



HIGH-LEVEL SCIENTIFIC SEMINAR: THE GEMINIVIRUS CHRONICLE AND 10 YEARS OF RICE PAN-GENOMICS RESEARCH

In line with its commitment to promoting scientific excellence and fostering knowledge sharing for food security, WAVE organised a scientific seminar on **24 April 2026**. The seminar brought together two renowned researchers to discuss key issues in plant health and genomics. Held at the **Scientific and Innovation Hub of Bingerville**, this hybrid event enabled the scientific community to explore the diversity, evolution and emergence of vector-borne phytoviruses, as well as pangenomics in rice.

Theme 1: Diversity, Evolution and Emergence of Vector-Borne phytoviruses: The Chronicle of Geminiviruses'

Professor Jean-Michel LETT, plant virologist at CIRAD

During his presentation, Professor Lett emphasised the ecological and molecular mechanisms that facilitate the emergence of phytoviruses, particularly geminiviruses, which are transmitted by insect vectors and are responsible for numerous diseases that affect tropical crops.

Based on his research into several viral complexes, Professor Lett demonstrated that the **emergence** of these diseases is closely associated with **biological invasions** and the **transcontinental spread** of **invasive viral strains**, as well as changes in vector populations.



Analysing the dynamics of viral dispersal has enabled the reconstruction of certain strains' migration routes and the identification of the main global dissemination areas. Professor Lett emphasised that *« the Mediterranean basin is the main area of dissemination of TYLCV variants and strains circulating worldwide, while the Middle East is probably the centre of TYLCV diversification »*, highlighting the importance of geographical circulation in the evolution of plant epidemics.

These results demonstrate that the emergence of viral plant diseases is the result of complex interactions between the virus, its vector, and the environments through which it travels. This confirms that **biological invasions play a decisive role in the spread of emerging diseases**.

Professor Lett also presented research into host changes through studying the **maize streak model**, which allows the dynamics of competition between different viral strains within agroecosystems to be analysed. Experimental results showed that some strains exhibited faster **viral accumulation** associated with greater vector transmission efficiency, thus conferring a major epidemiological advantage.

The data presented revealed that a viral strain can reach **86% transmission** efficiency compared to **60% for a competing strain**, illustrating how certain variants gradually gain the upper hand in natural populations.

However, the presentation also demonstrated that less competitive strains can sustain themselves within ecosystems thanks to specific biological mechanisms. This highlights the complexity of the epidemiological balances observed in the field.

Professor Lett emphasised that to **anticipate** the dynamics of emergence and **strengthen phytosanitary** surveillance systems, it is essential to understand the **biological traits of viruses**, their capacity for accumulation, their transmissibility and their adaptation to hosts.

This presentation thus sheds valuable light on the factors underlying the evolution of plant viruses, as well as on the scientific levers necessary to better prevent health risks to food and strategic crops.



Theme 2: Over 10 years of pan-genomics in rice: where have we come from, and where are we going?

Professor François SABOT, Director of Research at IRD



Through a synthesis of the advances made over the last twelve years, Professor Sabot reviewed the rise of pangenomics in rice, made possible by the reduction in sequencing costs and methodological advances in genomic analysis.

His presentation reminded us that pangenomics aims to explore all the genetic variations existing between individuals of the same species, beyond simple point mutations, in order to better understand the genetic determinants of certain agronomic traits.

"The diversity of one individual compared to another is much greater than we think, many genes do not exist in some individuals compared to others."

Through concrete examples, he showed that certain genetic variations specific to certain individuals can play a decisive role in traits such as tolerance to submersion, thus opening up important prospects for rice varietal improvement.

The presentation also insisted on the fact that a single reference genome is no longer sufficient to understand the biological complexity of a species, and that the study of multiple individuals becomes essential to better understand phenotypes of agronomic interest.

"In fact, to fully understand the evolution and diversity of a species, whether it's a virus, whether it's a plant, whether it's a man, you have to have a representation of all this variation. And for that, sequencing is the best way to obtain this information."

Finally, the methodological perspectives discussed have made it possible to glimpse the next steps in plant pangenomics, with approaches integrating more massive data and advanced mathematical tools.

A scientific space dedicated to sharing knowledge and building skills.

Through this seminar, WAVE has further reinforced its commitment to fostering environments conducive to high-level scientific dialogue and the exchange of knowledge and expertise on critical agricultural issues.

The discussions emphasised the importance of strengthening interdisciplinary research on plant diseases and genetic diversity in order to develop sustainable responses to health and food-related challenges in Africa.

By convening researchers, partners, and stakeholders from the agricultural sector to address these pressing issues, WAVE remains dedicated to promoting collaborative scientific research to enhance agricultural resilience and ensure food security.



Interactions with participants



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