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Investigation of Microbial Community Structure and Diversity in the Rhizosphere of Date Palm (*Phoenix Dactylifera* L.), Sukkari Cultivar

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Abstract: The rhizosphere microbial community of a plant plays a pivotal role in mediating plant and soil health. This study was conducted to unravel the rhizosphere microbial structure and community of Sukkari date palm trees. The soil collected from the rhizosphere was subjected to metagenomic analysis. The results revealed that most of the sequences (62%) were identified as bacteria: 48% were unknown bacteria, 5% were Actinobacteria, and 9% were Proteobacteria. Microorganisms belonging to eukaryotes were 25% of the microbial community, represented by 21% Streptophyta and 4% Ciliopora and 5% of the sequences were Archaea. These analyses were followed by functional enzyme analysis, which identified microbial metabolism in diverse environments related to nine carbohydrate and energy pathways; seven pathways were associated with degradation, and nine metabolic pathways were associated with amino acid metabolism. The comparison of community analysis with our previous study provided distinct differences even in the same plants with various cultivars.

Keywords: microorganism, bacteria, metabolites, Sukkari, DNA, rhizosphere, interaction, Phoenix dactylifera.

苏卡里品种枣椰树（凤蝶大号.）根际微生物群落结构和多样性调查

摘要：植物的根际微生物群落在调节植物和土壤健康方面发挥着关键作用。本研究旨在揭示完全地海枣树的根际微生物结构和群落。从根际收集的土壤进行宏基因组分析。结果显示，大部分序列（62%）被鉴定为细菌：48%为未知细菌，5%为放线菌，9%为变形菌。属于真核生物的微生物占微生物群落的 25%，以 21%的链霉菌和 4%的纤毛菌为代表，5%的序列是古生菌。这些分析之后是功能酶分析，该分析确定了与九种碳水化合物和能量途径相关的不同环境中的微生物代谢；7 条途径与降解有关，9 条代谢途径与氨基酸代谢有关。即使在具有不同品种的相同植物中，群落分析与我们之前的研究的比较也提供了明显的差异。

关键词：微生物，细菌，代谢物，完全地，脱氧核糖核酸，根际，相互作用，凤蝶。

1. Introduction

Date palm (*Phoenix dactylifera* L.) is an ancient crop cultivated for its fruit since 5000 years ago in the Middle East, North Africa, and Arabian Peninsula [1]. Saudi Arabia ranks second in the world, contributing to 25% of global date production with a total cultivable area of 172000 hectares [1]. Among the regions of Saudi Arabia, Al-Qassim is regarded as one of the most productive agricultural areas with extensive agricultural farming. Date palm trees and fruits are known to have great economic value in Saudi Arabia. The distinct quality and texture of date palm fruits in the Al-Qassim province, as compared with similar cultivars from other provinces, positively impact its market value. Numerous studies have been attempted on date palms regarding their microbial communities and their interaction with biochemical and physiological attributes [3, 4, 5]. In recent years, there has been a

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substantial increase in research into the role of soil microbial communities or metacommunities in agricultural systems. Similarly, microbiome investigations have shown that microbial communities that reside within the soil have a significant impact on plant growth and production and serve as a resource for mitigating desertification and relieving drought.

The microbial communities associated with the root system are shaped by various biotic and abiotic factors, which include soil type, geographical location, agronomic practices, plant–community diversity, and plant cultivars [6, 7]. The soil under a conventional ecosystem is distinguished by frequent crop turnover and fosters increased levels of microbial diversity. Conversely, desert oases hold low soil phylogenetic and functional microflora [8]. The rhizosphere of plants that are well-adapted to the local environment is the best source of native microbial isolates [9]. Thus, interpreting microbial genes and the gene products of rhizospheres is essential for revealing the soil metaphenome. The genome-enabled predictions and metabolomics of soil give an insight into the environmental significance of the soil microbiome and enable the development of innovative approaches to optimizing soil-carbon cycling, managing nutrient transport, and sustaining crop production [10].

In our previous study, we investigated soil samples from the rhizosphere of the Khalas date palm trees at the Al-Ahsa oasis in Saudi Arabia [11]. The metagenomics analysis showed that microbial enzymatic activities are related to carbon fixation and the metabolism of carbohydrates, amino acids, and sulfur. In the current study, we used a soil-metagenomics approach to explore the micro-organisms associated with the rhizosphere of another cultivar of the date palm called Sukkari from the Al-Qassim oasis. The results were compared for enzymatic activities from both microbial communities to explore possibilities of mitigating desertification using specific enzymatic or microbial inoculation. Previous studies have focused primarily on the use of 16S rRNA gene-amplicon sequencing for analyzing soil microbial communities. In the current study, metagenomics identified possible soil microbial communities that can be used in climate change remediation strategies and combating desertification and drought.

