

BforBB

Endogenous virus markers and plant genome NGS sequencing to address Musa biodiversity and enhance genetic resources for breeders

ABSTRACT

Sweet and starchy bananas are among the major food crops providing staple food and livelihoods for millions of small farmers across the tropics and subtropics in Africa, Asia, America and Oceania. However a large part of the global production relies on a limited number of edible cultivars clonally propagated, with a narrow genetic diversity as a consequence. The major gap to be addressed is to provide locally well adapted varieties to supply the increasing food demand and to reduce yield losses due partly to pest, diseases and viruses

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Flagship project : no

Project leader : Marie-Line Caruana

Project leader's institution : CIRAD

Project leader's RU : BGPI-PHIM

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Total budget allocated (including co-financing) : 110000 €

Funding : Labex

GOAL

A better knowledge of the Musa genetic diversity is essential to feed breeding programs. Nowadays, the banana diversity available for breeding programs shows an underrepresentation of some Musa sub-groups such as those of *M. balbisiana* genomes (B) where no more than twenty *M. balbisiana* diploids are available in collections, displaying moreover a narrow genetic diversity. In addition all the *M. balbisiana* resources naturally harbour banana streak virus sequences (eBSV) integrated within their genome. Some eBSV are able to spontaneously release active viruses leading to systemic infections. Then an in depth eBSV characterization of *M. balbisiana* resources is required especially since Duroy et al. (2016) established that eBSV can be used as phylogenetic markers to decipher the structure of *M. balbisiana* diversity.

The main objective of the proposal is to strengthen the Musa genetic diversity by characterising both the Musa and eBSV diversity among a large banana sampling of wild relatives and local landraces coming from mainland south East Asia.

ACTION

In this proposal, expeditions are planed with collaborators in Vietnam, Laos, Cambodia, Thailand and South China, to collect wild forms and also local landraces accordingly to national and international

regulations. We also propose to use herbarium specimens for relevant specimens in order to widen the sampling. Existing and newly collected samples as well as ancient herbarium specimens will serve as candidates to be genetically characterised for Musa as well as for eBSV.

Identification of new alleles for either known or never described eBSV, will contribute to refine the virus integration process in the geographical area where these integrations probably occurred.

RESULTS

The project will strengthen the knowledge on the diversity of wild relatives and local landraces with a main focus on the under characterized ancestral compartment from mainland South East Asia. Their lineage with modern cultivars will be inferred through their position in the global Musa phylogeny. In this way the uncommon use of eBSV as a phylogenetic marker will be relevant to assign the B genomes and clarify their diversity and the structure of the species.

This project will also promote scientific research on plant biodiversity in Asian countries and will contribute to the sustainable management and conservation of plant biodiversity in those countries.

PERSPECTIVES

As a long-term finalized output, this project should help to obtain genetic material containing B genome without any risk of eBSV awakening coupled with valuable agronomic adaptive traits to climate changes and disease/pest resistance.

This proposal will definitively contribute to the sustainable management and conservation of plant biodiversity in Asian countries where collections (cultivated stocks and ex situ Musa collections) will be carried out and will also promote scientific research on plant biodiversity in these countries.