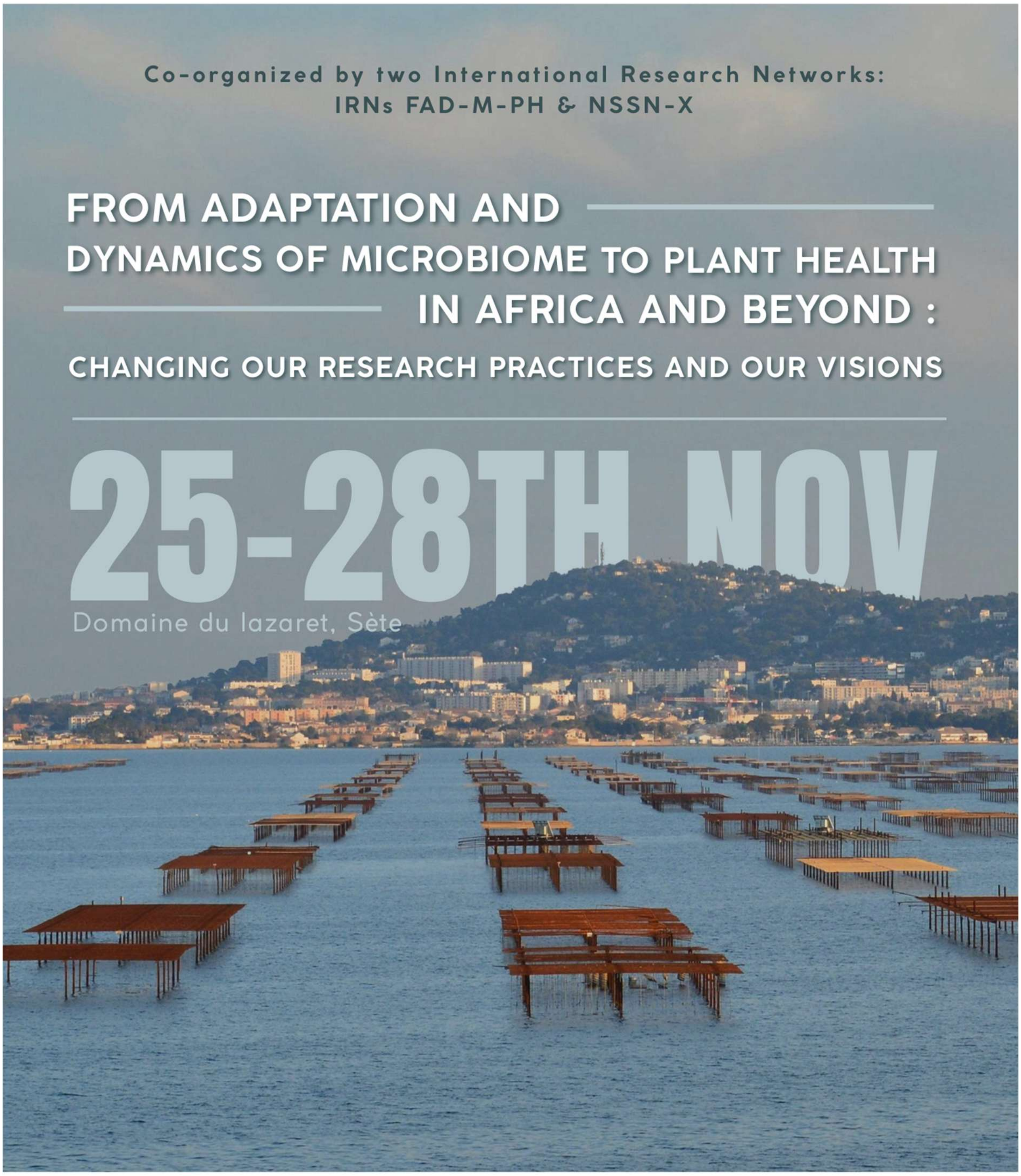

Co-organized by two International Research Networks:
IRNs FAD-M-PH & NSSN-X

FROM ADAPTATION AND DYNAMICS OF MICROBIOME TO PLANT HEALTH IN AFRICA AND BEYOND :

CHANGING OUR RESEARCH PRACTICES AND OUR VISIONS

25-28TH NOV

Domaine du lazaret, Sète

Partners

INRAE

147 rue de l'université
75338 Cedex 07
FRANCE
Tel. : +33(0)1 42 75 90 00
Fax : + 33(0)1 47 05 99 66

Website : **http://www.inrae.fr**

IRD

44 Bd de Dunkerque
13002 Marseille
FRANCE
Tél : +33(0)4 91 99 92 00

Website : **https://en.ird.fr/**

Montpellier University

163 rue Auguste Broussonnet
34090 Montpellier
FRANCE
Tel: +33(0)4 67 41 74 00

Website : **https://www.umontpellier.fr/en/**

Région Occitanie

201, avenue de la Pompignane
34064 Montpellier Cedex 02
FRANCE

Website : **https://www.laregion.fr/**

TSARA

contact@initiative-tsara.org

Website : **initiative TSARA**

Défi Octaave

contact-Octaave@agropolis.fr

Website : **Défi Octaave**

LabEx TULIP

Chemin de Borde Rouge - BP 52627
31326 Castanet Tolosan Cedex
FRANCE
Tel. : +33(0)5 61 28 55 52

Website : **LabEx TULIP**

Key Initiative CLAPAS

diana.fernandez@ird.fr

Website : **Key Initiative CLAPAS**

Scientific committee

Pr Naéssé	ADJAHOSSOU	ENSBAA (Univ)	BENIN
Dr Komi	ASSIGBETSE	IRD, Eco&Sols	FRANCE
Pr Yacoubou	BAKASSO	UAMN (Univ)	NIGER
Dr Mariam	BARRO	INERA	BURKINA FASO
Dr Adriana	BERNAL	ULA (Univ)	COLOMBIA
Dr Alice	BOULANGER	U de Toulouse, LIPME	FRANCE
Dr Antony	CHAMPION	IRD, DIADE	FRANCE
Pr Pierre	CZERNIC	U Montpellier, PHIM	FRANCE
Dr Ibrahim	HASHIM	TARI	TANZANIA
Dr Eugénie	HEBRARD	IRD, PHIM	FRANCE
Dr Valérie	HOCHER	IRD, PHIM	FRANCE
Dr Mathilde	HUTIN	IRD, PHIM	MADAGASCAR
Dr Souley	ISSAKA	UBBT (Univ)	NIGER
Dr Abalo	KASSANKOGNO	INERA	BURKINA FASO
Dr Agnieszka	KLONOWSKA	IRD, PHIM	FRANCE
Dr Laura	LOKO	ENSBAA (Univ)	BENIN
Pr Lyna	MUKWA	CPK	DEM. REP. CONGO
Pr Eddy	NGONKEU	U Yaoundé (Univ)	CAMEROUN
Dr Essowè	PALANGA	ITRA	TOGO
Dr Mame Penda	SARR DIAWARA	ISRA	SENEGAL
Dr Boris	SZUREK	IRD, PHIM	FRANCE
Dr Didier	THARREAU	Cirad, PHIM	FRANCE
Dr Issa	WONNI	INERA	BURKINA FASO
Dr Jeniffer	YANEZ	PUCE (Univ)	ECUADOR
Dr Arlette	ZAYIA	IRAD	CAMEROUN
Pr Innocent	ZINGA	U Bangui (Univ)	CENTRAL AFRICAN REP.

Organization committee

Dr	Komi	ASSIGBETSE	IRD, Eco&Sols
Dr	Elsa	BALLINI	Institut Agro, PHIM
Dr	Alice	BOULANGER	U de Toulouse, LIPME
Dr	Antony	CHAMPION	IRD, DIADE
Pr	Pierre	CZERNIC	U Montpellier, PHIM
Mrs	Cécile	GERDY	IRD, PHIM
Dr	Eugénie	HEBRARD	IRD, PHIM
Dr	Valérie	HOCHER	IRD, PHIM
Dr	Mathilde	HUTIN	IRD, PHIM
Dr	Agnieszka	KLONOWSKA	IRD, PHIM
Mrs	Clotilde	SABOT	IRD, PHIM
Dr	Boris	SZUREK	IRD, PHIM
Dr	Didier	THARREAU	Cirad, PHIM

Acknowledgments

Cécile Gerdy, Clotilde Sabot, Mélanie Pons, Morgane Guilhem IRD

Scientific program

	TUESDAY 25TH NOV.	WEDNESDAY 26TH NOV.	THURSDAY 27TH NOV.		FRIDAY 28TH NOV.
			NSSN-X	FAD-M-PH	
9h00		Keynote South O. Babalola	L. Brottier L. Gorgues C. Zarate B. Charleux	IRN review	
9h15				S. Issaka	
9h30				R. Longué	C. Tollenaere
9h45		A. Bernal		L. Loko	
10h00				J. Toffa	M. Barbier
10h15		I. Quibod		I. Zinga	L. Albar
10h30		Coffee break	Coffee break	Coffee break	Coffee break
10h45					
11h00		G. Onaga	C. Audran C. Blasco S. Marty S. Delafosse	E. Zongo	A. Perez Quintero
11h15				H. Founoune	Wrap-up
11h30		C. Nanoukon		IRN project	
11h45		M. Dominguez			
12h00				Lunch	Departure
12h15		Lunch			
12h30			Lunch		
12h45					
13h00	Arrival				
13h15					
13h30			Social event	IRN Workshop	
13h45					
14h00	Welcome note	Keynote Octaave D. Ortiz			
14h15					
14h30	Keynote North J. Leach				
14h45		M. Morrison			
15h00		L. Gagnevin		Social event	
15h15	P. Portier	M. Barro			
15h30		H. Raveloson			
15h45	C. Benezech	Coffee break			
16h00	Coffee break				
16h15					
16h30	H. Tall	N. Chen			
16h45					
17h00	L. Mukwa	I. Hashim			
17h15	M. Hutin	A. Klonowska			
17h30					
17h45	N. Arroyo Velez	M. Sarr			
18h00	Poster Session	Poster Session	Party		
18h15					
18h30					
18h45	Cocktail				
19h00					

Tuesday 25th

02:00pm Welcome note

02:30pm #1 **Jan LEACH - Colorado State University, USA**
Bacteria-Insect-Plant Interactions: Understanding How Microbiomes in Russian Wheat Aphid Honeydew Increases Aphid Virulence to Plants

03:15pm #2 **Perrine PORTIER – INRAe, Beaucouzé, France**
How to preserve viable Microbiota?

03:45pm #3 **Claire BENEZECH - Institut Agro, Montpellier, France**
Wheat genotype impacts plant responses to biosolutions

04:00pm Coffee break

04:30pm #4 **Hamidou TALL – ISRA, Sénégal**
Screening of rice varieties and accessions (Oryza sativa L. and Oryza glaberrima Steud) for resistance and genomic comparative to bacterial leaf streak in Senegal

05:00pm #5 **Lyna MUKWA – CPK, République Démocratique du Congo**
Molecular characterization of Ralstonia pseudosolanacearum causal agent of tomato wilt in western Democratic republic of Congo

05:15pm #6 **Mathilde HUTIN – IRD, Madagascar**
Bacterial Leaf Blight of rice : an emerging threat to rice cultivation in East Africa

05:45pm #7 **Noe ARROYO VELEZ – INRAe, Beaucouzé, France**
Prophage diversity reveals evolutionary history and dispersal of Xylella fastidiosa subsp. multiplex in France

06:00pm Poster session/cocktail

08:00pm Dinner

Wednesday 26th

09:00am #8 **Olubukola Oluranti BABALOLA - North West University, South Africa**
Adaptation and functional dynamics of plant associated microbiomes, in response to stresses for plant productivity, resilience, and sustainability

09:45am #9 **Adriana BERNAL - Universidad de los Andes, Colombia**
Understanding pathogen targets and microbiomes to manage cassava bacterial blight

10:15am #10 **Ian Lorenzo QUIBOD – IRD, Montpellier, France**
Continental drift: Population genomics of Rice Bacterial Leaf Blight in Africa and Asia

10:30am Coffee break

11:00am #11 **Geoffrey ONAGA – AfricaRice, Côte d'Ivoire**
Rice disease control in Africa

11:30am #12 **Chimène Nadège Mahoussi NANOUKON - Bénin**
Surveillance of Rice Bacterial Blight in Benin: Current Status, Challenges, and Perspectives

11:45am #13 **Marian DOMINGUEZ MIRAZO – IRD, Montpellier, France**
Advancing Phages as Bioindicators of Plant Health

12:15am Lunch

02:00pm #14 **Diana ORTIZ – INRAe, Montpellier, France**
Co-designing Resilient and Healthy Cropping Systems for Sustainable Agriculture

02:45pm #15 **Marie Therese MORRISSON – CIRAD, Montpellier, France**
Rethinking Plant Health: How Agrobiodiversity Sustains Cocoa Agroforestry in Côte d'Ivoire

03:00pm #16 **Lionel GAGNEVIN – CIRAD, Montpellier, France**
OCCIPHAGE: Exploring phage diversity for a sustainable biocontrol of Xanthomonas crop pathogens

03:15pm #17 **Mariam BARRO – INERA, Burkina Faso**
Agricultural practices' impact on major rice disease development and rice field soil fertility in western Burkina Faso

03:30pm #18 **Harinjaka RAVELOSON – FOFIFA, Madagascar**
Effect of cultural practices on two principal diseases: rice blast and bacterial leaf blight of rice in Madagascar

03:45pm Coffee break

04:30pm #19 **Nicolas CHEN - Institut Agro, Angers, France**
Putative host shift of Xanthomonas strains from cotton to cowpea in Burkina Faso

05:00pm #20 **Ibrahim HASHIM – TARI, Tanzania**
Emergence and Spread of Rice Bacterial Leaf Blight Disease in Tanzania: Implication for Control and Resistance Breeding

