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CONFÉRENCES
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Evolutionary and ecological genomics of polyploidy in plants: temporal dynamics across scales of biological organization from molecules to ecosystems

Génomique et Ecologie évolutive des plantes polyploïdes : Dynamique temporelle à différentes échelles d'organisation biologique, des molécules aux écosystèmes

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Conference Report
Rapport sur la conférence

Financial support: International Research Network "Polyploidy and Biodiversity" (IRN POLYDIV) CNRS INEE, University of Rennes, POLYDIV INRAE¸ Observatoire des Sciences de l'Environnement de Rennes (OSEREn), UMR Ecobio, Région Bretagne

French Summary / Resumé En Francais

La polyploïdie (résultant de duplication du génome entier) est un mécanisme central de diversification biologique chez les plantes, conduisant notamment à la spéciation. Il est à présent acquis que toutes les espèces végétales contemporaines contiennent des génomes dérivant d'un ou plusieurs cycles anciens et plus ou moins récents de polyploïdie. La polyploïdie est un sujet important en agronomie, en raison de sa prévalence chez les plantes cultivées. De même, d’un point de vue écologique, la polyploïdie s’avère particulièrement impliquée en biologie des invasions et dans les processus adaptatifs. L'un des principaux défis à relever pour expliquer le paradoxe des avantages ou inconvénients imposés aux organismes par le doublement des génomes, concerne la compréhension des connexions moléculaires, (génomiques et autres « omiques ») qui sous-tendent l'adaptation et les nouveaux phénotypes. Les deux dernières décennies ont ainsi vu l’explosion des études analysant les duplications génomiques des espèces actuelles. De nouvelles questions ont émergé sur notre vision rétrospective de l’histoire évolutive de ces génomes (par exemple, pourquoi et comment les génomes dupliqués reviennent à l'état « diploïde », les processus de fractionnement du génome, leurs conséquences adaptatives à court et à long terme). Cette Conférence, organisée par le réseau scientifique international Polyploïdie et Diversité (IRN POLYDIV), avait pour objectif de faire le point des dernières avancées et a permis de réunir des leaders mondiaux et scientifiques de renom issus de divers domaines de la biologie, allant du niveau moléculaire au niveau écologique. Le programme de la conférence a été conçu autour de quatre sessions principales, chacune étant étroitement liée aux autres par le biais de domaines de recherche émergents, comme suit : (1) La dynamique évolutive des génomes polyploïdes sur des périodes allant de l'époque contemporaine à des millions d'années ; (2) Les défis moléculaires liés à la présence de génomes multiples et les opportunités qui en découlent ; (3) Les progrès dans notre compréhension des processus moléculaires, génétiques et épigénétiques qui façonnent l'expression des gènes et, en fin de compte, les phénotypes, c'est-à-dire l'équation du génotype au phénotype ; et (4) Comment toutes les dynamiques englobées par les points (1) à (3) se traduisent-elles en adaptation, biodiversité et changements écologiques ? Soixante-quinze participants provenant de 12 pays différents ont échangé à travers 24 conférences invitées, 16 contributions orales sélectionnées et deux sessions posters. Les discussions ont montré comment les connaissances acquises grâce aux polyploïdes synthétiques de première génération et à de nombreux systèmes modèles naturels, permettent de mieux comprendre les multiples effets des cycles récurrents de fusion et de génomes au cours de l’histoire évolutive des plantes, et d’évaluer les immenses potentialités ouvertes par les nouvelles technologies dans l’accélération de l’acquisition des connaissances. La conférence a mis en évidence la manière dont les attentes théoriques pouvaient être intégrées aux observations issues de technologies en rapide évolution afin de donner tout leur sens aux données multi-OMICS, ainsi que le défi que représente la compréhension des liens entre l'architecture génomique 3D, l'adaptation polyploïde et les phénotypes. Les questions encore ouvertes concernent le rôle de la polyploïdie en tant qu’" impasses évolutives » ou au contraire, en tant que « catalyseur majeur de la diversification ». Les conséquences écologiques de la polyploïdie sont encore largement méconnues et méritent des travaux supplémentaires pour expliquer de manière satisfaisante la distribution des polyploïdes dans l'espace et dans le temps, et en particulier comment la polyploïdie peut augmenter la tolérance au stress et comment elle peut affecter les communautés soumises à des changements environnementaux. Le format et le riche programme de cette conférence Jacques Monod ont favorisé les débats, les discussions de nouvelles perspectives, ouvrant la voie à la prochaine décennie de recherche vers une synthèse biologiquement significative sur les conséquences de la polyploïdie. Les nouvelles approches appliquées aux problèmes classiques de l'évolution et de l'écologie promettent en effet une nouvelle ère de connaissances pouvant être appliquées en agriculture et en gestion des écosystèmes dans un monde en mutation. Dans cette optique, nous recommandons la tenue d'une nouvelle conférence Jacques Monod sur la Polyploïdie dans 4 ou 5 ans, permettant de faire le point sur les progrès attendus dans ce domaine.

