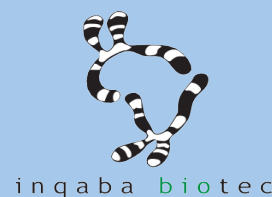


BAMENDA UNIVERSITY OF SCIENCE AND TECHNOLOGY AND THE UNIVERSITY OF BAMENDA



**PROCEEDINGS OF THE INTERNATIONAL CONFERENCE ON
FUNGI BARCODING FOR BIODIVERSITY CONSERVATION
(ICFBBC 2026) AT THE UNIVERSITY OF DOUALA AND ALVI
HOTEL DOUALA, CAMEROON, 14-17 JANUARY 2026**



JRS Biodiversity Foundation



Edited by: Tonjock Rosemary Kinge

Co-edited by: Tofel Haman Katamssadan, Samje Moses, & Balgah Roland Azibo

PROCEEDINGS OF THE INTERNATIONAL CONFERENCE ON FUNGI BARCODING FOR BIODIVERSITY CONSERVATION (ICFBBC 2026) IN DOUALA, CAMEROON, 14-17 JANUARY 2026

Date

14th to 17th January 2026

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University of Douala and Alvi Hotel, Douala, Cameroon

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- Bamenda University of Science and Technology (BUST), Mile 6 Nkwen, P.O. Box 277, Bamenda, Cameroon
- The University of Bamenda (UBa), Bambilli, P.O. Box 39, Bamenda, Cameroon

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-

Plenary Speakers

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- Prof. Mbouobda Hermann, University of Bamenda, Cameroon
- Prof. Tonjock Rosemary Kinge, Bamenda University of Science and Technology and University of Bamenda, Cameroon
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- Prof. Francisca Okungbowa, University of Benin, Nigeria
- Dr. Ethelyn Echeper Forchibe, Catholic University of Cameroon

ABSTRACTS FOR CONFERENCE SESSIONS

Session 1: Molecular Identification of Fungi

DNA Barcoding of Fungi: Bridging Taxonomy, Biodiversity, and Global Data Sharing

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Fungi represent a vital component of global biodiversity, contributing significantly to ecosystem functioning, agriculture, plant protection, and industrial biotechnology. Accurate identification of fungal species is essential for harnessing their benefits, managing plant pathogens, and conserving bioresources. DNA barcoding, which utilizes standardized genetic markers, such as the Internal Transcribed Spacer (ITS) region, has emerged as a powerful tool for rapid and precise fungal identification. This presentation highlights the principles and workflow of fungal DNA barcoding, including sample collection, DNA extraction, amplification, sequencing, and comparison with curated global databases, such as UNITE, GenBank, and BOLD Systems. Emphasis is placed on the applications of barcoding in agriculture, including the identification of beneficial mycorrhizal fungi, biocontrol agents, and plant pathogens, facilitating sustainable crop management and integrated disease control. Furthermore, DNA barcoding supports environmental biotechnology by enabling the discovery of fungi with industrially valuable enzymes, their application in bioremediation, and the conservation of rare or endangered fungal species. The presentation also explores the collaborative dimension of fungal barcoding, illustrating how researchers, farmers, and citizen scientists contribute to global biodiversity data sharing. Challenges, including incomplete reference databases, cryptic species, and technical limitations in metabarcoding, are discussed, along with future perspectives involving eDNA, high-throughput sequencing, and AI-driven predictive modeling. By bridging taxonomy, biodiversity, and global data sharing, fungal DNA barcoding emerges as a transformative approach for advancing sustainable agriculture, environmental management, and biotechnological innovation.

Keywords: Fungi, DNA barcoding, ITS region, Biodiversity, Agriculture, Plant protection, Environmental biotechnology

The Molecular Identification of mycorrhizal fungi: Arbuscular and Ecto-Mycorrhiza fungi across two sacred forests Coastal Kenya

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Mycorrhizal symbiosis is associated with adaptation of plants to terrestrial environments, survival and provision of essential benefits to diverse plant communities. The mycorrhizal association is the rule rather than the exception. The most common mycorrhizal associations are the belowground Arbuscular mycorrhiza fungi (AMF) and the Ectomycorrhiza (EM), with the former more widespread. The identification of the two types of mycorrhizae is predominantly by morphological characters. The ECM produce visible fruiting structures and a belowground vegetative mycorrhiza and mycelial network, and the entire life cycle of AMF is belowground with microscopic spores and sporocarps, mycorrhiza and extensive mycelial spread in the soil. There are numerous challenges in the use of morphological characters in the identification of ECM and AMF, hence, underestimating the diversity of these important ecological key functional groups. To a large extent, the use of molecular identification counteracts the challenges although not entirely, and it complements morphological identification. Molecular methods provide precise genetic identification and is able to detect the non-sporulating, non-fruiting, and unculturable mycorrhizal fungi. Our study used molecular identification complimented by morphology on both AMF and ECM. Total genomic DNA was extracted directly from 0.25 g of the soil samples using Quick-DNA™ Fecal/Soil Microbe Miniprep Kit in accordance with the manufacturer's protocol. The extracted DNA was quantified using NanoDrop 1000 spectrophotometer and stored at -20°C for further analysis. Genomic DNA was sent to Macrogen for sequencing using the Miseq Illumina sequencing platform. They used ITS3(F:5' GCATCGATGAAGAACGCAGC 3') and ITS4(R:5' TCCTCCGCTTATTGATATGC 3') and WANDA (F:5' CAGCCGCGGTAATTCCAGCT3') and AML2 (R:5' GAACCCAAACACTTTGGTTTCC 3') for ECM- fungi and AMF respectively. Demultiplexed paired-end sequences obtained from the sequencing centre were processed using QIIME2. Statistical analyses were performed using R v3.6.1. The molecular identification of ECM was able to detect fourteen (14) families using ITS3 and ITS 4. Contrary, only four families were identified using morphological features of fruiting bodies. The detection of ectomycorrhizal species showed new families reported for the first time in the area like Thelephoraceae, Gomphaceae, Sebacinaceae, Serendipitaceae, Lachnociadiaceae, Inocybaceae and hymenochaetaceae as additional ectomycorrhizal fungal communities. A total of five (5) records were not matching with existing records in the UNITE database. One (1) Lachnociadiaceae, one (1) Peniophoraceae, one (1) Thelephoraceae, one (1) Hymenochaetaceae and the order Boletales could not be matched with existing families in the database. Molecular identification detected a total of 53 AMF species comprised of eight (8) families and thirteen (13) genera using Wonder and AML2 primers. Contrary, morphological analysis described 7 families, 17 distinct morphotypes of AMF. In the molecular identification, there were five (5) records that were not matching with existing records in the UNITE database. Three (3) in the family Glomeraceae and two (2) in the order Glomerales were not matching with records in the database. The Results clearly indicate that molecular identification reveals a broader range of mycorrhizal species, including those absent from spore and morphotype surveys. It is however still essential to include the standard morphological procedures identification to build a reference database for identifying the below-ground mycorrhizal associations. It is also important for production of cultures for application in agriculture, forestry, restoration, rehabilitation and conservation purposes.

Keywords: Mycorrhiza, Diversity, Identification, Morphology, Molecular

Characterisation and Antifungal Potential Evaluation of Indigenous *Trichoderma* Isolates Against *Macrophomina phaseolina*: An *In Vitro* Study

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The fungus *Trichoderma* is an efficient soilborne biological control agent (BCA) for controlling plant pathogenic microorganisms, owing to its ability for competition, antibiosis and mycoparasitism. *Macrophomina phaseolina* is a soil-borne fungal pathogen responsible for the devastating loss of many economically important crops in subtropical regions of Africa, affecting up to 500 species at both the seedling and adult stages. Synthetic fungicides have been proven effective in controlling *M. phaseolina*; however, they often pose significant environmental and health risks to humans and animals. This study evaluated the antifungal efficacy of some *Trichoderma* isolates against *M. phaseolina in vitro*. The *Trichoderma* isolates were obtained from the cowpea rhizosphere soil using the serial dilution method in the laboratory. The *Trichoderma* isolates obtained from soil were culturally and genotypically identified based on the internal transcribed spacer (ITS) genes. The inhibitory potential of the *Trichoderma* isolates was tested against *M. phaseolina in vitro*. Culturally, all the fungal isolates were identified as belonging to the *Trichoderma* genus. Meanwhile, the genotypic characterisation identified the selected *Trichoderma* isolates as *Trichoderma asperellum*. The *in vitro Trichoderma* antifungal testing revealed that *T. asperellum* (Tric13), *T. asperellum* (Tric4), and *T. asperellum* (Tric12) exhibited significant inhibitory potential ($p < 0.05$) against *M. phaseolina*, with inhibition values of 82.51%, 82.41%, and 81.95%, respectively. Therefore, this study further established the efficacy of *Trichoderma* as an environmentally friendly biocontrol agent in controlling *M. phaseolina*.

Keywords: Biocontrol, biofungicide, *Macrophomina phaseolina*, *Trichoderma*, inhibition

Identification and phylogenetic relationship of fungi species associated with potato aphids in Bamenda, Northwest Region of Cameroon

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Potato (*Solanum tuberosum* L.) is one of the world's most important cultivated tuber crops in Cameroon. Potato aphids remain a major pest to potato plants, thus greatly reducing its productivity. Inadequate information still exists on identification of fungi species associated with potato aphids. The aim of the study was therefore to identify fungi species associated with potato aphids using molecular techniques to determine the entomopathogenic species which can be used to control potato aphids to increase potato productivity as well as increase food security. One hundred samples of aphid's cadavers were collected monthly from the field, put in zip lock bags and preserved in coolers. These samples were then transported to the laboratory and cultured on potato dextrose agar. After a period of 7 days, they were sub-cultured to obtain pure cultures. The pure cultures were obtained and molecularly identified using the ribosomal ITS and TEF regions. Results from cultural identification revealed fungi belonging to three genera: *Fusarium*, *Aspergillus* and *Penicillium* with different species in these genera. Sequence data analysis from the ITS gene regions revealed 6 fungi species namely, *Fusarium oxysporum*, *Aspergillus sydowii*, *Aspergillus niger*, *Curvularia affinis*, *Microascus murinus* and *Trichoderma erinaceum*. Also, 6 species with the translation elongation factor (TEF) were identified namely, *Cladosporium cladosporoides*, *Fusarium oxysporum*, *Fusarium Babinda*, *Trichoderma gamsii*, *Chaetomium cochiloides* and *Aspergillus niger*. Phylogenetic analysis produced a phylogram consisting of sequences of samples collected from the study area together with those from the GeneBank. Some of these fungi species have been reported to be entomopathogenic. Further research will screen entomopathogenic isolates that will serve as a biocontrol strategy against potato aphids which is an environmentally friendly method of pest control compared to synthetic pesticides.

