MITIGATING NEGATIVE DROUGHT EFFECTS OF SWEETPOTATO PRODUCTIVITY THROUGH TOLERANT CULTIVARS IN KENYA

God storage roots

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Country: Kenya
Crop: Sweet potato

Sweet potato: Introduction

- Grown in the tropics and subtropics
- In Sub-Saharan Africa 3rd most important root crop
- Important root & tuber crop in E. Africa
- A staple in Kenya during famine,
- Grown in Agro EZ ranging from 0-2200masl

Introduction continued

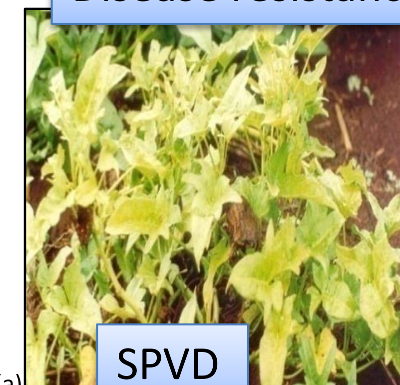
- Source of income to resource-poor
- Used for food and feed
- Remedy for β-carotene, Zn & Fe
- Being researched for bio-fuel production

Breeding objectives

Drought tolerance

Root nematodes resistance

Disease resistance

(a)


SPVD

(b)


Bacterial wilt

(c)


Alternaria blight

(d)


Fusarium wilt

Weevil resistance

Breeding targets cont'd

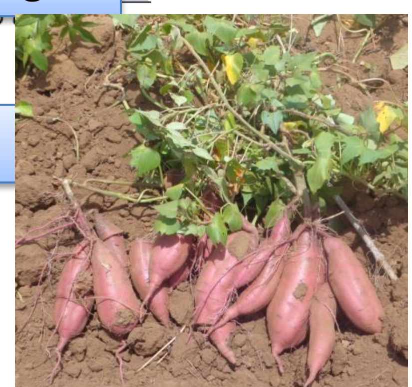
Biofortification

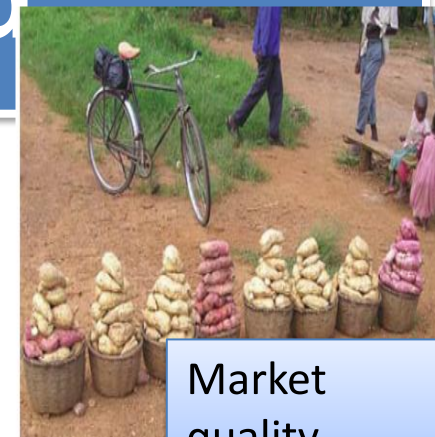
Ornamental

Sweetpotato doughnuts

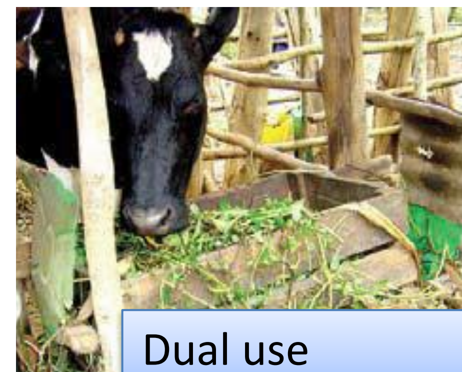
Processing

Improved yield





Market quality



Dual use

Why drought? Drought in SP can be devastating

Irrigated SP farm

Water stressed SP farm

Think of the variance of yield quantity and quality in this two farms!

Administering questionnaire (QN)

Administering QN & soil sampling

Drought

- Major constraint in Kenya
- S. potato sensitive during establishment & storage root initiation
- Affects yield severely: Rainfall seasonal & unreliable; high rate of evapo-transpiration
- Piece meal harvesting: lead to moisture loss, shortages of planting material and weevil exposure
- ***However drought tolerant sweet potato clones could be found***

Main goal

- To contribute to increased SP production by resource poor farmers, through breeding drought tolerant cultivars with other desirable traits.

