Sweetpotato combining ability and heterosis under drought stress

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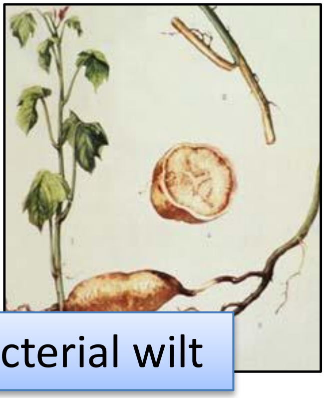
Introduction: Farmers’ concerns in Sweetpotato

Weevil Resistance

Disease resistance

SPVD



Bacterial wilt

Alternaria blight

Fusarium wilt

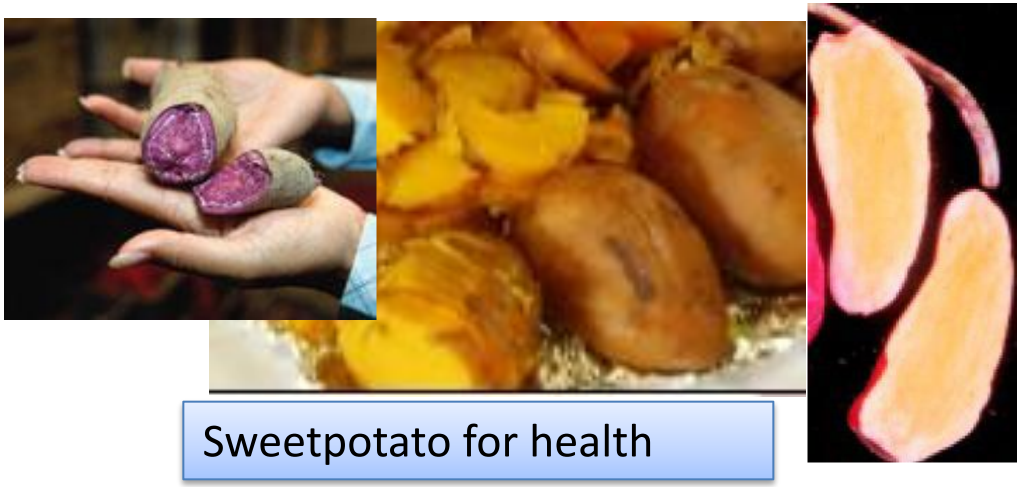
Sweetpotato breeding / socio-economic goals


Sweetpotato doughnuts


Sweetpotato crisps

Processing and value addition

Cooking qualities



Sweetpotato for health

Dual purpose use

Sweetpotato breeding / socio- economic goals

Market quality & transportation

Storage skills/facilities

Lack of clean, enough, timely seed

Drought tolerance

Improved yield

Why drought

- Drought is main abiotic constraint in SSA
- In Kenya, > 80% of land experiences drought
- Drought may result to 100% crop failure
- Hence the need for drought tolerance improvement
- Sweetpotato ($2n=6x=90$), hexaploid, with complex segregation ratios
- gene action of inheritance of drought tolerance not reported, hence this study

Drought stress causes

- Osmotic stress, cell dehydration, cell metabolic mal-functions
- Reduces photosynthesis, photosynthetic pigments, translocation and transpiration
- Production of reactive oxygen species which damage cell DNA, protein and lipids
- Lipid peroxidation leads to cell membrane solute leakages and malfunction, and cell metabolic imbalances
- Reduces stomatal conductance and CO_2 uptake, water use efficiency
- Reduces crop growth, lowers quantity and quality of yield and biomass

Excessive severe stress results in irreversible cell damage and death of entire crop

Drought tolerance trait is

- Polygenic, inversely related to yield, and is highly variable
- Involve morphological traits genes, Leaf rolling genes
- Root morphology and root/vine ratio, root thickness, root volume
- Osmotic adjustment, Leaf stay green

Cell dehydration due to drought triggers

1) ABA production which signals closure of guard cells

2) Mesophyll cell wall folding that reduce leave surface area

3) Replacement of water in vacuoles with compatible solutes, or less molecular weight molecules, and protein proline,

4) Production of anti-oxidant protein genes that include

- a) XVPer1 that protect DNA from reactive oxygen species,
- b) XVSAP1 that protects membrane leakage,
- c) both XPgols and ALDRXV4 which trigger formation of proteins that confer osmo-protection

Thus, drought tolerant genotype has the ability to

1. Tolerate cellular dehydration
2. Minimal water loss due to evapo-transpiration
3. Maintain favourable cell water status under moisture stress conditions
4. Escape drought
5. Recover from drought stress after a dry spell
6. Develop waxy thicker leaf layer and deep rooting

Thus:

