



ABSTRACT

*“Harvest the fruits of genomics
-to upgrade agriculture with new breeding tools”*

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The global food security is in menace because of the rapidly growing human population, the depletion of agricultural resources as arable land, water, and petroleum-based pesticide and fertilizer, and the climatic changes. The genetic improvement of crops is the most viable approach by which food production can try to keep pace with the anticipated growth of the human population. The efficiency of crop breeding relies on our knowledge on the biology of the ~60 species that uses about 95% of the arable land and a dozen of livestock. The most fundamental biological knowledge of a crop is stored in its genome.

Next generation sequencing (NGS) technologies, such as Illumina GA, SOLiD, and 454, made it feasible and economical acceptable to sequence genomes of all crops. However, as NGS often produces millions of shorter reads in a single run, it also meet computational and algorithmic challenges. BGI constructed a powerful platform mainly based on sequencing-by-synthesis technology, including >30 Illumina GA II, a 10,000-CPU cluster, and a software package, Short Oligonucleotide Analysis Program (SOAP). The genomes of cucumber (350 Mb), Brassica rapa (500Mb), potato (830Mb), duck (2 Gb), and even giant panda (2.3 Gb) have been assembled and analyzed, giving the first set of examples that NGS can be used in de novo sequencing of large plant and animal genomes. Large scale germplasm resequencing was conducted on rice, silkworm, and cucumber, which produced millions of SNPs and structural variations and identified hundreds of genes that likely underwent selection during domestications and breeding.

With the newly established Key Laboratory of Genomics (MOA), BGI, CAAS, and other agricultural research institutions will sequence 100 crops, 100 species of livestock and insects, core collection of every important species, and also perform genome-scan of over 400,000 accessions of various crops are stored in the National Seed Bank. Combined with genetic analysis and robust phenotyping, this huge resource will lead to high-throughput isolation of trait genes. The knowledge of trait genes will give rise to new breeding tools that can be used to deliberately design crops and animals that suit to various environment, agricultural practices, and applications.