

# LARGE SCALE GENETIC MAP INTEGRATION IN BRASSICA VIA DATABASE INTERACTION

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## Abstract

The value of genetic linkage maps for resolution of loci associated with crop traits is often dependent upon the availability of sufficient polymorphic marker loci that segregate in the relevant reference populations. Integrating different genetic maps helps to increase marker density and create more reliable marker orders. This allows intensive study of the orthologous relationships between *Brassica* and reference species such as *Arabidopsis*, as well as re-calculation of QTL positions associated with valuable crop traits. We describe the generation of a consensus genetic linkage map (BnaWAIT\_01\_2010a) for the 19 chromosomes of *Brassica napus*, which brings together various genetic maps collated in the genetic registry database, **CropStore<sub>DB</sub>** ([www.cropstore.org](http://www.cropstore.org)). For sequence-tagged marker loci, we also describe the process to extract sequence information from the DNA sequence registry database, **SeqStore<sub>DB</sub>**, and feed this into an in-house sequence alignment database, **AlignStore<sub>DB</sub>**. The genetic (population-level) information from **CropStore<sub>DB</sub>**, along with the sequence-level information from **SeqStore<sub>DB</sub>** and **AlignStore<sub>DB</sub>** is used to explore orthologous/homologous relationships between a query species such as *Brassica* and a reference species and/or any target sequence collection. The integration of data between these three databases also allows the provenance of additional features to be presented within the Ensembl genome browser, **BrassEnsembl** ([www.brassica.info/BrassEnsembl/index.html](http://www.brassica.info/BrassEnsembl/index.html)).

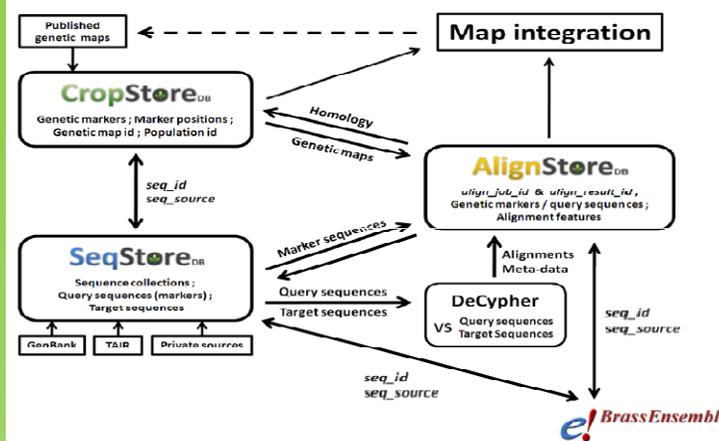


Fig.1. Schematic showing the interactions of the databases used for map integration

## Fig.2. Genetic map integration pipeline

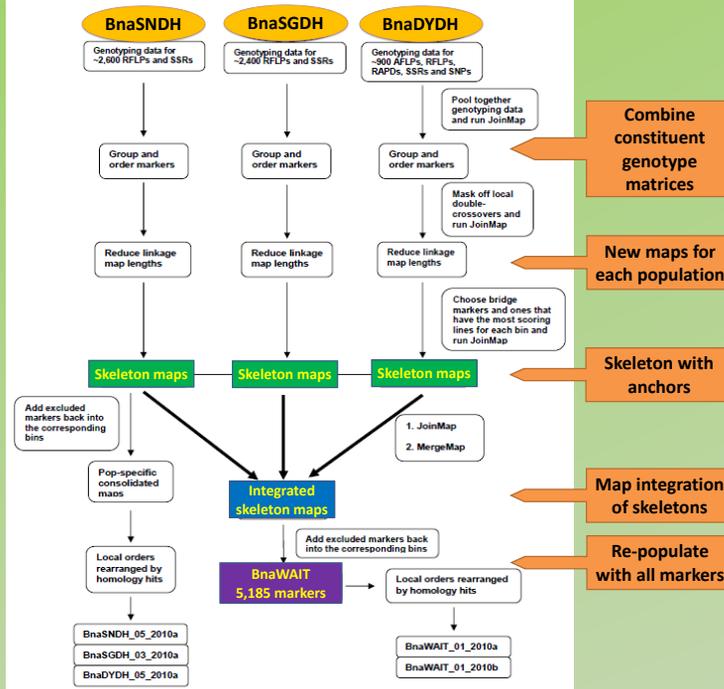


Fig.3. The distribution of map intervals for the BnaWAIT\_01\_2010a integrated map generated by JoinMap.

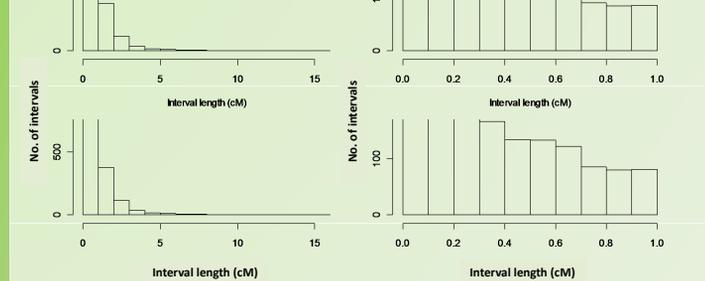
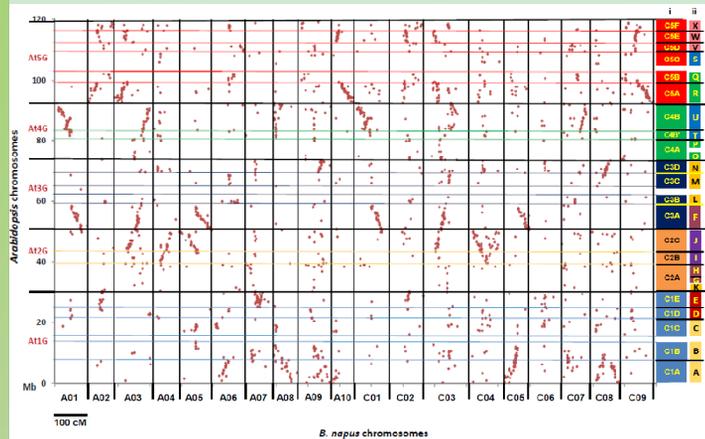


Fig.4. Genome duplication within the *Brassica napus* genome relative to the five *Arabidopsis* chromosomes. i) *Arabidopsis* blocks used in Parkin et al. (2005), ii) ancient karyotype (AK) blocks from Schranz et al. (2006) are shown alongside.



## Summary

1. Increased map density, with the mean map density of a locus per 0.86 cM, corresponding to a locus every 513 Kbp.
2. Good marker order consistency between the integrated map and each of the population-specific maps.
3. The map integration pipeline can be easily applied to other species.
4. Consistent with previous findings, we also found evidence of inversions and internal duplications within *Brassica* LGs relative to *Arabidopsis*.

## Future work

1. Integrate other *B. napus* maps and create integrated maps for the *B. rapa* A genome and *B. oleracea* C genome.
2. Investigate the distribution of recombination rates in *Brassica*.



## Data and Other Contributions

- CropStore<sub>DB</sub> : <http://www.cropstoredb.org/>
- The *Brassica rapa* Genome Sequencing Project Consortium
- BrassEnsembl: <http://www.brassica.info/BrassEnsembl/>
- Contact: [jun.wang@bbsrc.ac.uk](mailto:jun.wang@bbsrc.ac.uk) or [graham.king@bbsrc.ac.uk](mailto:graham.king@bbsrc.ac.uk)

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