05:15pm #21 **Agnieszka KLONOWSKA – IRD, Montpellier, France**
Bacillus isolates from rice roots suppress Pyricularia oryzae and mitigate blast disease in Burkina Faso

05:45pm #22 **Mame Penda SARR DIAWARA – ISRA, Senegal**
Genetic diversity and biological control of the pathogen Macrophomina in Senegal

06:00pm Poster session

08:00pm Dinner

Thursday 27th IRNs parallel sessions

Session IRN NSSN-X

09:00am #23 **Laurent BROTTIER – IRD, Montpellier, France**
Optimization of sample and strain collection management through the implementation of a Grist database

09:25am #24 **Lucille GORGUES – IRD, Montpellier, France**
Shuffling TALEs to Identify Resistance/Susceptibility Genes (STIRS)

09:50am #25 **Carlos ZARATE – INRAe, Castanet-Tolosan, France**
Genetic determinism of host range in plant pathogenic bacteria

10:15am #26 **Brice CHARLEUX – IRD, Montpellier, France**
Functional characterization of Os07g22730 as a downstream susceptibility gene in the TalB–OsERF#123 pathway of African Xanthomonas oryzae pv. oryzae

10:35am Coffee break

11:05am #27 **Corinne AUDRAN - INRAe, Castanet-Tolosan, France**
Exploring resistance by loss of susceptibility in Brassica oleracea

11:30am #28 **Camille BLASCO – IRD, Montpellier, France**
Expansion of Bacterial leaf Blight Disease of Rice Caused by Xanthomonas oryzae pv. oryzae in Tanzania

11:55am #29 **Soline MARTY - INRAe, Castanet-Tolosan, France**
Water availability in leaves defines the ecological niche and proliferation of Xanthomonas campestris

12:20am #30 **Sarah DELAFOSSE – IRD, Montpellier, France**
Diversity and prevalence of prophages and anti-phage defense systems in a major rice pathogen

12:15am Lunch

13:30pm Social activity

08:00pm Dinner/party

Thursday 27th IRNs parallel sessions

Session IRN FAD-M-PH

09:00am **Eugénie HEBRARD – IRD, Montpellier, France**
2022-2025: Our network review

09:15am #31 **Souley ISSAKA - Université de Tillabéri, Niger**
African Cassava Mosaic Disease (ACMD) epidemic in Niger

09:30am #32 **Régis LONGE SOPKE- Université de Bangui, République Centrafricaine**
Identification of natural hosts of MSV in the Central African Republic

09:45am #33 **Yêyinou Laura Estelle LOKO - UNSTIM, Bénin**
Potential of Metarhizium anisopliae and Beauveria bassiana to control Dinoderus porcellus (Coleoptera: Bostrychidae) infesting yam chips

10:00am #34 **Joelle TOFFA - UNSTIM, Bénin**
Plant-Microbiota-Insect Interactions: A novel strategy for improving the health and sustainability of vegetable crops in Benin

10:15am #35 **Innocent ZINGA - Université de Bangui, République Centrafricaine**
Aphid-borne cowpea mosaic in the Central African Republic: prevalence, diversity and search for control methods against Cowpea aphid borne mosaic virus (CABMV)

10:30am Coffee break

11:00am #36 **Aboubie Elisabeth ZONGO – INERA, Burkina Faso**
Molecular characterization of emerging viruses infecting Bambara groundnut (Vigna subterranea L. Verdc.) in Burkina Faso

11:15am #37 **Hassna FOUNOUNE – ISRA, Senegal**
Expansion Role of arbuscular mycorrhizal fungi in enhancing the crop productivity and sustainability of Sahelian agroecosystems

11:30am **Charlotte TOLLENAERE – IRD, Montpellier, France**
2026-2029: Next phase of our network

12:00am Lunch

13:30pm **IRN FAD-M-PH Workshop**

15:00pm Social activity

08:00pm Dinner/party

Friday 28th

09:30am #38 **Charlotte TOLLENAERE – IRD, Montpellier, France**
The co circulation and co infection of rice pathogens: evidence in the field and evolutionary consequences

10:00am #39 **Michel BARBIER – IRD, Montpellier, France**
The rice root knot nematode microbiota ***may be used for biocontrol purposes***

10:15am #40 Laurence ALBAR – IRD, Montpellier, France
Insights into rice crinkling disease: decoding transmission, host range and genetic resistance

10:30am coffee break

11:00am #41 **Alvaro PEREZ QUINTERO – IRD, Montpellier, France**
Repeat, evolve, repeat: The high evolvability of the Xanthomonas oryzae genome facilitates epidemic outbreaks in rice

11:15am Wrap up

12:00am The end

Oral Communications

#1 Keynote North

Bacteria-Insect-Plant Interactions: Understanding How Microbiomes in Russian Wheat Aphid Honeydew Increases Aphid Virulence to Plants

Jan E. Leach and Emily Luna
Colorado State University, Ft Collins, CO USA

In the phytobiome, plant phenotypes under biotic stresses emerge from complex interactions among hosts, pests, microbes, and the environment. We have shown that the Russian wheat aphid (RWA, Diuraphis noxia), a globally significant pest of small grains, depends on its associated microbiome to induce chlorosis on wheat. Bacteria from the aphid microbiome themselves are not pathogenic to these cereals, as direct inoculation of plants does not result in chlorosis, water-soaking or necrosis. Although few microbes are found in the aphid salivary glands or foreguts, many were detected in aphid honeydew, suggesting that stylets contaminated during feeding may introduce bacteria into the leaf interior. Mechanistic insight into how these microbes influence RWA virulence is emerging from plant transcriptome analyses following infiltration of RWA honeydew with high (High-HD) versus low (Low-HD) bacterial titers. Relative to Low-HD treatments, transcriptomes of High-HD treated plants exhibit transcriptional enrichment for biotrophic pathogen defense pathways, including salicylic acid (SA) biosynthesis and pathogenesis-related (PR) proteins. Intriguingly, regulation of pathways related to insect resistance, including jasmonate biosynthesis, signaling and degradation is more complex. The model emerging is that while expression of genes involved in jasmonate biosynthesis are upregulated, downstream JA signaling is suppressed and genes involved in degradation of JA are induced. These studies support the hypothesis that the RWA honeydew microbiome regulates aphid virulence by modulating the plant's defense mechanisms. Overall, these studies are revealing complexities in phytobiome interactions that may guide strategies to harness the potential of pest-associated microbiomes for improved pest control.

#2 **Perrine PORTIER – INRAe, Beaucouzé, France**

How to preserve viable Microbiota?

Culture collections, such as CIRM-CFBP, the French Collection for Plant-associated Bacteria (https://cirm-cfbp.fr/) have stored and distributed single strains for decades, bringing a much-appreciated service to scientists, permitting them access to reliable resources. Microbiology is nowadays shifting its focus more and more to whole communities. The closer study of these microbiota is impaired by technicalities and often limited to descriptive approaches. One way to overcome some of these hurdles would be to preserve these communities as viable entities. However, this is easier said than done, as microbiota are complex and heterogeneous communities comprising a significant fraction of non-cultivable organisms. Hence, the preservation of microbial community will have a heterogeneous effect on the members of the community, leading to heterogeneous survival, which may in turn affect the metabolic capacities of the whole community.

The MICROBE project (https://www.microbeproject.eu/) aims at paving the way for microbiome biobanking. Within the framework of this project, we focused on seed microbiota extracted from beans. Three partners of the MICROBE project, INRAE, CABI and AIT, teamed up to conduct parallel experiments to determine which preservation condition is least disruptive to the taxonomic composition and functional diversity of the preserved communities. For each tested condition, the taxonomic diversity, assessed by metabarcoding (16S rRNA, ITS, gyrB), and the functional diversity, assessed with Biolog EcoPlates, were measured before preservation and after 1 week, 3 months and 12 months of preservation.

The initial results indicate that some preservation conditions are more effective in preserving the functional diversity of the communities. This shows the importance of thoroughly considering, validating and recording the pre-analytical phase. The next steps are to compare the results from the functional assessment to metabarcoding data.

#3 **Claire BENEZECH - Institut Agro, Montpellier, France**

Wheat genotype impacts plant responses to biosolutions

C. Benezech, V. Fontaine, L.V. Meteignier, J.B. Morel, M.E. Saint Macary, E. Ballini

With growing ecological and economic pressures, there is increasing interest in finding alternative ways to boost plant production. One promising approach is the use of biostimulant products, which help plants better cope with abiotic stresses and improve nutrient assimilation. These biostimulants come from a wide range of sources natural, synthetic, or mixed including amino acids, enzymes, algal extracts, plant hormones, beneficial microbes, plant extracts, minerals, and nutrients. While their potential is clear, the exact mechanisms behind their effects are still not fully understood. This requires better characterization of the molecular responses they trigger in order to promote their safe use by farmers, with respect for both human and environmental health.

In our work, we aim to bridge this knowledge gap by characterizing the responses triggered by different biostimulants in durum wheat. These biostimulants activate various pathways that can enhance nutrient assimilation, improve drought tolerance, and boost seed quality. To achieve this, we combine molecular, metabolomic, and physiological approaches across four durum wheat varieties. Our analyses highlight that molecular, metabolomic, and physiological responses are strongly shaped first by the genotype, and then by the applied biosolutions.

We were able to show that specific molecular pathways are activated depending on both the biostimulant used and the plant's genetic background. We also identified correlations between transcriptomic, metabolomic, and physiological traits. To really push the "lab-to-field" transition forward, we are testing how biosolutions perform under a wide range of stresses from drought and nutrient shortages to temperature fluctuations and biotic challenges. By taking this broader view, we are uncovering key mechanisms underlying biostimulant activity and demonstrating their real potential to enhance plant resilience and productivity in the field.

#4 **Hamidou TALL – ISRA, Sénégal**

Screening of rice varieties and accessions (Oryza sativa L. and Oryza glaberrima Steud) for resistance and genomic comparative to bacterial leaf streak in Senegal

Akossan Bernadin Dossou, Hamidou Tall, Kandioura Noba, Boris Szurek, Mathilde Hutin, Sébastien Cunnac, Valérie Verdier, Onaga Geoffrey

Bacterial leaf streak caused by Xanthomonas oryzae pv. oryzicola (Xoc) is one of the most devastating diseases of rice worldwide, particularly in Asia and Africa, where it causes yield losses of up to 40%. Varietal resistance is one of the most effective strategies to control this disease. Screening of improved rice varieties (Oryza sativa L.) and isogenic lines (IRBBs) have allowed to identify the sources of resistance that controlled 80% of Senegalese Xoc strains. However, none of the isogenic IRBB lines or improved varieties tested are resistant to the strain S52-4-4, suggesting a mutation in this strain that

could constrain rice cultivation in Senegal. Comparative genomic and phylogenetic analysis revealed an evolutionary relationship between S52-4-4 and the strains BLS256 and CFBP2286, originating from the Philippine and Malaysia, respectively. Furthermore, the detection of an equivalent number of TAL effectors in the strains S52-4-4 and BLS256 provided evidence that these strains may share a common ancestor. These results, combined with the available genomic sequence and the characterization of S52-4-4 in this study, are useful for studying Xoc populations in Senegal and other countries. Nevertheless, the adaptation of S52-4-4 to all local varieties grown in Senegal requires a rapid response in terms of disease control.
Keywords: Screening, varieties and accession, Senegal, bacterial diseases, rice, Xanthomonas oryzae

#5 **Lyna MUKWA – CPK, République Démocratique du Congo**

Molecular characterization of Ralstonia pseudosolanacearum causal agent of tomato wilt in western Democratic republic of Congo

Lyna, F.T. Mukwa, Vincent Kamanda, Marie-Véronique Nomenjanahary, Hasina Rasoamanana, Stéphane Ramin-Mangata, Stéphanie Javegny, Jean-Jacques Chéron, Stéphane Poussier and Yann Pecrix

Solanaceous crops such as Solanum lycopersicum (tomato) and Solanum melongena (eggplant) are an important source of vitamins for the Congolese population and a key source of income for the farmers. In the Democratic Republic of Congo (DRC), interest in these crops is steadily increasing. In, 2022, tomato production was estimated at 233,000 tons in 2022, while for eggplant, despite being cultivated across all provinces, yields remain low and unsatisfactory. Unfortunately, the production of both crops is severly affected by a that appears during the rainy-season. Symptoms include wilting and complete necrosis of the plant, leading production losses in various locations. To understand the origin of these symptoms and provide advice to farmers for control measures, an epidemiological survey was conducted in seven locations in DRC. Samples were analyzed using both biological and molecular method for the pathogen characterization. Results showed, in all locations, the presence of a Gram negative bacterial, creamy to off-white colonies on Nutrient Agar media, sometimes with a slight yellowish tint color. A total of 22 bacterial wilt isolates were identified. Molecular characterization revealed that all isolates belonged to a single haplotype of Ralstonia pseudosolanacearum phylotype I sequevar 31. The genome of one representative strain, RUN6904, was sequenced and its type III effector (T3E) repertoire was characterized. Pathogenicity tests demonstrated the virulence of DRC isolates on tomato. However, the eggplant accession AG91-25 showed resistance, likely triggered by the RipAX2 T3E produced by the isolates. This research opens the way for eggplant varieties improvement for high yield production in DRC.
Key Words: vegetables crops, Kinshasa, income source, tomato, eggplant

#6 **Mathilde HUTIN – IRD, Madagascar**

Bacterial Leaf Blight of rice : an emerging threat to rice cultivation in East Africa

Xanthomonas oryzae pv. oryzae (Xoo), the causal agent of Bacterial Leaf Blight (BLB) of rice, leads to yield losses of up to 70% and threatens rice production. In 2019, we reported the first identification of BLB in Madagascar, a country where 90% of agricultural activity relies on rice production, and the emergence of the disease in Tanzania, one of the largest rice-producing countries in East Africa. Since then, annual surveys have shown a rapid and worrying spread of BLB in these countries, as well as in others (e.g. Kenya and Uganda), leading to the establishment of a collection of over 450 Xoo strains. Microsatellite genotyping of these strains revealed that they all belong to the same clonal complex in Madagascar and to another in continental East Africa. This finding suggests that Xoo was introduced to these two countries independently and recently. Moreover, our data indicate that pathogen haplotypes are maintained across farming seasons and that new haplotypes emerge annually. This suggests that the pathogen population has diversified over the past five years. Whole genome sequencing of 50 strains from these two countries indicates a possible introduction of Xoo from two different Asian countries. The recent introduction of Xoo in Madagascar, and the rapid spread of a few haplotypes belonging to the same clonal complex strongly suggest a role for infected seeds in BLB epidemiology. This is also supported by the molecular epidemiology study that we have conducted in Tanzania, Uganda and Kenya. We have also genotyped strains collected from different weed species growing in or around rice fields to better understand their role as reservoirs. Understanding disease epidemiology is critical to preventing new introductions, and reducing pathogen transmission is key to controlling disease spread and limiting its impact in the absence of resistant host varieties.

