Sweetpotato Speedbreeders

Progress towards the holy grain of a virus resistant sweetpotato

INTRODUCTION

Sweetpotato is grown for food and feed and is increasingly becoming an important cash crop for many farmers in sub-Saharan Africa. Sweetpotato virus disease (SPVD) is, however, one of the major bottlenecks in the expanded use of sweetpotato because it is devastating and can cause 50 to 90% yield loss in susceptible cultivars. Available methods do not adequately control SPVD. There is a need for farmers to have cultivars with desirable traits and durable resistance to SPVD. Development of SPVD resistance is under way in Uganda, led by CIP.

Fig 1. Sweetpotato virus disease (SPVD) - middle, *Sweet potato chlorotic stunt virus* (SPCSV) and *Sweet potato feathery mottle virus* (SPFMV) - infected plants; whiteflies (left) and aphids (right) are the vectors.

METHODS

Several steps have been involved in developing resistance to SPVD: 1) Developed reliable methods to detect the different known viruses (symptomatology, serology, indicator plants, real time polymerase chain reaction) 2) Developed a reliable method to discriminating between SPVD tolerant and resistant genotypes. 3) Prioritized the most important viruses to breed for. 4) Identified different sources of SPVD resistance 5) Developing an efficient breeding scheme to increase the SPVD resistance is underway.

Fig 2. Two sweetpotato crossing blocks (population Uganda A, population Uganda B) at Namulonge, Uganda

RESULTS

Reliable methods have been developed to detect SPVD in breeding populations: symptoms (scale 1 to 9; 1 = no symptoms; 9 = most severe symptoms), serology for confirmation where needed and real (quantitative) time PCR for discriminating between clones tolerant and resistant to SPVD (Table 1, Fig. 2). Emphasis is placed on developing resistance to SPFMV and SPCSV, the combination of which leads to SPVD. Breeding populations from two crossing blocks (population Uganda A, and population Uganda B, Fig. 2) generated at Namulonge, and introduced populations exhibited a wide range resistance, but skewed towards the susceptible category (SPVD score above 3.5) with very few genotypes in the highly resistant category (SPVD score 3.0 and below).

KEY TABLES OF RESULTS

Table 1. Identification of high yielding resistant sweetpotato clones at Namulonge, Uganda (SPVD = sweetpotato virus disease; SPFMV = Sweet potato feathery mottle virus; SPCSV = Sweet potato chlorotic stunt virus; ΔCt = difference in real time real time PCR threshold cycle/relates to virus titer); LSD = least significant difference; CV =coefficient of variation).

Access. code	Root yield (t/ha)	[1]SPVD (3 seasons)	Mean scores (3 reps, 1 season) SPVD	Alternaria		SPFMV [2](1/ΔCt)	SPCSV (1/ΔCt)
4.3	5.1	5.3	2.3	3.0		0.556	1.011
12.22	6.6	6.0	3.7	3.0		0.19	0.11
17.3	6.1	3.0	2.0	2.7	Resistant	0.053	0.067
20.8	14.3	4.0	2.3	5.3		0.053	0.053
21.4	16.2	3.3	2.0	2.7	Tolerant	0.144	0.463
23.11	19.9	2.3	2.7	3.7		0.273	0.162
24.7	5.4	2.7	1.0	1.3	Resistant	0.053	0.053
29.3	7.0	5.3	4.0	2.7		0.052	0.349
34.6	9.8	5.0	3.0	2.0		0.178	0.077
NSP11	17.4	2.7	2.3	2.0		0.113	0.064
Mean	10.7	4.1	3.1	2.9	Negative control	0.052	0.062
$LSD_{0.05}$	4.9	2.0	1.8	1.9			
CV (%)	27.3	29.8	35.1	39.6			

NEXT STEPS

Evaluation of introduced SPVD resistant clones and breeding populations generated in Uganda will continue under the high SPVD pressure environment at Namulonge to identify resistant genotypes. Molecular markers (DaRT) evaluated on populations in Peru will be validated on populations in Uganda. Bad parents will be eliminated from the crossing blocks to increase the frequency of genotypes with SPVD in the progeny.

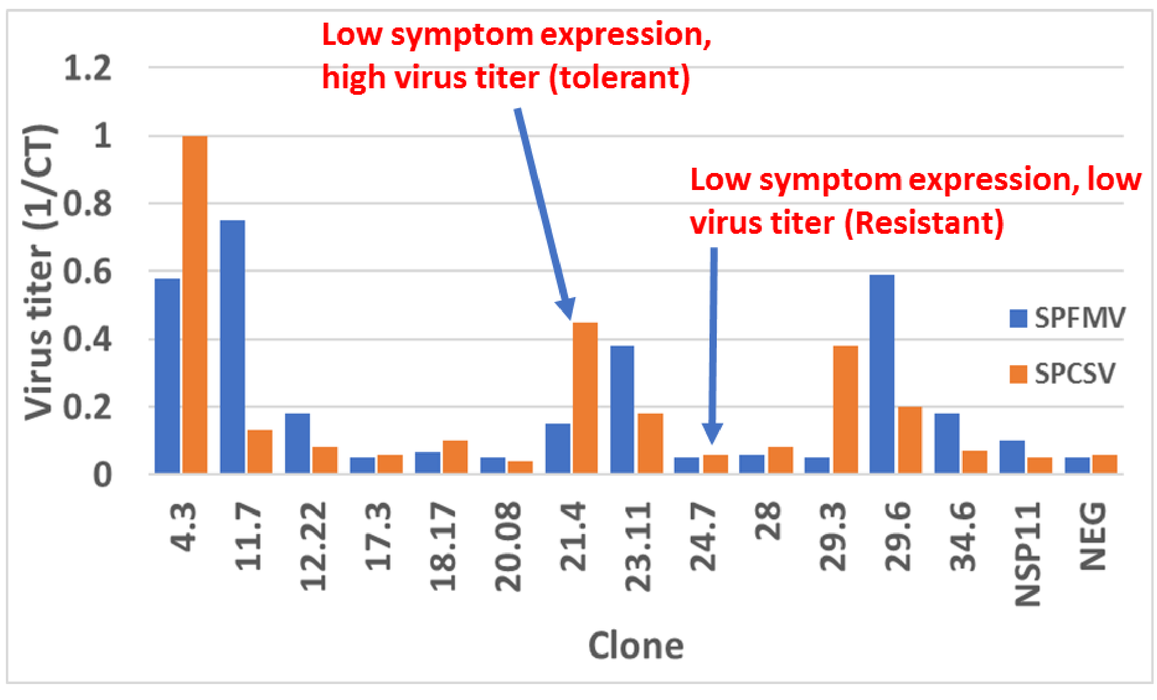

Fig 3. Discrimination of clones (genotypes) tolerant and resistant to viruses (CT = real time PCR threshold cycle; SPFMV (Sweet potato feathery mottle virus); SPCSV = Sweet potato chlorotic stunt virus; NSP11 = NASPOT 11 (virus resistant check clone); NEG = negative control

CONCLUSIONS

Good progress has been made in developing resistance to SPCSV and SPFMV (SPVD). However, developing molecular markers linked to SPVD resistance has been slow because of the complex nature of hexaploid sweetpotato. Routine SPVD screening protocals are working. Eliminating bad parents from crossing blocks is expected to increase the frequency of genotypes among populations generated in crossing schemes in sweetpotato population improvement.

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