© JUL 2026 | IRE Journals | Volume 10 Issue 1 | ISSN: 2456-8880
DOI: https://doi.org/10.64388/IREV10I1-1719880

Microbiological Assessment of Polyalthia Longifolia (Masquerade Tree) Rhizosphere Soil

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Abstract- ***Polyalthia longifolia (Masquerade tree) is a medicinal plant widely cultivated in tropical regions; however, information on the microbial communities inhabiting its rhizosphere remains limited. This study assessed the culturable bacterial and fungal populations associated with the rhizosphere of P. longifolia in selected areas of Sokoto State, Nigeria. Twelve rhizosphere soil samples were collected from seven locations at a depth of 0–15 cm using a soil auger. Soil samples were serially diluted to 10-6 dilution factor and cultured on Nutrient Agar (NA) for bacteria and Potato Dextrose Agar (PDA) supplemented with streptomycin for fungi. Bacterial isolates were identified using colony morphology, Gram staining, and standard biochemical tests, while fungal isolates were identified based on macroscopic and microscopic characteristics following lactophenol cotton blue staining. Four bacterial genera were isolated: Bacillus spp. (46.66%), Micrococcus luteus (26.66%), Corynebacterium spp. (15.00%), and Actinomycetes spp. (11.66%). The fungal community comprised Aspergillus flavus (29.79%), Aspergillus niger (27.66%), Sporotrichum spp. (21.28%), Candida spp. (10.64%), and Geotrichum spp. (10.64%). The predominance of Bacillus and Aspergillus species suggests that the rhizosphere of P. longifolia supports microorganisms involved in organic matter decomposition, nutrient cycling, and potentially beneficial plant-microbe interactions. These findings provide baseline information on the culturable rhizosphere microbiota of P. longifolia and highlight its potential as a reservoir of agriculturally and biotechnologically important microorganisms. Further studies employing molecular identification techniques and functional characterization are recommended to provide a more comprehensive understanding of the rhizosphere microbiome and its ecological significance.***

Keywords ***Polyalthia longifolia, Rhizosphere, Soil, Bacteria, Fungi.***

I. INTRODUCTION

Masquerade Tree" is a tall evergreen tree that is native to India and Sri Lanka. It is a member of the Annonaceae family (Moniruzzaman et al., 2015). It is generally recognized as Ashoka or False Ashoka (Katkar et al., 2010) About 120 species make up the genus Polyalthia, which is primarily found in Africa, South and South-East Asia, Australia, and New Zealand. Evergreen tree can grow up to a height of 15-20 meters tall. Young plants have straight trunks and weeping pendulous branch. The longest branch is seen at the base and shorter at the end of the trunk, giving an appearance of conical crown. Leaves are long, narrow dark green and glossy. Leaf blades are ovate-oblong to ovate-lanceolate with wavy margins. Reticulate veins rose on both surfaces of leaf. (Bunyapraphatsara, 2019). Transverse section of the leaf through the midrib showed bowl shaped abaxial parts and straight adaxial side. Petals are greenish yellow, narrowly triangular-lanceolate. Stamens are; connectives apically convex. Carpels are 20-25 in number with one ovule per carpel; stigmas are sessile. Fruits are borne in clusters of 10-20, usually ovoid in shape. Initially fruits are green in color but turns purple or black when ripe.Seeds are pale brown, ovoid, with a longitudinal groove. (Lemmens et al., 2019) One of the most significant native medicinal plants in Indian medical literature is Polyalthia longifolia. In India, almost all of this plant's parts are used medicinally to cure a variety of illnesses, and scientific studies have revealed that it has important medicinal characteristics (Subramanion et al. 2013). It has been used in traditional medicine to treat helminthiasis, diabetes, fever, skin conditions, and hypertension (Chioma and Reminus, 2023). It has been discovered that the leaves and the roots contain phytosterols and monounsaturated fatty acids, which helps in lowering cholesterol (Chioma and Reminus, 2023). The plant has traditionally been used to increase breathing, reduce blood pressure, stimulate and treat ailments such as uterine disorders, gonorrhea, leucorrhea, and menstrual issues (Subramanion et al. 2013). Currently, the scientific literature characterizes Polyalthia longifolia almost

exclusively through the lens of pharmacognosy and natural product chemistry, rather than soil ecology.

