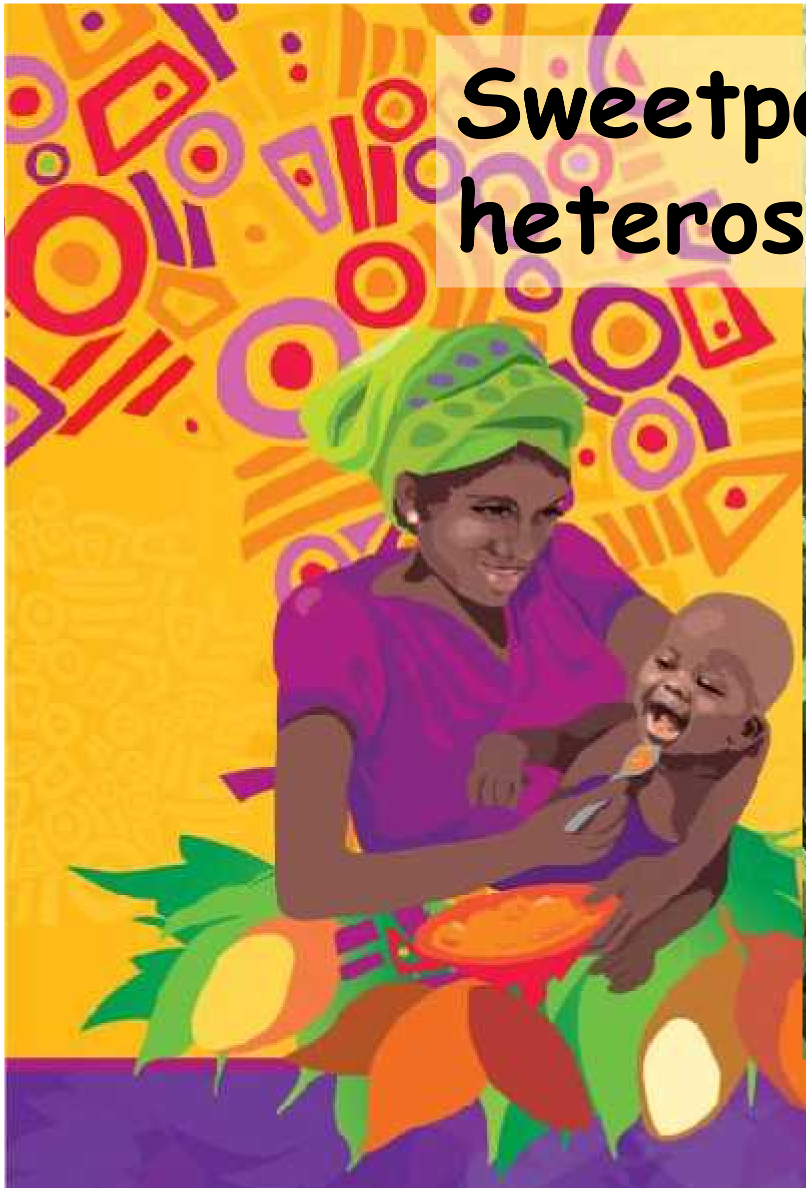
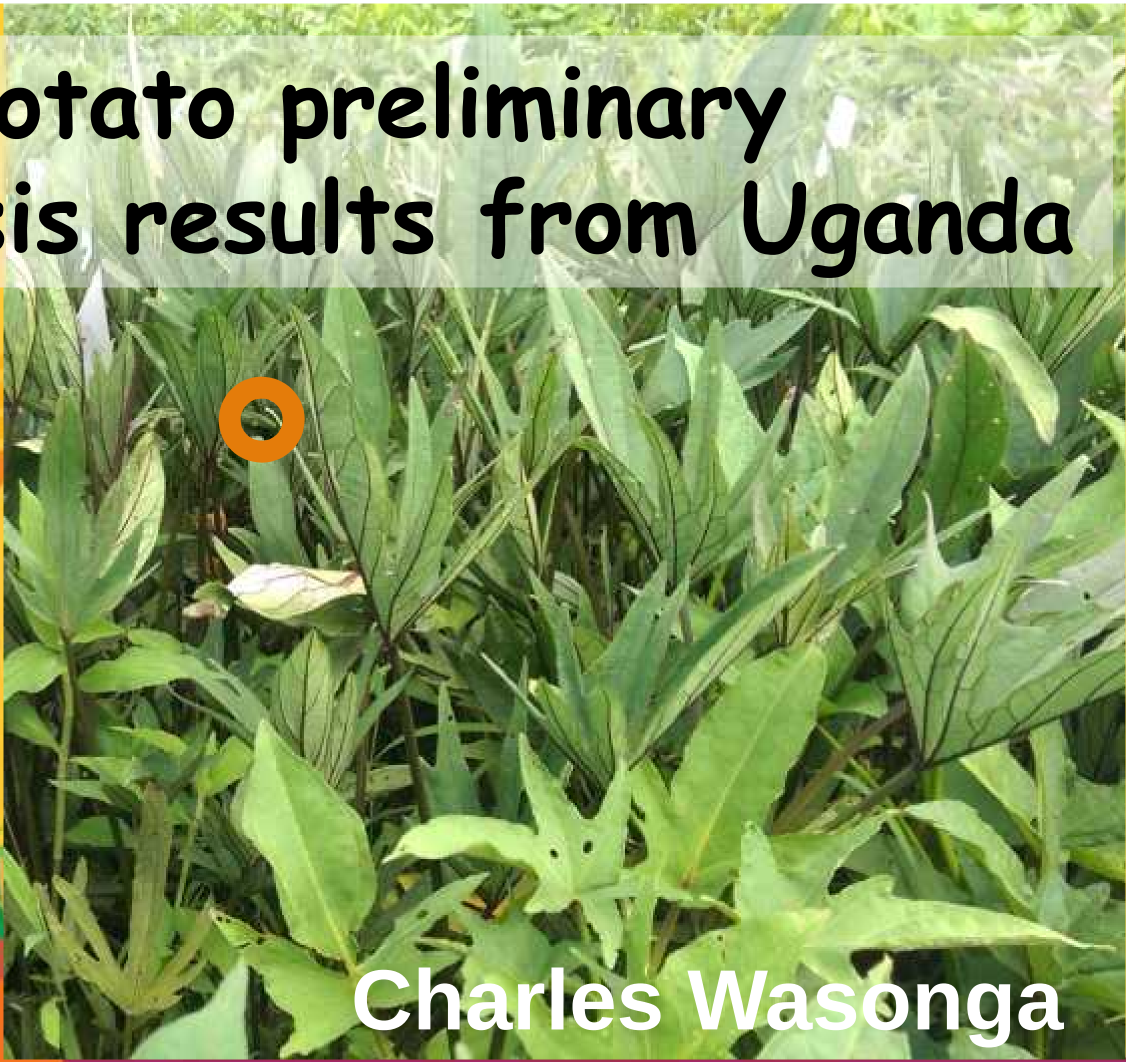
Sweetpotato preliminary heterosis results from Uganda





