



SMBE REGIONAL SYMPOSIUM OneBioAfrica 2026

**Strengthen One health networks
through molecular data sharing and
Bioinformatics in Africa**



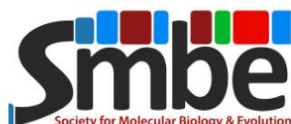
**Cotonou,
Republic of Benin**



**July 13-16th,
2026**

**PROGRAMME AND
BOOK OF ABSTRACTS**

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Credits:

Organizing committee. Chair: Boris armel OLOU.

Committee Members: Nourou Souleman YOROU, Basile Gbètondji HOUNWANOU, Abdoul Azize BOUKARY, Jean LEGEAY.

Scientific committee: Sévérin BIAOU, Sylvestre BADOU, Yaya IDRISOU, Rachel MEYER, Rodrigue Edéya Orobiyi PELEBE, Brice SINHOUENON, Olatunde OMOTOSO.

WELCOME TO OneBioAfrica 2026



Africa stands at a decisive moment. The challenges we face, emerging diseases, biodiversity loss, antimicrobial resistance, and ecosystem degradation are interconnected and require integrated, molecular-driven solutions within the One Health framework.

OneBioAfrica was initiated to strengthen Africa's capacity in molecular biology, bioinformatics, and evolutionary science, and to build a collaborative continental network capable of transforming genomic data into real-world health and conservation impact.

We bring together researchers, students, early-career scientists, and policymakers to share knowledge, exchange ideas, and shape the future of molecular science in Africa. Together, we are building resilient scientific networks that serve both people and the planet.

Dr. Boris Armel OLOU
Chair, OneBioAfrica Symposium



PROGRAMME

Sunday, 12 July 2026

Registration, Welcome Evening, and Networking

Time	Activity
16:00 – 18:30	Participant Registration and Badge Collection
18:30 – 19:00	Welcome Address and Opening Remarks
19:00 – 21:00	Welcome Cocktail, Snacks and Networking Session

Monday, 13 July 2026

Opening Ceremony, Invited Keynotes and Session 1

Time	Activity
08:00 – 09:00	Registration Continuation and Welcome Coffee
09:00 – 09:45	Official Opening Ceremony
09:45 – 10:00	Group Photo

Invited Keynote and Institutional Presentations

Time	Presentation
10:00 – 11:30	Plenary speaker Lecture – Prof. Sinsin (Benin)
11:30 – 12:30	Plenary speaker Lecture – Prof. Lara Urban (Switzerland)
12:30 – 14:00	Lunch Break

Session 1: Molecular Biology and Biodiversity Conservation

PRESENTATION

Session Chairs : Dr. Jean Legeay, Dr. Badou Sylvestre, Dr. Brice G. Sinhouenon

Time	Activity
14:00 – 14:15	Genetic diversity of the endangered tree <i>Pterocarpus erinaceus</i> poir., in Benin: insights for conservation
14:15 – 14:30	Molecular profiling of the rhizosphere mycobiome of <i>Afzelia africana</i> in Benin: implications for conservation and restoration
14:30 – 14:45	Sanitary quality of vegetables produced on market gardening sites in Parakou and Djougou in northern Benin
14:45 – 15:00	Integrating Herbarium Data and DNA Barcoding to Identify and Conserve Rare Plant Species in Rwanda (Online)

15:00 – 15:15	Deux nouvelles espèces de syncarides du Bénin et leur position phylogénétique au sein de la famille des Parabathynellidae
15:15 – 15:30	Identify the best substrate for <i>Pleurotus ostreatus</i> growing by rural women in central Benin
15 :30 – 15:45	Ectomycorrhizal morphotypes of <i>Isoperlinia doka</i> in Benin's soudanian woodland
15:45 – 16:00	Coffee Break
16:00 – 17:00	Plenary speaker Lecture: Long-Read Sequencing for One Health: Applications of the PacBio Portfolio in Human and Environmental Genomics (Kilsi Borgbara, Nigeria)
17:00 – 18:00	Panel Discussion: <i>Strengthening Molecular Biology and Biodiversity Conservation in Africa: Strategies for Expanding Access to Molecular Data and Building Molecular Biology Infrastructure Across African Universities</i>
18:00 – 18:15	Day 1 Wrap-up and Announcements

Tuesday, 14 July 2026

Session 2: Molecular Approaches in Human and Animal Health

Time	Activity
08:00 – 09:00	Morning Coffee and Networking
09:00 – 10:00	Plenary speaker Prof. Victorien Tamègnon Dougnon (Benin)
Session Chairs : Dr. Rodrigue E. O. Pèlèbè & Dr. Yaya Idrissou	
10:30 – 10:45	Soil surveillance for monitoring soil-transmitted helminth infections: method development and field testing in three countries
10:45 – 11:00	Combined effect of <i>ccr2</i> , <i>sdf1</i> and <i>trim5a</i> genetic variants on HIV-1 mother-to-child transmission in the north region of Cameroon
11:00 – 11:15	Progress report on molecular screening of potential zoonotic pathogens in mammals sold in bushmeat markets in Douala, Cameroon
11:15 – 11:30	Revealing the Silent Burden of Bovine Tuberculosis in Benin: A Comprehensive One Health Strategy
11:30 – 11:45	Prevalence, carbapenem resistance genes, and clonal distribution of <i>Acinetobacter baumannii</i> in West Africa: a systematic review and meta-analysis (Online)



12:30 – 14:00	Lunch Break
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Poster Session

Time	Presentation
14:00 – 15:00	Poster Session Coordinators: Dr. Abdoul-Azize Boukary & Dr. Basile G. Hounwanou Effect of Ejaculation Frequency, Extenders, and Cooling on the Sperm Quality of Djallonké Sheep in West Africa Environmental surveillance of soil-transmitted helminths and other enteric pathogens in settings without networked wastewater infrastructure Spatio temporal dynamics of the Monts Kouffé Forest Reserve (Benin) and prioritization of restoration areas Metabarcoding of Bacterial Communities on Floating Plastics in River Ngadda Health vulnerability in bushmeat exploitation and preventive measures for sustainable wildlife conservation Health vulnerability in bushmeat exploitation and preventive measures for sustainable wildlife conservation Prévention des zoonoses et problématique de la santé unique dans le département du Zou
15:00 – 15:40	SMBE Opportunities for African Researchers: Funding, Publications, Networking and Career Development Roundtable
15:30 – 16:00	Coffee Break
16:00 – 17:00	Roundtable Discussion: One Health Challenges in Africa; Funding Opportunities and Career Development for Early-Career African Researchers
17:00 – 18:00	Plenary speaker Dr. Rachel Meyer (USA)
18:00 – 18:15	Day 2 Wrap-up and Announcements

Wednesday, 15 July 2026

Bioinformatics Workshop

Time	Activity
08:00 – 08:30	Morning Coffee and Networking
08:30 – 09:00	Opening Remarks for the Bioinformatics Workshop

Hands-on Workshop: Bioinformatics, Microbial Ecology Analysis in R and Sequence Processing

Time	Activity
09:00 – 10:30	Plenary speaker Dr Andres Sauvêtre (France)
10:30 – 11:00	Coffee Break
11:00 – 12:30	Introduction to Microbial Ecology Data Analysis in R, Sequence Quality Control, Processing and Bioinformatics Pipelines
12:30 – 14:00	Lunch Break
14:00 – 15:30	Diversity Analysis, Visualization and Ecological Interpretation in R
15:30 – 16:00	Coffee Break
16:00 – 17:30	Practical Exercises, Questions and Interactive Discussion
17:30 – 18:00	Workshop Wrap-up

Thursday, 16 July 2026

Time	Presentation
Session Chairs : Dr. Séverin Biaou & Dr. Basile G. Hounwanou	
08:30 – 08:45	Unravelling soil fungal communities in dumpsites in kabale, western Uganda using culturomics
08:45 – 09:00	Antimicrobial Resistance in Poultry Production: Detection of ESBL and Carbapenemase Genes in <i>Escherichia coli</i> from Healthy Turkeys in Nigeria
09:00 – 09:15	Analyse des pratiques d'élimination des déchets ménagers dans les zones urbaines du Sud Borgou
09:15 – 09:30	Facteurs d'adoption des pratiques de restauration des paysages forestiers dans la préfecture de Kozah
09:30 – 09:45	Caractéristiques hydrochimiques et microbiologiques des eaux souterraines et risques sanitaires dans la commune de Parakou
09:45 – 10:00	Plant Biomarkers, Air Pollution and One Health Resilience: Urban Evidence from <i>Psidium guajava</i> in Douala (online)
10:00 – 10:30	Coffee Break
10:30 – 10:45	Contamination and pesticide multiresidue analysis in cotton production systems in Benin



10:45 – 11:00	Airborne mycobiome in the city of Parakou: Diversity, intra-annual dynamics and epidemiological implications in the One Health context
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Official Closing Ceremony

11:00 – 11:15	Awards ceremony: best oral presentation award
11:15 – 11:30	Awards Ceremony: Best Poster Presentation Award
11:30 – 11:45	Recognition of Invited Speakers, Partners and Organizing Committee
11:45 – 12:00	Certificate and Award Ceremony
	End of Symposium and Lunch

Our plenary speakers



Prof. Brice Augustin Sinsin

Affiliation: Laboratory of Applied Ecology,
University of Abomey-Calavi

Position: Chair of the National Academy of Science,
Arts and Literature of Benin (ANSALB)

Country: Benin

Recipient of the “Best African Scientist” award in 2017, Professor Brice Sinsin is one of Africa’s leading ecologists and conservation scientists. He is Professor of Ecology and Founder of the Laboratory of Applied Ecology at the University of Abomey-Calavi, Benin. He served as Rector of the University of Abomey-Calavi from 2012 to 2017, and in that position, he received many awards as best academic institution manager. For more than four decades, his research has focused on biodiversity conservation, rangeland management, wildlife ecology, natural resource management, and the sustainable use of ecosystems across West Africa. He trained more than 70 PhD students who had achieved their postgraduate degree under his supervision. He has authored more than 420 scientific publications and coordinated numerous national and international research projects. His work has significantly advanced biodiversity assessment, protected area management, and evidence-based conservation policies in Africa. He has been former Vice Chair for West and Central Africa of the IUCN World Commission on Protected Areas (WCPA), and acting or former Member of many Governing Boards for international institution like ICRAF’s Board of Trustee, and for regional organizations. He is Member of the National Academy of Science, Arts and Literature of Benin (ANSALB). At OneBioAfrica 2026, Professor Sinsin will share his extensive scientific and policy experience on emerging approaches to biodiversity conservation in Africa.