#7 **Noe ARROYO VELEZ – INRAe, Beaucouzé, France**

Prophage diversity reveals evolutionary history and dispersal of Xylella fastidiosa subsp. multiplex in France

Xylella fastidiosa is a xylem-inhabiting bacterium responsible for economically important plant diseases, including Pierce's disease of grapevine, citrus variegated chlorosis, and olive quick decline syndrome (Sicard et al., 2018). Originating in the Americas, this pathogen has now spread globally. Currently, three subspecies are formally recognized (fastidiosa, pauca, and multiplex), while two additional (sandyi and morus) have been proposed (Nunney et al., 2014; Schuenzel et al., 2005). In France, X. fastidiosa subsp. multiplex has been detected in PACA, Corse, and Occitania regions (Cunty et al., 2022; Denancé et al., 2017). Although control measures have limited its spread, the pathogen remains a constant threat to French agriculture, making it essential to understand the drivers of its evolution and dispersal.
Given the importance of prophages as drivers of bacterial evolution through horizontal gene transfer (HGT)(Varani et al., 2013), this study characterized their abundance and diversity in French X. fastidiosa subs. multiplex isolates. Across 67 genomes, we identified more than 500 prophage sequences (~7 per genome). Phylogenomic analysis grouped all prophages into 37 species-level clusters belonging to two distinct taxonomic lineages, neither of which showed relatedness to currently classified viral species. Interestingly, prophage diversity patterns were strongly influenced by geographic origin, supporting at least three independent introduction events into France. Comparative genomics further revealed overlap with prophages found in American isolates, providing insights into their potential origins. Finally, functional predictions of prophage-encoded proteins highlighted putative roles in host adaptation, suggesting they significantly contribute to X. fastidiosa survival.

#8 Keynote South

Adaptation and functional dynamics of plant associated microbiomes, in response to stresses for plant productivity, resilience, and sustainability

Olubukola Oluranti BABALOLA
North West University, South Africa

The plant microbiome represents a cornerstone of sustainable agriculture and environmental resilience. These intricate microbial communities, bacteria, fungi, and archaea, form dynamic and adaptive networks that sustain plant health, soil fertility, and ecosystem balance. In the Global South, where food systems face multiple pressures from climate change, resource degradation, and population growth, understanding and harnessing these microbiome dynamics offers transformative potential.

This keynote explores the adaptation and functional dynamics of plant-associated microbiomes, emphasizing how microbial communities evolve and respond to biotic and abiotic stresses such as parasitic weed infestation, drought, salinity, and nutrient scarcity. The discussion draws substantially on the ecological and genomic complexity of beneficial microbes in African agroecosystems. The contributions to microbial ecology, rhizosphere genomics, metagenomics and metabolomics have reshaped our understanding of how microbial adaptation drives plant productivity, resilience, and sustainability. The investigations into plant growth-promoting rhizobacteria and mycorrhizal fungi reveal how indigenous microbial resources can reduce chemical dependency, enhance nutrient efficiency, and foster climate-resilient crops.

This presentation highlights the imperative of South-led scientific leadership and cross-regional collaboration to translate microbiome science from theory into practice, moving from rhetoric to real results across the agricultural value chain. It argues for embedding microbiome-based innovations into national policies and global food security frameworks, aligning with SDG2 (Zero Hunger) and the broader agenda for sustainable development.

By connecting microbiome adaptation with plant health and ecosystem stability, this keynote underscores the promise of microbial intelligence as a pathway toward inclusive, climate-smart, and sustainable agriculture for the South and beyond.

#9 **Adriana BERNAL - Universidad de los Andes, Colombia**

Understanding pathogen targets and microbiomes to manage cassava bacterial blight

Darwin Castillo, Carlos Rodríguez, Paola Reyes, Santiago Cortés, Carlos Zarate, Erika Larrahondo, Jennifer Yanez, Sofia Contreras, Arley Cardenas, Ivan Ortiz, Fermin Rada, Rebecca Bart, Boris Szurek, Adriana Bernal Giraldo

Cassava is a vital staple crop that supports the food security of over 800 million people across Africa, Asia, and South America. Among its major threats, cassava bacterial blight (CBB) stands out as the most severe bacterial disease, leading to substantial yield losses under favorable environmental conditions. This disease is caused by Xanthomonas phaseoli pv. manihotis (Xpm), which relies primarily on type III effectors to establish infection.

In this study, we present two complementary biotechnological approaches for the management of CBB and potentially other cassava diseases. First, we employed interactomics and classical yeast two-hybrid screening to identify host protein targets of Xpm effectors in cassava cells. Selected interactions, particularly those involving the effectors XopAE and XopAO1, were validated in heterologous systems. Our results confirm that a small heat shock protein and a membrane homeostasis-related protein are bona fide targets of XopAE, while two candidate host targets were identified for XopAO1. These host proteins represent promising candidates for the discovery of natural resistance alleles in cassava germplasm or as targets for gene editing to enhance disease resistance.

The second approach focuses on leveraging the cassava microbiome for disease management. We analyzed the leaf microbiomes of healthy and CBB-infected plants from two distinct regions: the Colombian Caribbean coast and the Ecuadorian Amazon. Our results reveal distinct shifts in bacterial taxa associated with disease, suggesting a CBB-induced dysbiosis. A deeper understanding of these microbiome changes could inform microbiome-based strategies to mitigate disease and restore plant health.

#10 **Ian Lorenzo QUIBOD – IRD, Montpellier, France**

Continental drift: Population genomics of Rice Bacterial Leaf Blight in Africa and Asia

Cultivated rice was domesticated on two separate occasions: Oryza sativa in China ~ 9000 years ago and the other Oryza glaberrima in West Africa ~3000 years ago. Rice association with microorganisms was likely altered in the domestication process, which shaped the evolution and dispersal of diseases like rice bacterial leaf blight caused by the Xanthomonas oryzae pv. oryzae (Xoo). In this study, we employed population genomics to uncover the diversity and expansion of two genetically distinct bacterial blight pathogens across Asia (AsXoo) and Africa (AfXoo). For O. sativa, we identified two specific AsXoo lineages likely dispersed with either japonica or indica varieties. AfXoo, initially adapted to O. glaberrima, has recently overcome the resistance to O. sativa, contributing to current epidemics in West Africa. Furthermore, we characterize the genomic differences in the two phylogroups and their impact on the disease. Our research provides a comprehensive evolutionary history of bacterial blight, and its past and present impact on rice cultivation.

#11 **Geoffrey ONAGA – AfricaRice, Côte d'Ivoire**

Rice disease control in Africa

#12 **Chimène Nadège Mahoussi NANOUKON - Bénin**

Surveillance of Rice Bacterial Blight in Benin: Current Status, Challenges, and Perspectives

Chimène Nadège Mahoussi NANOUKON, Amed HAVIVI, Pamela LOUMEDJINON, Laurinzo DÉGUÉNON, Lambert Gustave DJEDATIN

Bacterial blight of rice, caused by Xanthomonas oryzae pv. oryzae (Xoo), is a highly destructive disease threatening rice production across West Africa, with yield losses ranging from 20% to 80%. Although data specific to Benin remain limited, studies in neighboring countries such as Madagascar and Tanzania indicate a rapid and alarming spread of the pathogen. In Benin, the disease has been confirmed in the northwestern region (Tanguiéta, Atacora Department). Beyond the work of Afolabi et al. (2016), who identified Xoo strains on wild rice (Oryza longistaminata), few studies have addressed the pathogen's distribution and impact. Recent field surveys conducted by our team revealed characteristic symptoms on cultivated varieties in several rice-growing zones of the Alibori Department (Banikoara and Malanville). National surveillance of bacterial blight in Benin remains limited, lacking systematic monitoring, regular alerts, and advanced diagnostic tools. Farmer awareness is low, and access to resistant varieties is constrained. The main challenges include: (i) weak diagnostic capacity and dependence on international laboratory confirmations; (ii) discontinuous epidemiological surveillance; (iii) frequent use of uncertified seeds and risky agronomic practices; and (iv) scarcity of resistant varieties adapted to local Xoo strains. To address these challenges, we recommend: (i) short-term actions: strengthening targeted surveillance, standardizing diagnostic protocols, and raising farmer awareness; (ii) medium-term measures: equipping national laboratories, screening local varieties, and integrating bacterial blight management into national phytosanitary programs; and (iii) long-term strategies: establishing a regional monitoring network, promoting applied research, and consolidating the seed system. A coordinated and multisectoral approach is crucial to contain the spread of X. oryzae pv. oryzae and ensure the sustainability of rice production in Benin.

#13 **Marian DOMINGUEZ MIRAZO – IRD, Montpellier, France**

Advancing Phages as Bioindicators of Plant Health

Marian DOMINGUEZ-MIRAZO, Clara TORRES-BARCELO

Monitoring plant health and predicting disease outbreaks remain major challenges for sustainable agriculture. This project explores a bold and largely uncharted idea: that bacteriophages (viruses infecting bacteria) can act as early bioindicators of plant disease. While phages are well known for shaping microbial dynamics in marine and human systems, their ecological roles in plant environments remain virtually unknown. We use rice bacterial blight, caused by Xanthomonas oryzae pv. oryzae, as a model to investigate how phage community structure relates to plant health status and disease progression. Our approach combines field sampling in rice-growing regions of Madagascar with metagenomic analyses of viral and microbial communities. We aim to determine whether specific phage patterns—such as diversity, abundance, or host range—are associated with disease presence, paving the way for early detection tools and phage-based biocontrol strategies. The project has just begun, with initial fieldwork and bioinformatic analyses laying the groundwork to connect phage ecology with epidemiological models of plant disease. By bridging microbiology, ecology, and plant pathology, this work seeks to open a new frontier in the use of microbial indicators for sustainable crop protection.

#14 Keynote Octaave

Co-designing Resilient and Healthy Cropping Systems for Sustainable Agriculture

Diana ORTIZ
Biodiversified agrosystems joint research unit INRAE-ABSys, Montpellier France

Current pest management strategies in cropping systems face critical limitations by often overlooking the complex ecological interactions essential for sustaining plant health, productivity and resilience This keynote introduces a paradigm shift grounded in the complementary concepts of salutogenesis and agroecological immunity, alongside the core principles of agroecological crop protection. It advocates for a systemic redesign that integrates diverse ecological, social, and economic interactions while respecting farmer knowledge and localized contexts.

The keynote underscores the transformative role of farmers, researchers, advisors, teachers, and other stakeholders as co-designers in agroecological transitions. Moving beyond top-down knowledge dissemination, it embraces collaborative participatory methods that foster adaptive, context-sensitive innovations. Emphasis is placed on participatory action research approaches that empower stakeholders to actively shape resilient and multifunctional farming systems.

Diversification is identified as a fundamental mechanism driving agroecosystem stability and natural pest regulation. Drawing on recent scientific assessments, the keynote highlights highly diversified agroforestry systems, largely shaped by farmer innovation, as models of resilience. These systems effectively mitigate threats such as water scarcity, soil degradation, biodiversity loss, and climate change. By integrating trees, crops, and livestock in multifunctional landscapes, agroforestry embodies both agroecological crop protection principles and the salutogenic approach to crop health, offering practical pathways toward sustainable and healthy cropping system design.

By integrating ecological principles, social learning, and participatory governance, this keynote proposes a strategic framework for co-constructing cropping systems that promote plant health, ecosystem functionality, and socio-economic autonomy, critical for advancing agroecological transitions and achieving sustainable food systems.

#15 **Marie Therese MORRISSON – CIRAD, Montpellier, France**

Rethinking Plant Health: How Agrobiodiversity Sustains Cocoa Agroforestry in Côte d'Ivoire

The dominant conception of plant health today remains rooted in a pathogenic approach focused on combating diseases and pests. This reductionist view has led to increasing dependence on chemical inputs to maintain productivity. In the context of an agroecological transition, it has become essential to initiate a paradigm shift by adopting a salutogenic approach to plant health. This approach shifts the question from "how to reduce aggressions" to "what conditions promote health," considering the plant as an organism integrated within a set of biotic, abiotic, and anthropogenic interactions. Health is therefore understood not as a fixed state but as a dynamic capacity for resilience and self-regulation within the agroecosystem. Within this framework, cocoa-based agroforestry systems in Côte d'Ivoire represent a particularly relevant study context. These systems exhibit a gradient of diversity, ranging from simplified monocultures to complex agroforests, and differ in their structure, floristic composition, spatial organization, and management methods, organic and conventional farming. We hypothesize that agrobiodiversity plays a central role in the health of cocoa trees through complementary mechanisms, including improved access to resources and regulation of biotic stresses via ecosystem services and functional management. The overall objective of this approach is to understand how the structure of agrobiodiversity and agricultural practices interact to influence the health of cocoa trees, in order to identify the ecological and social levers that can be mobilized to design sustainable cropping systems. To achieve this goal, the research was structured around three complementary components: an agronomic and floristic diagnosis carried out on 37 plots to characterize the diversity of cropping systems, document agricultural practices, and identify the empirical health criteria used by farmers; a detailed annual monitoring of 18 experimental plots to analyze the relationships between the structure of agrobiodiversity, farming practices, and indicators of cocoa tree health; and finally, an analysis of farming activities and practices to explore the decision-making processes and empirical knowledge mobilized by farmers in managing plant health and agrobiodiversity. This integrative approach, at the crossroads of agronomy, ecology, and the social sciences, highlights that the health of cocoa trees depends both on ecological regulation mechanisms and on empirical knowledge derived from farmers' experience. The results thus contribute to the development of a "health-centered agronomy," based on the co-construction of knowledge and the design of salutogenic, resilient, and sustainable agroforestry systems.