II. MATERIALS AND METHOD

Sample Collection

A number of 12 soil samples of P. longifolia rhizosphere were collected with the aid of an auger from four locations in Sokoto (Guiwa, Arkilla, Kosai and Alkammawa area) at depth of 0–15cm. The samples were packaged, labelled and transported to laboratory for microbial analyses.

Serial Dilution

Serial dilution of the soil samples was carried out based on the method described by Aziz (2021). One gram of each soil sample was suspended in 9ml of sterile distilled water to give a 1:10 (10-1) dilution and from the 10-1 dilution, 1ml was withdrawn using sterile syringe and dispensed into another 9ml of sterile distilled water to give a 10-2 dilution i.e. a 1:100 dilution and his process was continued until the concentration of 10-6 was formed.

Media Preparation

Nutrient agar (NA) was prepared as described Syahirah and Rabeta (2019). Approximately 2g of nutrient agar medium was weight and suspended into 1000ml of distilled water in a conical flask. The solutions were mixed and dissolved by continuous heating on a hot plate. After dissolution and homogenization, the media was sterilized in an autoclave at 121°C for 15 minutes. After the autoclave, the agar was allowed to cool before being poured into clean petri dishes. Potato dextrose agar (PDA) was prepared by suspending 39g of the powder into 1000ml of water. The suspension was also homogenized on a hot plate, sterilized at 121°C for 15 minutes and poured into petri dishes after cooling to about 40oC. 50g of Streptomycin was added to prevent bacterial growth.

Inoculation and Incubation

A small volume (0.5ml) of dilute microbial mixture was transferred to the center of an agar media plate and spread evenly over the surface with a sterile L-shaped bent glass rod. After inoculation, NA plates were incubated at 37ºC for 24 hours, while PDA plates were incubated for 7 days in the inverted position under aerobic condition (Aziz, 2021).

Isolation of bacteria and fungi

After the initial incubation, colonies exhibiting distinct morphologies specifically regarding size and color on both the NA and PDA media were selected. These isolates were sub-cultured onto fresh plates and incubated to establish pure cultures for downstream identification.

Identification of bacteria

Gram Staining

A smear was formed by placing tiny drop of sterile water in the center of a clean slide. The inoculation loop was flamed, allowed to cool, and used to touch a single bacterial colony, which was then gently mixed into the water droplet. The loop was flamed again, allowed to cool, and placed directly onto the center of the slide. The flat part of the loop was used to spread the droplet into a thin and even circle. The smear was allowed to dry completely at room temperature. The underside of the dry slide was passed through the upper flame of a Bunsen burner three times quickly (about one second per pass). This stuck the bacteria firmly to the glass so they would not wash away during staining. The prepared smear was placed on a staining rack over the sink, and the primary stain, crystal violet, was added to the smear for 1 minute. After 1 minute, the smear was washed under gentle tap water, and Gram's iodine was added for 1 minute. After 1 minute, the smear was washed under gentle tap water again. Decolorizer, acetone was added for fewer than 10 seconds. The slide smear was washed under gentle tap water again, and the counterstain, safranin was added for less than 1 minute. After 1 minute, the smear was washed under gentle tap water and allowed to air dry. The back side of the smear was cleared with tissue paper, a drop of immersion oil was applied, and the smear was focused on the microscope and observed under the oil immersion lens (100X) (Ansar et al., 2023).

Catalase test

Catalase test was done as described by Oyeleke and Manga (2008). A speck of bacterial growth was transferred with a loop to a drop of hydrogen peroxide on a slide and was observe for the formation

of bubble gas. The presence of catalase was indicated by bubbles gas (oxygen) that is positive while absence of bubbles indicates negative for catalase.

Methyl Red Test

MR test was done as described by Oyeleke and Manga (2008). A loopful of each isolate was inoculated onto the glucose phosphate peptone water medium and was incubated at 370C for 48 hours. Few drops of methyl red were added to the culture. MR positive test was indicated by formation of red color.

Indole test

To test for indole production, a bacterial colony was inoculated into a test tube containing 1% tryptophan broth and incubated at 37°C for 48 hours. Following incubation, 1.0 ml of chloroform was added, and the tube was shaken gently. Next, 2 ml of Kovac's reagent was introduced, and the mixture was gently agitated once more before being allowed to settle for 20 minutes. A positive result was indicated by the development of a red ring in the top layer, while a yellow ring signified a negative result (Udeani et al., 2009).

