

Prospects of using the *Brassica oleracea* gene pool in oilseed *B. napus* breeding

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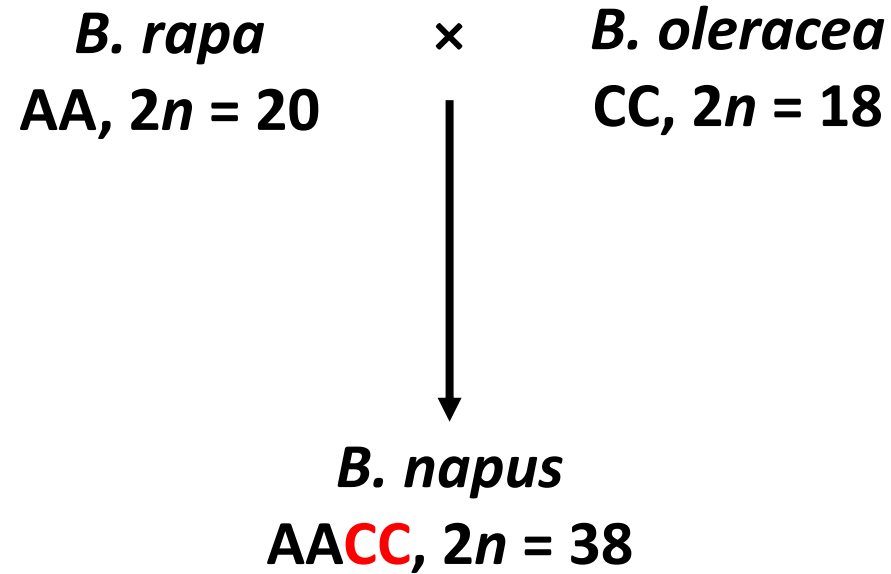
GCIRC Technical Meeting

April 8–10, 2025

Cambridge UK

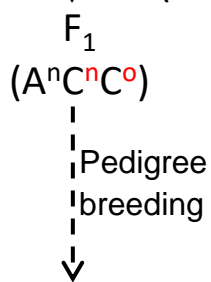
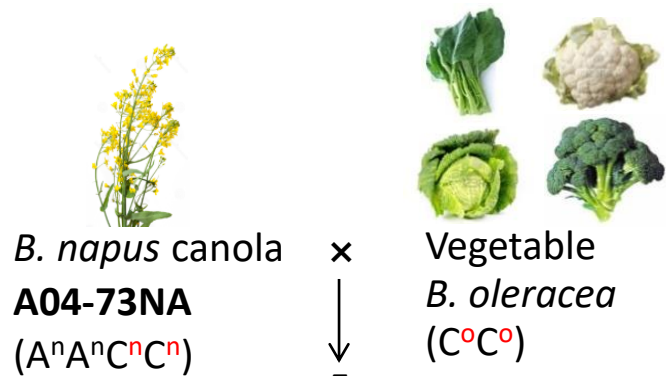


Use of *B. oleracea* in the breeding of *B. napus* canola



- C subgenome of *B. napus* is conserved and less variable than the A subgenome.

Introgression of allelic diversity from different variants of *B. oleracea*



Reconstituted
Canola
(AⁿAⁿCⁿCⁿ/AⁿAⁿC^oC^o)
lines = 228

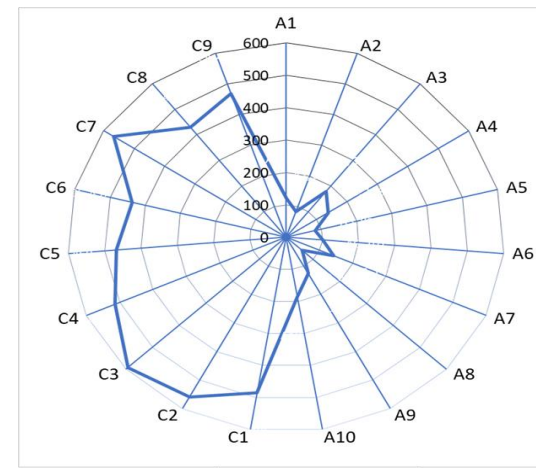


- Theoretically, the reconstituted canola lines will be carrying the A genome alleles of the *B. napus* parent A04-73NA, while their C genome will be carrying the alleles of the C genomes of *B. napus* or *B. oleracea*.
- This would allow to estimate the effect of the *B. oleracea* alleles in *B. napus*.