Keywords: Potato, Aphids, Fungi, Identification, Food, Security

Molecular Identification of fungal species isolated from diseased cabbages in the western highlands of Cameroon

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Some fungal species of cabbage are pathogenic contributing significantly to pre-harvest and post-harvest losses leading to food insecurity. Therefore, a study was carried out to identify fungal species on diseased cabbage in the Western highlands of Cameroon. One hundred samples of diseased cabbage were collected from Santa and Dschang. Fungal species were isolated from the leaves and molecular identification based on Internal Transcribed Spacer (ITS) and Translation Elongation Factor (TEF) gene regions were done. The results based on molecular identification of fungal isolates based on ITS regions revealed that a total of 45 fungal species belonging to 12 genera with *Trichoderma* being the highest with 16 isolates followed by *Fusarium* with 10 isolates. The fungal species identified from TEF regions showed that 51 species of fungal species were isolated from cabbage belonging to 8 genera with *Trichoderma* the most dominant (26 species) closely followed by *Fusarium* (16 species). The results revealed that TEF gene regions were better in identifying some fungal species like *Fusarium* sp. as compared to ITS gene region is a universal identifier. Also, *Trichoderma* sp. were better identified by the ITS gene region. The findings suggest that molecular identification methods, particularly TEF gene regions, provide superior resolution for distinguishing certain fungal species compared to ITS regions. This research contributes to understanding fungal diversity and its implications for managing cabbage diseases, thereby supporting food security efforts.

Keywords: Molecular identification, *Fusarium* sp, TEF gene, cabbage, Cameroon

Diversity and identification of coprophilous Ascomycota from cow dung from different cattle Ranches in the North West Region of Cameroon

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Coprophilous fungi are saprophytic fungi that live on animal dung. Dung is rich in nitrogen, water-soluble minerals, growth factors, undigested food components and carbohydrates making it a rich substrate for the growth of fungi and other microorganisms. Coprophilous fungi are an important component of the ecosystem, responsible for recycling the nutrients in animal dung, and the study of these microorganisms has been advocated for the experimental study of ecosystems. The aim of this work was to document on the diversity and identification of coprophilous Ascomycota fungi from cow dung from three cattle Ranches in the North West Region of Cameroon. Identification of these coprophilous fungi was carried out using morphological and molecular methods. Dry cow dung samples were collected from three different cattle Ranches. One kilogram of dry dung samples was collected from each cattle ranch. Dry dung samples were subjected to the moisture chamber method. Isolation of coprophilous fungi was done in Malt Extract Agar (MEA). A total of 16 coprophilous Ascomycota was isolated from cow dung. Highest diversity of coprophilous fungi was observed in cattle Ranch 3 (Upstation cattle Ranch) secondly cattle ranch 2 (Alahbukam Cattle Ranch) and the least in cattle Ranch 2 (Alahki cattle Ranch). Highest species diversity was also observed in cattle Ranch 1. Morphological and molecular identification showed most of the species from the group Ascomycota. *Paracremonium contagium*, *Purpureocilium lilacinus* and *Meyerozyma guilliermondii*, *Clonostachys epichloe*, *Clonostachys rosea* and *Gibberella fujikuroi* were isolated for the first time on animal dung in our studies.

Keywords: Diversity, coprophilous fungi, identification, molecular analysis, Ascomycota

Session 2: Phylogenetic Analysis of Fungi

Taxonomic Update of the Diversity of *Lentinus*, *Panus* and *Pleurotus* in Cameroon based on Extracellular Enzymes, Morphology and Molecular Characteristics

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The genera *Lentinus*, *Panus* and *Pleurotus* consist of mainly saprobe wood inhabiting mushrooms with decurrent lamellae, white spore print that cause wood white rot. Some of them are edible or medicinal. Their systematics had been complex, evolving from traditional (morphology, physiology) to modern (molecular phylogeny) classification with many taxonomic changing. Hence, in the modern context the taxonomic study in these genera need to be revisited especially in Africa and Cameroon in particular. The present study is a contribution to modern study of the taxonomy of *Lentinus*, *Panus* and *Pleurotus* in Cameroon using morphological, physiological and molecular characteristics. The physiological study consisted to determine the extracellular enzymes complex of the species and the type of wood rot the cause and was carried out by method of spot test on mycelia in culture. Morphological study based on macroscopic and microscopic features included samples collected by us and those from herbaria (Br, E and K(M)). Phylogenetic study was based on the ITS region of rDNA and parsimony and neighbour-joining analysis were done using 15 species of *Lentinus*, *Panus* and *Pleurotus* to which sequences of related species and genera were added. All species caused white rot, producing laccase and facultative tyrosinase or peroxydase at variable intensities. Morphologically 7, 8 and 6 species of *Lentinus*, *Panus* and *Pleurotus* were identified respectively. *Lentinus* species were distributed in three sections: Section *Dicholamellatae* (*L. brunneofloccosus*, *Lentinus* cf. *badius* and *Lentinus cystidiatus*), Section *Rigidi* (*L. cladopus*, *L. sajor-caju* and *L. squarrosulus*) and Section *Tigrini* (*L. retinervis*). Members of *Panus* are distributed in Section *Panus* (*L. courtetianus*, *L. strigosus*, and *L. cf. strigosus*), Section *Velutini* (*L. fasciatus*, *L. similis*, *L. velutinus* and *L. cf. ciliatus*) and one unidentified Section (*Lentinus* sp.₂). Species of the genus *Pleurotus* are divided into three sub-genera: sub-genus *Coremiopleurotus* (*P. fuscusquamulosus*), sub-genus *Pleurotus* (*P. flabellatus*, *P. luteoalbus*, *Pleurotus pulmonarius* and *Pleurotus* sp.) and sub-genus *Tuberregium* (*P. tuber-regium*). The molecular phylogenetic did not support the monophyly of *Lentinus* (*sensu lato*) and divided it into genera *Lentinus* and *Panus* in Polyporales. Several samples gave double banded ITS sequences indicating more than one polarity of these species and their high degree of polymorphism. The absence of sequences of many species did not permit the determination of relationship between species within sections of the two genera. *Pleurotus* was placed within Agaricales and confirmed the distribution of *Pleurotus* species in the up cited sub-genera. It put *Pleurotus pulmonarius* is in the same lineage with *Pleurotus sajor-caju* confirming the latter as a synonym of *Pleurotus pulmonarius*. Efforts are still needed for a good understanding of diversity and systematics position of taxa in these genera and related groups for the suitable of their biotechnological and industrial potentials in Cameroon and in the world in general.

Keywords: Wood rotting mushrooms, Extracellular enzymes, Systematics, phylogeny, Cameroon.

Phylogenetic Relationships of Fungi

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Understanding the phylogenetic relationships among fungi is vital for advancing our knowledge of biodiversity, ecological interactions, and the evolutionary history of these organisms. This presentation examines the methodologies and molecular techniques used in fungal phylogenetic analysis, emphasizing the significance of fungal barcoding. By analyzing key molecular markers, such as the Internal Transcribed Spacer (ITS) and the large subunit (LSU) rRNA genes, this study highlights recent findings that have reshaped our understanding of fungal taxonomy and classification. Case studies illustrate the complexities of phylogenetic relationships across diverse fungal groups, revealing insights into their ecological roles and evolutionary patterns. Furthermore, the implications of phylogenetic analysis for conservation strategies are discussed, underscoring the necessity for effective management of fungal diversity in ecosystems. Despite challenges such as incomplete sampling and data interpretation hurdles, advancements in genomics and bioinformatics offer new avenues for research. The future of fungal phylogenetics lies in integrating genomic data with ecological and morphological information to provide a more comprehensive understanding of fungi. This paper aims to contribute to ongoing discussions in the field by exploring the interconnectedness of fungi within broader biodiversity conservation efforts.

Keywords: phylogenetic relationships, fungi, fungal barcoding, biodiversity, conservation

Phylogenetic Relationship of *Ganoderma* species in Mezam Division, Northwest Region, Cameroon

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Ganoderma P. Karst is a pathogen that causes butt, root, and stem rot in trees, eventually leading to their death. However, this fungal species can be used to treat various human diseases. Due to morphological similarities among species, it is necessary to understand the phylogenetic relationships among *Ganoderma* species. This research aims to determine the Phylogenetic relationship of *Ganoderma* species in the Mezam Division, Northwest Region, Cameroon. Nine villages were sampled using opportunistic sampling. DNA was extracted from the ITS and TEF gene regions using the sorbitol-CTAB method. The ITS and TEF gene regions were amplified using ITS1, ITS4, EF595F, and EF1160R primers. Their identities were determined in GenBank using BLAST in NCBI, and a phylogenetic analysis was performed using MEGA version 11. The study identified 8 and 6 distinct *Ganoderma* species from the ITS and TEF gene regions, respectively. This includes *Ganoderma applanatum*, *G. brownii*, *G. cupreum*, *G. gibbosum*, *G. lucidum*, *G. multipileum*, *G. multiplicatum*, and *G. weberianum* from its ITS gene region, and *G. angustisporum*, *G. australe*, *G. eickeri*, *G. orbiforme*, *G. multiplicatum*, and *G. weberianum* from its TEF gene region. *G. multipileum*, *G. brownii*, and *G. gibbosum* are new records. Seven clades were obtained from the ITS gene regions, and six from the TEF gene, compared to GenBank. Isolates from Cameroon clustered with those collected from South Africa, China, Japan, the USA, and Brazil. The collected specimens significantly clustered together and formed a monophyletic group with other *Ganoderma* taxa, with solid support from ML values, implying that they have self-derived characters and that the Mezam division is diverse regarding *Ganoderma* species.

Keywords: *Ganoderma* species, identification, molecular characters, phylogenetic relationship, Mezam Division

TWAS YOUNG AFILIAE NETWORK (TYAN) INTERNATIONAL THEMATIC WORKSHOP SESSION

Integrating Authorship Ethics and Citation Practices: A Framework for Promoting Research Integrity in Scientific Manuscript Writing

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The credibility and reproducibility of scientific research rest upon two foundational pillars: ethical authorship and accurate citation practices. This presentation integrates the International Committee of Medical Journal Editors (ICMJE) authorship criteria—which define legitimate contribution, roles of first, corresponding, and co-authors, and warn against honorary, guest, and ghost authorship—with the technical rigor of citation styles commonly required in scientific manuscripts, specifically Vancouver and Harvard. In-text citations in Vancouver style employ consecutively numbered references (e.g., superscript¹ or bracketed [1]), while Harvard uses author-date format (e.g., Smith, 2020). Each system has distinct rules for multiple authors, corporate authors, secondary references, and unpublished work, affecting how credit is traced and acknowledged. Proper citation extends beyond in-text attribution to meticulously formatted reference lists, where Vancouver orders entries numerically as they appear, and Harvard alphabetizes by author surname. These conventions ensure transparency, prevent plagiarism, and allow readers to verify sources—a practice as critical as ethical authorship in maintaining trust. We also discuss the role of digital tools (e.g., Mendeley, EndNote) in managing citations across journal-specific formats and the importance of selecting reputable journals to avoid predatory publications. By aligning authorship ethics with disciplined citation methodology, researchers can uphold integrity, enhance manuscript quality, and foster a culture of accountability in academic communication.

