Re-analysis of heterotic gain in Uganda



Wasonga C., R. Mwanga, R. Eyzaguirre and W. Grüneberg

SWEETPOTATO ACTION FOR SECURITY AND HEALTH IN AFRICA

Objective



Establish yield gains in early generation sweetpotato clones derived from inter and intra population crosses of two East African genepools (Population Uganda A and Population Uganda B) hypothesized to be mutually heterotic

Materials and methods





Eight parents selected from each pool and crosses made between the genepools following A8xB8 factorial cross design, while within genepools A8xA8 and B8xB8, a diallel cross design was followed.

Seed obtained from crosses made between Pop Uganda A and Pop Uganda B



Small crossing block (Pop Uganda A)								
Big Crossing Block (Pop. Ug B)	A1 (Ejumula)	A2 (NASPOT 1)	A3 (Dimbuka- Bukulula)	A4 (NASPOT5/58)	A5 (NASPOT 7)	A6 (SPK004)	A7 (NAASPOT 10 O)	A8 (NK297L)
B1 (Resisto)	1C	2C	3C	4C	5C	6C	7C	8C
	212(53)	151[88]	123[106]	200[50]	261[112]	69[139]	94[87]	239[181]
B2 (Magabali)	9c	10c	11c	12c	13c	14c	15c	16c
	156[0]	184 [35]	368[50]	290[19]	150[243]	154[130]	229[222]	327[80]
B3 (NASPOT 5)	17c	18c	19c	20c	21c	22c	23c	24c
	310[224]	259[130]	377[253]	3[0]	360[185]	223[97]	197[97]	244 [27]
B4 (Wagabolige)	25c	26c	27c	28c	29c	30c	31c	32c
	51[4]	439[11]	482[482]	435[175]	216[69]	139[82]	408[63]	42[408]
B5 (Mugande)	33c	34c	35c	36c	37c	38c	39c	40c
	426[35]	323[31]	481[57]	16 [473]	122[166]	272[93]	85[39]	216[190]
B6 (NASPOT 11)	41c	42c	43c	44c	45c	46c	47c	48c
	375[219]	322[114]	178[149]	40[0]	233[168]	209[22]	135[20]	846[129]
B7	49c	50c	51c	52c	53c	54c	55c	56c
(New Kawogo)	136[82]	224[77]	53[226]	19[4]	259[17]	220[76]	32[3]	559[143]
B8 (Huarmeyano)	57c	58c	59c	60c	61c	62c	63c	64c
	890[77]	223[152]	1543[215]	471[73]	233[125]	205[132]	466[272]	495[227]

Crosses made within Pop Uganda A to generate seed



	A1	A2	А	A4	A5	A6	A7	A8
Parent	Ejumula	NASPOT 1	Dimbuka	NASPOT5/58	NASPOT 7	SPK004	NASPOT 10 O	NK259L
			Bukulula					
A1 Eiumula	v	217						
AI Ejumula	^	12271	850 (144)	204 (206)	264[190]	170 (025)	200 (22)	401 [200]
		[257]	030 [144]	394 [390]	304[180]	1/0 [025]	299 [22]	401 [209]
A2		X	62[0]	352[1089]	104[4]	60[54]	111[187]	78[17]
NASPOT 1								
A3 Dimbuka-								
Bukulula			х	622[702]	32[19]	74[6]	91[723]	311 [320]
A4		, i						
NASPOT5/58				x	435[177]	153[98]	9[5]	301[180]
A5 NASPOT								
7					x	88[17]	86[8]	310 [0]
A6 SPK004						x	221[8]	98 [0]
A7								
NASPOT 10								473[187]
0							x	
A8								
NK259L								x



Crosses made within Pop Uganda B and seed generated

Parent	B1	B2	B3	B4	B5	B6 NASPOT	B7	B8
	Resisto	Magabali	NASPOT 5	Wagabolige	Mugande	11	New Kawogo	Huarmeyano
B1 Resisto	x	256[0]	367[110]	124[15]	451[0]	142 [0]	666[311]	453[?]
B2 Magabali		х	154[248]	223[0]	170[50]	197[0]	680[512]	43[337]
B3 NASPOT 5			х	81[212]	131[110]	70[5]	64[81]	224[31]
B4								
Wagabolige				x	284[30]	820[380]	587[587]	803[154]
B5 Mugande					x	304[8]	194[122]	305[321]
B6 NASPOT								
11						x	65[2]	224[285]
B7 New								
Kawogo							x	1404[0]





20 clones planted per family

Three plants per clone

Two reps per environment

Four test environments -Namulonge (2014A, 2014B and 2015A) and Serere (2015A)

Data collection







Alternaria



SP weevil



Storage root and vine yield

Data analysis



Mid-parent mid-offspring heterosis was calculated using the formula:

Heterosis increment, %

= [Clone value - 1/2(P1+P2)] *100

(1/2(P1+P2)

Where P1 and P2 are means of parents one and two respectively

 NASPOT 5 and Huarmeyano and associated families were dropped from the final analysis. A recent genepool separation study had showed that NASPOT 5 did not belong to the population Uganda B while Huarmeyano did not belong to the two Ugandan SP populations

Results





	Nobservd	Mean	Minimum	Maximum	Median
Population					
AxA	28	8.168	2.405	11.59	8.575
BxA	48	8.884	2.152	13.43	9.232
BxB	15	8.547	2.355	13.31	8.525
PA	8	8.786	2.169	18.10	7.949
PB	6	6.553	0.775	20.24	3.829

Storage root yields of populations Uganda A (28 AxA families), Uganda B (15 BxB families) and crosses between populations Uganda A and Uganda B (48 BxA families) and also 6Bx8A parents. The results are means of four environments. The BxA families had a higher mean compared to AxA and BxB

The combination of 6x8 B and A parents through controlled crosses that had 48 families resulted in an overall heterosis increment of 16% for storage root yield over the mid-

parent.





