

Control of **homoeologous** chromosome pairing and recombination in oilseed rape

Collaboration between Birmingham and **Isobel Parkin's** group (AAFC Canada)

What is homoeologous pairing and recombination?

Why is the control of it important for *Brassica napus*?

How do we find the locus exerting most control over it?

Elaine Howell

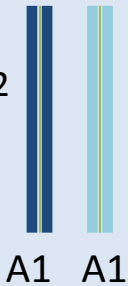


Meiosis

Diploid

1 pair
homologous
chromosomes

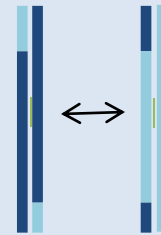
Replication - 2
chromatids
held together



Find
homologue:
DSBs, strand
invasion

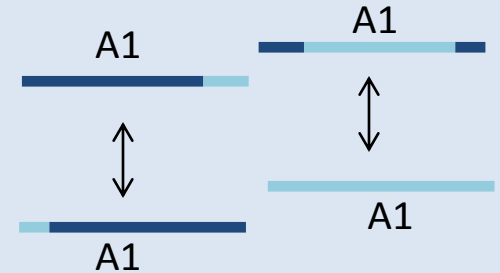


Crossover
between
homologous
chromatids

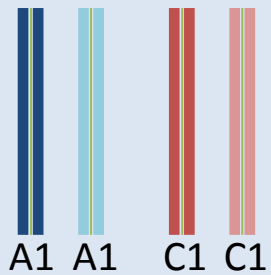


1st division
crossovers resolve
chromosomes separate

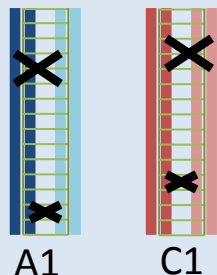
2nd division
chromatids separate
- 4 haploid products



Polyploid

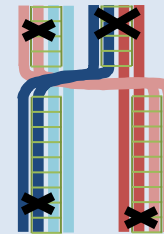
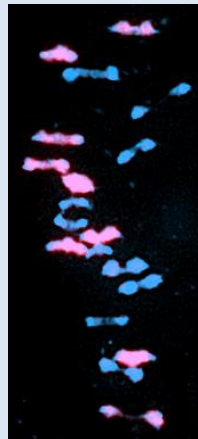


homologues and
homoeologues



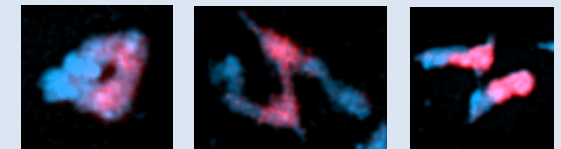
bivalents -
between
homologues

Normal *B. napus* at M1
19 bivalents 10A 9C



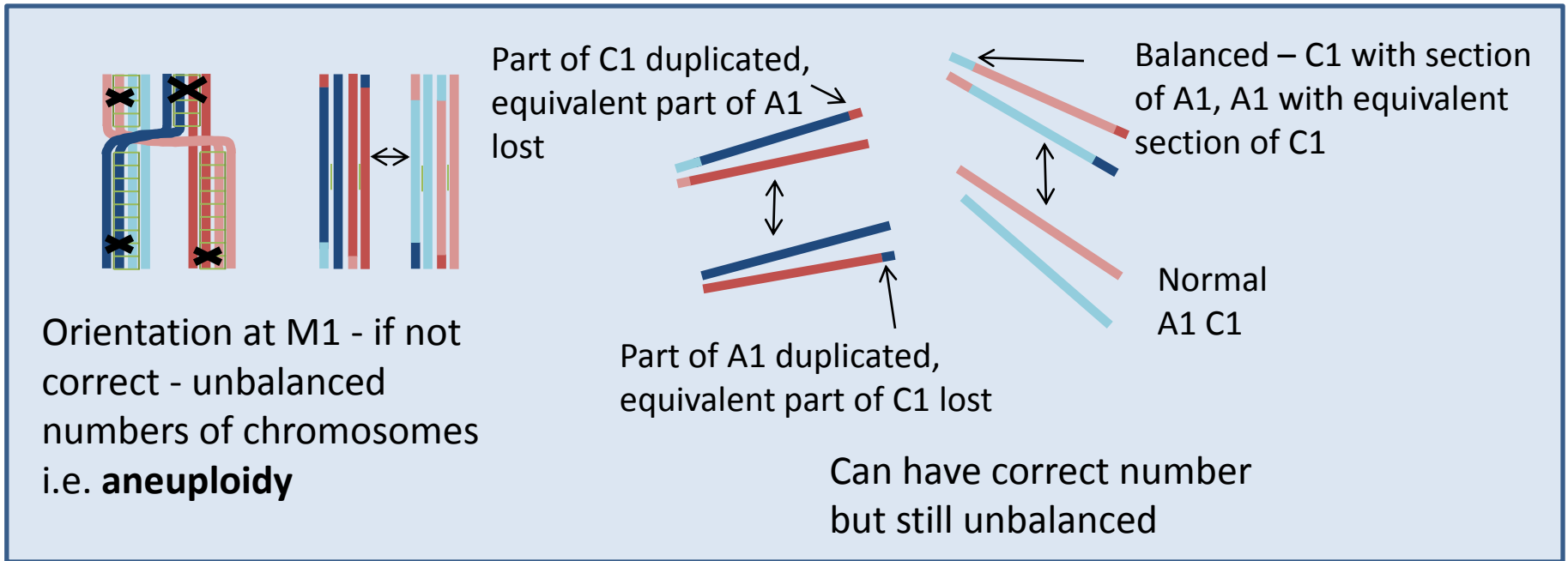
Pairing partner exchange
and crossovers between
homoeologues

