Breeding sweetpotato for resistance to Alternaria blight in Uganda

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Background

- Alternaria leaf petiole and stem blight (commonly referred to as Alternaria blight) occurs in most of the major sweetpotato growing regions of the world
- It is a minor disease in many parts of the world where sweetpotato is grown
- However, in East Africa, it is a serious production constraint in some areas due to the presence of aggressive *Alternaria* spp.

Background cont'd

- In Uganda, the major *Alternaria* species are *Alternaria bataticola* and *A. alternata*
- *A. bataticola* is the more aggressive species
- Yield losses due to Alternaria blight ranging from 25-54% have been recorded in different parts of the country
- Alternaria blight has been recorded in all regions of the country with the highest incidence and severity in the South-western highland agro-ecological zone and the Lake Victoria Crescent zone is a medium disease pressure zone

Background

- The differences in occurrence and distribution of the disease are attributed to climatic conditions which are favourable for pathogen infection and disease development
- Considerable differences in reaction to the disease among the among genotypes

Symptoms

Management of the Alternaria

- Plant disease free vines
- Rouge all infected plants
- Spraying with a fungicide (may not be economical)
- Plant resistant varieties

- Of the available control options, the most economical is the use of genetically based host plant resistance

- In order to breed for resistance to the disease, is essential to understand the mode of inheritance of resistance
- Thus the need for the study to understand the mode of inheritance of Alternaria blight

Objectives

The study was aimed at:

- Establishing farmer preferred sweetpotato traits, production constraints and Alternaria blight awareness
- Studying the mode of inheritance of Alternaria blight resistance
- determining the stability of selected F_1 genotypes across environments

Farmers awareness and perceptions of Alternaria blight and their preferred sweetpotato traits

Study was carried out in

- Kabale ("hotspot" for Alternaria blight)
- Luwero (medium Alternaria disease pressure)

- Individual household interviews and FGDs
  - 60 farmers per district were interviewed in the household interviews

Farmers preferred sweetpotato attributes

Attribute	Kabale		Luwero	
	% Respondents	Rank	% Respondents	Rank
Sweetness/taste	95.0	1	46.7	3
High yielding	91.7	2	96.7	1
Early maturity	80.0	3	68.3	2
High dry matter (mealy)	25.0	4	18.3	7
Disease resistance	20.0	5	46.7	3
Tolerance to drought	13.3	6	25.0	6
Good in-field root storability	6.7	7	38.3	5
Resistance to weevils	0.0	-	25.0	6
Orange fleshed (Vitamin A)	3.3	-	5.0	-

Production constraints

Constraint	Kabale		Luwero	
	%Respondents	Rank	%Respondents	Rank
Alternaria blight	76.7	1	12.8	6
Soil fertility (low)	45.0	2	6.7	-
Low yielding varieties	40.0	3	1.7	-
Caterpillars (dry season)	38.3	4	76.7	1
SPVD	28.3	5	61.7	2
Planting materials	23.3	6	28.3	5
Drought	15.0	-	61.7	3
Lack of market	6.7	-	11.7	-
Weevils	6.7		58.3	4

Farmer's perceptions of Alternaria blight

- 98.3% of farmers in Kabale knew the disease
- 86.2% of farmers in Luwero knew the disease
- Of those who knew the disease
  - 94.8% of farmers in Kabale & 89.5% in Luwero considered Alternaria a production constraint
- Yield losses due to Alternaria blight ranges from 10 to 100%

Genetic analysis of resistance to Alternaria blight

Methodology

- Parents of known levels of resistance were planted in a crossing block
- Crossing carried out using the NCII mating design
- 16 parents (resistant as females; moderate resistance & susceptible as males)
- due to incompatibility parents were divided into two sets (compatibility groups)
- 20 families from set 1 & 12 families from set 2
- Rapid multiplication technique used to generate enough planting material for replicated trials at 2 locations

Field evaluation of the progeny

- Trails established at 2 sites
  - Kachwekano ZARDI (a “hot spot” for Alternaria blight)
  - Namulonge/NaCRRI
- Row-column design used
- 30 genetically unique siblings per family were selected
- Total of 960 genotypes evaluated
- 5 cuttings per genotype were planted on 1.5m ridges
- 2 replications per site

Field evaluation cont'd

- Inoculation with Alternaria was done at 1 MAP
- Plants scored for Aternaria blight severity starting 3 weeks after inoculation and then at 3-week interval to get 4 data sets
- The Alternaria scores were used to calculate the AUDPC

Data analysis

- Genetic information determined on family mean basis
- Model 1 in SAS version 9.3 was used for analysis with parents as fixed effects & sites as random effects
- ANOVA was performed to provide information about **combining ability** & contribution of the components of the **trt SS to the gene action** underlying Alternaria blight resistance expression

NC II ANOVA MS & SS at Namulonge & Kachwekano Set 1

Source	DF	AUDPC
Site	1	54033.21***
Rep(Site)	2	9333.53***
GCA_f	3	22084.00***
GCA_m	4	16814.72***
SCA	12	4434.22**
Site*GCA_f	3	6717.50***
Site*GCA_m	4	3880.14***
Site*SCA	12	1135.04^{NS}
Error	38	620.70
Treatment SS		186721.50
%SS due to GCA		71.5
%SS due to SCA		28.5

Summary

- Significance of the GCA_f MS indicated that additive genetic variance contributed by the female parents is very important in controlling expression of Alternaria resistance
- Significance of GCA_m MS indicated that the male parents contributed significant additive genetic effects to the expression of Alternaria blight resistance
- Significance of SCA MS indicated that non-additive gene action is also important in the expression of Alternaria blight resistance
- The GCA SS contributed 71.5% and SCA SS contributed 28.5% of the treatment SS indicating that additive gene action is more important than non-additive gene action

Other data collected

At harvest

- Total number & mass of storage roots (marketable & non-marketable)
- Shoot mass
- Weevil damage
- Storage root skin colour
- Storage root flesh colour
- Storage root defects (Cracking)
- Dry matter composition

- **SPVD**

Evaluation of selected sweetpotato F_1 genotypes at three sites in Uganda

Selection genotypes

- 21 genotypes were selected and evaluated at 3 locations (NaCRRI, Kachwekano & Serere) and 3 reps
- 5 promising genotypes selected for further evaluation

Thanks for listening