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Investigating Two Date Palm Cultivars Microbial Pathways

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Abstract: The cultivars of Sukkari and Khalas are known for their economic value in Saudi Arabia. However, the rhizosphere microbial community associated with the two cultivars has never been analyzed. This study aims to identify the possible microbial community and associated environment enzymatic activity with the two dates palm cultivars' rhizosphere and analyze it using metagenomics. The results showed a distinct microbial community in each of the two cultivars. Khalas cultivar rhizosphere was associated with 86% of the sequences identified as bacteria compared to 62% of bacterial sequence associated with Sukkari cultivar rhizosphere. On the other hand, 25% of the Sukkari rhizosphere was associated with eukaryotes sequences. The functional Enzyme analysis identified common environmental metabolic pathways between date palm cultivars related to carbon fixation, carbohydrates, and amino acids. The environmental metabolic pathways related to degradation were only identified in the Sukkari cultivar rhizosphere. These findings might indicate distinguished microorganisms associated with each date palm cultivar rhizosphere and might be exploited to enhance soil health and agricultural practices.

Keywords: metagenomics, pathways, interaction, microorganisms.

研究兩種棗椰樹品種的微生物途徑

摘要：蘇卡里和卡拉斯的品種在沙特阿拉伯以其經濟價值而聞名。然而，從未分析過與這兩個品種相關的根際微生物群落。本研究旨在確定兩個棗椰樹品種的根際可能存在的微生物群落和相關的環境酶活性，並使用宏基因組學對其進行分析。結果表明，這兩個品種中的每一個都有不同的微生物群落。卡拉斯栽培品種根際與 86% 的細菌序列相關，而與蘇卡里栽培品種根際相關的細菌序列為 62%。另一方面，25% 的蘇卡里根際與真核生物序列有關。功能酶分析確定了與碳固定、碳水化合物、氨基酸相關的棗椰樹品種之間常見的環境代謝途徑。與降解相關的環境代謝途徑僅在蘇卡里 栽培品種根際中發現。這些發現可能表明與每個棗椰樹品種根際相關的顯著微生物，並可能被用來增強土壤健康和農業實踐。

关键词：宏基因组学，途徑，相互作用，微生物。

1. Introduction

In a previous study, we found that Plant Growth-Promoting Rhizobacteria (PGPR) regulated phytobeneficial traits through reciprocal protein stimulation via microbe plant interactions, both during and post-colonization [1]. The study [2] showed that plants could discriminate among bacterial strains, laying the foundation for detailed mechanistic explorations of plant-microbiota interactions. In the current study, we hypothesis that microbial communities in the date palm cultivar rhizosphere are species-specific and agricultural practices might contribute to soil health in conjunction with the diversification of plants species. In addition, we explore the rhizosphere metagenomics in two date palm cultivars to study environmental pathways.

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2. Materials and Methods

Soil rhizosphere samples were collected from two date palm cultivars, Khalas and Sukkari, and metagenomics analysis was performed as described in [3]. Enzyme Commission (EC) codes are used to check associated genes and proteins in the website of the KEGG GENES Database (https://www.genome.jp/kegg/annotation/enzyme.html) The EC generates microbial metabolism environment pathways using the iPath3.0 web application [4].

3. Results and Discussion

The taxonomic assignment of reconstructed metagenome-assembled genomes using the metaWRAP pipeline showed domination of environmental bacteria of the taxonomic representation Bacteroidetes, Planctomycetes, Actinobacteria, Chloroflexi, Proteobacteria, and Eukaryotes for both dates palm cultivars Sukkari and Khalas (Fig. 1).

The primary pathways found in both date palm cultivars (Sukkari and Khalas) were Carbon fixation pathways, Pyruvate metabolism, Pentose phosphate pathway, Glyoxylate Phenylalanine, and Purine metabolism and Nitrogen metabolism. The results showed that the most significant pathways were carbohydrates and energy metabolisms since these pathways are essential to microbial community and soil health. These pathways consisted of Carbon fixation pathways, Glycolysis pathway, which converts glucose into pyruvate and generates small amounts of ATP (energy), then incorporated into Pyruvate metabolism. In parallel to glycolysis, the other energy source is the Pentose phosphate pathway used by bacteria to generate NADPH and sugar. In addition, environmental pathways of Glyoxylate and dicarboxylate metabolism are also involved in the biosynthesis of carbohydrates from fatty acids (Fig. 2).

On the other hand, methane and sulfur metabolisms, Benzoate, and Xylene degradation were the secondary pathways found in the current study were higher in Sukkari than Khalas, which approve specificity reported in a previous study [5]. Anaerobic bacteria degrade carbon in methanogens which produce methane as a metabolic by-product [6]. Whereas Sulfur is reduced or oxidized by bacteria from proteins, sulfate esters of polysaccharides, steroids, phenols, and sulfur-containing coenzymes metabolize and become available to plants. In addition, two bacterial pathways were involved in Benzoate and Xylene degradation, which is known to facilitate other nutrients such as carbon and acetyl CoA to bacteria. In addition, nitrogen metabolism is associated with Ascomycota, which represents 10% of soil sample taxonomy. Since Ascomycota contribute significantly to soil phosphate transporter, nitrogen immobilization and degradation of complex sugars and polysaccharide synthesis [7]. The abundance of eukaryotic microorganisms in the Sukkari rhizosphere might explain why the environmental degradation pathways were higher in Sukkari cultivar than Khalas. Thus indicate specificity in microbial rhizosphere among date palm cultivars. Other factors might contribute to the microbial diversity associated with agricultural practices, such as irrigation type or fertilization.

