Genomic regions associated with yield traits in elite rice lines mapped

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(Phys.org)—A team of researchers with the Chinese Academy of Sciences and the China National Rice Research Institute has successfully mapped the genomic regions associated with yield traits in several elite rice lines as part of a study to determine the genomic architecture of heterosis. In their paper published in the journal *Nature*, the team

describes the laborious process they used and why they believe that their work could lead to finding a universally shared genomic region that contributes to heterosis. James Birchler with the University of Missouri offers an in depth look at the work done by the team in a News & Views piece in the same journal issue.

Scientists have known for some time that when two plant species are bred together, the result is often a plant that is more fertile than either of its two parents—a phenomenon known as heterosis. Plant specialists have taken advantage of this feature to produce ever higher crop yields for a wide variety of crop plants, one of which is rice. Oddly, the genetic reasons for heterosis occurrence has never been found, though researchers have put a lot of effort into understanding it, as they believe it could lead to even higher yields or the introduction of other positive features. In this new effort, the researchers embarked on an ambitious project that they hoped would finally solve the mystery.

The study consisted of collecting rice plant samples that represented 17 elite lines—they subsequently bred them to produce a first generation and then over 10,000 second-generations hybrids. The researchers studied each as they grew and produced rice and cataloged their features. Next, the team performed DNA sequencing on every one of the lines, which allowed them to compare genomic regions. As they did so, they wound up splitting the hybrids into three main groups based on the strategies that had been used to breed them.

The researchers report that they were unable to identify the exact genomic architecture of heterosis, but they were able to isolate and map several genomic regions with the groups that could be associated with heteroic effects on rice grain yields. While this was not the outcome they had been hoping for, the work is still considered groundbreaking, Birchler notes, because it has shed a lot of light on the types of traits that are responsible for the phenomenon.

Abstract

Increasing grain yield is a long-term goal in crop breeding to meet the demand for global food security. Heterosis, when a hybrid shows higher performance for a trait than both parents, offers an important strategy for crop breeding. To examine the genetic basis of heterosis for yield in rice, here we generate, sequence and record the phenotypes of 10,074 F2 lines from 17 representative hybrid rice crosses. We classify modern hybrid rice varieties into three groups, representing different hybrid breeding systems. Although we do not find any heterosis-associated loci shared across all lines, within each group, a small number of genomic loci from female parents explain a large proportion of the yield advantage of hybrids over their male parents. For some of these loci, we find support for partial dominance of heterozygous locus for yield-related traits and better-parent heterosis for overall performance when all of the grain-yield traits are considered together. These results inform on the genomic architecture of heterosis and rice hybrid breeding.