General Description of the Meeting

The “Evolutionary and Ecological Genomics of Polyploidy in Plants” Conference was organized by the International Research Network (IRN) “Polyploidy and Biodiversity” (POLYDIV), supported in France by CNRS, University of Rennes and INRAE, and 8 partner teams from 7 countries (France, Belgium, Sweden, Switzerland, Czech Republic, England, USA). The Conference was held in Roscoff (France) from Sept 15th to Sept. 19th, and was structured into four topical sessions, each of which included invited talks (20 minute each) and selected oral contributions (15 minute each):

Session I: Evolutionary dynamics of polyploid genomes
Session II: How do plants adapt to genome doubling and beyond?
Session III: Molecular (genetic & epigenetic) processes shaping the regulation of duplicated genomes
Session IV: Ecological consequences of polyploidy

In addition, there were two poster sessions. Representation of gender, career status, geographic regions, and institutions were considered during abstract selection. The presentations were exceptional, state-of-the-art, leading to rich and stimulating discussions and exchanges regarding the future of the field. Multiple participants commented on the exceptional quality of this conference.

Participants: The conference was attended by 75 participants, including 33 Ph.D. students and post-docs, from France, USA, Czech Republic, Germany, Belgium, UK¸ China, Switzerland, Sweden, Netherlands, Spain, Italy. There were 24 invited speakers, 16, selected contributed talks, 34 posters.

Invited speakers (9 from France, 8 from Europe, 7 from outside Europe; 10 female): AINOUCHE Malika (University of Rennes, UMR CNRS Ecobio, France), BARKER Michael (Department of Ecology & Evolutionary Biology, University of Arizona, USA), BONNEMA Guusje (Department of Plant Sciences WIR Wageningen, Netherlands), CASACUBERTA Josep, (Center for Research in Agricultural Genomics, Barcelona, Spain), CHOULET Frédéric (INRAE INRAE Clermont-Ferrand, France), CONOVER Justin (University of Arizona, Tucson, USA), D’HONT Angélique (CIRAD, Montpellier, France), GLEMIN Sylvain (UMR CNRS Ecobio, University of Rennes, France), HU Guanjing (Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, China), Ales KOVARICK (Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno), LEITCH Andrew (Queen Mary University of London, U.K.), LEITCH Ilia (Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, London, U.K), LASCOUX Martin, (Uppsala University, Sweden), MANDAKOVA Terezie, (Mazaryk University, Brno, Czech Republic), MASON Annaliese(INRES - Pflanzenzüchtung Bonn, Germany), NOVIKOVA Polina (Max Planck Institute for Plant Breeding Research, Köln, Germany), ROUSSEAU-GUEUTIN Mathieu (IGEPP, INRAE, Le Rheu, France), SERRA Heïdi, (Genetics, Reproduction and Development Institute (iGReD), CNRS UMR 6293, Inserm U1103, Université Clermont Auvergne, France), SOLTIS Pamela (Florida Museum of Natural History, University of Florida, USA), PARISOD Christian (Department of Biology - University of Fribourg, Switzerland), SALMON Armel (University of Rennes, UMR CNRS Ecobio, France), VAN DE PEER Yves (VIB UGent Center for Plant Systems Biology, Ghent,Belgium), VEKEMANS Xavier (Unité Evo-Eco-Paléo (EEP) – UMR 8198CNRS / Université de Lille, France), WENDEL Jonathan (Iowa State University, Ames, USA), WINCKER Patrick (Genoscope, Evry, France)

