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Chrysophyllum albidum DETERIORATION ENTAILS DECLINE IN *Pseudomonas* AND INCREASE IN *Acetobacter* ABUNDANCE

***Ogbuji, N. G., Ataga, A. E., Ukwu, I. A. and Nwosu, U. C.**

Department of Plant Science and Biotechnology, University of Port Harcourt, Port Harcourt, Rivers State, Nigeria.
Corresponding Author's Email: nkechi.ogbuji@uniport.edu.ng
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Abstract

Microorganisms that inhabit fruits can affect the quality of fruits during storage. Some of these organisms are beneficial while others are deleterious (pathogenic). This paper analyzed African star apple (*Chrysophyllum albidum* G. Don-Holl) microbiota to detect the bacterial and fungal community structure using high-throughput sequencing (HTS) technology. Healthy and diseased fruits of *C. albidum* were obtained from Choba market in Port Harcourt, Rivers State, Nigeria. Bacterial and fungal DNA were extracted from the samples and subjected to 16S and 18S rRNA sequencing respectively. Metagenomic analyses of bacterial and fungal strains from the samples revealed total operational taxonomical units (OTUs) as 341 and 4366 respectively. Among the bacteria, the phylum Proteobacteria was dominant while all identified fungi belong to the phylum Ascomycota. There was a significant reduction in the abundance of *Pseudomonas* in the diseased sample compared to the healthy sample. Conversely, relative abundance of *Acetobacter* increased in the diseased sample compared to the healthy sample. The fungal genera, *Acidomyces*, *Geosmithia* and *Magnaporthe* were also obtained. Additionally, the bacterial genera, *Candidatus* Portiera, *Blautia*, *Brevibacterium*, *Tetragenococcus* and *Acinetobacter* which were present in the healthy fruits were not obtained from the diseased sample. These findings can help predict microbial community structural dynamics involved in the spoilage of African star apple and thus how the spoilage can be prevented or controlled.

Keywords: African star apple, Bacteria, *Chrysophyllum albidum*, Fungi, Metagenomic analysis

Introduction

Chrysophyllum albidum G. Don-Holl, commonly called Africa star apple, is a forest food tree species that bears large berries. It is a nutritional and medicinal plant with up to 800 species which belongs to the order Ericales (Ehiagbonare *et al.*, 2008) and family Sapotaceae (Ganglo, 2023). The fruit tree is widely distributed in Africa. In Nigeria, it is distributed in all the regions of the country and has local names such as "udara" (Igbo); "agbalumo" (Yoruba) and "khada" (Hausa) (Madubuike and Okereke, 2009; Idowu *et al.*, 2006). The fruit has commercial value as the pulp is consumed by inhabitants of both rural and urban areas in Nigeria. *C. albidium* is cultivated in home gardens, tree-based gardens and in cash crop farms (Onyekwelu *et al.*, 2011). Native fruit trees contribute immensely to food availability and health care during food crisis (famine) as they possess nutritional and medicinal values (Okwu *et al.*, 2018). *C. albidum* is used as an ethno-medicine in many African countries because of its potential pharmacological activities due to the presence of trace elements and phytochemical components (Idaguko and Orabueze, 2023). The seed oil and leaves have been reported to have antibiotic activity against pathogenic *Staphylococcus aureus* (Onuigbo *et al.*, 2023) and enteric bacterial pathogens such as *Escherichia coli*, *Salmonella typhi*, *Klebsiella pneumonia*, *Proteus mirabilis*, *Shigella dysenteriae* and *Proteus vulgaris* (Odewade and Odewade, 2023). A novel nano-heterogeneous biocatalyst has been derived from the seed coat which significantly improved the yield and oxidation stability of biodiesel (Esonye *et al.*, 2023). The leaves, seeds and fruits are potent antimicrobials (George *et al.*, 2018; Akin-Osanaiye *et al.*, 2018) used for the management of diseases such as diarrhea, stomachache, dermatological problems etc. (Idowu *et al.*, 2006). The seed also has potential as an additive to animal feed (Akin-Osanaiye *et al.*, 2018).