Prof. Nourou Souleman Yorou

Affiliation : Agence béninoise pour la recherche et l'innovation (ABRI)

Position: Executive Director of ABRI

Country: Benin

Expert Session: Fungal taxonomy and Evolution

Professor of Tropical Mycology at the University of Parakou in Benin. After completing his doctoral thesis in 2008 at the University of Munich in Germany, he worked as a postdoctoral fellow and then led an independent research group at the University of Munich before returning permanently to his home country Benin in 2014. Since then, he has headed the research unit on tropical mycology and plant-fungi interactions. His work focuses on the taxonomy, ecology, and distribution of ectomycorrhizal fungi. He has coordinated more than 15 research projects on the diversity and sustainable use of fungi in tropical Africa. He has also worked to promote mycology in tropical Africa through numerous national and international training courses, seminars, and conferences, as well as training many PhD students in Benin and West Africa. He is the author and co-author of more than 200 scientific papers and two books on edible fungi in Benin and West Africa. He was awarded the Mary Ethel Dodge Medal for outstanding early career contributions to Mycology, and is also a corresponding member of the Belgian Royal Academy for Overseas Sciences. In 2015 he was appointed as the Director General of the Beninese Agency for Research and Innovation.



Prof. Victorien Tamègnon Dougnon

Affiliation : École Polytechnique d'Abomey-Calavi, University of Abomey-Calavi

Position: Executive Director of the Benin Agency for E-Education

Country: Benin

Expert Session: Antimicrobial Resistance, Environmental Microbiology

Full Professor of Microbiology at the Department of Human Biology, École Polytechnique d'Abomey-Calavi, University of Abomey-Calavi (Benin). His research focuses on antimicrobial resistance, environmental microbiology, and the valorization of African medicinal plants for the development of innovative alternatives to antibiotics. He has established extensive international collaborations and contributes to multidisciplinary research addressing major public health challenges in Africa. Beyond his research and teaching, Prof. Dougnon holds several leadership positions. He currently serves as Director of the École Polytechnique d'Abomey-Calavi, one of Benin's leading engineering schools, and Director General of the Beninese Agency for Distance Education (AbT-E). He is also a member of the Academic Commission of the Sèmè City Foundation and the Scientific Council of the Laboratory for Environmental Studies and Monitoring (LESE), where he serves as an environmental microbiology specialist. His career reflects a strong commitment to scientific excellence, higher education, innovation, and sustainable development.



Dr. Lara URBAN

Affiliation: University of Zurich

Country: Switzerland

Expert Session: Genomics and Artificial Intelligence for Planetary Health

Statistical geneticist and ecologist with a PhD in computational genomics from the University of Cambridge and the European Bioinformatics Institute (EMBL-EBI) and independent research experience with the national Department of Conservation as a Humboldt Fellow in New Zealand. Since 2022, Lara has led her own research group, now as a professor at the University of Zurich and its Food Safety and One Health Institutes, and previously as Helmholtz Principal Investigator at the Helmholtz AI Institute with a faculty position at the Technical University of Munich. Lara was named the Young Scientist of the Year by the German Association of University Professors in 2023, and serves as a member of the German governmental One Health Council, the Swiss Biorisk Alliance advisory board, the Swiss Pathogen Surveillance Platform nanopore expert group, and of the Swiss delegation of the Codex Alimentarius Commission.



Dr. Jean Legeay

Affiliation: African Genome Center, Université Mohamed 6 Polytechnique

Position: Researcher

Country: Morocco

Expert Session: Molecular Biology and Biodiversity Conservation

Researcher at the African Genome Center, Université Mohamed 6 Polytechnique, Morocco. He received a PhD from the University of Lorraine, France, in 2019, on the topic of the effect *Phytophthora* pathogens on the diversity of trees in tropical rainforests. His research interest is the interaction of microbes with plants, especially in the context of developing solutions for dryland agriculture. His current projects involve the development of inoculates that would allow crops to form protective sheaths around roots, and the effect of the cadmium on the soil microbiome. He has given courses in microbial ecology and statistics in Parakou, Benin, in 2024 and 2025 and in Kano, Nigeria, in 2025.



Kilsa Borgbara

Affiliation: Inqaba Biotec West Africa

Country: Nigeria

Expert Session: Molecular Biology and genomics

Kilsa Borgbara is the Laboratory Manager and PacBio Applications Specialist at Inqaba Biotec West Africa, where he oversees genomics, molecular biology, and bioinformatics operations across the region. He has extensive experience in next-generation sequencing (NGS), long-read sequencing, molecular diagnostics, laboratory development, quality management systems, and bioinformatics applications for research and public health.

At Inqaba Biotec, Kilsa leads initiatives to expand access to advanced genomic technologies, including PacBio long-read sequencing, while supporting researchers across Africa with genomics and bioinformatics solutions. His work spans pathogen genomics, infectious disease research, biodiversity studies, molecular diagnostics, and capacity building in genomic sciences. Kilsa is passionate about advancing genomics and bioinformatics capabilities in Africa and promoting the application of sequencing technologies to address challenges in the African continent.



Dr. Rachel Meyer

Affiliation: University of California, Santa Cruz

Country: United States of America

Expert Session: Ecology and Evolutionary Biology

Associate Adjunct Professor of Ecology and Evolutionary Biology at the University of California, Santa Cruz. She earned her PhD from the City University of New York and the New York Botanical Garden focusing on eggplant domestication, followed by an NSF Plant Genome Postdoctoral Fellowship at New York University. Rachel then served as an AAAS Science and Technology Policy Fellow at the National Science Foundation, where she pivoted to focusing on the intersection of interdisciplinary biodiversity science and public policy. Prior to joining UCSC, she was the Executive Director of the UC Conservation Genomics Consortium that launched the CALeDNA program. She continues research on plant genomes and ethnobotany while also growing CALeDNA and serving as the Chief Scientific Officer for eDNA Explorer, a global eDNA web tool. She has been running eDNA training workshops in Africa for four years.



Dr. Andres Sauvêtre

Affiliation: IMT Mines Alès, France

Country: France

Expert Session: Environment and Society within the One Health Framework

Dr. Andrés Sauvêtre is an agronomist and holds a PhD in Plant Biology and Biotechnology from the Autonomous University of Barcelona (Spain), and Helmholtz Zentrum München (Germany). He is a researcher at IMT Mines Alès and the research unit HydroSciences Montpellier in France, where he develops nature-based solutions for sustainable wastewater treatment and water reuse. His research focuses primarily on the fate, transformation and removal of organic micropollutants in constructed wetlands and wastewater treatment systems. He investigates plant uptake and metabolism, contaminant transfer to agroecosystems, and the contribution of wastewater biofilms, plant-associated microbial communities and endophytic microorganisms to micropollutant degradation. In parallel, he develops bioaugmentation strategies using selected microorganisms to enhance micropollutant removal and improve the resilience and efficiency of constructed wetlands. Using environmental microbiology and molecular approaches, he also studies the dissemination of antibiotic-resistant bacteria and antibiotic resistance genes in constructed wetlands and treated wastewater. His work explores how microbial community structure and plant–microbiome interactions influence both treatment performance and environmental health risks. By integrating micropollutant research, microbial ecology, antibiotic resistance and ecological engineering, his work contributes to the One Health approach by supporting safer wastewater treatment and reuse while protecting human, agricultural and ecosystem health.



Plenary speakers abstracts

eDNA to assess habitat health and the web tools to do it

Rachel Meyer

Ecology and Evolutionary Biology, University of California, Santa Cruz, United States of America

Abstract

California shares most of the same challenges commonly occurring across Africa: changing temperature and rainfall, declines in invertebrates, increased urbanization and natural resource extraction, encroaching invasive species, and maximized use of arable land. These pressures rarely act on ecosystems, wildlife, or people in isolation—shifts in habitat quality ripple into animal populations, zoonotic disease risk, water security, and human livelihoods, making them a fundamentally One Health problem. To create sustainability, habitat improvement and conservation need integration with land uses that support human needs. Environmental DNA (eDNA) is a powerful One Health tool for this integrated view, because a single sample simultaneously captures signals across the tree of life—vertebrates, invertebrates, plants, microbes, and pathogens—linking ecosystem condition to the species and health risks that bear on animals and people alike. To advance this work, California is developing eDNA tools, and CALeDNA program scientists are collaborating with African scientists to innovate in ways where we all benefit from each other's ideas and approaches. In this talk, we'll review the latest approaches to building environmental health assessment frameworks that integrate eDNA with other data like remote sensing and land management records, operationalizing One Health by connecting biodiversity, land use, and human context in one analysis. We'll examine case studies from the CALeDNA program in California, Rwanda, and South Africa, shared on our tool, the eDNA Explorer—a web platform where scientists worldwide share eDNA projects and integrate data, turning shared infrastructure into a cross-continental One Health resource for people, animals, and ecosystems together.