Contributed talks: BAFORT Q. (VIB UGent Center for Plant Systems Biology, Ghent,Belgium), DUAN T, HUANG Y., SCHRANZ E (Wageningen University, Netherlands). DOUBLET V., GERCHEN JF, LLOYD A. PETRIKOVA E. ALMEIDA - SILVA F (VIB UGent Center for Plant Systems Biology, Ghent, Belgium), EL-MESSAOUDI M, LI X., SHARBROUGH J., HAN T., HARRINGTON A, LEE K, MORTIER F (VIB UGent Center for Plant Systems Biology, Ghent, Belgium)

Observer: Vera DOMINGUES (UK) Senior editor for Nature Ecology & Evolution

Scientific Program

One of the most important realizations of the genomics era is that whole genome duplication, resulting from polyploidy, is a central mechanism of biological diversification in plants, leading to adaptation and speciation. We now understand that all modern plant lineages have genomes that derive from one or more ancient as well as more recent cycles of polyploidy, each followed by a diverse spectrum of ecological and evolutionary processes that lead to the generation of new clades and novel adaptations.

Accompanying the growth in our understanding of the importance of polyploidy has been a parallel appreciation of its relevance to multiple disciplines and from multiple scales of biological organization. Polyploidy now is an important topic in agronomy, due to the prevalence of whole genome doubling in crops. Similarly, from an ecological perspective, polyploidy is an important topic in invasion biology. A key challenge in recent years and into the future has been the need to understand the molecular, genomic, and other 'omics' connections that underlie adaptation and novel phenotypes, that is, the genotype-to-phenotype connection. Thus, the last couple of decades have witnessed an explosive growth in probing the molecular genetic consequences of whole genome doubling in contemporary species. Additional mysteries have arisen from "looking backward" through evolutionary time; for example, why and how do duplicated genomes return to a "diploid" state, and what are the short term and long-term adaptive consequences of these processes?

Our goal was to convene global leaders and key scientists from across various biological perspectives, from the molecular to ecological levels. The program of the conference was designed with the foregoing conceptual breath and focus. The Conference included four primary sessions, each of which is inextricably linked to the others through emerging research areas, as following: (1) The evolutionary dynamics of polyploid genomes over evolutionary time frames from contemporary to millions of years; (2) The multiple molecular challenges of coping with and opportunities that arise from life with multiple genomes; (3) The astonishing progress in our understanding of the molecular, genetic and epigenetic processes shaping gene expression, and ultimately, phenotypes; that is, the genotype to phenotype equation; and (4) How do all of the dynamics encompassed by (1) through (3) translate into adaptation, biodiversity and ecological changes?

The Conference started with two introductions: **Malika Ainouche** presented the historical context of polyploidy research, and highlighted why after a century of discovery, Polyploidy (resulting from whole genome duplication, WGD) has become a major topic in Plant sciences, Evolutionary Biology and Ecology from both fundamental and applied perspectives. Among the most remarkable advances resulting from the expanding access to complex polyploid genome information is our increased understanding of the mechanisms involved in the particularly dynamic nature of polyploid genomes and the realization that early views about polyploidy prevalence represented only the "emerged part of the iceberg", as now we understand that all modern "diploids" appear to derive from ancestral polyploids. **Jonathan Wendel** complemented this presentation using the cotton genus as a model system to demonstrate the insights that can be derived from interdisciplinary mergers across disciplines, from taxonomy to genomics to ecology, and biological scales of organization, from the molecular to the ecological. A brief description of all invited talks and their content follow.

Session I: Evolutionary dynamics of polyploid genomes

The session focused on the early evolutionary processes following polyploidization, highlighting the role of reticulate histories resulting from hybridization, chromosomal restructuring and the contribution of polyploidy to genome size diversity.

Pamela SOLTIS and Douglas SOLTIS. *Polyploidy and Rapid Changes: Lessons from Recently Formed Natural Polyploids*. In this 'tag-team talk', insights gleaned from polyploidy as an ongoing natural process in many plant groups was presented, illustrating both commonalities and peculiarities across systems.