Fruit surfaces and internal tissues serve as habitats for several microorganisms. Apart from the pathogenic species implicated in disease epidemiology, the role played by other microorganisms that make up the microbiome of fruits is not fully understood (Sui et al., 2024). Microbial-induced decay of post-harvest fruits, which occurs mostly during storage, leads to significant economic losses (He *et al.*, 2024). Factors such as: fruit type, farming practice, application of agrochemicals, and ripening phase of fruits determine the distribution of microorganisms on fruits (Leff and Fierer 2013; Pinto *et al.*, 2014; He *et al.*, 2024). Microorganisms naturally associated with fruits may be beneficial and induce disease resistance in the host plant (e.g. *Pseudomonas*, *Metschnikowia, Cryptococcus*) or pathogenic to plants leading to great economic losses (e.g. *Erwinia*, *Botrytis*, *Phoma*) (Kumar et al., 2016; Opara and Asuquo, 2016, Abdelfattah *et al.*, 2016). There is limited information on the dynamics of fruit microbiome, fruit immune response and fruit health after harvest (Kithan-Lundquist *et al.*, 2025). The use of conventional microbiological methods that involves culture-dependent techniques to analyze the microbial community of fruits may have hindered the generation of adequate information on the composition of microbial communities and the impact of the organisms that make up these communities. These techniques do not take into cognizance the non-culturable members of the populations. High-Throughput Sequencing (HTS) technologies and bioinformatics analyses provide a better platform that can yield more accurate results. Amplicon sequencing is one of the approaches used to study the soil, phyllosphere and rhizosphere microbiomes through HTS technologies (Buee *et al.*, 2009; Mendes *et al.*, 2013; Abdelfattah *et al.*, 2017). A specific region of the genome, such as a part of the 16S rRNA gene for bacteria (e.g. the V3-V4 region) and of the 18S rRNA gene (e.g. the Internal Transcribed Spacer [ITS] region) for fungi, is amplified by polymerase chain reaction (PCR) and sequenced with high throughput technology to determine the microbial community of a sample.

The health issues of a host plant largely depend on the microbiota associated with it (Berg *et al.*, 2017). Microorganisms on fruit surfaces can be transferred from the soil to the plants by animals, e.g. insects (Stefanini *et al.*, 2015). Ready-to-eat-foods such as fruits are a good source of microbes for human (Leff and Fierer, 2013; Wassermann *et al.*, 2017), with some forming part of the gut microbiota (David *et al.*, 2014; Derrien and van Hylckama Vlieg, 2015). *C. albidium* like other fruits is colonized by various microorganisms, some of which can be pathogenic. The interactions between microorganisms of the phyllosphere can determine the microbial community structure on fruit surfaces and can directly or indirectly affect various evolutionary and ecological processes (Friesen *et al.*, 2011; Alvarez-Perez and Herrera, 2013).

The attention for food safety is greatly increasing especially for ready-to-eat products such as fruits and vegetables used for salads, since these are consumed raw without prior heat treatment (Santos *et al.*, 2023). The microbial diversity of fruits is inadequately explored and information on Africa star apple microbiota is limited hence the need for this study. The objectives of the study are to (1) determine the microbiota associated with Africa star apple fruits, and (2) determine whether the microbiota differ in the healthy and diseased fruits. Both the fungal and bacterial communities of the fruits were assessed.

Materials and Methods

Sampling and Microbial DNA Extraction

Sampling was done in Choba market in Port Harcourt, Rivers State, Nigeria. The coordinates of the market are 4° 53′ N and 6° 54′ E. One hundred and fifty milligrams of healthy and diseased *Chrysophyllum albidum* fruit pulps were separately weighed and transferred into 1.5 ml of nucleic acid buffer in micro-centrifuge tubes. Samples were sent to Laragen Incorporated, USA for analysis. Fungal and bacterial DNA were extracted following Laragen's Validated proprietary bacterial/fungal DNA extraction protocol. Each sample was replicated three times. *C. albidium* fruits are shown in Figure 1.