Keywords: One Health; Biodiversity assessment; Ecosystem health; Remote sensing; Land-use change; eDNA Explorer

Genomic Technology and AI for One Health Surveillance

Lara Urban

University of Zurich, Switzerland

Abstract

The increasing emergence and spread of infectious diseases, antimicrobial resistance, and other biological threats highlight the need for integrated approaches to health surveillance across humans, animals, and the environment. Advances in genomic technologies, combined with artificial intelligence (AI), are creating new opportunities to detect, characterize, and monitor biological threats at unprecedented scale and resolution. This presentation will explore how genomic data and AI-driven approaches can contribute to One Health surveillance, enabling the integration and interpretation of complex biological information across health sectors and ecological contexts. Particular attention will be given to the potential of genomic technologies to support pathogen detection and surveillance, while AI and computational methods can facilitate the analysis

of large and heterogeneous datasets and improve the identification of emerging risks. The presentation will also consider the importance of translating these technological advances into effective surveillance systems that support evidence-based decision-making and preparedness. By bringing together genomics, computational science, and One Health perspectives, these approaches offer promising opportunities to strengthen biological surveillance and develop more responsive and integrated health systems. Building scientific and computational capacity, particularly through collaboration across disciplines and regions, will be essential for ensuring that these technologies can contribute effectively to One Health surveillance globally.

Keywords: Genomic surveillance; Artificial intelligence; One Health; Pathogen surveillance; Computational genomics; Emerging infectious diseases; Bioinformatics.

IUCN STAR Metrics for Reducing Threats to Endangered Species in Benin

Brice A. Sinsin

Laboratory of Applied Ecology (LEA), Faculty of Agronomic Sciences, University of Abomey-Calavi, Benin

Abstract

Biodiversity loss in Benin is driven by multiple pressures, including habitat degradation and fragmentation, agricultural expansion, overexploitation of biological resources, mining, invasive species, pollution, and climate change. In this context, the IUCN Species Threat Abatement and Restoration (STAR) metrics provide a framework for quantifying the potential contribution of threat reduction and habitat restoration actions to lowering species extinction risk. The approach integrates species' extinction risk, the extent of current and restorable areas of habitat, and the relative contribution of different threats to population decline. In 2021, the Laboratory of Applied Ecology of the University of Abomey-Calavi was commissioned by IUCN to apply the STAR tool in Benin to support biodiversity assessment, conservation prioritization, and decision-making. The approach was applied to several threatened wildlife species, including the red-bellied guenon (*Cercopithecus erythrogaster erythrogaster*), lion, buffalo, hippopotamus, and elephant. The results demonstrate the value of STAR metrics for identifying and spatially prioritizing major threats, highlighting areas where conservation interventions could generate the greatest potential benefits, and informing national biodiversity conservation priorities. By linking species extinction risk with specific threats and restoration opportunities, STAR provides a practical decision-support framework for targeting conservation investments and strengthening biodiversity management in Benin.

Keywords: IUCN STAR metrics; threatened species; threat abatement; habitat restoration; biodiversity conservation; Benin.

Microbial Communities in Constructed Wetlands for Wastewater Treatment and Reuse: From Micropollutant Removal to Bioaugmentation

Andrés Sauvêtre¹, Nassim Ait-Mouheb², Monica Brienza³, Serge Chiron⁴, François Lestremat¹, Boris Olou^{1,5}, Viviane Radl⁶, Peter Schroeder⁶, Dorde Tadic⁴, Anna Wegrzyn⁷

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2 *UMR G-eau, University of Montpellier, INRAE, Montpellier, France*
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4 *Hydrosiences Montpellier, Univ Montpellier, IMT Mines Alès, IRD, CNRS, Montpellier, France.*
5 *Research Unit Tropical Mycology and Plant-Soil Fungi Interactions (MyTIPS), Faculty of Agronomy, University of Parakou, BP 123 Parakou, Benin;*
6 *Research Unit Comparative Microbiome Analysis, Helmholtz Zentrum München, German Research Center for Environmental Health, Ingolstädter Landstr. 1, 85764 Neuherberg, Germany*
7 *Environmental Biotechnology Department, Faculty of Energy and Environmental Engineering, Silesian University of Technology, Gliwice, Poland., Konarskiego 18, 44-100 Gliwice, Poland*

Abstract

Constructed wetlands are nature-based wastewater treatment systems that provide an efficient and low-energy solution for wastewater treatment and water reuse while supporting nutrient recovery and ecosystem services. However, important challenges remain regarding the removal of organic micropollutants and the environmental dissemination of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARG), raising concerns about the safe reuse of treated wastewater. Addressing these challenges requires a better understanding of the microbial communities that drive treatment processes. These microbial communities play a central role in contaminant transformation, micropollutant degradation, nutrient cycling and the ecological functioning of treatment wetlands. Our work highlights how microbial ecology, supported by targeted molecular tools, can provide new insights into the functioning of constructed wetlands. Wastewater biofilms, plant-associated microbiomes and endophytic microorganisms are investigated using complementary culture-dependent and molecular approaches, including the isolation and identification of endophytic microorganisms. Building on these insights, the potential of microbial ecology to support innovative strategies for improving treatment performance is discussed, including the bioaugmentation of constructed wetlands with selected endophytic bacteria and fungi to enhance micropollutant removal. By integrating environmental microbiology, targeted molecular tools and ecological engineering, this research contributes to the development of more efficient and safer nature-based wastewater treatment systems for water reuse.

Keywords: Constructed wetlands; Microbial ecology; Wastewater reuse; Micropollutant removal; Antibiotic resistance; One Health; Bioaugmentation

ABSTRACTS

SESSION: MOLECULAR BIOLOGY AND BIODIVERSITY CONSERVATION

Genetic diversity and population structure variation of the endangered tree *Pterocarpus erinaceus*, in Benin: Insights for Conservation and Management

Séverin Bioau^{1, *}, Valère Kolawolé Salako², Noulékoun Florent^{3,4}, Kpedetin Ariel Frejus Sodedji⁵, Gbètondji Basile Hounwanou⁶, Thierry Dehouegnon Houehanou¹, Gérard Nounagnon Gouwakinnou¹

¹ *Research Unit of Biodiversity Conservation at the Interface People, Land Use and Climate Changes (UR-BiPLaC), Laboratoire d'Ecologie de Botanique et de Biologie Végétale, Université de Parakou (UP), Parakou, Benin*

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⁵ *Non-Timber Forest Products and Orphan Crop Species Unit, Laboratory of Applied Ecology (LEA), University of Abomey-Calavi (UAC), Cotonou, Benin*

⁶ *Research Unit Tropical Mycology and Plant- Soil Fungi Interactions, Faculty of Agronomy, University of Parakou, Parakou, Benin*

* Corresponding author: sbbiaou@gmail.com

Abstract

Understanding the diversity and genetic structure of endangered species is essential for effective conservation. Many interventions focus on habitat or population protection while overlooking adaptive potential linked to genetic variability. This study assessed genetic diversity and population structure of *Pterocarpus erinaceus* Poir. in Benin. 68 accessions were genotyped using 1,527 SNP markers, and genetic parameters were estimated. Population structure was examined through principal component and admixture analyses to inform conservation strategies. Hill diversity profiles show that populations of *P. erinaceus* in the Sudanian zone (SZ) and Sudano-guinean zone (SGZ) of Benin are genetically richer in alleles and evenness than those in the Guinean zone (GZ). Observed heterozygosity exceeds expected heterozygosity across all subpopulations. However, the low effective population size ($N_e = 48.93$) indicates a high risk of inbreeding and genetic erosion. Population structure analysis identifies three distinct genetic clusters ($K = 3$), with evidence of admixture but significant differentiation (F_{ST}). Most genetic variation (99.14%) occurs within populations rather than between them. Despite relatively high within-population diversity, the species remains genetically vulnerable. These findings highlight the need to prioritize in situ conservation of SZ and SGZ populations and enhance gene flow to increase effective population size. Preserving diversity within each population is fundamental to the long-term survival of this valuable species.

Keywords: Species conservation; population evolution; Genetic analysis; Genomics; West Africa

Ectomycorrhizal morphotypes of *Isoperlinia doka* in Benin's woodland

Soloum Clément Teteli^{1,2*}, Boris Armel Olou¹, Nourou Soulemane Yorou¹, Annemieke Verbeken²

¹Research unit in Tropical Mycology and Plants-Soil Fungi Interactions (MyTIPS), Faculty of Agronomy, University of Parakou, 123 Parakou, Benin

²Research Group Mycology, Ghent University, Gent, 9000, Belgium

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Abstract

Ectomycorrhizal symbioses are critical for tree resilience in African woodlands, yet remain poorly documented. This study assessed EcM colonization of *Isoperlinia doka* across a climatic gradient in Benin and characterized associated fungal morphotypes using integrative morpho-molecular approaches. Root samples were collected from 12 forest reserves spanning both Sudanian and Sudano-Guinean zones. EcM morphotypes were examined under microscope following Agerer (1987–2006) criteria, while fungal identification was achieved through ITS rDNA sequencing using Sanger sequencing, with taxonomic assignment based on NCBI GenBank and UNITE databases. Mycorrhization rate was 52.8%, with a strong climatic gradient: 77.8% in the Sudano-Guinean zone versus 27.8% in the Sudanian zone. This contrast highlights the influence of rainfall and soil moisture on symbiotic establishment. The identified EcM morphotypes of *I. doka* belong to seven genera, namely *Lactifluus*, *Russula*, *Thelephora*, *Amanita*, *Inocybe*, *Sebacina*, and *Scleroderma*. These genera represent key functional groups known to enhance nutrient acquisition, drought tolerance, and pathogen resistance in host trees. This first morphotype reference for *I. doka* in West Africa provides a baseline for understanding fungal diversity in dry tropical forests. The results demonstrate that EcM symbiosis is widespread but strongly modulated by climate, with reduced colonization in drier northern sites. Such findings suggest that assisted inoculation with locally adapted EcM isolates could be necessary to improve reforestation success under water-limited conditions. By linking fungal diversity to ecological gradients, this study provides essential knowledge to design mycorrhiza-informed restoration strategies in African woodlands facing increasing anthropogenic and climatic pressures.

