

EDITORIAL

Insights in Plant-Microbe Interaction through Genomics Approach (Part 1)

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For the last few decades, the constant striving to understand the mechanism of plant-microbe interaction has increased manifold, even though a lot of inaccessible information is yet to unfold. Ingress into such covered information can be a notable aid for mankind, particularly by helping plants fight against pathogens and other stresses. Crops are continuously exposed to many stresses, which may be abiotic or/and biotic. At times the interactivity of microbes with plants assists plants to stand against various environmental stresses; on the contrary, sometimes they act as stresses for plants. Plants are always at higher risks as most of the microbes interact with the plants to feed or to survive [1, 2]. There is an extensive range of beneficial microorganisms which play vital role in plant growth, development and survival [3]. These are most often known as agriculturally important microbes which not only help plants to get proper nutrients but also regulate the plant and other microbe interactions. Knowing the nature of microbe and its connection with particular plants be useful to control diseases in plants. There are several mechanisms for plant-microbe interactions which vary from plant to plant and microbe to microbe as well [4]. The interaction can materialize in any part of the plants, may it be underground or above the soil. It can also be both endophytic and epiphytic, depending on the microbes. In addition to these two major participants, it also relies on the environment neighboring the area where the interaction occurs.

Zooming into the high definition resolution of the genomic arrangements with the help of emerging and advanced techniques in the post-genomics era has been of primary focus. Comparative genomics studies have successfully revealed the genetic make-up of both plants and microbes in the past using powerful molecular approaches. In the last few decades, the advancement in the sequencing, as well as data analysis techniques have provided the most efficient way of studying the genetic variation, differential expression, gene regulatory networks, and many more [5]. Microarray technologies created a new world for the scientists which has been almost replaced by the Next generation sequencing (NGS) and before the NGS has been used to even its full capabilities, we have single cell genomics in the picture which promises to provide the genomic resolution up to the single cell level. Technologies such as CRISPR-Cas-9 (Clustered regularly interspaced short palindromic repeats- CRISPR-associated protein 9) have been a boon to the world of research, especially in the field of plant pathology. Keeping in mind all these points, the current issue is aiming at shining light into the current scenario as well as past researches that brought so much useful information to improve crop protection.

The review article by Agrahari *et al.* [6] describes the importance of studying plant-microbe interaction and its use to crop improvement. The article discusses the post-genomic era omics approaches such as next-generation sequencing (NGS) in association with marker assisted selection, cloning and recombination techniques, Genome-wide association studies (GWAS) and also CRISPR-Cas-9 technology. A brief overview of various models such as zig-zag model, invasion model, spatial immunity model, *etc.* has been provided to understand plant defense responses against various pathogens. To fight against various abiotic and biotic stress conditions, deployment plant-associated microbial population has the potential to help up to a great extent. Last but not the least, the article describes the beneficial microbes and their applications in crop improvement. Another article by Anupriya *et al.* [7] describes the genomics and molecular aspects of white rust disease along with how the white rust resistance can be transferred in the susceptible varieties of oilseed Mustard. This review broadly defines the nucleotide binding leucine rich repeat receptor (NLR) signaling and its application to exhibit oomycetes resistance in plants with special reference to effector molecules, *Albugo candida* secretome. It also describes various efficient approaches such as NLR repertoire enrichment, r-avr gene interaction, RNAi, and CRISPR-Cas technologies, which are being used to understand the pathogen-resistance mechanism. Shukla *et al.*, [8] in their article, have reviewed biotechnological approaches for bioremediation of xenobiotics. They specifically discuss potential extremophiles, basically microorganisms living in extreme conditions. This review provides information on the previous studies regarding the extremophiles (microbes) and the pollutants which can be degraded. The use of extremozymes such as amylases, proteases, *etc.* are highly stable and can act as good novel catalysts. There are reports of more than 3,000 such enzymes which have been isolated from various extremophiles and have immense importance industrial uses.

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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”.

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