analysis could be adapted to infer the dynamics of other not fully characterized *Nicotiana* retrotransposon families.

*Speaker

Detection of homologous syntenic blocks within the hexaploid *Spartina maritima* genome.

Morgane Milin* , Oscar Lima¹, Malika Ainouche¹, and Armel Salmon¹

¹UMR CNRS 6553 ECOBIO - Université de Rennes 1 – CNRS : UMR6553 – France

Abstract

The detection of homologous (orthologous, homoelogenous and paleologous) regions is crucial to understand the short-term and long-term consequences of whole genome duplication, and their impact on the ecology and adaptation of species. The genus *Spartina* Schreb. (Poaceae, Chloridoideae), characterized by recurrent hybridization and polyploidization events, shows a wide range of ploidy levels from tetraploid to dodecaploid, in a well-understood phylogenetic frame. In this study, we focus on the hexaploid *Spartina maritima* ($2n=6x=60$), a salt-marsh native European species, which is involved (as male parent) in the formation of the neo-allododecaploid *S. anglica*, following its hybridization with the introduced North-American species *S. alterniflora*. We are using the first reference genome assembly in *Spartina maritima* to perform various comparative analyses. Comparisons at the genomic scale involving a RBBH procedure (Reciprocal Best Blast Hit) and dotplot analyses were first performed to determine the genomic composition of the *S. maritima* genome. Homologous regions, (a) within the assembled hexaploid *S. maritima* genome and (b) between *S. maritima* and four selected grass genomes (Diploid: *Oryza sativa*, *Sorghum bicolor*, *Eragrostis curvula*; Tetraploid: *Eragrostis tef*) were detected as contiguous RBBH representing homologous syntenic blocks. This set of orthologs is used: 1) to assess to the divergence between *S. maritima* subgenomes (homeologs), and 2) to detect retained or lost gene copies compared to other grasses, *Eragrostis* (Chloridoideae), *Sorghum* (Panicoideae) and *Oryza* (Oryzoideae) which would represent candidates for fractionation. Their functional category, location in the genome, and if one or the other subgenome is preferentially retained would be assessed. Our results will also improve our understanding of the deep history of the meso-hexaploid *Spartina* lineage that formed 6-10 mya.

*Speaker

Nutrients shape plant community structure based upon genome size.

Joseph Morton^{*1,2}, Andrew Leitch¹, Ilia Leitch², and Erika Hersch-Green³

¹School of Biological and Behavioural Sciences, Queen Mary University of London, London, UK – United Kingdom

²Jodrell Laboratory, Royal Botanic Gardens Kew, Richmond, UK – United Kingdom

³Department of Biological Sciences, Michigan Technological University, Houghton, Michigan, USA – United States

Abstract

Genome size (GS) varies 2400-fold across angiosperms and, as nucleic acids are some of the most nitrogen- (N) and phosphorus- (P) demanding molecules of the cell, species with larger genomes will likely be less tolerant of nutrient limitation. Interactions between N, P and GS may therefore be an important drivers of plant growth and community composition. Both experimental lab and field trials have shown that species with larger GS are more productive and competitive on plots fertilised with N and P compared to plots without fertilisation, but these sites are similar in climatic conditions and functional group composition. We explore GS-nutrient interactions across a range of fertiliser trial sites in the Nutrient Network, to examine if this relationship varies with both climate and community composition. Overall, community-weighted mean genome size (cwGS) was found to be significantly higher on plots treated with both N and P. The response of cwGS to both N and P varied substantially between sites, however, and the magnitude of this response was found to be climate dependent, decreasing with both temperature and precipitation seasonality. GS also varied significantly between functional groups, and observed changes in plot cwGS may therefore have been driven by changes in the community composition, which are also determined by both nutrients and climate independent of GS. These results support previous findings, but also identify important interactions with other factors limiting plant growth. Further research in this field should therefore incorporate both climatic and functional trait data, to fully ascertain the importance of GS as a character influencing community composition in complex and varied natural systems.

*Speaker

Genomic substrates of chromosome rearrangements and dysploidy during plant evolutionary diversification.

Manuel Poretti*¹, Christian Parisod¹, and Martin A. Lysak²

¹University of Fribourg – Switzerland

²Masaryk University – Czech Republic

Abstract

Chromosome rearrangements (CRs) promote the reduction of genome size and chromosome numbers (i.e., descending dysploidy) 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 will use comparative genomics of closely related species with contrasted genome sizes and differently progressed descending dysploidy to identify the molecular mechanisms underlying CRs. We aim to sequence, analyze and compare genomes of nine *Biscutella* species (Buckler Mustards; Brassicaceae) differing by genome sizes (0.7 to 1.2 Gbp) and chromosome numbers ($x = 6, 8, 9$). We will combine genome sequence data with long-range scaffolding and molecular cytogenetics to obtain accurate chromosome-scale assemblies and annotate them using transcriptomics data. Comparative genomics will then quantify small- vs large-scale restructuring events and how much they affect coding vs non-coding regions of chromosomes. This will not only identify underlying molecular mechanisms, but will further address the impact of gain vs loss of gene and transposable elements sequences on genome size evolution and dysploid CRs during species diversification.