Keywords: Ectomycorrhiza, *Isoperlinia doka*, morphotypes, ITS barcoding, West Africa

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

Gbètondji Basile Hounwanou^{1*}, Jean Legeay², Boris Armel Olou¹, Nourou Soulemane Yorou¹

¹Research Unit in Tropical Mycology and Plant-Soil Fungi Interactions, University of Parakou, BP 123, Parakou, Benin.

²African Genome Center (AGC), University Mohammed VI Polytechnic, Morocco

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Abstract

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: eDNA; native tree; regeneration; Next generation sequencing; tropical Africa

Patterns of Macrofungal Diversity and Substrate Association in a Protected Semi-Arid Forest Ecosystem of Northeastern Nigeria

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Abstract

Macrofungi play fundamental ecological roles in forest ecosystems through organic matter decomposition, nutrient cycling, and the maintenance of ecosystem functioning. Despite their importance, information on their diversity and substrate preferences remains limited in many tropical dry forests of sub-Saharan Africa. This study assessed the diversity, composition, and substrate-associated distribution of macrofungi in the protected Kanawa Forest Reserve, Gombe State, northeastern Nigeria. Field surveys documented a total of 35 macrofungal species belonging to three classes, four orders, and thirteen families. The assemblage was dominated by members of the class Agaricomycetes, followed by Basidiomycetes and Dacrymycetes, although several taxa were represented by only a few individuals. Species diversity across substrates was evaluated using standard ecological indices, including the Shannon–Wiener diversity index (H'), species richness (M), Pielou's evenness index (E), Simpson's diversity index ($1-D$), dominance (D), and Shannon evenness (e^H/S). The results revealed a relatively balanced distribution of species among the recorded families. Leaf litter supported the highest species richness (18 species), followed by dead wood (6 species),

standing dead wood (5 species), and living trees (2 species). It also exhibited the greatest abundance and diversity values ($D = 0.2194$; $1-D = 0.7806$; $H' = 2.004$; $e^H/S = 0.7846$), highlighting its importance as the primary substrate for macrofungal colonization and decomposition. Distribution patterns ranged from very low (34%) to very high (12%) occurrence classes, with leaf litter harboring the highest proportion of highly decomposing species. These findings emphasize the ecological significance of conserving protected forest habitats to sustain fungal biodiversity and the ecosystem processes that underpin forest resilience.

Keywords: Macrofungal diversity; Forest ecosystems; Shannon–Wiener index; Substrate association; Decomposition; Tropical dry forests.

Spatio-temporal dynamics of the Monts Kouffé Forest Reserve (Benin) and prioritization of restoration areas

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Abstract

Deforestation and land-cover change represent major ecological challenges in West African forest reserves, where increasing anthropogenic pressure and climatic variability threaten biodiversity and ecosystem services. This study analyzes land-cover change in the Monts Kouffé Forest Reserve (Benin) between 2005 and 2025 to assess landscape transformations and identify priority areas for restoration. Satellite imagery from Landsat 7 (2005) and Landsat 8 (2015, 2025) was processed on the SEPAL platform and analyzed in Google Earth Engine. Preprocessing included spectral band selection and vegetation indices, combined with climatic and topographic variables. Land-cover classification distinguished three ecologically relevant classes: dense forest, woodland/wooded savannah, and savannah. Results show a sharp decline in dense forest, from 54,680 ha (29.96%) in 2005 to 11,368 ha (6.23%) in 2025, while savannah expanded from 38,399 ha (21.04%) to 102,341 ha (56.07%). Net forest loss reached 63,944 ha, corresponding to an annual deforestation rate of -2.93%. Diversity indices decreased over time, reflecting ecological homogenization, reduced evenness, and increased dominance of savannah. Spatial metrics indicated fragmentation of forest patches and expansion of savannah mosaics. A multi-criteria analysis integrating climate and slope identified heterogeneous high-priority sectors for reforestation. These findings highlight significant landscape transformations over two

decades and emphasize the urgency of conservation actions supported by spatial analysis. By combining remote sensing, ecological indices, and spatial prioritization, this study provides a baseline for guiding reforestation planning and biodiversity conservation strategies in the Monts Kouffé Forest Reserve and similar West African ecosystems.

Keywords: Deforestation, LCC, Reforestation prioritization, Mont Kouffé, Benin

Integrating Herbarium Data and DNA Barcoding to Identify and Conserve Rare Plant Species in Rwanda

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Abstract

The conservation of rare and endemic plant species requires accurate taxonomic identification and reliable information on their spatial distribution and genetic diversity. In Rwanda, where increasing anthropogenic pressures threaten natural ecosystems, integrating traditional botanical resources with modern molecular techniques offers new opportunities for biodiversity conservation. This study highlights the use of herbarium data combined with DNA barcoding as a complementary approach for identifying and conserving rare plant species. Herbarium collections provide valuable historical and geographical records that facilitate the reconstruction of species distributions and the assessment of changes in plant diversity over time. DNA barcoding enhances species identification by resolving taxonomic uncertainties, particularly among cryptic or morphologically similar taxa. The integrated approach implemented at the National Herbarium of Rwanda supported the detection and documentation of rare and endemic species, including orchids and other under-documented plants occurring in fragmented habitats such as remnant forests and wetlands. In addition, molecular analyses improved taxonomic resolution and enabled the assessment of genetic diversity, providing essential information for conservation planning and restoration initiatives. By linking traditional botanical knowledge with molecular tools, this approach strengthens biodiversity monitoring, supports evidence-based decision-making, and contributes to the development of effective conservation strategies. The integration of herbarium resources and DNA barcoding therefore represents a valuable framework for safeguarding Rwanda's plant diversity and can serve as a model for biodiversity conservation in other rapidly changing African landscapes.

Keywords: DNA barcoding; Herbarium collections; Plant conservation; Rare species; Biodiversity monitoring; Rwanda.

Combined effect of CCR2, SDF1 and TRIM5 α genetic variants on HIV-1 mother-to-child transmission in the North Region of Cameroon

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Abstract

HIV-1 mother-to-child transmission (MTCT) is multifactorial, including host genetic factors. Prior studies on CCR2-64I, SDF1-3'A and TRIM5 α polymorphisms related to HIV infection in children focused solely on mother or on children, overlooking the combined effect of mutation in both mother and child. The objective of this study was to seek the combined effect of CCR2, SDF1 and TRIM5 α polymorphism on MTCT in Cameroon North Region. A case-control study was conducted among children under 15 years, born from HIV-infected mothers. Genomic DNA was extracted and genotyping conducted by PCR-RFLP. Analyses were performed with IBM-SPSS version 26 and STATA version 19. Odd Ratios with 95% Confidence Interval were used as association measure. Overall, 113 mother/child pairs participated. Amongst the children, 25 were HIV-infected and 88 HIV uninfected. The allelic frequencies for CCR2-64I, SDF1 3'A and TRIM5 α -136Q were 28.0%, 7.0% and 9.0% respectively in HIV-uninfected children. These frequencies were not different significantly in HIV-infected children. There was no association between the number of child mutations and HIV acquisition. Taken individually, the CCR2-64I, SDF1 3'A, and TRIM5 α -136Q polymorphisms do not appear to protect against mother-to-child transmission of HIV-1. However, when the number of mutations in mother is considered, the strength of the relationship between the number of child mutation and children HIV infection increases with the number of maternal mutations, with Chi-square increasing from 0.29 for no maternal mutation to 1.70 for at least 2 mutations. Gene's combination will help to better appreciate their contribution in MTCT.

Keywords: HIV; MTCT; polymorphism.

Exogenous Melatonin Modulates Morphological Traits and Drought-Responsive Genes (SNAC1 and DREB1A) in Tomato (*Solanum lycopersicum*) under Drought Stress (Nigeria)

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Abstract

Drought stress is one of the major environmental constraints limiting tomato (*Solanum lycopersicum*) production worldwide, particularly in regions increasingly affected by climate change. The application of plant biostimulants such as melatonin has emerged as a promising strategy to enhance crop resilience against water

deficit. This study evaluated the effects of exogenous melatonin on the morphological performance and expression of drought-responsive genes in three tomato accessions subjected to five treatments: a well-watered control, drought stress (DR), and drought stress supplemented with three melatonin concentrations (DM50, DM100, and DM150). Morphological and physiological responses were assessed alongside quantitative PCR (qPCR) analysis of two key stress-responsive genes, *SNAC1* and *DREB1A*. Drought stress markedly inhibited plant growth and reduced chlorophyll content, confirming its detrimental effects on tomato development. However, melatonin application significantly mitigated these adverse effects by improving plant physiological performance and enhancing stress tolerance. Gene expression analysis revealed substantial upregulation of drought-responsive genes under melatonin treatments. Compared with untreated drought-stressed plants (*SNAC1* = 4.47-fold; *DREB1A* = 1.28-fold), melatonin increased expression levels to 146.02-fold and 2.66-fold, respectively, demonstrating a strong transcriptional activation of stress-defense pathways. These findings indicate that melatonin functions as an effective biostimulant by stabilizing plant physiology and regulating key molecular mechanisms involved in drought adaptation. The study highlights the potential application of melatonin as a sustainable strategy for improving tomato productivity and resilience in water-limited agricultural environments.