2. Material and methods

2.1. Study Site

The Al-Qassim region is in an arid zone characterized by low rainfall, extreme temperatures, and barren, salt-affected soils. However, agricultural activities in Al-Qassim depend on groundwater and the use of chemical fertilizers to enhance soil fertility and crop productivity. Farmers use techniques to increase the economic value of some areas of Saudi Arabia more than others. Al-Qassim, the area of this study, is in central Saudi Arabia, approximately 400 km northwest of Riyadh, the capital. The Al-Qassim region encompasses an area of 65,000 sq. km and lies approximately 600–750 m above sea level, with gliding from west to east in general. The weather in Al-Qassim is a typical desert climate characterized by cold and rainy winters, hot summers, and low humidity (around 20%) [12].

2.2. Sample Collection

Samples were collected from soil adhering to date palm roots (Sukkari cultivar) at seven different sites in Al-Qassim province. The collected soil samples were pooled for DNA extraction and preceded for further analysis.

2.3. DNA Extraction, Metagenomics Library Preparation, and Sequencing

Soil samples were subjected to microbial DNA extraction using Soil Kit Qiagen DNeasy PowerMax. Extracted DNA was digested, and adaptors were attached in a single step, using the tagmentase enzyme included in the Nextera DNA Flex library preparation kit (Illumina). The sequencing library was prepared using the Nextera DNA Flex library preparation kit (Illumina), strictly following the manufacturer's instructions. Furthermore, the library was dual-indexed to allow for post-sequencing demultiplexing. The pool was sequenced in a fraction of an Illumina NovaSeq6000 PE150 lane to obtain ten gigabases of raw data.

2.4. Quality Control (QC) and Pre-Processing of Sequencing Data

The MetaWRAP pipeline [13] was used for the bioinformatic analysis, including QC, taxonomy assignment, abundance estimation, and functional annotation. Raw metagenomic shotgun sequencing files consisted of forward (R1) and reverse (R2) reads, sorted by library and their quality scores. The indices and sequencing primers were trimmed during the demultiplexing step.

2.5. Taxonomic Profile Exploration and Assignment

An analysis was conducted to explore the taxonomic profile of the whole dataset; we applied the novel assembly-free approach of CCMetagen [14] based on mapping the reads directly to a reference database. The assembly was inputted to map against the NCBI-Nucleotide database (nr/nt) using the KMA tool [15], and alignment was performed without similarity reduction. This tool includes an extra mapping step, wherein each mapped sequence was scored with the ConClave sorting scheme algorithm to reach the best score. Then, CCMetagen processed the results from the alignment to generate a Krona interactive pie chart [16].

2.6. Metagenomic Assembly

DNA sequence reads with high quality were filtered and assembled using the MetaWRAP pipeline by joining them into larger contigs and assigning them to different bins associated with draft genomes. Metagenomes were assembled using MEGAHIT software [17] and implemented in the metaWRAP-Assembly module using default parameters. During the assembly, the shorter contigs (< 1000 bp) were discarded. QUAST software [18] was employed to evaluate the assembled contigs for samples. The resulting assemblies were binned using the metaWRAP-Binning module using three different softwares: metaBAT2, MaxBin2, and CONCOCT [19–21]. To consolidate and produce the highest-quality bin, the metaWRAP-Bin_refinement module was utilized to choose the best version of each bin, based on completion (> 70%) and contamination (< 10%) values [22]. The metaWRAP-Bin_refinement module used a hybrid approach that took the three bin sets obtained during the initial binning step to produce an improved binning set. Then CheckM software [22] was run on the improved bin set to generate completion and contamination rank plots, which were used to evaluate the success of the binning refinement process in both samples (Fig. 3 and 4). Additionally, the metaWRAP-Blobology module was used to visualize the results of the binning refinement in each sample. This module plotted the GC content vs. the abundance of all the contigs across the metagenomic sample, including phylogenetic information [23]. The taxonomy of each contig was estimated using MegaBLAST [24].

Furthermore, we ran the metaWRAP-Quant bins module to estimate the abundance of each bin in each metagenomic sample. This module used Salmon software [25] to index the metagenomic assembly and align the reads from each sample back to the assembly. The abundance table was generated using the length-weighted average of the bin's contig abundances. We used the metaWRAP-Reassemble_bins module and reassembled the reads with metaSPAdes [26]. For each bin, three sets of reads were used: reads mapping perfectly (strict mapping), reads mapping with less than three mismatches (permissive mapping), and reads from the original bin. After reassembly, we used the software CheckM to evaluate its success.

3. Results

3.1. Quality Control and Pre-Processing of Sequencing Data

Using the metaWRAP-QC was accomplished with 100% reads. The brief details of the reads are furnished in Table 1. The data was then subjected to assembly statistics based on contigs of size ≥ 1000 bp unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs) (Table 2).

