Chrysophyllum albidum Deterioration Entails Decline in Pseudomonas and Increase in Acetobacter Abundance

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Abstract

Microorganisms inhabiting fruits can affect the quality of fruits during storage. Some of these organisms are beneficial while others maybe deleterious (pathogenic). This paper analyzed African star apple (Chrysophyllum albidum) microbiota to detect the bacterial and fungal communities 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 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 when 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, Tetragnococcus and Acinetobacter which were present in healthy fruits were not present in the diseased sample. The current study has helped in recognizing the microbial community structure of healthy and diseased fruits of C. albidum. 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.

Introduction

Africa star apple (Chrysophyllum albidum G. Don-Holl) is a nutritional and medicinal plant with up to 800 species and belongs to the family Sapotaceae and order Ericales (Ehiagbonare et al. 2008). 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 posses nutritional and medicinal values (Okwu et al. 2018). 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).

Many microorganisms colonize the phyllosphere of plants (fruit surfaces, flowers, leaves and stems) (Abdelfattah et al. 2016). Factors such as: 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). 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 paucity of information on the composition of microbial communities and the impact of the organisms that make up these communities (Massart et al. 2015). This may be due to the use of conventional microbiological methods that involves culture-dependent techniques to analyse the population. These techniques do not take into cognizance the non-culturable members of the populations. High-Throughput Sequencing (HTS) technologies and bioinformatic 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 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. albidum* 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 microbial diversity of fruits is understudied (Leff and Fierer 2013); more information on fruits and vegetable-associated microbiota is required for food safety (Blau et al. 2018). 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 in November 2019. 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 1.5ml 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 DNA extraction protocol. *C. albidium* fruits are shown in Fig. 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 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 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, 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).

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

<table>
<thead>
<tr>
<th>Samples</th>
<th>Target region</th>
<th>Raw Sequences</th>
<th>High quality reads</th>
<th>OTUs</th>
</tr>
</thead>
<tbody>
<tr>
<td>SSA1</td>
<td>V3-V4</td>
<td>50542</td>
<td>1560</td>
<td>113</td>
</tr>
<tr>
<td>SSA2</td>
<td>V3-V4</td>
<td>20767</td>
<td>12428</td>
<td>228</td>
</tr>
<tr>
<td>SSA1-18S</td>
<td>ITS1&amp;2</td>
<td>74825</td>
<td>3373</td>
<td>636</td>
</tr>
<tr>
<td>SSA2-18S</td>
<td>ITS1&amp;2</td>
<td>348111</td>
<td>333273</td>
<td>3730</td>
</tr>
</tbody>
</table>

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)

**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. 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 (Fig. 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 (Fig. 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 (Fig. 3).

**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 65% of the OTUs followed by *Candidatus* Portiera (Fig. 4). For the diseased fruit sample, *Pseudomonas* was the most abundant genus (with relative abundance of approximately 85%), 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* (Fig. 4).

The significant groups of genera obtained were biocontrol (*Pantoea, Bacteroides*), phytopathogenic (*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.

**Discussion**

The microbiota of fruits plays an important role in fruit preservation because they establish interactions with the host and post-harvest phyto-pathogens. Additionally, they can also play a role in the maturation and ripening of fruits (Buchholz et al. 2018; Ravanbakhsh et al. 2018). 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. 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. A large number of sequences obtained were found to be closely related to the plant growth-promoting bacterial genera Pseudomonas, Acetobacter and Gluconobacter, the parasitic genus, Candidatus Portiera, the phyto-pathogenic genera Geosmithia spp. and Magnaporthe spp., and the acidophilic genus, Acidomyces.

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 (Kumar and Chordia 2017). On the other hand, some Pseudomonas species live as parasites on plants (Moore et al. 2006). Symptoms they produce on plants include: leaf spots, stem spots, blight, galls, cankers and soft rots (Höfte and De Vos 2007). Other genera obtained from the bacterial community of C. albidium were: Acetobacter, Gluconobacter, Gluconoacetobacter, Bacteroides, Akkermansia, Prevotella, Candidatus Portiera, Pantoea, Enterobacter, Staphylococcus, Trabulsiella, Rheinheimera, Blautia, Brevibacterium, Tetragnococcus, Catenibacterium, Anaerococcus, Streptococcus and Acinetobacter. The genera, Candidatus Portiera, Staphylococcus, Blautia, Brevibacterium, Tetragnococcus, 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.

