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A systematic dissection in oilseed rape provides insights into the genetic architecture and molecular mechanism of yield heterosis

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Background:

Heterosis, discovered by Charles Darwin, refers to the superior performance of hybrid F1 relative to their inbred parents and its exploitation contributes tremendously to crop production in modern agriculture. Several hypotheses have been proposed to explain heterosis mainly including dominance, over-dominance (or pseudo-overdominance), and epistasis. However, systematic dissection and verification of these hypotheses are rarely documented and only a few of heterosis genes have been identified.

Objective:

To dissect the genetic and molecular basis of heterosis in oilseed rape, yield heterosis has been systematically characterized at the phenotypic, genetic and molecular levels, by using a representative cross of Zhongshuang11×No.73290.

Methods:

At the phenotypic level, the level of heterosis for 24 yield, component and related traits has been accurately evaluated in multiple years and locations and compared across these traits. At the genetic level, the genetic architecture of heterosis for these traits has been dissected by large-scale mapping of heterotic QTL and construction of trait-QTL network. In addition, dominance hypothesis has been verified by manipulation of two heterotic QTL-NILs. At the molecular level, one heterosis gene has been identified and its regulatory mechanism has been dissected systematically.

Results:

Here comparison of heterosis level across different traits showed that the strong heterosis of composite traits (such as yield) could be attributed to the multiplicative effects of moderate heterosis of component traits, whether at the genome or locus level. Yield heterosis was regulated by a complex trait-QTL network that was characterized by obvious centre-periphery structure, hub QTL, complex up/down-stream and positive/negative feedback relationships. More importantly, we showed that best-parent heterosis on yield could be produced in a cross of two near-isogenic lines by the pyramiding and complementation of two major heterotic QTL showing partial-dominance on yield components. The causal gene (BnaA9.CYP78A9) of QC14 was identified, and its heterotic effect results from the heterozygous status of a CACTA-like transposable element in its upstream regulatory region, which led to partial dominance at expression and auxin levels, thus resulting in non-additive expression of downstream responsive genes involved in cell cycle and proliferation, eventually leading to the heterosis of cell number.

Conclusions:

Taken together, the results at the phenotypic, genetic, and molecular levels were highly consistent, which demonstrated that the pyramiding effect of heterotic QTL and the multiplicative effect of individual component traits could well explain yield heterosis in oilseed rape. These results provide in-depth insights into the genetic architecture and molecular mechanism of yield heterosis.

Reference:

Ye, J., Liang, H., Zhao, X., Li, N., Song, D., Zhan, J., Wang, X., Tu, J., Varshney, R.K., Shi, J. and Wang, H. (2023). A systematic dissection in oilseed rape provides insights into the genetic architecture and molecular mechanism of yield heterosis. *Plant Biotechnol. J.*, https://doi.org/10.1111/pbi.14054.