Endophytic bacteria and fungi communities associated with date palm enhance plant growth and performance under salt stress

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Abstract:
Statement of the problem: Date palms (*Phoenix dactylifera* L.) inhabit harsh desert environments and remain viable even in areas with saline soils and survive long periods with limited water supply. Despite the high tolerance to abiotic stress, its growth was impaired by the inclusion of salt water in the irrigation system due to water scarcity in hyper-arid environments. Research studies on date palm have begun to probe the complex responses to abiotic stresses using genome-wide omics-based technologies and those examining root and soil microbiomes effects on stress tolerance. The purpose of this study is to unravel the bacterial communities according to irrigation sources and the colonization of date palm roots with the mutualistic fungus *Piriformospora indica*, in enhancing plant growth and the preservation of Na+ and K+ ions balanced homeostasis under salinity stress. The transcriptome analysis using RNAseq technology will allow to discover the genes and pathways involved in salinity tolerance.

Methodology and Technology employed: We investigated the effect of irrigation sources (non-saline freshwater vs saline groundwater) on date palm root-associated bacterial communities using 16S rDNA metabarcoding. The colonization of date palm roots with the mutualistic fungus *Piriformospora indica*, was performed to identify candidate genes and pathways involved in salinity tolerance. At a large scale, we used RNAseq technology to identify the transcriptome of date palms subjected to salinity stress and colonized with *P. indica*.

Findings: The multivariate analyses displayed strong structuring of bacterial communities according to irrigation sources, and both soil EC and irrigation water pH were the major factors affecting bacterial communities. The genera Bacillus, Micromonospora and Mycobacterium were dominated while saline water irrigation, whereas contrasting pattern was observed for Rhizobium, Streptomyces and Acidibacter. The colonization of date palm with the mutualistic fungus *Piriformospora indica*, enhanced the levels of antioxidant enzymes and altered the expression levels of essential Na+ and K+ ion channels in roots like HKT1;5 and SOS1 genes. The transcriptome analysis using RNAseq technology displayed significant differentially expressed genes (DEGs) involved in cellular processes, metabolic processes, response to salt stress, cellular and catalytic activity, metabolism, sugar metabolism, oxidoreductase activity, signal transduction mechanisms, and posttranslational modification pathways.

Conclusion & Significance: Our study provides a complete understanding of DEGs involved in salinity stress at the transcriptome level in date palms colonized with *P. indica*. Endophytes can be exploited as an essential plant bio-stimulant for improving date palm production for economic sustainability in saline-degraded or saline irrigated lands.

Biography:

Khaled Masmoudi is a Professor and Assistant Dean for Research & Graduate Studies at the College of agriculture & Veterinary Medicine, UAEU. His research focuses on studying the molecular mechanisms underlying plant responses to harsh environments such as salinity, drought and extreme temperatures. He uses a combination of genetic, biochemical, genomic and transcriptomic approaches to analyze various levels of gene regulation and to understand stress signaling pathways and stress tolerance. Plant biotechnology is the driver of innovative solutions in sustainable agriculture and can contribute to the major challenge of food security, environmental sustainability and climate change. He published more than 120 scientific papers in peer-reviewed journals and many book chapters.

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