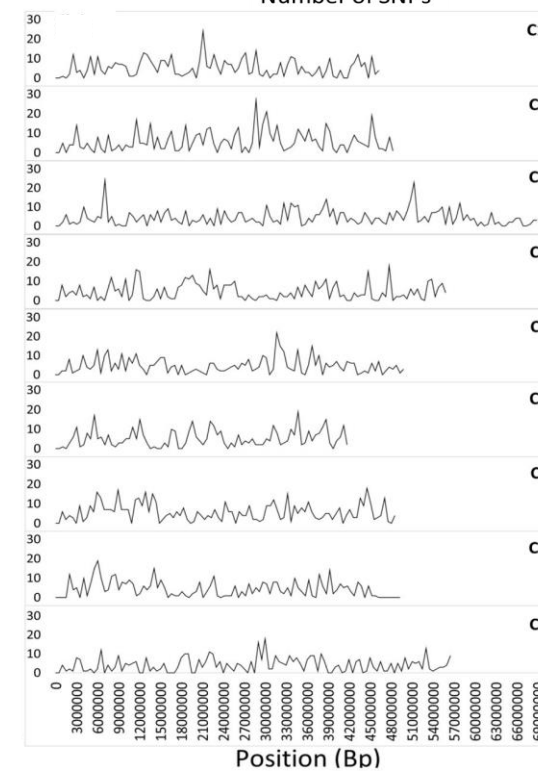
SNP genotyping



Distribution of 5,743 SNPs in A & C genomes

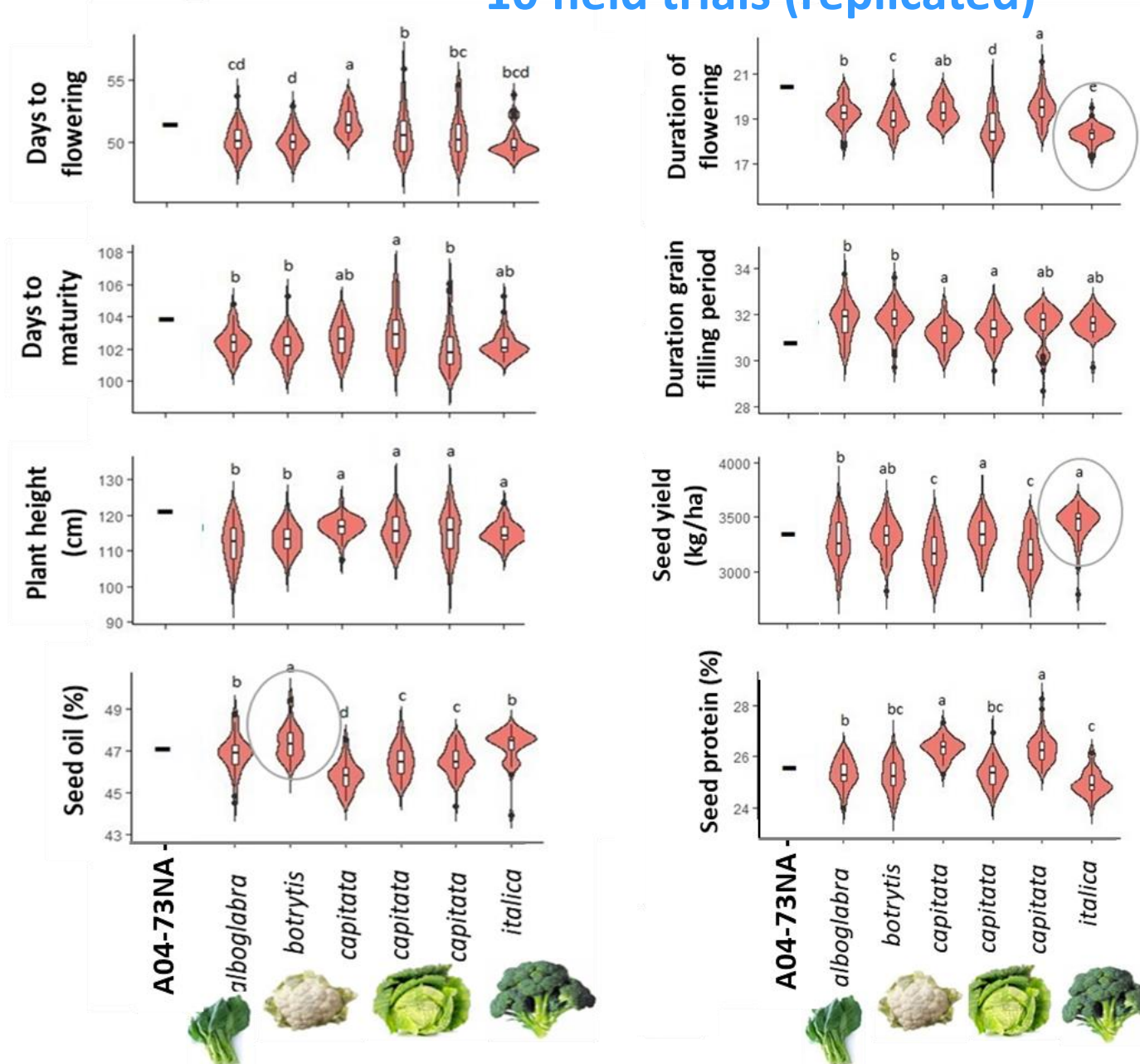


About 80%
SNPs from
the C
genome



