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Natural variation and genetic bases of pod shatter resistance in Brassica species

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Background:

Canola pods are highly sensitive to shattering, significantly reducing yield. However, the extent of seed loss varies across environments depending on genotypic attributes (pod strength, canopy architecture, resistance to lodging and diseases), method of harvesting (windrow vs direct heading), time of harvesting (early, 'optimal' time vs late) and environmental conditions at the time of harvest. Shattered seeds grow in the field and become a weed in the next crop; hence must be controlled. Breeding for pod shatter resistance is one of the major breeding objectives of commercial Brassica breeding programs.

Objective:

We investigated the natural variation of pod shatter resistance in different species of *Brassica*: *B. rapa* (n = 89), *B. napus* (n = 197) and *B. carinata* (n = 82). The accessions were evaluated for pod shatter resistance under natural field conditions using pod rupture energy as a proxy for pod strength.

Methods:

To understand the genetic basis underlying shatter resistance, we phenotyped and genotyped three intercross populations of *B. napus* (BLN2762/Surpass400, R1/R2, ZS11/R1) and two genome-wide association panels (Australian and Chinese diversity panels). Pod shatter resistance was measured with either pendulum or a random impact test. Mapping populations were genotyped with the *Brassica napus* 60K Illumina Infinium™ SNP array /DArTseq/DNA resequencing.

Results:

The genetic analyses showed multiple loci (Quantitative trait loci, QTLs) located on different chromosomes across the *Brassica* genomes associated with resistance to pod shatter. We further developed mapping populations derived from crosses of *B. rapa* x *B. napus*, *B. rapa* x *B. carinata*, and *B. napus* x *B. carinata* and used them for genetic analysis. One of the interspecific breeding lines (*B. rapa/B. napus*): BC94052, showed improved pod shatter resistance. We developed F2 and F2:3-derived populations for genetic analysis from the cross between BC94052 and an advanced breeding line, BC94051. Through genome scan, interval, and inclusive composite interval mapping analyses, we identified seven QTLs associated with pod rupture energy on A02, A03, A05, A09 and C01 chromosomes. Both parental lines contributed alleles for pod shatter resistance. We identified five pairs of significant digenic epistatic QTLs for additive x additive, additive x dominance and dominance x dominance interactions between A01/C01, A03/A07, A07/C03, A03/C03, and C01/C02 chromosomes for rupture energy. QTL effects on A01/C01 and A03/A07 were in the repulsion phase.

Conclusions:

Comparative analysis identified several candidate genes underlying main QTL and epistatic QTL interactions for pod shatter resistance, including SHATTERPROOF, FRUITFUL, and INDEHISCENT genes. SNP variants within these candidate genes were identified using the DNA resequencing data of 363 accessions of *B. napus*. Our research suggested that natural variation for pod shatter resistance exists within each *Brassica* species and was controlled by multiple loci having additive and digenic epistatic effects.