#16 **Lionel GAGNEVIN – CIRAD, Montpellier, France**

OCCIPHAGE: Exploring phage diversity for a sustainable biocontrol of Xanthomonas crop pathogens

Lionel GAGNEVIN, Carlos ZARATE-CHAVES, Maria NEORALOVA, Chloé COSSIN, Amandine MAURIN, Ralf KOEBNIK, Charlotte BRIVES, Alice BOULANGER, Clara TORRES-BARCELO, Rémy FROISSART and Boris SZUREK

Bacteriophages, viruses that specifically infect bacteria, are promising biocontrol agents against phytopathogens such as Xanthomonas spp., which threaten crops of high economic importance. Current control relies on copper-based compounds, whose long-term accumulation raises environmental concerns, highlighting the need for sustainable alternatives. The Occiphage project aimed to explore the diversity of phages in the Occitanie region and assess their potential against two key bacterial pathogens: Xanthomonas phaseoli pv. manihotis (Xpm), the agent of cassava bacterial blight, and X. campestris pv. campestris (Xcc), responsible for black rot in Brassicaceae. Environmental samples from wastewater and irrigation water were screened for lytic phages. In total, 67 virulent phages active against Xpm and 9 against Xcc were isolated, with host range evaluation identifying candidates effective against most pathogen strains. Genomic sequencing of representative isolates revealed their diversity and provided a foundation for understanding phage–host interactions. This work establishes a framework for phage-based biocontrol and highlights the potential of bacteriophages as sustainable alternatives to chemicals in managing Xanthomonas diseases. KEYWORDS: Agriculture, Biocontrol, Phytopathogenic bacteria

#17 **Mariam BARRO – INERA, Burkina Faso**

Agricultural practices' impact on major rice disease development and rice field soil fertility in western Burkina Faso

Mariam BARRO, Alexandre P OUEDRAOGO, Abdoul Latif DISSA, Issa WONNI, Agnieszka KLONOWSKA and Charlotte TOLLENAERE

In Burkina Faso, rice farmers often resort to intensive agricultural practices, such as excessive use of pesticides and chemical fertilizers. However, these practices have negative effects on human, animal, and environmental health. Finding agroecological farming practices that are accessible to producers is essential. Hence this study, which aims to sustainably increase rice productivity through agroecological management of rice diseases. In this context, we first assessed the physicochemical properties of soils in irrigated rice cultivation (Bama) and lowland rice cultivation (Badala) before conducting field trials with farmers using different fertilization and rotation practices. Next, we evaluated the impact of the different practices on yields and the main rice diseases. The results show that practices T0 (control) and T3 (rotation with mineral fertilization) have higher yields, respectively 3.2 and 3.43 t/ha in 2023, and 2.73 and 3.28 t/ha in 2024, with higher average incidence and severity of blast disease and leaf streak disease, unlike the rotation practices without mineral fertilizers or pesticides (T1 and T5), which had the lowest average incidence. Soils cultivated using these ecological practices (T1 and T5) are richer in organic matter. There are therefore agroecological practices that reduce the development of rice diseases while improving soil fertility.

#18 **Harinjaka RAVELOSON – FOFIFA, Madagascar**

Effect of cultural practices on two principal diseases: rice blast and bacterial leaf blight of rice in Madagascar

Rice is the staple food crop in Madagascar with a consumption of 130 kg average per capita per year. The rice production did not cover the needs for the population, so the country imports rice every year to fill the gap. Rice diseases are one of the constraints impacting rice yield in this country. Among them, rice blast (RB), caused by the fungal pathogen Pyricularia oryzae and bacterial leaf blight (BLB) caused by the bacterial pathogen Xanthomonas oryzae pv. oryzae. These two diseases have become serious threats to rice cultivation, in which rice farmers did not have many means to manage them. The reason why understanding the effect of different cultural practices on these two diseases constitutes essential elements in the formulation of control strategies.

These two diseases have different histories in Madagascar. RB has been observed for a long time, while BLB was recently identified from 2019. The team working on rice diseases emphasizes the diagnosis of these diseases and exploiting the different methods available and affordable in the country's situation. Then, many studies have been conducted to understand the effect of different cultural practices to each disease. It was found that some cultural practices promote the attack of the disease and others reduce it. However, it must be mentioned that many studies are still necessary, especially when considering co-infection on an organ, a plant or a plot by Pyricularia oryzae and Xanthomonas oryzae pv. oryzae. Knowing that the attack of multi-pathogens generates great methodological challenges. Taking into account all information obtained on the effect of cultural practices on these two diseases, combined with that available elsewhere on studies of these two pathogens, will enable to progress in reducing the impact of them on the rice production.

#19 **Nicolas CHEN - Institut Agro, Angers, France**

Putative host shift of Xanthomonas strains from cotton to cowpea in Burkina Faso

Nanwinyele E. Some, Martial Briand, Kadidia Koita, Marie-Agnès Jacques, Issa Wonni, Nicolas W. G. Chen

Native to tropical Africa, cowpea (Vigna unguiculata) is a key legume in sub-Saharan Africa, particularly in Burkina Faso, where it plays an important role in combating food insecurity. However, a recent outbreak of cowpea bacterial blight has been observed in several production areas and seed stations, causing significant losses. As part of a new collaboration between France and Burkina Faso we have initiated a project aiming at better characterizing this disease and propose appropriate control methods. We performed field analyses across six provinces, which showed that intercropping cowpea with maize reduces global disease incidence, while an association with common bean aggravates it. Phylogenomic analysis and phenotyping of eight strains isolated from symptomatic cowpea leaves identified Xanthomonas citri pv. malvacearum (responsible for cotton bacterial blight) as the causative agent. This finding suggests that these bacteria acquired the ability to infect cowpea via cross-species transmission from neighboring cotton fields. By investigating the genome of these strains in relation to their ability to infect cotton and cowpea, our analyses provide insights into the molecular determinants of this presumed host shift.

#20 **Ibrahim HASHIM – TARI, Tanzania**

Emergence and Spread of Rice Bacterial Leaf Blight Disease in Tanzania: Implication for Control and Resistance Breeding

Ibrahim Hashim, Boris Szurek, Florence Auguy, Claire Neema, Reuben Mihayo and Leah Philipo

Rice is a main staple crop globally and in Sub-Saharan Africa (SSA), with its production ranking second worldwide. However, the crop suffers from significant yield losses, especially due to bacterial leaf blight (BLB), caused by Xanthomonas oryzae pv. oryzae. In Tanzania at first time the notable outbreak of BLB was observed in 2019 in Dakawa, Morogoro, which rapidly spread to other major rice-producing regions. Our observation showed that BLB is exacerbated by irrigated rice environments favorable for disease proliferation, use of susceptible variety and is further intensified by excessive application of nitrogenous fertilizer. Additionally, seed transmission has been identified as a key factor in long-distance disease spread, while insufficient knowledge among farmers regarding proper disease identification and management poses a significant barrier to effective control. The outbreak of BLB in Tanzania and how it spread from one area of the country to another has changed our way of thinking and focus the need for further research into the role of seed transmission and the improvement of Tanzanian rice germplasm for BLB resistance. A strategic focus on enhancing farmer awareness of BLB disease, implementation of proper rice fertilization practices, and surveillance of disease spread is very crucial. This comprehensive approach will contribute to better disease management, improved rice yield, and sustainable rice production in Tanzania.

Keywords: Yield Losses, Seed Transmission, Excessive Nitrogen Use, Lack of Knowledge

#21 **Agnieszka KLONOWSKA – IRD, Montpellier, France**

Bacillus isolates from rice roots suppress Pyricularia oryzae and mitigate blast disease in Burkina Faso

SANGA I., BOULARD G., COCIANCICH S., KASSANKOGNO A., WONNI I., SONDO M., BARRO M. and KLONOWSKA A.

Rice blast, caused by Pyricularia oryzae, is a major constraint to rice production in Burkina Faso and calls for sustainable control options. We screened 44 cultivable bacterial isolates obtained from rice roots across multiple agro-ecological zones for antagonism and biocontrol activity against P. oryzae, and assessed their distribution in field microbiomes. In vitro dual-culture assays identified several Bacillus sensu lato and one Burkholderia isolate with strong inhibition of P. oryzae mycelial growth; three Bacillus strains (ABIP 1178, ABIP 2939, ABIP 3006) consistently exceeded 50% inhibition. These strains also showed moderate antagonism toward Bipolaris oryzae and Curvularia lunata. In planta, root inoculation of the susceptible cultivar FKR64 with selected Bacillus and Priestia isolates reduced blast severity, achieving up to 25% lower area under the disease progress curve compared with controls. Phylogenetic analysis of 16S rRNA sequences placed the most effective antagonists within the Bacillus subtilis clade - some closely related to B. velezensis, B. amyloliquefaciens, and B. aerius - and identified an effective Priestia isolate related to P. aryabhattai/zanthoxyli. Complementary in silico analysis of rice root microbiomes from fields with contrasting blast incidence revealed higher relative abundance of Bacillus and Priestia amplicon sequence variants in healthy fields, including ASVs closely matching our effective isolates, suggesting a role in natural disease suppression. Together, these results highlight native Bacillus subtilis-clade and Priestia strains as promising candidates for biocontrol and microbiome-informed crop protection strategies in West African rice systems.

#22 **Mame Penda SARR DIAWARA – ISRA, Senegal**

Genetic diversity and biological control of the pathogen Macrophomina in Senegal

Macrophomina is an important soil and seed-borne pathogen. It has a broad geographic distribution, and a large host range. The aim of this work is to determine the genetic diversity among a set of 189 isolates from Senegal and the CBS collection, and also to test in vitro and in vivo, antifungal activity of neem (Azadirachata indica) and henna (Lawsonia inermis) extracts on the pathogen Macrophomina. To achieve this goal, a multigene DNA analysis was conducted for 5 loci ITS, TEF, ACT, CAL and TUB. The efficacy of the aqueous extracts was tested on the mycelial growth of the fungus in vitro at two concentrations of 10 and 15% in the lab. In addition, a field trial was set up using a split split plot design with 03 replicates in a plot naturally infested by the fungus with 05 cowpea varieties. Based on these results we found a novel species of Macrophomina occurring on Abelmoschus esculentus, Arachis hypogaea, Hibiscus sabdarifa and Vigna unguiculata in Senegal. No consistent correlation was found among genotype, host and geographic location, and both species could even occur on the same host at the same location. In vitro evaluation of neem and henna extracts on the fungus showed a good

inhibition in mycelial growth with a rate of 65.03% and 69% respectively at concentrations of 15% and 10%. A variety-dose interaction was noted in the field trial and depending on the concentration of the extract, the varieties reacted differently. This work allow us to more characterize the pathogen Macrophomina in Senegal and with the 05 species of Macrophomina around the world, further research is required to determine their presence in Senegal, but also their virulence and geographic distribution compared to M. phaseolina. The antifungal activities of these two extracts are good prospects for using plant extracts on a large scale to limit production losses.

Key words: Macrophomina-soilborne pathogen-diversity-neem-henna-extracts.

#23 **Laurent BROTTIER – IRD, Montpellier, France**

Optimization of sample and strain collection management through the implementation of a Grist database

L. Brottier, F. Auguy, D. Belmadi, A. Saidani, H. Bouzayen, A. Dereeper, S. Cunnac

At the IRD in Montpellier, the XPLAIN team has developed a database using the Grist tool (https://www.getgrist.com/) to ensure the traceability of data relating to Xanthomonas pathogen collections: from sampling data (GPS location, collection dates, sample photos, regulations) to metadata from assembled genomes. This work provides a flexible system that (i) facilitates data entry by research team members and their partners, (ii) provides summary data dashboards, and (iii) ensures data traceability and lays the foundations for a sequencing data management plan (DMP) . This research data management solution is now being considered more broadly within the PHIM unit with a view to extending it to other pathogens (particularly fungi) for the purpose of collection management, but also more broadly for the epidemiological monitoring of plant diseases. Grist is now operational in the XPLAIN team thanks to the design of a suitable biological database model, a new project, “CLAPAS BioloGrist,” was launched in 2025 in collaboration with the MIVEGEC unit, which is also interested in this solution. One of the key objectives was to connect the KoboToolBox tool to the Grist database, in order to enable the entry of sampling data in the field using tablets, but also to develop a protocol for the semi-automatic submission of microbial genome sequencing data to public databases (ENA/SRA). An IRD instance has been set up to centralize the various Grist databases (https://biologrist.ird.fr/).

#24 **Lucille GORGUES – IRD, Montpellier, France**

Shuffling TALEs to Identify Resistance/Susceptibility Genes (STIRS)

Gorgues Lucille, Zárate-Chaves Carlos, López Camilo Ernesto, Szurek Boris, Perez-Quintero Alvaro

Plant pathogenic bacteria develop attack strategies (arms), to which plants respond by establishing defense mechanisms, creating a dynamic evolutionary arms race (Zuluaga et al., 2017). Strategies for genome editing for resistance is are inspired by this process, relying either on identifying and introducing resistance (R) genes or on modifying or inactivating susceptibility (S) genes (Olalekan Shittu and Henry Obiazikwor, 2018). A major question remains: how is this evolutionary process established, and can it be predicted? The Xanthomonas/plant pathosystem is an ideal model to study this dynamic, particularly through TAL effectors, which are able to manipulate the host genome by inducing susceptibility genes while evading resistance genes (Ji et al., 2016; Read et al., 2016; Triplett et al., 2016). Redirecting this process by creating a random TAL effector library would allow a genome-wide scan of the host, where random gene induction could lead to the discovery of novel susceptibility and resistance genes. To achieve this, we are developing a large-scale screening method to assess the virulence potential of TAL collections in rice and cassava. This approach could also be extended to other Xanthomonas pathosystems (tomato, citrus, banana, cabbage, etc.), thereby providing a better understanding of evolutionary mechanisms and constituting a step forward in genome editing.