Charles Wasonga

SWEETPOTATO ACTION FOR SECURITY AND HEALTH IN AFRICA

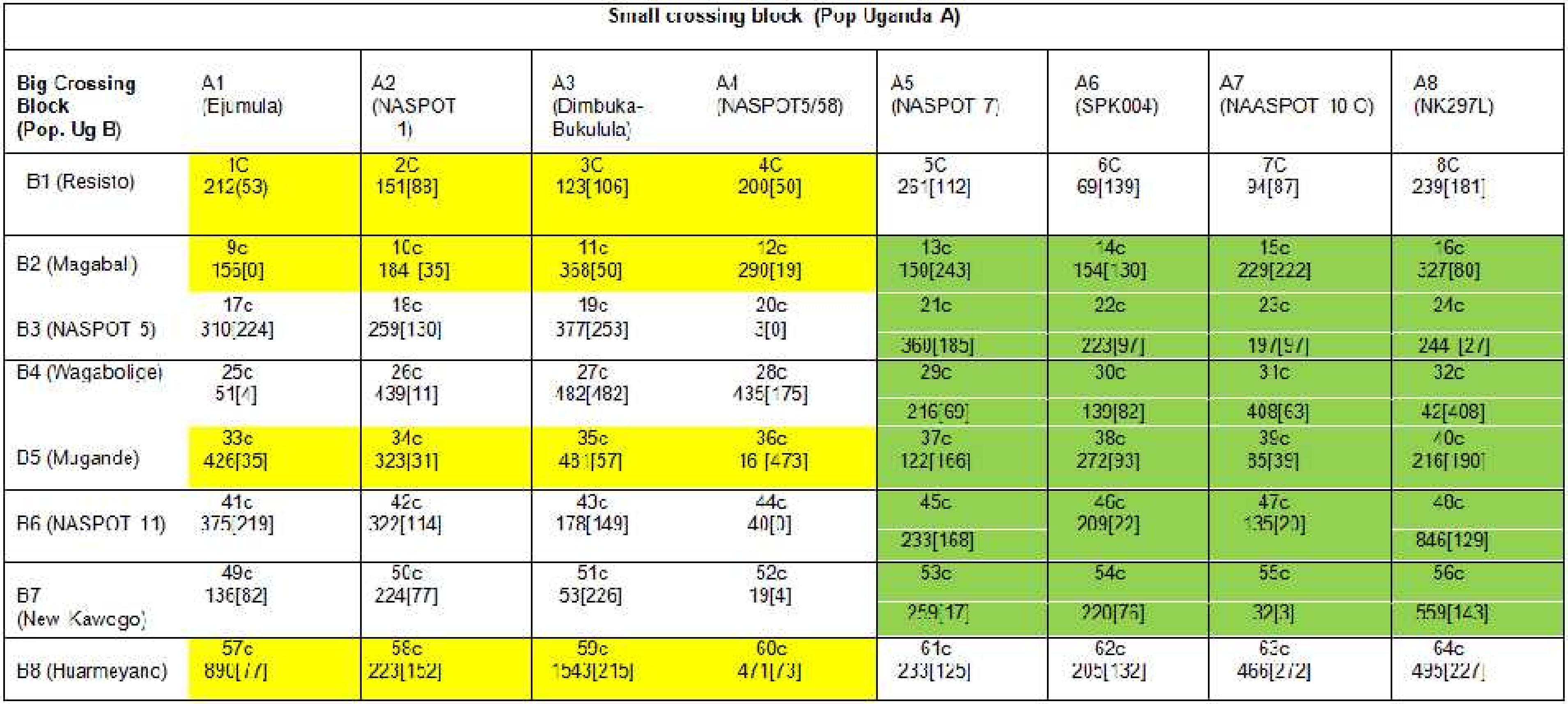
Objectives

The objective of this study was to 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

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

Controlled crosses between the target parents were made by hand

Seed generated from crosses 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 C)	A8 (NK297L)
B1 (Resisto)	1C 212(53)	2C 151[83]	3C 123[106]	4C 200[50]	5C 261[112]	6C 69[139]	7C 94[87]	8C 239[181]
B2 (Magabali)	9c 155[0]	10c 184 [35]	11c 358[50]	12c 290[19]	13c 150[243]	14c 154[130]	15c 229[222]	16c 327[80]
B3 (NASPOT 5)	17c 310[224]	18c 259[130]	19c 377[253]	20c 3[0]	21c 360[185]	22c 223[97]	23c 197[97]	24c 244 [27]
B4 (Wagabolige)	25c 51[4]	26c 439[11]	27c 482[482]	28c 435[175]	29c 216[69]	30c 139[82]	31c 408[63]	32c 42[408]
B5 (Mugande)	33c 426[35]	34c 323[31]	35c 481[57]	36c 16 [473]	37c 122[166]	38c 272[93]	39c 35[39]	40c 216[190]
B6 (NASPOT 11)	41c 375[219]	42c 322[114]	43c 178[149]	44c 40[0]	45c 233[168]	46c 209[22]	47c 135[20]	48c 846[129]
B7 (New Kawogo)	49c 136[82]	50c 224[77]	51c 53[226]	52c 19[4]	53c 259[17]	54c 220[76]	55c 32[3]	56c 559[143]
B8 (Huarmeyano)	57c 890[77]	58c 223[152]	59c 1543[215]	60c 471[73]	61c 233[125]	62c 205[132]	63c 466[272]	64c 495[227]

