

BGI Study Results on Resequencing 50 Accessions of Rice Cast New Light on Molecular Breeding

According to a report in *Nature Biotechnology* (online), supported by the National Natural Science Foundation of China, on December 12, 2011, Shenzhen, China—BGI, the world's largest genomics organization, announced that a study on resequencing 50 accessions of cultivated and wild rice was published online today in *Nature Biotechnology*. The study provides one of the largest genome variation data sets for wild and cultivated rice, which is valuable for breeding and for identifying agronomically important genes in rice. This data also yields new insights for geneticists and biologists to deeply explore the domestication history of cultivated rice.

Rice feeds more than half the world's population, and accounts for over 20 percent of the world's total calorie intake. At various times and places in history, some wild rice species formed particularly close relationships with human populations resulting in a range of biological and genetic changes owing to a process known as domestication, a special artificial selection. This process has played an important role in rice cultivation with divergence of many genes controlling important agronomic traits.

Asian cultivated rice (*Oryza sativa*) is thought to have been domesticated from divergent populations of Asian wild rice, *O. rufipogon* and *O. nivara*, about 10,000 years ago. For decades, geneticists have tried various ways to identify the major causative genes responsible for the significant phenotypic traits changed during the domestication, such as grain size, color, shattering, seed dormancy, among others.

“If we want to clearly understand the genome variation between cultivated and wild rice, it's better to know the comprehensive catalog of genome variation in both cultivated and wild rice,” said Xu Xun, Vice President of Research and Development Department at BGI, and the leading author of the paper. “The high-quality variation data will greatly facilitate the identification of functional variations and be useful for marker-assisted breeding and gene mapping of rice.”

In this study, researchers sequenced 40 cultivated accessions selected from the major groups of Asian cultivated rice and 10 accessions of their wild progenitors. They next investigated genome-wide variation patterns in rice and obtained 6.5 million high-quality single nucleotide polymorphisms (SNPs).

“This is one of the largest high-quality SNP data sets obtained in rice,” said Liu Xin, Senior Bioinformatician of BGI and the co-leading author of this paper. “It could provide molecular markers for designing rice SNP arrays and for breeding to identify important rice genes that could potentially improve the quality and yield of rice.”

Because of the low levels of variation and skewed allele frequency spectra, some favorable alleles associated with important biological features tend to be rare and are difficult to detect. Using these population SNP data, researchers successfully identified thousands of genes with significantly lower diversity in cultivated but not in wild rice, which indicated the candidate regions were selected during domestication. The validity of this approach was further evidenced by the successful identification of the two well-known rice domestication genes, *progl* and *sh4*. In addition, the results also support the view that japonica and indica, two major subspecies of cultivated rice, were independently domesticated, and further suggest japonica was domesticated from the Chinese strain of *O. rufipogon*.

“The millions of SNP data generated in this study not only provide tremendous opportunity to unravel the domestication history of rice, but they also could serve as a valuable source for researchers to rapidly identify agronomically important genes in rice,” said Xu. “We hope that this new data accelerates the global effort to improve the quality and yield of rice in order to better address the challenges of a growing world population and food shortages.”