*Speaker

Investigation of the immediate effects of allopoloidization using *Chlamydomonas reinhardtii*

Lucas Prost^{*1,2}, Quinten Bafort^{1,2}, Griet Casteleyn¹, Antoine Van De Vloet^{1,2}, Yves Van De Peer^{*1}, and De Clerck Olivier²

¹VIB-UGent Center for Plant Systems Biology, Ghent University – Belgium

²Phycology Lab, Ghent University – Belgium

Abstract

Allopolyploids are organisms that have multiple genome sets originating from at least two parental species. Allopolyploid plants seem to have wider ecological ranges than their diploid progenitors and have the ability to exploit new habitats. Little is known about the mechanism behind this change in environmental tolerance. The allopolyploid plasticity hypothesis suggests that allopolyploids can maintain a high fitness in various ecological contexts by using specific adaptive gene copies or expression levels of one of the parents depending on the conditions. Studies testing this hypothesis show contradictory results. These studies typically use naturally occurring allopolyploids and the putative diploid descendants of the parent species, neglecting the fact that these may differ considerably from the true diploid parents. We intend to tackle this issue using experimental evolution with *Chlamydomonas reinhardtii*. Cryopreservation will allow direct comparison of the ancestors with allopolyploid descendants. We plan to evolve different haploid strains in divergent stressful conditions. Once the strains show adaptation, they will be merged to obtain allopolyploids. The fitness of the newly-formed allopolyploids will be tested in the parental stressful conditions and gene expression of the haploid and allopolyploid strains will be compared. We expect the allopolyploid to maintain a high fitness in both conditions by using either adaptive parental gene copies or expression levels.

*Speaker

Polyploidy and genome size variation in plant species from Kerguelen Islands

Thierry Robert*¹, Françoise Hennion*², Françoise Lamy³, Najat Takvorian⁴, Valérie Gouesbet⁵, Angélique D'hont⁶, and Sonia Siljak-Yakovlev⁷

¹Laboratoire Ecologie Systématique et Evolution, Université Paris-Saclay. – Sorbonne Université – France

²UMR ECOBIO, Université de Rennes1 – CNRS-Université de Rennes1 – France

³Laboratoire Ecologie, Systématique et Evolution, Université Paris-Saclay – Université de Versailles Saint-Quentin-en-Yvelines – France

⁴Laboratoire Ecologie, Systématique et Evolution, Université Paris-Saclay – Sorbonne-université – France

⁵UMR ECOBIO, Université de Rennes1 – CNRS-Université de Rennes1 – France

⁶Structure et Evolution des génomes – CIRAD : UMRAGAP – France

⁷Laboratoire Ecologie, Systématique et Evolution, Université Paris-Saclay – CNRS – France

Abstract

Polyploid species are very common in the arctic region, a feature believed to be linked to a larger adaptive potential than non-polyploids. Data on variation in genome size and ploidy level is much more scarce for the sub-Antarctic flora despite strong ongoing climate change in this area. Here, we focused on plant species of Kerguelen Islands that harbour a probably very ancient, flora with a high rate of endemism. A first overview of genome size and ploidy levels of 9 native species in Kerguelen is presented. Furthermore, genetic diversity and genome size variation of the strict Kerguelen endemic, *Lyallia kerguelensis* Hook.f., supposed to have survived Pliocene-Pleistocene climate change, was investigated. We showed:

i). All studied species are polyploids, from tetraploid to octoploid. This is in agreement with what has been observed for species of high latitudes in the Northern Hemisphere but also in the Falkland Islands and South Georgia in the sub-Antarctic.

ii) SSR markers revealed extremely low genetic variability. Pertaining to the commonly high mutation rate of microsatellite sequences, this strongly suggested that *L. kerguelensis* has undergone a very strong and protracted demographic bottleneck likely due to past major glaciation events (the most recent one occurred between about 28 ka and 19 ka ago).

iii) In contrast, and surprisingly, the variability in genome size of *L. kerguelensis* was very high. We suggest the contrasting patterns observed with SSR markers and genome size may be the result of recent, and may be on-going, transposable element activities. The mechanisms underlying this unusual feature remain to be elucidated. As a first step, a research is actually developed that aims at assessing the intraspecific variability in transposable elements content of the genome of *L. kerguelensis*.

*Speaker

Genetic determinants controlling heat induced diploid pollen formation

Cédric Schindfessel*¹ and Danny Geelen¹

¹Department of plants and crops, Ghent University – Belgium

Abstract

Meiosis lays at the basis of sexual reproduction and the creation of new genotypes, selection upon which leads to adaptation to a changing environment. The meiotic process is influenced by temperature, and in Arabidopsis, heat stress during male meiosis leads to the development of restituted (diploid) gametes, that are putatively a driving factor for sexual polyploidisation and genome wide duplication. To address the question whether heat stress induced diploid pollen formation depends on specific genetic factors, we conducted a screen of 200 Arabidopsis ecotypes for hyper and hyposensitivity to high temperature. The analysis uncovered a large variation in heat stress sensitivity, with accessions producing anywhere between 0% and nearly 100% dyads after 24h at 32°C. These data were used as the input for a genome wide association study (GWAS), revealing multiple QTLs that await validation. Mapping analysis and genetic complementation tests between the most sensitive accessions point towards the major involvement of CyclinA1;2/TAM in governing the high dyad phenotype after heat stress. The methodology and an intermediate update on the results will be presented.

*Speaker