- The study aimed at determining the ratio of GCA : SCA to depict gene action
- GCA mean performance of a parent genotype over several cross combinations; associated with additive gene effects,
- SCA mean performance of crosses that perform better and is typically associated with non-additive gene effects (dominance)
- In this study, diallel mating design method II (parents, F_1's, no reciprocals) was used

Materials and Method

Seedlings germination

Field evaluation

Crossing block

- Field evaluation: KARI Kiboko, Screen house evaluation: KARI Muguga
- 24 parents planted for crossing
- Specific crosses done; 3500 true seedlings harvested from 24 parents
- A half diallel of 6x6 of crosses with ≥20 seeds
- Seeds scarified, germinated, established, multiplied in screen house

6x6 half diallel

ID	Parental name	Fresh root yield t ha^{-1}	Drought tolerance
P1	1990621	14.3	T
P2	Resisto	16.5	I
P3	Bosbok	19.5	I
P4	A56	18.7	S
P5	Excel	20.1	S
P6	W119	15.9	T

Crop at 4 months

(a) Drought stressed

(b) No drought

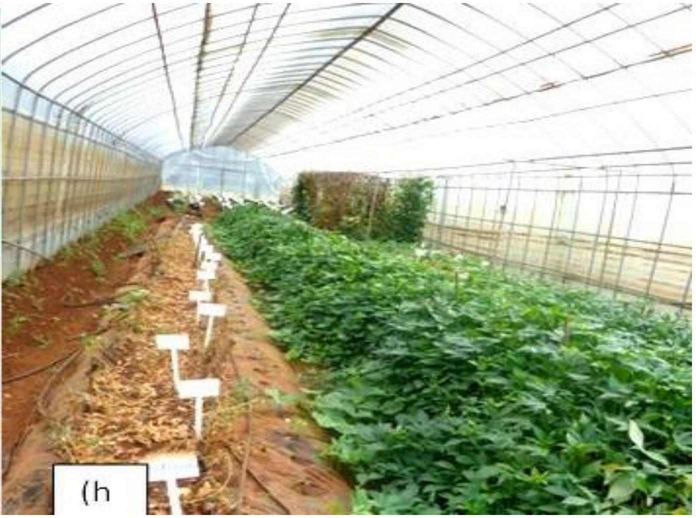
- Site: KARI Kiboko drought research station, 900masl, Rainfall= 500/year, annual temp: 30oC
- Design: Split plot; whole plot= water regime, subplot: genotypes
- Planted during dry season
- Cuttings=25 cm, 4-6 nodes, inserted 20-30 cm, at 60^{o} on 25 cm high ridges, spacing 30x 90 cm; DAP applied at planting (50 kg of P_2O_5 ha^{-1})
- Drought stressed= no irrigation supplementation
- No drought+ supplemented with irrigation
- Replication=2, seasons=3, Harvested =5 months

Data collected on:

- number of plants harvested per cross
- fresh root yield per cross (FSR)
- fresh vine weight per cross(FV)
- number of storage roots per cross (NSR)
- number of marketable storage roots (NMSR)
- total fresh biomass per cross (Bio)
- Harvest index (HI) and % root dry matter (%RDM) estimated
- Data analysed using SAS
- Best 10 clones presented below
- DSI calculated; DSI = $\frac{1-Ys/Yp}{1-\bar{Y}s/\bar{Y}p}$ (Fischer and Maurer, 1978).
- Ranking done; rank y=$\sum_{\boldsymbol{k=1}}^{\boldsymbol{n}} \mathbf{x}$,

Screen house experiments

- Design: RCBD, replication= 5, repeated= 3, April 2012 and Dec. 2012
- Shoots of 10 cm from F_1 parents planted 5 cm deep;
- High density black polythene sheet box (15 x 0.45 x 0.45 m); 0.4 m deep sterile soil; spacing 15cm x15cm
- Two tensiometers to a depth 30 cm
- Watered to field capacity (zero tensiometer reading) for first 15 days after planting, application was stopped after
- Days to permanent wilting point (DPWP) counted
- Light intensity, relative maximum and minimum temperature collected using data logger