Keywords: Ethical authorship, citation, plagiarism, digital tools, integrity

Co-occurrence of Microplastics and Trace Metals in Coastal Bangladesh: Implications for Aquatic Ecosystems, Biodiversity, and Food Safety

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Trace elements and microplastics (MPs) are emerging global threats to aquatic biodiversity and human health, particularly in vulnerable coastal regions. This study provides an integrated assessment of these pollutants in the coastal ecosystems of Bangladesh, focusing on trace metal contamination in cultivated fish from Bhola Island and MPs in sediments from the Karnaphuli River estuary and Kuakata beach. Analysis of ten fish species via Atomic Absorption Spectrophotometer revealed detectable levels of metals (Fe, Zn, Cu, Co, Mn, Ni, Pb, Hg, Cd), though health risk indices (EDI, THQ, TTHQ <1) and carcinogenic risk values (<10⁻⁶) indicated no immediate threat to consumers at current intake levels. Concurrently, microplastic surveys identified significant contamination, with sediment concentrations reaching 59.5 items kg⁻¹ in estuaries and 284 items kg⁻¹ at beaches, dominated by PET, PE, PS, and nylon, and with Pollution Load Index (PLI) confirming widespread pollution. Multivariate analyses traced metal origins to both natural and anthropogenic sources, while MP morphology and polymer profiles highlighted distinct pollution pathways. Together, these findings underscore the intertwined pressures of chemical and plastic pollution on aquatic biodiversity and local food security, urging integrated monitoring and management in the context of climate change and coastal vulnerability.

Keywords: Trace elements, microplastics, coastal ecosystems, food security, Bangladesh

From Pest Control to Agroecosystem Resilience: Lessons from Climate-Smart Push-Pull Farming in Kenya

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Sustainable crop protection is fundamental to food security, ecosystem stability, and biodiversity conservation, particularly in climate-vulnerable agroecosystems of sub-Saharan Africa. The fall armyworm (*Spodoptera frugiperda*) continues to pose a major threat to maize production, with management practices often dominated by synthetic pesticides that raise economic, environmental, and health concerns. This presentation draws on field-based evidence from a modified climate-smart push-pull cropping system evaluated in the semiarid lands of Kenya, highlighting ecologically grounded approaches to pest management. The study assessed drought-tolerant push crops, including green leaf *Desmodium* (*Desmodium intortum*) and edible legumes, in combination with alternative pull crops (*Brachiaria* grass and Napier grass) under rainfed dryland conditions. Results demonstrated significantly reduced fall armyworm incidence and damage severity in push-pull systems compared to maize monocropping, confirming the effectiveness of climate-adapted intercropping strategies for pest suppression. *Desmodium* consistently performed as the most effective push crop, while *Brachiaria* and Napier grasses showed comparable suitability as pull crops, offering flexibility for adoption across diverse farming contexts. Beyond pest control, the push-pull system reduced dependence on chemical insecticides, enhanced crop diversification, and strengthened agroecosystem resilience. Such systems create biologically complex production landscapes that support long-term crop health and productivity. While fungal barcoding was not directly applied in this research, the presentation highlights its relevance as a complementary tool for crop protection, particularly in characterizing fungal communities associated with pest suppression, soil health, and plant resilience. By positioning crop protection as an ecological intervention, this keynote underscores the importance of integrating agronomic innovation with biodiversity-informed tools to advance sustainable agriculture in dryland regions.

Keywords: Push-Pull, Agroecology, Biodiversity, Crop Protection, Sustainability

Session 3 and 4: Fungi sequence analysis, bioinformatics and Fungi genetics

Expanding the *Coltricia* lineage from West Africa through DNA barcoding

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Coltricia (Hymenochaetales, Hymenochaetaceae) is a cosmopolitan group of wood-inhabiting fungi known for its ecological role in nutrient cycling and ectomycorrhizal associations, particularly in tropical ecosystems. Species diversity of *Coltricia* in tropical West Africa is poorly explored, with only four species previously documented from the region. Recent field surveys were conducted in Benin, Guinea, and Togo, leading to the collection of six *Coltricia* specimens. Through a combination of morphological and molecular analyses, two new species, *Coltricia langeri* and *Coltricia mosseboi*, were identified and described. Phylogenetic analyses based on sequence data of the internal transcribed spacer (ITS), large subunit ribosomal DNA (28S), and translation elongation factor 1-alpha (*EF1a*) regions confirmed the placement of these new species within *Coltricia*. Our results also revealed the polyphyletic nature of *Coltricia* and its close relationship with *Coltriciella*, challenging current generic boundaries. A dichotomous key to the six *Coltricia* species now known from tropical Africa is provided. This study expands the known diversity of *Coltricia* in Africa to six, contributing to the understanding of fungal diversity in tropical forests. The discovery of these new species highlights the need for further exploration and conservation of fungal species in West African ecosystems.

Keywords: *Coltricia*; ectomycorrhizal associations; fungal biodiversity; tropical West Africa; wood-decay fungi

Molecular profiling of the rhizosphere mycobiome of *Azelia africana* in Benin: implications for conservation and restoration

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Azelia africana (African oak) is a keystone tree with high socio-economic importance across tropical Africa. Yet, the species regeneration in wild is challenged by poor mycorrhization and vulnerability to fungal pathogens. We used high-throughput DNA sequencing to characterize the rhizosphere mycobiome of *A. africana* across three forest reserves in Benin and to identify indicator species relevant for conservation interventions. From 120 soil cores (30 composite samples), we profiled fungal community composition and functional guilds, then used constrained correspondence analysis to test the influence of tree traits on community structure. Co-occurrence network analysis mapped interaction patterns within the fungal assemblage, and random forest models identified site-predictive taxa. The results reveal a taxonomically and functionally diverse fungal community, with a high representation of plant pathogens that varied significantly among sites. Tree height partially explained variation in community composition for both ectomycorrhizal and pathogenic guilds. Particularly, *Russula* spp., *Ganoderma enigmaticum*, and *Ganoderma parvigibbosum* were associated with taller trees. *Thelephora* emerged as the core ectomycorrhizal genus across site, with *Thelephora maroana* being the most represented species. Network analyses showed higher node density and connectivity among pathogenic taxa, suggesting more complex and potentially resilient pathogen networks. Indicator ASVs included *Thelephora* and *Ganoderma* spp. for Pendjari Forest and *Fusarium* spp. for Lama Forest. This study provides the first molecular baseline of soil fungal communities associated with *A. africana* in these tropical West African forests. Our findings identify candidate mycorrhizal taxa for inoculation trials and highlight pathogen taxa that need monitoring, offering actionable molecular targets to inform restoration strategies and improve the long-term conservation of this threatened keystone species.

Keywords; *Azelia africana*, molecular profiling, conservation, restoration, Benin

Diversity of Arbuscular Mycorrhizal Fungi on three land - use types in the Bamenda Highlands, Cameroon

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Land use types significantly impact Arbuscular Mycorrhizal Fungi (AMF) diversity with forests and wildlife-grazed areas which are less disturbed generally showing distinct communities and higher richness compared to plantations which are monocropping intensive agriculture. Another factor which has an influence on AMF community composition and species richness is soil properties. Understanding the effects of land use changes on arbuscular mycorrhizal fungal (AMF) communities may greatly benefit ecosystem conservation and restoration. The aim of the study was to understand the effect of land use changes and soil physiochemical properties on AMF community in three land use types: forests, grazing land and eucalyptus plantation in the Bamenda Highlands of Cameroon. The SPUN soil sampling technique was used to collect soils from the three land use types and community investigation was done using SSU gene region with illumina MiSeq sequencing platform. The effect of soil physiochemical properties on AMF diversity in the three land use types was also investigated. Our results showed that AMF species richness was higher in Forest followed by grazing land and least with Eucalyptus plantation. The concentrations of soil OC, OM, N, Mg, SBE, and BS was highest in Forest, C/N, Ca and CEC was highest in grazing land and Na and P was highest in plantation. These were important soil factors accounting for the AMF community change. *Gigaspora* was the dominant genus of AMF indicator species in Forest, *Acaulospora* in grazing land and *Glomus* in Eucalyptus plantation. A total of 12 species of AMF were identified in the three land use types. Overall, our results indicated that there were differences in AMF species richness in the three land use types and the AMF species identified will help in restoring these three land use types.

Keywords: Identification, species richness, SSU, Next generation sequencing

Assessment and Utilization of Mycorrhizal Fungal for the Conservation and Restoration of the sacred forest of the western highlands

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Mycorrhizal fungal networks are essential for forest organization, regeneration, and ecosystem stability through their role in nutrient acquisition and seedling establishment. This study assessed the diversity and utilization potential of mycorrhizal fungi for the conservation and restoration of sacred forests in the Western Highlands of Cameroon. The study was conducted in the Bamendjo, Bamenjinda, and Bamessingue sacred forests located at about 2000 m asl in the Bamoutos Department. These forests represent some of the last remnants of natural forest in an increasingly agricultural landscape and are under growing anthropogenic pressure. Thirty soil samples were collected evenly across the three sites and analyzed for soil physicochemical properties and mycorrhizal diversity. Molecular techniques, including DNA extraction and Illumina sequencing, were employed for fungal identification where SSU was amplified using WANDA/AML2 primers. Soil properties differed significantly among sites, with Bamessingue soils recording the highest C/N ratio (25.09), organic matter (9.93%), and organic carbon (5.76%). A total of 14 Arbuscular Mycorrhizal Fungi (AMF) samples were identified such as *Acaulospora*, *Archacospora*, *Claroideoglossum*, *Dentiscutata*, *Diversispora*, *Entrophospora*, *Gigaspora*, *Glomus-Sensu-Lato*, *Pacispora*, *Paraglossum*, *Racocetra*, *Rhizophagus*, *Scutellospora* and *Setoglossum*. The results provide baseline data to support the integration of native mycorrhizal fungi into nursery practices. This approach is expected to reduce seedling mortality and enhance restoration success in sacred forest ecosystems.

