Editorial

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With the advent of high-throughput sequencing platforms, such as Illumina's Genome Analyzer, HiSeq, MiSeq and NextSeq, Roche/454's Genome Sequencer FLX, Thermo-Fisher Scientific's SOLiD, Ion Torrent and Ion Proton, PacBio's Real-Time Sequencer and more recently Oxford Nanopore's MinION, it has become feasible to sequence entire genomes and transcriptomes at an exponential pace. This has huge implications in plant breeding and genetics. The reviews presented in this volume summarize recent developments in next-generation sequencing (NGS) and bioinformatics tools and their application in understanding and improving agronomic traits.

Next-generation sequencing (NGS) coupled with high-performance computing have revolutionized the field of plant breeding and genetics (Bhadauria and Banniza, 2014; Bhadauria et al., 2016). This volume compiles recent advances in the NGS as well as the application of NGS in understanding and improving agronomics traits such as yield, drought tolerance and disease resistance.

In this volume, the review by Sharma et al. (pp 1-36) outlines the evolution of DNA sequencing techniques and platforms, including the first generation (Sanger's chain-termination method and Maxam-Gilbert's chemical cleavage method), second-generation (Illumina's GA, HiSeq and MiSeq as well as Roche/454's GS FLX), third-generation single molecule real-time sequencing (PacBio's SMRT RS) and the more recent fourth-generation sequencing platform Oxford Nanopore's MinIon. The application of NGS in the genome sequencing and evolution of rice, maize and sorghum (pp 37-50) and orchids (pp 51-70) shed light on the challenges in the post-NGS era, such as genome assembly and annotation. Gomez-Casati and colleagues (pp 89-104) describe the application of omics (gene expression and regulation as well as quantitative proteomics approaches, such as iTRAQ) in fruit development and ripening, and plant disease resistance. Bioinformatics resources for plant genomics are detailed and discussed in two reviews (pp 71-104). The NGS-based genotyping-by-sequencing approaches are useful to map polymorphism in experimental populations and germplasm, which then can be used to track genomic regions controlling quantitative traits, such as fusarium head blight and stripe rust resistance in wheat (pp 105-108) and rice (pp 109-126). Sequencing of the transcriptome from infected plant tissues (dual RNA-seq) can provide molecular insight into host defence and pathogen virulence during incompatible and compatible interactions, thereby facilitating in designing crops with improved resistance (pp 127-142). In addition to genome and transcriptome sequencing, the NGS can also be used in sequencing of small RNA (20-24 nucleotides; pp 143-170) and transcription factor binding sites (ChIP-seq; 171-180) in genomes. Structural variations, such as abnormal chromosome number, chromosomal rearrangement, copy number variation, presence or absence variation, mobile element insertion and deletion and homologous exchange play key role in phenotypic diversity of agronomic traits, such as biotic and abiotic stress tolerance. Zhang and colleagues looked into the application of NGS in mapping such structural variations (pp 181-194). The final article discusses soil biodiversity (pp 195-198).

References

Bhadauria, V., and Banniza, S. (2014). What lies ahead in post-genomics era: a perspective on genetic improvement of crops for fungal disease resistance? Plant Signal Behav. 9, e28503.

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