

SafePGR
Videonference report 18/02/2014

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WP Management

28-30 May 2014 : joint events in Gran Canaria Island

- International Conference “Boosting sustainable development from high biodiversity”. The objective is to present and refine the 4 challenges in conciliating conservation and sustainable management of tropical and subtropical biodiversity in OR and OCT’s.
- Mid-term conference of NetBiome’s 2010 Call for projects. The objective is to present the intermediate reports of the on-going research projects
- NetBiome-CSA Workgroups 1st workshop. The objective is to draft challenge outline and decide work programme.

The coordinators of NetBiome projects are invited to attend these events. NetBiome-CSA is a new project whose objective is to mobilize stakeholders, their knowledge and resources for initiative such as policy and priority analysis, multi-stakeholders dialogues, exchange of good practices, training and issuing of recommendations.

Two questions were discussed during the videoconference:

- Who will represent SafePGR at the meeting ? It is agreed that the project will be represented by either C. Pavis or one of the workpackage coordinators depending on availability and discussion topics of the working groups.
- What are our ideas concerning the new NetBiome-CSA project? Potential topics for a follow up project were discussed thoroughly during SafePGR’s intermediate meeting last October. It is now important to see if some of them could fit in a future call for project, however it is less than sure that there will be another call for projects. The factsheet of NetBiome CSA is available on the project’s website.

Human resources

- Lydiane Bonheur's contract is extended until 31/08/2014.
- Charlotte Julian's contract is extended until 30/04/2014, then Charlotte will work again on the project for the whole of July 2014.

Equipment

Deep freezer is now fully operational !

Financial resources

Madeira is now ready to reimburse Montpellier for travel costs to Montpellier (coordination meeting, October 2013).

WP 1

Analysis of the diversity of the generated sequences

Guadeloupe

- **Sugarcane and banana badnaviruses** : sequence analysis does not highlight any new species or additional diversity to known viral species (SCBV, BSV)
- **Sugarcane ampeloviruses**: 84/165 samples are infected. Direct sequencing performed on 5 PCR products shows a low level of diversity (2%). This might result from primers used being too specific. It is agreed that (i) no more testing or sequencing should be performed with these primers, (ii) Bordeaux will design a new primer pair taking into account available information from ESTs and deep seq on the variability of the virus and (iii) this new primer pair will be evaluated in Guadeloupe to see if it has broader polyvalence and detects more isolates/infections.
- **Sweet potato**:
 - 4 begomovirus sequences homologous to sequences available from databases
 - All tentative rhabdovirus sequences are plant sequence contaminations
- **Yam**:
 - **Macluraviruses**: sequences generated for 14/16 infected samples. S. Winter's antiserum was tested in ELISA on Guadeloupe's infected samples but no sample came positive. A proper positive control and new batch of antiserum will be provided by S. Winter and another attempt will be made before drawing any conclusion.
 - **Closteroviruses**: direct sequencing tested for 7 out of 47 infected samples gave good results. The rest of the samples will be analyzed by direct sequencing. Denis analyzed the sequences. They show a good level of diversity (up to 10%).
 - **Potyvirus**es : Sequences generated for 16 / 95 infected samples. All sequences match essentially with YMV. It is agreed that there is no point generating more sequences.
 - **Potexvirus**es : sequences were generated from all infected plants. Analyses show that they belong to 2 distinct species
 - **Secovirus**es: 2 primer pairs were designed by Armelle for the detection of RNA1 and RNA2. Overall analyses show a high level of diversity (up to 20%), therefore it is agreed that PCR products should be cloned then sequenced. *Azores*

Azores

- **Banana** : no positive samples for either tobamovirus, badnavirus and potyvirus.
- **Sweet potato** :
 - **Potyvirus**es : 35/42 positive samples using Armelle's primers. Not yet sequenced. Will be done in time.

Madeira

- **Banana** : Will proceed with cloning and sequencing when indexings are completed.
- **Sweet potato** :
 - Potyviruses : PCR products to be sequenced
 - Betaflexiviridae: sequences display 80% homology to SPCFV

WP2

- For the dsRNA metagenomics approach, [plant samples collected by partners have to be processed onsite using the dsRNA CF11 purification method](#), as agreed during the coordination meeting. [Partners will generate cDNAs from dsRNAs and send them to Montpellier no later than end of June.](#)
- Guadeloupe's share is very high (740 samples in total) and available human resources do not allow for all samples to be processed on time. It is agreed that [Guadeloupe's target is to provide at least 150 cDNA](#) for each the following crops : banana, sugarcane and yam. Other partners will be able to provide cDNAs according plans.
- Azores is not sure of the quality of the extractions, have problems with the CMV control. Has to improve the extraction.
- For the viral particles approach, plant samples are being processed in Montpellier. Almost all plant samples have been already provided by partners.

WP3

- The pipeline is ready. Efforts have been made to allow easy visualization of the annotation results and comparison of viral sequences.
- Marie is interested to play with the data, and will be trained by Sébastien or Sandy.

Publication of the results

- New Mastrevirus in sugarcane. Submitted by Montpellier to PLoSOne.
- New Potexvirus in vanilla. Writing of the paper scheduled by Michel in 2014.
- New Macluraviruses in Yam. Data to be shared with S. Winter for a co-publication. Planning?
- New Secoviruses in yam: Bordeaux to complete partial sequencing of RNA1 and 2 and Guadeloupe to complete diagnostics. Pierre-Yves puts together a first draft of the paper when all these are complete and circulated it. Plan to submit during first semester 2014.
- New Potexviruses in yam. Bordeaux to complete genome sequence by 5'RACE. Available data include diagnostic method, prevalence study and diversity. Once genome sequence is complete, Pierre-Yves starts putting together a first draft of the paper and circulates it. Plan to submit during first semester 2014.
- Insert viral status of the CRBs accessions in OLGA catalogue.

Until now, we plan to write separate papers on diagnostics and virus characterization. Later on if data are OK, we may envisage a more comprehensive paper on overall comparison of diagnostic methods (comparison of classical techniques and deep sequencing in vanilla e.g.).

Concerning the papers on virus characterization, we have to review regularly the advances on each new virus species. A feedback is necessary, in order to decide if we continue or not the molecular characterization on the different new viruses. [Pierre-Yves to review progress on a regular basis.](#)

Next videoconference planned between 15 and 25 June 2014 ([Claudie to organize a Doodle](#))

- Feed-back of the Canaria meeting
- 6 months extension of the project
- Final meeting scheduled in Guadeloupe in March 2015