Ilia LEITCH. *The impact of polyploidy on genome size diversity and when it matters*. Professor Leitch provided a global overview of how the immense, ~2,400-fold range of plant genome sizes is distributed across the plant tree of life and the contrasting role that polyploidy has played in contributing to such diversity in the different land plant lineages. She also highlighted the ecological impacts of such genome size diversity, focusing on examples were increases in genome size due to polyploidy may have played a role in influencing how and where plants grow and compete, and hence impact the global distribution of species.

Armel SALMON. *Duplicate, diploidize, duplicate, hybridize, duplicate and invade": lessons from meso and neopolyploid genome evolution in Spartina (Chloridoideae, Poaceae*). Dr. Salmon reported on the genome dynamics of two iconic polyploid grasses (*Sporobolus alterniflorus* and *S. maritimus*) involved in neopolyploid speciation, and showed that an ancestral *Sporobolus* genome (n = 2x = 20) duplicated 9.6-24.4 million years ago, an event followed by descending dysploidy resulting in a genome with an unexpected base chromosome number (n = 15). This diploidized genome duplicated again 2.1-6.2 MYA to form a tetraploid lineage (2n = 4x = 60), thus reshuffling the ploidy of these species previously thought hexaploids.

Terezie MANDAKOVA. *Decoding apomixis in Boechera: The roles of hybridization, chromosome dynamics, and polyploidy*. Dr Mandáková presented recent advances in understanding apomixis in the genus *Boechera* (Brassicaceae), focusing on the role of hybridization, chromosome dynamics, and polyploidy. She highlighted recurrent hybridization events and centric fission, leading to apomixis-associated chromosomes. Using telomere-to-telomere genome assemblies and cytogenetics, she demonstrated how genomic stress and repetitive sequence amplification drive chromosomal reorganization, offering insights into the evolution of apomixis and its potential application in crop breeding.

Andrew LEITCH. *Ecological and evolutionary processes acting on plant species depend on their genome size*. Professor Leitch illustrated how the calculated rates of DNA loss per generation (<500 bp/generation) following polyploidy is difficult to reconcile with the observations of genome downsizing post-polyploidy. He proposes that a solution to this problem might be that genome downsizing is an emergent property of polyploidy, which after time has an ecological advantage to plants growing in nutrient poor habitats

Angélique D'HONT. *Genome sequencing reveals a complex history of admixture during sugarcane domestication and cultivar diversification*. Dr. D'Hont shared a novel approach based on repeated k-mers (proxies for transposable elements) to analyze polyploid history in the sugarcane (*Saccharum*) complex. The results demonstrate that sugarcane was domesticated from hybrids between distinct subgroups of the wild *S. robustum* species, and that they diversified by hybridization with distinct subgroups of the wild species *S. spontaneum*. She also described the discovery of an unknown ancestral contributor to modern cultivars.

Michael BARKER. *Ecology of polyploid plants in the Anthropocene*. Professor Barker explored the ecological consequences of polyploidy at a global scale by synthesizing large biodiversity datasets to test the idea that polyploidy species may be more resilient in the face of environmental stress. The analysis demonstrated that plant communities in more variable and extreme climates, such as those at high latitudes, have a higher proportion of polyploids, and that polyploid species also have significantly larger geographic ranges, broader climatic niches, and a lower risk of extinction when compared to their diploid relatives. These macroecological findings support the hypothesis that polyploidy is adaptive in stressful environments and may facilitate their differential survival during periods of rapid climatic change.

Selected talks: BAFORT Q. - The impact of whole genome duplication on somatic evolution in plants. DUAN T. - Separating phases of allopolyploid evolution with resynthesized and natural *Capsella bursa-pastoris*. HUANG Y. - Convergent and divergent genomic features of independent post-polyploid chromosomal diploidization in plants. SCHRANZ E. - Phylogenomic synteny analysis tracks conserved ancient polyploid-derived triplicated genomic blocks across Asteraceae genomes

Session II: How do plants adapt to genome doubling and beyond?

In this session, we discussed how polyploids overcome the challenges of ensuring regular meiosis and fertility, and the molecular and cytological mechanisms related to chromosome pairing, homologous and homeologous recombination.

