

Preface

Feeding the world's population has become one of the major challenges in recent decades. Crop improvement requirements as well as food resource management are being tackled to overcome the limits of plant-based production. On the other hand, scientific and technological advances let us characterise plant resources and develop more productive crops. Genome sequencing approaches are now being applied to diverse plant species for several purposes, including marker development, phylogenomics, gene function analyses, and evolutionary and structural genomics studies.

In this special issue, which is the first thematic volume of the Turkish Journal of Agriculture & Forestry, one review and 13 research articles cover the topics of genomics and transcriptomics. Türkteş et al. review the second-generation sequencing (sometimes also referred to as “next-generation sequencing”) of plant genomes with a detailed approach section and a comparative plant-genome sequencing outputs section. In this review, genome sequencing technologies and analysis tools are also explained, including the latest plant-genome studies. Temel et al. develop a linkage map for lentil by utilising transcriptome-based single nucleotide polymorphism (SNP) discoveries. They detect 50,960 putative SNPs in two lentil genotypes. In another article in this special issue, Suresh et al. utilise RNA-Seq analyses for large-scale identification of microsatellites or simple-sequence repeat (SSR)/SNP markers in a faba bean symbiotic nitrogen-fixation crop. Rajesh et al. identify expressed resistance gene analogue (RGA) sequences from coconut RNA-Seq data. They phylogenetically analyse sequences of 243 RGAs, which cluster into six distinct classes, further measuring the expression of selected transcripts. Genomic tools are used to identify genetic resources by Qureshi et al. in maize to control *Fusarium* stalk rot. In this study, variations among lines are detected using SSRs. Simović et al. use statistical analyses of morphological characteristics to find a mosaic of genetic variations in different Norway maple ecotypes. Likewise, Mishra et al. find significant morphological and biochemical variance in different strawberry genotypes, highlighting their potential for breeding.

We trust that this special issue on crop genomics and transcriptomics will promote further advancement of research in the area of plant genomics.

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