Specific objectives

1. To determine production constraints & farmers preferences on grown cultivars
2. Evaluation for drought tolerance of sweetpotato population
3. Screening sweet potato drought mechanism
4. Genetic studies to determine gene action + inheritance for drought tolerance

Obj.1. To determine production constraints & farmers preferences (PRA + Survey)

- Western, Central and Eastern Kenya
- 5 counties: Homabay, Murang'a, Kirinyaga, Machakos, Makueni
- Two districts per county
- Two agricultural divisions per district
- Farmers interviewed across division randomly
- 30 questionnaires administered in each division (5x2x2x30=600) + focused group discussions
- Data collected, and is being analysed with SPSS

Results

Deliberating sweetpotato constraints

Positive reports

- aware of OFSP/ usefulness
- Attitude change;(SP for income, health, food and feed)
- Increased requests for improved OFSP

Farmers constraints

poor yields

Drought menace

Lack of storage skills/facilities

Weevil menace

Lack of Clean, enough and timely cuttings

Constraints cont’d

Market & transportation

Preferred cooking qualities

Value addition

Obj.2. Sweetpotato population evaluation for drought tolerance

- 84 cultivars; farmers field + genebank of Kenya + CIP Nairobi,
- Evaluation; 2 drought sites; 2 seasons
- Design: split plot replicated twice
- 2 managed environment: droughted, non droughted.
- At start of experiment; Soil fertility analysed, soil moisture content determined, Tensiometers installed to monitor soil water, and data logger put in place to collect data on temperature humidity and light intensity and rain gauge installed to determine amount of iirigation water.
- Water Drought introduced 6 WAP, after establishment
- Data collected: Biomass (root +vine), no. of roots, chlorophyl content, soil moisture, leaf and vine pubescence , HI, stress indices,
- Data analysed
- Parental clones selected and crossing block established

Cont’d

- Rapid drought box screening in greenhouse: Clones : RCBD design,
- Watered for two weeks
- Data collected: days to permanent wilt