At M1, held
together at Xs
seen as chiasmata



Homoeologous
bivalents and
quadrivalents etc.

Results of homoeologous recombination



Infrequent in cultivated *B. napus*
Frequent in resynthesized *B. napus*

Useful genetic variation in the diploids -> resynthesize *B. napus* lines -> cross with normal *B. napus* but instability is a problem.

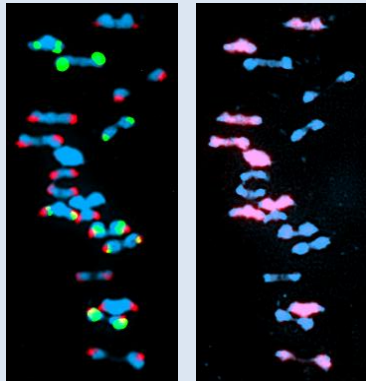
Find locus exerting most control over homoeologous recombination

- introduce it into diploids or find it in the diploid gene pool
- create **more stable resynthesized lines**
- adds to information - how polyploids cope during meiosis

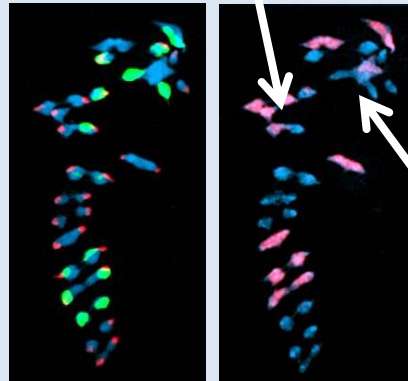
Cytogenetics

Examine spreads of **male meiocytes** at **M1** stage from **anthers**.

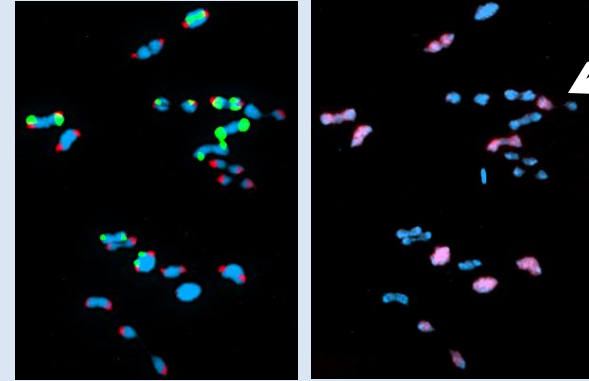
FISH with two probes, reprobe with GISH (label C genome DNA)