#25 **Carlos ZARATE – INRAe, Castanet-Tolosan, France**

Genetic determinism of host range in plant pathogenic bacteria

Plants coexist with countless microbes, yet only a few are pathogenic, raising the key question of what defines a pathogen and its host range. In phytopathogenic bacteria, host specificity is thought to be determined by type III effectors (T3Es), which act collectively as repertoires known as effectomes. Using synthetic biology, we construct synthetic minimal effectomes (SMEs) and test them in an effectorless Xanthomonas campestris pv. campestris strain to assess their ability to restore fitness in host and nonhost plants. This approach reduces the complexity of large, redundant effector repertoires by systematically evaluating subsets of effector combinations. Our aim is to uncover general rules of effectome function, explore how effectomes and plant immunity co-evolve, and assess their role in host range and pathogen emergence. Beyond addressing a central question in phytopathology, this work also delivers innovative tools and resources to advance research on plant-microbe interactions.

#26 **Brice CHARLEUX – IRD, Montpellier, France**

Functional characterization of Os07g22730 as a downstream susceptibility gene in the TalB–OsERF#123 pathway of African Xanthomonas oryzae pv. oryzae

Xanthomonas oryzae pv. oryzae (Xoo), the causal agent of bacterial leaf blight (BLB), is one of the most devastating bacterial pathogens of rice. The virulence of Xoo largely relies on Transcription Activator-Like Effectors (TALEs), type III effectors that act as plant transcription factors by binding to specific DNA sequences in host promoters to activate susceptibility (S) genes (Perez-Quintero and Szurek, 2019). Within the African Xoo lineage, the TALE TalB has been identified as a major virulence determinant. TalB directly induces the AP2/ERF transcription factor gene OsERF#123, which has been validated as a susceptibility gene contributing to disease development (Tran et al., 2018). Recent transcriptomic analyses revealed that Os07g22730 is transcriptionally activated downstream of OsERF#123, raising the hypothesis that it may function as a secondary susceptibility factor in the Xoo-rice interaction, an observation not previously reported in this pathosystem.

To test this hypothesis, we engineered artificial TALEs (ArTALEs) specifically designed to target distinct binding sites in the Os07g22730 promoter. These ArTALEs were expressed in a TALE-deficient Xoo strain and inoculated onto the susceptible rice variety Azucena. Preliminary results showed that artificial induction of Os07g22730 enhanced disease symptoms, strongly suggesting a role in promoting susceptibility. Complementary approaches using mutant rice lines further supported a role for this gene in disease development.

Together, these findings identify Os07g22730 as a potential downstream target of the TalB–OsERF#123 pathway and as a contributor to susceptibility in the African Xoo-rice interaction. This work expands our understanding of the molecular mechanisms underlying African Xoo virulence. I will present our preliminary results on the functional characterization of Os07g22730 and discuss its role in susceptibility.

Key-words: ERF#123, Host-pathogen interaction, Rice, Susceptibility genes, TALEs, Xanthomonas oryzae

#27 **Corinne AUDRAN - INRAe, Castanet-Tolosan, France**

Exploring resistance by loss of susceptibility in Brassica oleracea

Xanthomonas campestris pv. campestris (Xcc) is the causal agent of black rot, a devastating disease that represents a major threat to Brassica crop production worldwide. A key feature of the pathogenicity of Xanthomonas is the delivery of transcription activator-like effectors (TALEs) into plant cells via the type III secretion system. Once inside the nucleus, TALEs act as transcription factors that reprogram host gene expression, often inducing susceptibility genes that favour bacterial growth and disease development.

We characterised the repertoire of TAL genes (the TALome) in Xcc and investigated their contribution to virulence in Brassica oleracea and other plants. Among these, the TALE Tal12a emerged as a virulence determinant, promoting both symptom development and bacterial proliferation in cauliflower. Transcriptomic analyses, TALE-binding elements prediction, and heterologous expression assays in Nicotiana benthamiana revealed that Tal12a induces a large number of host genes, including transcription factors, auxin-related genes and SWEET family sugar transporters. Functional assays showed that BoIAA7c and BoSWEET14c contribute to symptom development, though neither promotes bacterial growth.

These findings identify the first susceptibility genes in cauliflower and reveal that Tal12a promotes disease through a complex transcriptional reprogramming, involving direct and indirect target induction, with several genes functioning as minor susceptibility factors.

#28 **Camille BLASCO – IRD, Montpellier, France**

Expansion of Bacterial leaf Blight Disease of Rice Caused by Xanthomonas oryzae pv. oryzae in Tanzania

Blasco C, Auguy F, Brottier L, Hashim I, Mihayo R, Philipo L, Hutin M, Neema C, Szurek B

Xanthomonas oryzae pv. oryzae is the causal agent of the bacterial leaf blight disease, which dévastâtes rice crops in many countries. BLB is now prevalent in most rice-producing countries in Asia and West Africa. Recently, BLB has been detected in East Africa, with reports emerging from Tanzania in 2019 (Schepler-Luu et al., 2023). Subsequent surveys have documented the spread of this disease across different regions of Tanzania, as well as into Kenya and Uganda. In this study, we investigated the dynamics of the BLB epidemic at multiple spatial scales in Tanzania. We examined the population genetic structure of Xanthomonas oryzae pv. oryzae by genotyping strains isolated from infected leaves collected across different regions of Tanzania between 2019 and 2025. Genetic analysis was performed on Xoo populations at scales ranging individual fields to entire regions. Our results suggest that Xoo was first introduced in to Tanzania in the Morogoro region before spreading widely to other regions. The importation of contaminated seed material represents one hypothesis for the dissemination of the disease. Field-level analyses of genetic diversity in populations provide valuable insights into the factors shaping epidemic spread useful information for understanding the factors that shape the spread of the epidemic.

#29 **Soline MARTY - INRAe, Castanet-Tolosan, France**

Water availability in leaves defines the ecological niche and proliferation of Xanthomonas campestris

Plants have developed complex immune responses able of restricting the proliferation of most microbes they encounter. In the case of pathogenic microbes, disease symptoms are often linked to the formation of water-soaked lesions, resulting from the accumulation of water in the apoplast. While it is well established that humidity is a key factor in plant disease development, the molecular mechanisms behind this phenomenon remain largely unknown. Recent studies highlight the role of the pathogenic bacterium Pseudomonas syringae in manipulating water availability within the apoplast, suggesting that water may be a direct effector of plant immunity. In this work, we explore the potential link between water availability and plant immunity using the vascular pathogenic bacterium Xanthomonas campestris pv. campestris (Xcc) which infects hydathodes of Brassicaceae plants. We identified Arabidopsis mutant plants affected in their leaf development which exhibit higher levels of apoplastic water and support enhanced proliferation of Xcc within the mesophyll. In those mutants, Xcc gained the capacity to establish infection from stomata. Mechanically blocking guttation recapitulated the phenotypes, i.e. caused both watersoaking and increased proliferation of Xcc in both Arabidopsis and cauliflower. These results raise several key questions: Is water accessibility in the apoplast a key effector of plant immunity? Can Xcc favour high-humidity conditions to promote its proliferation?

#30 **Sarah DELAFOSSE – IRD, Montpellier, France**

Diversity and prevalence of prophages and anti-phage defense systems in a major rice pathogen

Bacteriophages, viruses that infect and replicate within bacteria, are major drivers of bacterial evolution. Through lysogenic infection, where they integrate their genome in the form of a prophage within the bacterial genome, they promote horizontal gene transfer. To counteract phage infection, bacteria have developed anti-phage defense systems, leading to a dynamic evolutionary arms race between phages and their hosts. This work aims to address two main questions : How diverse are prophages and anti-phage defense systems across the phylogeny of a bacterial species? And, in the case of a widely distributed rice pathogen, how are these features distributed, and do they correlate with phylogeny or geographic origin ? Xanthomonas oryzae is a widely distributed bacterial species that poses a major threat to global rice production. Its diverse pathovars infect different host plants and tissues, with some causing devastating diseases such as bacterial leaf blight and bacterial leaf streak on rice, leading to significant yield losses on one of the world's most important staple crops. Moreover, the distinct lineages of Xo exhibit significant genetic differences. While the genomic architecture of Xo lineages is currently being investigated, the role of phage-related genomic features in shaping this diversity remains unexplored. Prophages and anti-phages defense systems are known to influence genome evolution, but their impact has mostly been studied in other bacterial taxa ; while such research on phytopathogenic bacteria remains scarce.

We analyzed prophage number, size, and diversity across 336 Xo genomes. In parallel, we investigated the number and distribution of defense systems to assess anti-phage strategies within and between populations. Most Xo genomes harbor one to two prophages, a pattern that is consistent across populations. In total, 426 prophages were identified, spanning 83 species. On the other hand, a total of 2,576 defense systems, encompassing 84 subtypes, were identified, with each Xo strain carrying between 4 and 14 defense systems, their number and types varying according to population.

Our results indicate a dichotomy in transmission dynamics of phage-related genomic elements within Xo. Prophage diversity does not follow the phylogeny of the host genomes but instead reflects the geographic origin of the strains, suggesting that prophages are acquired predominantly through horizontal transfer. In contrast, anti-phage defense systems exhibit high subtype specificity within each population and align with host phylogeny, consistent with stable vertical inheritance. Together, these findings provide the first systematic view of phage-related genomic features in Xanthomonas oryzae.

#31 **Souley ISSAKA - Université de Tillabéri, Niger**

African Cassava Mosaic Disease (ACMD) epidemic in Niger

Cassava (Manihot esculenta) is an important source of starch, protein and vitamins for nearly 800 million people worldwide. It makes a major contribution to food security in Niger. However, its cultivation is limited by numerous biotic constraints, including African Cassava Mosaic Disease (ACMD) caused by the African Cassava Mosaic Virus (ACMV); very few studies have been devoted to the epidemiology and variability of the virus. The present work aims to: (i) study the epidemiology of the virus responsible and (ii) map ACMD in Niger. It involved surveying cassava-growing areas, collecting samples of diseased cassava, indexing the samples collected on a susceptible variety and mapping the geographical distribution of viral isolates. Preliminary results show, on the basis of observations, that ACMD is present in all country’s cassava-growing areas, with incidences varying according to site and variety. Incidences ranged from 25% to 90%, and tuber losses varying from 40% to over 80%. The presence of the disease in the farms surveyed was confirmed by the results of biological indexing. Actualy, a wide range of samples carrying symptoms of the disease are awaiting serological and molecular analysis to elucidate the diversity of the virus in the study area. Ultimately, the ACMV isolates identified will help to : characterize the germplasm of the national centers, identify sources of resistance to ACMD and develop high-performance cassava varieties adapted to the ecology of the study area and other endemic sites.

#32 **Régis LONGE SOPKE- Université de Bangui, République Centrafricaine**

Identification of natural hosts of MSV in the Central African Republic

Maize streak disease is the viral disease causing the most production loss in maize cultivation in sub-Saharan Africa. As its name suggests, it is caused by the maize streak virus (MSV), belonging to the genus Mastrevirus of the family Geminiviridae. In the Central African Republic, MSV has been studied very little in maize or in non-cultivated plant species. As part of the crop ecosystem, these wild species play an important role in the development and management of viral diseases in general. Seven (7) PCR products were sequenced. BLASTn results indicate homology with the sequences of the C1, V1, and intergenic region (LIR) genes of MSV from Rwanda, Zambia, South Africa, Kenya, and the Philippines, with nucleotide identity percentages ranging from 92 to 99.46 %. Phylogenetic analyses indicate that MSV-CF sequences cluster together regardless of their hosts. They differ from Panicum streak virus (PanSV) sequences, the Mastrevirus infecting Panicum maximum, including an isolate from the Central African Republic characterized in 2009. These results indicate that Panicum maximum and Imperata cylindrica are hosts of MSV in the Central African Republic.

#33 **Yêyinou Laura Estelle LOKO - UNSTIM, Bénin**

Potential of Metarhizium anisopliae and Beauveria bassiana to control Dinoderus porcellus (Coleoptera: Bostrychidae) infesting yam chips

The beetle Dinoderus porcellus Lesne is a serious storage insect pest that causes important losses by destroying stocks of yam chips. In the aim to found an alternative control method to the use of synthetic insecticides for its management, the virulence of the entomopathogenic fungi Beauveria bassiana (Balsamo) Vuillemin (isolate Bb115) and Metarhizium anisopliae (Metschnikoff) Sorokin (isolate Met 31) against adults of D. porcellus was evaluated under laboratory conditions (25 ± 2 ◦C and 70 ± 5% RH). Then, the effectiveness of the most virulent entomopathogenic fungus as biological agent against D. porcellus was assessed under farmer storage conditions. For each entomopathogenic fungus isolate, four conidial concentration (0, 105, 107, and 109 conidia/mL) at the dose of 1 µL were inoculated topically on D. porcellus adults (3–5 days old). Observations focused on insect mortality, cadaver sporulation and weight loss of yam chips. Lethal dose and lethal time values were estimated using probit analysis. Both fungal isolates at all conidial dose caused more than 50% mortality on day 7, with the highest mortality (94.44%) achieved using B. bassiana at the 109 conidia/mL. LT50 values for B. bassiana and M. anisopliae isolates were 2.63 and 3.35 days, respectively, while their LT90 values were 6.15 and 9.87 days, respectively. Yielding the lower LD90 values and the highest rates of cadaver sporulation, B. bassiana isolate appeared as the most virulent against D. porcellus. After 3 months of storage, comparatively to the control, the B. bassiana isolate at the highest conidial dose (109 conidia/mL) significantly reduced D. porcellus populations, and weight loss of yam chips. This study revealed the potential of B. bassiana and M. anisoplae isolates as biological control agent against D. porcellus for yam chips protection.