Guusje BONNEMA. *Contribution of homoeologous exchange and interploidy introgression to crop domestication of polyploid Brassica*. Dr. Bonnema presented the results on their models polyploid *Brassica* system, showing that turnip and wild *B. oleracea* are the progenitors of the *B. napus* A and C genomes, respectively. Frequent interploidy introgression from diploids has increased diversity and contributed to trait variation. In addition, homoeologous exchanges are exceptionally common and are relevant to traits; these are mostly located within distal chromosome arms, with a bias for A replacing C segments.

Martin LASCOUX. *The role of hybridization and genome doubling in the evolution of an allotetraploid weed*. Professor Lascoux discussed how hybridization and whole genome doubling in neopolyploids in the *Capsella* genus change in the overall pattern of gene expression, and that the vast majority of expression alteration was due to hybridization, with genome doubling playing almost no role.

Justin CONOVER. *Population genetics of homoeologous exchanges*. Dr. Conover presented a new population genetic framework for analyzing how allele and genotype frequencies change due to homoeologous exchanges in allopolyploids. This work laid the mathematical foundation for exploring these dynamics in natural populations, and demonstrated one way in which natural selection can get a 'second chance' to purge deleterious mutations that have been fixed within one subgenomes.

Heidi SERRA. *How does meiosis adapt to allopolyploidy? Insights from Arabidopsis suecica.* Dr. Serra described how newly formed allotetraploid *Arabidopsis suecica* stabilizes meiosis over generations, from instability and infertility in the early generations, including homoeologous exchanges, but with some lines rapidly evolving improved meiotic stability. This was shown to reflect distinct evolutionary trajectories driven by strong selective pressure.

Annaliese MASON. *Synthetic* Brassica *hybrids provide insight into meiotic stabilisation in polyploids.* Professor Mason used synthetic *Brassica* hybrids to provide insight into meiotic stabilization in polyploids. She showed that fertility and meiotic behavior in newly formed allopolyploids are highly genotype-dependent, that synthetic allopolyploids inherit specific genetic variants from their lower-ploidy progenitor species that affect meiotic stability, and that generational selection for fertility can improve meiotic behavior in some *Brassica* hybrid lines.

Polina NOVIKOVA. *Mechanisms of recurrent polyploidization cycles*. Dr. Novikova discussed the *Arabidopsis lyrata* species complex, the most polyploidy-rich complex in the genus. This group is characterized by multiple autopolyploidization events in central and northern Eurasia, and these allopolyploidization events also generated the *A. kamchatica* species-complex. She demonstrated how environment and genetics interact to explain this enrichment in polyploids, the latter including high frequencies of unreduced gametes, and the sharing of adaptive meiosis alleles within the polyploidy pool.

Selected talks: DOUBLET V - Adaptation to whole genome duplication across scales. convergent evolution among Angiosperm plant species. GERCHEN JF - Population genomic evidence of inter-ploidy gene flow in natural plant populations. LLOYD A. - A role for MSH4 in meiotic adaptation in allopolyploid *Arabidopsis suecica*. PETRIKOVA E. - Polyploidy in action: disentangling the consequences of genome doubling in *Arabidopsis arenosa*.

Session III: Molecular (genetic & epigenetic) processes shaping the regulation of duplicated genomes

In this session, we examined how polyploidy affects regulation of development, stress tolerance, and the role of repetitive sequences and transposable elements in polyploid evolution. Polyploid speciation combines two different gene regulatory networks and/or alters gene dosages and stoichiometries. How this massive gene expression alteration is controlled, and its developmental and phenotypic and ecological effects, remains mysterious. This field represents a cutting edge in polyploidy research.

Mathieu ROUSSEAU. *Crucial role of the formation pathway and of meiotic recombination on polyploid diversification and speciation success*. Dr. Rousseau discussed the several routes that may lead to allopolyploid speciation, but drew special attention to the poorly explored unilateral pathway, which involves the formation of an allotriploid individual. This latter can be partially fertile and in *Brassica* modified meiotic recombination permits the generation of genetically diverse progenies. In only a few generations, this can lead to euploid, meiotically stable and highly diversified populations, showing that the triploid bridge increases the chance of allopolyploid speciation success.