Keywords: Melatonin; drought stress; *Solanum lycopersicum*; gene expression; *SNAC1*; *DREB1A*; biostimulant.

Microbial contamination in peri-urban market gardening sites in Benin

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Abstract

Market gardening plays a crucial role in food security and the livelihoods in Benin. It occupies an important place in the local economy and provides a vital source of fresh food for the population. This study aims to improve the sanitary quality of vegetables produced on market garden sites in Djougou in Benin by exploring microbiological contaminants, as well as the impact of irrigation practices on human health and food security. A descriptive cross-sectional study with an analytical focus was conducted on market garden sites in Djougou, Benin. Purposive sampling was used to select market gardeners. Data were collected using a KAP (Knowledge, Attitudes, and Practices) questionnaire on Kobocollect. 127 samples of vegetables, irrigation water, and fertilizers were collected. Microbiological contaminants studies were conducted by performing bacterial culture, isolation, and identification on Vitek systems. The resistance profile of

isolated *E. coli*, *Salmonella* strains was determined using the Kirby-Bauer method. Molecular analyses, such as PCR, were used to detect virulence genes. The results revealed a lack of training in agricultural hygiene among vegetable growers, high microbial contamination at all stages of vegetable production, highlighting that water and fertilizers are the main sources of vegetable contamination. Furthermore, the *E. coli* strains isolated from vegetables exhibited high resistance for amoxicillin 66.7% of strains, ceftriaxone, with 66.7% of resistant strains, and for sulfamethoxazole trimethoprim, with 55.6% of resistance and intermediate susceptibility to cephalosporin.

Keywords: Agricultural practices; Benin; microbiological contaminants; sanitary quality; vegetables

Identify the best substrate for *Pleurotus ostreatus* growing by rural women in central Benin

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Abstract

Facing food insecurity in developing countries, the cultivation of edible mushrooms represents a promising alternative. This study aims to identify the best substrate for *Pleurotus ostreatus* cultivation by rural women in central Benin. Specifically, it evaluates the performance of rice straw, sawdust, and soybean residues, analyzes the impact of moisture on productivity, and studies the perceptions of women in Parakou (Tourou, Baka, and Gah-non). Methodologically, statistical model selection was based on the Akaike Information Criterion (AIC), while the Kruskal test was used to rank the means. Biological efficiency was calculated to compare the substrates. The results show that soybean residues are colonized the fastest by mycelium, with an optimal initial moisture content of 60%. Both soybean residues and rice straw prove effective for cultivation, although rice straw requires a longer cycle. Sawdust is less efficient but could be improved through composting. The best yields increase with the moisture level, ideally above 60% without exceeding a critical threshold of 95%. Finally, the survey reveals that the women of Parakou are familiar with mushrooms but were unaware of the possibility of cultivating them. Motivated by income improvement, they express a strong interest in receiving training, justifying their future inclusion in agricultural learning projects.

Keywords: Mushroom cultivation; *Pleurotus ostreatus*; Rural women; Substrate performance; Water content

Two New Syncarid Species from Benin and Their Phylogenetic Position within the Family Parabathynellidae (Crustacea: Malacostraca)

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Abstract

Bathynellacean crustaceans are among the least studied components of subterranean aquatic biodiversity, particularly in West Africa. During an extensive sampling campaign conducted across Benin, two previously undescribed syncarid species belonging to the order Bathynellacea Chappuis, 1915 were discovered and characterized. One species belongs to the genus *Racovitzaibathynella* Serban & Coineau, 1994, while the second belongs to the genus *Cteniobathynella* Schminke, 1973. These findings represent the first records of Bathynellacea in Benin and significantly expand the known distribution of this group in Africa. Prior to this study, only two species of *Racovitzaibathynella* had been reported from South Africa and one from Chad and Israel. The newly described taxa, *Racovitzaibathynella beninensis* Camacho & Lagnika sp. nov. and *Cteniobathynella boutini* Camacho & Lagnika sp. nov., exhibit a unique combination of diagnostic morphological characters while sharing several generic features typical of their respective lineages. Phylogenetic reconstruction based on the 18S ribosomal RNA gene revealed a distinct Afrotropical clade comprising the newly identified African species, clearly separated from European, Australian, and Asian clades. These results provide new insights into the evolutionary history and biogeography of Parabathynellidae and highlight the importance of subterranean ecosystems in Benin as reservoirs of previously undocumented biodiversity.

Keywords: Bathynellacea; Parabathynellidae; 18S rRNA; subterranean aquatic fauna; new species; phylogeny; Benin.

Strides to institutionalise eDNA into fish biodiversity monitoring in Malawi; case of endangered fish species

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Abstract

Conventional methods for assessing aquatic biodiversity often rely on capture-based sampling, which may further disturb or threaten vulnerable fish populations. Environmental DNA (eDNA) has emerged as a non-invasive and highly sensitive approach for biodiversity monitoring, offering significant potential for the conservation of endangered aquatic species. This study represents an important step toward institutionalizing eDNA-based monitoring of fish biodiversity in Malawi through a case study conducted in the Bua River catchment. A total of 19 sampling sites were surveyed, resulting in the collection of data

on 14 fish species. Among the recorded species, *Enteromius paludinosus* was the most abundant, accounting for 30.1% of the observations, followed by *Enteromius trimaculatus* (16.1%), *Oreochromis shiranus* (14.0%), *Petrocephalus catostoma* (10.0%), and *Clarias gariepinus* (8.5%). To establish a comprehensive molecular reference framework, 155 invertebrate specimens and 72 eDNA water filter samples were collected. The eDNA filters, invertebrate specimens, and fish tissue samples were submitted to the Centre for Biodiversity Genomics at the University of Guelph, Canada, for molecular analyses. Fish and invertebrate specimens have already been successfully sequenced and incorporated into the **BOLD Tree of Life** reference database, thereby strengthening DNA reference libraries for Malawi's freshwater biodiversity. The analysis of eDNA water samples is currently underway and is expected to further enhance biodiversity detection and support the long-term integration of eDNA into national aquatic biodiversity monitoring and conservation programs.

Keywords: Environmental DNA (eDNA); fish biodiversity; freshwater conservation; molecular monitoring; BOLD System; Malawi.

An integrative approach to the study of fimicolous fungi in Cameroon's pasture ecosystems: Molecular identification and valuation of *Chlorophyllum hortense* and *Chlorophyllum globosum*

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Abstract

Fimicolous fungi constitute an important yet poorly documented component of pasture ecosystems in Sub-Saharan Africa, where they contribute significantly to nutrient cycling and ecosystem functioning through the decomposition of animal dung. This study investigates the diversity and biotechnological potential of fimicolous fungi in Cameroon using an integrative approach that combines classical morpho-taxonomic characterization with molecular identification based on internal transcribed spacer (ITS) region sequencing. Particular attention was given to two representative species, *Chlorophyllum hortense* and *Chlorophyllum globosum*, selected for their ecological significance and potential socioeconomic value. Molecular analyses enabled accurate taxonomic identification and strengthened species delimitation, providing a reliable framework for future biodiversity assessments. Beyond their ecological role in organic matter decomposition, these fungi were evaluated for their potential valorization and their traditional uses within local communities. Biochemical investigations revealed promising nutritional and pharmacological properties, suggesting potential applications in sustainable mushroom cultivation (myciculture), functional foods, and herbal medicine. By integrating molecular tools with ecological and ethnomycological knowledge, this study highlights the importance of conserving fungal diversity while promoting the sustainable use of biological resources. The findings support the development of natural resource management strategies that simultaneously enhance biodiversity conservation, food security, and local

livelihoods, thereby contributing to a One Health approach that links ecosystem health with human well-being.

Keywords: Fimicolous fungi; ITS sequencing; *Chlorophyllum hortense*; *Chlorophyllum globosum*; myciculture; biodiversity conservation; One Health.

ENVIRONMENT AND SOCIETY WITHIN THE ONE HEALTH FRAMEWORK

Unravelling soil fungal communities in dumpsites in kabale, western uganda using culturomics

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Abstract

Inadequate waste disposal systems have long been a perennial problem, with no clearly safe solution in sight in most developing countries. Dumpsites harbour microbial pathogens in the soil ecosystem that can cause disease outbreaks upon their seepage into the water bodies. However, there is a paucity of investigation on the diversity of fungi in dumpsites in Uganda. Hence, this research aims at evaluating the diversity and distribution patterns of fungi associated with top soils from fifteen different dumpsites in Kabale, South West, Uganda. Culturomics approach was employed in this investigation. Isolation of the fungal species was done using five different culture media, i.e., Potato Dextrose Agar (PDA), Malt Extract Agar (MEA), ChromAgar (CA), FastFung (FF), and Sabouraud Dextrose Agar (SDA). Fungal isolation was carried out using the soil dilution plate technique. ITS rRNA gene sequencing was used to identify purified isolates. FF emerged as the most effective agar, yielding the highest number of fungal isolates, followed by PDA, MEA, CA, and SDA. In all, 54 different isolates were obtained. *Trichoderma*, *Fusarium*, and *Aspergillus* sp were the most prevalent. Also, pathogenic and opportunistic fungi such as *Simplicillium lamellicola*, *Mortierella multispora*, and *Torulaspora delbrueckii* were isolated. All *Aspergillus* isolates were further screened for azole resistance (itraconazole, voriconazole, posaconazole, and Amphotericin B). Results showed that most *Aspergillus* species had lower MICs; however, *A. clavatus* had an MIC of 1.5 ug/mL. This work further emphasises the need for regular monitoring of dumpsites for fungi, which can pose a public health concern.