#34 **Joelle TOFFA - UNSTIM, Bénin**

Plant-Microbiota-Insect Interactions: A novel strategy for improving the health and sustainability of vegetable crops in Benin

Joelle Toffa, Yasmine Gbenontin, Yêyinou Laura Estelle Loko

Vegetable crops are of major economic and nutritional importance in Benin, yet their production is severely constrained by insect pests, leading to considerable yield losses. To support the development of locally adapted integrated pest management (IPM) strategies, this study investigated the interactions between tomato plants, their microbiota, and insect pests, focusing on the endophytic potential of the indigenous fungus Beauveria bassiana. A participatory survey involving 255 tomato farmers across 12 communes in southern Benin facilitated the collection of plant samples. Root segments (~4 mm), cultured on PDA medium, revealed the presence of B. bassiana, which was mass-produced for further assays. Two tomato cultivars were inoculated by seed soaking in conidial suspensions (1×10^7 and 1×10^9 conidia/mL). Endophytic colonization was confirmed in roots, stems, and leaves, with roots showing the highest colonization levels. A bioassay with Helicoverpa armigera larvae showed significantly reduced survival (1.5±0.2 days) compared to control (8.4 ± 0.9 days), along with decreased foliar consumption (89.17±10.33 mm^2 ; 820.3±92.77 mm^2). Mycelial growth on dead larvae confirmed fungal pathogenicity. These findings underscore the potential of entomopathogenic and endophytic fungi in enhancing plant health. Their integration into vegetable crops systems offers an environmentally sound alternative to chemical pesticides, there by fostering more sustainable and resilient agricultural practices in Benin. Keywords : Tomato plants, microbiota, endophyte, insect pests, biocontrol

#35 **Innocent ZINGA - Université de Bangui, République Centrafricaine**

Aphid-borne cowpea mosaic in the Central African Republic: prevalence, diversity and search for control methods against Cowpea aphid borne mosaic virus (CABMV)

Zinga Innocent, Silla Sembella, Longue Sopke Regis Dimitri, Kola Doli Alain Romaric

Cowpea (Vigna unguiculata) is a legume grown and consumed by hundreds of millions of people in Africa and beyond. Its cultivation is seriously hampered by Cowpea aphid-borne mosaic virus (CABMV) in Africa in general. CABMV is caused by cowpea potyviruses and spread by the aphid vector (Aphis craccivora) and the use of infected seeds. Epidemiological surveillance continues and indicates that some CABMV species are expanding their geographical ranges. Despite the studies carried out, the diversity of CABMV species in some countries remains unknown, particularly in the CAR. This study carried out on cowpea fits well into the program for the selection and popularization of cowpea cultivars in the CAR. This work integrates studies on the gromorphological and phytosanitary performance of cowpea cultivars, the biological and molecular characterization of emerging cowpea mosaic viruses and that of the control of CABMV by thermotherapy. The study of the agromorphological and phytosanitary performance of cowpea cultivars in agrosystems made it possible to preselect 4 cowpea accessions in the production areas in the CAR. Following a behavioral evaluation of the species at the three sites, all located in the country's two agro-climatic zones, and using data and leaf samples collected from cowpeas, we analyzed growth parameters, yield components and disease epidemiological factors. Our results show that plant emergence rates are higher than the recommended potential standard (97%> 75%), agro-ecological zones are affected by the disease and show a diversity of leaf symptoms. Principal component analysis of quantitative variables revealed a high-performance elite accession such as Kahkir (1.3 t/ha), which could be used in the CAR breeding and extension program. Biological and molecular characterization of emerging CABMV viruses from different accessions grown in CAR identified a CABMV size of around 1000 bp with the CABMV-specific primer pair (Poty-GP1-5'CP-R/Poty-GP1-5'CP-F, UN6-F/P106-R) and around 325 bp with the universal primer pair (UN5/UN6). Full nucleotide sequencing confirmed the presence of 7 CABMV variants in RCA (CA1, CA5, CA11, CA15, CA28, CA30, CA33), making it a locus of CABMV diversity. Phylogenetic and recombination analyses showed that CABMV isolates from the CAR are closely related to those from Burkina Faso (MF277036, MF277037, MF277031 and MF277034), Uganda (KT726938) and Nigeria (Y17822). The study of CABMV control by thermotherapy at different temperature ranges for a fixed time (15 min) on infected seeds revealed a delay in the expression of CABMV symptoms and an increase in seed yield in plants emerging from infected seeds compared with plants emerging from infected seeds not treated with heat. Similarly, this study showed that 65°C represents the optimal treatment temperature. These results confirm the need for intervention in the implementation of heat therapy control strategies under CABMV epidemic conditions.
Keywords: Cowpea mosaic, CABMV, selection, epidemiology, thermotherapy

#36 **Aboubie Elisabeth ZONGO – INERA, Burkina Faso**

Molecular characterization of emerging viruses infecting Bambara groundnut (Vigna subterranea L. Verdc.) in Burkina Faso

Bambara groundnut (Vigna subterranea L.Verdc.) is an African legume with high agronomic, nutritional, and economic potential. However, its crop remains neglected and its productivity is limited by various constraints, including viral diseases that are insufficiently documented. Our work (Zongo et al., 2019) has nevertheless identified emerging viruses in samples collected in the Sudanian and

Sudano-Sudanian zones of the country. Analysis of the capsid protein sequences showed the presence of potential new species provisionally named Bambara groundnut potyvirus 1 (BGPV1) and Bambara groundnut potyvirus 2 (BGPV2). However, these results, based on partial sequences, do not allow the exact identity of the detected viruses to be confirmed. We therefore present here a complementary study conducted with the aim of confirming the precise identity of these potential new viruses through complete sequencing of the viral genomes.

To this end, new samples were collected in the zone (Sudanian) with a high prevalence of these viruses. A total of 38 samples were collected and subjected to specific molecular amplification (RT-PCR). Analysis of partial sequences revealed that seven isolates had 95-99% nucleotide identity with BGPV1, while 12 isolates had similar identities with BGPV2, confirming the presence of both viruses in the samples analysed. Nanopore sequencing was then performed on two samples. Although the sequencing provided promising results, complete genome reconstruction by nanopore was not achieved. Nevertheless, the partial sequences generated show that the BGPV2 genome is very similar to that of Bean common mosaic virus (BCMV) and that these two viruses are co-infecting, which complicates bioinformatic analysis.

This work confirms the genetic diversity of potyviruses infecting bambara groundnut in Burkina Faso and represents an important step toward the complete characterization of these newly identified viruses. Work is continuing to obtain the complete genomes and establish the definitive taxonomic classification of these new viruses, which is an important step towards the implementation of a sustainable and agroecological integrated control strategy for Bambara groundnut viruses.

#37 **Hassna FOUNOUNE – ISRA, Senegal**

Expansion Role of arbuscular mycorrhizal fungi in enhancing the crop productivity and sustainability of Sahelian agroecosystems

FOUNOUNE Hassna, Ndeye Maguette Hane, FALL Abdoulaye Fofana

In Sahelian regions, particularly in Senegal, climate change exacerbates soil degradation, reduces fertility, and undermines the sustainability of agricultural production systems. To address these challenges, the adoption of agroecological practices offers promising pathways toward integrated and resilient production systems. Among these practices, the management and utilization of the soil microbial community, particularly arbuscular mycorrhizal fungi (AMF), could play a key role. AMF enhance plant mineral and water nutrition and contribute to improving the productivity of Sahelian agroecosystems. We present here some results highlighting the agronomic role of AMF: (i) the contribution of AMF to the bioavailability of micronutrients (iron and zinc) in cultivated millet (Pennisetum glaucum). Results show that Fe, Zn, P, and K concentrations are significantly higher in the shoot biomass of mycorrhizal plants compared to non-inoculated controls; and (ii) the dynamics of AMF within agroforestry systems based on Guiera senegalensis (a native shrub). Findings reveal that root mycorrhization intensity in crops associated with Guiera is significantly lower 8.1% for peanut and 2.7% for millet, compared with systems without Guiera (19.9% for peanut and 8.2% for millet). Several hypotheses are proposed to explain these patterns, which will also be correlated with crop yield data (ongoing work). Overall, these studies highlight the key role that AMF can play in soil biofunctioning and crop production. They contribute to maintaining soil fertility, enhancing plant stress tolerance, and supporting resilient agroecological strategies.

Keywords: Arbuscular mycorrhizal fungi (AMF) ; Sahelian agroecosystems ; Micronutrient bioavailability; Guiera senegalensis ; Millet ; Peanut.

#38 **Charlotte TOLLENAERE – IRD, Montpellier, France**

The co circulation and co infection of rice pathogens: evidence in the field and evolutionary consequences

Estelle Billard, Abalo Itolou Kassankogno, Nils Poulicard, Martine Bangratz, Aurore Comte, Phonsiri Saengram, Abdoul Kader Guigma, Eugénie Hébrard, Charlotte Tollenaere

Multiple pathogens may co-occur at different spatial scales (i.e. co-circulation), and this is a prerequisite for co-infection (i.e. the infection of a single host by different pathogen species). Both co-circulation and co-infection have the potential to affect disease dynamics, but such population-scale consequences remain poorly explored. Rice grown in Burkina Faso is affected by multiple pests. We conducted a field survey to document the frequency of co-occurrence of multiple diseases, based on symptom observation during a multi-year and multi-site survey. Specifically, the rice yellow mottle virus (RYMV) and the bacteria Xanthomonas oryzae (Xo) were detected simultaneously in many fields, particularly in an area identified as a disease hotspot. These two pathogens have been shown to interact in experimental settings, resulting in a lower viral load in presence of the bacteria. We hypothesized that such co-circulation and virus-bacteria interactions could affect viral evolution, leading to a distinct composition of viral populations in plants co-infected with the bacteria, compared to the plants infected by the virus only. To test this hypothesis, we performed a stratified random sampling in two sites, during two consecutive years (2021 and 2022). Molecular detection applied jointly to RYMV and Xo revealed a much higher frequency of samples co-infected by the two pathogens, than inferred from the observations of the two types of specific symptoms on the same plants. We then characterized the genetic diversity of RYMV in collected samples revealing a locally high diversity within fields, and significant structuration between the two sites. In addition, we found some evidence for an association of some RYMV lineages with the presence of Xo, suggesting reciprocal influence of co-infecting pathogens on the genetic structuration of other pathogen species. Further research is required to explore the consequences of multiple infections on the evolution of pathogen populations.

#39 **Michel BARBIER – IRD, Montpellier, France**

The rice root knot nematode microbiota may be used for biocontrol purposes

Meloidogyne graminicola is a plant-parasitic nematode widespread in Southeast Asian rice fields, where it causes important yield losses. To control plant-parasitic nematodes, nematicidal molecules such as Methyl Bromide have long been used, but their negative effects on health and environment make their marketing increasingly restricted. An alternative control solution is the use of biocontrol agents. In Cambodia, 90% of the rice fields are flooded during the rainy season, but flooding is known to drastically change the soil physico-chemical parameters and microbial communities. These changes can impact the colonization and efficiency of the organisms marketed as biopesticides. During our work in Cambodia, we searched for rice field suppressive soils against M. graminicola, which are soils that reduce the impact of the disease in fields due to their biological nature. These soils are then a potential source of biocontrol agents. Once identified, we incubated the juvenile larvae of M. graminicola in these soils, and we applied a cultivable approach on the juveniles to isolate predatory microorganisms. The cultivation allowed us to isolate seven bacterial genera presenting an in vitro nematicidal effect. These bacteria, adapted to local culture conditions and specific to M. graminicola, represent promising biocontrol agents to replace harmful nematicides.

#40 **Laurence ALBAR – IRD, Montpellier, France**

Insights into rice crinkling disease: decoding transmission, host range and genetic resistance

The rice crinkling disease has been reported in West Africa and is increasingly affecting rice production in South America. The causal agent is a bipartite virus, Benyvirus oryzae, also known as Rice stripe necrosis virus. RSNV is transmitted to rice by the soil protist Polymyxa graminis, an obligate endoparasite of rice roots whose spores can persist in the soil for up to a decade. To date, no sustainable control strategy has been developed. To improve our understanding of this still poorly characterized pathosystem, several complementary research approaches are being pursued. A controlled infection system using P. graminis has been established in our greenhouses to characterize the infection process, contribute to assess host range and identify potential resistance sources. In addition, vector-free inoculation methods, based on mechanical inoculation or infectious viral clones are being developed, to study the viral infection process and host specificity independently of the vector. Finally, a resistance major QTL identified in the African cultivated rice, Oryza glaberrima (Gutierrez et al., 2010) is currently being characterized to pinpoint the gene responsible for resistance.

#41 **Alvaro PEREZ QUINTERO – IRD, Montpellier, France**

Repeat, evolve, repeat: The high evolvability of the Xanthomonas oryzae genome facilitates epidemic outbreaks in rice

All living beings evolve but they don’t do so at the same speed. The “evolvability” of an organism can be determined by genomic features like the presence of repetitive regions and, as such, it is a trait subject to natural selection. We show that the genome of the bacterial pathogen Xanthomonas oryzae, causing Bacterial Leaf Blight in rice, is abnormally repetitive and highly evolvable, likely due to selection imposed by resistance in the host plant. As a consequence, X. oryzae has an increased ability to break down resistance, adapt to different rice varieties, and cause epidemics. We hypothesize that the spread of epidemic X. oryzae strains is likely favored by genomic changes involving repeats that can lead to changes in virulence.

Posters

P1 **Natalia HERNANDEZ ALCÁNTARA**

Characterization of rhizosphere bacteria and their effect as growth promoters in two varieties of Coffea arabica L. under water deficit conditions.