Table 1 Quality control and pre-processing of sequencing data showed a total of 100% reads from paired-end sequencing (i.e., forward (R1) and reverse (R2) reads)

% reads that passed filters	Number of reads after filtering	Number of reads before filtering
100%	37,751,837	37,758,313

Table 2 Assembly statistics based on contigs of size ≥ 1000 bp unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs)

Assembly	Sample
# contigs (≥ 0 bp)	84811
# contigs (≥ 1000 bp)	84810
# contigs (≥ 5000 bp)	3668
# contigs (≥ 10000 bp)	809
# contigs (≥ 25000 bp)	79
# contigs (≥ 50000 bp)	12
Total length (≥ 0 bp)	1.66E + 08
Total length (≥ 1000 bp)	1.66E + 08
Total length (≥ 5000 bp)	32330261
Total length (≥ 10000 bp)	12952359
Total length (≥ 25000 bp)	2973332
Total length (≥ 50000 bp)	777412
# contigs	84811
Largest contig	93021
Total length	1.66E + 08
GC (%)	63.86
N50	1953
N75	1314
L50	21654
L75	48128
# N's per 100 kbp	0

3.2. Taxonomic Profile Exploration and Assignment

The analysis was conducted to explore the taxonomic profile of the whole dataset. The results revealed that 62% of the sequences belonged to bacteria (Fig. 1). Subsequently, we used the metaWRAP-Classify_bins module to assign taxonomy to the reassembled bins. We estimated the taxonomy of each bin for each sample using MegaBLAST to align against the NCBI_nt as the reference database (Table 3). Functional annotation was performed using the metaWRAP-annotate_bins module and module PROKKA [27] to conduct the functional annotation and translation of genes in each bin. The Swiss-Prot database from UniProt was used for taxonomic division: bacteria identification [28, 29].

3.3. Metagenomic Assembly and Binning

The abundance table was computed based on marker genes and the fraction of the dataset mapped against the reference database's marker genes. Microbial reads belonging to taxa with no available reference data are reported in the table as unclassified. Table 3 represents each taxonomic unit in each sample (Fig. 1). Additionally, the metaWRAP-Blobology module was used to visualize the results of the binning refinement in each sample. This module plotted the GC content vs. the abundance of all the contigs across the metagenomic sample, including phylogenetic information [23]. The taxonomy of each contig was estimated using MegaBLAST [24] and the NCBI_nt

database (Fig. 2).

Table 3 Bin taxonomy assigned using Mega-BLAST for the identified soil microorganisms

Genomic bins	Q1
bin.5.orig.fa	Bacteria
bin.4.orig.fa	Bacteria
bin.2.orig.fa	Bacteria
bin.1.orig.fa	Bacteria; Proteobacteria
bin.6.orig.fa	Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales; Flavobacteriaceae
bin.3.orig.fa	Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis

3.4. Taxonomic Profile Exploration

The taxonomy of each contig was estimated using MegaBLAST [16]. Fig. 1 shows a taxonomic analysis of the rhizosphere soil in which 62% of the sample sequences were assigned to bacteria, 48% were unknown, 5% were Actinobacteria, and 9% were Proteobacteria. Eukaryotes account for 25% of the taxonomy—represented by 21% Streptophyta and 4% Ciliopora—and 5% Archaea.

Fig. 1 A pie chart representing the taxonomy of each contig, estimated using MegaBLAST [23] and the NCBI_nt database. The taxonomic representation showed that 62% of the sample sequences were assigned to bacteria: 48% unknown bacteria, 5% Actinobacteria, and 9% Proteobacteria. Eukaryotes were 25% of the sequences, represented by 21% Streptophyta and 4% Ciliopora; Archaea were 5% of the sequences

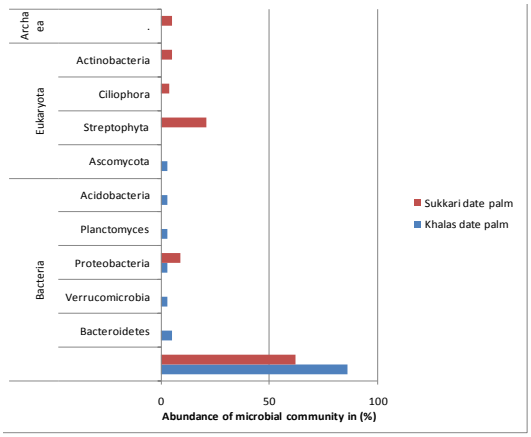

Fig. 2 Comparison of relative abundances of microbial community between Sukkari and Khalas date palm rhizosphere soil

3.5. Enzyme Commission Enzyme Codes (EC), Pathways, and Functional Annotation

The analysis resulted in 44 enzyme codes associated with 95 metabolites. The Sma3sv2 program produced functional annotations with the most probable gene name, the most probable description, and the putative Enzyme Commission enzyme codes (EC). The iPath3.0 web application [30] was used for visualization and analysis of metabolic pathways from the EC numbers (EC) to show functional annotations with putative Enzyme Commission codes associated with microbial metabolism in diverse environment pathways (Fig. 3). Further details of the list and the correlation between Enzyme Commission codes (EC), PubMed, GenBank, NCBI Protein, and KEGG GENES are presented in Appendix, Table A1.