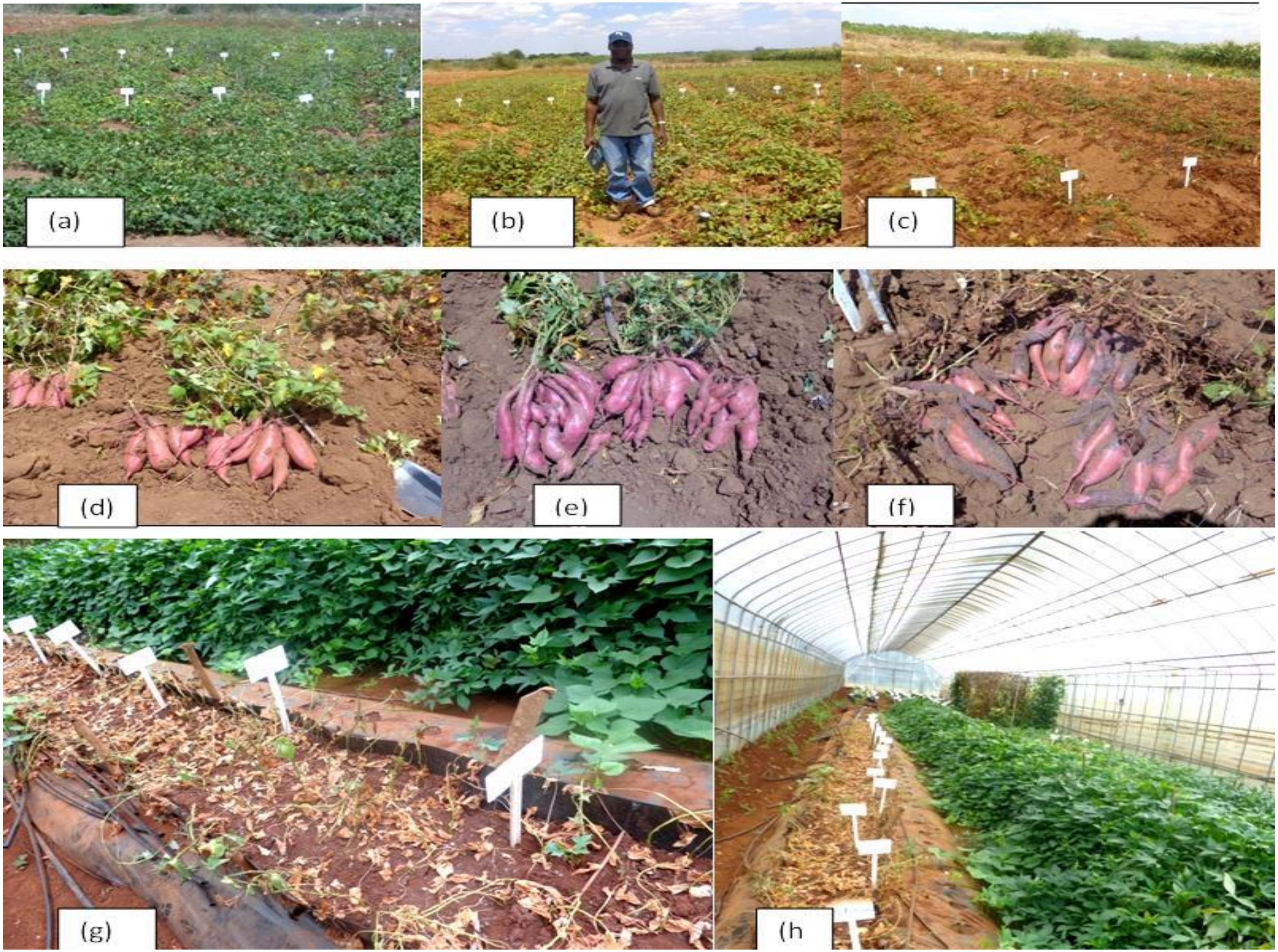
Heterosis

- Mid parent heterosis, $H_{F1n}=X_{F1}-1/2(X_{P1}+X_{P2})$,
  - X_{F1} is the yield of nth F_1 progeny from the cross of its two parents,
  - X_{P1} = yield of parent one, X_{P2} = yield of parent two.
- The best parent heterosis; $H_{F1n}=X_{F1}-(X_B)$,
  - where, X_{F1} is the yield of the F_1 progeny from the cross of its two parents,
  - and X_B is the yield of best parent of the F_1 progeny

Statistical analysis

- Analysis with SAS 9.2.1
- GCA and SCA effects computed using Griffing's model (1956) : $Y_{ij} = \mu + g_i + g_j + s_{ij} + \varepsilon_{ij,}$
  - where, Y_{ij}= average value of the progeny derived from the crossing of ith female parent with jth male parent,
  - μ = overall mean, g_i = the GCA effects of the ith female parent,
  - g_j = the GCA effects of the jth male parent,
  - s_{ij} = the SCA effects for the cross between the ith female parent and the jth male parent,
  - and ε_{ij}= experimental error with ijth genotype in the environment
- GCA and SCA ratios estimated using general predicted ratio (GPR);
  - GCA/SCA = $(2MS_{GCA})/(2MS_{GCA} + MS_{SCA})$ (Baker 1978); where, ratios close to one indicate additive effects are important, while ratios close to zero indicate dominance effects are important

photographs showing (a) no drought stress experiment (b) moderately drought stressed (c) severe drought stress (d) and (e) storage roots harvested from no drought stress plots (f) and (g) rapid drought screening box experiments in greenhouse and planting materials bulking



