DMP du projet "SURFING"

*Plan de gestion de données créé à l'aide de DMP OPIDoR, basé sur le modèle "Horizon 2020 FAIR DMP (anglais) - Personnalisé"
fourni par INRAE - Institut national de recherche pour l'agriculture l'alimentation et l'environnement.*

Renseignements sur le plan

Titre du plan	DMP du projet "SURFING"
Langue	fra
Date de création	2018-02-14
Date de dernière modification	2020-09-10
Identifiant	MSCA-IF-ST-2017

Renseignements sur le projet

Titre du projet	SURFING
Résumé	Interspecific hybridization and genome doubling (allopolyploidy) are key factors in plant adaptation and speciation. These intriguing genomic processes cause extensive structural rearrangements and reprogramming of functional regulatory pathways inherited from parental species. Furthermore, hybrid species have shown broad phenotypic diversity. However, mechanisms responsible for genome stabilization after allopolyploidy remain poorly understood. The aim of my project is to provide an interdisciplinary overview of the effects of polyploidy on structural and functional dynamics in a major crop, oilseed rape (Brassica napus). This polyploid species is an excellent system to unravel the long-term and immediate evolutionary effects of ancient and recent polyploid events. In my project, I will use a novel approach that combines (epi)genomics and transcriptomics in phenotypically contrasting polyploids to investigate the role of structural and (epi)genetic regulation in genome stabilization. This work includes, amongst others, the transfer of knowledge to the host lab of cutting-edge molecular and in silico DNA methylation analysis methods. More specifically, I will determine the effects of structural and functional dynamics on B. napus (1) meiotic behavior and fertility, (2) gene expression and (3) glucosinolate content. My findings will open new avenues for using standing variation to modify and ultimately enhance agronomic traits.
Sources de financement	• European Commission : 719908

Produits de recherche :

1. Default research output (Jeu de données)

Contributeurs

Nom	Affiliation	Rôles
		• Coordinateur du projet • Personne contact pour les données • Responsable du plan

Droits d'auteur :

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1. Data summary

WP1 Structural evolutionary dynamic of resynthesized _B. napus_ and identification of the genomic regions explaining their meiotic instability and low fertility

In resynthesized allotetraploid oilseed rape (_B. napus_), **major structural rearrangements** are observed as soon as after the first meiosis. **Altered meiosis** and **poor fertility** is also reported. To better understand the origin of these rearrangements and their impact on meiosis and fertility, the host team has produced in the last decade various resynthesized _B. napus_ populations by crossing two genotypes of _B. oleracea_ with two genotypes of _B. rapa_ (including reciprocal crosses and different pathways to achieve chromosome doubling: i.e. unreduced gametes or colchicine). The different resynthesized individuals that were obtained were then advanced by single plant descent (now at generation S8). All the material produced (~ 400 individuals) was **phenotyped for their fertility** (i.e. number of seeds/100 flowers) **and their meiosis** (i.e. number of chromosomes, number of univalent/multivalent/pollen/mother cell). I propose to genotype about half of these individuals (generation S1, S3, S6, S8 with DNA extracted and stored in the host lab) using the Illumina 60K array developed for _B. napus_. From this dataset, **rearrangements** and **breakpoints** regions **will be identified.** These unique and extensive datasets will provide answers on the **drivers of genome stability in _B. napus_**. **Impact on fertility of large rearrangements**, including their genomic positions in the genome will also be investigated.

°Phenotyping data on fertility and meiotic behavior (already existing in the host laboratory and will be made available via Zenodo repository or https://data.inra.fr/),

°Genotyping data will be made available in the form of table (excel format in data.inra.fr, raw datasets are available upon request).

WP2: Intertwined role of structural rearrangements and duplicate gene expression evolution on _B. napus_ phenotypic diversity

This second WP aims at determining the role of hybridization, genome doubling, and long term polyploid evolution on gene expression and phenotypic diversity in oilseed rape. To that purpose, RNA seq data (Illumina Paired End reads) were recently obtained in collaboration with Prof. I. Bancroft (University of York, UK) through an ERA-CAPS grant. This dataset in addition with DNA Seq and metabolomic profiling of the same individuals will provide the opportunity to answer these challenging questions: **(1) What are the functional and regulatory pathways preferentially altered after WGD and their long term dynamics? (2) What exactly is the role of epigenetics in plant speciation?**

°Transcriptomic datasets obtained in collaboration with Prof. I. Bancroft (University of York, UK) through an ERA-CAPS grant (data.inra.fr and bioinformatic cluster on site),

°DNA-Seq datasets obtained through a "France Génomique" grant, that enabled the host laboratory to identify the different homoeologous exchanges that occurred in each individual. (Illumina PE 70X, deposited in NCBI with accession number PRJEB29460 and bioinformatic cluster on site),

°Database of transposable elements and repetitive motifs using the REPET pipeline (fasta and gff files in Zenodo or https://data.inra.fr/ and bioinformatic cluster on site).

2. FAIR data

Creation of DOI for bioinformatics packages (stored on Github /**juliefc**/) via Zenodo.org. All scripts are uploaded with a README file.
Creation of DOI for data deposited on Zenodo.org and https://data.inra.fr/. Datasets belonging to the same project/manuscript will be granted the same DOI.
All DOI will be cited in the published articles.

All datasets produced in the context of this project will be made publicly available. Metadata, documentation and code will be made available via Zenodo.org or https://data.inra.fr/ with assigned DOI. All other datasets, typically sequencing datasets, assembled genomes and genes will be made available via NCBI with an identifier and accession numbers also referenced in published articles.

Datasets are made interoperable by using appropriate databases and specific vocabularies of the research field.

Datasets will be licenced under Creative Commons Attribution 4.0. Data will be made available as soon as the articles supporting the conclusions of the datasets will be accepted for publication.

3. Allocation of resources

The costs of making the data FAIR are supported by INRA as the institute is providing all the online tools needed. Beneficiary and supervisors in the host laboratory are responsible for data management of the project.

4. Data security

Data are safely stored in publicly available repositories but also in house on a bioinformatics server which is daily saved.

5. Ethical aspects

There are no ethical or legal issue that can impact data sharing of this project.

6. Other

We are also following the INRA procedure for data management.