Seed generated from crosses within Pop Uganda A

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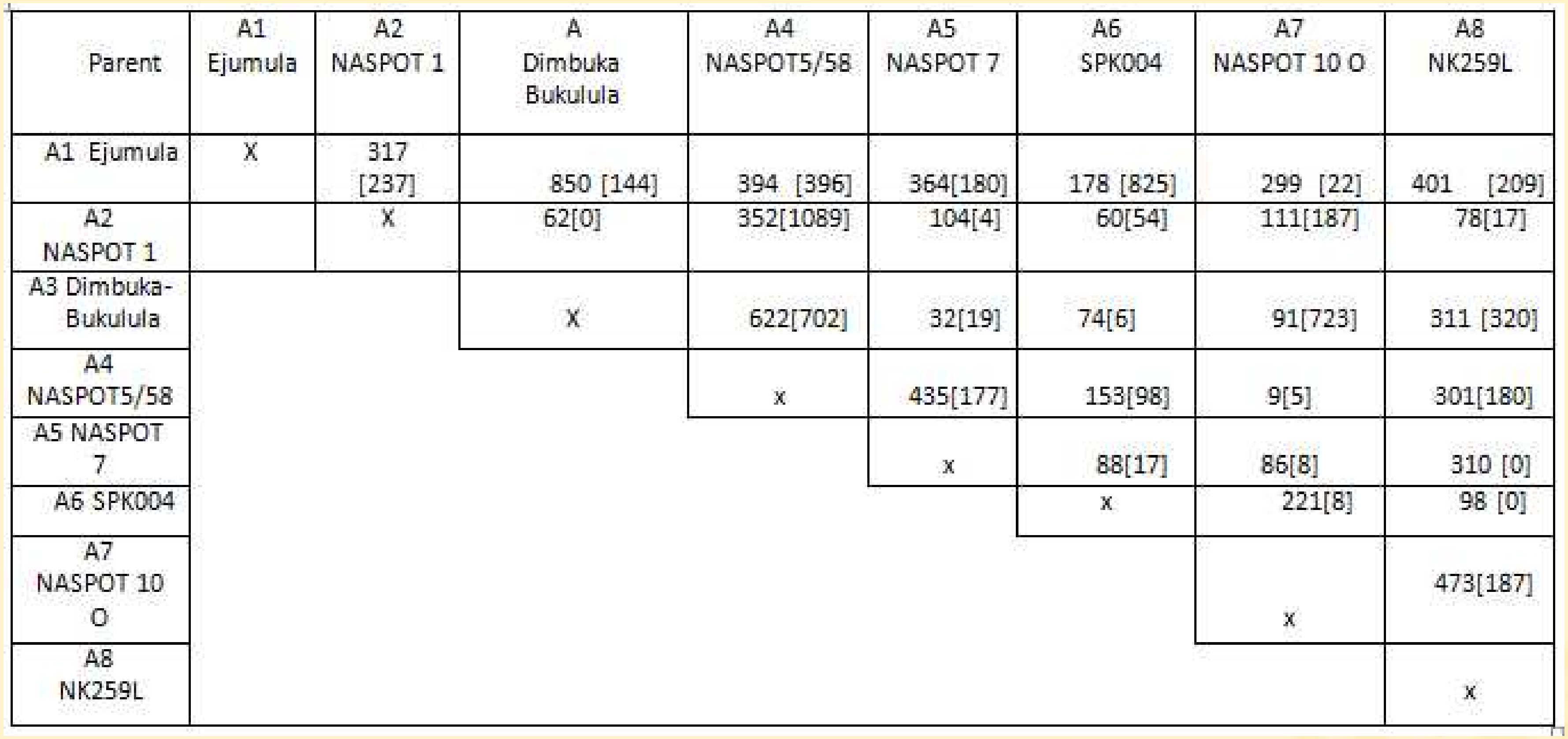
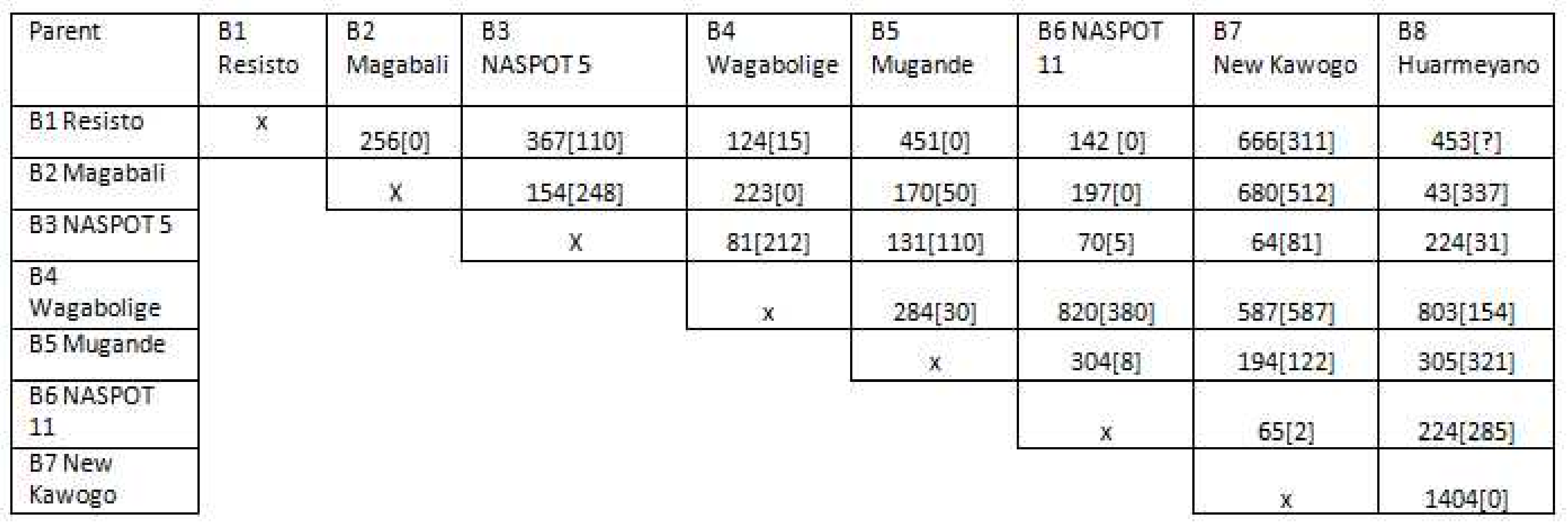