Results

- The GCA and SCA effects for all traits were significant while their interaction with environment effect was only significant for BIO under drought
- All the GCA/SCA ratios were greater than 0.5 in both environments except for total fresh biomass (BIO) and marketable number of roots (MNR), which were 0.4 and 0.27, respectively under drought

GCA/SCA under no drought stress environment

Source	**df**	**Mean Squares**				
		FSR	BIO	HI	MNR	%RDM
Environment (E)	2	2425.01***	2983.21***	0.026**	1226.20 ns	1.08 ns
Replication	3	306.91**	330.45**	0.024***	9499.40***	0.18 ns
Genotype (G)	20	842.17***	822.91***	0.022***	1235.40*	50.02***
G x E	40	12.16 ns	12.19 ns	0.002 ns	153.10 ns	0.20 ns
GCA	5	559.67***	497.49***	0.022**	1143.20*	77.55**
SCA	15	965.31***	941.26***	0.023**	1234.90*	48.98**
GCA*E	10	6.56 ns	6.16 ns	0.002 ns	192.70 ns	0.34 ns
SCA*E	30	14.83 ns	14.58 ns	0.002 ns	167.00 ns	0.20 ns
Error	60	47.03	48.94	0.003	580.30	0.63
GCA/SCA ratio		0.54	0.51	0.66	0.65	0.76
R2		0.89	0.90	0.86	0.63	0.98

GCA/SCA under drought stress environment

Source	df	Mean Squares				
		FSR	BIO	HI	MNR	%RDM
Environment (E)	2	2.67*	65.32***	0.18***	936.60**	0.78 ns
Replication	3	3.18**	2.04	0.02*	807.90**	0.27 ns
Genotype (G)	20	9.66***	20.28***	0.05***	1792.30***	48.35***
G x E	40	0.49 ns	6.93***	0.02***	66.1 ns	0.80 ns
GCA	5	10.15***	8.15**	0.06***	423.50*	82.12**
SCA	15	10.19***	24.65***	0.09***	2235.00**	44.23**
GCA*E	10	0.76ns	6.93***	0.01 ns	90.50 ns	0.95 ns
SCA*E	30	0.50 ns	7.78***	0.02**	68.50ns	0.86 ns
Error	60	0.70	1.61	0.01	182.90	0.53
GCA/SCA ratio		0.67	0.40	0.57	0.27	0.79
R2		0.84	0.87	0.80	0.79	0.96

Combining ability effects under drought stress environment

- Parent P6 had + significant GCA effects for all traits except HI
- Parents P1, P3, P4 and P5 had negative significant storage root SCA effects
- GCA effects on FSR were P6>P2>P1>P5>P3>P4
- G15 and G7 had the highest significant SCA effects on FSR.
- G15, G5 and G12 had the highest significant SCA effects (0.14–0.2) for HI.
- SCA effects for marketable number of roots on all progenies were negative

GCA and SCA for root yield traits (t ha^{-1}) under drought stress environments

SCA effects	Crosses	FRW	BIO	HI	MNR	%RDM
G1	A56 x Resisto	-0.45	-0.43	-0.05	-6.80	0.09
G2	A56 x W119	1.16***	1.28	0.01	-9.10*	1.41***
G3	A56 x1990621	-1.37***	-1.71*	-0.03	-4.71	0.26
G4	A56 x Bosbok	-0.13	-0.58	0.06	-12.72**	-0.59*
G5	A56 x Excel	1.46**	-1.67	0.16*	-40.60***	0.51
G6	Resisto x W119	-1.64***	-3.16***	-0.02	-4.91	0.81**
G7	Resisto x 1990621	1.46***	1.15	0.09*	-4.82	1.90***
G8	Resisto x Bosbok	1.38***	1.46*	0.05	-0.50	3.77***
G9	Resisto x Excel	-2.32***	-4.23**	0.01	-29.91***	-2.30***
G10	W119 x 1990621	1.17***	0.91	0.10*	-2.31	-3.60***
G11	W119 x Bosbok	-2.05***	-3.19***	-0.07	-8.22*	2.90***
G12	W119 x Excel	0.26*	-3.04*	0.14*	-21.31**	-1.30**
G13	1990621 x Bosbok	-0.02	-0.72	0.04	-3.60	-0.88
G14	1990621 x Excel	-0.35	-2.13	0.12	-40.73***	9.27***
G15	Bosbok x Excel	2.17***	-1.13	0.20**	-42.10***	-2.11***
GCA effects for parents						
P1	1990621	-0.02	0.16	0.00	-3.70*	0.892***
P2	Resisto	0.41**	-0.59	-0.03	-3.72*	-0.433**
P3	Bosbok	-0.35**	-0.07	-0.04*	2.51	-0.273*
P4	A56	-0.54***	-0.18	0.06**	-0.43	1.684***
P5	Excel	-0.23*	-0.04	-0.01	2.01	-2.324***
P6	W119	0.73***	0.73*	0.03	3.41*	0.454**

