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An advanced *Brassica carinata* genomics platform for Brassica crop improvement

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Background:

Brassica carinata is an important agricultural crop of *Brassica* cultivated for edible oil and biofuel markets. Unlike the efforts devoted to key staple food, fibre and oilseed crops, few genomic resources were developed specifically to support the genetic improvement of *B. carinata*. The lack of high-quality reference genomes and pan-genome sequences hindered the genomics-based breeding of B. carinata.

Objective:

We aim to sequence two highly homozygous accessions to obtain high-quality reference genomes and construct a pan-genome platform for *B. carinata* and provide the genome-wide variations map and uncover the key genes underlying agronomic traits with focus on pod shatter resistance.

Methods:

Two accessions of *B. carinata*, with distinct plant architecture and pod shatter resistance, were sequenced by a combination of Illumina short-reads, Oxford Nanopore Technology long-reads, and Hi-C reads. The genome assemblies were verified and improved using published a genetic linkage map and GOGGs analysis. We also sequenced Illumina short-reads for additional 82 B. carinata accessions and constructed a pan-genome for *B. carinata* on genome sequences of 86 representative accessions. Based on the pan-genome platform, we further identified candidate genes associated with important traits, and mapped the physical position of massive published QTL.

Results:

We constructed two high-quality reference genomes for *B. carinata*, with a total length at ~ 1.07 Gb and contig N50 more than 24 Mb, and subsequently reported the first pan-genome of B. carinata based on genome sequences of 86 representative accessions. Using this pan-genome platform, we identify 1,767 candidate genes for important traits of *B. carinata*. Focusing on pod shatter resistance, a unique trait of *B. carinata*, we characterize several key genes and reveal their evolutionary divergence within *Brassica*. The hub gene for pod shattering resistance of *B. carinata*, is identified and further verified by co-expression and QTL-seq analyses. We further present the divergence times of nine *Brassica* A, B and C subgenomes and their expansion of gene families and identify species-specific genomic variations for *B. carinata*. Our analysis also revealed that *B. nigra* (the B genome donor) is implicated as the maternal parent during natural hybridization in the formation of *B. carinata*.

Conclusions:

Our pan-genome of *B. carinata* contained comprehensive genetic information and enabled the identification of key genes for favourable traits. The hub gene controlling the pod shattering resistance of B. carinata can be a target for introgression into Brassica crops. The pan-genome platform enabled the comprehensively genome-wide comparisons of *B. carinata* to identify massive SNP/Indels/SVs unique to *B. carinata*, which can be developed as molecular markers to guide breeding. We performed the comparative evolutionary analysis of the Brassica subgenome and provide critical information that adds to the limited genomic resources of evolutionary relationships for *B. carinata*. This comprehensive study provides a valuable resource for understanding the genetic architecture of *B. carinata* traits and the genomic-assisted breeding of *Brassica* crops.