Keywords: antifungal resistance; culturomics; dumpsites; fungi; public health.

Effect of *Moringa oleifera* Extracts on Insect Pests and White Rot of Common Bean (*Phaseolus vulgaris* L.) under Field Conditions in Central Cameroon

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Abstract

The extensive use of synthetic pesticides in agriculture has raised growing concerns regarding environmental contamination, biodiversity loss, and the emergence of resistance in target organisms, highlighting the need for sustainable and eco-friendly crop protection strategies. Plant-based biopesticides have emerged as promising alternatives due to their biodegradability and reduced environmental impact. This study evaluated the efficacy of *Moringa oleifera* seed extracts in controlling insect pests and white rot disease caused by *Sclerotinia sclerotiorum* on common bean (*Phaseolus vulgaris* L.) under field conditions in Central Cameroon. Field trials were conducted over two cropping seasons using both aqueous and organic seed extracts of *M. oleifera*. The effects of the treatments on pest infestation and disease severity were assessed and compared with untreated controls. Results demonstrated that both aqueous and organic extracts significantly reduced damage caused by insect pests and mitigated the impact of *S. sclerotiorum* on bean plants. The treatments contributed to improved plant health and reduced disease pressure throughout the growing period. These findings support the potential use of *M. oleifera* seed extracts as environmentally friendly biocontrol agents for integrated pest and disease management in bean production systems. The adoption of such plant-based alternatives could contribute to sustainable agriculture by reducing reliance on synthetic pesticides while promoting environmental, animal, and human health within a One Health framework.

Keywords: *Moringa oleifera*; biopesticides; biological control; *Sclerotinia sclerotiorum*; common bean; integrated pest management; One Health.

Antimicrobial Resistance in Poultry Production: Detection of ESBL and Carbapenemase Genes in *Escherichia coli* from Healthy Turkeys in Nigeria

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Abstract

Antimicrobial resistance in *Escherichia coli* represents a growing concern for poultry health and public safety. While this issue has been widely studied in chickens, limited information exists on multidrug-resistant *E. coli* in turkeys in Nigeria. This study aimed to determine the occurrence, antimicrobial resistance patterns, and β -lactamase genes of *E. coli* isolated from turkeys in commercial farms in Ibadan,

Nigeria. A total of 225 cloacal swabs were collected from turkeys across five farms during the period of 2024-2025. Isolates were identified using PCR targeting the *uidA* gene. Antimicrobial susceptibility testing followed Clinical and Laboratory Standards Institute (CLSI, 2025) guidelines, while multiplex PCR assay was used to detect ESBL and carbapenemase genes. Sixteen (7.1%) isolates were confirmed as ESBL and carbapenemase producers, all exhibiting multidrug resistance with multiple antibiotic resistance index (MARI) values ranging from 0.5 to 0.9. The isolates showed the highest resistance to sparflaxacin, augmentin, and streptomycin (93.75%). Detected ESBL and carbapenemase genes in isolates included *bla*TEM (100%), *bla*CTX-M (56.25%), *bla*SHV (6.25%), *bla*OXA-48-like (56.25%), and *bla*NDM-1 (6.25%). This study provides the first report of ESBL- and carbapenemase-producing *E. coli* in turkeys in Nigeria. The co-existence of critical resistance genes highlights the urgent need for antimicrobial stewardship, routine surveillance, and enhanced biosecurity in turkey production systems.

Keywords: Antimicrobial resistance; Carbapenemases; Esbl gene; *Escherichia coli*; Turkeys

Analyse des pratiques d'élimination des déchets menagers dans les zones urbaines du département du sud du borgou (Parakou, N'Dali, Tchaourou)

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Abstract

Face à une urbanisation rapide et une croissance démographique soutenue, les villes africaines rencontrent des difficultés dans la mise en œuvre de politiques durables de gestion des ordures ménagères. Cette situation engendre des pratiques d'élimination anarchiques, qui nuisent à la qualité de vie urbaine. Cette étude examine les pratiques d'élimination des déchets dans les villes de Parakou, N'Dali et Tchaourou (Borgou, Bénin), en analysant les comportements des ménages et les facteurs qui influencent leurs choix en matière de gestion des déchets. Une approche mixte (quantitative et qualitative) a été adoptée, combinant une enquête auprès de 258 ménages via KoboCollect, des entretiens semi-directifs avec des acteurs locaux, et une analyse statistique par modèle logit multinomial. Les résultats révèlent que l'incinération est la pratique dominante (69,8 %), suivie de l'enfouissement (16,3 %), des dépôts sauvages (10,1 %) et de la collecte organisée (3,9 %). Ces pratiques informelles s'expliquent par l'absence d'infrastructures adaptées et de services accessibles. L'analyse montre que le niveau d'instruction, le revenu, le statut résidentiel (locataire ou propriétaire) et la distance aux points de collecte influencent de manière significative les choix des ménages. Ces constats soulignent l'urgence d'adapter les politiques de gestion des déchets aux réalités socioéconomiques et spatiales locales. L'amélioration de l'accès aux services de collecte et la promotion d'initiatives communautaires sont essentielles pour une gestion durable des ordures ménagères. En perspective, cette approche pourrait être étendue à d'autres villes du Bénin et d'Afrique, ou servir à évaluer l'impact des politiques mises en œuvre dans des contextes similaires.

Mots-clés : Gestion, Ordures, Production, Elimination, Ménage

Facteurs d'adoption des pratiques de restauration des paysages forestiers dans la préfecture de Kozah (Nord-Togo) : enjeux pour la résilience climatique et la transition socio-écologique

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Abstract

In the face of the accelerating degradation of forest landscapes in West Africa, forest landscape restoration (FLR) is an essential strategy for strengthening ecological and socioeconomic resilience in the context of climate change. In Togo, the Kozah Prefecture is characterized by significant human pressure, leading to rapid ecosystem transformation and the weakening of production systems.

Cette étude vise à analyser les facteurs d'adoption des pratiques de RPF à travers une approche intégrée combinant télédétection, Systèmes d'Information Géographique (SIG), enquêtes socioéconomiques et modélisation économétrique. L'analyse diachronique de l'occupation des terres entre 1995 et 2025 révèle une expansion des zones agricoles et des jachères (+135,7 %) ainsi qu'une forte régression des formations boisées, passées de 85,1 % à 2,8 % du territoire. Les plantations et les zones d'habitation ont également connu une augmentation importante, traduisant une intensification des pressions anthropiques. Les pratiques étudiées, notamment l'agroforesterie, la régénération naturelle assistée et les techniques de conservation des sols, présentent des effets positifs sur la fertilité des sols, la lutte contre l'érosion, la qualité de l'eau, la biodiversité et la production de biomasse ligneuse. Toutefois, 93 % des ménages déclarent une baisse de fertilité des sols et 86 % une diminution des rendements agricoles. L'analyse économétrique montre que l'adoption des pratiques de RPF est principalement influencée par la sécurité foncière (OR=14,5 ; $p<0,05$), les contraintes biophysiques telles que la topographie (OR=10,8 ; $p<0,05$) et la perception de la baisse des rendements (OR=5,08 ; $p<0,05$). D'autres variables, notamment la taille des parcelles, le genre ou la situation matrimoniale, présentent une influence marginale. Ces résultats soulignent que l'adoption des pratiques de restauration dépend autant des conditions socioéconomiques et institutionnelles que de leur efficacité écologique, d'où la nécessité de politiques de restauration intégrées et adaptées aux réalités locales.

Mots-clés : Pratique de restauration des paysages forestiers (RPF) ; facteurs d'adoption ; résilience climatique ; dynamiques des unités d'occupation des terres ; préfecture de Kozah.

Caracteristiques hydrochimique et microbiologique des eaux souterraines et évaluation des risques sanitaires associés à Parakou (Bénin)

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Abstract

Cette étude a pour objectif de caractériser les valeurs hydrochimique et microbiologique des eaux souterraines et d'évaluer les risques sanitaires dans la zone d'étude. Une approche méthodologique comprenant l'échantillonnage de 14 forages et de 17 puits, l'enquête sur 379 personnes et l'analyse des échantillons d'eau au laboratoire a été mise en œuvre. Les résultats ont montré que 32 % des eaux de forage et 44 % des eaux de puits ont présenté des valeurs supérieures en nitrate ; 20 % et 57 % des forages et des puits ont respectivement des teneurs en sulfates hors la norme OMS. Quant aux valeurs microbiologiques, 100 % des puits et 64% des forages sont polluées par *Escherichia coli*; 94 % des puits et 42 % des forages sont polluées par les germes banales et 65 % des puits sont pollués par les coliformes fécaux. En effet, 25 % ont souffert d'une gastro-entérite et 32 % ont souffert de la fièvre typhoïde. L'état de dégradation des eaux souterraines analysées nécessite une attention particulière.

