Life Sciences

# New Progress in Understanding Genetic Basis of Heterosis in Rice

On Sep 8, 2016 (Beijing time), a group of biologists reported online in *Nature* their new progress in understanding the genetic basis of heterosis in rice, an issue that has long confused scientists. This research paper, entitled "Genomic architecture of heterosis for yield traits in rice", has been resulted from a joint research conducted by Prof. HAN Bin's group and Prof. HUANG Xuehui's group from the Institute of Plant Physiology and Ecology (SIPPE), Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences (CAS), in cooperation with Prof. YANG Shihua's group from the China National Rice Research Institute.

Scientists have made great, intensive and continuous efforts to increase in crop breeding to meet the demand of global food security. Exploiting the heterosis phenomenon in hybrid crop breeding is one of the most efficient ways for many crops including rice, maize and sorghum. However, the genetic cause of heterosis in crop has long been a puzzle despite the fact that the heterotic phenomenon has been discovered for more than a century and various genetic models have been suggested to explain it.

This joint work reported large-scale genomic mapping for yield-related traits and evaluation of the heterotic effects by analyzing over 10,000 rice lines produced from 17 elite rice lines. The large data of genomics and phenomics from a well-designed composition of populations made it possible, for the first time, to identify the genetic contributors comprehensively and find out the exact causes of heterosis. The researchers found that modern rice varieties can be classified into three major types, reflecting the major breeding systems. Within each group a few genomic regions and gene alleles from female parents linked to heterosis effects for improved yields were identified, but these loci varied across the three groups. The key heterosis-related genes often controlled several yield-related components simultaneously, serving as the major contributors of heterosis. For the individual yield components, the heterozygous state of the heterosis-related genes generally
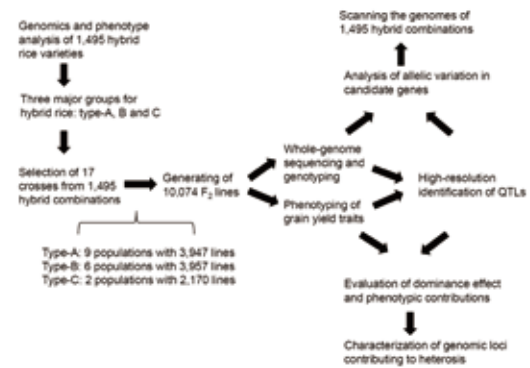
The experimental design and analysis procedure in this study
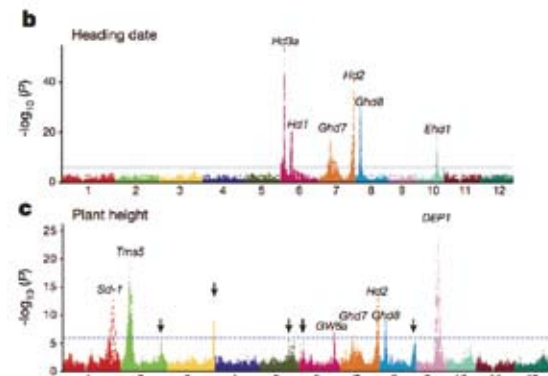
Large-scale sequencing, genotyping and genetic mapping in 10,074 F$_2$ lines. (Images provided by SIPPE)

acted through the way of dominance complementation.

Taking all the components into account, the co-authors revealed, hybrids with yield heterosis resulted from an optimal combination of multiple yield-related components, contributing to better performance of overall yield in crop productions.

These results, informing on the genomic architecture of heterosis for yield traits in rice, might be useful for crop improvement programmes.