	Nobservd	Mean	Minimum	Maximum	Median
Yield_parameter					
Biomass	48	41.77	21.48	54.63	42.16
Storage root	48	8.88	2.15	13.43	9.23
Vine	48	32.88	13.81	44.99	33.75

Storage root, vine and biomass yields of 48 BxA SP families. The results are means of four environments. Vine production was higher than storage root





- For the 48 BxA SP families evaluated, heterosis increment associated with storage root was higher than that of vine and biomass production.
- The combination of 6x8 B and A parents through controlled crosses that produced 48 families resulted in an overall heterosis increment of 16% for storage root over the midparent.

-	C	Δ	C	H	Λ	
		-		Contraction of the	1	1.54

Big Crossing Block	Small crossing block (Pop Uganda A)								
(Pop Uganda B)	A1	A2	A3	A4	A5	A6	A7	A8	
	(Ejumula)	(NASPOT 1)	(Dimbuka- Bukulula)	(NASPOT 5/58)	(NASPOT 7)	(SPK004)	(NASPOT 10 O)	(NK297L)	
	<u>14.0</u>	<u>8.0</u>	<u>3.2</u>	<u>2.3</u>	<u>18.1</u>	<u>7.9</u>	<u>14.6</u>	<u>2.2</u>	
B1 (Resisto)	1c	2c	3c	4c	5c	6с	7c	8c	
<u>3.6</u>	<u>12.0</u> (<mark>36</mark>)	<u>9.7</u> (68)	<u>10.2</u> (197)	<u>7.1</u> (<mark>139</mark>)	<u>10.2</u> (-6)	<u>10.4</u> (82)	<u>13.4</u> (48)	<u>11.4</u> (297)	
B2 (Magabali)	9c	10 c	11c	12c	13c	14c	15c	16c	
<u>7.3</u>	<u>5.3</u> (- <mark>50</mark>)	<u>8.8</u> (14)	<u>9.7</u> (85)	<u>6.4</u> (33)	<u>9.6</u> (- <mark>24</mark>)	<u>8.4</u> (10)	<u>12.0</u> (10)	<u>8.2</u> (73)	
B4 (Wagabolige)	25c	26c	27c	28c	29c	30c	31c	32c	
<u>4.0</u>	<u>12.8</u> (42)	<u>8.7</u> (45)	<u>6.3</u> (73)	<u>4.0</u> (28)	<u>5.3</u> (- <mark>52</mark>)	<u>3.8</u> (- <mark>36</mark>)	<u>7.7</u> (- <mark>18</mark>)	<u>8.3</u> (170)	
B5 (Mugande)	33c	34c	35c	36c	37c	38c	39c	40c	
<u>3.3</u>	<u>8.1</u> (-6)	<u>7.0</u> (23)	<u>7.5</u> (129)	<u>11.2</u> (299)	<u>6.8</u> (- <mark>36</mark>)	<u>5.7</u> (3)	<u>5.3</u> (- <mark>41</mark>)	<u>2.2</u> (- <mark>21</mark>)	
B6 (NASPOT 11)	41c	42c	43c	44c	45c	46c	47c	48c	
<u>20.2</u>	<u>13.1</u> (- <mark>23</mark>)	<u>9.5</u> (- <mark>33</mark>)	<u>8.6</u> (-27)	<u>11.2</u> (0)	<u>12.2</u> (-37)	<u>9.5</u> (- <mark>32</mark>)	<u>9.4</u> (- <mark>46</mark>)	<u>10.1</u> (-9)	
B7 (New Kawogo)	49c	50c	51c	52c	53c	54c	55c	56c	
<u>0.8</u>	<u>9.0</u> (22)	<u>10.4</u> (144)	<u>12.4</u> (538)	<u>9.8</u> (573)	<u>9.6</u> (5)	<u>8.9</u> (109)	<u>9.6</u> (22)	<u>8.4</u> (<mark>433</mark>)	

6Bx8A parents and family mean storage root yields and heterosis increments. The values for storage root yield (in t/ha) are underlined while the values for heterosis increment (%) are shown in brackets.

63% of cross combination and families (30 out of 48 families) had heterosis increments of >0% for storage root and that 23% of cross combination and families (11 families), exhibited heterosis increments of >100%. Four families had SRY heterosis increment above 400%





Variations in mean storage root heterotic yield increments within and between families descending from six population Uganda B female parents crossed with eight population Uganda A parents. The results are means of four environments. For each parent there were eight families.

Heterosis increment was high and more variable for Resisto, Wagabolige, Mugande, and New Kawogo families from gene pool B





Variations in mean storage root heterotic yield increments within and between families descending from eight population Uganda A male parents crossed with six population Uganda B parents. The results are means from four environments. For each parent there were six families.

From pool A (males) large heterosis increments were obtained from Dimbuka Bukulula, NASPOT 1, NASPOT 5/58 and NK259L

Conclusions and future



- Exploitable heterotic yield increment for storage root is achievable through the combination of parents from the two East African sweetpotato genepools in addition to improving for other important quality and adaptation traits such as SPVD resistance.
- Large variations in heterosis yield increment between the BxA families suggests differences among the parents with respect to combining ability. Identification of testers for each population and crossing all genotypes in the two populations with the testers might help to separate heterotic groups for population improvement.
- Work has commenced to make crosses between parents in the two crossing blocks with a view to identifying parent combinations that produce families with high heterosis increments