Mots clés : eaux souterraines ; hydrochimique ; pollution ; risques sanitaires

Plant Biomarkers, Air Pollution and One Health Resilience: Urban Evidence from *Psidium Guajava* in Douala, Cameroon

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Abstract

Accelerating urbanization across Africa is intensifying particulate air pollution, threatening ecosystem integrity, urban livability, and public health within the One Health framework. Urban vegetation provides critical natural mitigation infrastructure by intercepting airborne particulates and improving environmental quality; however, resilience thresholds of tropical species remain insufficiently understood. Generating such evidence is essential for designing climate-resilient African cities and cost-effective nature-based solutions. This study investigated physiological responses of *Psidium guajava* to dust pollution across urban (PK14), residential (Entrée Kotto), and suburban (Lendi) zones of Douala, over a 12-month period. Leaf dust load and key stress biomarkers; total chlorophyll, ascorbic acid, relative water content (RWC), leaf extract pH, and Air Pollution Tolerance Index (APTI) were assessed as indicators of plant health and environmental stress. Results revealed a threshold-dependent response. Moderate dust loads ($\leq 2.4\%$) significantly enhanced chlorophyll accumulation ($\beta = 1.607$, $p = 0.017$) and optimized leaf pH, indicating adaptive compensation under low-to-moderate stress. Beyond this threshold, elevated dust exposure caused marked physiological decline, with peak dust loads reaching 3.9% in the urban site and significant reductions in water status (RWC; $r = -0.74$, $p = 0.01$). APTI values ranged from 6.0–9.7, identifying *P. guajava* as a sensitive bioindicator suitable for urban air-quality surveillance. Seasonal rainfall moderated dust deposition, whereas highly urbanized locations

experienced greater stress intensity. These findings demonstrate that plant biomarkers can provide low-cost early-warning tools for pollution monitoring in data-scarce cities while supporting strategic urban greening, ecosystem quality, climate adaptation, and One Health outcomes across rapidly growing African urban centres.

Keywords: Air pollution tolerance index; Dust pollution; Hormesis; Photosynthetic efficiency; Tropical urbanization

Airbone mycobiome in the city of Parakou: Diversity, intra-annual dynamics and epidemiological implications in the One Health context

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Abstract

Fungi are a very diverse group of organisms that play a major role in the functioning of ecosystems and are important for human and animal health, food production, and nature conservation. However, very little data is available on the actual diversity of airborne fungi and their implications for health. This study highlights the major fungal taxa of importance for human health according to seasonal variation, while also establishing links with domestic animals and air quality in Parakou within a One Health framework. Using a cyclone air sampler combined with DNA barcoding and probabilistic species identification, a large number of fungal sequences were obtained. A total of 1,444,992 DNA sequences were generated and grouped into 55,225 operational taxonomic units, revealing a remarkably high diversity. Overall, 169 species were identified, distributed across 115 genera, 69 families, 33 orders, 12 classes, and 5 phyla. The Ascomycota phylum was the most dominant with 105 species, followed by Basidiomycota with 53 species. Diversity indices showed a clear seasonal pattern, with higher diversity during the rainy season (85 genera) compared to the dry season (30 genera), along with some heterogeneity at the genus level. Notably, high concentrations of spores from pathogenic genera such as *Aspergillus*, *Alternaria*, *Candida*, *Cladosporium*, *Cryptococcus*, *Fusarium*, and *Mycosphaerella* were detected, suggesting potential health risks. Aerial sampling combined with molecular identification proved to be an efficient and cost-effective approach for monitoring airborne fungal diversity and could significantly enhance large-scale biodiversity assessment programs.

Keywords: Airborne fungi; Fungal diversity; DNA barcoding; One Health.

Metabarcoding of Bacterial Communities on Floating Plastics in River Ngadda within Maiduguri metropolis Using PacBio Full-Length 16S rRNA Sequencing

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Abstract

Plastic pollution in freshwater systems creates novel microbial habitats termed the plastisphere, with important ecological and public health implications. This study investigated the bacterial communities associated with floating plastic debris and adjacent surface water in River Ngadda, an urban river in Maiduguri, Nigeria, using PacBio full length 16S rRNA gene sequencing. Floating polyethylene plastics and surrounding water samples were collected, and DNA was extracted and sequenced to achieve high resolution taxonomic profiling. Comparative analyses revealed distinct microbial assemblages between plastic surfaces and the water column. Plastic associated communities exhibited higher observed amplicon sequence variant (ASV) richness and greater Faith's phylogenetic diversity, indicating enhanced microbial complexity on plastic substrates. Pseudomonadota dominated both environments; however, Cyanobacteriota were selectively enriched on plastic surfaces.

Health vulnerability in bushmeat exploitation and preventive measures for sustainable wildlife conservation in community forests of Benin

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Abstract

Bushmeat is a vital resource for communities in West Africa, providing them with both protein and income. However, the handling and consumption of this meat pose risks to public health and biodiversity conservation. Based on the “One Health” framework, this study aims to evaluate the health risks associated with the exploitation of bushmeat in communal forests in Benin. 205 individuals were interviewed using a snowball sampling method. Firth and Lasso binary logistic regression analysis of the data showed that behaviors relating to bushmeat handling and consumption vary across localities. Despite a general awareness of the inherent dangers, the results indicate that local populations have not yet been able to reduce their dependence on this practice. Firth's binary logistic regression analysis shows that age and level of secondary education have a statistically significant effect ($p < 0.05$) on population exposure to diarrhea. Conversely, hunters show a statistically significant ($p < 0.05$) effect regarding exposure to allergy and haemorrhoid. The Lasso binary logistic regression analysis shows that, to combat communicable diseases, the population relies on traditional treatments, which involve the use of certain plant parts due to their local availability and accessibility, as well as other substances such as alcohol consumption and the use of large amounts of chili peppers when cooking bushmeat. Furthermore, the study identifies symptoms associated with bushmeat consumption and proposes alternative strategies to reduce dependency on this resource, integrating health, ecological and socio-economic concerns within a transdisciplinary “One Health” approach.

Keywords: Alternative strategy; Bushmeat; One Health; Perception; Zoonotic diseases

Prevention of zoonoses and the challenges of one health in the Zou departement (Benin Republic)

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Abstract

Zoonoses such as rabies, tuberculosis and antimicrobial resistance continue to have a major impact on public health in Benin, where 75% of infectious diseases are of animal origin. This study analyses strategies for the prevention and control of zoonoses, specifically rabies, in the Zou department. The methodology adopted combines the analysis of secondary data from veterinary and environmental services, supplemented by field surveys and interviews with institutional and local stakeholders. The results reveal a high prevalence of animal bites in the Zou department, with a predominance of cases linked to dogs (82.50% in 2025). Over the last three years (2023, 2024 and 2025), the municipalities of Abomey, Bohicon and Quinhi recorded the highest number of cases. Close cohabitation between human populations and domestic animals, combined with inadequate healthcare coverage, facilitates the emergence of diseases. Low rates of rabies vaccination, poor living conditions, rapid urbanisation and climate change exacerbate these health risks. Increased vaccination of domestic animals, community awareness campaigns on hygiene and coordinated epidemiological surveillance appear essential for the sustainable management of zoonoses in this region.

Keywords: Benin, One Health, prevention, rabies, zoonoses

Contamination and pesticide multiresidue analysis in cotton production systems in Benin

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Abstract

High quantity of chemical pesticides spraying in conventional cotton production systems may affect negatively natural ecosystems components. This study examined the contamination levels of soil in Benin's cotton production system in West Africa by residues of pesticides used in cotton farming. One hundred and fourteen soil samples from six conventional and organic cotton production systems were collected and analysed. Multi-class pesticide residues were extracted from the soil samples, and analysed using respectively modified QuEChERS extraction and LC-MS/MS chromatography methods. Results showed an overall soil contamination to emamectin benzoate (18.5 µg/kg), imidacloprid (116.3 µg/kg), profenofos (12.7 µg/kg), acetamiprid (10.8 µg/kg), triasophos (12.6 µg/kg), abamectin (14.3 µg/kg), and deltamethrin

(10.4 µg/kg). Especially, emamectin benzoate was detected with a high contamination in Banikoara district (18.5 µg/kg). Nevertheless, these contaminations were not deemed threatening from a toxicological perspective. Soils in conventional cotton cultivation displayed lower organic matter levels but higher concentrations of pesticides, whereas soils in organic cotton cultivation were less degraded and contaminated. Consequently, it is imperative to conduct environmental risk assessments and monitor key pesticide metabolites to establish sustainable cotton production systems in Benin.

Keywords : Conventional cotton production systems; Environmental impact; Pesticides; Soils contamination

Community Practices and Laboratory Investigations of Hydatid Disease in Western Libya: Towards a One Health Prevention Strategy

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Abstract

Cystic echinococcosis is a neglected zoonotic disease with major health and economic impacts. In Libya, CE remains hyperendemic due to home slaughtering, poor disposal of infected organs, and close human–animal interactions. This doctoral research integrates community-based surveys with laboratory investigations to design a national prevention strategy. A quasi-experimental design was adopted. 1,270 participants for a knowledge, attitudes, and practices study, alongside 294 dog stool samples and 378 livestock tissue samples. KAP results revealed that only 30% of participants had adequate knowledge, while risky practices such as feeding dogs infected offal and irregular vegetable washing sustained transmission. Samples have been collected from dogs and livestock in western Libya. Laboratory analyses (ELISA, PCR) are planned as the next step to confirm. The study highlights the urgent need for a comprehensive prevention strategy integrating veterinary sectors, aligned with One Health.

Water quality and distribution of intestinal parasitic forms in surface waters in Yaoundé-Cameroon (Central Africa)

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Abstract

Intestinal parasites and environmental diseases are the consequences of complex interactions between the etiological agent, the host and the environment. A work aimed at studying the distribution of resistance forms of intestinal pathogens in relation to the physico-chemical quality of water. This study was carried out from march to june 2022 during the short rainy season in the Yaounde. Water sampling for physico-

chemical and parasitological analyses was carried out according to standard methods at 30 stations in the lowlands of Yaounde. Distilled water and saline centrifugation techniques were used to identify helminths eggs and larvae in water. The results of the physico-chemical analyses showed that waters were warm, with a neutral pH, a low turbidity and low ammoniacal nitrogen content. Results of the parasitological analyses shown the presence of 11 species of helminths with a dominance of *Strongyloides stercoralis* larvae (195 Larvae/L) and *Toxocara leonina* (115 Eggs/L).