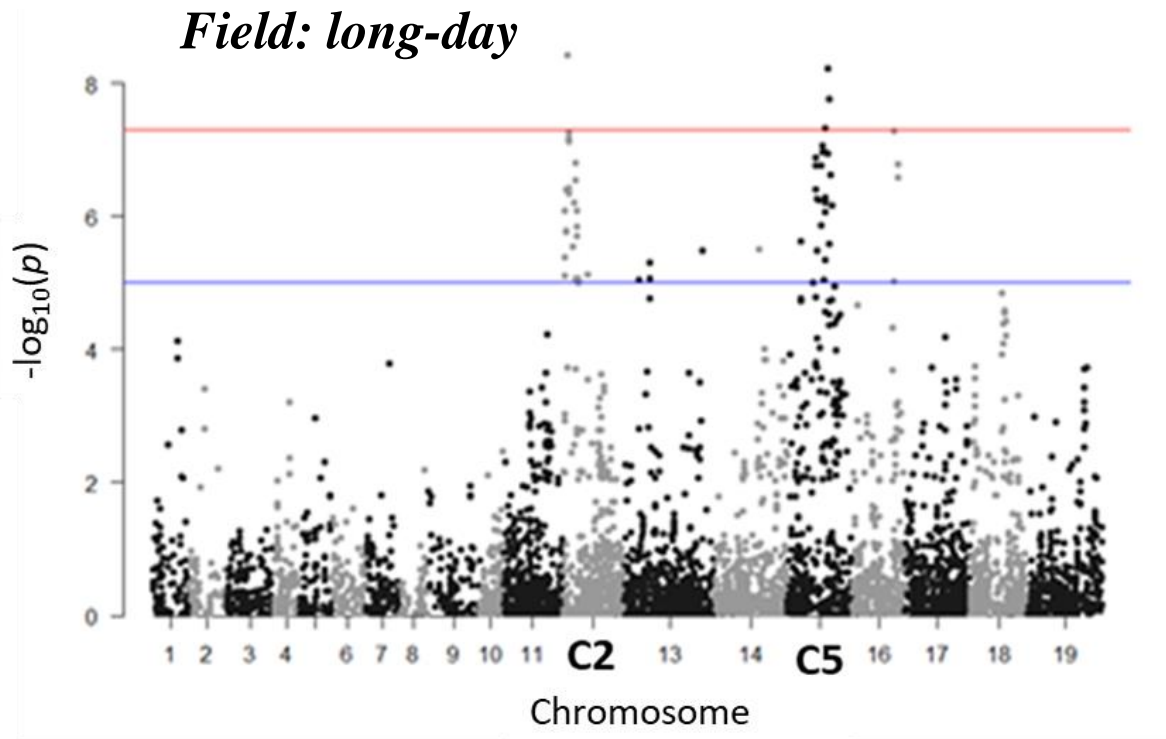
Distribution
of the SNPs
on nine C
genome
chromosomes

Performance of the populations derived from Canola \times *B. oleracea* crosses in 10 field trials (replicated)