Sequencing and Bioinformatic Analysis

Amplified products were sequenced on Illumina miseq platform at Laragen Incorporated, California, USA. The sequences were demultiplexed using the standard

Figure 1: ***Chrysophyllum albidium* fruits (George *et al.* 2018)**

Illumina pipeline. Next-generation sequencing Short Reads (*ngsShoRT*) trimmer (Chen *et al.*, 2014) was used to remove low quality reads. Data processing was performed on QIIME v.1.9.0 (Caporaso *et al.*, 2011). Sequences were clustered using UCLUST algorithm (Edgar *et al.*, 2011) at 97% similarity threshold against GREENGENES database (DeSantis *et al.,* 2006) for the 16S reads and UNITE database (Abarenkov *et al.*, 2010) for the 18S reads. Sequences assigned to chloroplasts and mitochondria were expunged. For each OTU, the most abundant sequence was selected as the representative sequence. Alpha diversity indices were constructed to determine the microbial diversity of *C. albidium* samples. Bar charts were built using R software. The datasets generated from *Chrysophyllum albidium* samples were deposited on National Centre for Biotechnology Information Database under Sequence Read Archive (SRA) Bio-project number PRJNA933374.

Results

Diversity and richness of microbial communities

After data analysis, a total of 350,634 high quality sequences (336646 eukaryotic and 13988 prokaryotic sequences) assigned to 4,707 OTUs (for fungi and bacteria) were obtained (Table 1). OTUs were assigned to 7 phyla, 16 classes, 26 orders, 38 families, and 24 genera. Number of OTUs in individual samples ranged from 113 to 3730. SSA2 had the highest number of OTUs for the prokaryotic sequences while the highest number of OTUs was detected in SSA2-18S for the eukaryotic sequences (Table 1).

Composition of *Chrysophyllum albidium* Microbiota at the Phylum and Class Levels

The relative abundance of reads assigned at the phylum level were 98.4%, 99.88%, 99.85% and 100% for samples SSA1, SSA2, SSA1-18S and SSA2-18S, respectively.

Table 1: Total prokaryotic (V3-V4) and eukaryotic (ITS1&2) sequences obtained from *Chrysophyllum albidium* microbiota

Samples	Target region	Raw Sequences	High quality reads	OTUs
SSA1	V3-V4	50542	1560	113
SSA2	V3-V4	20767	12428	228
SSA1-18S	ITS1&2	748825	3373	636
SSA2-18S	ITS1&2	348811	333273	3730

SSA1: Healthy African Star Apple (16S gene)
SSA2: Diseased African Star Apple (16S gene)
SSA1-18S: Healthy African Star Apple (18S gene)
SSA2-18S: Diseased African Star Apple (18S gene)

Proteobacteria dominated the bacterial phyla with 93.15% of assigned reads, followed by Firmicutes (4.46%) and Bacteroidetes (1.08%). The individual relative abundance was 92.56% (SSA1) and 93.74% (SSA2) for Proteobacteria, 1.03% (SSA1) and 1.13% (SSA2) for Bacteroidetes, and 4.36% (SSA1) and 4.56% (SSA2) for Firmicutes (Figure 2). Ascomycota was the only fungal phylum obtained from the samples; accounting for 99.85% of the total reads obtained from SSA1-18S and 100% of the total reads from SSA2-18S. Only 0.15% of all the fungal sequences obtained were unassigned at the phylum level (Figure 2).

Among the bacterial classes,

Gammaproteobacteria highly dominated with 72.99% of the total reads obtained, followed by Alphaproteobacteria (20.09%), Bacilli (2.42%), Clostridia (1.96%) and Bacteroidia (1.03%) while fungal sequences assigned to Dothideomycetes (99.51%) were most abundant (Figure 3).