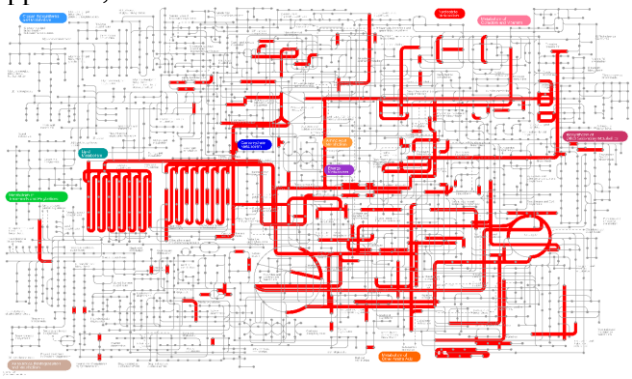

Fig. 3 Microbial metabolism in diverse environment pathways for Commission enzyme codes (EC), shown in red, using the iPath3.0 web application [30]; the lines allow us to navigate and find reactions involved in these metabolic processes on the pathway map

3.6. Marker Genes Approach

To explore the taxonomic profile of the other organisms that were potentially present in the soil samples (i.e., non-bacterial microorganisms), MetaPhlAn 3.0 [30] was used to generate the microbial community profile of samples. It takes metagenomic raw reads as input and maps them against a reference database comprising clade-specific marker sequences of bacteria, archaea, eukaryotes, and viruses. Consequently, only a small fraction of the dataset is mapped against the marker genes reference database. The results of this analysis include an estimation of the fraction of the metagenome, which consists of unknown microbes.

We applied bioinformatic pipelines to characterize the metagenomic information of the organisms in the soil samples. Most of the metagenomic reads were identified as bacterial organisms; however, we argue that low and uneven coverage along the metagenomes, together with a lack of information in the available databases, prevented us from obtaining refined bins from the dataset and, consequently, assignments at lower taxonomic levels. Therefore, assembly-free and marker genes-based approaches were included to identify the organisms present in the metagenomic sequencing data, although these did not improve the

taxonomic assignment.

3.7. Functional Annotation

Functional annotations with the most probable gene name, the most probable description, and the putative Enzyme Commission enzyme codes (EC) were used to explore possible pathways, followed by the EC classification scheme for enzymes based on the chemical reactions they catalyze. The iPath3.0 web application [29] was used to visualize and analyze the environmental metabolic pathways from the EC numbers in order to find reactions involved in soil metabolic processes (Table 4).

Table 4 Soil EC functional annotation associated pathways using iPath3.0 web application, associated pathways (extracted from the EC data listed in Appendix, Table A1)

Microbial metabolism in diverse environments
Benzoate degradation
Beta-Alanine metabolism
Chloroalkane and chloroalkene degradation
Chlorocyclohexane and chlorobenzene degradation
Galactose metabolism
Glyoxylate and dicarboxylate metabolism
Lysine degradation
Methane metabolism
Nitrogen metabolism
Phenylalanine metabolism
Purine metabolism
Pyruvate metabolism
Ascorbate and aldarate metabolism
D-Arginine and D-ornithine metabolism
Amino acids metabolism
Aminobenzoate degradation
Arginine and proline metabolism
Bisphenol degradation
Carbohydrate metabolism
Carbon fixation pathways in prokaryotes
Carotenoid biosynthesis
D-Alanine metabolism
Dioxin degradation
Fluorobenzoate degradation
Glycine, serine, and threonine metabolism
Glycolysis/Gluconeogenesis
Glyoxylate and dicarboxylate metabolism
Lipids metabolism
Methane metabolism
Naphthalene degradation
Pentose and glucuronate interconversions
Pentose phosphate pathway
Phenylalanine metabolism
Propanoate metabolism
Sulfur metabolism
Toluene degradation
Xylene degradation

4. Discussion

The Saudi Arabian government aims to develop the agricultural sector despite the challenges in soil quality and the demand for water resources. Among the agricultural regions of Saudi Arabia, Al Qassim Province has a good reputation for producing the Sukkari cultivar of date palm trees. Sukkari is the sweetest date variety and is grown as an irrigation crop whose mature tree can yield up to 1,000 kilograms of fruit per year. Al Qassim is regarded as one of the leading date palm-producing regions in Saudi Arabia, providing an important source of income for the government and farmers.