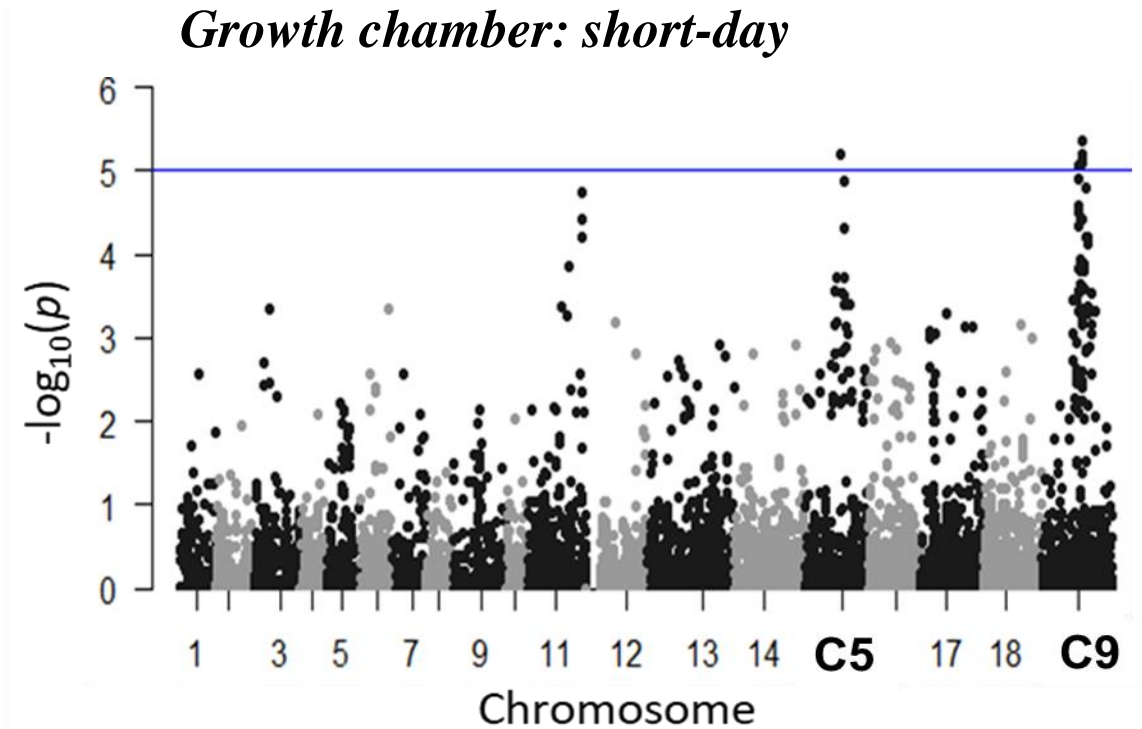


➤ Wide variation was found in the populations for different traits

Mapping of flowering time



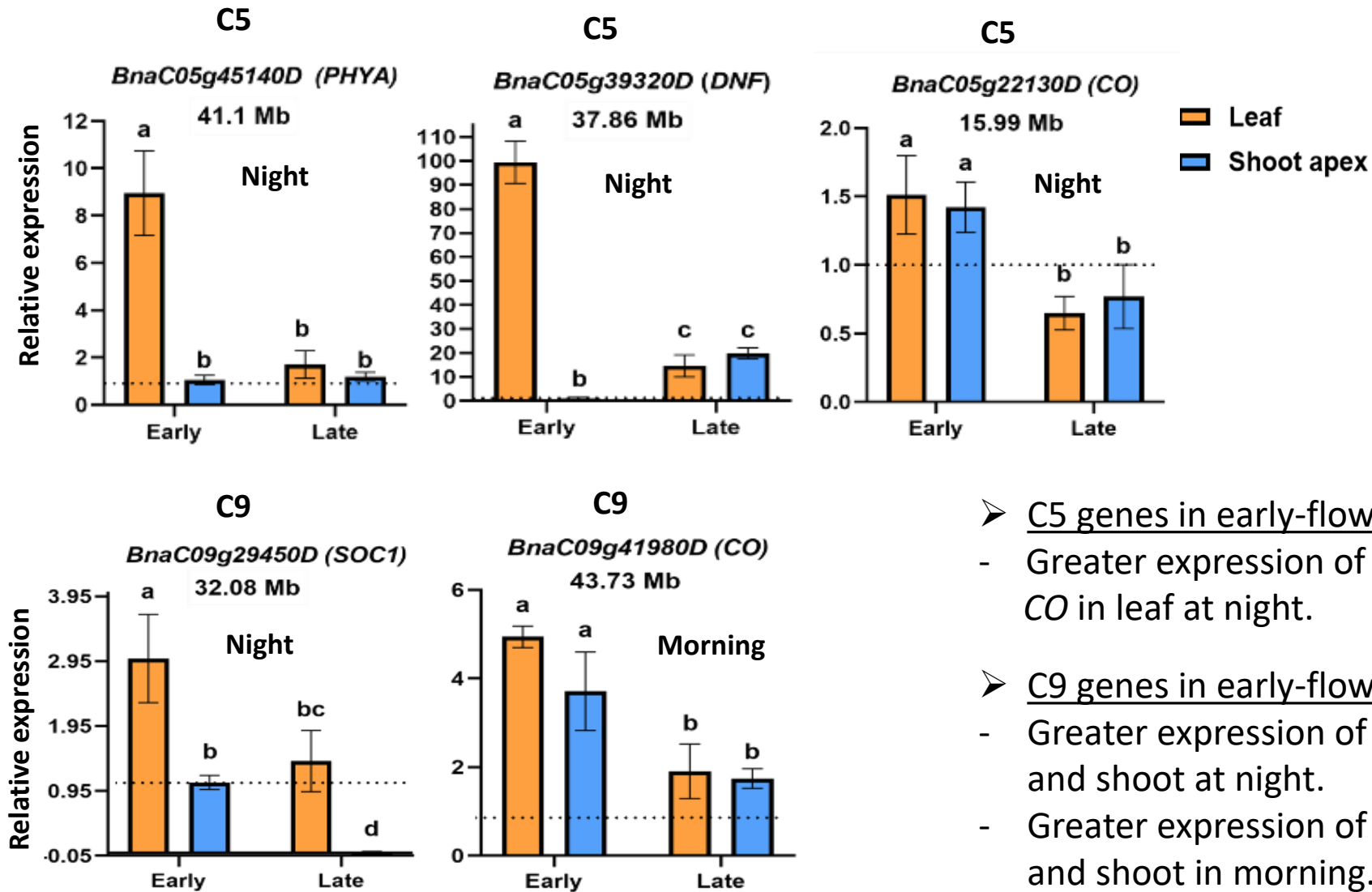
C2 QTL: 5.1–10.75 Mb; C5 QTL: 26.1–31.8 Mb