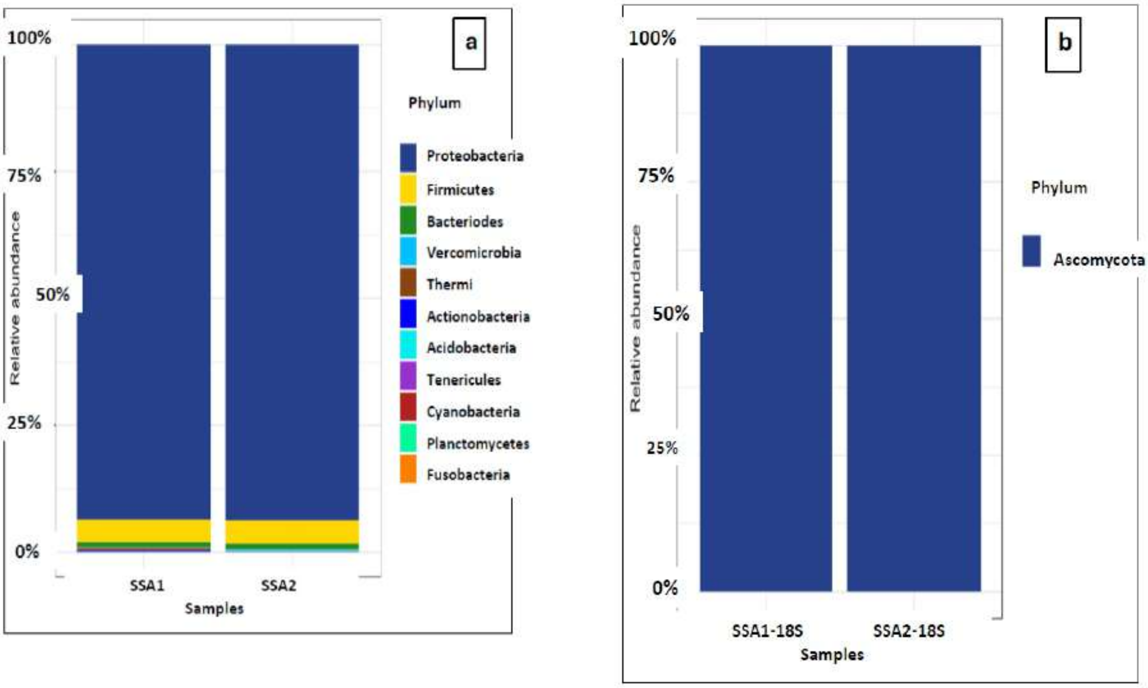

Figure 2: Distribution of bacterial phyla (a) and fungal divisions (b) across the healthy and diseased *Chrysophyllum albidium* fruits

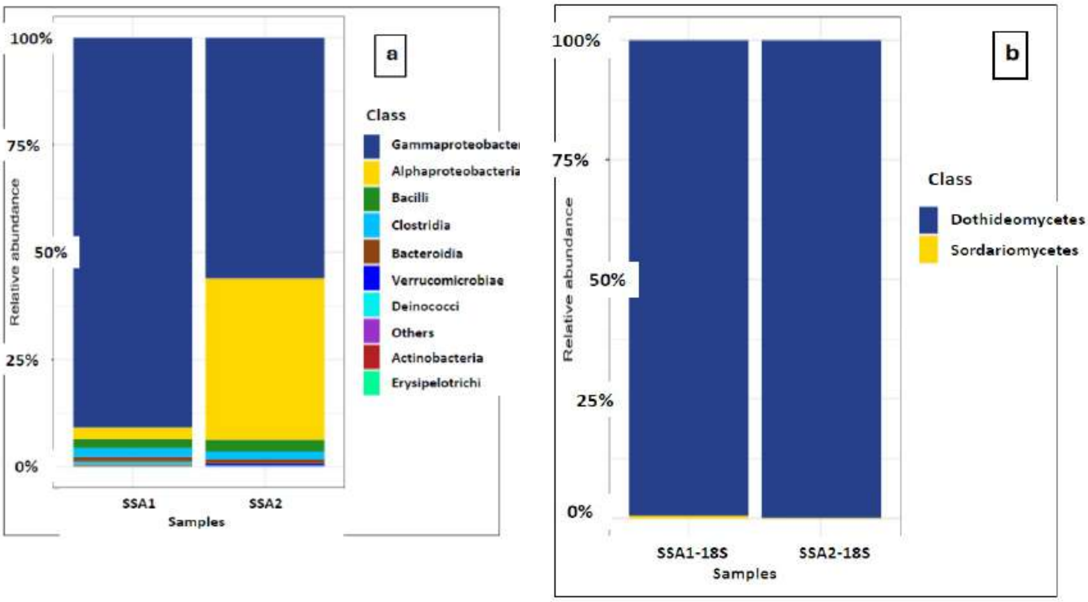

Figure 3: Distribution of bacterial (a) and fungal (b) classes across the healthy and diseased *Chrysophyllum albidium* fruits

Composition of *Chrysophyllum albidium* Microbiota at the Genus Level

The total number of bacterial genera obtained was 21 while the total number of fungal genera was 3. The bacterial genus *Pseudomonas* was predominant and obtained about 75% of the total OTUs while *Acetobacter* (24%), *Gluconobacter* (5%) and *Candidatus* (3%) were also of high abundance. The most abundant bacterial genus obtained from the healthy fruit sample was *Pseudomonas,* representing about 85% of the OTUs followed by *Candidatus* Portiera (Figure 4). For the diseased fruit sample, *Pseudomonas* was the most abundant genus (with relative abundance of approximately 65%, followed by *Acetobacter*.

