



Progress MAS for SPVD resistance

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SPVD resistance breeding - General

Still no progress in breeding populations (major problem, we don't deliver as promised), but major progress on the marker front!!!

This target is divided now in 4 components:

- (i) identification of marker associations and marker validation,**
- (ii) pre-breeding with germplasm resources exhibiting confirmed SPVD resistance, but exhibiting poorly in agronomical performance,*
- (iii) search for less SPVD susceptibility in advanced breeding lines and varieties with good agronomical performance,*
- (iv) HEBS – more inbreeding in two pools and offspring testing (not at HQ - Namulonge)*

4. SPVD resistance breeding / Populations & Nextgen Markers

Population VJ08 and off springs for marker association - 2 groups of clones (resistant / susceptible) each with 12 clones AFLP, SSR

Population VZ08 for marker validation – for observed marker associations and new marker associations - Inoculum plants for SPVD has been completed. The 500 clones of VZ08 are phenotyped in 2016 for SPCSV and SPFMV. The capacity to phenotype SPCSV and SPFMV resistance (500 clones per year) is a bottleneck at CIP – the new ELISA reader will help.

New marker validation (nextgen markers)

RTB cross cutting - two small groups of clones (resistant / susceptible) to Andrzej Kilian from Diversity arrays Technology / Australia and to University of Canberra. The number of markers for silicoDArT were 48,682. We have in our 2 x 12 bulks (resistance versus susceptible) in total 29,133 DArT markers. After using the call rate as a first step to find clean DArT markers about 18,600 DArT markers are remaining -> we will use now the TASSEL program for association 2 groups and 12 clones in each group (all tracing back to population VJ08)

4. Marker & SPVD resistance

Marker progress for SPVD resistance analysis through SASHA (AFLP and SSR markers) and RTB cross cutting with logistic form GT4SP (fast throughput silicoDArT markers)

Two small sets of VJ08 clones were formed (a **resistant set and susceptible set of clones, each comprising 12 clones**)

- (i) AFLP marker associations with SPCSV (E44M34.533, E33M48.460, E36M34.400, E33M48.343, and E39M32.440, band absent in the resistant bulk and present in the susceptible bulk; E39M34.156, band was present in the resistant bulk and absent in the susceptible bulk,
- (ii) SSR markers associated with susceptibility to SPCSV (IBS204-172, IBS169-162, Ib-286-125, IbJ559-262, IbJ559-269, IbJ116a-229, and IBS149-225).
- (iii) DArT marker associations with SPCSV 758044, 7563062, 7572542, 753123, and 7574925.

4. SPVD resistance breeding IV

Very important is that we have the right test population(s) in place after we have validated old and the larger number of new next-gen markers with the VZ08

The right populations are in Africa! And for this I suggest the current large hybrid population Robert is developed and which should be put into field evaluations without pre-selection for SPVD in multiplication!!! -> we see all roads are connected (all breeding methods are connected), because:

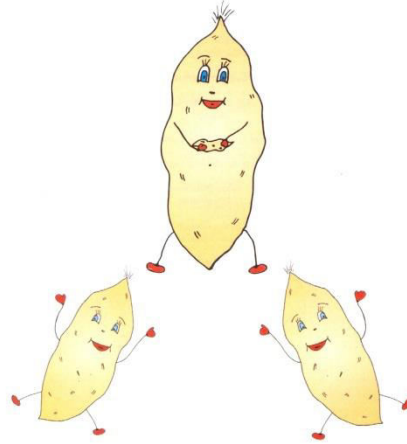
This new hybrid population from genepool A and B in Uganda will allow us to select the best family makes (parents) with respect to yield and SPVD resistance as well as to validate MAS for virus resistance in sweetpotato in an applied breeding program => with this we can enter into MAS for SPVD in sweetpotato breeding testing >10,000 clones in early breeding stages (it will be simply a cost question for a bunch of DArT markers and perhaps very few or no remaining old AFLP and SSR markers

4. MAS & SPVD resistance

Next steps:

Validation of markers with population VZ08 – this population is related to VJ08 (same male parent) – mid of 2017 – about 500 clones

Testing markers in applied breeding material at Namulonge – the best would be the current AxB crosses on large scale – intention to select among parents in A and B genepool on basis of the offspring performance AxB (yield and SPVD) – additionally now comparing predicted and observed response to SPVD resistance by using markers in applied breeding material – about 10,000 clones



Thank-you for your Attention