Screening for drought at KARI Kiboko, Kenya

Irrigated sp	**Water stressed**

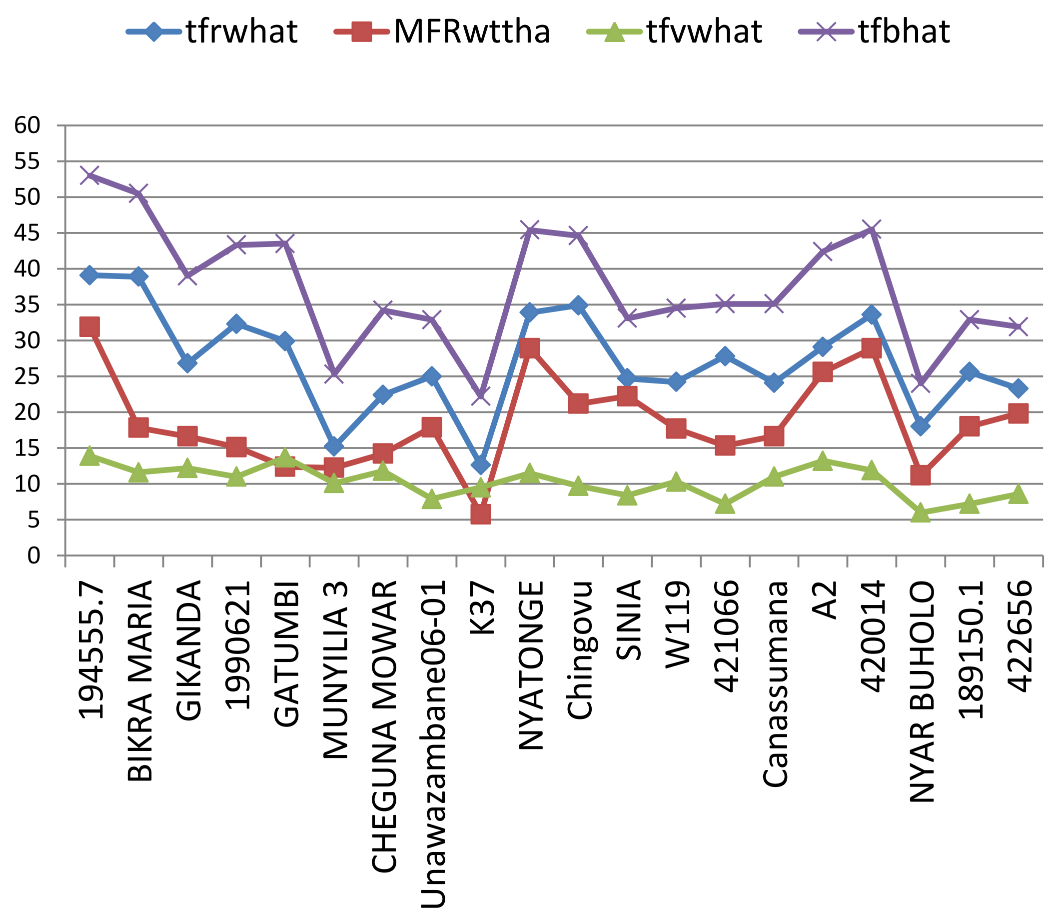
Rapid screening procedure

Results

Parameter	tnotperhatho	tfrwhat	percrdm	tfvwhat	tfbhat	DTD	HI
Minimum	18.52	0.1852	13.9	0.1852	0.8642	46	0.022
Mean	125.2	17.59	28.06	8.732	26.33	65.11	0.6504
Maximum	298.8	65.28	36.23	35.8	89.2	98	0.9773
Environ1	103.3	8.2	28.08	2.63	10.83		0.7093
Environ2	147	26.99	28.03	14.83	41.82		0.5914
Environ	0.08	0.007	0.838	0.006	0.002	<.001	0.026
Cultiva	<.001	<.001	<.001	<.001	<.001	<.001	<.001
Environ.Cultiva	<.001	<.001	0.657	<.001	<.001	<.001	<.001
cv%	25.9	37.3	9.2	35.5	27.8	10.7	16

- Number of roots did not differ with environment, shows probably total of roots are determined early during sp establishment.

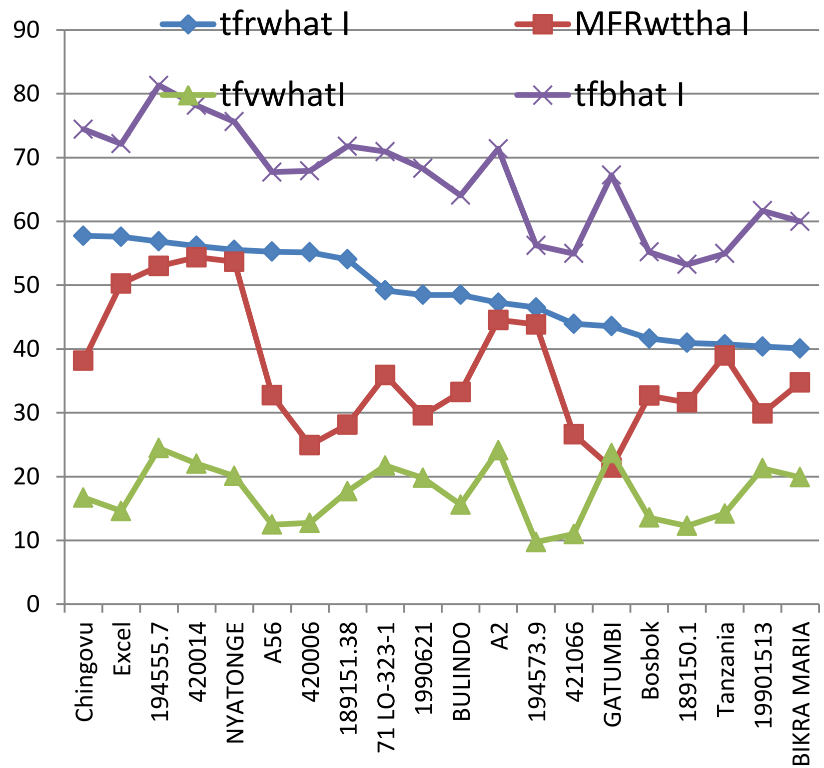
Best 20 High performing cultivars across environment