Parent	A1 Ejumula	A2 NASPOT 1	A Dimbuka Bukulula	A4 NASPOT5/58	A5 NASPOT 7	A6 SPK004	A7 NASPOT 10 O	A8 NK259L
A1 Ejumula	X	317 [237]	850 [144]	394 [396]	364[180]	178 [825]	299 [22]	401 [209]
A2 NASPOT 1		X	62[0]	352[1089]	104[4]	60[54]	111[187]	78[17]
A3 Dimbuka-Bukulula			X	622[702]	32[19]	74[6]	91[723]	311 [320]
A4 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 O							x	473[187]
A8 NK259L								x

Seed generated from crosses within Pop Uganda B



Parent	B1 Resisto	B2 Magabali	B3 NASPOT 5	B4 Wagabolige	B5 Mugande	B6 NASPOT 11	B7 New Kawogo	B8 Huarmeyano
B1 Resisto	x	256[0]	367[110]	124[15]	451[0]	142 [0]	666[311]	453[?]
B2 Magabali		X	154[248]	223[0]	170[50]	197[0]	680[512]	43[337]
B3 NASPOT 5			X	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]

Seed resulting from combinations of crosses with the 16 parents germinated and 20 seedlings/clones raised in screen house for each of 120 families generated

The trial was established at two sites (Namulonge and Serere) during seasons one and two of 2014