SESSION: MOLECULAR APPROACHES IN HUMAN AND ANIMAL HEALTH

Environmental surveillance of soil-transmitted helminths and enteric pathogens in settings without networked wastewater infrastructure

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Abstract

Soil-transmitted helminths (STH) are one of the most prevalent infections world-wide. Current surveillance strategies for STH focus on identifying and quantifying eggs in stool samples via microscopy, which exhibits poor specificity and sensitivity. Wastewater-based epidemiology is a surveillance tool used to monitor pathogen circulation, and could replace stool-based approaches for STH detection. Here, we report evaluation of sampling strategies for soil and wastewater STH surveillance in rural and peri-urban settings without networked sanitation. We used multi-parallel qPCR assays to detect STH DNA in soil collected from high foot-traffic locations and three types of wastewater samples (passive Moore swabs, grab samples, and sediment from drainage ditches) in Comé, Benin and Tamil Nadu, India. We detected STH in soil (India = 32/95, Benin = 39/121) and wastewater (India = 24/60, Benin = 8/64) with a detection frequency across all sample types of 36% in India and 25% in Benin. We evaluated which sample locations and types allowed

for more sensitive detection of STH DNA and determined that STH prevalence varied by sample site but did not vary significantly within a given sample site locations (e.g., samples collected from multiple locations within one market). Further, we determined that wastewater sediment samples outperformed grab and Moore swab sample types for STH detection. Finally, we expanded our methods to include detection of other enteric pathogens using multiplexed qPCR for wastewater samples. Our results establish sampling strategies for environmental and wastewater surveillance of a wide range of enteric pathogens in settings without networked sanitation.

Keywords: enteric pathogens; molecular surveillance; soil-transmitted helminths; wastewater-based epidemiology.

Progress report on molecular screening of potential zoonotic pathogens in mammals sold in bushmeat markets in Douala, Cameroon

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Abstract

The bushmeat trade in tropical Africa is increasingly recognised as a major public health concern due to the emergence of several zoonotic diseases carried by wildlife, such as Ebola, monkeypox and, most recently, SARS-CoV-2. In Central Africa, bushmeat markets frequently bring humans into contact with wildlife, potentially facilitating the transmission of pathogens. In this context, it is essential to document the diversity of microorganisms associated with wildlife sold for human consumption in order to better understand potential zoonotic risks. Thus, 298 buccal, cutaneous and anal swabs were collected from 202 live, fresh and smoked mammalian specimens sold at the Dakat bushmeat market in Douala, using a DNA collection and preservation kit (Swab Collection and DNA Preservation System, Norgen, Canada), employing an opportunistic sampling strategy. After extraction and PCR amplification, high-throughput sequencing was performed. Bioinformatic processing involved sequence cleaning and filtering using OBITools, taxonomic assignment through the SILVAngs platform and additional data quality filtering using the R package metabar. We then limited our focus to eukaryotic organisms, many of which have already been identified as human pathogens by other researchers. The next step will be to compile a list of bushmeat pathogens in Cameroon and study microbial diversity based on parameters such as host, condition or sample type.

Keywords: bushmeat, Cameroon, metabarcoding, molecular screening, zoonotic risk.

Exploration des biomarqueurs oxydatif et inflammatoire associés aux symptômes d'anxiété chez les adolescents au Bénin

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Abstract

Les troubles anxieux chez les adolescents constituent un enjeu majeur de santé publique, particulièrement dans les contextes socio-environnementaux vulnérables. Cette étude vise à évaluer le rôle des biomarqueurs du stress oxydatif et de l'inflammation comme médiateurs biologiques entre expositions aux facteurs socio-environnementaux et symptômes d'anxiété chez des adolescents au Bénin. Un design analytique sera utilisé, intégrant des données psychosociales et biomarqueurs. Les marqueurs inflammatoires comme la TNF α seront quantifiés par ELISA ; et celui du stress oxydatif le Nrf 2 par Western blot. Des modèles de médiation seront appliqués pour tester les relations causales entre les expositions, les biomarqueurs et les symptômes. Cette approche interdisciplinaire s'inscrit dans le champ des approches moléculaires en santé humaine et contribue à combler le déficit de données en Afrique subsaharienne principalement au Bénin. En intégrant des données psychosociales et moléculaires, cette recherche éclairera des interventions adaptées pour la santé mentale des adolescents en Afrique de l'Ouest, où des données sont urgemment nécessaires. « Cette recherche a été financée [en partie] par une subvention de démarrage de l'Afrique Research Support Hub (ARSH) offerte par le Centre de recherche sur la population et la santé en Afrique (APHRC) et financée par Wellcome par le biais d'une subvention de projet à l'APHRC. »

Mots-clés : ELISA; Nrf2; TNF α ; Santé mentale; Western blot

Prevalence, Carbapenem Resistance Genes, and Clonal Distribution of *Acinetobacter baumannii* in West Africa: A Systematic Review

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Abstract

Carbapenem-resistant *Acinetobacter baumannii* is classified by the World Health Organization as a critical priority pathogen because of its multidrug resistance and association with healthcare-associated infections. In West Africa, limited diagnostic capacity and inadequate antimicrobial stewardship may facilitate the spread of carbapenem-resistant *Acinetobacter baumannii* (CRAB). However, regional epidemiological data remain fragmented. A systematic review was conducted according to PRISMA 2020 guidelines. PubMed, Scopus, Web of Science, Google Scholar, and African Journals Online (AJOL) were searched up to March 2026. Studies reporting CRAB prevalence, resistance genes, or molecular epidemiology in ECOWAS countries were included. From 1,309 records identified, 78 studies from nine countries met the inclusion criteria. Due to substantial heterogeneity ($I^2 = 85.5\%$), a narrative synthesis was performed. CRAB prevalence ranged from 12.5% to 100% across settings. The predominant carbapenemase genes were *blaOXA-23*, *blaOXA-58*, and *blaNDM-1*. Molecular typing showed the predominance of the international clone IC2 (ST2-Pasteur). No molecular epidemiological data were identified for Guinea, Guinea-Bissau, and Liberia.

CRAB is increasingly disseminated across West Africa, highlighting the urgent need for coordinated regional surveillance, genomic monitoring, and strengthened antimicrobial stewardship programs.

Keywords : *Acinetobacter baumannii*; antimicrobial resistance; carbapenemase; CRAB; West Africa.

Molecular Diagnosis of Tuberculosis in human and Dromedaries in Algeria

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Abstract

Background: Tuberculosis in dromedaries in Algeria has been little studied to date. The objective of this study was to determine the prevalence of tuberculosis in dromedaries in three Algerian slaughterhouses using samples of lesions suspected of tuberculosis, detected on carcasses during post-mortem visual inspection. **Methodology:** The study also used laboratory diagnostics to isolate and identify the causative agents of the infection. A total of 102 carcasses were suspected of having tuberculosis out of a total of 3,342 dromedary carcasses inspected. The lesions were located as follows in the carcasses: 64 out of 102 were in the lungs, 37 in the liver, and 1 in a bronchial lymph node. In France, five and six samples of suspected tuberculosis lesions, respectively, tested positive by bacilloscopy (4.9%) and culture (5.88%; 95% CI 2.19–12.36). Spoligotyping on the same DNA extracts confirmed the presence of four *Mycobacterium bovis* strains with the same spoligotype SB0941 and one strain with spoligotype SB2562, a profile newly described in this study, which is phylogenetically close to the previous profile. Using suspected tuberculosis lesions from dromedary camels, a non-tuberculous mycobacterium was identified as *Mycobacterium virginiense* MO-233 (sequence ID:

Nr149186) using 16SrDNA sequencing. Our study reported *M. bovis* TB in 0.1 % of 213 TB cases for the humans.

Having demonstrated the presence of *M. bovis* tuberculosis in the population of In Algeria, it is now necessary to implement control measures to reduce transmission between animals and humans.

Keywords: Dromedary, Humans, Mycobacterium, Spoligotyping, Tuberculosis

Reproduction technology (sperm harvesting, extenders, freezing) in Djallonké sheep in West Africa

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Abstract

This study evaluated the impact of harvesting frequency, extenders, and cooling on the semen quality of Djallonké rams. Optimal freezing conditions were established to create a local sperm storage protocol. Fifteen Djallonké rams, aged 15 to 24 months, were selected and divided into three experimental groups ($n = 5$), with each group corresponding to semen collection intervals of 48 hours, 72 hours, and 96 hours. Semen was collected via electroejaculation over a six-month period, yielding a total of 278 samples. Parameters (volume, color, pH, motility, concentration, and morphology) were evaluated using the CASA system. Dilutions were performed in the laboratory. A seven-day cooling process was implemented, followed by cryopreservation in liquid nitrogen for two weeks. The data were analyzed using the General Linear Model procedure in SAS® 9.2. The results showed that the best sperm quality was recorded at 96-hour intervals (0.57 ± 0.23 ml), with better overall sperm motility (4.00 ± 3.83) and progressive motility estimated at 63.98%, with 30.99% of sperm immobile. The average sperm pH was 6.8 ± 1.00 and the color was creamy white. The optimal extender for sperm survival was the commercial extender Oviplus. However, sperm from Djallonké rams have low cold resistance due to thermal shock and exhibit a mortality rate exceeding 90% during cryopreservation. Overall, a 96-hour interval has proven to be optimal for assisted reproductive technology protocols. However, semen loses its fertilization capacity after three days of storage at $+4^{\circ}\text{C}$ and remains difficult to freeze at -196°C .

Keywords: Sperm harvesting frequency – Extenders – Freezing – Sperm characteristic – Ram's spermatozoa