Frederic CHOULET. *Dynamics of transposable elements in the hexaploid wheat and wild relatives*. Dr. Choulet discussed polyploidy in bread wheat, which has undergone two recent events of polyploidization, joining together A-B-D subgenomes, originating from three distant species. TEs are not conserved between A-B-D but maintained a stable copy number following polyploidy despite complete turnover. Comparative phylogenomics demonstrates that TE dynamics do not follow burst/silencing cycles but that instead, transposition rate appeared constant and polyploidy did not trigger genomic shock.

Josep CASACUBERTA. *Differential LTR-retrotransposon dynamics across polyploidization, speciation, domestication and improvement of cotton (Gossypium)*. Dr. Casacuberta described the evolutionary dynamics of LTR-retrotransposons during following allopolyploidization in cotton. He showed how amplification and deletion are highly variable among LTR-retrotransposon lineages and also between species and subgenomes, of the polyploids. In cotton some lineages have impacted in the differential evolution of centromeres and others have generated gene expression variability that may have been selected during domestication and crop improvement.

Guanjing HU. *Dynamics of duplicated gene regulatory networks governing cotton development and stress tolerance*. Dr. Hu described gene regulatory network (GRN) modulation following polyploidization in cotton. Analysis of duplicated gene expression and network relationships during fiber development revealed novel subgenomic asymmetries. D-biased homoeologs drive higher expression from the D subgenome, while A subgenome TFs preferentially regulate the fiber GRN. Stress tolerance analysis under salt and cold conditions revealed nuanced patterns for further investigation.

Ales KOVARICK. *Bimodal centromeres in pentaploid dogroses shed light on their unique meiosis*. Dr. Kovarik, described the unusual meiotic behavior of polyploid “dog roses” (*Rosa* sect. *canina*). Most sexually reproducing species have an even chromosome copy number, but the dog rose plants do not. Using reference grade genome assemblies, he described how the transmission of five subgenomes to the offspring is mediated by the unusual behavior of the dog rose chromosome in meiosis.

Selected talks: ALMEIDA-SILVA F - Evolution of gene expression following gene and genome duplications in high-resolution, spatially resolved plant transcriptomes. EL-MESSAOUDI M - Assessing the immediate genomic and epigenomic impact of polyploidy in *Arabidopsis thaliana*, LI X - Polyploidy as a lens into *cis*-regulatory evolution: insights from soybean and peanut. SHARBROUGH J, Energy production capacity increases following genome doubling.

Session IV: Ecological consequences of polyploidy

The genomic processes set in motion as a consequence of polyploidy have organism-wide effects that reverberate through physiology and phenotype. As a consequence, polyploidy has fundamental implications for our understanding of plant species ecology, community assembly and ecosystem functioning. Massive data sets and meta-analyses allow for new insights to be derived from ecological genomics-focused questions, adaptation to novel ecological niches, evolution of new functions, and competitive interactions that mold species composition and community assembly.

Yves VAN DE PEER. *The rise of polyploids during environmental catastrophes*. Professor Van de Peer contrasted the high prevalence of polyploid organisms with the realization that instances of ancient polyploidy are surprisingly rare, presenting a paradox. Using broad phylogenomic sampling of angiosperms, he showed how waves of polyploidization are correlated with events such as the Middle Miocene Disruption, the Eocene-Oligocene transition (EOT), the Paleocene-Eocene Thermal Maximum (PETM), the Cretaceous-Paleogene (KPg extinction, and different oceanic anoxic (OAE) events. He proposed that polyploid organisms have an increased chance of survival during times of great environmental turmoil.

Patrick WINCKER. *Genome variability in single-cell marine alga.* Dr. Wincker shared the story of the cosmopolitan marine microalga *Pelagomonas calceolata* has high transcriptomic plasticity, as well as ploidy changes that are broadly distributed in natural populations from across the species' range. He described how he is exploiting ploidy variability to detail its potential role in adaptation to diverse environments.

Sylvain GLEMIN *Consequences of polyploidy and selfing on fitness and ecological strategies in the* Capsella *genus*. Dr. Glemin considered population and mating system conditions that would favor polyploids vs. diploids. He shared a study comparing fitness and competitive ability of four *Capsella* species with different mating systems and ploidy levels within the range of the obligate outcrossing species, *C. grandiflora*. Genome sequencing data were used to estimate the mutation load In agreement with predictions, selfing species have lower fitness and competitive ability than outcrossers and polyploid selfers performed better than the diploid selfers. His results highlight the possible roles of ecological context in the evolution of selfing and polyploid species.