Citrate test

A speck of each isolate was inoculated into Koser's citrate medium and was incubated at 370C for 72 hours. A positive citrate test was confirmed by formation of blue color (Oyeleke and Manga, 2008).

Urease test

A loopful of each isolate was inoculated unto Christensen's urea agar and was incubated at 370C for 24 hours. Liberation of red color indicates urease-positive test while initial yellow color indicates negative.

Oxidase test

Following the method described by Chesebrough (2003), a loopful of bacterial culture on a clean slide was treated with a few drops of 1% aqueous tetramethyl-p-phenylenediamine hydrochloride. The immediate development of a purple color within 5 seconds indicated a positive result.

Identification of fungi

The fungal morphology was studied macroscopically by observing the colony features (color, shape, size and hyphae), and microscopically using a lactophenol cotton blue-stained slide mounted with a small portion of the mycelium (Gaddeyya et al., 2012)

III. RESULTS AND DISCUSSION

Table 1: Bacteria Isolated from the Rhizosphere of Polyalthia longifolia

S/N	Bacteria	Number of colonies	Frequency of Occurrence (%)
1	Corynobacterium spp	9	15
2	Baccilus spp	28	46.66
3	micrococcus luteus spp	16	26.66
4	Actinomycetes spp	7	11.66

The root-soil interface, or rhizosphere, is a selective chemical zone modulated strictly by plant root exudates. This phenomenon historically termed the "rhizosphere effect" accounts for the structural assembly and recruitment of specific beneficial or tolerant soil microbiota from the surrounding bulk soil (Thomas et al., 2022). The overwhelming selection of Gram-positive phyla (Bacillota and Actinomycetota) observed in this dataset reflects the unique physiological demands of surviving adjacent to Polyalthia longifolia roots. Accounting for nearly half of the total population (46.66%), Bacillus species represent the dominant Plant Growth-Promoting Rhizobacteria (PGPR) cohort in this system. The inherent structural advantage of Bacillus lies in endospore formation. This protects them against shifting abiotic pressures such as desiccation, localized osmotic shocks, and toxic heavy metals or secondary metabolites within the soil matrix (Forni & Borromeo, 2023). Root exudates are highly rich in labile organic acids, amino acids, and sugars. Bacillus spp. possess rapid growth kinetics and specialized chemotactic machinery that allow them to preferentially migrate toward, and form robust biofilms along, root surfaces.

Micrococcus species secured a significant secondary position (26.66%). Often characterized as robust, non-spore-forming cocci, their survival in high numbers points toward targeted biochemical compatibility. Micrococcus species excel at degrading complex organic carbon residues and xenobiotics. They are vital links in soil carbon and nitrogen cycling, breaking down intermediate root turn-over compounds. Many rhizospheric Micrococcus strains produce high concentrations of carotenoid pigments that shelter them from oxidative stress induced by reactive oxygen species (ROS) frequently generated during plant-microbe signalling or environmental stress periods. The presence of Corynebacterium spp. (15.00%) introduces an intriguing metabolic dimension. While less celebrated in baseline bio-fertilizer discussions than Bacillus, these coryneform rods are deeply integrated into the degradation cycles of soil organic matter. They frequently specialize in processing stubborn, aromatic hydrocarbons and long-chain fatty acids present within root cell walls and exudate fluids, converting them into bio-available nutrients for both the host plant and neighboring microflora.

At 11.66%, Actinomycetes represent the smallest isolated fragment. However, this quantitative frequency must be interpreted through the lens of methodology rather than absolute ecological insignificance. Actinomycetes (such as Streptomyces) are slow-growing, filamentous organisms. On standard agar media, they are easily outcompeted, masked, or physically overgrown by the rapid, spreading colony development characteristic of Bacillus spp. Despite lower isolation frequencies, Actinomycetes function as the primary defense shield of the rhizosphere. They produce an array of secondary metabolites—including antimicrobials and extracellular lytic enzymes (chitinases, glucanases)—that degrade fungal cell walls. This suppresses soil-borne phytopathogens (like Fusarium or Pythium) before they can breach the root epidermis (Dileep et al., 2013).

