

Application of Next Generation Sequencing Technologies in Revealing Plant-Microbe Interactions

Ramesh Kothari^{1*}, Ravindra Pal Singh¹ and Vishal Kothari²

¹Department of Biosciences, Saurashtra University, Rajkot-360005, Gujarat, India

²Department of Biotechnology, Junagadh Agricultural University, Junagadh, Gujarat, India

Abstract

Advancements in genomic (DNA and RNA) sequencing have dramatically accelerated research in the domain of host microbiome during current decade. Extensive application of next generation sequencing (NGS) technologies has identified the core microbiome of the human gut that is being used for improving health. Microbial communities of plant host have been recognized as a potential biological factor essential for shaping, acclimation, growth and health of the host. Nevertheless, we are far away to understand precise composition of the microbial communities and their function in the plant host. The purpose of this article is to highlight specific area of microbial - plant association that can be deeply analysed by using NGS and spectral technologies.

Keywords: Plant bacterial interaction; Next generation sequencing; Secondary genome; Quorum sensing; Associated bacteria

Main Text

Microbial communities associated with different parts of the plant make rhizospheric, phyllospheric and endospheric specific microbiome [1]. These communities influence health and development of plant by building of beneficial, neutral or detrimental association [2]. Majority of microbial communities do not interact with the host while some of them exert specific role in the plant health as well as its development [3,4]. For example, they are known to fix environmental nitrogen and produce various plant growth promoting substances. It has also been observed that associated bacterial communities employ quorum sensing (QS) system to communicate with plant host [5,6]. Homologous receptor of QS-LuxR system has been identified in several plant hosts that are responded to bacterial QS signaling molecule and subsequently modulating development of root and root structures [7]. The specific questions to understand host microbiome and their interaction are “what are the precise compositions of microbial communities in/on the host?” and “what are the core functional microbial communities of the host at given environmental conditions?” Addressing these questions is necessary to support plant growth and development in order to fulfil future consumption demand.

DNA (metagenomic), RNA (metatranscriptomics) and amino acid (metaproteomics) sequencing of metagenomic samples of the whole microbial communities of the host along with spectral analysis of their metabolites will be a prudent way to address above questions [8]. A study used the metagenomic study of rhizospheric samples from green house grow *Lotus japonicus* and determined that the plant had showed better growth in the presence of phytic acid and their rhizospheric microbiome consists of some gene clusters relating to phytic acid utilization, such as alkaline phosphatase and citrate synthase [9]. Another study has found that the rhizospheric microbial community is selected on the basis of functional cores genes related to the metabolism of nitrogen, iron, phosphorus and potassium [10]. These genes are potential benefits of host, such as growth promotion and nutrition. Identification of potential genes has also been used to modulating plant health by transferring active beneficial microbiomes by mixing disease suppressive soils with disease conducive soils or alleviated drought stress in *Arabidopsis thaliana* [11,12]. A comparative study of metagenomics and metaproteomics study of rhizosphere and phyllosphere of rice plant revealed the complexity of microbial communities and certain genes are differentially expressed

in both microbiomes [13]. Metatranscriptomics and metabolomics studies of the plant microbiome are powerful tools that can provide comprehensive picture of the active core microbiome of the host at given condition. Metatranscriptomics analysis of the rhizospheric microbiome of the *Arabidopsis* revealed several transcripts that were differentially expressed at different stages of the host. For example, disease suppression genes (streptomycin synthesis) were considerably induced at bolting and flowering stages [14].

Microbial metabolomics is the study of the set of metabolites present within microbial communities. By monitoring the global outcome of interactions of the complete set of metabolites of host microbial communities and their host can likely provide a more perfect picture of the actual physiological state of the microbiome. The dynamic metabolic flux of microbial communities and plant rhizosphere is extensively studied in context to rhizobial interaction [15]. Moreover, chemical interaction through bacterial QS (AHL) signaling molecule is recently highlighted due to their assessment in plant growth, development, and performance (Hartmann et al. 2014). LuxR solo receptors have been identified in both associated bacterial communities and plant host [16,17]. Bacterial LuxR solos are generally studied in pathogenic bacteria and rhizobia. In case of pathogenic bacteria, LuxR solos respond to plant produced unknown low-molecular weight compounds that induce pathogenicity related genes whereas in case of rhizobia, plant produced compounds modulate symbiosis island transfer and nodulation [15]. It is just beginning to understand interkingdom chemical communication of bacterial communities and their host and much information of this interaction remain unclear so far. Thus, the studying bacterial metabolites will pay the way to divulge this chemical communication with the perspective of controlling the disease and enhancing the growth of the host.

Definitely, the NGS technologies has revalorized our understanding

***Corresponding author:** Ramesh Kothari, Department of Biosciences, Saurashtra University, Rajkot-360005, Gujarat, India, Tel: 912812586419; E-mail: kothari1971@gmail.com

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of microbial communities through provision of high throughput sequencing at low cost, however, function of host microbiome is remain unclear. Thus, obtaining integrated information of microbial communities via different meta-omics technologies should be future goal to draw high-resolution regulatory maps of the activities and physiological potential of host microbiome. Such approach will lead to explain differentially expressed genes (stress, defense or climate change) of microbially mediated host process at given environmental condition. This information will be helpful for future perspective as a modulating microbiome for minimizing diseases incidence and enhancing gross plant productivity.

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