The rhizosphere of the Sukkari date palms was analyzed using metagenomics. The taxonomic assignment revealed the dominance of environmental bacteria contributing to 62% of the sample sequences, 48% of which were unknown bacteria and 14% belonging to a known community accounting for 5% Actinobacteria and 9% Proteobacteria (specifically class Alphaproteobacteria; order: Sphingomonadales; family: Sphingomonadaceae; genus: Sphingopyxis). Eukaryotes accounted for 25% of the sample, represented by 21% Streptophyta and 4% Ciliophora, and archaea accounted for 5%, as shown in Fig. 1. [33] demonstrated that date palm recruits Gammaproteobacteria and Alphaproteobacteria invariably to the edaphic and geographical location. Similarly, our study recruited Alphaproteobacteria, which is abundant at the phylum level and would thus serve as a source of nitrogen for other microorganisms [33]. Sphingomonas was found in the rhizosphere of different plant species, such as kiwifruit (*Actinidia deliciosa*), and was proposed to be used as a bacterial biofertilizer contributing to plant growth [30, 34]. The high abundance of Sphingomonas in the rhizosphere of Sukkari can be related to its efficiency as a plant growth-promoting rhizobacterium. Additionally, Streptophyta fungi are known to have symbiotic relationships with plants and can increase certain plant growth hormones, notably indole-3-acetic acid, which has been shown to exhibit increased protection against plant pathogens, increased growth hormones, and greater nutrient uptake [34, 36]. This indicates that the Sukkari rhizosphere colonizes plant growth-promoting microbes.

The phylum Actinobacteria is Gram-positive, with a high GC content and a remarkable range of morphologies [36]. In their natural environment, Actinobacteria can exhibit specific interactions, such as specialized metabolites, and can facilitate interactions between different microbial species [38, 39]. Actinobacteria are also found in close association with various eukaryotic hosts, such as plants. In a symbiotic relationship, the introduction of plant stress hormones to the soil can activate antibiotic production by Actinobacteria, which can protect plants against phytopathogens. [4] demonstrated the phylogenetic affiliation of several Gram-negative bacteria, along with 26% of the Actinobacteria in the date palm rhizosphere. In analogy, our study also evinced 5% of Actinobacteria. These could be responsible for the changes in the metabolic profile of root exudates due to their antibiotic production. These molecules play an important role in shaping the rhizosphere microbiome and inhibiting opportunistic pathogens, thus protecting the host [40]. [41] utilized Actinobacteria to enhance

soil fertility and date palm yield, suggesting their usage by the host, thereby eliminating external inoculant application.

Of the Proteobacteria, 3% were represented by the Flavobacteriaceae class from the phylum of Bacteroidetes, which is a major phylum of Gram-negative bacteria. Members of the Flavobacteriaceae family are found in a wide variety of marine, freshwater, and soil habitats, and some are associated with plants [42]. The order Sphingomonadales, which contains the families Erythrobacteraceae and Sphingomonadaceae, is a relatively less studied phylogenetic branch within the class Alphaproteobacteria, an extraordinarily diverse and ancient group of bacteria [43]. Sphingomonadales bacteria have come a long way after being recognized as a novel genus [44], a novel family [45], and a novel order [46] in terms of the characterizations of genetic relationships and evolution.

Proteobacteria are a phylum of Gram-negative bacteria that are very common in soil environments and are related to a wide range of functions involved in carbon, nitrogen, and sulfur cycling [47], nitrogen fixation [48], and the utilization of macromolecules such as polysaccharides and protein. In the current study, we identified the *Sphingopyxis* genus in the soil sample. *Sphingopyxis* is known to produce ectoine, polyhydroxyalkanoates, and carotenoid secondary metabolites, and to possess biodegradative capabilities for various environmental contaminants.

Archaea belong to the least well-known major group of soil-inhabiting microbes; they exist independently or cohabitate with other organisms. Although archaea are widely distributed in common environments, most of them are found in soil and resist cultivation in laboratories. Using molecular methods enhances the ability to explore archaea's taxonomic and metabolic diversity [44–53]. Knowledge of their exact habitats, associations, and genetic potential will enable the identification of the key functions of archaeal soil [54].

The microbial communities of the Sukkari and Khalas date palm varieties were analyzed in the current study. However, bacteria were abundant in both rhizospheres, and there were differences in the compositions of the other phyla, as shown in Fig. 2. Proteobacteria were present in both cultivars but were more abundant in the Sukkari date palms. Further Actinobacteria and archaea were found in Sukkari, which could not be observed in the Khalas rhizosphere. The difference in the eukaryotic community was obvious as eukaryotes are dominated by Streptophyta and Ciliophora in Sukkari and by Ascomycota in Khalas. Ciliophora are diverse; few are pathogenic while others form relationships with bacteria or algae that can help increase the environmental resiliency of the bacteria [50]. This suggests that changes occur in the Ciliophora members to develop an association with bacteria in the rhizosphere. Furthermore, Acidobacteria, Planctomyces, Verrucomicrobia, and Bacteroidetes were noticed in the Khalas date palms.