19 bivalents
10 **AA** and 9 **CC**



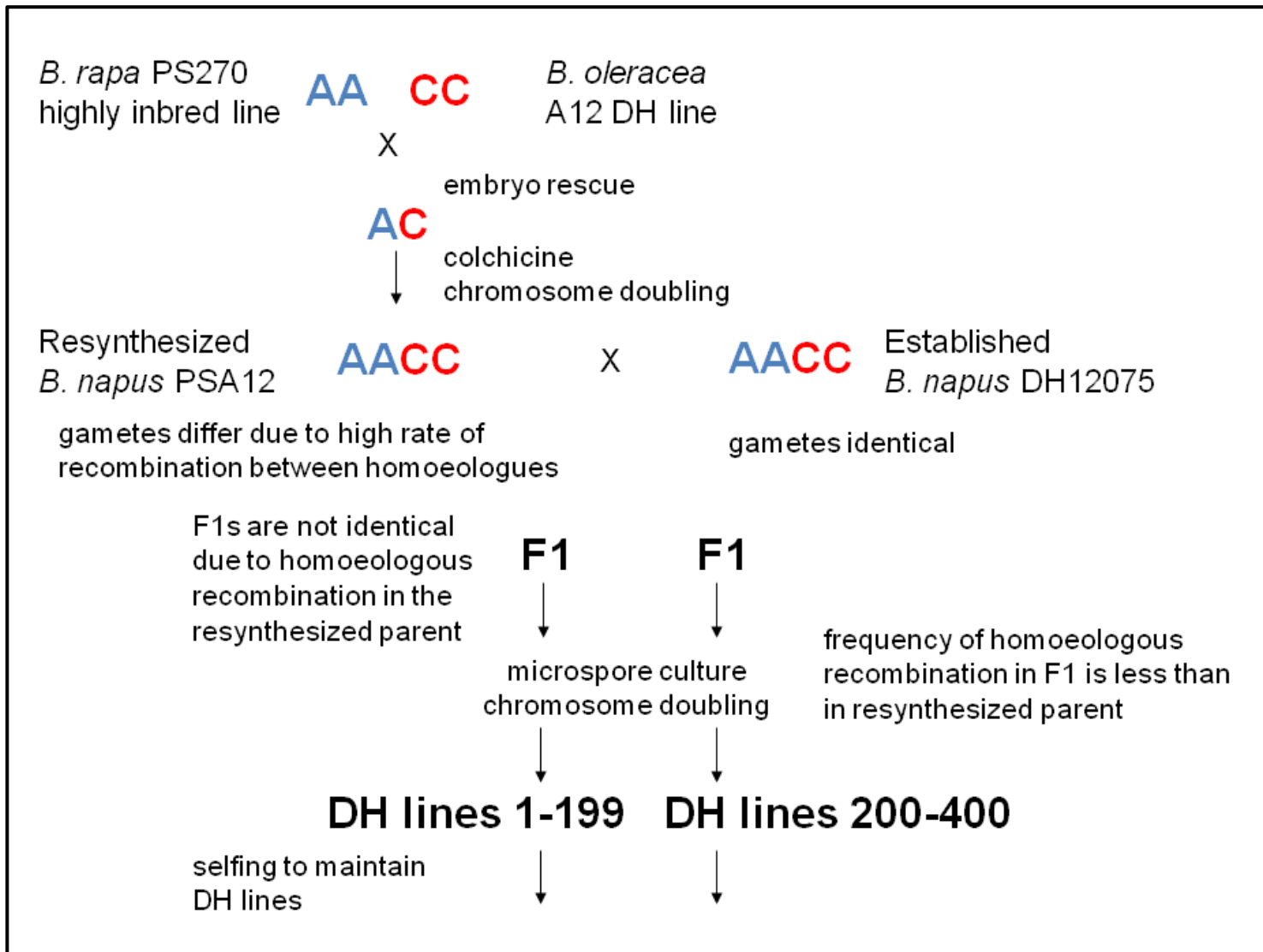
Plant with
homoeologous
recombination



Plant gained one A
chromosome and lost one C
(often form a bivalent)

- Score spreads, (50+) per plant, for homoeologous interactions.
- Calculate minimum number of pairing partner exchanges that occurred to produce the different configurations in each spread.
- Mean number per spread per plant.

BnaSGDH Population – Isobel Parkin (AAFC)



Map: 90 lines
RFLP SSR data
from AAFC

Cytogenetics:
31 lines, random

QTL
Cartographer:
One region on
A09 strongly
associated
with the trait

Current work

Selected Lines – with recombination points between flanking RFLP/SSR markers of the QTL -> cytogenetic analysis 19 lines -> 2 groups

SNP data (Illumina Brassica 60K chip - AAFC) for 124 lines – including all these.

Narrowed the region

Remainder of lines screened with flanking markers (AAFC) – 16 more.
SNP data -> 3 in the narrow region -> cytogenetic analysis

Will confirm and further narrow the region

Test crosses (AAFC) - with many lines

**Should confirm the region
and provide data on the sites of recombination**

Finding candidates?

Genome sequences:

B. napus ($A_n A_n C_n C_n$) – DH12075 parent of population – draft (AAFC)

B. rapa ($A_r A_r$) – Chiifu

B. oleracea ($C_o C_o$) – TO1000

SNP sequences defining the region

-> align to the genomes -> identify genes within the region.

Known meiotic genes? Other likely genes?

mRNAseq - anthers containing meiocytes at **early prophase**

Which genes in the region are expressed/not expressed?

Reduce potential number and may recognise unannotated genes.

Pilot study with *B. napus*, *rapa* and *oleracea* parents.

Larger experiment with DH lines planned. (Differential expression?)

Acknowledgements and Thanks to:



BBSRC 2012 - 2015



Maria Cuacos - RNA-seq data analysis

PIs:

Sue Armstrong, Chris Franklin, Zewei Luo

Collaborators:

Erin Higgins, Isobel Parkin, (AAFC Canada)

Graham King (Southern Cross University Australia)

BBSRC 2003 - 2006

PIs:

Mike Kearsey, Gareth Jones (Birmingham)

Graham King (Rothamsted)

Collaborators:

Isobel Parkin, Derek Lydiate (AAFC Canada)

Colleagues in the Brassica community particularly those at Warwick HRI and in the Meiosis lab. Birmingham