Climate change has intensified the frequency and duration of drought periods, compromising agricultural productivity, especially in coffee (Coffea arabica), a crop of major economic importance worldwide and fundamental for Colombia. Several varieties of this species are sensitive to water stress. An ecological alternative to mitigate this impact is the use of plant growth-promoting bacteria (PGPB), microorganisms capable of alleviating abiotic stress. In this study, five rhizospheric bacteria isolated from Plukenetia volubilis with potential as PGPB were characterized. Their ability to form biofilms, colonize roots, and promote in vitro growth in Arabidopsis thaliana was evaluated through morphological measurements (leaf area, fresh weight, and root length), as well as amplification of the acdS and amoA genes. Based on these results, a bacterial consortium was designed and evaluated on the C. arabica varieties Castillo and Cenicafé 1, which underwent a 45-day drought period followed by a 15-day recovery phase. During this period, physiological parameters such as leaf water potential, stomatal conductance, photosynthetic rate, transpiration, maximum quantum efficiency of PSII, as well as biomass and other functional traits, were measured. The results showed that the bacterial consortium had no significant effect on the Castillo variety, but did have a significant effect on Cenicafé 1, as there was an increase in the volumetric concentration of water in the soil, accompanied by more positive water potentials and higher photosynthetic rates. This study constitutes a pioneering contribution to the evaluation of bacterial consortia on the response and recovery of coffee varieties under drought conditions, highlighting the need for new trials to validate the impact of PGPB on other varieties and promote their application in agricultural scenarios affected by climate change.

P2 **Santiago CORTES CALDERON**

*Analysis of Protein–Protein Interactions of the Effector XopAE and Their Implications ince Cassava Bacterial Blight Developmen*t

Santiago Cortés Calderón, Carlos Rodríguez Mantilla, Sofia Contreras, César Trujillo Beltrán, Paola Reyes Caldas, Barbara Hanna Zimmermann and Adriana Jimena Bernal Giraldo

Cassava (Manihot esculenta) is a staple crop for global food security but is highly vulnerable to cassava bacterial blight (CBB), caused by Xanthomonas phaseoli pv. manihotis (Xpm). This pathogen deploys nearly 30 type III-secreted effectors, among which XopAE is essential for full virulence. XopAE is a conserved protein within Xpm populations and has been associated with suppression of plant basal immunity (PTI). Previous findings suggested that one of its potential targets in cassava is MePATL3, a SEC14-GOLD family patellin involved in vesicular trafficking.
In this study, we aimed to validate and characterize the interaction between XopAEXpm and MePATL3. Yeast two-hybrid (Y2H) assays in Saccharomyces cerevisiae indicated a positive interaction, we aimed at confirming the interaction by pulldown assays, using His-tagged XopAEXpm purified through cobalt-affinity chromatography. Additionally, transient expression of MePATL3 in Nicotiana benthamiana was optimized and verified by Western blot at 48 h post-infiltration. Considering that patellins participate in vesicular trafficking, defense signaling, and may undergo phosphorylation and ubiquitination, we further explored whether MePATL3 stability was altered upon interaction with XopAEXpm.

Overall, our findings support that XopAEXpm directly interacts with MePATL3, potentially modulating vesicle-mediated defense responses and thereby contributing to CBB pathogenicity. These insights shed light on molecular mechanisms of Xpm virulence and may contribute to the development of improved strategies for cassava resistance.

P3 **Jorge OLIVEROS ROJAS**

Plant Growth Promoting Rhizobacteria and Their Role in Tomato Salt Stress Tolerance: A Sustainable Biotechnological Alternative

Jorge Oliveros Rojas; Camilo Racedo Pulido; Maira Bernal López and Adriana Bernal Giraldo

As one of the most important crops worldwide, tomato (Solanum lycopersicum) contributes significantly to both economic value and food security. Nevertheless, its production is highly constrained by soil salinity, an abiotic stress that reduces plant growth and yield. This problem is further aggravated by climate change and inadequate agricultural practices, making salinization an increasing challenge for global agriculture. In this context, the use of plant growth-promoting rhizobacteria (PGPR) emerges as a promising strategy. These beneficial bacteria can assist plants in coping with biotic and abiotic stresses, enhancing their development and stress tolerance. This study evaluated the impact of five bacterial morphotypes with previously characterized PGPR properties under laboratory conditions on the growth and physiological performance of tomato plants subjected to salinity stress. Plants were exposed to three NaCl concentrations (0, 100, and 300 mM), and growth parameters such as plant height, leaf area, and biomass (fresh and dry weight of leaves, stems, and roots) were measured, along with physiological variables including stomatal conductance and photosystem II efficiency. Results showed that bacterial morphotypes 2 and 3 exhibited superior performance under salt stress compared to the negative control and other morphotypes. The tested bacterial morphotypes demonstrated a significant capacity to mitigate NaCl effects, promoting more robust plant growth even under high salinity conditions. Specifically, their growth-promoting action was reflected in increased biomass accumulation, suggesting that certain bacterial isolates may play a crucial role in enhancing abiotic stress tolerance in horticultural crops. Overall, the findings support the potential of morphotypes 2 and 3 as effective PGPRs with sustainable applications to improve tomato resilience against salt stress. This biotechnological strategy represents a promising alternative to address the increasing salinization of agricultural soils, thereby contributing to more sustainable horticultural production and global food security.

P4 **Camilo RACEDO**

Development of an agricultural bio input based on plant growth-promoting bacteria

Camilo Racedo, Layla Castellanos, Juan Diego Díaz, Felipe Salcedo, Chad Leidy & Adriana Bernal

Global food production faces unprecedented threats from climate change and soil degradation, jeopardizing both present yields and future agricultural resilience. Current common practices used to increase food production are based on chemical fertilizers and intensification of pesticide application; while these options have ensured agricultural productivity for decades, they are slowly poisoning our soil and ground water, and neglecting ecological, microbial, and physicochemical aspects of soil health, creating long-term imbalances in nutrient cycling and microbiome diversity. The use of plant growth promoting rhizobacteria (PGPR) constitutes a positive alternative to improve food production without generating negative effects on our soils. For these reasons, our research looks for a way to create an ecologically safe and efficient agricultural bio input based on PGPR as its main component. For this, we isolated autochthonous PGPR from Colombian crops and created multifaceted synthetic communities (SynComs) based on their biochemical capacities and in planta performance. Additionally, to translate these SynComs from the lab to the field we have developed a biochar-based formulation with the help of affordable preserving solutions to maintain microorganism viability without the use of refrigeration or special containers to create a durable biofertilizer which can be easily transported and implemented in agricultural settings. We obtained SynComs capable of promoting plant growth in the model plant Solanum lycopersicum in culture rooms and a formulation which protects microbial viability for at least 30 days.

P5 **Léa JOBERT**

Rhizosphere soil-borne legacy of infected rice plants and its impact on next generation

The discovery of disease-suppressive soils, in which microbiome-mediated mechanisms protect crops from soil-borne pathogens (1), has highlighted the critical role of the microbiome in crop protection. Due to its promising applications in more sustainable agriculture, this protective capacity is now the subject of an increasing number of studies. One of the key ecological processes involved is the concept of soil-borne legacy, whereby previous plant-microbe interactions influence the performance of subsequent plants (2). While plants are influenced by their associated microbiomes, they also actively modulate the composition and function of microbial communities through specific metabolites - a phenomenon often referred to as the “cry for help” (3).

In this study, we investigated the influence of the rhizosphere microbiota of rice plants exhibiting foliar disease symptoms in a Cambodian field on subsequent generations of plants. Based on a visual assessment of foliar symptoms, we collected and mixed the rhizospheres of plants classified as “diseased” or “healthy”, respectively. These mixed rhizospheres were then used to sow new rice plants in a controlled greenhouse environment and were subsequently challenged with Xanthomonas oryzae pv. oryzae, the causal agent of bacterial leaf blight.

Phenotypic analyses revealed that plants grown in the rhizosphere microbiota collected from diseased field plants were smaller, yet exhibited increased resistance to foliar pathogens compared to those grown in the rhizosphere of healthy plants. Amplicon sequencing of the roots and rhizospheres of the field confirmed distinct community structures in the initial rhizosphere mix, suggesting a microbiota-driven priming effect. Ongoing analyses aim to determine which taxa were inherited and could explain the observed phenotype.

These findings support the idea that plants exposed to pathogens can condition their rhizosphere microbiota to enhance resistance in the next generation, providing a promising new approach to crop protection strategies.

P6 **Laurence ALBAR**

Gene editing allows the generation of durable resistance against RYMV in rice

Gene editing offers new opportunities to develop resistant lines by targeting susceptibility factors involved in plant-pathogen interactions. The translation initiation factor eIFiso4G.1 is a susceptibility factors required by rice yellow mottle virus (RYMV), one of the most devastating rice pathogens in Africa, to complete its cycle in the host plant. Editing of OseIFiso4G1 can contribute to the development of sustainable resistance to RYMV. CRISPR-Cas9 technology was used to generate lines with knock-out (KO) mutations in the susceptibility factor eIFiso4G.1 and its paralog, eIFiso4G2. In addition, we also generated lines with short deletions in the central region of eIFiso4G1 which is involved in the interaction with the virus. The different lines were evaluated for resistance to representative isolates of RYMV, for resistance durability and for plant growth under controlled conditions. We showed that KO mutations in eIFiso4G.2 do not affect susceptibility, whereas KO mutations and some (but not all) deletions in eIFiso4G.1 confer high resistance. Our results suggest that, despite a putative effect on plant growth, KO mutations in eIFiso4G1, may drastically reduce the risk of resistance-breakdown compared to known resistance alleles found in natural rice diversity. The 3D structures of edited eIFiso4G1 with deletions were modeled and compared to natural resistance alleles to better understand the interaction with the Vpg of RYMV and predict resistance efficiency. Overall our results confirm that CRISPR-Cas9 is a promising strategy for generating RYMV resistance in elite rice varieties.

P7 **Martine BANGRATZ**

Nanopore sequencing to explore genetic diversity of rice viruses in West Africa and South America

Martine Bangratz, A. Comte, M. Barro, A.K. Guigma, L.P. Carrasco, H. Tall, C. Tollenaere, N. Poulicard

Rice is the most important cereal crop for human consumption worldwide. Changes in farming practices, intensification and climate change, are increasingly exposing rice to the risk of epidemics and the potential emergence of new diseases, particularly viral ones (Anderson et al., 2004). Currently, 20 viruses are known to infect rice worldwide, with the majority circulating in Asia. Only 3 have been identified in Africa and 2 in the Americas (Wang et al., 2022, Fouad et al., 2024). In recent years, the use of high-throughput sequencing technology from Nanopore (ONT, Oxford Nanopore Technologies) has become increasingly used for detecting plant viruses (Sun et al., 2022). This technology (Liefting et al., 2021) enabled us to characterise several known and unknown viruses from different families with distinct genomic organisations. Specifically, we first shed light on the intra-host diversity of the rice yellow mottle virus (Solemoviridae), which is endemic to Africa and induces severe yield losses. We also obtained the complete genome sequences of known viruses that has received little attention despite their significant impact on rice production. These include the rice hoja blanca virus (Phenuiviridae), which is endemic to America, and the rice stripe necrosis virus (Benyviridae), which is present on both continents. Finally, we have identified and characterized previously unknown viruses, belonging to the Potyviridae and Rhabdoviridae families. These viral genomics data are essential for developing effective diagnostic tools to detect and monitor the spatio-temporal evolution of viral diseases in rice fields from Africa and South America.

P8 **Penda NDOYE**

Comportement symbiotique de cinq variétés de niébé inoculées avec cinq souches de Rhizobiums en condition semis contrôlée (serre) au Sénégal.

Le niébé (Vigna unguiculata L. Walp.) est une légumineuse d’intérêt nutritionnel et écologique en Afrique de l’Ouest, grâce à sa capacité à établir une symbiose efficace avec les bactéries fixatrices d’azote du genre Bradyrhizobium. Cependant, les rendements observés sont très variables et montrent que les conditions édapho climatiques sont déterminantes. De plus, des études ont montré que le niébé pouvait s’associer à une grande diversité de Bradyrhizobium et que cette diversité pouvait être relativement spécifique à la zone agroécologique tout en étant modifiée par inoculation. Afin d'assurer un potentiel symbiotique à la zone de culture et aux variétés appréciées par les producteurs, il est possible d'inoculer le niébé avec des souches efficaces, compétitives et adaptées.

Ainsi, dans le cadre de notre thèse inscrite dans le projet BioMicNet (Réseau de recherche et d'innovations en inoculation microbienne des cultures comme levier de la transition agro-écologique du Sénégal), nous nous intéressons à la caractérisation de l'efficacité de la réponse du niébé à l'inoculation. Pour cela, nous nous basons principalement sur des aspects agronomiques en particulier variétal et symbiotiques pour une amélioration de la productivité du niébé au Sénégal. L'objectif est d'identifier les combinaisons variété-souche les plus performantes, un essai a été conduit en serre du 26 juin au 27 août 2025. Cinq variétés de niébé (Sam, Mélakh, Yacine, Baye Ngagne et Kelle) particulièrement appréciées par les producteurs de trois zone agroécologiques du Sénégal, pour leurs propriétés agronomiques ont été inoculées avec cinq souches de Bradyrhizobium (LCM3257, LCM3682, LCM4767, 1.3 et 1.5) préalablement testées en conditions contrôlées (Chambre de culture) ainsi qu'un traitement mixte. Les observations ont porté sur des paramètres liés à la symbiose et à la croissance : nombre et poids sec des nodules, poids sec des racines, poids sec de la biomasse aérienne, poids sec total de la plante et taux de chlorophylle comme indicateur du statut azoté de la plante (mesuré tous les huit jours pendant trois semaines à partir du 25e jour après semis). Cette expérimentation visait à évaluer le comportement symbiotique de chaque variété en fonction des souches inoculées et à identifier les couples symbotiques les plus efficaces en conditions semi-contrôlées.