The definitive driver behind this bacterial profile is the specialized phytochemistry of P. longifolia. The plant is renowned for generating aggressive antimicrobial, cytotoxic, and antioxidant compounds (Aliyu, 2023). When these bioactive chemicals are deposited into the rhizosphere through root exudation, they act as an antimicrobial filter. Many Gram-negative, sensitive bacteria face immediate growth inhibition. In contrast, the isolated genera (Bacillus, Micrococcus, Corynebacterium, and Actinomycetes) possess rigid cell structures (thick peptidoglycan walls) and advanced efflux pumps or enzymatic machinery capable of neutralizing or utilizing these specialized plant defense compounds (Kernou et al., 2023). Thus, the resulting community is not random; it represents a tailored, mutually selected core microbiome where the host plant trades carbon resources for protection, nutrient availability, and physiological growth support.

Table 2: Fungi Isolated from the Rhizosphere of Polyalthia longifolia

S/N	Fungi	Number of Colonies	Frequency of Occurrence (%)
1	Sporotrichum spp	10	21.28
2	Aspergillus niger	13	27.66
3	Aspergillus flavus	14	29.79
4	Candida spp	5	10.64
5	Geotrichum spp	5	10.64

The fungal community isolated from the rhizosphere of Polyalthia longifolia on potato dextrose agar (PDA) was dominated by Aspergillus flavus (14 colonies; 29.79%), followed closely by Aspergillus niger (13 colonies; 27.66%), while Sporotrichum spp. accounted for 21.28% (10 colonies), and Candida spp. and Geotrichum spp. each represented 10.64% (5 colonies). This distribution indicates that the rhizosphere of P. longifolia supports a fungal community dominated by fast-growing saprophytic fungi capable of utilizing the abundant organic substrates typically found in the rhizosphere. The rhizosphere is recognized as one of the most biologically active zones in soil because root exudates, sloughed-off cells, and decomposing organic matter provide nutrients that selectively enrich microbial populations. Consequently, fungal

composition in the rhizosphere is shaped by plant species, soil physicochemical properties, climatic conditions, and interactions among microbial communities (Philippot et al., 2013; Compant et al., 2019).

The predominance of Aspergillus flavus (29.79%) suggests that this species is well adapted to the rhizosphere environment of P. longifolia. Species of Aspergillus are among the most ubiquitous soil fungi and possess exceptional metabolic versatility that enables them to colonize nutrient-rich rhizosphere habitats. They produce a wide array of extracellular enzymes, including cellulases, pectinases, proteases, xylanases, and phosphatases, which facilitate decomposition of plant residues and mineralization of organic matter. These enzymatic capabilities contribute significantly to nutrient cycling and enhance soil fertility. Furthermore, several Aspergillus species are known to solubilize insoluble phosphates and produce siderophores that improve nutrient availability to plants. The abundance of A. flavus may therefore reflect its competitive advantage in utilizing root exudates and organic substrates available in the rhizosphere. Similar dominance of Aspergillus species has been reported in rhizosphere soils of numerous tropical trees and medicinal plants, where they often constitute one of the major fungal genera recovered using culture-dependent techniques (Lugtenberg et al., 2017; Compant et al., 2019).

Although A. flavus contributes positively to nutrient turnover, its ecological significance should also be interpreted cautiously because certain strains are capable of producing aflatoxins, which are among the most potent naturally occurring mycotoxins. However, not all environmental isolates produce aflatoxins, and many soil isolates function primarily as saprophytes or endophytes without expressing toxigenic traits. Consequently, the presence of A. flavus in the rhizosphere should not automatically be interpreted as an indication of pathogenicity or toxin contamination, but rather as evidence of its ecological adaptability and competitiveness within soil microbial communities (Amaike and Keller, 2011; Frisvad et al., 2019).

Aspergillus niger was the second most abundant fungus, accounting for 27.66% of the total isolates. The high frequency of A. niger further supports the view that the rhizosphere of P. longifolia favors fungi capable of rapid colonization and efficient decomposition of organic substrates. A. niger is widely recognized for its production of organic acids, particularly citric acid and gluconic acid, which contribute to phosphate solubilization and increased nutrient availability. In addition, this fungus produces numerous hydrolytic enzymes that facilitate degradation of cellulose, hemicellulose, lignin-associated compounds, and other complex organic materials. The ecological functions of A. niger therefore extend beyond decomposition to include enhancement of nutrient acquisition and maintenance of soil fertility. Numerous studies have also demonstrated the plant growth-promoting potential of selected A. niger strains through phytohormone production, phosphorus solubilization, and improvement of plant tolerance to abiotic stress (Tiquia-Arashiro and Grube, 2019; Sharma et al., 2023).

