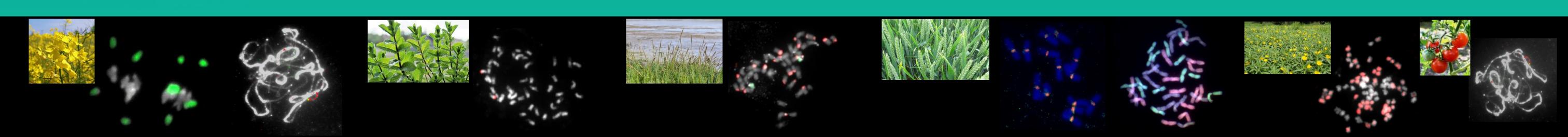


PLATEFORME DE CYTOGENETIQUE MOLECULAIRE VEGETALE





UMR 1349 IGEPP INRAE Centre Bretagne-Normandie 35653 LE RHEU CEDEX

https://igepp.rennes.hub.inrae.fr/l-igepp/plateformes/cytogenetique-moleculaire

https://www.biogenouest.org/plateformes/

OBJECTIFS ET MISSIONS DE LA PLATEFORME

L'objectif de cette plateforme est de participer au développement chez les plantes supérieures des programmes d'études de génomes faisant appel à l'hybridation *in situ* Fluorescente (FISH) pour accroître :

- la caractérisation cytogénétique du matériel végétal impliquant les hybrides interspécifiques afin de valoriser les gènes d'intérêt présents au sein des espèces apparentées, notamment les gènes de résistance,
- la compréhension de la structure des génomes chez des espèces polyploïdes.

Cette plate-forme a également une mission de formation et d'information des chercheurs et techniciens pour un transfert de technologie.

ACCESSIBILITÉ

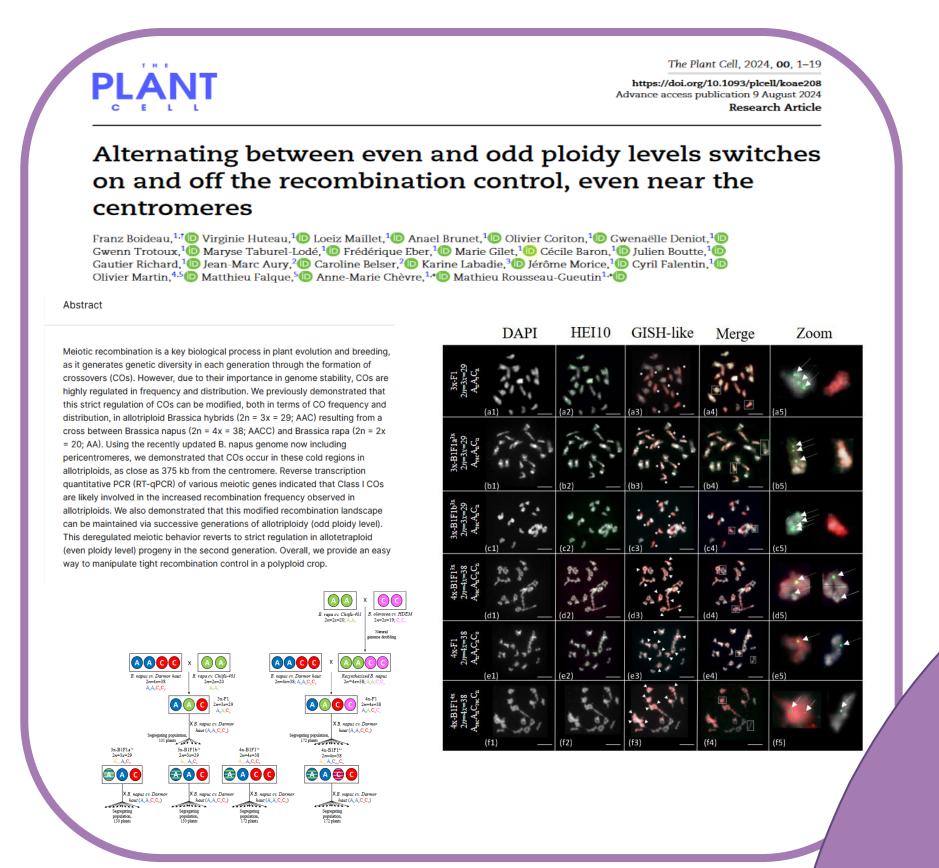
- ☐ La plateforme est accessible à la communauté scientifique publique et privé
- Réalisation de différentes techniques de cytogénétique dans le cadre de collaborations de recherche ou prestations
- ☐ Développements méthodologiques en lien avec vos besoins
- ☐ Organisation de formations à la demande

ÉQUIPEMENTS

- Deux stations de microscopie Zeiss équipé en fluorescence
- Système d'imagerie : Camera ORCA-Flash4 (Hamamatsu)
- Logiciel d'acquisition Zen software Zeiss
- Cytomètre de flux Cyflow Sysmex



