

Evolution of genomes: structure-function relationships in the polyploid crop species *Brassica napus* (Evo-genapus)

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ERA-NET for Coordinating
Action in Plant Sciences



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Brassica napus

Brassica rapa, AA, $2n=20$
(Wang et al. 2011)



Brassica oleracea, CC, $2n=18$
(Liu et al 2014)



?

Synthetics for mimicking the origin of natural *B. napus*!

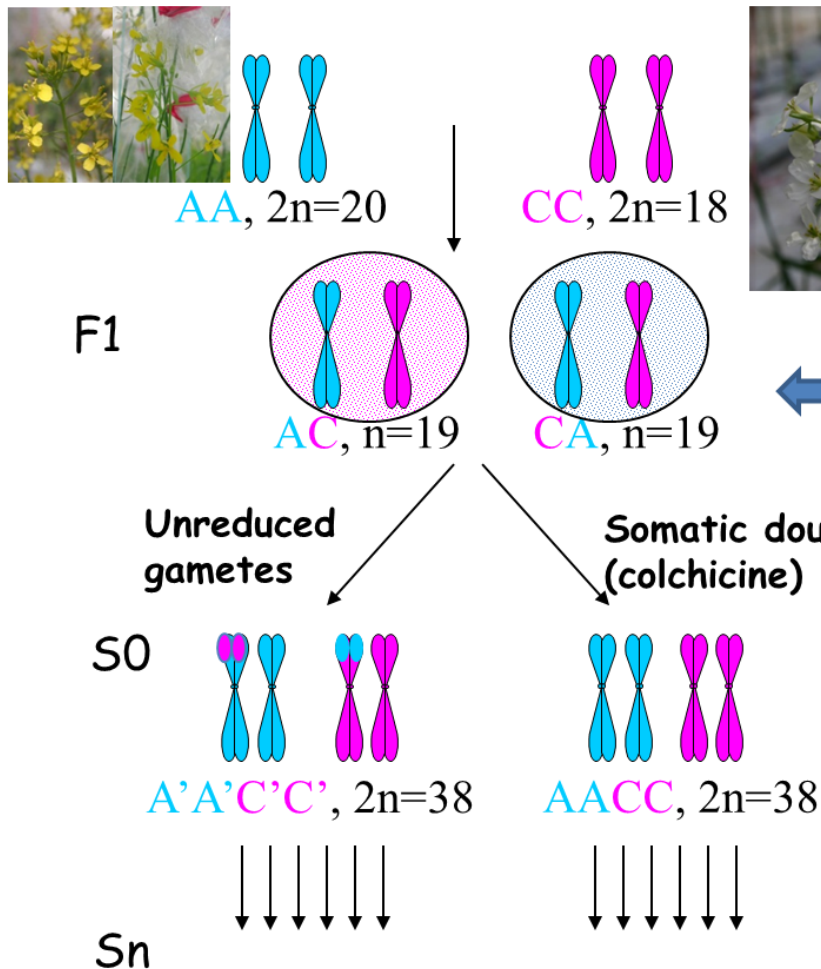


Brassica napus, AAC, $2n=38$
(Chalhoub et al. 2014 subm.)



- recent hybrid ($<0.1\text{My}$)
- A regular meiosis: 10II AA + 9II CC
- Disomic inheritance
- A good fertility