FRW = fresh root weight in tha^{-1}, Bio = fresh total biomass weight in t ha^{-1}, HI = Harvest index, MNR = marketable number of storage roots in thousands ha^{-1}, %RDM = percent root dry matter, and *, **, *, = significant at P≤0.05, P≤0.001, P≤0.0001 respectively**

Combining ability under no drought stress

- Parent 6 (W119) had +significant GCA effects for all traits
- Parent P2, had - significant GCA effects under storage root yield
- Parent P4 had +significant GCA effects for HI (0.02) and %RDM (1.39)
- Parent P1 had + significant GCA on %RDM.
- GCA on FSR: P6>P2>P1>P5>P3>P4
- G15, and G7 had the highest significant SCA effects (16.32-20.99) FSR
- Fresh total biomass SCA effects for G15, G7, and G10 were significant
- G12, G7, and G2 had the highest significant SCA effects (0.08 – 0.12) HI

Combining ability under no drought stress

SCA effects	Crosses	FRW	BIO	HI	MNR	%RDM
G1	A56 x Resisto	-0.92	-0.74	-0.02	-14.2*	0.79**
G2	A56 x W119	10.48*	8.75**	0.08***	10.6	1.92***
G3	A56 x1990621	-6.9*	-5.85	-0.05*	7.81	-1.27***
G4	A56 x Bosbok	-7.92**	-7.54*	-0.03	-3.32	-1.14***
G5	A56 x Excel	6.05	8.42	0.01	3.61	-0.55***
G6	Resisto x W119	-9.05**	-9.26**	-0.04*	-0.60	1.58***
G7	Resisto x 1990621	16.32***	15.54***	0.09***	9.31	2.05***
G8	Resisto x Bosbok	9.51**	12.67**	0.01	22.20**	4.16***
G9	Resisto x Excel	-21.33***	-21.35**	-0.13**	-1,01	-3.59***
G10	W119 x 1990621	14.80***	15.01***	0.05*	8.61	-4.20***
G11	W119 x Bosbok	-15.23***	-15.06***	-0.08***	-3.30	1.84***
G12	W119 x Excel	16.22**	13.52*	0.12**	27.81*	-2.95***
G13	1990621 x Bosbok	-9.72**	-10.33**	-0.04*	-10.20	-2.35**
G14	1990621 x Excel	2.54	3.79	0.01	43.61**	6.66***
G15	Bosbok x Excel	20.99***	20.95**	0.02	12.71	-2.38***
GCA effects for Parents						
P1	199062.1	-0.33	0.15	0.00	-6.11*	0.99***
P2	Resisto	-1.52**	-3.66**	-0.04***	-8.40**	-0.13
P3	Bosbok	6.44	0.68	-0.01	2.21	-0.40***
P4	A56	4.53	-2.73**	0.02*	5.12	1.39***
P5	Excel	-0.44	-0.45	0.00	0.81	-2.36***
P6	W119	0.39***	6.01***	0.03**	6.31*	0.51***

Performance of F1 and their parents on days to permanent wilting point (DPWP)

Parental crosses		DPWP	SCA effects
G1	A56 x Resisto	68	-2.71**
G2	A56 x W119	81	8.31***
G3	A56 x1990621	72	0.40
G4	A56 x Bosbok	67	- 5.32***
G5	A56 x Excel	79	13.31***
G6	Resisto x W119	63	-13.30***
G7	Resisto x 1990621	90	15.31***
G8	Resisto x Bosbok	85	10.11***
G9	Resisto x Excel	70	-1.20
G10	W119 x 1990621	83	5.30***
G11	W119 x Bosbok	67	-10.51***
G12	W119 x Excel	87	7.02***
G13	1990621 x Bosbok	67	-9.31***
G14	1990621 x Excel	71	0.30
G15	Bosbok x Excel	91	13.10***
Parents			GCA effects
P1	1990621	70	0.91***
P2	Resisto	69	1.30
P3	Bosbok	78	-0.80***
P4	A56	60	-3.90
P5	Excel	60	0.61
P6	W119	80	1.82**
Mean	-	74	-
$LSD_{0.05}$	-	4.12	-
% CV	-	2.83	-

Heterosis under drought stress environment

- Clones G8-8, G15-8, and G15-5, showed the highest mid parent (269.6, 184.5 and 196.3) and best parent (223.4, 117.8, and 126.9) heterosis on fresh storage root yield under drought stress.
- Clone G7-10 had the highest mid parent (75.8) and best best-parent (81.4) heterosis on the basis of fresh total biomass yield.
- Heterosis for the best 35 F1 recombinants identified based on performance of all F1 crosses on storage root weight and total fresh biomass under drought environment