20 clones planted per family

3 plants per clone

Two reps per site

Incidences and severity of SPVD scored

Incidences and severity of alternaria scored

Incidences and severity of weevil damage scored

Storage root and vine yield recorded

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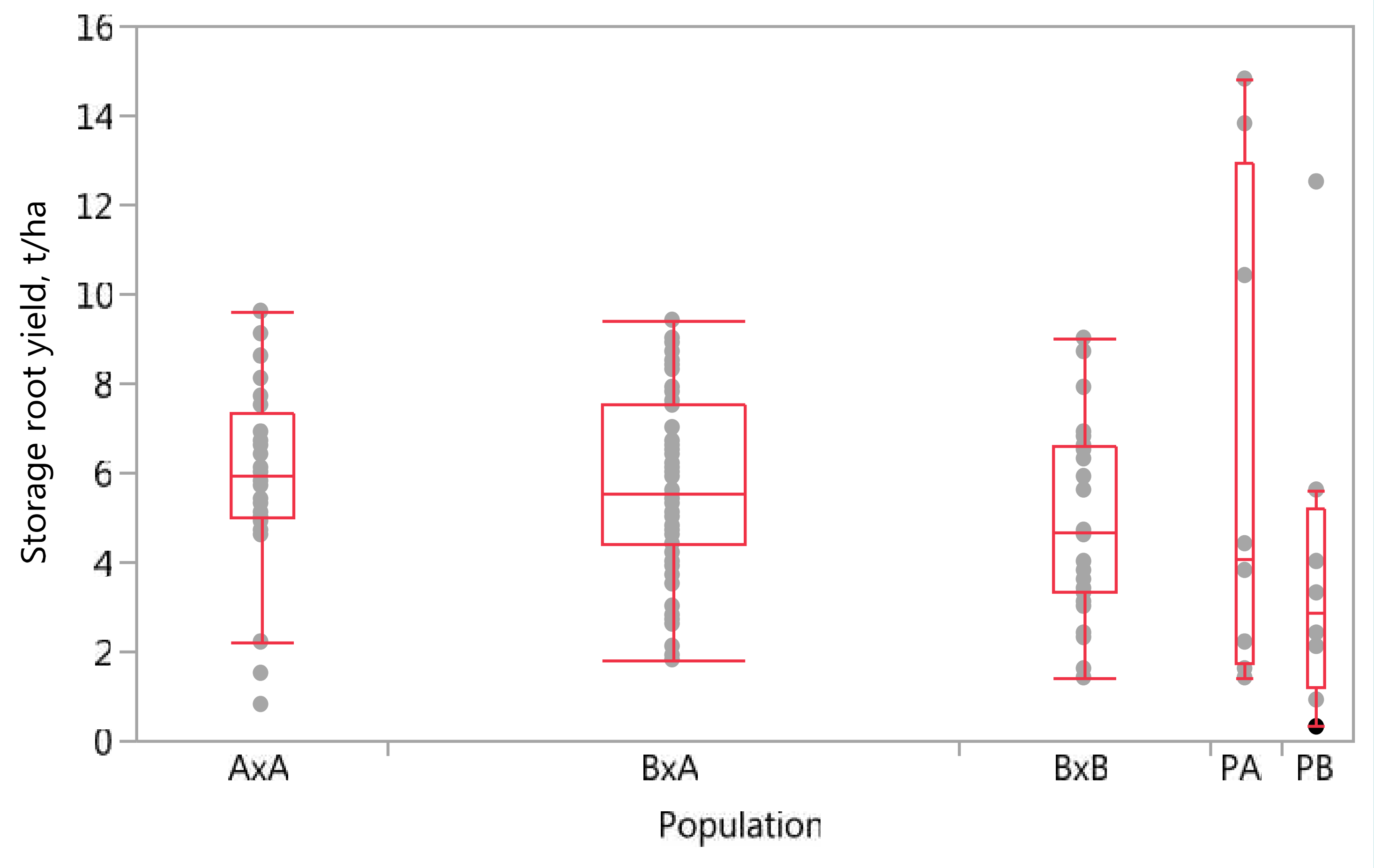
Data analysis

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

Heterosis increment, %

$$= \frac{\underline{[\text{Clone value} - \tfrac{1}{2}(P1+P2)] * 100}}{(\tfrac{1}{2}(P1+P2)}$$

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



Quantiles

Level	Minimum	10%	25%	Median	75%	90%	Maximum
AxA	0.8	2.13	5.025	5.9	7.35	9.15	9.6
BxA	1.8	2.9	4.4	5.5	7.5	8.5	9.4
BxB	1.4	2.23	3.325	4.55	6.575	7.98	9
PA	1.4	1.4	1.75	4.1	12.95	14.8	14.8
PB	0.3	0.3	1.2	2.35	5.2	12.5	12.5

Means and Std Deviations

Level	Number	Mean	Std Dev	Std Err Mean	Lower 95%	Upper 95%
AxA	28	5.97143	2.14508	0.4054	5.1357	6.803
BxA	64	5.66094	1.97979	0.2475	5.1664	6.155
BxB	28	5.01429	2.10532	0.3979	4.1979	5.831
PA	8	6.55000	5.57520	1.9711	1.8890	11.211
PB	8	3.88750	3.86687	1.3671	0.6547	7.120