C5 QTL: 28.7–30.8 Mb; C9 QTL: 29.1–36.4 Mb

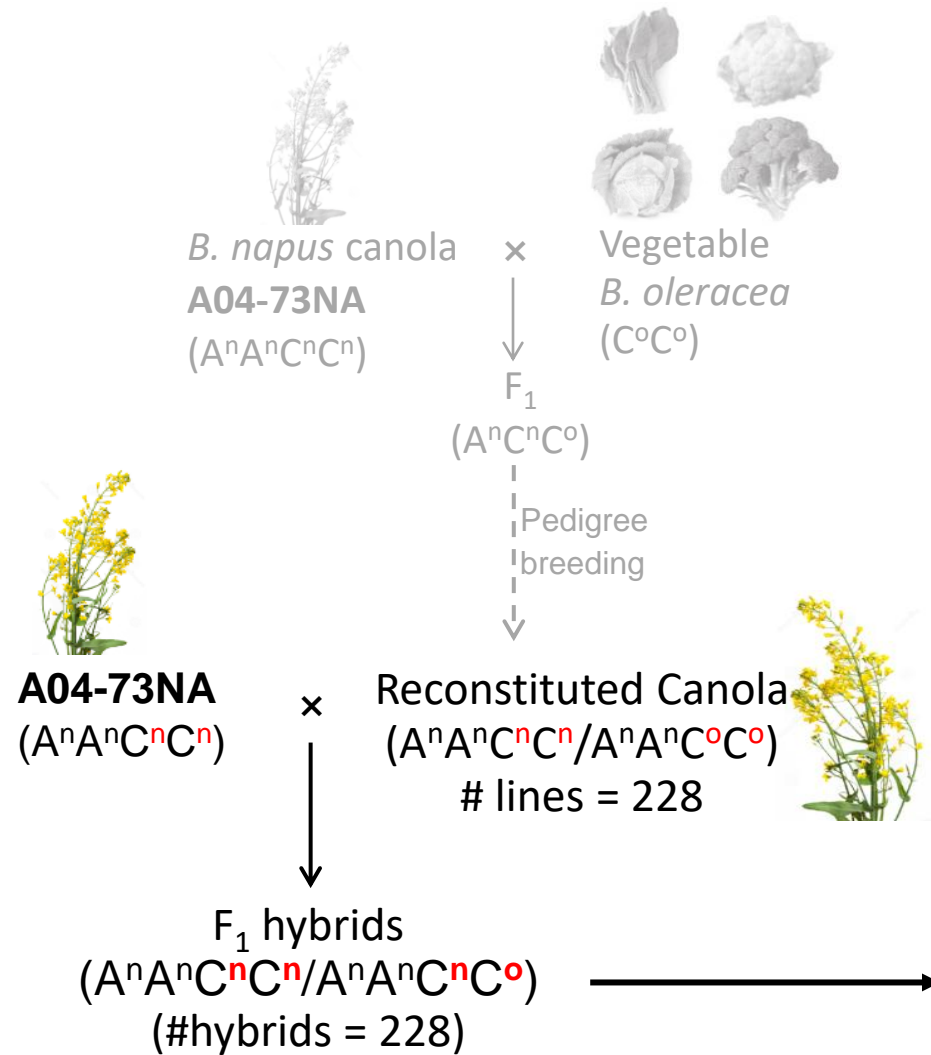
- C5 allele of the cabbage cv. Bindsachsener improved the earliness under both short- and long-day conditions.
- C9 allele of the cabbage cvs. Badger Shipper/Balbro improved the earliness only under short-day condition.

Relative expression of flowering genes from C5 and C9 in the early- and late-flowering lines under 10 h photoperiod condition

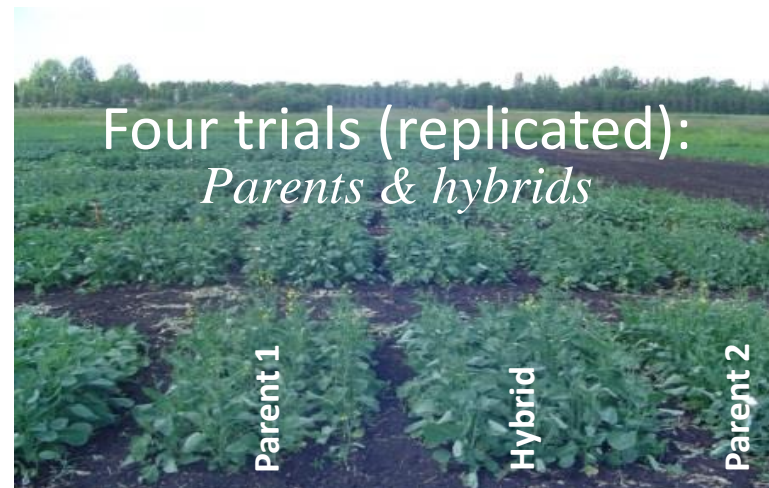


- C5 genes in early-flowering lines:
 - Greater expression of *PHYA*, *DNF* and *CO* in leaf at night.
- C9 genes in early-flowering lines:
 - Greater expression of *SOC1* in both leaf and shoot at night.
 - Greater expression of *CO* in both leaf and shoot in morning.