4.1. Exploring In-Depth Genes, Proteins, and Associated Microbes

As reported in previous studies, bacteria regulate phytobeneficial traits through reciprocal protein stimulation via microbe plant interactions both during and after colonization, which is essential for plants' health sustainability and provides protection against biotic and abiotic stresses [55]. Furthermore, multi-scale functional annotations with the most probable gene names and putative EC were used to visualize the environmental metabolic pathways involved in soil metabolic processes. The Enzyme Commission codes that were used to check associated genes and proteins showed several microbial pathways associated with the rhizosphere of Sukkari trees. The identified metabolic soil pathways are essential to plant health and soil sustainability and are associated with mycorrhizal and ectomycorrhizal fungi. The soil environmental pathways associated with the microbial community in the Sukkari rhizosphere were nine carbohydrate and energy pathways: carbohydrate metabolism, carbon fixation pathways in prokaryotes, glycolysis/gluconeogenesis, glyoxylate and dicarboxylate metabolism, ascorbate and aldarate metabolism, galactose metabolism and glyoxylate and dicarboxylate metabolism, lipid metabolism, carotenoid biosynthesis, and methane metabolism.

The Sukkari rhizosphere revealed a high diversity of bacterial phyla, namely Firmicutes, Bacteroidetes, Actinobacteria, and Cyanobacteria Actinobacteria was not present in the non-rhizosphere soil sample. In addition, seven pathways were associated with dioxin degradation, aminobenzoate degradation, benzoate degradation, bisphenol degradation, fluorobenzoate degradation and chloroalkane, lysine degradation, chloroalkene degradation, and chlorocyclohexane and chlorobenzene degradation. Additionally, nine metabolic pathways were associated with amino acid metabolism: beta-alanine metabolism, glycine, serine, and threonine metabolism; arginine and proline metabolism, nitrogen metabolism, phenylalanine metabolism, purine metabolism, pyruvate metabolism, D-arginine and D-ornithine metabolism, D-alanine metabolism. These identified metabolic soil pathways essential to plant health and soil sustainability and associated with the 14% known bacteria in the sample, which consists of 5% Actinobacteria, 9% Proteobacteria (specifically, Sphingomonadaceae; Genus: Sphingopyxis), with the 25% eukaryotic microorganisms, represented by 21% Streptophyta and 4% Ciliopora, and the 5% Archaea in the sample.

The Proteobacteria in the sample are involved in carbon, nitrogen, and sulfur cycling, nitrogen fixation [47], and utilizing macromolecules such as

polysaccharides and proteins.

Proteobacteria use macromolecules such as polysaccharides and proteins for their metabolism and cycle carbon, nitrogen, and sulfur. However, not much is known about them yet because they are so diverse that studying them through lab analysis is very difficult [56, 57].

Similarly, Archaea contribute to various nitrogen and carbon geochemical cycles [2, 37, 58] and are considered a substantial component of the complex microbiome. Archaeal communities have much more varied and important roles in biogeochemical cycles across different environments than previously thought [35]. However, in the current study, we were unable to identify the species of archaea in the soil sample. We did identify the *Sphingopyxis* genus, which is known to produce ectoine from glycerol, polyhydroxyalkanoates, and carotenoid secondary metabolites, and to possess bio-degradative capabilities for various environmental contaminants. The main chemical composition of the *Sphingopyxis* genus is that it produces sugars such as trehalose and amino acids, for example, Cys, Met, Trp, or His 1–10. In addition to being able to break down proteins into peptides, these sugars can also be used for nutrition. Several studies have examined the composition and diversity of archaeal communities in the rhizosphere, comprising rice and wetland plants and no other plant groups [31, 32]. Our study observes the existence of an archaeal community in the tree rhizosphere.

5. Conclusion

This study provided an overview of the metagenomic profile of *Sukkari* palm trees and its comparison with *Khalas* date palm trees. The revealed results of rhizospheric metagenomic analysis are, however, higher for bacteria in both cultivars. The study provided insight into the presence of several other microbial communities, including actinobacteria, streptophyta, archaea, and cilipora, with marked differences between both cultivars. Additionally, eukaryotic microorganisms associated with the identified metabolic soil pathways comprised 25% of the sample, illustrating the entanglement of soil microbes in a wide array of pathways. The current study also demonstrates the influence of microbial communities on crucial environmental and soil pathways. The rhizosphere of the *Sukkari* date palm cultivar's microbial community contributes either directly or indirectly to the soil metaphenome, which in turn firmly influences agricultural sustainability. Thus, studying the metagenomics of *Sukkari* shed light on how farming practices and soil quality influence microbial communities. These results can be used further to identify soil–plant interactions specific to species and to enhance soil health with microbial communities related to environmental sustainability.