Sporotrichum spp. represented 21.28% of the fungal population, making them the third most abundant genus isolated. Although Sporotrichum species are less frequently reported than Aspergillus in rhizosphere studies, they are well known as saprophytic fungi associated with decomposition of lignocellulosic materials. Their ability to produce cellulolytic and ligninolytic enzymes enables them to participate actively in the degradation of plant litter and recycling of carbon within soil ecosystems. Their occurrence in the rhizosphere of P. longifolia therefore suggests an active role in decomposition processes and maintenance of soil organic matter dynamics. The relatively high occurrence of Sporotrichum may also indicate the presence of abundant organic residues beneath the tree canopy, creating favorable ecological conditions for lignocellulose-degrading fungi.

The lower occurrence of Candida spp. (10.64%) is not unexpected because yeasts generally occur in lower abundance than filamentous fungi in most soil ecosystems. Nevertheless, their presence is ecologically significant. Rhizosphere-associated

yeasts are increasingly recognized for their ability to produce phytohormones such as indole-3-acetic acid, synthesize vitamins, solubilize phosphate, and produce antimicrobial metabolites that suppress plant pathogens. Certain Candida species also contribute to nutrient mineralization and may interact synergistically with bacteria and filamentous fungi in promoting plant growth. Their relatively lower frequency may reflect their preference for localized nutrient-rich microsites surrounding roots rather than widespread colonization of bulk soil (Botha, 2011; Fonseca and Inácio, 2022).

Similarly, Geotrichum spp. accounted for 10.64% of the fungal isolates. Members of this genus are commonly found in soil rich in decaying organic matter and are recognized for their ability to degrade cellulose, pectin, and other plant-derived polymers. Their occurrence suggests active decomposition of root-derived organic materials within the rhizosphere. Although Geotrichum species have received comparatively less attention in rhizosphere ecology than Aspergillus or Penicillium, they contribute to nutrient turnover and organic matter decomposition and may participate in complex microbial interactions that influence soil health and plant productivity.

The predominance of filamentous fungi over yeasts observed in this study agrees with the general ecological pattern reported for most agricultural and forest soils. Filamentous fungi possess extensive hyphal networks that enable efficient exploitation of heterogeneous soil environments, facilitating access to dispersed nutrient sources and enhancing competitive ability. In contrast, yeasts are typically confined to microsites containing readily available soluble nutrients and therefore often occur at lower frequencies in culture-based studies (Baldrian, 2017).
It is also important to recognize that the observed fungal composition may have been influenced by the use of PDA as the isolation medium. PDA is a nutrient-rich, general-purpose medium that favors rapid growth of opportunistic fungi such as Aspergillus while underrepresenting slow-growing or nutritionally specialized taxa. Consequently, culture-dependent methods usually recover only a fraction of the actual fungal diversity present in soil. High-throughput sequencing studies have consistently demonstrated that many rhizosphere fungi remain unculturable under standard laboratory conditions. Therefore, while the present findings provide valuable information on the culturable fungal community associated with P. longifolia, they likely underestimate the total fungal diversity present in the rhizosphere (Nilsson et al., 2019; Tedersoo et al., 2022).

The fungal community structure observed in this study suggests that the rhizosphere of P. longifolia supports microorganisms capable of active organic matter decomposition, nutrient cycling, and potentially beneficial plant–microbe interactions. The dominance of Aspergillus species indicates efficient decomposition and mineralization processes that may contribute to maintaining soil fertility around the tree. At the same time, the detection of genera such as Candida, Geotrichum, and Sporotrichum highlights the functional diversity of the rhizosphere microbiome.