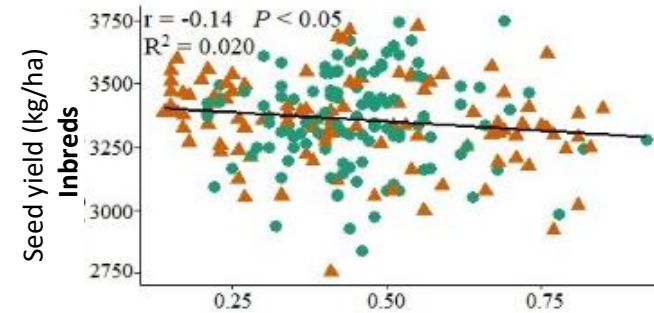
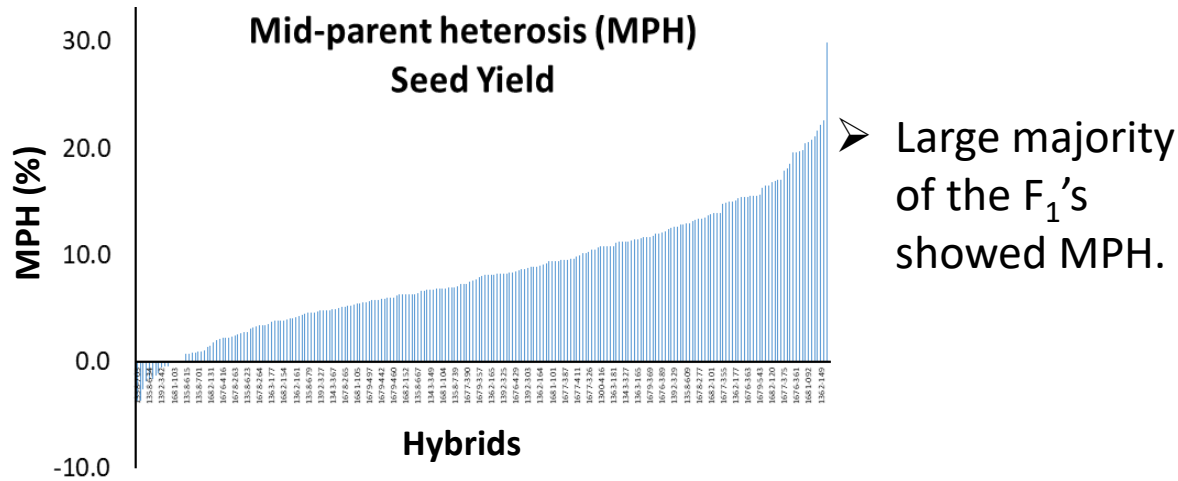
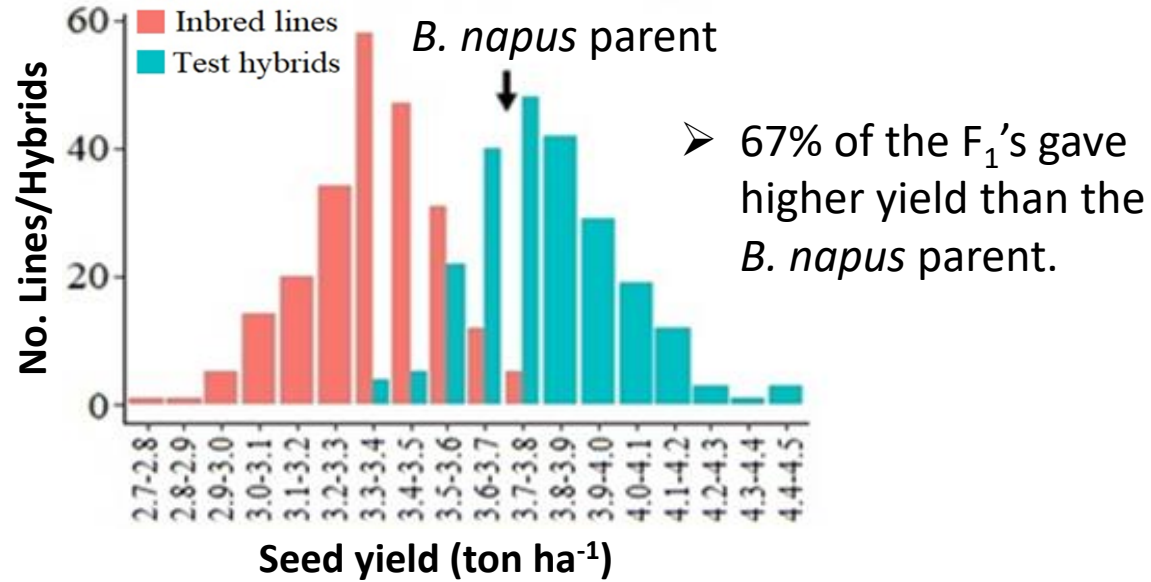
Evaluation of the *B. napus* lines derived from *B. napus* × *B. oleracea* interspecific crosses for seed yield in F₁ hybrid



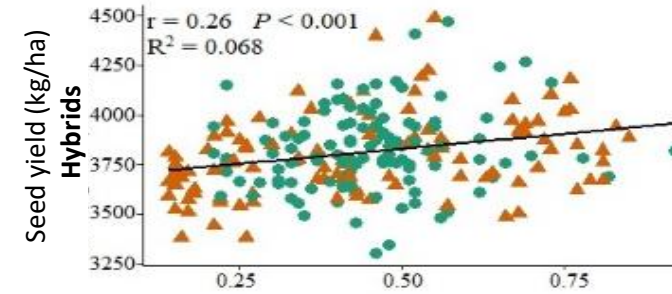
- Theoretically, the heterozygosity in the F₁ hybrids will be for the C genome alleles of *B. napus* and *B. oleracea*, and this would allow to estimate the effect of the *B. oleracea* alleles on heterosis in *B. napus* canola.