Less than 1% of the total fungal sequences obtained from the diseased *C. albidium* fruits were classified at the genus level while 51.26% of the total fungal sequences obtained from the healthy fruits were classified at the genus level. The fungal genus *Acidomyces* was most abundant in the diseased (0.07%) and healthy fruit samples (51.08%). Other fungal genera obtained were *Geosmithia* and *Magnaporthe* (Figure 4).

The significant groups of genera obtained were bio-control (*Pantoea, Bacteroides*), phyto-pathogenic (*Pantoea*, *Candidatus* Portiera, *Gluconobacter*), plant growth-promoting bacteria (*Pseudomonas*, *Gluconacetobacter, Enterobacter*, *Brevibacterium*), probiotic (*Blautia*), and human gut and intestinal microbiota (*Bacteroides*, *Akkermansia*, *Blautia*, *Ruminococcus*, *Prevotella*) species.

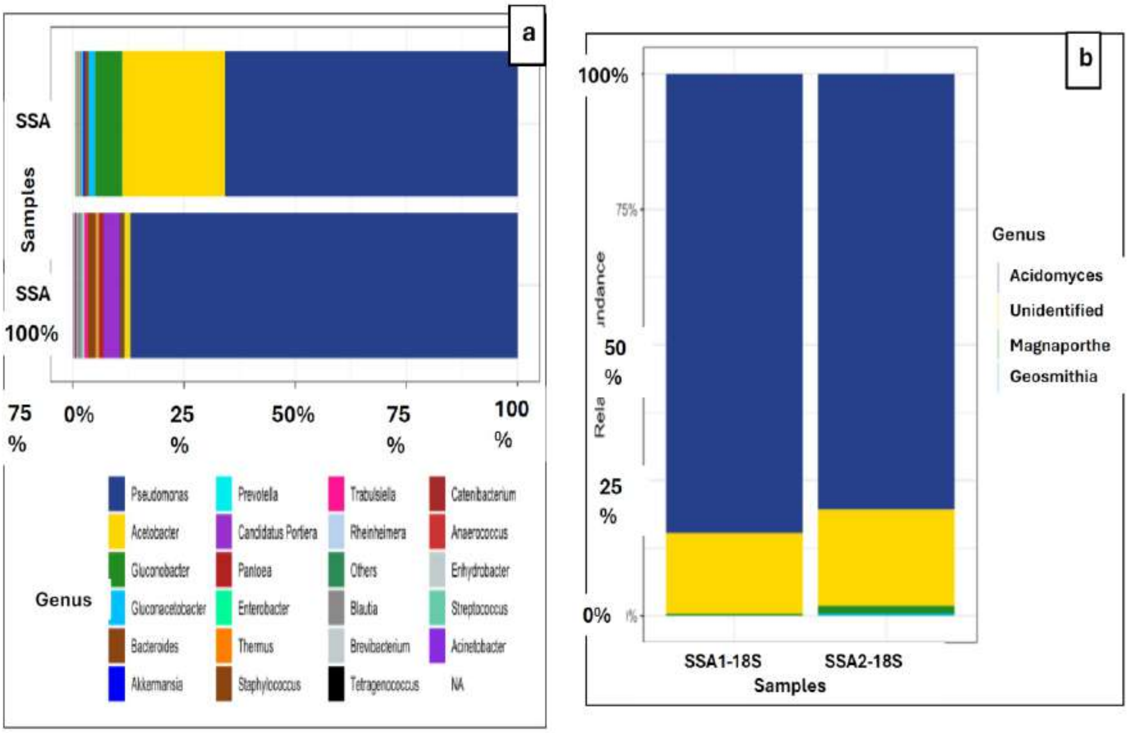

Figure 4: Distribution of bacterial (a) and fungal (b) genera across the healthy and diseased *Chrysophyllum albidium* fruits

Discussion

The microbiota of fruits plays an important role in fruit preservation as the organisms establish interactions with the fruit tissues (Solanki *et al.*, 2024; Kithan-Lundquist *et al.*, 2025). Additionally, they can also play a role in the maturation and ripening of fruits (Buchholz et al., 2018; Ravanbakhsh *et al.*, 2018; Zhang *et al.*, 2021). A better understanding of fruits' microbiota composition and the interactions among the organisms in the communities may give an insight into developing improved methods of fruit storage to reduce the incidence of post-harvest diseases of fruits. This study describes the use of metagenomics to identify and classify Africa star apple microbiota.

