

Progress towards breeding for sweetpotato weevil resistance in Uganda



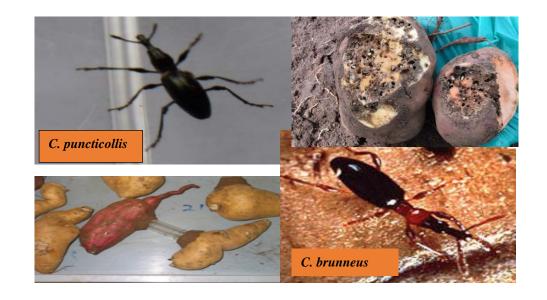
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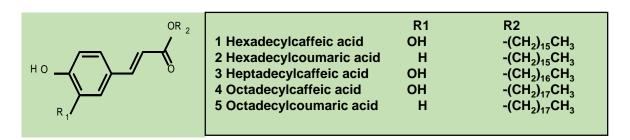


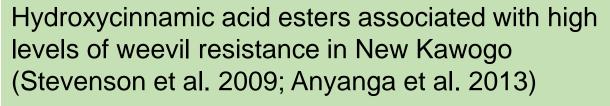
Approaches employed by NaCRRI-NCSU-NRI-CIP

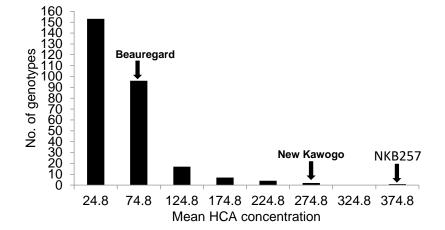


- Exploiting biochemistry and other resistance factors for selection of resistance
- Weevil resistance germplasm development
- Exploiting no choice bioassays for precision selection of resistance
- Long term population improvement for weevil resistance
- Exploiting use of marker assisted breeding

Key Results to date







beveloped this population (201 progerty)
Broad sense heritability (H2=0.49)

Developed NKR population (287 progeny)

Transgressive segregation in the NKB mapping population

Identified 4 SSR associated with field-based SPW resistance

Identified 3 SSR associated with Hydroxycinnamic acid ester-based weevil resistance

Marker	Total variance (%)	Most significant allele	R ²	ProbF
IBSSR03	38.5	IBSSR03B219	0.0525	0.039
IBS62		IBS62B120	0.0654	0.004
lbL16		lbL16NK183	0.0446	0.028
lbL10		IbL10B197	0.0671	0.004
IBS11		IBS11NKB253	0.0510	0.023
IbE5		IbE5B218	0.0580	0.011
lbJ544b		lbJ544bNKB197	0.0460	0.030

Current and future research





- Collected, characterized 208 accessions of putatively weevil resistant germplasm
- Screened germplasm collection for weevil resistance
- Established crossing block for long term population improvement
- Generated 10,000 polycross and 2,000 controlled cross seed
- Conducted no choice bioassay for selection of weevil resistance
- To profile total HCA in the germplasm collection at NRI, UK
- Conduct seedling nursery trials for routine population improvement
- Develop GBS platform for SNP discovery and QTL analysis with NCSU (PEARL & GT4SP projects)
- Initiate genomic selection for weevil resistance (PEARL & GT4SP)

Need to integrate breeding, genomics, microbiology with tested crop management options for sustainable management of SPW in Africa