Les résultats montrent que les variétés ne répondent pas toutes de la même manière à l'inoculation. En effet, l'impact de l'inoculation sur la croissance végétale pour la variété Baye Ngagne, la souche LCM3682 ressort comme la plus efficace, car elle est la seule à améliorer significativement la biomasse totale de la plante tout en contribuant à une meilleure teneur en chlorophylle. Chez la variété Kelle, les souches 1.3 et LCM3257 améliorent le statut chlorophyllien, mais aucune souche n'a eu d'effet significatif sur la biomasse totale. Pour Mélakh, la souche LCM3682 améliore l'état chlorophyllien, tandis que le traitement mixte favorise la croissance globale. Chez Yacine, les traitements mixte, LCM3257 et LCM3682 améliorent significativement le taux de chlorophylle, et la souche LCM3257 induit une légère augmentation du poids aérien sans affecter le poids total. Enfin, la variété Sam n'a montré aucune réponse notable à l'inoculation, ni sur la croissance végétative ni sur le taux de chlorophylle dans les conditions de serre.

Les résultats obtenus en serre constituent une base de sélection des couples prometteurs. Cependant, afin d'évaluer les effets des conditions édapho-climatiques, des génotypes de niébé et de Bradyrhizobium, des essais ont également été lancés cet hivernage en station avec les mêmes traitements, dans trois zones agroécologiques contrastées du Sénégal : Bambey (centre), Dahra (nord) et Nioro (sud), représentatives du gradient pluviométrique national. Dans cette étude, les performances agronomiques des variétés seront étudiées en fonction des souches. La fixation d'azote sera quantifiée avec des analyses N15 et la compétitivité des souches inoculées et co-inoculées avec les souches indigènes sera étudiée par metabarcoding. Après sélection des couples symbiotiques performants, ces derniers seront testés en association avec des champignons mycorhiziens arbusculaires afin d'évaluer l'effet synergique en station puis en milieu paysan. Cette approche intégrée vise à confirmer, en conditions réelles, le potentiel agronomique des souches identifiées en prenant en compte formulation de l'inoculum et élaboration d'un protocole d'application sur des variétés d'intérêt pour les producteurs et adaptées à leurs zones de cultures. En définitif, cette thèse vise à contribuer à la promotion d'une fertilisation biologique durable et adaptée aux contextes locaux.

P9 **Mairame SY**

Microbiodiversité symbiotique efficiente pour le développement des cultures dans différentes Zones Agroécologiques du Sénégal

L’agriculture sénégalaise, majoritairement familiale, constitue un pilier essentiel de la sécurité alimentaire nationale. Cependant, elle demeure confrontée à de nombreuses contraintes : dégradation des sols, faible fertilité, changements climatiques et dépendance accrue aux engrais chimiques. Ces facteurs limitent la productivité des principales cultures vivrières et maraîchères et aggravent la vulnérabilité des petits exploitants. Face à ces défis, la valorisation de la microbiodiversité symbiotique, en particulier celle des champignons mycorhiziens arbusculaires (CMA), offre une alternative écologique et durable pour renforcer la résilience et la durabilité des systèmes agricoles.
Cette thèse vise à évaluer et valoriser la diversité des CMA dans trois zones agroécologiques représentatives du Sénégal (Bassin arachidier Sud, Bassin arachidier Nord et zone des Niayes) et à développer des inocula locaux efficaces pour cinq cultures d’intérêt socio-économique majeur : l’arachide, le niébé, le mil, l’oignon et la tomate.
La démarche méthodologique repose sur quatre grandes étapes. D’abord, une caractérisation morphologique et moléculaire des CMA isolés des sols et racines collectés dans les zones étudiées permet d’établir un inventaire de la microbiodiversité symbiotique. Ensuite, des expérimentations en conditions semi-contrôlées sont conduites afin d’évaluer la réponse des différentes variétés de cultures à l’inoculation de CMA, en analysant les paramètres de croissance, de nutrition minérale et de mycorhization. Les souches les plus performantes sont ensuite multipliées et formulées en inocula adaptés, avant d’être testées en conditions réelles de culture dans les exploitations paysannes. Des analyses statistiques multifactorielles permettent enfin de comparer les performances des différentes symbioses selon les zones et les espèces cultivées.
Les résultats attendus concernent la caractérisation de la diversité mycorhizienne locale, la sélection de souches indigènes performantes, et la formulation d’inocula microbiens adaptés aux conditions sénégalaises. Leur utilisation devrait améliorer significativement la croissance et le rendement des cultures, réduire la dépendance aux engrais chimiques, et renforcer la résilience des systèmes agricoles face aux stress climatiques.
Ce travail contribuera à la transition agroécologique du Sénégal en promouvant une agriculture durable fondée sur la valorisation de la biodiversité microbienne locale. Il ouvrira également des perspectives pour l’intégration de ces biotechnologies symbiotiques dans les politiques agricoles et les programmes de développement rural, tout en participant à la préservation des écosystèmes et de la sécurité alimentaire nationale.
Mots-clés : Microbiodiversité symbiotique, champignons mycorhiziens arbusculaires, inocula, agroécologie, fertilité des sols, Sénégal."

P10 **Abdoulaye Fofana FALL**

Effect of Guiera senegalensis and Fertilization Practices on Pearl Millet and Groundnut Productivity and Mycorrhizal Functioning in the Sahel

Declining soil fertility and irregular rainfall limit crop productivity in the Sahel. This study investigated the combined effects of Guiera senegalensis shrub proximity and fertilization practices on the productivity and mycorrhizal functioning of pearl millet (Pennisetum glaucum) and groundnut (Arachis hypogaea). Field experiments were conducted using six distances from Guiera (0, 1, 2, 3, 4, and 5 m) and five fertilization treatments: control (no input), horse manure (5 t/ha), mineral fertilizer (MF), 50% MF + 50% manure (MF50+M50), and Guiera litter (5 t/ha). For groundnut, fertilization significantly increased both fodder and grain yields, with horse manure (484 kg/ha) and mineral fertilizer (469 kg/ha) outperforming the control (380 kg/ha). For millet, the combined MF50+M50 treatment produced the highest grain yield (805 kg/ha), an 81% increase compared to control, and yield was highest directly beneath Guiera senegalensis canopies. Mycorrhizal assessments revealed complex interactions: while Guiera presence enhanced soil mycorrhizal infectivity; particularly in groundnut plots; it reduced root colonization rates in both millet and groundnut. This suggests potential competition or modulation effects between shrub and crop root symbioses. Overall, integrating Guiera senegalensis with balanced organic–mineral fertilization improved crop yields and enhanced soil microbial potential, offering a promising pathway for resilient and microbiome-friendly agroecosystems in the Sahel.

P11 **Théo PERCHE**

Integrated Study of Tripartite Interactions Between Plant-Bacillus-Xanthomonas Under Environmental Stress

Théo Perche, Bethel D. Tadesse, Mayuri Sadoine

Understanding how plants and microorganisms adapt to environmental stresses is central to improving crop resilience. Calcium (Ca^{2+}) signaling is a major regulatory mechanism in both plants and bacteria, controlling processes such as plant stress responses, bacterial motility and biofilm formation. However, the molecular details of Ca^{2+} signaling in plant-microbe interactions remain poorly understood.

The PhD project aims to investigate Ca^{2+} signaling as a cross-kingdom communication pathway within a tripartite system involving the plant Arabidopsis thaliana, the beneficial bacterium Bacillus subtilis, and the pathogenic bacterium Xanthomonas campestris pv. campestris. The objective is to elucidate how Ca^{2+} dynamics influence bacterial behavior and plant responses under abiotic stresses such as drought, salinity, and temperature fluctuations.

Using genetically encoded fluorescent biosensors combined with microfluidics and advanced microscopy, we will monitor real-time Ca^{2+} fluctuations, reactive oxygen species production, and nutrient signaling at the plant–microbe interface. Transcriptomic analyses and genome editing tools will identify and validate key genes involved in Ca^{2+}-dependent signaling, bacterial motility, and biofilm development.

This integrative approach will generate novel insights into Ca^{2+} signaling in the context of plant-microbe interactions both beneficial and pathogenic, ultimately contributing to the development of sustainable biocontrol strategies to enhance plant resistance against Xanthomonas infections.

Participants

NOM	Prénom	Research Unit	Institute	City	Country
ALBAR	Laurence	PHIM	IRD	Montpellier	FR
ARROYO VELEZ	Noe	IRHS	IRHS-INRAE	Beaucouzé	FR
AUDRAN	Corinne	LIPME	INRAE	Castanet-Tolosan	FR
BABALOLA	Olubukola	FSS	North-West U	Mmabatho	ZA
BALLINI	Elsa	PHIM	Institut Agro M	Montpellier	FR
BALS	Julie	LIPME	INRAE	Castanet Tolosan	FR
BARBIER	Michel	PHIM	IRD	Montpellier	FR
BARRO	Mariam	INERA	Centre U Manga	Koudougou	BF
BENEZECH	Claire	PHIM	PHIM	Montferrier	FR
BERNAL	Adriana	LIMMA	U de los Andes	Bogota	CO
BLASCO	Camille	PHIM	IRD	Montpellier	FR
BOULANGER	Alice	LIPME	INRAE	Castanet-Tolosan	FR
BROTTIER	Laurent	PHIM	IRD	Montpellier	FR
CHAMPION	Antony	DIADE	IRD	Montpellier	FR
CHARLEUX	Brice	PHIM	IRD	Montpellier	FR
CHEN	Nicolas	IRHS	Institut Agro	Angers Cedex 01	FR
CORTES CALDERON	Santiago	LIMMA	U de los Andes	Bogotá D.C.	CO
DELAFOSSE	Sarah	PHIM	IRD	Montpellier	FR
DIAZ PINO	Cristian	PHIM	IRD / U Colombia	Montpellier	FR
DOMINGUEZ MIRAZO	Marian	XPLAIN	PHIM	Montpellier	FR
FOUNOUNE	Hassna	LNRPV/ISRA	ISRA	Dakar	SN
GAGNEVIN	Lionel	PHIM	CIRAD	Montpellier	FR
GORGUES	Lucille	PHIM	IRD	Pezenas	FR
GRENIER	Solene	LIPME	INRAE	Castanet-Tolosan	FR
HASHIM MOHAMEDI	Ibrahim	TARI	TARI	Morogoro	TZ
HEBRARD	Eugenie	PHIM	IRD	Montpellier	FR
HERNANDEZ ALCANTARA	Natalia	LIMMA	U de Los Andes	Bogotá	CO
HOCHER	Valérie	PHIM	IRD	Montpellier	FR
HUTIN	Mathilde	PHIM	IRD	Montpellier	FR
ISSAKA	Souley	UP/DPDC	UBBT	Tillabéri -Niger	NE
JOBERT	Léa	PHIM	IRD	Montpellier	FR
KACZMAREK	Thomas	PHIM	IRD	Montpellier	FR
KLONOWSKA	Agnieszka	PHIM	IRD	Montpellier	FR
LASSOIS	Ludivine	Plant Sciences	Agro-Bio Tech	Gembloux	BE
LEACH	Jan	Agric Biol	Colorado State U	Fort Collins	US
LOKO	Laura		UNSTIM	Dassa-Zoumé	BJ
LONGUE SOKPE	Régis	LaSBAD	U Bangui	Bangui	CF
MARTY	Soline	LIPME	INRAE	Castanet Tolosan	FR
MORRISSON	Marie	UMR ABSYS	CIRAD	Montpellier	FR
MUKWA	Lyna		Clinique des Plantes	Kinshasa	RDC
NANOUKON	Chimène	LGBA	UNSTIM	Dassa-Zoumè	BJ
NDOYE	Penda	G.ABT	U de liège	Gembloux	BE
NEEMA	Claire	PHIM	Institut Agro M	Montpellier	FR
NOEL	Laurent	LIPME	CNRS-INRAE	Castanet-Tolosan	FR
OLIVEROS ROJAS	Jorge	LIMMA	U de los Andes	Bogotá D.C.	CO

ONAGA	Geoffrey	GDI	AfricaRice	Bouake	CI
ORTIZ	Diana	ABSys	INRAe	Montpellier	FR
PERCHE	Théo	UMR 5240	INSA Lyon	Villeurbanne	FR
PEREZ QUINTERO	Alvaro	PHIM	IRD	Montpellier	FR
PORTIER	Perrine	IRHS	INRAE	Beaucouzé	FR
QUIBOD	Ian	XPLAIN	IRD	Montpellier	FR
QUINTANA CUEVA	Alexis		PUCE	Valence	EC
RACEDO	Camilo	LIMMA	U de Los Andes	Bogotá	CO
RAVELOSON	Harinjaka	CRR /DP SPAD	FOFIFA	Antsirabe	MG
ROUTABOUL	Jean-Marc	LIPME	INRAE	Castanet-Tolosan	FR
SADOINE	Mayuri	UMR5240	INSA Lyon	Villeurbanne	FR
SARR	Mame		ISRA	Bambey	SN
SY	Mairame	ULB	ULB	Bruxelles	BE
SZUREK	Boris	PHIM	IRD	Montpellier	FR
TADESSE	Bethel	SPMIR	INSA Lyon	Villeurbanne	FR
TALL	Hamidou	ISRA	ISRA	Tambacounda	SN
TOFFA	Joelle	ZASVE	ENSBBA-UNSTIM	Dassa-zoumé	BJ
TOLLENAERE	Charlotte	PHIM	IRD	MONTPELLIER	FR
TORRES-BARCELO	Clara	PHIM	INRAE	Montpellier	FR
ZAMORA-LEDEZMA	Ezequiel	FAGROCLIM	UTM	Portoviejo	EC
ZARATE	Carlos	LIPME	INRAE	Castanet-Tolosan	FR
ZINGA	Innocent		LaSBAD	Bangui	CF
ZONGO	Elisabeth		INERA/CNRST	Ouagadougou	BF