Resynthesised *B. napus*



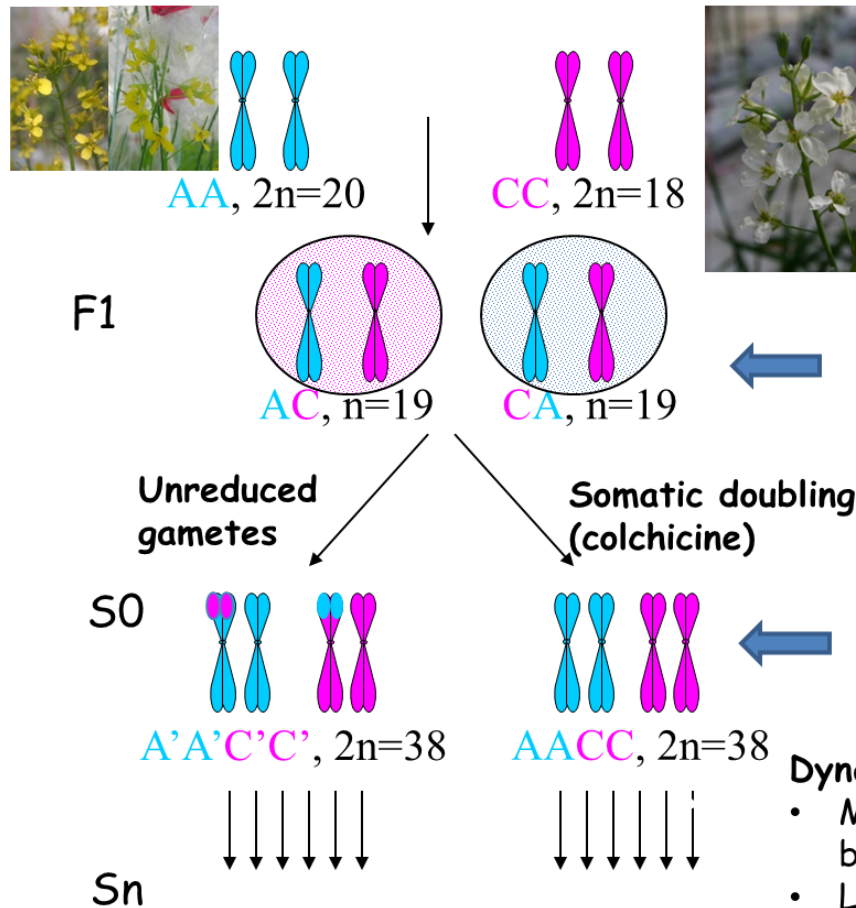
Functional burst:

- Methylation (Salmon et al in prep)
- Immediate silencing of C genome rDNA (Książczyk et al 2011)
- RNA (cDNA AFLP) (Salmon et al in prep)
- si RNA (Palacios 2014)
- Proteins (Albertin et al 2006;2007)

No burst of TE (Sarilar et al 2013)

-> **Dynamic in advanced generations**
especially for self-incompatibility
(Hadj-Arab 2011)

Resynthesised *B. napus*



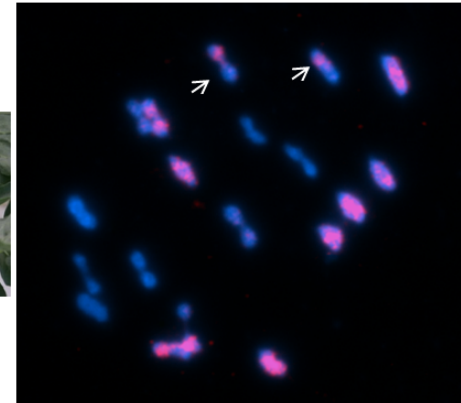
Structural rearrangements from the first meiosis:

- F1: Numerous structural rearrangements but of small sizes from unreduced gametes (Szadkowski et al 2011)