A high diversity was observed in the diseased fruit pulp for both fungal and bacterial sequences. Pertaining to the fungal composition of the Africa star apple pulp, members of the phylum *Ascomycota* which were largely represented by the class Dothideomycetes and family Teratosphaeriaceae dominated all the samples (99.93% of the total sequences). The genus *Acidomyces* was predominant in all the samples followed by *Magnaporthe* and *Geosmithia*, which are phyto-pathogenic genera. The relative abundance of the phyto-pathogens (*Geosmitha* and *Magnaporthe*) was higher in the diseased *C. albidium*, pulp. This may be as a result of spoilage activities. Bacterial community of Africa star apple was dominated by the phyla Proteobacteria (93.15%) mostly represented by the class Gammaproteobacteria and family Pseudomonadaceae. Members of Gammaproteobacteria are known to play vital role in the degradation and absorption of organic compounds, sulfide and ammonia (Zhang *et al.,* 2020). Other phyla obtained were Firmicutes and Bacteroidetes. The relative abundance of the three most abundant phyla were higher in the diseased *C. albidium* pulp indicating a higher diversity of bacterial organisms informing spoilage activities. Proteobacteria increased from 92.56% in the healthy pulp to 93.74% in the diseased pulp. Bacteroidetes and Firmicutes increased from 1.03% to 1.13% and 4.36% to 4.56% respectively. A large number of sequences obtained from this study were found to be closely related to the plant growth-promoting bacterial genera *Pseudomonas*, *Acetobacter* and *Gluconobacter*, the parasitic bacterial genus, *Candidatus* Portiera, the phyto-pathogenic fungal genera *Geosmithia* spp. and *Magnaporthe* spp., and the acidophilic fungal genus, *Acidomyces*. There was a significant shift in the relative abundance of the genus *Pseudomonas* in the healthy and diseased *C. albidium* pulp. The relative abundance decreased from 85% (in the healthy pulp) to 65% (in the diseased pulp). Some *Pseudomonas* species are known to enhance plant growth and this decrease may be attributed to decrease in fruit health. There was also a notable shift in the relative abundance of the genus *Acetobacter* in the healthy and diseased *C. albidium* pulp. The relative abundance increased from 2.5% (in the healthy pulp) to 25% (in the diseased pulp). These shifts can inform farmers on fruit spoilage and aid in the development of sustainable control strategies and better fruit storage.

More than three quarters of the bacterial species obtained belong to the genera *Pseudomonas* and *Acetobacter*. *Pseudomonas* spp., as representatives of Dothideomycetes, was present in all samples and was remarkably high in quantity in healthy *C. albidium* fruits. *Pseudomonas*, *Acetobacter* and *Gluconobacter* representing Pseudomonadaceae and Acetobacteraceae dominated the diseased *C. albidium* fruit, followed by *Gluconoacetobacter*, *Bacteroides*, *Akkermansia*, *Prevotella*, *Pantoea* etc. *Pseudomonas* has been found in plant tissues and rhizosphere of plants where they enhance plant growth (Thakur *et al.*, 2023; Aparicio *et al.*, 2025). On the other hand, some *Pseudomonas* species including, *Pseudomonas cerasi, P congelans, P graminis, P syringae* have been isolated from plants where they live as parasites causing diseases and displayed symptoms such as wet spot on trunks of wood, wood browning, leaf spots, etc. (Porotikova *et al.*, 2025). Other genera obtained from the bacterial community of *C. albidium* were: *Acetobacter, Gluconobacter*, *Gluconacetobacter*, *Bacteroides*, *Akkermansia*, *Prevotella*, *Candidatus Portiera*, *Pantoea*, *Enterobacter*, *Staphylococcus*, *Trabulsiella*, *Rheinheimera*, *Blautia*, *Brevibacterium*, *Tetragenococcus*, *Catenibacterium*, *Anaerococcus*, *Streptococcus* and *Acinetobacter*. The genera, *Candidatus* Portiera, *Staphylococcus*, *Blautia*, *Brevibacterium*, *Tetragenococcus*, *Catenibacterium* and *Acinetobacter* were present only in the healthy Africa star apple fruit pulp (SSA1) while *Gluconacetobacter* and *Prevotella* were obtained only from the diseased fruit pulp (SSA2). There was a respective decline in *Pseudomonas* and increase in *Acetobacter*, *Gluconobacter* and *Akkermansia* abundance in the healthy fruit pulp when compared to the diseased fruit pulp. The bacterial community from the diseased fruit was more diverse in comparison to the other samples.

