

EDITORIAL

Insights in Plant-Microbe Interaction through Genomics Approach (Part IV)

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The last part of the thematic issue consists of two review and two research articles. Some of the articles, with important insights into genomics approaches to understand plant-microbe interactions, have already been published in the first three parts of the issue [1-3]. The issue starts with the article by Pagano *et al.*, which presented a review on the genomic tools that are being used for the enhancement in the production of soybean [4]. Going through this article would lead researchers to know in detail about the soybean production, in general, as well as the cutting-edge approaches such as gene-editing technology that has the potential to reveal more insight into the right modification of soil microbes, rhizobial genomes, and soybean microbiome. The authors extensively discussed the Nitrogen fixation, genome research, microbial associations, rhizobial inoculants and microbial genomic research in soybean.

Baruah and co-authors presented an article to provide understanding about the role of promoters of genes, which are known to be pathogen-sensitive during plant defense mechanisms [5]. This article goes deep into the conceptual analysis of key motifs and promoter elements in the genes obtained from the TransGene promoter database. The titles and abstracts of the published articles for the genes were collected, and text mining was performed by the authors to provide frequent keywords in the form of the word cloud. With the help of Plant CARE, the promoter elements were identified and presented in the form of a chord diagram containing connections between the promoters and respective elements. The article suggests various important and frequently connected factors that influence the pathogen-induced promoters in the plant defense. WRKY and GT-1 are the most significant transcription factors found along with cis-acting elements ABRE, MYC and MYB and also the elements such as W-box, Gbox, WUN motif, and TC-rich repeats.

Ratnaparkhe and co-authors performed a whole-genome sequencing and comparative analysis to provide better insight into the development of rust-resistant soybean cultivars [6]. The study aimed at the identification of genomic variations between the rust-resistant line EC241780 and susceptible cultivar JS-335. A whole-genome pair-end re-sequencing using Illumina HiSeq2500 platform was carried out on the genomic DNA of soybean genotype EC241780 leaf samples. Following the sequencing, the read was mapped; SNPs, as well as InDels, were identified and annotated. The authors also performed the haplotype analysis using *Glycine max* accessions and identified a rust resistance locus. The authors briefly discussed the Rpp (Resistance to *P. pachyrhizi*) genes that play a vital role in plant-microbe interaction. Comparative analysis identified three genes encoding for NBS-LRR family protein, which are Glyma18G51715, Glyma18G51741 and Glyma18G51765 and the most prominent candidate for Rpp1 locus.

Kangabam and co-authors did a metagenome analysis on soil samples collected during post-monsoon and winter season with the objective to present a seasonal profile of the Loktak Lake that had undergone different anthropogenic impacts [7]. The authors provided a well-description of the sampling sites with information such as ecosystems and keystone taxa in the form of a table. The MISEQ library was prepared, followed by sequencing, cluster generation and analysis of metagenomic data. Summary of measured environmental variables such as pH, temperature, salinity, *etc.* has been provided with their mean and standard deviations across the post-monsoon and winter season. Co-occurrence microbial interaction sub-networks have also been constructed to find that the network density and heterogeneity alter across the season. It also indicated that temperature among all the variables was the maximum number of Operational Taxonomic Units connections both in the case of monsoon and winter data. Bringing all the variables together provided a great understanding of the seasonal profile of microbial communities across different land uses patterns in Loktak Lake, which will help in biodiversity markers for improving the aquatic ecosystem.

AUTHORS' CONTRIBUTIONS

All authors JS, AV, HBS, contributed in writing this Editorial article for the research topic “Insights in plant-microbe interaction through genomics approach (Part IV)”.

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