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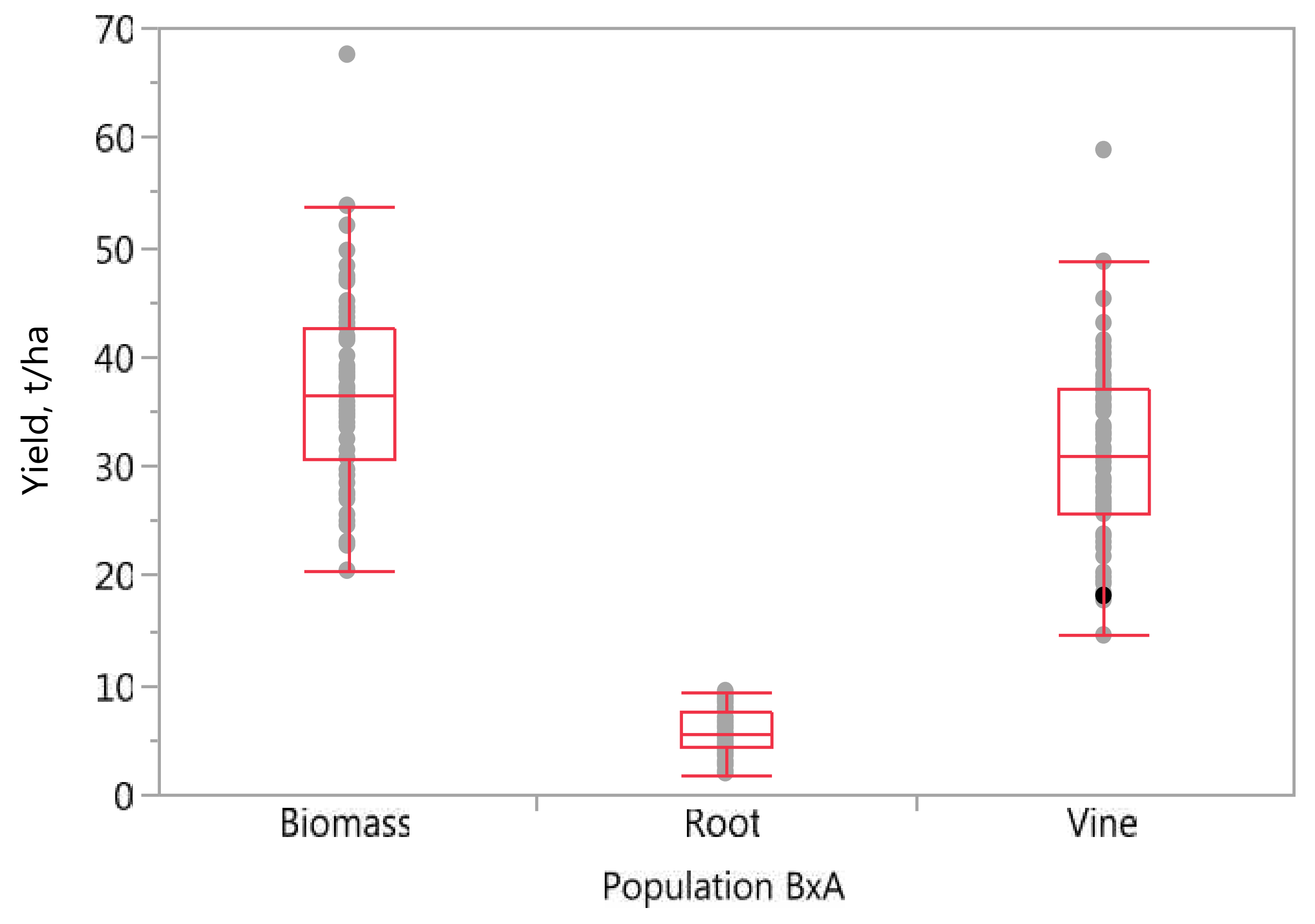

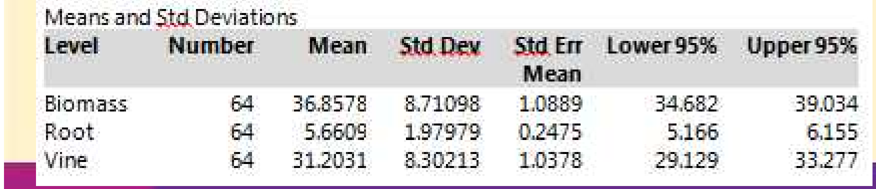
Means and Std Deviations

Level	Number	Mean	Std Dev	Std Err Mean	Lower 95%	Upper 95%
Biomass	64	36.8578	8.71098	1.0889	34.682	39.034
Root	64	5.6609	1.97979	0.2475	5.166	6.155
Vine	64	31.2031	8.30213	1.0378	29.129	33.277

Level	Minimum	10%	25%	Median	75%	90%	Maximum
Biomass	20.4	25.2	30.625	36.5	42.575	47.75	67.5
Root	1.8	2.9	4.4	5.5	7.5	8.5	9.4
Vine	14.5	19.6	25.675	30.95	37.025	40.5	58.8