Keywords: Arbuscular mycorrhizal fungi, Sacred forests, Forest restoration, Soil fertility, Western Highlands Cameroon

Session 5: Fungi Host Identification and Multidisciplinary

How Fungi Can Rethink Fertilizer Use in Agriculture

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Fertilizer has played a central role in ensuring global food security, yet its increasing use is associated with nutrient losses, water pollution, greenhouse gas emissions, and rising production costs. At the same time, modern agriculture has achieved major productivity gains through mineral fertilizers, but these gains increasingly come with environmental, economic, and biological costs, including nutrient losses, soil degradation, and declining nutrient-use efficiency. Fungi, a crucial component of agricultural systems remains largely overlooked. This keynote highlights the role of fungi as an invisible workforce that underpins nutrient acquisition, soil structure, and crop resilience. Through extensive hyphal networks, fungi act as nutrient brokers, enhancing the uptake of phosphorus, nitrogen, and micronutrients while mediating carbon flows between plants and soil. However, intensive fertilizer regimes can disrupt these symbiotic relationships, reducing biological contributions to nutrient efficiency. Research and field examples show that excessive fertilizer use can disrupt fungal partnerships, reducing their benefits over time. This talk explores how smarter nutrient strategies, timing, placement, reduced disturbance, and crop diversity or defense can work with fungi. Supporting this biological workforce can help farmers maintain yields, improve soil health, and reduce reliance on costly inputs.

Keywords: Fungi; Fertilizer; Nutrient efficiency; Sustainable agriculture

Abundance of arbuscular mycorrhizal fungi associated with the rhizosphere of plants during crop rotation between *Sorghum bicolor* L. Moench and *Glycine max* L. Merrill

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This study aimed to evaluate the influence of biofertilizers applied during crop rotation between *Sorghum bicolor* and *Glycine max* on the diversity of native arbuscular mycorrhizal fungi in the soil. The experimental design was a split-plot design. Four treatments were applied: the control, plants fertilized with *Bradyrhizobium japonicum*, *Trichoderma asperellum*, and the *Bradyrhizobium japonicum* + *Trichoderma asperellum*. Two cultivation campaigns were carried out on the same cultivation site. At the cultivation site. Before planting, the physicochemical characteristics of the soils of the site were determined. For the analysis of AMF diversity, soil from the rhizosphere of *S. bicolor* and *G. max* plants, as well as plant roots, were collected randomly. mycorrhization indices and morphological characterization of the arbuscular mycorrhizal fungi associated with the rhizosphere of each plant under the two cultivation campaigns were carried out according to the applied treatments. The results obtained showed that the soil pH was acidic, with a value of 5.8, very low in assimilable phosphorus, rich in calcium ions, and with a clayey texture. The highest mycorrhization frequencies were observed in *S. bicolor* during the first cultivation campaign at month 3, reaching 97.50% in plants fertilized with *B. japonicum* and *T. asperellum*. In the second cultivation campaign, under both non-rotation and rotation conditions, values of 100% were recorded at month 3 in the presence of *B. japonicum* and *T. asperellum*, respectively. The relative abundance of arbuscular mycorrhizal fungal spores was 6.25% under rotation conditions with *B. japonicum* and 4.9% under non-rotation conditions with *T. asperellum*. Seven genera of arbuscular mycorrhizal fungi (AMF) were identified in the soils using data from <https://invam.ku.edu>: *Acaulospora* sp., *Claroideoglosum* sp., *Entrophospora* sp., *Funneliformis* sp., *Gigaspora* sp., *Glomus* sp., and *Scutellospora* sp., belonging to 7 families: Acaulosporaceae, Claroideoglomeraceae, Gigasporaceae, and Glomeraceae.

Keywords: *Sorghum bicolor*, *Glycine max*, crop rotation, and arbuscular mycorrhizal fungal diversity

Diversity of arbuscular mycorrhizal fungi along an altitudinal gradient on Mount Cameroon

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Mount Cameroon is a major biodiversity hotspot that is increasingly threatened by anthropogenic activities and environmental degradation, resulting in the loss of both aboveground and belowground biodiversity. This study aimed to evaluate the influence of environmental factors on the diversity and distribution of arbuscular mycorrhizal fungi (AMF) across different vegetation levels on the southwestern slope of Mount Cameroon. Soil and root samples were collected during the dry season (February 2024) using a mixed sampling design along an altitudinal gradient. Sampling was conducted at two soil depths (0-20 cm and 20-40 cm). At each site, a floristic survey of dominant plant species was carried out. Soil physicochemical properties, mycorrhizal colonization rates, and AMF spore density and morphology were analyzed using standard laboratory methods. The results showed high mycorrhizal colonization rates, reaching 100% in several dominant plant species from submontane, montane, and subalpine vegetation types. Soils were predominantly silty-clayey with acidic pH values ranging from 4.5 to 6.4 (H₂O). AMF spore densities varied with altitude and soil depth, with higher densities recorded in submontane forests. In total, nine AMF genera were identified, including *Glomus*, *Gigaspora*, *Acaulospora*, *Funneliformis*, *Rhizophagus*, and *Scutellospora*, with *Glomus* being the most dominant and widely distributed genus across all vegetation levels. These findings highlight the strong influence of altitude, vegetation type, and soil depth on AMF community structure and emphasize the importance of integrating molecular identification and DNA barcoding approaches to improve the characterization and conservation of fungal biodiversity in tropical mountain ecosystems.

Keywords: Arbuscular mycorrhizal fungi, biodiversity, altitude gradient, Mount Cameroon, fungal conservation.

Macrofungal Diversity in Gashaka Gumti National Park Nigeria

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National parks, like Gashaka Gumti-National Park were established to protect, preserve, conserve and manage representative samples of indigenous flora and fauna. Diversity studies of macrofungi have grown during the recent years, because they are important components of biodiversity serving as key primary colonizers in ecosystem, deadwood decomposition and with variety of uses as food, pharmaceutical and medicinal qualities. This study reports on the wet season diversity and distribution of macrofungi in Gallery Forest and Savanna woodland vegetation of Gashaka Gumti-National Park in Northern Nigeria based on fruit body characteristics. A total of 37 species of macro fungi distributed across 21 families were encountered. The Gallery Forest recorded the highest number of species (21 species) compared to Savanna woodland (17 species) during the sampling period. The distribution of species across families showed that Mycenaceae had the highest number of species, followed by Agaricaceae, Bolbitiaceae, Xylariaceae and Tricholomataceae while twelve of the other families had only one species each. This revealed that macrofungi utilized wide range of substrates where the soil had 21 (53.85 %) species, followed by log with 18 (48.72 %), leaf litter 5 (10.26 %) and one (5.13 %) species from fruit shell. The availability and the types of substrates are important drivers of macrofungal composition with majority (78.38 %) of macrofungal species occurring on a single type of substrate (substrate-specific). The list of macrofungi in this study provides the baseline information on the assessment of changes in macrofungal diversity in the National Park.

Keywords: Identification, mushrooms, substrate, distribution

Spore Density and Diversity of Arbuscular Mycorrhizal Fungi Across Various Cropping Systems in Smallholder Farms in Makueni County, Kenya

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Arbuscular mycorrhizal (AM) fungi are key soil symbionts that improve plant nutrient uptake, drought tolerance, and soil structure traits, making them particularly important in semiarid smallholder farming systems such as those in Makueni County, Kenya. At the same time, smallholder farmers are widely recognized for producing approximately one-third of the world's food and for their significant contribution to below-ground biodiversity. Their diverse cropping systems play a crucial role in improving soil health and sustaining biodiversity. Against the background, this study examined the role of cropping systems in shaping the AM fungi spore density and genera in the dryland area of Makueni County, Kenya. Soil samples from 34 farms were collected after harvesting during the main growing season. AM fungal spores were extracted using the wet-sieving and decanting method and morphologically identified. These results showed that key components of the cropping systems significantly influenced spore density and diversity of AM fungi. A total of five genera were detected: *Acaulospora*, *Scutellospora*, *Gigaspora*, *Dentiscutata*, and *Racocetra*. Multi-species intercropping supported a higher number of genera compared with monocropping. Notably, multi-species systems involving pigeon peas were strongly associated with the genus *Dentiscutata*. Farms amended with farmyard manure exhibited higher spore density and greater genus richness than farms without soil amendments. However, the genus *Racocetra* was recovered exclusively from farms that had been amended with inorganic fertilizers. These findings underscore the potential of cropping systems to enhance soil biodiversity and strengthen microbial network interactions. While further research across different climatic regions and cropping systems is necessary, the application of DNA barcoding is recommended for more accurate identification of AM fungi species

Keywords: Arbuscular mycorrhizal fungi, morphology-based taxa, community structure, smallholder farming systems

Agaric Mushrooms Diversity and Ethnomycology in Primary and Secondary Montane Forests of Kedjom-Keku, North-West Region of Cameroon

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Fungi are important components of forest ecosystems where they play several roles as saprotrophs (nutrient recyclers), mutualists (partners of vascular plant species) or parasites (Regulator of the population). In Cameroon, less than 3% of fungal species have been documented and the majority of studies were done in lowland forests and very few information is available on the biodiversity of these organisms in montane and sub-montane forests as well as the traditional knowledge of the natives on these organisms. The aim of this work was to study the diversity of Agaricoid fungi in the montane forest of Kedjom-Keku in the North West Region of Cameroon. Samples were collected at an interval of 15 days in three months from mid-March to mid-June 2018 on two permanent plots of 50 m x 50 m in the primary and secondary forests. The samples collected were identified based on their morphology such as colour, shape, size of the gill, stipe, cap and spore and a herbarium of dry samples was constituted. Jaccard similarity index was calculated to compare the mushroom diversity in the two forest types. Ecology of species was accessed by determining their substrate and mode of life. Ethnomycological information was accessed from 100 administered questionnaires on local names, uses and myth of collected mushroom species from natives and data such as species, genera, and family richness's and data on descriptive statistics was calculated in Excel 2013. A total of 215 samples were collected representing 2 orders, 16 families, 34 genera and 76 species. Out of the 76 species collected, 30 species and 27 species were strictly collected in the primary and secondary forests respectively and 19 species were common to both forests. In the primary forest, the richest genera were *Mycena*, *Crepidotus*, *Marasmiellus* and *Agaricus* and the richest families were; *Marasmiaceae*, *Mycenaceae* and *Agaricaceae* while in the secondary forest, the richest genera were *Mycena*, *Marasmius* and *Gymnopus* and richest families were *Agaricaceae*, *Marasmiaceae* and *Mycenaceae*. For the ecology, 56.6% of the species were collected on wood, 42.1% of the species on soil and 1.3% of the species on litter; all the species were saprotrophic. For ethnomycology, local names, uses and myths of collected mushroom samples were gotten from the natives of Kedjom-keku. The species richness was higher in the primary forest than the secondary forest making it ideal for conservation of macrofungi. Extension and long-term monitoring of fungal diversity in such ecosystems are needed using modern tools for fungi identification for a better understanding of the contribution of fungi in the conservation of forest ecosystems.

Keywords: Montane forests, Macrofungi, Diversity, Ethnomycology, Conservation, Tropical Africa

Study and Comparison of Nutritional Profiles of Some Wild Edible Species of *Termitomyces* and *Pleurotus* of Cameroon.