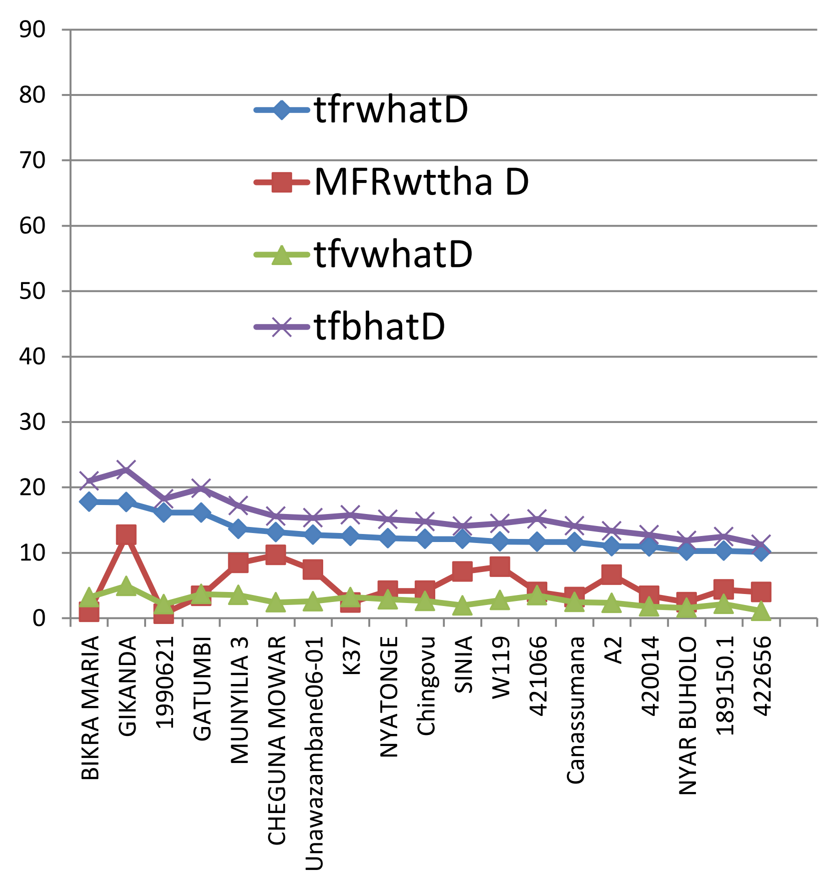
- TFRW: AE=12-40 t/ha
- IRR=39-58 t/ha (1000-1600g/plant)
- Not IRR= 9-18 (250-500 g/plant)

Performance per environment

Irrigated



Drought



Performance under both environment

drought	Irrigation	Both
189150.1	189151.38	194555.7
422656	194573.9	420014
Canassumana	420006	421066
CHEGUNA MOWAR	19901513	199062.1
GIKANDA	71 LO-323-1	A2
K37	A56	BIKRA MARIA
MUNYILIA 3	Bosbok	Chingovu
NYAR BUHOLO	BULINDO	GATUMBI
SINIA	Excel	NYATONGE
Unawazambane06-01	Tanzania	
W119		

- HI was higher in high yielding cultivars relative to poor yielding cultivars.
- Cultivars that took more days to permanent death, also drought tolerant

Correlation of stress indices

	Stress susceptibility Index	Mean productivity	Tolerance index	STI	Geometric nm mean produ.	Yield index	Yield stability index	Harmonic mean	Percent reduction
SSI	-								
MP	0.2037	-							
TOL	0.684	0.7274	-						
STI	0.2037	1	0.7274	-					
GMP	0.0838	0.9472	0.527	0.9472	-				
YI	-0.5059	0.5956	-0.1179	0.5956	0.7538	-			
YSI	-0.9907	-0.1823	-0.6728	-0.1823	-0.0623	0.5237			
HARM	-0.0228	0.8403	0.3279	0.8403	0.9685	0.8321	0.0432	-	
perred	0.9907	0.1823	0.6728	0.1823	0.0623	-0.5237	-1	-0.0432	-
	1	2	3	4	5	6	7	8	9

% reduction, SSI, HARM,MP, STI, GMP, YI had similar stress estimates, which agreed with tolerance of the cultivars

Obj. 3 Study on sweetpotato drought tolerance mechanism

- 8 cultivars selected from population evaluation and evaluated in the greenhouse (2 controls, 2 drought tolerant, 2 intermediate and 2 susceptible.
- Design: split plot design: 4 water regimes X 8 cultivars, replicated 3 times.
- Water never applied through out, cut off at , 1, 2 and 3 month after planting, 2Clones planted under Irrigation and managed drought stress, 2sites , 2 seasons (off-season)
- Drought introduced at establishment
- Design: Split plot design, whole plots=water supply, subplot=genotypes
- Data collected: Yield (Fresh and DM, No. of roots, vine length and branching, days to permanent wilt

The experiments

	Cultivar
1	441725
2	Resisto
3	194555.7
4	Excel
5	1990621
6	NYAR BUHOLO
7	Unawazambane06-01
8	A56

Trend observed: Moisture stress introduced at third month did not affect the yields and biomass relative to optimum regime

