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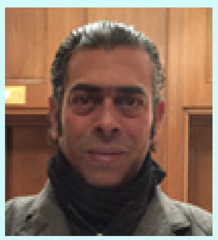
Metagenomics of Microbial Communities Associated with the Rhizosphere of the Saudi Desert Medicinal Plants



Mohammed N Baeshen
University of Jeddah
Saudi Arabia

COLUMN ARTICLE

Abstract

Some wild desert medicinal plants were prescribed in folkloric medicine for treating various disorders. Recent studies indicate that these plants have medicinal properties. Current ongoing studies subjected these plants to detailed genomic and metabolomic studies along with its associated microflora. Therefore, it's very important to study the rhizosphere microbial communities associated with these plants. The rhizosphere microbial communities must be subjected to deep, high-throughput sequencing (metagenomic sequencing), followed by high-level computational analysis of the sequenced data sets. This may result to constitute valuable resources that could be screened for enzymes of environmental and industrial importance. Identifying novel organisms and /or novel genes would be exploited biotechnologically for medicinal uses, biodegradation, biomining, biofuel production, etc. This work will make available large genomics data sets to the global research community.

INTRODUCTION

Plant associated microbial communities have already shown tremendous potential for fixing nitrogen, enhancing the plant growth, and helping plants tolerate abiotic stress [1,2]. It is now well know that all healthy land plants harbour a multitude of microbes in their roots and internal tissues. These can affect the plant growth and development (e.g. the stimulation of root development), or induce important phenotypes such as drought tolerance [3,4].

Given their established beneficial roles, plant-associated bacteria may also play an important role in helping plants to adopt in a changing or variable environment (acclimatize). More studies are required to investigate the degree of specificity between plant host species and their microbial communities across a variety of environmental conditions.

Metagenomic approaches have recently been employed for comparing microbial communities from different soils [5-8] including soils collected from cold deserts, hot deserts, forests, grasslands, and tundra [9]. These studies fulfilled the expected results and led to the characterization of microbiome composition and functional attributes across the various environments studied. More specifically, the study by Fierer., *et al*. [9] revealed that biotic stress genes are less abundant in the desert soils than in the other soils, which led them to suggest that abiotic conditions, "are more important in shaping the desert microbial communities". They also concluded that metagenomic approaches can be useful in understanding how the microbial diversity and gene functions could vary across terrestrial biomes.

The only studies includes molecular approaches of some plants and its associated community were applied lately in the department of biology at King Abdulaziz Univesity – Saudi Arabia [10-13], and some of these studies that concerns the genomic analysis of these plants would serve

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as an anchor or reference for the present proposal and other future studies, especially when comparing the genomes with the surrounding physical conditions of the environment. Also, studying the metagenomics of the rhizosphere microbiome will give more than our expectations to those who has been studies by means of classical molecular biology which don't target the unculturable microorganisms at the known laboratory conditions.

CONCLUSION

Until today, there are no published studies on the desert plant associated rhizosphere in Saudi Arabia, and researches subjected to develop a better understanding of the phylogenetic diversity of the rhizobacteria associated with these plants, and a better understanding of their genetic and metabolic potential are not available. Therefore, employing metagenomics approaches to the study of the microbial communities associated with medicinal desert plants is expected to help us characterizing these microbial communities in terms of structure and function and identifying important genes in the microorganisms associated to plant communities. These genes can then be used toward the production of valuable new products for industrial, nutritional, and pharmaceutical applications against diseases. Studies can also be conducted to identify the stress-related genes and their upstream regulatory mechanism in these microbial communities that are native in harsh environment of arid and semi-arid regions in Saudi Arabia. This could open new routes for engineering crops to feed the world's exploding population.

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