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Termitomyces and *Pleurotus* are among the mushroom species commonly consumed by the populations of Cameroon. To demonstrate their nutritional value, the nutritional quality of eighteen (18) samples of different species of *Termitomyces* and seven (07) of *Pleurotus* were analyzed. Measurements were taken of ash, water, carbohydrate, crude fiber, lipid, protein and energy content. The results indicate that these mushrooms are rich in lipids (11.75 g/100 g DM), proteins (25.89 g/100 g DM), crude fiber (13.91 g/100 g DM), water (86.82 g/100 g FM), ash (6.51 g/100 g DM), carbohydrates (27.57 g/100 g DM) and energy (324.13 kcal/100 g). Highly significant differences ($P < 0.05$) were observed between species. For example, *Termitomyces* sp.5 (28.78 g/100 g DM) is rich in ash, while *P. pulmonarius* (28.52 g/100 g DM) stands out for its high lipid content and *T. griseiumbo* (49.38 g/100 g DM) has a remarkable level of protein. In terms of carbohydrates, *P. ostreatus* (55.51 g/100 g DM) stands out, while *P. tuber-regium* (26.79 g/100 g DM) has a notable proportion of crude fiber. In terms of energy, *P. pulmonarius* (459.76 kcal/100 g DM) still stands out. These results demonstrate the significant nutritional potential of these mushrooms, which are used to reduce nutritional deficiencies and facilitate intestinal transit due to their fiber content. The domestication of these mushrooms would appear to be a good alternative to both reduce the risks of depletion of this resource and also its sustainable management.

Keywords: Mushroom, nutritional value, nutritional deficiencies, domestication, sustainable management.

Phenology of *Pleurotus* species and Host Trees in Ngel-Nyaki Montane Forest for Sustainable Conservation

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This study was carried out to observe the fruiting activities of some *Pleurotus* species and phenology of their host trees for sustainable conservation in the Ngel-Nyaki Montane Forest ecosystem. A general survey for *Pleurotus* species was carried out in the montane forest and points of observed or spotted *Pleurotus* species and their hosts were marked using Global Positioning System (GPS). Points of the *Pleurotus* species and purposefully selected matured life trees of the *Pleurotus* hosts were tagged and monitored twice for the monthly fruiting of *Pleurotus* species and host trees phenology. Rapid Rural Appraisal (RRA) and household survey was also conducted to assess local knowledge about the periods whereby *Pleurotus* species in the montane forest (Ngel-Nyaki) are always available. Descriptive statistics was used to present data on the monthly fruiting and phenological activities using R studio statistical packer version 4.2. Species similarity between rainy and dry seasons was determined using the Jaccard's similarity coefficient (Cj). *Pleurotus* species were observed fruiting mostly within late rainy season and early dry season to late dry season and early rainy season. The four (4) different *Pleurotus* species (*Pleurotus pulmonarius*, *Pleurotus ostreatus*, *Pleurotus eryngii* and *Pleurotus djamor*) spotted were observed fruiting in the months of October, 2021 to December, 2021. One of these *Pleurotus* species (*Pleurotus djamor*) was observed fruiting again as from April, 2022 to June, 2022 while the other three started fruiting but from May to July, 2022 for *Pleurotus eryngii* and *Pleurotus ostreatus* while *Pleurotus pulmonarius* was lastly spotted fruiting in June, 2022. *Pleurotus eryngii* were spotted again growing from November to December, 2022. Jaccard's similarity coefficient (Cj) had a value of 1.0. The respective host trees were: *Polyscias fulva*, *Ficus lutea* and *Anthonotha noldeae*. The phenological activities of the host tree species were same to that of *Pleurotus* species having its peak in mid dry season. Information on these very important events could really go a long way to assist conservators to curb the over exploitation of these *Pleurotus* species and their host trees especially those that produce edible fruits. Conservators are hereby encouraged to carry out more studies on *Pleurotus* species fruiting and phenological activities of host trees to master these very important events for better protection of the wild.

Keywords: Phenology, *Pleurotus* species, Host Trees, Ngel-Nyaki, Montane Forest Sustainable Conservation

Taxonomic Diversity of Coprophilous and symbiotic fungi in rangelands of Adamawa Region of Cameroon

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The Adamaoua region of Cameroon, characterised by its vast savannah landscapes, is home to a crucial but still largely unexplored fungal biodiversity. This study focuses on the taxonomic diversity of fungi that play an essential ecological role in these ecosystems: coprophilous and symbiotic fungi. Coprophilous fungi are saprotrophs that grow exclusively on the excrement of herbivores. They play a fundamental role in the nutrient cycle, notably by breaking down the cellulose and lignin ingested by livestock and recycling nitrogen and phosphorus. The Adamaoua region, with its intense pastoral activity, provides a rich and constant substrate. Species richness is often correlated with the animal's diet and the seasonal microclimates of the rangelands, highlighting the importance of these organisms in the health of pasture soils. At the same time, symbiotic fungi, particularly mycorrhizal fungi, are vital to the flora of the savannah. They form mutualistic associations with plant roots, facilitating the absorption of water and minerals in exchange for sugars produced by photosynthesis. It contributes to plant resilience in the face of frequent water and nutrient stress in savannah areas. However, information on this fungal diversity in Adamaoua is non-existent. The present study was to document the macrofungi of rangeland of this region. Fungi collections were done in Mai 2025 to October 2025 and collected samples identified base on the macroscopic and microscopic characters while their substrate and mode life where noted. In total, 270 samples of mushrooms for 43 species, 28 genera, 12 families and 4 orders were collected. Species included coprophilous (31,34 %), ectomycorrhizal (25,37 %) and Termite associated fungi (7,46 %). These results give and over view of fungi in the Sudano-Guinean agroecological zone of Cameroon. However biotechnological studies are needed to determine their potential application in industry.

Keywords: fungi, diversity, coprophilous fungi, agroecological zone, symbiotic fungi

Evaluation of Mycoremediation Potentials of Some Fungal Species on Oil-Based Drill Cuttings in the Niger Delta, Nigeria

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This study evaluates the mycoremediation potential of five indigenous fungal species (*Artolenzites acuta*, *Trametes elegans*, *Ganoderma lucidum*, *G. resinaceum*, and *G. australe*) for the degradation of oil-based drill cuttings (OBDC) from the Niger Delta, Nigeria. The research was conducted in two phases: first, optimizing fungal spawn production on rice bran, corn cob, and a mixed substrate; and second, assessing the baseline contamination profile of treated and untreated OBDC before fungal inoculation. Spawn production results revealed that the mixed substrate (rice bran + corn cob) supported the highest mycelial growth, with *A. acuta* and *T. elegans* exhibiting the fastest colonization rates. Baseline characterization of OBDC showed that despite prior industrial treatment, residual contaminants remained critically high, including Total Petroleum Hydrocarbons (TPH: 4000 mg/kg) and heavy metals such as lead (161.74 mg/kg). A mycoremediation experiment was subsequently initiated by inoculating OBDC with fungal spawn under controlled conditions. Although final degradation results are pending, this work establishes a robust methodological framework for fungal-based bioremediation and highlights the promising potential of selected fungal species to remediate complex hydrocarbon and heavy metal contamination in oil-polluted environments. The findings support the development of sustainable, eco-friendly remediation strategies for the Niger Delta region.

Keywords: Mycoremediation, Oil-based drill cuttings, Fungal species, Niger Delta, Hydrocarbon degradation, Heavy metals

Evaluating the Performance of Oyster Mushrooms Grown on Various Organic Waste Substrates in Bamenda Town, Western Highlands of Cameroon

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Mushroom production in Cameroon is still at infancy due to unsustainable production techniques. An evaluation of the performance of three oyster mushrooms species (*Pleurotus ostreatus*, *Pleurotus sajor-caju* and *Pleurotus florida*) grown on three organic substrates (sawdust, corncobs and rice-husk) was carried out in view of optimizing mushroom production in Bamenda town. Bulked substrates were each supplemented with kernel cake on which slake lime and water was added to normalize pH and water respectively. The mixed substrates were subsequently filled in polythene bags following a 2-factor factorial experiment with 10 replicates per treatment, arranged in a Completely Randomized Design. Following sterilization and cooling of the substrates, these were then inoculated with the different mushroom spawns. The inoculated substrates were immediately incubated under relatively dark conditions. Data collected on mushroom yield and components was analyzed following ANOVA and correlation. Both mushroom species and substrate type significantly influenced mushroom yield. The substrates significantly ($P < 0.005$), number of fruiting bodies ($r = 0.37$; $P > 0.01$) and primordia formation ($r = 0.33$; $P > 0.03$). The good performance of corncobs can be explained by the physical and chemical properties of the substrate. It equally took minimum days for mycelia growth and primordial formation when grown on corncobs (19.9 days). Corncobs can therefore be recommended to mushroom farmers as the best substrate for maximum production of oyster mushrooms. In terms of their growth cycles, no significant variations ($P > 0.05$) for the mushroom species under the different growth substrates was observed. Practically, the selection of the type of organic matter substrate for mushroom cultivation in Bamenda town is critical. While mushroom species adopted may be dictated on spawn availability.

Keywords: Organic substrate, Oyster mushroom, yield, Bamenda.

Effects of Basalt Rock on the Growth Rate and Yield of Green Peeper in Bambili

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The ability to increase green pepper output by local farmers and small home garden owners are constrained by many factors amongst which is the inability to purchase inorganic fertilizers. The study was carried out in Bambili, Mezam division North West region of Cameroon using a Randomized Complete Block Design (RCBD) with four treatments and three replications in order to assess the effects of basalt rock on the growth rate, disease incidence and yield of green peeper. Treatment zero (T0) serves as the control, Treatment one (T1) was made up of poultry manure, Treatment two (T2) with basalt rock powder and Treatment three (T3) made up of a mixture of basalt rock and poultry manure. Data was analyzed using ANOVA and comparing the means using LSD at $p < 0.05$. There was a significant difference in most of the growth and yield parameters with the highest plant height which was recorded in T2 composed of basalt while the least in T0 that is control, number of leaves was highest in T1 (manure treatment) with the least being control, while the highest leaf area index was gotten in T2 (Basalt treatment). For stem girth, a progressive increase was recorded as the number of weeks increased after planting with the highest still recorded at the level of T2 and control with the least. The analysis of variance at ($p < 0.05$) showed a statistically significant difference in the stem girth in different blocks from the 4th week to the 7th week after planting. Yield parameter such as highest fruit weight was recorded in T2 (42g) and control T0 being the lowest (15g) and the highest number of fruits was with T2 (19.33 cm) while T0 recorded the least number of fruits, with fruit diameter (11cm).

Keywords: Basalt rock, growth rate, disease incidence, yield, Bambili.