Firmicutes has been recorded as one of the core phyla of the human intestinal microbiota, and Ruminococcaceae and Lachnospiraceae are the most abundant families of this phylum (Biddle et al. 2013). Some species of Blautia and Brevibacterium have been reported to posses bio-control and plant-growth promoting potentials. 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 since its establishment to contribute to the alleviation of metabolic and inflammatory diseases and for its antimicrobial activity (Chakravarthy et al. 2018). Blautia is part of the microbiome of the intestines and feces of mammals. It is a genus of anaerobic bacteria with probiotic characteristics (Liu et
al. 2021). Some species of the genera *Ruminococcus* and *Clostridium* have been re-classified under *Blautia*. The probiotic effects of this genus includes: host health regulation ability, biological transformation and metabolic syndrome alleviation.

Some species of the genus, *Gluconacetobacter* are plant growth-promoting bacteria. A strain of *Gluconacetobacter* species, *Gluconacetobacter diazotrophicus* Pal5 has been shown to reduce the effects of low nitrogen stress and water unavailability (drought) in maize plants, by initializing plant defense mechanisms (Tufail et al. 2021). Therefore, this strain can be successfully used in sustainable agriculture. Hence, seed inoculation with *G. diazotrophicus* can be a very effective means of inducing water deficit and nitrogen stress tolerance in maize plants. *G. diazotrophicus* has also been reported to be involved in *Xanthomonas albilineans* pathogenic interactions with sugarcane (Arencibia et al. 2006). The organism produces elicitor molecules which trigger defense response in sugarcane leading to plant resistance to *X. albilineans*. This helps to control the pathogen from being transmitted to emerging shoots.

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-Ai14T and VTH-Ai15 which were reported to have plant growth-promoting ability (Vu et al. 2019). Based on their 16S rRNA gene sequences, a phylogenetic tree was constructed and this showed that the two isolates were closely related to *Acetobacter nitrogenifigens* RG1T although they formed an independent cluster.

*Bacteroides* spp. are Gram-negative obligate anaerobes known to colonize the colon and are members of the human gut microbiome (Zafar and Saier 2021). In humans, some members of the genus *Bacteroides* play double roles (pathogenic and beneficial) depending on their location in the host. Such species are often beneficial in the gut but act as opportunistic pathogens when present in other parts of the body. Oral administration of fatty acids (oleic acid and palmitic acid) from *Bacteroides thetaiotaomicron* prevented the increase in inflammation, reduced the populations of *Escherichia faecalis* and *E. coli*, and eliminated *Candida glabrata* from the human gut (Charlet et al. 2022). In situations where the contents of the colon contaminate the extra-intestinal host environment, *Bacteroides* spp. such as *B. fragilis* successfully adapts to the new habitat and cause infections (Patrick 2022). Such infections can arise from the bursting of a swollen appendix or from a gastro-intestinal surgery, which if not treated, can develop into bacteraemia and subsequent death of the individual. Metabolism of oligosaccharides and polysaccharides, providing nutrients such as vitamins to members of the intestinal microbiome and also nutrition to the host are key roles of *Bacteroides* spp. (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 (Ayesha et al. 2015). 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 maybe due to specific metabolic requirements and symbiotic relationships. One of such bacterium is *Candidatus Liberibacter asiaticus* (CLas) (Krystel et al. 2019). *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 (Haapalainen, 2014). 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, 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. The symptoms vary depending on the host plant infected (Coutinho and Venter 2009). Symptoms include die-back, leaf blotches, leaf spots, and fruit, bulb and stalk rot. *P. ananatis* is also capable of infecting humans and occurs in various environments (Andrea et al. 2007). Some strains are ice-nucleating, an attribute that has been used in the food industry and also to biologically control some insect pests of crops. *P. ananatis* can be used as a biological control agent. The species has been reported to promote growth in pepper and potato. It has both anti-fungal and anti-bacterial properties.

*Enterobacter* spp. are plant growth-promoting rhizobacteria. Microorganisms colonize the rhizosphere of plants and this results in changes in plant growth and development. *Enterobacter* spp. are soil bacteria that enhance the development of plant roots and protect plants against pathogenic infections (Jha et al. 2011). 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 been reported 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. *Rheinheimera* 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 baumannii* and *Klebsiella pneumonia* which exhibit multi-drug resistance (Presta et al. 2017).

Some *Acidomyces* species have been reported to be acidophilic, living in highly acidic habitats. These are: *Acidomyces acidophilus* (Selbmann et al. 2008), and *Acidomyces acidothermus* (Yamazaki et al. 2010; 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.

**Declarations**

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Competing Interests

The authors have no relevant financial and non-financial interests to disclose.

Author Contributions

All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Nkechi Gloria Ogbuji, Anthony Eromosele Ataga, Ifeyinwa Albright Ukwu and Ugochukwu Chibuike Nwosu. The first draft of the manuscript was written by Nkechi Gloria Ogbuji and all authors commented on the previous versions of the manuscript. All authors read and approved the final manuscript.

References


**Figures**
Figure 1

*Chrysophyllum albidium* fruits (George et al. 2018)

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

Figure 4

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