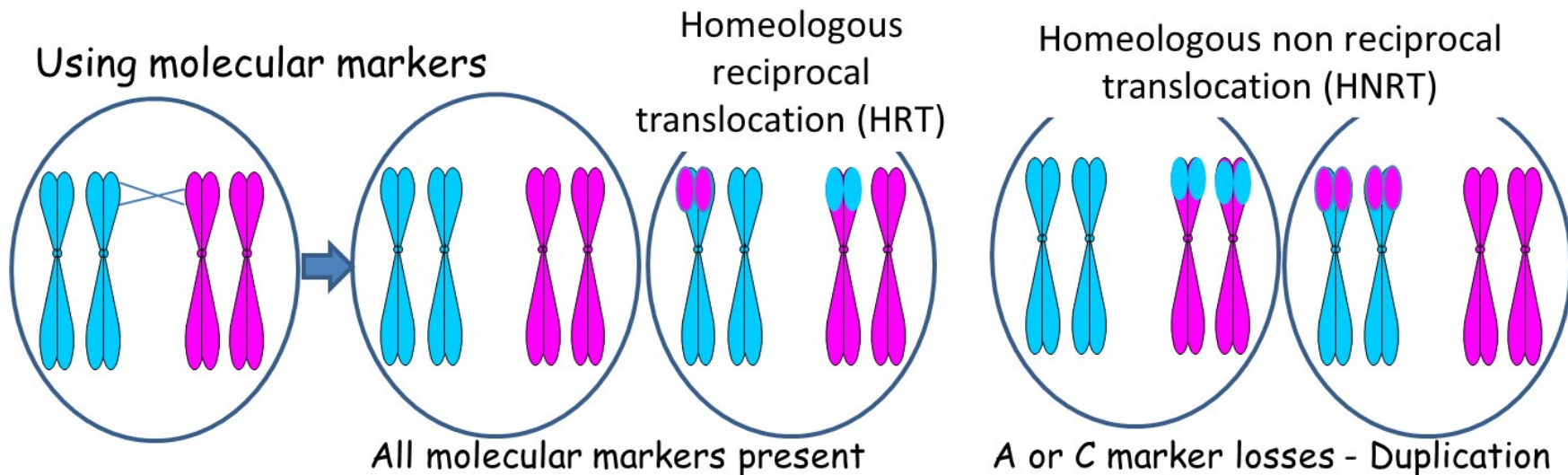
- S0: frequent rearrangements of large size (Szadkowski et al 2010)

Dynamic in advanced generations but always:

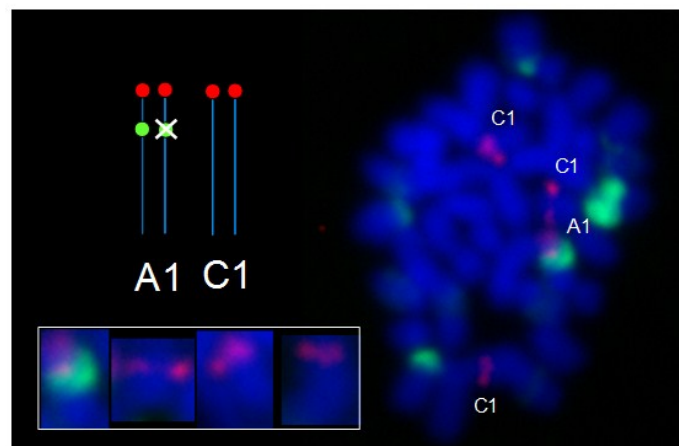
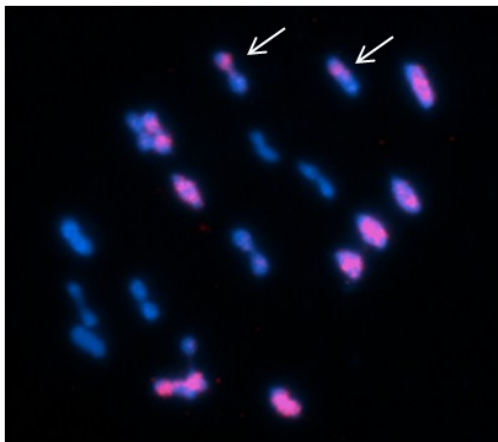
- Meiotic instability: 0 to 60% of cells with 19 bivalents
 - Lost of C genome markers > to A genome
 - Poor seed set (0 to 100 seeds/100fl)
- [oilseed rape 1500 to 2500seeds/100flo]