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Appendix

Table A1 The correlation between Enzyme Commission codes (EC), PubMed, GenBank, NCBI Protein, and KEGG Genes

PDB	KEGG Genes	NCBI Protein	GenBank	PubMed	EC
				4052375	E1.5.5.1
				925004	
	[eco:b3469]			9364914	E7.2.2.12
	[eco:b3469]			9405611	
	[eco:b3469]			9830000	
	[ath:AT2G19110]			15670847	
	[ath:AT4G30110]			15475410	
				1955861	E1.5.1.43
	[vch:VC1624]			19196710	
				22025614	
	[eco:b2255]	AAL23678	AY057445	15695810	E2.1.2.13
1YRW	[eco:b2255]			15807526	
2BLL 2BLN	[eco:b2255]			15809294	
1Z73 1Z74 1Z75 1Z7B 1Z7E	[eco:b2255]			15939024	
	[eco:b2255]			17928292	
	[eco:b2255]	AAL23678	AY057445	15695810	E1.1.1.305
1U9J	[eco:b2255]			15491143	
2BLL 2BLN	[eco:b2255]			15809294	
1Z73 1Z74 1Z75 1Z7B 1Z7E	[eco:b2255]			15939024	
	[eco:b2255]			17928292	
				5845847	E1.1.1.120
				5845848	
				5845849	
				4387016	
				13462997	E1.1.1.48
				14251301	
				11752437	E1.13.11.80
2NP9				17507985	
2PG8				18004875	
				14342329	E4.2.1.51
				14323651	
				4887851	
				320001	E1.1.1.1
				13605979	
				14367287	E2.6.1.21
				13263311	
				4953710	
				4710577	
				1158891	
	[ag:AAA22252]	AAA22252	J04460	2914916	
	[ag:AAA68028]	AAA68028	U26732	9696787	
				9485439	
1DAA	[ag:AAA22252]	AAA22252	J04460	7626635	
					E1.3.1.76
1KYQ	[sce:YBR213W]			11980703	
	[ag:ABI49649]	ABI49649	DQ875599	17259310	E3.5.99.11
				5010303	E3.5.1.26

					6061403	
					5778645	
		[pae:PA3286]			22753057	E2.3.1.207
		[ag:BAA21844]	BAA21844	AB001599	9260954	E2.6.1.76
		[hin:HI0949]			9514614	
		[hel:HELO_2589]			9864317	
		[ag:AAK12084]	AAK12084	AF316874	11823218	
		[ag:AAB57634]	AAB57634	U66614	9141677	
		[mtu:Rv1336]			18842002	E2.5.1.113
3DWG	3DWI	[mtu:Rv1336]			18771296	
3DWM						
3DKI		[mtu:Rv1336]			18799456	
3FGP		[mtu:Rv1336]			19101553	
					7040984	E3.2.2.21
					7040983	
					352392	
					7041972	
					8590654	E3.5.1.87
		[sme:SMc01820]	AAT66633	AY646850	16254442	
					11849938	
		[ag:ABC88406]	ABC88406	DQ310789	527937	E4.1.3.32
		[ag:ABC88406]	ABC88406	DQ310789	16894175	
		[eco:b3368]			2407234	E2.1.1.107
1KYQ					11980703	
					6870241	E1.2.1.67
		[hel:HELO_2590]			9864317	E4.2.1.108
		[ag:AAK12085]	AAK12085	AF316874	11823218	
		[ag:AAB57635]	AAB57635	U66614	9141677	
		[hel:HELO_2590]	CBV42474	FN869568	20849449	
		[sce:YOR125C]	AAB36435	S81938	8621692	E1.14.99.60
		[hsa:10229] [mmu:12850]	AAC69451	AF032900	10501970	
			AAC69179	AF053770		
		[eco:b0662]			10802164	
		[pae:PA0655]			11435415	
		[sce:YOR125C]			16624818	
		[ag:CAD48582]	CAD48582	AJ508908	11409545	E4.2.1.149
		[eco:b0036]			11551212	
		[ag:CAD48582]	CAD48582	AJ508908	15731894	
		[ag:BAA31547]	BAA31547	AB010956	9346293	E4.1.2.42
		[ag:BAA31547]	BAA31547	AB010956	9642221	
					10390816	
		[axy:AXYL_00071]	BAA86032	AB026892	10952004	
					12686135	
					4402936	E1.1.1.2
					4393513	
					2914844	E6.2.1.27
					9446680	E7.1.1.2
					20595580	
3M9C	3M9S				20505720	
					22392981	
		[ag:ABI15166]	ABI15166	AF257324	17395717	E1.1.3.45
2IPI					17242508	
		[pam:PANA_4161]			1400305	E1.3.99.31
		[msm:MSMEG_3607]			26560079	E1.1.1.403
					4884138	E3.1.1.1
					4981346	
					5353595	
					13208632	
					5785220	
					6208846	
					5785222	
					13108854	E1.2.1.28
		[vvu:VV1_2124]			16492767	E2.3.2.29
					13986017	E1.1.1.127
					14321384	E3.8.1.3
					5928195	
		[ag:CAA06926]	CAA06926	AJ006231	9721273	E1.2.1.68
					6037552	E2.3.1.31
					4878817	E3.4.11.9
					6749499	
					3627107	

