

APPLICATION OF NEXT-GENERATION SEQUENCING TECHNOLOGIES IN PLANT GENETICS

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The advent of remarkable technology, next-generation sequencing (NGS) has opened a new horizon in molecular biology. This technology is considered as the second revolution after the introduction of PCR machine. NGS technologies allow direct and cost-effective sequencing of multiple DNA fragments in parallel to produce millions of short sequence reads in an impressive speed and cost-effective manner compared with Sanger sequencing. The result of these studies provides the knowledge for basic research. Additionally, these data could be applied to improve crop yield. At present, different platforms are available in the market including SOLiD/Ion Torrent PGM from Life Sciences, Genome Analyzer/HiSeq 2000/MiSeq from Illumina, and GS FLX Titanium/GS Junior from Roche Company. These technologies are routinely being applied in a variety of aspects, including *de novo* sequencing, mate-pair, whole-genome sequencing, targeted resequencing, transcriptome profiling and epigenetic. To date, the NGS platforms have been used to sequence the genome of cucumber, coca, apple, barely, banana and tomato in combination with Sanger sequencing. Also, wild strawberry, muskmelon, watermelon, chickpea and orange genomes were sequenced using next generation sequencing platforms alone. Whole-genome sequencing provides a reference genome for crop research studies. Resequencing of multiple cultivars and land races has become affordable by NGS and the resulted data could be used for phylogeny studies, single nucleotide polymorphism (SNP) discovery and the study of functional genes. In addition, the NGS technologies have enabled researchers to sequence mRNA (RNA-seq), rRNA, tRNA, and other non-coding RNA from plants in different conditions including biotic and abiotic stresses and developmental stages. The generated data set can be applied for gene discovery, gene functional studies and molecular marker development. RNA-Seq has been used as a powerful and cost-efficient tool for advanced research in many areas. Compared with microarray, RNA-Seq is more efficient in gene expression profiling; because it avoids many limitations of microarray such as, the dependence on prior knowledge of the organism, cross-hybridization and dye based issues. This technology has been used in transcriptome profiling studies for various plants, including maize, rice, soybean and potato. The generated data set provide a baseline for future experiments and create a sequence resource. In epigenetic, large scale chromatin immunoprecipitation (ChIP) assay and DNA methylation analysis are other important applications of next generation sequencing technologies. In spite of the remarkable progress in sequencing technologies, highly repetitive and also heterozygous or polyploid genomes in plants still remain an issue. Although NGS makes genome sequences available, the data analysis and biological explanations are the limitations of this technology.