Detection of homoeologous recombination: BAC FISH



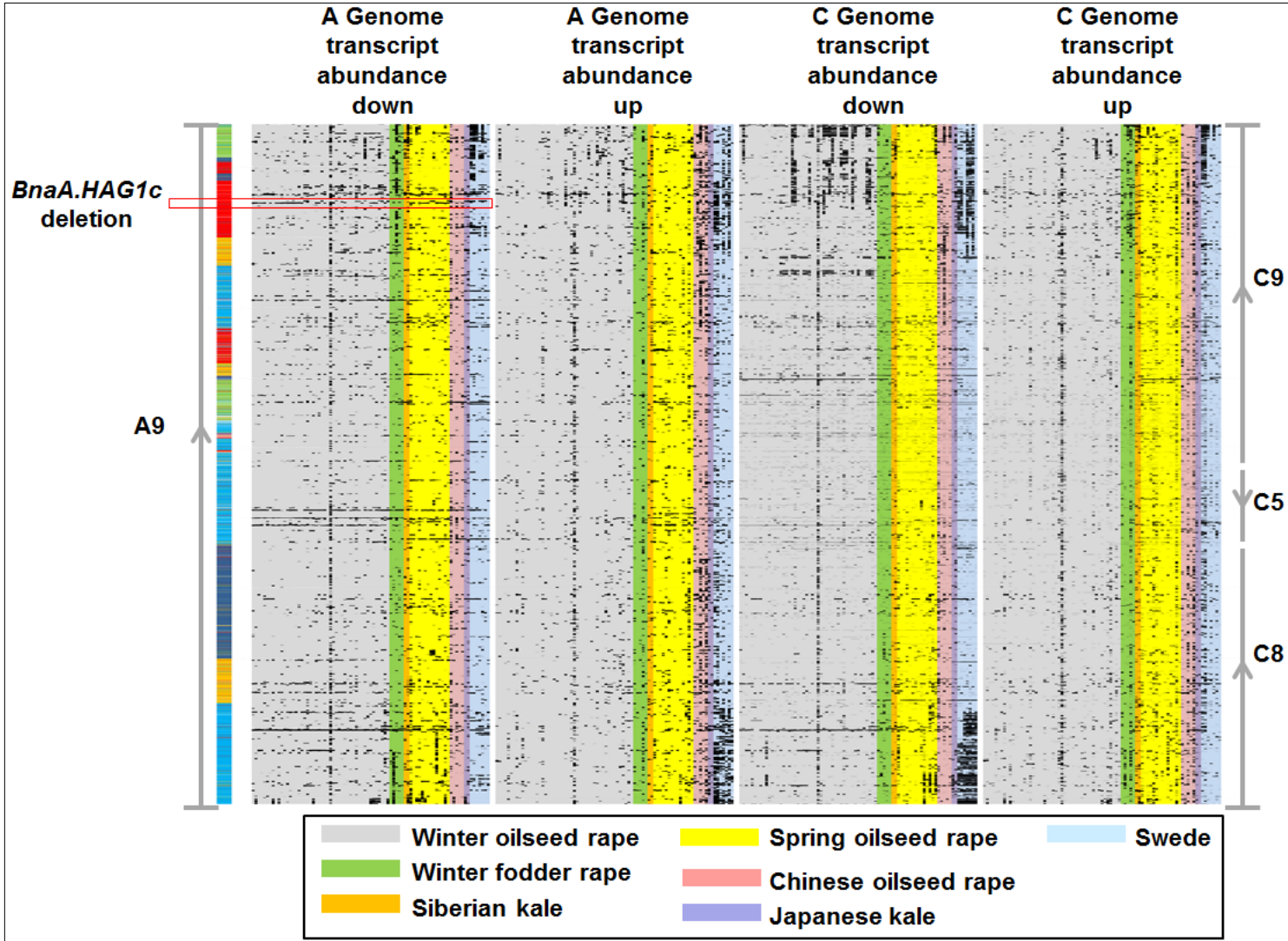
Using BAC FISH analyses



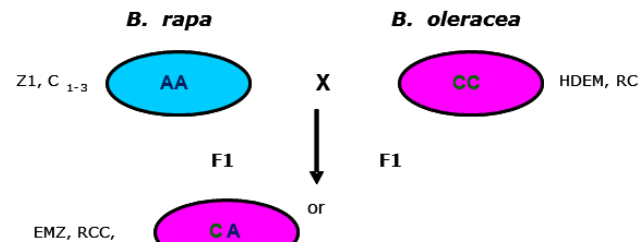
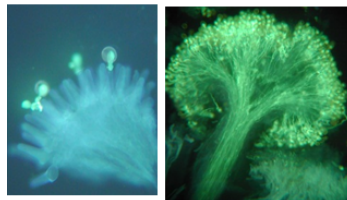