				2139778	
	[ag:BAA13010]	BAA13010	D86080	23893114	E6.3.1.18
				21969545	E1.3.98.6
	[mba:Mbar_A1458]			24669201	
				4291491	E1.1.1.30
				4954074	
				14415394	
4HL6	[eco:b2371]	ABG35152	DQ668372	23935849	E2.8.3.19
	[ag:ABG35152]				
1KYQ	[sce:YBR213W]			11980703	E4.99.1.4
				12195810	
				16748573	E3.5.1.4
				14800883	
				7008792	E2.1.1.63
				7000780	
				2987862	
				2825131	
				2670886	
				2394694	
				1993655	
				2065659	
				10913091	E4.2.2.26
	[sde:Sde_3284]			22281843	
				24795372	
		AHW45238	KJ094505	25335746	
	[ag:ABI15166]	ABI15166	AF257324	528393	E1.3.3.14
	[ag:ABI15166]	ABI15166	AF257324	17395717	
2IPI				17242508	
				13276340	E3.2.1.14
				9791107	
				10760150	
				12039789	
				21633084	
				14245411	E4.1.2.14
				5561473	
				13712218	E1.8.1.8
	[amq:AMETH_4929]			8385013	E1.1.99.36
				9485460	
				10784035	
				14690248	
				12827287	
				1261545	E1.14.13.22
				11551214	
	[ag:AAY29689]	AAY29689	AY935522	17636255	E1.14.11.55
	[sco:SCO1867]			18849444	
3EMR	[ag:AAY29689]	AAY29689	AY935522	20498719	
				14089442	E4.1.3.16
				5780845	
				5580656	
				3942759	
				23317005	E1.1.1.385
				13756049	E3.5.1.18
	[eco:b4088 b4086 b4087]			9401019	E7.5.2.8
				5332668	E2.3.1.30
				5550822	
	[ag:CAP12609]	CAP12609	AM900040	11376004	E2.1.1.307
	[ppu:PP_0405]			23831760	E2.7.1.221
				4349113	E1.14.13.16
				4313	
				26237670	E4.1.99.23
	[elm:ELI_4215	AKV89410	KT347435	26246619	
	ELI_4216]	AKV89411	KT347436		
	[mta:Moth_1723	AKV89416			
	Moth_1722]	AKV89417			
				13061511	E1.2.1.10
				7458347	
	[ag:CAA43226]	CAA43226	X60835	8419288	
	[bxe:Bxe_C1188]			19476337	
	[ttj:TTHB247]			22316175	
				6597561	E3.4.16.4
				3888533	

	[ag:AAD50979]	AAD50979	AF170343	10613872	E1.8.4.10
	[sme:SMc00092]	AAD55759	AF158023	10464198	
				12072441	
	[alv:Alvin_2447]	AAF27544	AF163765	10939523	
				6539772	E1.13.11.37
1TMX	[ag:AAV71144]	AAV71144	AY822041	15772073	
				16232466	
				2857161	E6.2.1.25
	[ag:BAC20179]	BAC20179	AB075600	12835921	E4.1.3.41
	[eco:b1745]			9696779	E3.5.3.23
1YNF 1YNH 1YNI	[eco:b1745]			15703173	
				2865249	
				3534538	
	[pae:PA0899]	AAC46013	AF011922	9393691	
				5777325	E3.5.1.28
				809432	
				803507	
				6126517	
				13712439	E2.6.1.18
				5762452	
	[bxe:Bxe_C1188]			19476337	E1.2.1.87
	[bxe:Bxe_C1188]			21838275	
	[ttj:TTHB247]			22316175	
				5309907	E4.1.1.61
	[ag:AAN39377	AAN39377	AF548005	15458418	E1.14.13.208
	AAN39376]	AAN39376	AF548005		
	[ag:AAN39377	AAN39377	AF548005	12399500	
	AAN39376]	AAN39376	AF548005		
		AAK00600	AF220510	11222587	
		AAK00599			
				20452977	
				5938934	E3.4.11.2
				931983	
				873921	
				357150	
				6105876	
				13428783	E3.2.2.4
	[sav:SAV2564]			15850982	E1.14.99.44
	[sao:SAOUHSC_02881]	AAX46185	AY841893	15933032	
	[eco:b2762]			7588765	E1.8.4.8
	[bja:blr0467]	AAA26192	M60874	1850420	E7.6.2.5
		CAA54967	X78037	7862087	
				9889977	
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	[eco:b0677]			4861885	E3.5.1.25
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