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Mining the strong pod shattering resistance gene in Ogu restorer lines

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Background:

The R gene of Ogu CMS restorer line is derived from the large genome segment of radish introduced into rapeseed. The redundant radish segment with the restoration gene carries a lot of adverse traits, such as high glucosinolate content and poor fertility.

Objective:

Some Ogu restorer lines also introduce strong pod shattering resistance genes original from radish into rapeseed genome. We expect to clone the unique resistant gene contributing to specific aligned layer bridge (LLB) structure in the abscission layer.

Methods:

We adopted two indoor methods (Random Impact Test and anatomical analysis) to investigate the pod shattering resistance. The shattering resistance index (SRI) was gained for each line by the method of Random Impact Test. The lignified- layer bridge (LLB) structure was observed by anatomical analysis of fresh samples. The genetic locus of LLB structure was mapping by BSA-sequencing with F2 population. The complete genes information was gained genome and predicted genes by highly accurate circular consensus sequencing (CCS) reads (HiFi; PacBio) using the HiFiasm assembly tool. Transcriptome was adopted to analysis the expression difference of genes within the locus.

Results:

In the previous study, we identified a strong pod shattering resistant Ogu restorer line OR88 (Chu et al., 2022) with pod shattering index (SRI) > 0.8. The elite line OR88 with strong shatter resistance and specific aligned layer bridge (LLB) was identified in field and indoor. By genetic mapping, the single LLB gene was located to a 0.688 Mb region on C09, near the Ogura CMS restorer gene Rfo. In order to clone the strong pod shattering resistance gene, we used highly accurate circular consensus sequencing (CCS) reads (HiFi; PacBio) with the HiFiasm assembly tool sequencing two comparable Ogu restorer lines OR88 (resistant line) and OR5 (unresistant line). We got all 2398 genes involved in the 15.7Mb introgression segment of radish into the rapeseed C09 genome. By comparing the transcriptome of the gynoecium development stage, we found 41 significantly different expression genes within the interval. Among the candidate genes, a LOB gene was expected as a key gene for functional verification which could affect the development of lateral organ boundaries.

Conclusions:

Our novelty discovery will contribute an elite Ogu restorer line with strong pod shattering resistance, and we will mine unique resistant gene for the LLB structure. It will help us to a better understanding and application in pod shattering improvement in rapeseed.

References:

Chu W, Liu J, Cheng HT, Li C, Fu L, Wang WX, Wang H, Hao MY, Mei DS, Liu KD, Hu Q. (2022). A typical lignified layer bridge controlled by a single recessive gene is associated with high pod shatter resistance in *Brassica napus L. The Crop Journal*, 10(3), 638-646 Doi: https://doi.org/10.1016/j.cj.2021.09.005.