Obj. 4. Genetic studies

- Half diallel in G.House
- 23 parents selected + crossed (tolerant +susceptible to drought)
- F1 seedlings established in G.house, planted in field, evaluated in field 2environment +3 seasons
- Design: Split plot design
- Data: Yield (Fresh and DM, No. of roots, vine length and branching)

Half Diallel

	A56	Resisto	W119	2E+06	Excel	Bosbo k
A56						
Resisto	1					
W119	2	6				
199062.1	3	7	10			
Excel	4	8	11	13		
Bosbok	5	9	12	14	15	

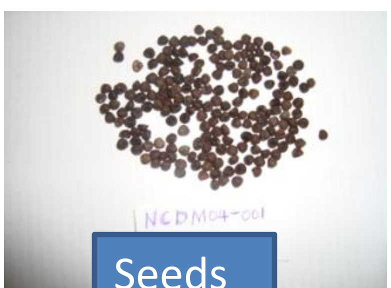
- Estimate GCA & SCA
- Determine and partition genetic variance
  - Additive variance
  - Dominance variance
  - Genetic gain for drought tolerance

Seedling establishment

- Parents + F1's evaluated in 2 sites + 2 seasons

Seedlings multiplication

Field evaluation



Seeds

GCA and SCA estimation model

- $Y_{ij} = \mu + g_i + g_j + s_{ij} + \varepsilon_{ij,}$ (Griffing's, 1956) , where:
  - Y_{ij} = average value of the progeny derived from the crossing of i^{th} female parent with j^{th} male parent,
  - μ = overall mean,
  - g_i = the GCA effects of the i^{th} female parent,
  - g_j = the GCA effects of the j^{th} male parent,
  - S_{ij} = the SCA effects for the cross between the i^{th} female parent and the j^{th} male parent
  - ε_{ij} = experimental error.
- Assumption: $\sum g_i = 0$ and $\sum s_{ij} = 0$

Estimated mean square and general interpretation of a half diallel (Griffing 1956)

Source of variation	d.f	Expected mean square
Replicatio n	r-1	
Cross	[p(p-1)/2]-1	$\sigma^2_e + r\sigma^2_{cross}$
GCA	(p-1)	$\sigma^2_e + r\sigma^2_{sca} + r(p-2)\sigma^2_{gca}$
SCA	P(p-3)/2	$\sigma^2_e + r\sigma^2_{sca}$
Error	(r-1){[p(p-1)/2]-1	σ^2_e

- Where: r and p refer to number of replications and parents per diallel respectively
- σ^2_{gca} = Covariance of half-sib families = ¼ σ^2_a
- σ^2_a = additive genetic variance
- σ^2_{sca} = Covariance of full-sib families – (2 * (Covariance of half-sib families) = ¼ σ^2_a
- σ^2_d = dominance genetic variance
- σ^2_e = error variance
- σ^2_{cross} = [½ - 1/(n + 1)] σ^2_a + σ^2_d

Cross	No. performed well in both N IRR and IRR
A56 X W119	3
A56 X Bosbok	3
Resisto X 199062.1	3
Resisto X Excel	3
W119 X 1990621	3
W119 x Bosbok	4
Excel x Bosbok	4

Promising progenies

A56 X W 119

Resisto X Excel

Promising progenies cont'd

W119 X Bosbok

Resisto X199062.1

Beyond the study: SP breeding program

PhD studies/Thesis

Advance screening the good materials and eventually release/ seed material propagation

Parent A				×	Parent B				YR 1: Parental crosses
F_{A1}	F_{A1}	F_{A1}	F_{A1}	↓	F_{B1}	F_{B1}	F_{B1}	F_{B1}	Seedling established
F_{A1} clones	F_{A1} clones	F_{A1} clones	F_{A1} clones	↓	F_{B1} clones	F_{B1} clones	F_{B1} clones	F_{B1} clones	YR 2: F1 Evaluation
F_{A1} clones	F_{A1} clones	F_{A1} clones	F_{A1} clones	↓	F_{B1} clones	F_{B1} clones	F_{B1} clones	F_{B1} clones	YR 3: Multi-location trials
	F_{A1} clones	F_{A1} clones		↓		F_{B1} clones	F_{B1} clones		YR 4:Good clones selected
				↓					
		F_{A1} clones				F_{B1} clones			YR 5:Advanced trials selection and release