SafePGR

TOWARDS SAFER PLANT GENETIC RESOURCES THROUGH IMPROVED VIRAL DIAGNOSTIC

Objectives

Plant Biological Resources Centers (BRCs) provide final users (farmers, extension officers) with genetic resources best suited to their needs. They also provide breeding programs with genitors that are critical for the development of crops adapted to environmental and societal changes. Their capacity to guarantee the sanitary status of the resources they conserve and distribute is essential to prevent the spread or emergence of diseases.

The main species conserved and propagated by the plant BRCs of Guadeloupe, Madeira, Azores and Reunion Island are vegetatively propagated and prone to virus accumulation.

Although sanitation methods exist for recovering virus-free plants from infected ones, only a small fraction of plant virus diversity is known and detection tools only exist for a limited number of viruses.

Cultivated biodiversity in Guadeloupe: a female yam genotype at flowering stage (Dioscorea alata)

The general objective of the SafePGR project was to improve the knowledge of the diversity of viruses infecting the crops addressed by the partner's BRCs, in order to develop or optimize diagnostic techniques, ultimately permitting the safe movement of plants between project partners and beyond.

Approaches

Training for metagenomic methods - Intermediate meeting in Cirad Montpellier, October 2013.

Six crops were targeted (banana and plantain, sugarcane, yam, sweet potato, garlic and vanilla) and 7 research groups from Biological Resources Centers and virology labs of France and Portugal were involved in:

i) The analysis of the molecular diversity of the main viral families infecting the 6 targeted crops

ii) The optimization of classical diagnostic methods taking into consideration data generated through the analysis of viral diversity

iii) The development of new diagnostic methods based on metagenomics and deep-sequencing technologies

Stakeholders such as plant protection agencies, diagnostic laboratories and regional councils were associated to the transfer of the results and diagnostic methods generated by the project.

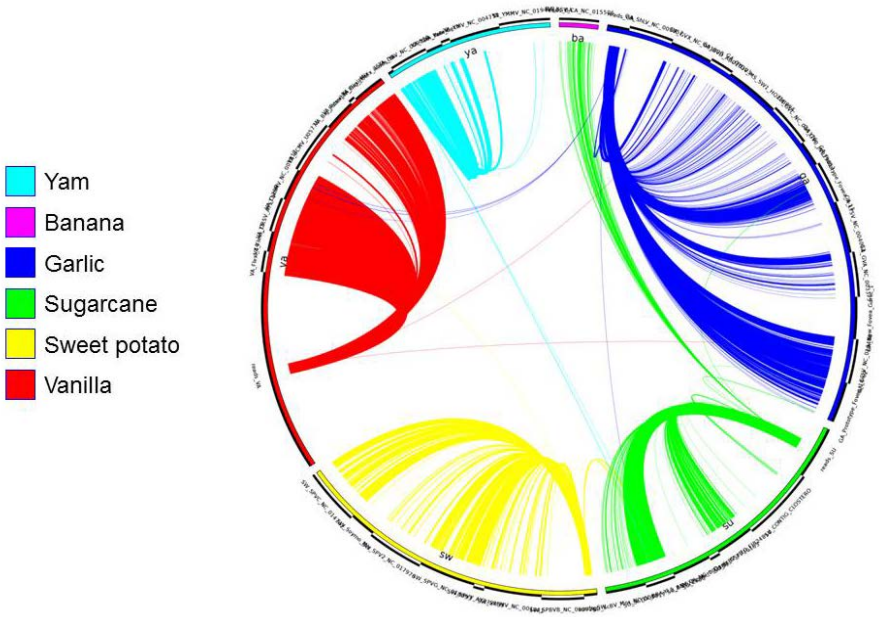
7 partners

INRA (Institut National de la Recherche Agronomique), ASTRO Research Unit - Guadeloupe (Fr) / CIRAD (Centre de Coopération Internationale en Recherche Agronomique pour le Développement), AGAP Research Unit - Guadeloupe (Fr) / CIRAD, BGPI Research Unit (Fr) / CIRAD, PVBMT Research Unit - Reunion Island (Fr) / INRA, BFP Research Unit (Fr) / Biotechnology Centre, University of Azores – Azores (Pt) / University of Madeira, ISOPlexis Gene Bank – Madeira (Pt)

Total budget: 1 444 121 € / Total Grant: 553 227 €

Main outputs

- 21 novel viruses discovered and characterized
- Overall presence of 40 viral species in the 6 plant species targeted by the project
- Complete genome sequences of 8 identified viruses of sugarcane and yam and 16 partial sequences of yam viruses deposited in GenBank
- Adaptation of a pipeline for bioinformatics analyses, which performs automatically the cleaning of the nucleotide sequences generated for each sample, their assembly and the identification of viral sequences among them through comparisons with international sequence databases
- A comprehensive approach was adopted combining bioinformatics, metagenomics and classical molecular methods for the characterization of known and novel virus species
- Viral diagnostic tools for the detection of all the novel viruses discovered throughout the project
- Optimized diagnostic tools for 10 already known viruses
- Safer exchanges of germplasm through improved efficiency of sanitation
- Significant contribution to the development of high throughput sequencing in plant virus diagnostics
- Transfer of sanitation methods to the yam and sugarcane sanitation programs carried out in Guadeloupe and Montpellier, respectively
- The results are now irrigating a project of a quality seed production sector, with economic actors



Outcomes of the analyses of viral nucleotide sequences generated by metagenomics approaches using next generation sequencing (NGS).

- Young researchers & capacity building: 3 MSc trained, 3 temporary staff now have permanent positions
- Web : http://www2.antilles.inra.fr/safepgr/