Heterosis under drought stress environment

				Fresh storage root weight		Total fresh biomass	
Cross	Family	Clone ID	Rank	MH	BH	MH	BH
Excel x Bosbok	G15	10	1	177.1	112.2	19.6	15.8
Excel x Bosbok	G15	9	2	173.1	109.1	16.5	12.8
Excel x Bosbok	G15	8	3	184.5	117.8	6.1	2.7
Excel x Bosbok	G15	5	4	196.3	126.9	-2.1	-5.2
Excel x Bosbok	G15	4	5	168.2	105.3	3.0	-0.2
Excel x Bosbok	G15	1	6	151.0	92.2	-62.7	-63.9
1990621 x Excel	G14	6	7	117.6	66.6	12.3	20.3
1990621 x Excel	G14	2	8	140.8	84.4	-19.5	-13.8
W119 x Bosbok	G11	9	9	126.1	108.4	11.6	16.8
W119 x Bosbok	G11	4	10	104.1	88.1	25.8	31.8
W119 x Bosbok	G11	3	11	96.6	81.3	-7.2	-2.8
W119 x Bosbok	G11	2	12	99.0	83.4	-7.9	-3.6
W119 x Bosbok	G11	1	13	98.6	83.1	-22.9	-19.3
W119 x Excel	G12	2	14	4.1	21.9	30.5	35.5
W119 x 1990621	G10	8	15	99.0	83.4	7.5	25.4
W119 x 1990621	G10	7	16	129.6	100.9	-11.0	-14.3
W119 x 1990621	G10	6	17	125.0	96.9	12.8	8.6
W119 x 1990621	G10	5	18	128.5	110.6	9.1	27.3
W119 x 1990621	G10	3	19	96.9	81.6	15.9	35.3
W119 x 1990621	G10	2	20	137.1	107.5	-16.8	-19.9
Resisto x Bosbok	G8	5	21	3.5	14.1	43.3	46.8
Resisto x Bosbok	G8	1	22	60.0	42.5	-53.4	-56.3
Resisto x Excel	G9	9	23	142.4	103.6	-45.9	-44.0
Resisto x Excel	G9	7	24	140.5	102.0	39.4	44.5
Resisto x Excel	G9	4	25	135.2	97.6	-8.1	-4.8
Resisto x 1990621	G7	10	26	107.7	85.0	75.8	81.4
Resisto x 1990621	G7	5	27	124.2	99.7	15.4	19.1
Resisto x 1990621	G7	2	28	114.0	90.6	9.8	13.3
Resisto x W119	G6	7	29	-5.4	-8.9	-25.2	-32.8
Resisto x W119	G6	6	30	23.1	25.9	36.8	43.2
Resisto x W119	G6	3	31	22.7	25.6	31.2	38.2
A56 x Bosbok	G4	10	32	84.1	69.7	-5.4	10.4
A56 x Bosbok	G4	9	33	116.6	99.7	-9.0	6.2
Resisto x Bosbok	G8	8	34	269.6	223.4	-12.1	-15.4
A56 x Bosbok	G4	6	35	88.1	73.4	15.9	35.3

Heterosis under no drought stress environment

- Clone G4-9, G4-10 and G4-6, showed the highest mid parent (247.6, 233.7, and 231.5) and best parent (209.2, 199.6, and 194.9) heterosis on fresh storage root yield.

- Clone G4-9, G4-10 and G7-5 had the highest mid parent (164.6, 153.8, and 153.6) and best parent (233.6, 110.3, and 112.3) heterosis on the basis of fresh total biomass yield

- Heterosis for the best 35 F1 recombinants identified based on performance of all F1 crosses on storage root weight and total fresh biomass under no drought stress environment