IV. CONCLUSION

This study successfully assessed the culturable microbial communities associated with the rhizosphere of Polyalthia longifolia (Masquerade tree) in selected locations within Sokoto State, Nigeria. The results demonstrated that the rhizosphere harbours a diverse population of bacteria and fungi, reflecting the biologically active nature of the root-soil interface. Among the bacterial isolates, Bacillus spp. were the most predominant, accounting for 46.66% of the total bacterial colonies, followed by Micrococcus luteus (26.66%), Corynebacterium spp. (15.00%), and Actinomycetes spp. (11.66%). The dominance of Bacillus species suggests that the rhizosphere of P. longifolia provides a favourable environment for plant growth-promoting bacteria capable of nutrient cycling, organic matter decomposition, and suppression of soil-borne pathogens. Similarly, the fungal community was dominated by Aspergillus flavus (29.79%) and Aspergillus niger (27.66%), followed by Sporotrichum spp. (21.28%), while Candida spp. and Geotrichum spp. each accounted for 10.64% of the isolates. The predominance of these fungi indicates

an active community of saprophytic microorganisms involved in the decomposition of organic matter and nutrient mineralization within the rhizosphere. Although A. flavus is known to include aflatoxin-producing strains, its occurrence in the rhizosphere should be interpreted primarily as evidence of its ecological adaptability, as toxigenicity cannot be inferred without further molecular and biochemical analyses.

Overall, the study confirms that the rhizosphere of P. longifolia serves as an important ecological niche supporting microorganisms with potential roles in nutrient recycling, soil fertility maintenance, and plant health. The findings provide baseline information on the culturable rhizosphere microbiota of P. longifolia in Sokoto State and contribute to the growing body of knowledge on plant-associated microorganisms. However, because the study relied on conventional culture-dependent techniques and phenotypic identification, the actual microbial diversity present in the rhizosphere is likely greater than that reported. Future investigations using molecular approaches, combined with functional assays for phosphate solubilization, enzyme production, phytohormone synthesis, and antagonism against plant pathogens, would provide a more comprehensive understanding of the ecological roles and biotechnological potential of these fungal isolates.

REFERENCES

[1] Aliyu, N. D. (2023). Green synthesis of eco-friendly potassium nanoparticles and its application in Amaranthus viridis, Solanum lycopersicum and Hibiscus sabdariffa. Science World Journal, 18(4), 149–152.

[2] Amaike, S., & Keller, N. P. (2011). Aspergillus flavus. Annual Review of Phytopathology, 49, 107–133. https://doi.org/10.1146/annurev-phyto-072910-095221

[3] Ansar Ahmad Paray, Manju Singh, Mohsin Amin Mir, & Amandeep Kaur. (2023). Gram staining: A brief review. International Journal of Research and Review, 10(9), 336–341. https://doi.org/10.52403/ijrr.20230934

[4] Aziz, M. K. (2021). A book on experiments of microbiology (Experiment 14, pp. 26–30).

[5] Baldrian, P. (2017). Forest microbiome: Diversity, complexity and dynamics. FEMS Microbiology Reviews, 41(2), 109–130. https://doi.org/10.1093/femsre/fuw040

[6] Botha, A. (2011). The importance and ecology of yeasts in soil. Soil Biology and Biochemistry, 43(1), 1–8.

[7] Bunyapraphatsara, N. (2019). A manual of the trees of Thailand (Vol. 2). Department of National Parks, Wildlife and Plant Conservation.

[8] Cheesbrough, M. (2003). District laboratory practice in tropical countries (Part 2). Cambridge University Press.

[9] Chioma, D., & Reminus, O. (2023). Phytochemical analysis of Polyalthia longifolia (fresh leaves). Direct Research Journal of Chemistry and Material Science, 11(7), 49–52.

[10] Compant, S., Samad, A., Faist, H., & Sessitsch, A. (2019). A review on the plant microbiome: Ecology, functions, and emerging trends in microbial application. Journal of Advanced Research, 19, 29–37. https://doi.org/10.1016/j.jare.2019.03.004

[11] Dileep, N., Junaid, S., Rakesh, K. N., Prashith Kekuda, T. R., & Noor Nawaz, A. S. (2013). Antifungal activity of leaf and pericarp of Polyalthia longifolia against pathogens causing rhizome rot of ginger. Journal of Science, Technology and Arts Research, 2(1), 56–59.

[12] Fonseca, Á., & Inácio, J. (2022). Ecology and biodiversity of yeasts in terrestrial environments. In C. P. Kurtzman, J. W. Fell, & T. Boekhout (Eds.), The yeasts: A taxonomic study (6th ed.). Elsevier.