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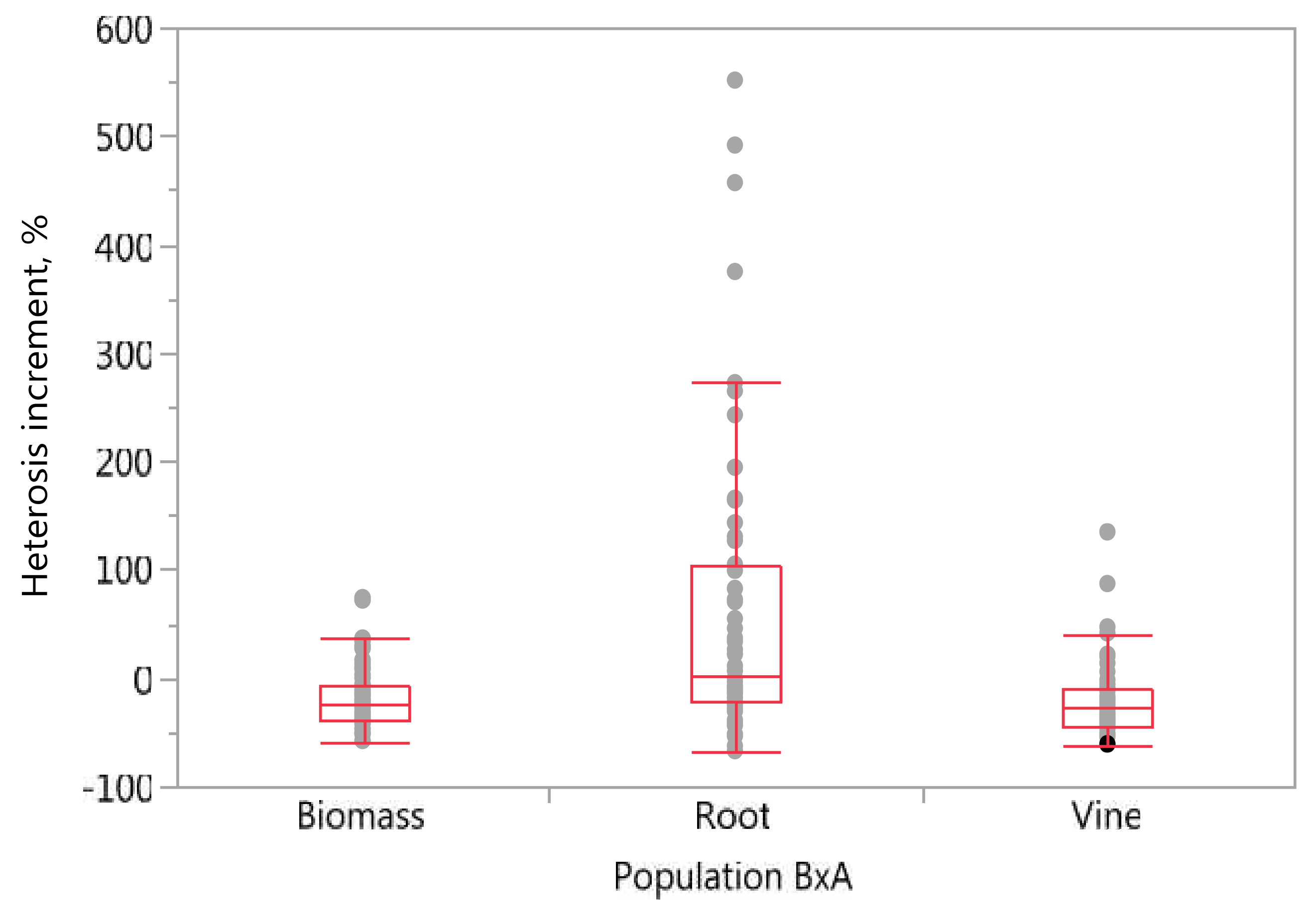
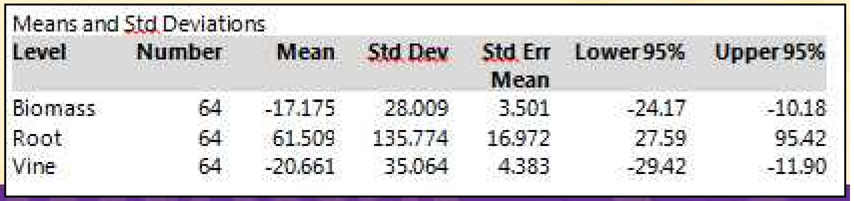


Level	Minimum	10%	25%	Median	75%	90%	Maximum
Biomass	-58.3	-47.55	-37.6	-23.15	-6.575	27.85	73.7
Root	-67.6	-44.3	-21.3	2.85	103.075	253.3	551.1
Vine	-62.7	-54.3	-43.9	-26.4	-8.175	20.95	134.3


Means and Std Deviations

Level	Number	Mean	Std Dev	Std Err Mean	Lower 95%	Upper 95%
Biomass	64	-17.175	28.009	3.501	-24.17	-10.18
Root	64	61.509	135.774	16.972	27.59	95.42
Vine	64	-20.661	35.064	4.383	-29.42	-11.90