Xavier VEKEMANS *Plant self-incompatibility systems, mating system evolution, and the success of polyploid lineages*. Professor Vekemans considered the question of whether polyploidy drives evolution of self-fertilization. Taking into account genetic determination of systems controlling plant reproduction and the mechanism of polyploidization, he presented results from two studies describing maintenance or loss of the sporophytic self-incompatibility system of Brassicaceae in association autopolyploidy and allopolyploidy. He confirmed observations in Brassicaceae suggesting a general pattern of maintenance of an outcrossing mating system with self-incompatibility in autopolyploids derived from a diploid self-incompatible parent, while allopolyploids show loss of the SI system, often followed by evolution of high selfing.

Christian PARISOD. *Evolutionary consequences of whole-genome duplications through time Whole-genome duplication and ecological radiation*. Professor Parisod described recurrent whole-genome duplication events (including experimental ones) in *Biscutella laevigata* to identify common patterns indicative of invariant processes associated with polyploidy. He demonstrated that whole-genome duplication *per s*e induces minimal phenotypic and transcriptional changes, whereas post-polyploidy evolution fostered adaptive genetic changes and transcriptional responses to environmental cues that recurrently increased stress tolerance.

Selected talks: HAN T. - Ecological and genomic drivers of polyploid adaptation in yellowcress herbs (*Rorippa*, Brassicaceae). HARRINGTON A - Climatic rarity and similar niche shifts underlie variable patterns of range size in *Clarkia* polyploids. LEE K - Ploidy level drives geographic variation in leaf traits of a common invader and palatability to a generalist herbivore; MORTIER F - Nutrient consumption and Coexistence: How Nutrient Competition determines Polyploid Establishment in greater duckweed (*Spirodela polyrhiza*).

Conclusion and Recommendations

The Conference ended with a fruitful and animated discussion among all participants, concluding remarks by J. Wendel and M. Ainouche, and a view to the future, by C. Parisod. This latter presentation covered a range of topics illustrating how the conference integrated molecules to ecosystems and a large diversity of model organisms. He emphasized how knowledge gained from early generation synthetic polyploids and numerous natural model systems provides for a better understanding of the cascading effects and consequences of genome merger and duplication, and the new understanding enabled by modern technology. The conference demonstrated how polyploid research embraces the whole breadth of biology and can fundamentally advance our understanding of life across levels of organization. He drew on examples from the many presentations to emphasize how gene flow and local adaptation are drivers of species distribution across heterogeneous environments, and highlighted how the conference illustrated the promises of multi-OMICS technologies towards an integrated understanding of the genotype to phenotype challenge. Prof. Parisod also noted how the conference highlighted how theoretical expectations could be integrated with observations from rapidly evolving technologies to make full sense of multi-OMICS data, and the challenge of understanding the connections of 3D genome architecture to polyploid adaptation and phenotypes. Questions for the future were also highlighted, including the many concerning the extent to which polyploidy is “genome blender”, generates “hopeful monsters” or “walking zombies”, yields “evolutionary dead ends” or, in contrast, is a major “catalyzer of diversification”, and how the conference made it clear that the ecological consequences of polyploidy are still largely not understood, and which deserve further work to satisfactorily explain the distribution of polyploids in space and time, and particularly how polyploidy possibly increases stress tolerance, and how it may affect communities under environmental changes. The format and the rich program of this Jacques Monod Conference fostered insightful discussions and perspectives paving the way for the next decade of research towards a biologically meaningful synthesis on the consequences of polyploidy.

The foregoing encapsulates many of the questions for the future. Many of these areas represent exciting opportunities for new insights, taking advantage of the explosive growth in technologies that enable insight into the details of genomic function and computational tools that permit co-analysis of massive genetic and epigenetic data sets. Application of these exciting new tools to classic evolutionary and ecological problems promises an era of transformative insights into the workings of nature that also have practical applications from agriculture to ecosystem management in a changing world.

With this in mind, we recommend that the many vital and timely topics discussed during this scientific conference be revisited in 4-5 years with a new Jacques Monod Conference. This would be an exciting opportunity to take stock of the inevitable progress in the field and the many stimulating and important ideas presented during this, the 2025, version.