Some species of *Blautia* and *Brevibacterium* have been reported as bio-control and plant-growth promoting organisms. *Bacillus gibsonii* and *Brevibacterium frigoritolerans* were reported to have suppressed Fusarium stalk rot of maize in Pakistan (Batool *et al.*, 2019) and improved growth in both healthy and diseased maize plants. *Blautia, a member of* the *Lachnospiraceae family*, has gained a great attention for its antimicrobial activity (Chakravarthy *et al.*, 2018). Some species of the genus, *Gluconacetobacter* are plant growth-promoting bacteria (Tufail *et al.*, 2021). *G. diazotrophicus* has also been reported to trigger defense responses against the harmful bacterium *Ralstonia pseudosolanacearum*, causal agent of bacterial wilt disease (Srebot *et al.*, 2023). The organism triggers induced systemic resistance (ISR) particularly the salicylic acid (SA) and jasmonic acid/ethylene (JA/Et) signaling pathways. The genus *Acetobacter* consists of some members with plant-growth-promoting ability. A study on determination of acetic acid bacteria diversity in Vietnam gave rise to two bacterial strains, isolates VTH-Ai14^T and VTH-Ai15 which were reported to have plant growth-promoting ability (Vu *et al.*, 2019). *Bacteroides* spp. are Gram-negative obligate anaerobes known to colonize the colon in humans (Zafar and Saier, 2021).

A species of the genus *Candidatus* Portiera, *Candidatus* Portiera *aleyrodidarum* is an obligate parasite vectored by the cotton whitefly, *Bemisia tabaci* (Gennadius) and other whiteflies (Lei *et al.*, 2023). A survey of bacterial communities associated with *B. tabaci* showed the predominance of the phylum, Proteobacteria of which the genus "Candidatus Portiera" was the most predominant obligate endosymbiont (Goretty *et al.*, 2019). Many economically and medically important bacteria cannot be cultured on any known laboratory media may be due to specific metabolic requirements and symbiotic relationships. One of such bacterium is Candidatus Liberibacter asiaticus (CLas) (Carter *et al.*, 2023). Candidatus liberibacter species are Gram-negative bacteria that live as phloem-limited obligate parasites in plants, and are associated with several plant diseases. These bacteria are transmitted by insects called psyllids, or jumping plant lice, which feed on plant phloem sap (Oraby *et al.*, 2025). CLas causes devastating losses in citrus production and it is transmitted by the vector, psyllid (ACP, *Diaphorina citri*). There are no resistant cultivars or any effective treatment for citrus plants infected by CLas. Studies on the pathogenicity and control of CLas on plants has been hampered by lack of pure cultures. Available information on the bacterium was mostly generated from *in-vivo* studies performed on infected plants and this is resource and time demanding.

Pantoea belonging to the family Enterobacteriaceae consists of species of Gram-negative bacteria that cause destructive diseases in rice plants (He *et al.*, 2024; Andriani *et al.*, 2025), thereby leading to devastating economic losses of rice production globally. Most important rice diseases such as bacterial leaf blight, grain discoloration, inhibition of seed germination and stem necrosis have all been reported to be caused by species of the genus *Pantoea* (Azizi *et al.*, 2020). *Pantoea ananatis* is a Gram-negative, motile, facultative anaerobe that causes diseases in several forest trees and economically important agricultural crops. *P. ananatis* has been recorded on both monocots and dicots. Symptoms include chlorosis, panicle blight, lesions on leaves, leaf streak, die-back, leaf blotches, leaf and fruit spots, bulb and stalk rot (Alhusays *et al.*, 2024; Bruno *et al.*, 2025). *P. ananatis* can be used as a biological control agent. The species has been used as a biocontrol agent against *Erwinia amylovora*, the causal agent of fire blight (Lee *et al.*, 2024).