Heterosis under no drought stress environment

Genotype identity				Fresh storage root weight		Total fresh biomass	
Cross	Family	Clone ID	Rank	MH	BH	MH	BH
Excel x Bosbok	G15	10	1	139.3	131.8	105.3	94.2
Excel x Bosbok	G15	9	2	145.0	137.3	113.1	101.6
Excel x Bosbok	G15	8	3	91.7	85.6	67.0	58.0
Excel x Bosbok	G15	5	4	198.4	189.0	149.0	135.6
Excel x Bosbok	G15	4	5	193.4	184.2	145.9	132.7
Excel x Bosbok	G15	1	6	179.1	170.3	134.6	122.0
1990621 x Excel	G14	6	7	12.3	-14.1	16.5	-8.1
1990621 x Excel	G14	2	8	13.0	-13.6	14.6	-9.6
W119 x Bosbok	G11	9	9	120.1	80.1	81.6	62.0
W119 x Bosbok	G11	4	10	111.0	72.7	66.1	48.2
W119 x Bosbok	G11	3	11	114.2	75.3	71.1	52.7
W119 x Bosbok	G11	2	12	134.8	92.2	84.9	65.0
W119 x Bosbok	G11	1	13	145.7	101.1	89.8	69.3
W119 x Excel	G12	2	14	4.3	12.4	-5.2	1.2
W119 x 1990621	G10	8	15	215.4	180.5	146.4	210.7
W119 x 1990621	G10	7	16	101.4	90.2	84.6	74.6
W119 x 1990621	G10	6	17	82.5	72.4	64.0	55.2
W119 x 1990621	G10	5	18	187.5	155.7	124.0	182.4
W119 x 1990621	G10	3	19	222.8	187.2	147.0	211.5
W119 x 1990621	G10	2	20	81.4	71.3	64.7	55.8
Resisto x Bosbok	G8	5	21	10.2	24.0	12.3	22.6
Resisto x Bosbok	G8	1	22	-14.0	-27.2	-20.5	-29.9
Resisto x Excel	G9	9	23	79.7	56.3	82.1	69.1
Resisto x Excel	G9	7	24	84.3	60.3	75.3	62.8
Resisto x Excel	G9	4	25	74.8	52.0	63.4	51.7
Resisto x 1990621	G7	10	26	185.7	145.2	132.7	94.8
Resisto x 1990621	G7	5	27	210.9	166.8	153.6	112.3
Resisto x 1990621	G7	2	28	188.3	147.5	139.1	100.1
Resisto x W119	G6	7	29	20.9	16.1	3.5	4.8
Resisto x W119	G6	6	30	-11.1	-6.7	3.8	2.6
Resisto x W119	G6	3	31	-14.9	-10.3	-7.5	-8.9
A56 x Bosbok	G4	10	32	233.7	196.9	153.8	110.3
A56 x Bosbok	G4	9	33	247.6	209.2	164.6	233.6
Resisto x Bosbok	G8	8	34	82.5	72.3	63.7	54.9
A56 x Bosbok	G4	6	35	231.5	194.9	148.5	213.4

Clone Performance under drought and no drought

Parameter	Best in Drought	Range	Best in No drought	range
Storage root yield	G10,G12,G7,G5	6.01-6.82	G15,G8, G5, G10, G2	45.6-63.2
Total biomass	G2,G15, G12	10.1-10.5	G5,G12, G15	65.8-78.9
Harvest index	G7,G10 and G12	0.66-0.71	G10, G12 and G14	0.74-0.81
Marketable storage roots	G10,G12 and G13	32-41 thous/ha	G10, G12 and G14	92-102.7
Parents storage root yield	P6>P2>P1>P5>P3>P4	3.2-5.2	P5>P1>P4>P3>P2>P6	23.3-37

Promising clones

Resisto X Bosbok (8-5)

W119 X 199062.1 (10-7)

Promising progenies cont'd

Excel X Bosbok (15-6)

Resisto X199062.1 (7-10)

