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Expanding a novel gene pool of Brassica napus with massive introgression of related oilseed species and exploring its intersubgenomic heterosis

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In our previous studies, we have constructed a novel dynamic gene pool of B. napus (ArArCcCc) with introgression of the Ar and Cc subgenome from hundreds of accessions of B. rapa (ArAr) and B. carinata (BcBcCcCc). To further expand this gene pool, and explore its breeding value and intersubgenomic heterosis for rapeseed hybrid breeding, we aimed to select new-type B. napus lines with favorable traits, good general combining ability and further introgress genomic components from hundreds of B. juncea. By recurrent selection and extensive phenotyping, we screened lines with high oil content, high oleic acid content, high linoleic acid content, high linolenic acid content, large seed size, good pod traits (high number and pod density in main inflorescence and high seed number per pod). These lines were used for intercrossed to pyramid multiple favorable traits and self-pollination or microspore cultivar for homogenizing. For these homozygous lines, we performed genotyping and phenotyping assisted with genomic selection. By testing hybrid between new-type B. napus and elite traditional B. napus testers on yield and yield related traits, we evaluated their intersubgenomic heterosis in different environments and genotyped them by sequencing for hybrid genomic selection. Results showed strong intersubgenomic heterosis and affected significantly by environments. Genomic prediction accuracy also varied with environments and trait architecture. With cycles of phenotypic and genotypic selection, the breeding value of the gene pool would be increased for hybrid breeding.