Enterobacter spp. are plant growth-promoting rhizobacteria. Microorganisms colonize the rhizosphere of plants and this leads to changes in plant growth and development. *Enterobacter* spp. are soil bacteria that enhance the development of plant roots and protect plants against pathogenic infections (Fasusi *et al.*, 2021; Kumar *et al.*, 2022). Colonization and biofilm formation by these bacterial genera holds a potential for the development of bio-control agents and bio-fertilizers that may help the host plants in fighting diseases. *Enterobacter cloacae* has also been reported as a pathogenic organism on *Capsicum annuum* L. (chili pepper) seedlings in Chi-huahua, Mexico where it affected up to 4% of the seedlings under greenhouses conditions (García-González *et al.*, 2018). Initial symptoms appeared as lesions with small spots on leaves and brown necrotic regions at the tips of margins. Over time, the spots became necrotic and surrounded by chlorotic halo. As the disease advanced, defoliation occurred.

Rheinheimera belongs to the family *Chromatiaceae* and class Gmmaprotoebacteria. *sp.,* strain EpRS3 was isolated from *Echinacea purpurea* rhizosphere (Chiellini et al., 2014) and is known for its ability to produce antibacterial compounds which have detrimental effect against the protist *Euplotes aediculatus*, strain EASCc1 (Chiellini *et al.*, 2019). The protist was reported to harbor the obligate parasitic bacterium, *Polynucleobacter necessarius* and the endosymbiont "*Candidatus* Nebulobacter yamunensis. In liquid culture, *Rheinheimera* sp. EpRS3 produces and releases bioactive molecules hampering the survival of *E. aediculatus*. The bioactive molecules also affected the *P. necessarius* endosymbionts which went into degradation and vacuolization after the experimental treatments. In addition, the strain can inhibit the growth of different bacterial pathogens such as: *Acinetobacter baumanni and Klebsiella pneumonia* which exhibit multidrug resistance (Presta et al., 2017).

Some *Acidomyces* species have been reported to be acidophilic, living in highly acidic habitats. These are: *Acidomyces acidophilus* (Kuzmina *et al.*, 2025), and *Acidomyces acidothermus* (Hujslová *et al.*, 2013). These organisms can degrade organic molecules and are potential candidates for bioremediation. The fungus, *Magnaporthe oryzae* is one of the most devastating pathogens of rice (Zhou, 2016) and wheat (Rabby *et al.*, 2022) plants. Infection leads to severe symptoms and causes great yield losses on affected plants. The pathogen induces disease lesions by by-passing a host protein.

Consistent and aggressive feeding by the walnut twig beetle (*Pityophthorus juglandis*), the vector of a filamentous Ascomycete in the genus, *Geosmithia* causes stem and branch cankers on species of *Juglans* and *Pterocarya*. This has led to severe disease spread and death of *Juglans nigra* trees in western USA (Margaret *et al.*, 2020). The insect vector can be spread passively to long distances by human assistance. Through human assistance, diseases and vectors are easily introduced to new areas at points of entry such as airports and seaports. The species, *Geosmithia morbida* was the first species reported as a plant pathogen among other species within the genus.

Conclusion

The result from this study has provided an insight into the bacterial and fungal communities associated with *C. albidium* fruit. However, the problem of sparse information or incompleteness of information in databases exists. A lot of genera and species are yet to be included on metagenomics databases and this brings about challenges in taxonomic assignments. Many sequences are thereby unclassified or unassigned at different taxonomic levels. On these databases, sequences of bacterial origin are presently more abundant than fungal sequences; therefore, the correct taxonomic assignment of bacteria sequences is easier. The high incidence of unidentified fungi which occurred at the order, family and genus levels shows that the fungal diversity of *C. albidium* fruit is yet to be completely characterized. The fungal diversity obtained in this study serves as a basis for future research. Genetic variation is limited within the ITS1&2 regions; this hampered the precise identification of many taxa detected in the fungal community. In future studies, we shall look at more variable regions that can provide detailed information and enable complete characterization of these organisms.

Conflict of Interest

Authors declare that no conflict of interest exists.

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