EXEMPLES DE RÉSULTATS:



(5) Immunolocalisation Reviewed by: gene duplications, and transposable element content may have a large impact of the genomic structure, which could generate new phenotypic traits. Comparing tw genome vs. the B. rapa 'Chiifu' genome, using comparative genomics and cytogeneti approaches. First, we showed that large genomic variants on chromosomes A05, A06 A09, and A10 are due to large insertions and inversions when comparing B. rapa 'Z1 and B. rapa 'Chiifu' at the origin of important length differences in some chromosol be 55 and 29 Mb, respectively. To validate these observations, we compared using fluorescent in situ hybridization (FISH) the two A06 chromosomes present in an Fi hybrid produced by crossing these two varieties. We confirmed a length difference of 17.6% between the A06 chromosomes of 'Z1' compared to 'Chiifu.' Alternatively citation: using a copy number variation approach, we were able to quantify the presence of a higher number of rDNA and gypsy elements in 'Z1' genome compared to 'Chiifu' on different chromosomes including A06. Using flow cytometry, the total genome size of 12 Brassica accessions corresponding to a B. rapa available core collection was estimated and revealed a genome size variation of up to 16% between these accessions as well as of new accessions belonging to different cultigroups of B. rapa and highlighted the potential impact of differential insertion of repeat elements and inversions of large genomic regions in genome size intraspecific variability.

Genome Size Variation and

Comparative Genomics Reveal Intraspecific Diversity in *Brassica*

Comptage chromosomique et

cytométrie en flux

Caractérisation et identification de translocations

chromosomiques

Plateforme Cytogénétique moléculaire Végétale

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Caractérisation cytogénétique de materiel végétal

New Results

A Follow this preprint

Genomic relationships among diploid and polyploid species of the genus Ludwigia

L. section Jussiaea using a combination of molecular cytogenetic, morphological, and crossing investigations

D. Barloy, L. Portillo-Lemus, S. A. Krueger-Hadfield, V. Huteau, O. O. Coriton doi: https://doi.org/10.1101/2023.01.02.522458

Abstract and Figures

CSH Cold Spring Harbor Laboratory bioRxiv

The genus Ludwigia L. section Jussiaea is composed of a polyploid species complex with 2x, 4x, 6x and 10x ploidy levels, suggesting possible hybrid origins. The aim of the present study is to understand the genomic relationships among diploid and polyploid species in the section Jussiaea. Morphological and cytogenetic observations, controlled crosses, genomic in situ hybridization (GISH), and flow cytometry were used to characterize species, ploidy levels, ploidy patterns, and genomic composition across taxa. 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), which also participated for one part (2x) to the Ludwigia ascendens genome (4x). Ludwigia grandiflora subsp. hexapetala (10x) resulted from the hybridization between L. stolonifera (4x) and Ludwigia grandiflora subsp. grandiflora (6x). One progenitor of L. grandiflora subsp. grandiflora was identified as L. peploides (2x). Our results suggest the existence of several processes of hybridization, leading to polyploidy, and possibly allopolyploidy, in the section Jussiaea due to the diversity of ploidy levels. The success of GISH opens up the potential for future studies to identify

other missing progenitors in Ludwigia L. as well as other taxa.

L. stolonifera (4x)

L. grandiflora subsp. grandiflora (6x)

L. grandiflora subsp. hexapetala (10x)

L. helminthorrhiza (2x)

L. adscendens (4x)

olution

Evolution structurale des génomes chez les espèces polyploïdes

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Received: 8 October 2021 Accepted: 15 January 2022

New Phytologist (2022) doi: 10.1111/nph.18004

recombination.

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Key words: Brassica napus, chromosome

Epigenomic and structural events preclude recombination in

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mapping or oligo fluorescence in situ hybridization.

Meiotic recombination is a major evolutionary process generating genetic diversity at each

generation in sexual organisms. However, this process is highly regulated, with the majority of

crossovers lying in the distal chromosomal regions that harbor low DNA methylation levels. Even in these regions, some islands without recombination remain, for which we investigated

 Genetic maps were established in two Brassica napus hybrids to detect the presence of such large nonrecombinant islands. The role played by DNA methylation and structural variations in this local absence of recombination was determined by performing bisulfite sequencing and

whole genome comparisons. Inferred structural variations were validated using either optical

Hypermethylated or inverted regions between Brassica genomes were associated with the

absence of recombination. Pairwise comparisons of nine B. napus genome assemblies

revealed that such inversions occur frequently and may contain key agronomic genes such as

DNA methylation or structural variations in B. napus. It is thus essential to take into account these features in breeding programs as they may hamper the efficient combination of favor-

We conclude that such islands without recombination can have different origins, such as

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