

BAXEPI

Unravelling the emergence of the Banana Xanthomonas Wilt through a novel approach

ABSTRACT

The Banana Xanthomonas Wilt (BXW), caused by *Xanthomonas vasicola* pv. *musacearum* (Xvm), has devastated the banana plantations all over the Great Lakes region from 2001, causing very negative social impacts and biodiversity loss within the *Musa* germplasm.

Year : 2016

Project number : 1605-025

Type of funding : AAP

Project type : AAP OS

Research units in the network : BGPI-PHIM PVBMT

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Flagship project : no

Project leader : Emmanuel Wicker

Project leader's institution : CIRAD

Project leader's RU : IPME-PHIM

Budget allocated : 20000 €

Total budget allocated (including co-financing) : 20000 €

Funding : Labex

GOAL

This project, involving an international research consortium, aims at gathering the basic data for unravelling the evolutionary mechanisms of BXW emergence. We thus assembled reliable collections, and developed new genotyping tools. We then addressed the host jump from enset to banana in Ethiopia, and reconstructed the BXW invasion routes.

ACTION

Sampling the Xvm diversity in contrasted agrosystems

Developing and assessing genotyping tools

Analyzing the emergence

RESULTS

A big international Xvm collection was assembled

Xvm populations were sampled in the « enset belt » of Ethiopia, the presumptive area of origin, on enset, banana, maize and *tripsacum* sp, in various cropping systems.

Xvm populations were also sampled from banana crops from Eastern and Central African countries: DRC, Kenya, Rwanda, Tanzania, Uganda.

We developed a Multi-Locus VNTR Analysis (MLVA) scheme, MLVA-19, specific to Xvm, and whose

discriminatory power is adapted to outbreak analysis at geographical scales ranging from the field to the country.

A global map of the Xvm lineages (DAPC clusters) was built up, revealing unexpected pathogen diversity, notably in Ethiopia and Uganda

The center of Xvm diversity is Ethiopia, and the emergence spread from this country to Uganda, for further invade the Great Lakes region.

Two Xvm core-collections (BANCOLL, ENSCOLL) were proposed to banana and enset geneticists and breeders working on host resistance

Key isolates to be sequenced were identified and listed.

PERSPECTIVES

Transnational network for surveillance of banana wilt pathogens

Population genomics of host adaptation of *X. vasicola*