Ecosystem services of cocoa agroforestry systems around a forest concession in South Cameroon

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Agroforestry systems are common in rural landscapes in the Congo Basin. They contain significant biodiversity and contribute to agricultural production, human health and food security. However, when the source of cocoa, timber and oil palm exported to the European Union, alignment with zero-deforestation regulations is challenging. This study examines how do cocoa and oil palm agroforestry systems in Southern Cameroon contribute to the socio- ecological sustainability of rural communities, in terms of ecosystem services, resilience and land governance. Based on qualitative and statistical analysis of interviews with 108 households and 7 focus group discussions in villages cultivating cocoa, and a floral inventory of 65 plots covering 15 ha, the results show these systems have a high level of floristic richness, characterized by a high diversity and density of conserved and introduced species. The majority of systems were inherited and are highly valued for their provision of multiple products and services, derived from 71 native and exotic species. Ecosystem services provided include food and medicinal products and cash crops, cultural identity values including land tenure, regulating and supporting services of shade, water, wind and climate regulation, and soil fertility. The diversity and complexity of architectural profiles increase with proximity to the forest. Households perceive four main constraints to manage systems: lack of financing, difficulties accessing phytosanitary products to treat cocoa pests and diseases, labour shortages and lack of technical knowledge to increase production and income. These limit further valorization of the agroforestry systems and farmers ability to respond to international regulations.

Keywords: Ecosystem service, agroforestry system, biodiversity, forest concession.

Ecosystem-Based Adaptation Strategies to Climate Variability and Livelihood Resilience Amongst Farmers in Santa Sub-Division, Northwest Region, Cameroon

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In the international climate policy arena, Ecosystem-based Adaptation has become the preferred adaptation approach in building resilience to climate change in the least developed and developing countries. Ecosystem-based adaptation is the use of biodiversity and ecosystem services as part of a strategy to help people adapt to climate change. Ecosystem-based Adaptation (EbA) approaches, like agroforestry and soil conservation, can significantly boost resilience, but their specific effectiveness in Santa's unique socio-ecological setting isn't well understood. There's a crucial need to examine how current EbA practices impact farmers' livelihood resilience in the face of climate change. Specifically, this work has categorized existing EbA practices, assessed livelihood resilience, and examined EbA's contribution to farmers' resilience. The study made use of a mixed methods data collection approach and data analysis was done using descriptive and inferential statistics for quantitative data as well as theme-based analysis for qualitative data. Findings revealed that, while agroforestry was widely adopted, conservation agriculture emerged as the most prevalent EbA strategy (92% adoption). The findings also indicated that natural capital significantly contributes to climate resilience. Furthermore, conservation agriculture, diversification of agricultural systems, and restoration of degraded lands were identified as the primary EbA strategies enhancing farmer resilience, contrary to the initial hypothesis that emphasized agroforestry's leading role in both adoption and contribution to resilience. This study highlights that while agroforestry is widely adopted, conservation agriculture is the most prevalent and impactful EbA strategy for enhancing farmer resilience in Santa, contributing significantly to natural capital. Given its proven effectiveness, we recommend that future adaptation initiatives prioritize and scale up the implementation of conservation agriculture, alongside promoting the diversification of agricultural systems and the restoration of degraded lands, to robustly bolster farmer resilience against climate change. Further research should delve into the socio-economic factors influencing the adoption and sustained practice of these key EbA strategies.

Keywords: Ecosystem-based Adaptation (EbA), Resilience, Livelihood, Farmers

Establishing a Biodiversity Baseline for Key Insect Taxa in the Tchabal Mbabo - Gashaka Gumti National Park (GGNP) Transboundary Landscape

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Transboundary landscapes are vital corridors for biodiversity conservation, yet they often suffer from significant data gaps due to logistical and political complexities. The Tchabal Mbabo massif in Cameroon and Gashaka Gumti National Park (GGNP) in Nigeria form a crucial, yet understudied, transboundary ecosystem. This project, supported by the JRS Biodiversity Foundation, focuses on establishing a comprehensive biodiversity baseline within the critical transboundary link between Tchabal Mbabol (TM) and Gashaka Gumti National Park (GGNP). The overall objective of the study targets three major animal groups: mammals, birds and insects. The Cameroonian research team will focus on insect diversity, specifically targeting three key insect groups that serve as vital integral components of ecosystem functioning: butterflies (Lepidoptera), bees (Anthophila), and rove beetles (Staphylinidae). Butterflies and bees provide crucial pollination services, while staphylinids serve as sensitive bioindicators of soil and leaf-litter health. By utilizing standardized sampling protocols including Pollard-walk transects, pan trapping, and pitfall/Winkler extraction, this study aims to document species diversity, abundance and distribution across the TM-GGNP landscapes. The resulting data will be integrated into open-access biodiversity databases which will be invaluable to informing targeted cross-border conservation strategies, assessing the impacts of environmental change, and fostering collaborative transboundary management. A core component of this initiative is regional capacity building, involving the recruitment and training of students in advanced entomological field methods and specimen curation. This presentation highlights how targeted invertebrate surveys and international collaboration are fundamental to safeguarding the biodiversity of African montane and forest-savanna mosaics.

Keywords: Transboundary Biodiversity, Lepidoptera, Anthophila, Staphylinidae, TM-GGNP, JRS Biodiversity Foundation.

POSTERS

Identification and phylogenetic relationship of fungal species associated with cassava leaves (*Manihot esculenta* Crantz.) in Bamenda, (Northwest Region) Cameroon.

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Cassava (*Manihot esculenta* Crantz.) is one of the major food crops in Cameroon. Its cultivation is faced with several pests and diseases, yet proper identification of the pathogenic agents is ongoing. This study aims to identify Fungi species from Cassava leaves and determine its phylogenetic relationship. Random sampling was used to collect symptomatic leaves in 20 cassava farms in Bamenda and cultured on potato dextrose agar (PDA). Mycelia of 31 pure isolates were harvested and used for molecular analysis. DNA was extracted using the sorbitol - CTAB (Cetyltrimethylammonium Bromide) method and amplified using the complete Internal Transcribed Spacer (ITS) and partial Translation Elongation Factor (TEF) gene regions. Sequences were edited using Chromas and Basic Local Alignment Search Tool (BLAST) was performed in the National Center for Biotechnology Information (NCBI). Neighbor-joining in MEGA 10.2 (Molecular Evolutionary Genetics Analysis) was used to generate phylograms at 1000 bootstrap. Six fungi genera were identified based on colony characteristics (*Aspergillus*, *Candida*, *Colletotrichum*, *Fusarium*, *Penicillium* and *Trichoderma*) while twenty-one fungi species were identified following molecular identification. From the ITS, nineteen fungi species were identified and grouped into fifteen genera (*Aspergillus*, *Candida*, *Clonostachys*, *Colletotrichum*, *Curvularia*, *Epicoccum*, *Fusarium*, *Geotrichum*, *Mucor*, *Nigrospora*, *Paecilomyces*, *Penicillium*, *Phoma*, *Pichia*, *Trichoderma*) while thirteen fungi species were identified from TEF belonging to ten genera (*Aspergillus*, *Cladosporium*, *Clonostachys*, *Curvularia*, *Epicoccum*, *Fusarium*, *Geotrichum*, *Lentinus*, *Penicillium*, *Trichoderma*). These species formed phylograms with four monophyletic groups. This study identified Fungi species from cassava leaves and determined its phylogenetic relationship which is important to devise control measures.

Keywords: Identification, fungi species, cassava leaves, cultural, molecular, phylogeny.

Identification of the fungal pathogens that cause leaf spot disease on waterleaf (*Talinum triangulare*) in Mezam Division of Cameroon

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The cultivation of *Talinum triangulare* (water leaf) improves the life quality of families, provides additional income to farmers and has medicinal properties. However, the cultivation of this leafy vegetable in Cameroon has suffered a major blow from leaf spot disease. The objective of this study is to identify the fungal pathogens that cause leaf spot disease on water leaf in Mezam Division of Cameroon. Samples for characterization were collected from 9 farms in 4 Sub Divisions of Mezam Division. For morphological identification, small pieces of infected leaf parts were inoculated on prepared plates of potato dextrose agar. After 7 days of incubation, pure cultures were made, and isolated fungi were identified according to recommended references. For molecular characterization, DNA was extracted from the samples using the Quick-DNA™ Fungal/Bacterial kit. The genomic segments ITS (internal transcribed spaces) was sequenced, purified and analyzed on the ABI 3500xl Genetic Analyzer. DNASTAR was used to analyze the AB1 files generated by the ABI 3500XL Genetic Analyzer and results were obtained by a BLAST search (NCBI). For morphological characterization, 13 morpho types were identified with morpho types 1, 3 and 10 being the most dominant. For molecular identification, 7 fungal species were identified, with *Fusarium oxysporum*, *Yarrowia phangneensis*, *Wickerhamomyces anomalous* and *Geotrichum candidum* being the most dominant isolates. The combination of morphological and molecular characters was fundamental for identification of the fungal species.

Keywords: Characterization, morphological, molecular, disease, water leaf.

INTERNATIONAL CONFERENCE ON FUNGI BARCODING FOR BIODIVERSITY CONSERVATION (ICFBBC 2026) AT THE UNIVERSITY OF DOUALA AND ALVI HOTEL DOUALA, CAMEROON 14-17 JANUARY 2026

PRECONFERENCE WORKSHOP PROGRAMME

DNA Extraction, PCR Amplification and Sequence Analysis

Wednesday 14th and Thursday 15th January 2026

Venue for Day 1: Molecular Cell Biology Laboratory of the Department of Biochemistry, University of Douala

Venue for Day 2: Alvi Hotel Conference Hall

Number of Participants: 50 Maximum

WORKSHOP DATES: 14-15 TH January 2026		
WORKSHOP AGENDA		
Day 1: Wednesday 14 th January 2026		
Time	Activities	Responsible
8.30-9:00	Registration and installation	Secretariat
9-9.30	Opening <ul style="list-style-type: none"> - Word from the Host - Word from the organizers - Welcome of facilitators - Family picture 	HOD/Biochemistry Prof. Tonjock R. Inqaba (Brice Tibab) Prof. Tofel H.
9.30-9.40	Presentation of the program	Prof. Tonjock R.
9.40-10.00	Self-introduction/ Set up discipline rules for the workshop	Prof. Samje Moses
10.00-10.15	Keynote Talk 1: Inqaba Presentation	Inqaba (Brice Tibab)
10.15-10.45	Keynote Talk 2: Sample preparation for DNA extraction	Prof. Tonjock R.