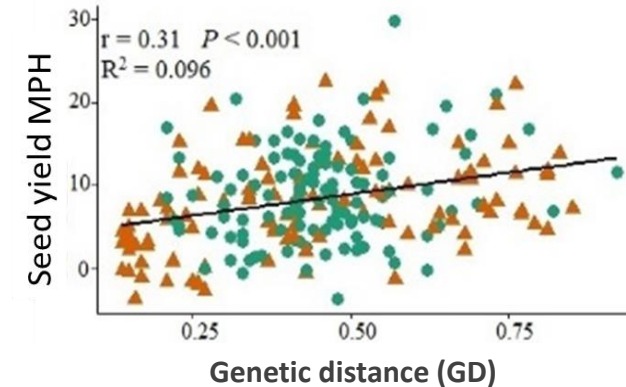
Seed yield of the F₁ hybrids of the *B. napus* lines derived from six *B. napus* × *B. oleracea* interspecific crosses



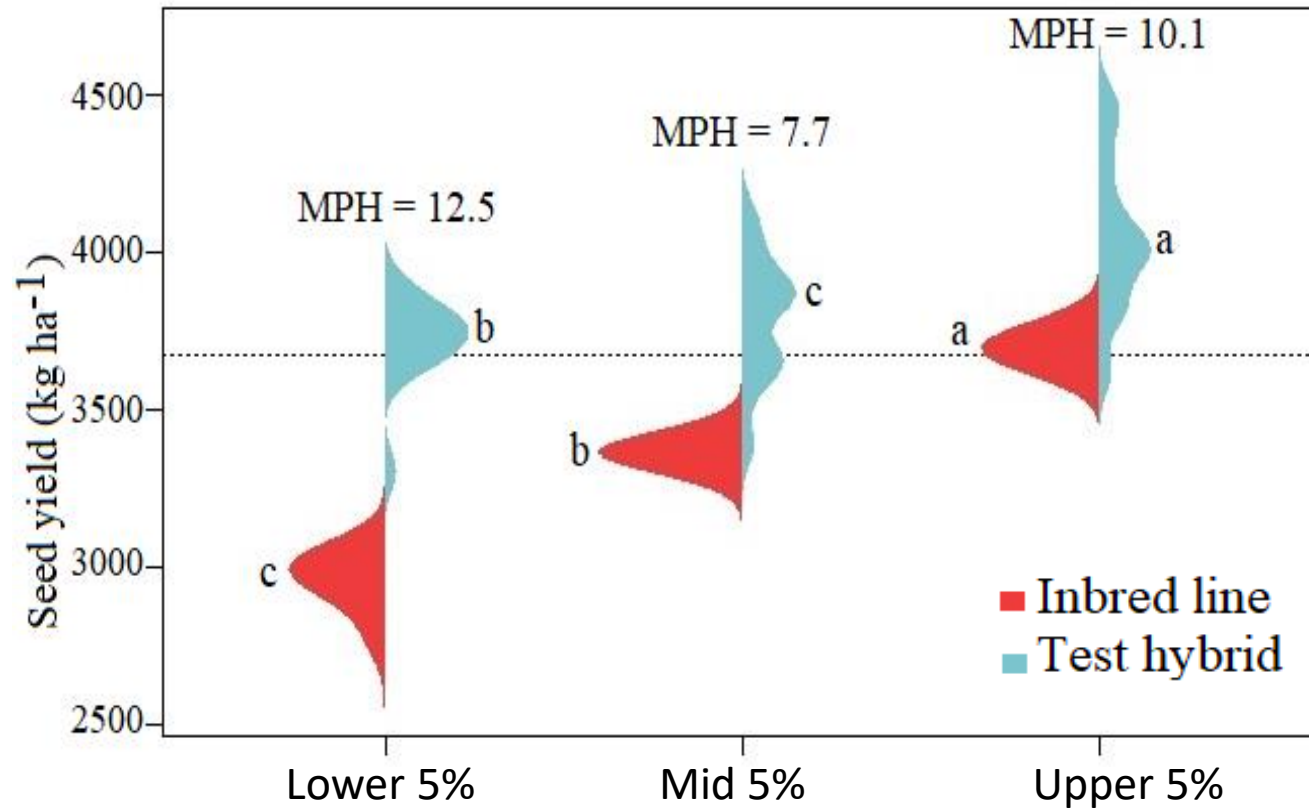
➤ Genetic distance (GD) showed a weak negative correlation with seed yield in the inbred population.



➤ GD showed a positive correlation with seed yield in the hybrid population ($r = 0.26$) as well as with MPH ($r = 0.31$).



