

Dissection of Genome Using High Throughput for Crop Improvement

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The effects of climate changes in the short and long run coupled with the increasing world population require more efforts in crop productivity and improvement in order to prevent severe hunger and food insecurity worldwide and more specifically in developing countries. Qin, *et al.* (2016) reported that crop improvement is vital issue owing to the pressure of the population. Moreover, abiotic, disease and pest outbreak will be exacerbated and there will be decrease in yields of many crops. Genomic dissection is considered as a determining factor to face with these challenges. The use of recent advances in molecular genetic techniques, including analysis of gene expression, marker mapping, and quantitative trait loci (QTLs) analysis contributes greatly to better understanding the genetic and phenotypic basis of plant stress-tolerance and, in some cases, also lead to the development of crop plant with enhanced tolerance to biotic and abiotic stress. The molecular genetics have been a boost to accelerate crop improvement. The era of genetic markers has been of great importance in terms of increasing the selection of agronomic characters in various plant breeding programs. Edwards and Batley (2010) indicated that the information about DNA sequence facilitates the gene detection and molecular markers associated with various and interesting agronomical characters which is of paramount importance in crop improvement. This has been proven earlier on by Ben Miflin (2000) who demonstrated that genetic improvement is the area to consider for the major breakthroughs in crop improvement. Generally crop genes that confer an important function are used to improve the same agricultural character in related crop plants (Zhao, *et al.* 2014; Zheng, *et al.* 2015). In addition, Edwards and Batley (2010) also pinpoint that the knowledge of the gene underlying a trait permits the transfer of the trait between cultivars and even species using genetic modification. They further stated that the gene conferring the promising trait may be incorporated into a cultivar by using marker-assisted selection (MAS) breeding instead.

The high throughput of next-generation sequencing is a technology capable of sequencing thousands of millions of nucleotides. It also provides opportunities to create new markers which help in the identification of genes of interesting agronomic traits. Edwards and Batley (2010) reported that the identification of all genes in a crop species allow to get the understanding of the mechanism by which interesting traits are governed. The Next generation sequencing systems have been employed also for gene expression through genomic dissection to identify candidate genes for crop improvement. The rapid of candidate genes is now possible through bioinformatics analysis using the information available from reference genome sequences for several crop species (Edwards and Batley, 2010)

The ultra-high throughput sequencing systems namely the Roche GS FLX; the SOLiD system from Applied Biosystems (ABI) (Carlsbad, California, USA); and Solexa Genome Analyzer technology, which is commercialized by Illumina (San Diego, California, USA) and High Throughput Illumina Strand-Specific RNA Sequencing systems have been used. Wang, *et al.* (2011) reported that Illumina Inc. (San Diego,

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CA) offers one of the most extensively used sequencing technologies for transcriptomic analysis. Similarly, it has been reported by many researchers that gene expression profiling using cDNA microarrays and DNA chips or biochips is an adequate method to investigate gene expression under abiotic stresses such as salinity, drought and cold stresses (Kasuga, 1999, Bräutigam and Gowik, 2010, and Dang, *et al.* 2014).

The genome of many crops have been sequenced in some crops viz Rice (Goff, *et al.* 2002), cacao (Scheffler, *et al.* 2009), apple (Velasco, 2009), banana (Hribova, *et al.* 2009), however, genome sequencing in some crops are not yet available such as barley and wheat (Edwards and Batley, 2010), sweetpotato (Isobe, *et al.* 2017).

Thus, the identification of genes and molecular markers eliciting the agronomic characteristics is vital means to quicken the breeding process and lead to improved varieties with improved yield and nutritional values, resistance to abiotic and biotic conditions.

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