Detection of homoeologous recombination: transcriptomics

Differential gene expression across 83 accessions of natural *B. napus* (cultivars of various crop types)



Poor seed set by resynthesised *B. napus*



Somatic doubling
(Colchicine treatment)

diplogamete

pollen

S0
Allotetraploid

S1

120plants

S2

120plants

120plants

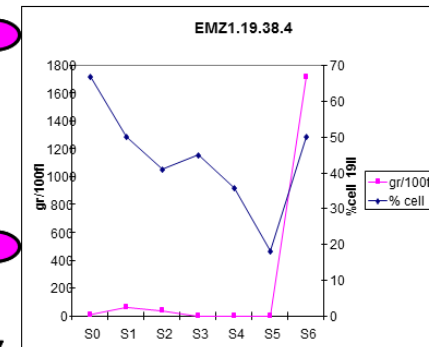
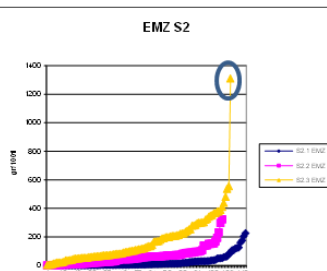
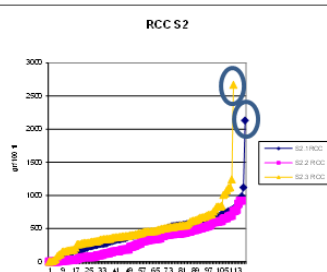
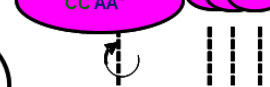
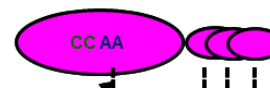
120plants

S3

120plants

120plants

120plants



4 plants from more than 3500 observed with the same fertility as oilseed rape

Hypothesis

We **hypothesise** that the genome evolution observed in resynthesised *B. napus* represents an accelerated form of the genome evolution that is ongoing in cultivated *B. napus* derived in nature.

We aim to **test** this hypothesis by characterising molecular evolution on a genome-wide scale in a large panel of natural and resynthesised *B. napus*, including derived populations, relating the observed variation in genome structure to trait variation of relevance for rapeseed as a crop.

Objectives

1. Establish the *B. napus* pan-transcriptome, comprising ordered unigenes (EST assemblies) representing the nascent *B. napus* genome.
2. Quantify the frequency of copy number variation (of transcribed sequences) and homoeologous exchanges present in *B. napus* formed in nature.
3. Quantify the frequency of copy number variation (of transcribed sequences) and homoeologous exchanges present in resynthesised *B. napus*, comparing it with the frequency observed in *B. napus* formed in nature.
4. Understand how genome structural evolution affects trait variation, for a range of traits of importance in this crop.

Material for testing effects on agronomic traits

Selfing or
outcrossing

Synthetics AACC
 $2n=38$

Natural *Bn*
x synthetics

RCC and EMZ

Set of fertile
plants

Set of poorly
fertile plants

Express x R53
Express x 1012-93
Express x V8 (semisynthetic)

DH mapping
populations

Selection of plants contrasted for traits of interest (from flower traits to seed production and vigour) -> identification of genomic regions and of structural and/or functional regulations involved

Core collections of natural *B.napus*
Characterization of natural variability -> identification of structural and/or functional regulations involved

Progress

1. Project due to start **30/6/14** (DI staff costs at UoY: Zhesi He)
2. UoY have acquired genome sequences and CDS models for *B. rapa* Chiifu V2 (China), *B. oleracea* TO1000 (Canada), *B. napus* Darmor-bzh (France).
3. JLU recruiting PhD student
4. JLU, INRA identifying lines and collating trait data

Acknowledgements

Rod Snowdon



Anne-Marie Chevre



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Funding from:

- BBSRC BB/L027844/1
- DFG SN17/1
- INRA BAP-SPE



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