[13] Forni, C., & Borromeo, I. (2023). The utilization of seed priming as a tool to overcome salt and drought stresses: Is still a

long way to go? Seeds, 2(4), 406–420. https://doi.org/10.3390/seeds2040031

[14] Frisvad, J. C., Hubka, V., Ezekiel, C. N., Hong, S.-B., Nováková, A., Chen, A. J., Arzanlou, M., Larsen, T. O., Sklenář, F., Mahakarnchanakul, W., & others. (2019). Taxonomy of Aspergillus section Flavi and their production of aflatoxins. Studies in Mycology, 93, 1–63. https://doi.org/10.1016/j.simyco.2018.06.001

[15] Gaddeyya, G., Niharika, P. S., Bharathi, P., & Kumar, P. K. R. (2012). Isolation and identification of soil mycoflora in different crop fields at Salur Mandal. Advances in Applied Science Research, 3, 2020–2026.

[16] Katkar, K. V., Suthar, A. C., & Chauhan, V. S. (2010). The chemistry, pharmacologic and therapeutic applications of Polyalthia longifolia. Pharmacognosy Reviews, 4(7), 62–68.

[17] Kernou, O. N., Azzouz, Z., Madani, K., & Rijo, P. (2023). Application of rosmarinic acid with its derivatives in the treatment of microbial pathogens. Molecules, 28(10), 4243. https://doi.org/10.3390/molecules28104243

[18] Lemmens, R. H. M. J., Soerianegara, I., & Wong, W. C. (Eds.). (2019). Plant resources of South-East Asia: Timber trees. Backhuys Publishers.

[19] Moniruzzaman, M., Ferdous, A., & Bokul, F. W. (2015). Evaluation of antinociceptive activity of ethanol extract of bark of Polyalthia longifolia. Journal of Ethnopharmacology, 172, 364–367.

[20] Nilsson, R. H., Larsson, K.-H., Taylor, A. F. S., Bengtsson-Palme, J., Jeppesen, T. S., Schigel, D., Kennedy, P., Picard, K., Glöckner, F. O., Tedersoo, L., & others. (2019). The UNITE database for molecular identification of fungi. Nucleic Acids Research, 47(D1), D259–D264. https://doi.org/10.1093/nar/gky1022

[21] Oyeleke, S. B., & Manga, S. B. (2008). Essentials of laboratory practical in microbiology. Tobest Publisher.

[22] Philippot, L., Raaijmakers, J. M., Lemanceau, P., & Van der Putten, W. H. (2013). Going back to the roots: The microbial ecology of the rhizosphere. Nature Reviews Microbiology, 11(11), 789–799. https://doi.org/10.1038/nrmicro3109

[23] Sharma, A., Kumar, V., Shahzad, B., Ramakrishnan, M., Sidhu, G. P. S., Bali, A. S., Handa, N., Kapoor, D., Yadav, P., Khanna, K., & others. (2023). Beneficial soil fungi and their role in sustainable agriculture. Frontiers in Microbiology, 14, 1186326. https://doi.org/10.3389/fmicb.2023.1186326

[24] Subramanion, L. J., Choong, Y. S., Saravanan, D., Deivanai, S., Latha, L. Y., Vijayarathna, S., & Sasidharan, S. (2013). Polyalthia longifolia Sonn.: An ancient remedy to explore for novel therapeutic agents. Research Journal of Pharmaceutical, Biological and Chemical Sciences, 4(1), 714–730.

[25] Syahirah, J., & Rabeta, M. S. (2019). Antioxidant and antimicrobial activity of lemuni noodle. Food Research, 3(1), 7–13. https://doi.org/10.26656/fr.2017.3(1).090

[26] Thomas, P., Rajendran, T. P., & Franco, C. M. M. (2022). Cytobacts: Abundant and diverse vertically seed-transmitted cultivation-recalcitrant intracellular bacteria ubiquitous to vascular plants. Frontiers in Microbiology, 13, Article 806222. https://doi.org/10.3389/fmicb.2022.806222

[27] Udeani, C. K. T., Obroh, A. A., Okwuosa, N. C., Achukwu, U. P., & Azubike, N. (2009). Isolation and characterization of bacterial isolates. African Journal of Biotechnology, 8(22), 6301–6303.