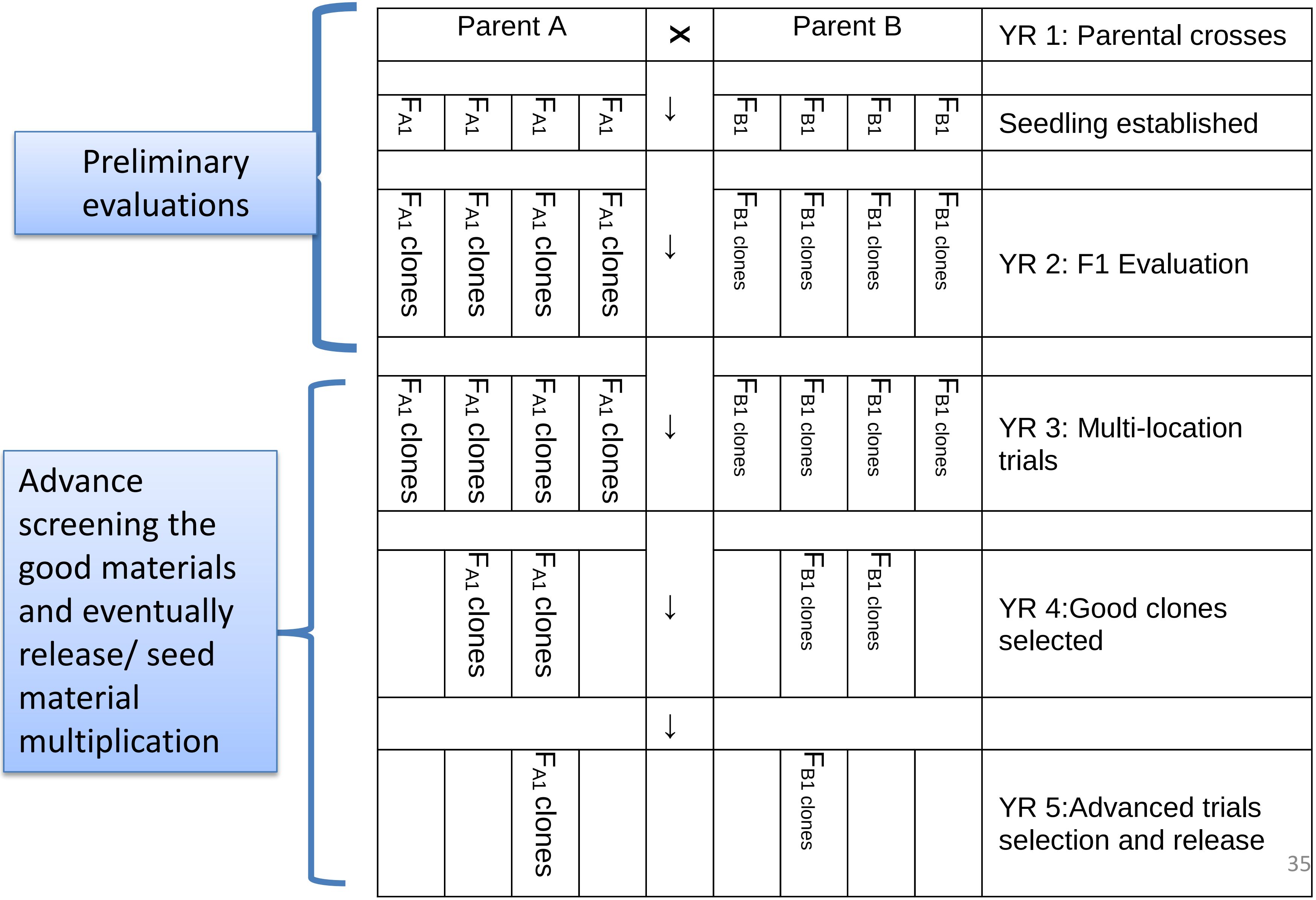
Discussion and conclusion

- DSI showed P3 and P4 susceptible to drought, P5 semi-tolerant, P6 tolerant
- G15 and G10 yielded highest, had significant - %RDM SCA effects under drought, but + SCA effects under no drought stress, suggesting root dry matter content was negatively correlated with yield and drought tolerance
- Thus drought suppresses assimilate production, which affect the sizes of the storage roots. Therefore, gene or genes that enhance assimilate production could be responsible for drought tolerance in sweetpotato, especially under drought escape.
- Best two crosses G15 (P3 x P5) and G5 (P4 x P5) whose parents P3 and P4, were susceptible but combined well with drought susceptible P5 to produce high yielding and drought tolerant progenies suggests, drought susceptible parents probably carried minor (recessive) drought tolerance genes, which combined well in specific F_1 progenies to enhance drought tolerance.

- Thus, genes for drought tolerance in sweetpotato are homozygous recessive; the susceptible parents were either carriers of the homozygous or heterozygous recessive. Further studies may be conducted to confirm the inheritance of genes responsible for drought tolerance in sweetpotato. Thus donors of drought tolerance genes may actually be drought susceptible themselves
- Additive gene action was more predominant than non-additive gene action
- Most families with positive significant SCA effects on storage root yield had negative significant SCA effects on % RDM,
- However, G7 and G8 had high storage root yields, +SCA effects on % RDM and thus could be exploited for drought tolerance, high yield and high root dry matter
- The high DPWP indicated that persistent but slowed vine growth was one of the mechanisms of drought tolerance.

- +/- SCA effects for total biomass under drought implied effective photosynthate translocation to storage roots under increasing moisture stress was one of the drought tolerant mechanisms
- Genotypes that had high heterosis (for biomass or storage roots) under no drought but low or negative heterosis under drought meant they were unstable across environments and could be evaluated for use in areas with reliable rainfall regimes.
- Therefore, since sweetpotato clones are released as highly heterozygous F_1 progeny, then a breeding programme should factor in heterosis and SCA effects for significant genetic gain advances in breeding sweetpotato for drought tolerance.
- Finally, this study uniquely combines yield performance, combining ability estimates of the crosses made, DPWP, and heterosis under drought and no drought stress to unmask the gene action and the possible genes allelism for drought tolerance in sweetpotato

What next?



Preliminary evaluations

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

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

Way forward

- Onfarm participatory evaluation of the best 60 clones to select best 10 clones
- Multi-location onfarm trials on selected 10 clones with > farmers groups
- Best 5 clones entered to national performance trials for release
- Put up proposals for funding of the work –AGRA and other Donors

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Thank you