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# Accelerating the development and utilization of new-type *Brassica napus* gene pool by genomics-based approaches

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**Background:**

In recent decades, the gene pool of *Brassica napus*, has been significantly enriched benefiting from worldwide efforts on the successful introduction of abundant Brassica subgenome variation. An important issue in this respect is how to accelerate the utilization of such variation for rapeseed breeding with advancing genomics-based approaches.

**Objective:**

We aimed to identify the whole genomic variation of a new-type B. napus gene pool that we developed for decades with introgression of pan-genomic variation from B. rapa, B. carinata and *B. juncea*, and analyse the elite alleles, novel genes, and haplotypes for important per se traits and its heterosis. By developing genomic selection models, the breeding value and the selection efficiency of pre-breeding would be improved and increased.

**Methods:**

A panel of 300 diverse lines from the new-type B. napus gene pool, and a set of tetra-parent joint mapping populations with 735 DH lines were grown in more than three environments for field trials to evaluate their yield and seed quality traits. More than 400 hybrids generated from new-type B. napus lines as male parents, were also grown in field trials for heterosis analysis. Whole-genome sequencing technologies including Illumina and ONT sequencing were used to analyse the genomic variation of the new-type B. napus lines and hybrid testers. Both the new-type B. napus diverse lines and their derived hybrid populations were used as training population. Novel diverse lines and hybrids were developed and used as a test population for each year. GWAS, QTL mapping and selection sweep analysis were used to detect links between markers and traits. GBLUP, rrBLUP, Bayes, neural networks and other machine learning methods were used for genomic prediction analysis.

**Results:**

The whole genome-wide variation, including abundant SNP and Indel polymorphisms, genomic structural variation and exotic introgression segments have been investigated in the new-type B. napus lines. Hundreds of causal QTLs accounting for flowering time, plant height, branch numbers, yield and yield component traits, biomass, seed quality traits, have been detected. Novel QTLs harboured in new-type B. napus genomes, such as those accounting for low glucosinolates have been identified and compared with published ones. Genomic prediction models with the genetic effects of the structural variation, exotic introgression, and QTLs, were tested to improve prediction accuracy. Under the guidance of the genomic evaluation of the new-type B. napus panel by comparison with conventional B. napus, we developed novel diverse lines and hybrids for practical pre-breeding.

**Conclusions:**

Massively introducing subgenomic variation from progenitors or related species significantly broadened the genetic basis of B. napus gene pool. However, strong “genome shock”, linkage drags, and unfavourable/undomesticated traits for Brassica oil crops constrained the utilisation of novel germplasm in rapeseed breeding. With population-based recurrent selection, we could rapidly stabilize genomes with the reconstruction processes. With genomic-based knowledge, we could precisely identify and use the novel genetic variation contributing to per se traits and heterosis. This would significantly accelerate the exploration on the breeding value of B. napus gene pool and assist the genomic breeding of rapeseed.