Performance of the top-, medium-, and poor-yielding inbred lines derived from *B. napus* × *B. oleracea* crosses and their F₁ hybrids



- Hybrids of all three groups showed a similar level of MPH.
- However, hybrids of the top 5% inbred lines gave significantly greater yield than the hybrids of the other two groups, indicating the importance of both additive and non-additive effect genes for increased seed yield in hybrids.

MPH = percent mid-parent heterosis. Dashed line: B. napus parent. The same letter for the inbred or hybrid indicates the values are not significantly different at $p < 0.05$.

Introgression of allelic diversity from *B. oleracea* Chinese kale

B. napus Hi-Q — × — *B. oleracea* (Chinese kale)

RIL-144
(Reconstituted
B. napus)

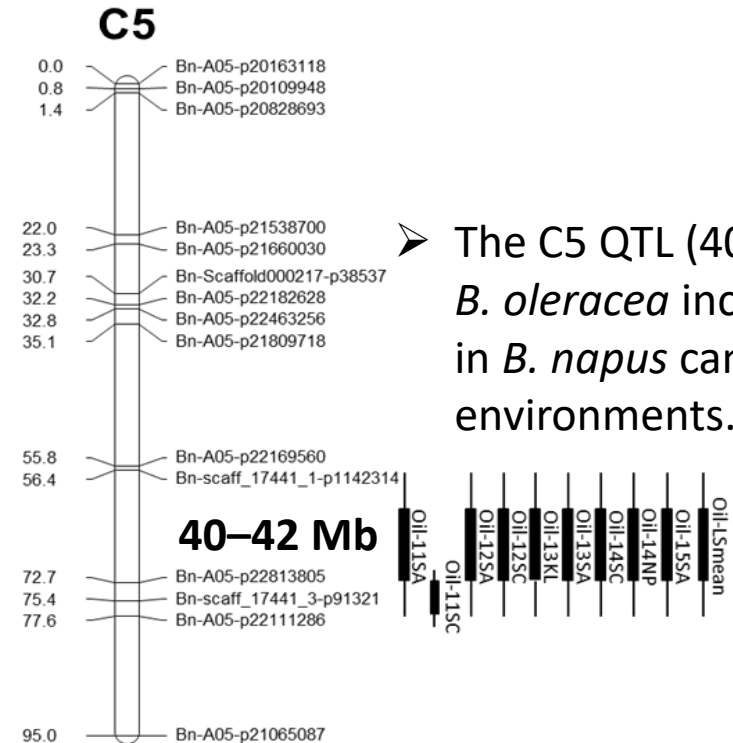
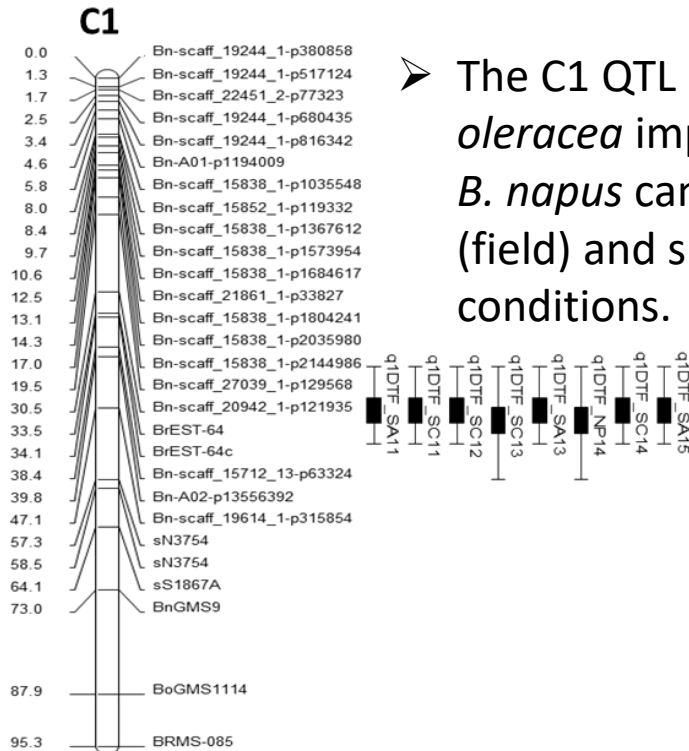
× — **Hi-Q (*B. napus*)**

DH population

Nine field trials
(*replicated*)



➤ Theoretically, the DH population will be segregating only for the C genome alleles.



Conclusions

- Favourable alleles for agronomic and seed traits can be found in *B. oleracea* for use in canola breeding.
- *B. oleracea* alleles can contribute to seed yield heterosis and consequently to high yield in F₁ hybrids.

Funding



Industry Partners

Acknowledgements

Thanks to all students and staff of the University of Alberta Canola Breeding-research group,
and collaborators from seed companies & other institutes

The image features a white background with clusters of bright yellow flowers and green buds on the left and right sides. The flowers are in various stages of bloom, with some fully open and others as small buds. The text is centered in a blue, cursive font.

Thank you for attention