

# Studies shown gene present and absent complementation may contribute to the heterosis of maize

Partly funded by NSFC, a group of researchers in China Agricultural University and BGI in China, together with international collaborators from Iowa State University, University of Minnesota and University of Copenhagen completed studies on a whole genome map of single nucleotide polymorphism, insertion/deletion variation and the gene content variation among elite maize lines in China. The results, published online in *Nature Genetics*, provide a valuable resource for genetic studies and molecular breeding of this important crop.

This research team resequenced a group of six elite commercial maize inbred lines, some of which are the parents from popular heterotic groups. The study obtained 1.26 billion 75-bp paired reads which were aligned to the maize reference genome using SOAP software v2.18, and uncovered 1,272,134 SNPs and 30,178 indel polymorphisms (IDPs), providing a collection of markers with high-density through the genome. 101 chromosomal intervals with low-sequence-diversity were identified in the maize genome, containing a number of candidate genes related with maize improvement during selection.

The team also investigated the situation of presence/absence variations (PAVs) in maize lines by mapping the sequences of Mo17 and other inbred lines to the reference genome of B73. Different numbers of PAVs were identified for each heterotic group. Using SOAP de novo to assemble reads absent in B73 but present in other maize lines, the team found many putative genes missing in the current version of B73 reference genome.

Based on the discoveries that SNPs and IDPs have potential disabling effect on gene function and that different sets of PAVs present in different heterotic groups, the team hypothesized that the complementation effect of presence/absence variations and other deleterious mutations could have contributed on heterosis.

“The maize genome is large and complex while with abundant genetic resources in population. With the development of next generation sequencing technology, it has become feasible to resequence entire large genomes and thereby to carry out genome-wide surveys of genetic variation. The complement of more maize genomics data resource will have great contribution to the maize research community, said Dr. Xu Xun, the project investigator of BGI in China.

“The study will provide additional clues to the molecular basis of heterosis and will be helpful to researchers to identify quantitative trait loci that are important for crop improvement, the team wrote.