10.45-11.15	Coffee Break	
11.15-11.35	Keynote Talk 3: DNA extraction/ Q and A	Inqaba (Mih Brandon)
11.35-12.00	Keynote Talk 4: PCR Amplification/ Q and A	Inqaba (Mih Brandon)
12.00-13.00	Lunch break	
13.00-14.00	Hands-on DNA Extraction	Inqaba (Mih Brandon)
14.00-15.00	Agarose Gel Electrophoresis	Inqaba (Cybelle Mezajou)
15.00-15.30	Coffee Break	
15.30-16.30	PCR amplification	Inqaba (Cybelle Mezajou)
16.30-17.30	Agarose Gel Electrophoresis	Inqaba (Cybelle Mezajou)
	Day 2: 15th January 2026	
9-9.30	Debriefing of Day1 Activities	Prof. Tonjock R.
9.30-10.00	Keynote Talk 5: From sequence editing to generation of phylogenetic tree / Q and A	Dr. Olou Boris
10.00-11.00	Sequence editing	Dr Olou Boris/Prof Tonjock
11.00-11.30	Coffee Break	
11.30-12.30	Sequence editing	Dr Olou Boris/Prof Tonjock
12.30-14.00	BLAST Search and Download of Sequences	Dr. Olou Boris/Prof Tonjock
14.00-15.00	Lunch Break	
15.00-16.00	Sequence Alignment	Dr. Olou Boris/Prof. Tonjock R.
16.00-17.00	Phylogenetic Tree Generation	Dr. Olou Boris/Prof Tonjock

17.00-17.30	Next step and Feedback from facilitators and participants	All
17.30-18.00	Closing and certificate awards -Word from the host -Word from the organizers -Word from the representative of the participants -Closing remarks Family picture with certificates	All Facilitators
	END OF WORKSHOP	

CONFERENCE PROGRAM

International Conference on Fungi Barcoding for Biodiversity Conservation (ICFBBC)

16 - 17th January, 2026
Alvi hotel
Douala, Cameroon

15:00-18:00: 12 th and 13 th January, 2026 Arrival of conference participants	
8:00 - 17:30 14 th and 15 th January, 2026 Registration Pre-conference Workshop on DNA Extraction, PCR Amplification and Sequence Analysis Award of Certificate	
Friday 16th January, 2026	
8:00 - 9:00	Meeting Start: Registration
9:00 - 10:00	Opening Ceremony coordinated by Prof. Tofel Haman Welcome from Conference Organizer, Prof. Tonjock Rosemary Kinge Welcome from Bamenda University of Science and Technology by Prof. Balgah Roland Azibo Conference Overview from the Committee Chair: Prof. Tonjock Rosemary Kinge Who's here and why: Acknowledging those present, reviewing the knowledge, talent and expertise in the room MC: Prof. Samje Moses / Prof. Tofel Haman

	Getting to know each other: Exchange of pleasantries GROUP PHOTOS
10:00 - 10:30	Keynote Talk 1: DNA Barcoding of Fungi: Bridging Taxonomy, Biodiversity, and Global Data Sharing (Online) Prof. Francisca Iziegbe Okungbowa, University of Benin, Nigeria
10:30 -11:00	Coffee Break/ Poster Session and networking
11:00 - 11:30	Keynote Talk 2: The Molecular Identification of mycorrhizal fungi: Arbuscular and Ecto-Mycorrhiza fungi across two sacred forests Coastal Kenya Dr. Joyce Mnyazi Jefwa, Pwani University, Kenya
11:30 - 12:00	Keynote Talk 3: Characterization and Antifungal Potential Evaluation of Indigenous <i>Trichoderma</i> Isolates Against <i>Macrophomina phaseolina</i> : An <i>In Vitro</i> Study Dr. Olusola L. Oyesola, Covenant University, Nigeria
12:00 - 13:00	Session 1: Molecular Identification of Fungi Session Chair: Prof. Mbouobda Hermann, University of Bamenda, Cameroon Secretary: Prof. Njouonkou Andre Ledoux, University of Bamenda, Cameroon Presenter 1: Dr. Nsah Francoline Sama, University of Bamenda, Cameroon Presenter 2: Chia Genevieve Kain, University of Bamenda, Cameroon Presenter 3: Sirri Vera Nsoh, University of Bamenda, Cameroon PANEL DISCUSSION 1
13:00- 14:00	Lunch
14:00- 14:30	Keynote Talk 4: How Fungi Can Rethink Fertilizer Use in Agriculture Prof. Mbouobda Hermann Desire, University of Bamenda, Cameroon
14:30- 15:30	Session 2: Phylogenetic Analysis of Fungi

	<p>Session Chair: Prof. Djuani Astride Carole, University of Yaounde 1, Cameroon Secretary: Dr. Oba Romuald, University of Bertoua, Cameroon</p> <p>Presenter 5: Prof. Njouonkou Andre Ledoux, University of Bamenda, Cameroon Presenter 6: Dr. Godswill Ntsomboh Ntsefong, University of Yaounde 1, Cameroon Presenter 7: Dr. Bih Joan Ndeh, University of Bamenda, Cameroon</p> <p>PANEL DISCUSSION 2</p>
15:30- 17:30	<p>TYAN TITO SESSION</p> <p>Moderator 1: Prof. Tonjock Rosemary Kinge Moderator 2: Prof. Akomoneh Elvis</p> <p>Presenter 8: TYAN Presentation: Dr. Tasrina Rabia Presenter 9: Prof. Abul Bashar Mir Md Khademul Islam, Dhaka University, Bangladesh Presenter 10: Dr. Tasrina Rabia, Atomic Energy Centre Dhaka, Bangladesh Presenter 11: Dr. Phyllis Muturi Wanbui, Embu University, Kenya (online)</p> <p>TYAN Panel discussion on: Tips on obtaining scholarships, fellowships and grants/ Available scholarships, fellowships and grants by Prof. Mbouobda Hermann, Prof. Tofel Haman, Prof. Samje Moses, Dr. Olou Boris, Prof. Njouonkou Andre, Dr. Tasrina Rabia, Prof. Khademul Islam, Prof. Akomoneh Elvis</p> <p>Questions/Answers</p>

Saturday 17th January, 2026	
8:45- 9.00	Attendance Meeting Start Opening remarks/ Announcements/Recap of the previous day
9:00- 9.30	Keynote Talk 5: Expanding the Coltricia lineage from West Africa through DNA barcoding Dr Boris Armel Olou, University of Montpellier, France/University of Parakou, Benin
9:30 - 11.00	Session 3 and 4: Fungi sequence analysis, bioinformatics and Fungi genetics Session Chair: Prof. Samje Moses Secretary: Dr. Febnteh Eric

	<p>Presenter 1: Gbètondji Basile Hounwanou, Fungi for Nature, Benin</p> <p>Presenter 2: Dr. Nkemnkeng Francoline, University of Bamenda, Cameroon</p> <p>Presenter 3: Moforcha Lilian Zemenjuh, University of Buea, Cameroon</p> <p>Presenter 4: Ajiya B. Cleophas, Gombe State University, Nigeria</p> <p>Presenter 5: Michael Sakha, Kenyatta University, Kenya</p> <p>Presenter 6: Fru Sandra Funghwa, University of Bamenda</p> <p>PANEL DISCUSSION 3</p>
11:00-11:30	Coffee Break
11:30-14:00	<p>Session 5: Fungi Host Identification and Multidisciplinary</p> <p>Session Chair: Prof. Tofel Haman</p> <p>Secretary: Dr. Nkemnkeng Francoline</p> <p>Presenter 1: Prof. Djeuani Astride Carole, University of Yaounde 1, Cameroon</p> <p>Presenter 2: Wokdjou Romulus, University of Yaounde 1, Cameroon</p> <p>Presenter 3: Dr. Oba Romuald, University of Bertoua, Cameroon</p> <p>Presenter 4: Dr. Febnteh Eric, University of Bamenda, Cameroon</p> <p>Presenter 5: Zouberou Mouanfou, University of Ngaoundere, Cameroon</p> <p>Presenter 6: Shu Ngwa Conglad, University of Port Harcourt, Nigeria</p> <p>Presenter 7: Dr. Ayongwa Gideon Che, Bamenda University of Science and Technology, Cameroon</p> <p>Presenter 8: Kohongong Salamatou Mboh, University of Bamenda, Cameroon</p> <p>Presenter 9: Dr. Etchike Alex, University of Dschang, Cameroon</p> <p>Presenter 10: Foncham Linda Konnant, Bamenda University of Science and Technology, Cameroon</p> <p>PANEL DISCUSSION 4</p>
14:00-14:30	JRS Grantee Presentation: Dr. Forchibe Ethelyn Echep
14:30-14:45	Announcements/ Evaluation session
14:45-15:00	Prizes to best oral and poster presenter/Vote of thanks/Award of Certificates /Closing
15:00-16:00	Late Lunch

END

BIOGRAPHY OF KEYNOTE SPEAKERS



PROF. TONJOCK ROSEMARY KINGE

Tonjock Rosemary Kinge is an Associate Professor of Mycology and Phytopathology and the Head of Department of Plant Sciences, Faculty of Science in the University of Bamenda, Cameroon. Her research is focused on; fungi diversity, fungi pathology, biodiversity conservation, ethnomycology, molecular biology and multidisciplinary. She is the leader of the Fungal Biodiversity, Ecology, Ethnomycology and Phytopathology Research Group (Fbeep group). Rosemary is the Next Einstein Fellow Ambassador and the British Society for Plant Pathology Ambassador in Cameroon. Rosemary was a TWAS-CAS postgraduate fellow from Kunming Institute of Botany, China from 2008-2009, a postdoctoral fellow from the University of the Free State, Bloemfontein, South Africa from 2016-2017. A Fulbright scholar from the University of Florida, Gainesville, USA from 2017-2018 and an Alexander von Humboldt experienced research fellow from the University of Bayreuth, Germany from 2021-2022. Rosemary is the coordinator for the western zone for Cameroonian Professional Research Oriented Women (CaPROWN) and a mentor for higher women in Cameroon. Rosemary won the *2024 Humboldt Alumni Networking Award for innovative mentoring* and founded the association; *“Promotion of Female Academic Excellence in STEM through Innovative Networking”* (PROFAESTEM), which has as vision to build capacity in empowering, supporting, promoting, inspiring, integrating and strengthening females in STEM from Master, PhD and post-doctorate levels to excel in STEM. As an international speaker, she has given numerous public lectures and keynote addresses worldwide. She is a member of several scientific organizations including the Cameroon Academy of Young Scientists (CAYS) where she is the technical and logistic secretary. She is an Affiliate of the African Academy of Sciences (AAS), an affiliate of TWAS Young Affiliate Network (TYAN) and a member of OWSD. Also, Rosemary is a fellow of the African Science Leadership Programme (ASLP) and the public relation officer for the Cameroon Bioscience Society. Rosemary belongs to several international organizations where she holds key leadership positions. Rosemary has won many travel grants, research grants, workshop and conference grants. She mentors females in STEM and is passionate in capacity building of the younger generation. She is editor of Conservation Letters and a reviewer for many journals. She has published over 70 articles in international peer-reviewed journals.



