Ad hoc support

Tracing the evolution of pathogens and their virulence determinants through ancient herbarium samples

ABSTRACT

It is now possible to access the DNA of older isolates of a pathogen by screening samples of its host plant available in herbarium collections. Such data will provide information on the "ancient" genetic diversity of phytoviruses and phytobacteria involved in current diseases and will allow us to jointly estimate their mutation rates and date the divergence events of the major pathogens isolated today.

The identification and extraction of such "fossil" viral and bacterial sequences appear to be essential to better estimate the origin of contemporary phytopathogenic agents and to better understand their evolution over the past thousands or tens of thousands of years.

The plants treated will be citrus and cassava.

Year : 2016
Project number : 1600-014
Type of funding : SP
Project type : PC
Research units in the network : BGPI-PHIM PVBMT
Start date : 2016-03-01
End date : 2017-02-28
Flagship project : no

Project leader : Boris Szurek
Project leader's institution : IRD
Project leader's RU : IPME-PHIM

Budget allocated : 14580 €
Total budget allocated (including co-financing) : 14580 €
Funding : Labex

GOAL

This initiative aims to carry out the relational (creation of a consortium) and methodological exploratory phase of a future project to be submitted in 2017 to international funding calls (CRP-RTB, CEE...). The main objective of this project will be to identify nucleic acids of ancient pathogens from herbarium samples and to use them to reconstruct the evolutionary history of these pathogens (viruses and bacteria).