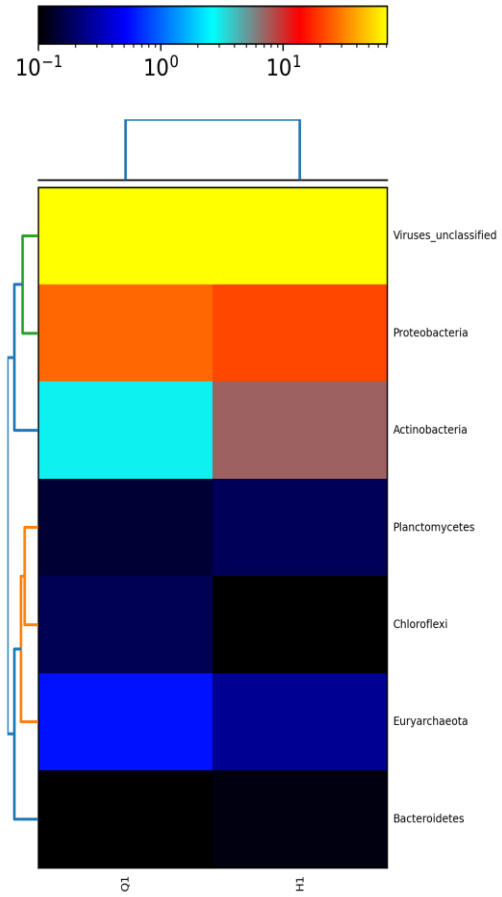

Fig. 1 Two dates palm cultivars' Sukkari and Khalas rhizosphere metagenomics results with distinct differences in microbial community abundance. Taxonomic assignment of reconstructed metagenome assembled genomes used the metaWRAP

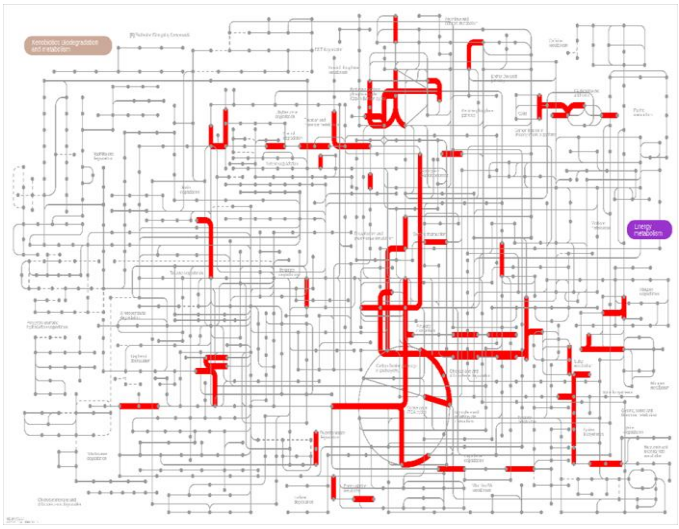

Fig. 2 Common microbial metabolism environmental pathways for both cultivars Khalas and Sukkari based on Enzyme Commission represented by red using iPath3.0 web-application

4. Conclusion

The metagenomics profile of Sukkari and Khalas date palm cultivars showed similar species in the rhizosphere microbial community regarding bacterial but different abundance.

The rhizosphere microbial community was higher in bacteria for both the cultivars and exceeded 60% of the microbial community. The rhizosphere microbial community in Sukkari date palm showed 20% fewer bacteria compared to Khalas cultivar. Thus, explain the rich eukaryotes in the Sukkari rhizosphere microbial community (21% Streptophyta, 4% Ciliopora, and 5% Archaea) compared to Khalas cultivar.

The functional Enzyme analysis identified common environmental metabolic pathways between date palm cultivars related to Carbon fixation, carbohydrates, amino acids, and different environmental metabolic pathways in the Sukkari cultivar rhizosphere related to degradation. These findings might indicate that the distinguished microorganisms for each cultivar rhizosphere are species-specific or might indicate different agricultural practices that contributed to the various microbial communities.

Studying date palm metagenomics sheds light on how farming practices and soil quality influence the microbial community. These results can be used further to identify soil-plant interactions specific to species and enhance soil health with microbial communities related to agricultural and environmental sustainability.

5. Limitations and Further Study

The limitation of the current study is that we do not know whether the climate and soil type might influence or contribute to microbial communities more than date palm cultivars.

Future research will consider climate, soil type, agricultural practices, and plant species to eliminate any possible interference with the study results.

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