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

OBJECTIFS

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.

ACTIONS

Sampling the Xvm diversity in contrasted agrosystems
Developing and assessing genotyping tools
 Analyzing the emergence

RESULTATS

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

Responsable :

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