PROF. (MRS) FRANCISCA IZIEGBE OKUNGBOWA

Francisca Iziegbe Okungbowa is a professor of mycology, and phytopathology, with research focus primarily on biocontrol (especially of fungal pathogens), fungal bioresources, food security and environmental sustainability studies. Her research also extends to gender and STEM. After obtaining her PhD degree from the University of Benin, Prof. Okungbowa had postdoctoral trainings in molecular biology (Indian Institute of Chemical Biology, Kolkata), molecular mycology (University of Manchester, UK) and biocontrol of pathogens of selected agriculturally important plants (Institute of Sustainable Agriculture, Cordoba, Spain), using various scholarships. She holds a Postgraduate Diploma in Education (PGDE) from the National Teachers Institute (Kaduna, Nigeria) and Certificates in Adult Education (Canadian College of Educators, Mississauga, Canada), Digital Transformation (Instituto Tecnológico de Canarias, Spain), and an intermediate level (B2) proficiency certificate in Spanish Language (Mujeres Por Africa, Madrid, Spain). She has been Head of Department of Plant Biology and Biotechnology and President Organisation for Women in Science for the Developing World (OWSD) University of Benin Branch. She belongs to several scientific bodies such as the Botanical Society of Nigeria, American Phytopathological Society, American Society for Microbiology, African Mycological Association (currently the Vice President), International Mycological Association (Executive Board member) and others. She is a past Research Fellow of the Third World Academy of Science (TWAS, Italy), Council of Scientific and Industrial Research (CSIR, India), International Society for Human and Animal Mycology (ISHAM, Netherlands) and Science by Women (Spain). She has supervised several postgraduate and numerous undergraduate students, served as external examiner to various universities, and presently a reviewer and editorial board member of several journals. Prof. Francisca Okungbowa has published over 80 scientific articles (including book chapters and journal articles) and presented papers at various local and international conferences. Currently the Director, Centre for Sustainable Development Goals, she delivered the 235th Inaugural Lecture of the University of Benin, Nigeria titled “They are good; they are bad: periscoping the biological entities called fungi” in February 2020. She is the leader of the multidisciplinary Plant Protection and Bioresources Research Group (PPB-RG) at the same university. Her hobbies include volunteering, playing golf, sight-seeing, and reading books (novels, nature, cookery, healthy living, inspirational and religious).



PROF. MBOUOBDA HERMANN DESIRE

Mbouobda Hermann Desire is an Associate Professor of Biochemistry/Biotechnology and Phytopathology. He did his PhD in plant defense mechanism of cocoyam in the University of Yaounde 1. He is currently Vice-Dean Programming and Academic Affairs, Faculty of Science, the University of Bamenda, Cameroon. His teaching activity involves enzymology, biotechnology, phytopathology, molecular biology and genetics. His research activity is focused on; Use of local microorganism's (indigenous microorganisms and Phosphate solubilizing fungi) manures and Endophytes to improve some local crops; Phytoprotection (formulated biopesticides and biomannures); plants and pathogen biodiversity; Plant defense mechanism, stimulation and inoculation. Founding member of the Laboratory of Phytoprotection and Valorisation of Genetic Resources, Biotechnology Center, University of Yaounde 1 and Laboratory of Biology, Department of Biology, Higher Teaching Training College (HTTC), University of Bamenda. He is member of several scientific organizations notably financial controller of Cameroon Bioscience Society (CBS), member of Bioveg (Plant Biotechnology: plants improvement and food security) of AUF. He did his Post graduate in the University of Caddi-ayad, Marrakech Morocco (2007-2008). Resource Person for the elaboration of a document on the situation of the environment in Central Africa commented by the International Union to Nature Conservation (UICN) Ref: 0892/09 (2008-2009): Resource Person for the elaboration of sectorial national review of Chad (Protection des végétaux et gestion des pesticides, Africa Emergency Locust Project [Chad], commented by Chad Government in collaboration with Work Bank. Ref: N° 275/MAI/SE/SG/AELP/IO. (2010): Consultant to finalize the report on the environment in Central Africa commentate by International Union to Nature Conservation (UICN) (2011) External Expert to evaluate Global Environment Outlook Africa (GEO-6), Healthy Planet Healthy People, by United Nations Environmental Programme (UNEP) (2015). He is reviewer for some journals, has published more than 50 articles in international peer-reviewed journals. He is involved in PhD and MSc defenses with other states universities (University of Yaounde 1, University of Dschang and University of Douala). He currently supervises many PhD and master Students in some Cameroon States Universities.



DR. BORIS ARMEL OLOU

Boris Armel Olou is a mycologist specializing in fungal diversity, integrative taxonomy, and biodiversity conservation, with a strong focus on the application of molecular tools to document and protect tropical fungi. He is affiliated with the University of Montpellier (France) and the Research Unit in Tropical Mycology and Plant-Soil-Fungus Interactions (MyTIPS) at the University of Parakou, Benin, where his work integrates field-based research, molecular phylogenetics, and conservation science. His research combines classical taxonomy, ecology, and DNA barcoding to address major knowledge gaps in fungal diversity, particularly in West Africa. He has extensive experience in sequence editing, barcode data analysis, and phylogenetic tree reconstruction, contributing to the discovery and description of numerous fungal species and to the expansion of reference barcode datasets for underrepresented tropical regions. His work focuses especially on wood-inhabiting fungi, ectomycorrhizal fungi, and wild edible mushrooms. Over the past decade, Dr. Olou has conducted mycological fieldwork across a wide range of ecosystems in West and Central Africa, as well as in Europe, combining biodiversity inventories with molecular analyses to address key gaps in fungal knowledge. He has held research and guest scientist positions at several international institutions, including African Genome Center (AGC), University Mohammed VI Polytechnic (Morocco), Goethe University Frankfurt (Germany), Meise Botanic Garden (Belgium), Technical University of Munich (Germany), IMT Mines Alès (France), Rhine-Waal University of Applied Sciences (Germany), and the University of Kassel (Germany). These experiences have strengthened his interdisciplinary perspective and his ability to work across diverse research environments. A key component of Dr. Olou's work is capacity building. He has facilitated and organised multiple training programmes on DNA barcoding, environmental DNA (eDNA), next-generation sequencing, and bioinformatics, with a strong emphasis on practical, end-to-end workflows. His training approach guides participants from raw sequence data through quality control, alignment, and phylogenetic inference, ensuring that molecular outputs are clearly linked to taxonomy, ecology, and biodiversity conservation. At **ICFBBC 2026**, Dr. Olou brings both technical expertise and a strong commitment to collaborative learning. Through his facilitation of sessions on **sequence editing and phylogenetic tree construction**, he aims to help participants confidently translate fungal barcode data into robust evolutionary and conservation insights, reinforcing the critical role of fungi in global biodiversity research.



DR. JOYCE MNYAZI JEFWA

Joyce Mnyazi Jefwa is a Senior Lecturer and Researcher at Pwani University in Kilifi, Kenya. She is based in the Department of Biological Science. She holds a PhD in Botany from the University of Pretoria, MSc in the Conservation of Soil Fertility from the University of Kent at Canterbury, Bachelor of Education Science (Botany Major and Zoology) from Kenyatta University in Kenya, and a Post graduate Diploma in Biosafety and Biotechnology from the Ghent University, Belgium. She is also skilled Taxonomy, micropropagation, mushroom spawn production and mycorrhizal inoculum production. Her research focus is on Plant and fungi with focus on mycorrhiza and mushrooms, Taxonomy, Ecology and Conservation. Conservation, restoration, utilization, domestication of plant and Fungi. She worked at the National Museums of Kenya where she initiated the Mycology section and started the mycorrhizae and mushroom laboratory and a Fungarium facility. She worked at CIAT and partly IITA, integrated soil microbial component in the Integrated Soil Fertility Management (ISFM) programme. She has served in different capacity in professional bodies and associations.



DR. ETHELYN ECHEP FORCHIBE

Dr. Ethelyn Echip Forchibe is an entomologist and educator whose work contributes to bridging high-level academic research and grassroots community impact. She ensures her research directly results in real-world, tangible benefits for local farmers. Dr. Forchibe holds a PhD and a Master of Philosophy degree in Entomology from the University of Ghana, and a Bachelor of Science in Zoology from the University of Buea, Cameroon. A recipient of numerous prestigious accolades, she has served as a Visiting Scientist at the University of Cambridge, is a two-time German Academic Exchange (DAAD) Scholar, and has secured grants from the BBSRC, IFDC-GhanaVeg, and the JRS Biodiversity Fund. Her expertise spans integrated crop protection, sustainable pest management for improved food production, and biodiversity conservation. Her commitment to capacity building extends directly to transforming lives on the ground. She has facilitated numerous professional workshops and has trained over 200 farmers and individuals across Africa on sustainable, climate-smart pest management strategies. Most recently, she contributed to training students across Africa and Asia on Higher Education didactics during the 2025 International Geo-training Summer School at Osnabrück University, Germany. Currently, Dr. Forchibe serves as a Lecturer and Researcher at the Catholic University of Cameroon (CATUC), Bamenda, where she mentors the next generation of agricultural scientists. Her current research investigates the diversity and consumer perception of orphaned crops in the North West region of Cameroon, alongside studying insect diversity for transboundary conservation in key ecological areas (Tchabal Mbabo and Gashaka Gumpti National Park) between Nigeria and Cameroon. She is committed to continually honing her skills, and her journey is guided by the powerful belief that *"true success is an internal journey of courage and persistence."*



DR. OLUSOLA LUKE OYESOLA

Olusola Luke Oyesola is a plant pathologist, lecturer, and food security researcher whose work sits at the intersection of crop disease management, fungal biology, and climate change. With a strong commitment to translating science into practice, he is recognized for advancing interdisciplinary approaches that link plant health, biodiversity conservation, and sustainable livelihoods, particularly within tropical and sub-Saharan African contexts. Dr. Oyesola holds a PhD in Plant Pathology and currently serves as a lecturer in the Biological Sciences Department, Covenant University, Nigeria, where he teaches and mentors undergraduate and postgraduate students in plant disease management, mycology, climate-smart agriculture, biodiversity conservation, and industrial biotechnology. His academic training and professional experience have equipped him with a comprehensive understanding of pathogen biology, host-pathogen interactions, and the ecological and climatic drivers that shape emerging and re-emerging plant diseases in both agricultural and natural ecosystems. His research portfolio focuses on fungal pathogens affecting economic crops in Nigeria. Notably, his work integrates field ecology, laboratory-based diagnostics, and policy-relevant frameworks to address real-world challenges such as food insecurity, habitat degradation, and disease risks under climate variability. Dr. Oyesola has contributed to competitive research grants aimed at addressing plant fungal disease management. Beyond research, Dr. Luke is demonstrating strong leadership in academic and professional service. He has participated in interdisciplinary teams spanning plant science and conservation biology, and he actively supports capacity building through training and mentorship. His work reflects a commitment to strengthening local scientific capacity while engaging global research and conservation networks. Central to his professional vision is the belief that plant health is foundational to food security, ecosystem resilience, biodiversity conservation and human well-being. He is passionate about promoting excellence, innovation, and ethical responsibility in science, while advocating for evidence-based decision-making in agriculture, forestry, and conservation. His work emphasizes collaboration across disciplines and sectors as a pathway to addressing global environmental challenges.