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Exploring diversity of Brassica juncea genomes to improve B. napus varieties

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Brassica juncea Czern et Coss. is a crop plant species used for condiment, oilseed and vegetables and more diverse in morphology than B. napus L.. Meanwhile, the former have a stronger tolerance to abiotic stresses such as drought and heat than the latter. Canada and Australia, among others, developed canola quality oilseed Brassica juncea to substitute for rapeseed. However, more research is needed to insight into diversity of Brassica juncea genomes to improve canola varieties although genome sequencing of tuberous mustard, the subspecies tsatsai of B. juncea was reported in 2016.

We carried out de novo sequencing of oilseed B. juncea ssp juncea var. SCHZ using combination of Pacbio and HiSeq platforms, Hi-C technology and the ultrahigh-density genetic map consisting of15543 markers. The total length of final assembly is 889,060,942bp, distributed across 18 chromosome-level pseudomolecules and representing ca. 92% of the estimated genome size. We annotated 83,146 high-confidence protein-coding genes along with 30,587 genes encoding small noncoding RNAs. Moreover, we conducted pan sequencing of ten B. juncea accessions from the Asian countries which are suspected to be the place of origin of B. juncea. These accessions have an estimated genome size of 1,019~1,085Mb and an assembled total length of 868,441,953~ 915,317,291bp , and encode 79,206~ 83999 protein-encoding genes. Together with two de novo sequenced ones SCHZ and T84-66, they were used for analysis of core genes and genetic variation. A total of 20,629 core gene families composed of 52,206~ 58,949 genes was identified in B. juncea, with 9,886~ 18,094 dispensable and 15~809 accession-specific gene families. Comparison to the new high-quality reference genome of SCHZ found extensive genetic variation including SNPs, InDels, SVs, CNVs. Re-sequencing of some 500 B. juncea accessions was completed. Detection of their genetic variation is underway. The detected variation loci will be used for phylogenetic analysis and genetic dissection of major traits.

Superior traits can be easily transferred into B. napus canola cultivars through the interspecific cross between B. juncea and B. napus. In the future we will compare homologous or homoeologous genes from these two species to uncover the best alleles for practical canola breeding.