Heterosis in Sweetpotato – what do we know, options and where to go?

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Cali - 20/10/2014

Heterosis and Heterosis increments

Offspring is superior to the mid-parent performance – heterosis increment or heterotic gain

$\bar{F}1 > \frac{(P1+P2)}{2}$ where $\bar{F}1$ is the family mean and P1 and P2 is the parental performance

$\bar{F}1$ offspring in clonally propagated crops is the family derived from a cross – such F1s are segregating we need estimates of the mean across all clones of a family <u>without selection</u>! – note in heterotic cross combinations / families you still can select for "the best" clone

Why? For better population improvement (for increasing the frequencies of good crosses) – it is not for developing hybrid varieties (each clone is a already a hybrid variety)

Target: Generate and select systematically from better / "fortified" populations through the advantages of heterosis exploiting breeding scheme <=> reciprocal recurrent selection, respectively.

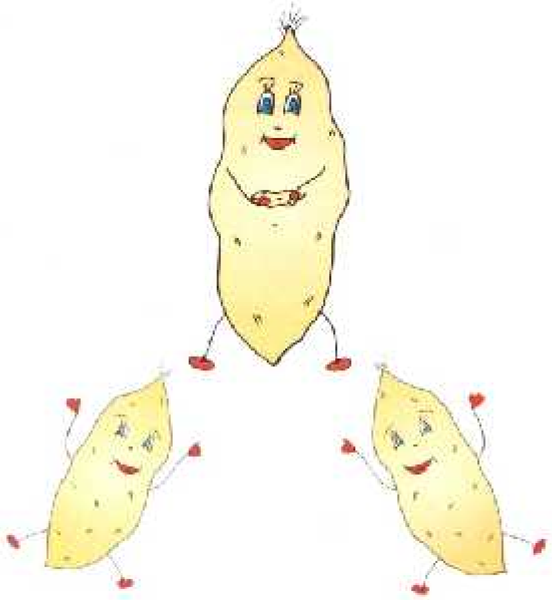


Fig. Illustration of Heterosis

What do we have for sweetpotato?

A) Comments / publications from heterosis gurus:
(Hull, Melchinger) – but they do not work with clonally p. crops

B) Heterosis increment studies in sweetpotato:

1) **Mega-clones** (important clones across regions) **– 4 x 12 crosses (48 families) –** without separation of genepools, without selection of recombining ability, without inbreeding.
2) **PJ1 x PZ1 population (two populations at CIP developed independently since 2004) - 231 families clones (49 PJ parents and 31 PZ parents)** - with separation of genepools, without selection of recombining ability, without inbreeding.
3) **A x B population with 8 x 8 parents (64 families) from Namulonge tested at Namulonge)** - with separation of genepools, without selection of recombining ability, without inbreeding.
4) **A x B population with 8 x 8 parents (64 families) from Namulonge tested at Umbelusi / Mozambique)** - with separation of genepools, without selection of recombining ability, without inbreeding.

(5) PJ and PZ populations (tracing back to 49 PJ parents and 31 PZ parents - with separation of genepools, without selection of recombining ability, with inbreeding, ready to cross PJ" x PZ" **to determine the gain of one complete reciprocal recurrent selection cycle**

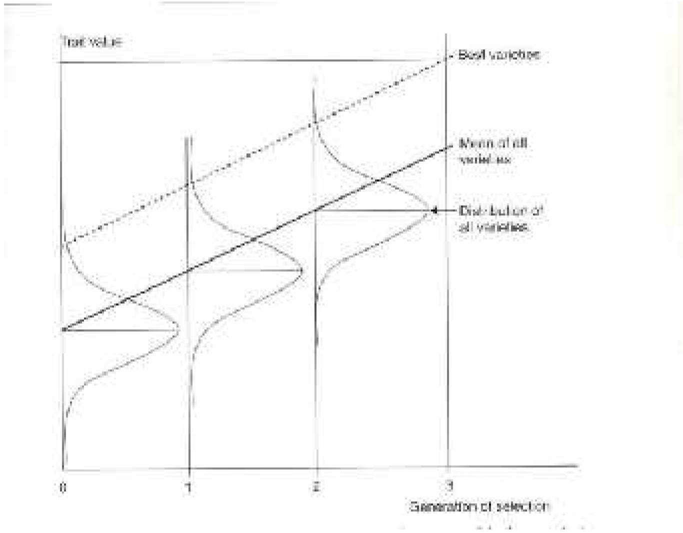


Illustration what we want – this is efficiently generating better populations !!!

Better for yield and yield stability (exploiting the phenomena heterosis) and better for quality and biotic stress resistance (by allowing more inbreeding within mutually heterotic genepools)

Heterosis increments in sweetpotato - Family means in offsprings derived from 4x12 cross combinations

Are there offspring means clearly superior to mid-parent performance?

Yes

Go decision to estimate offspring means with parents in applied breeding material by

PJ05 x PZ06

Table 1. Storage root yield (t/ha) of four male and 12 female sweetpotato parents (underlined), their offspring means and heterosis increments of offspring on basis of mid-parent – mid-offspring estimates (italics) evaluated at two locations, San Ramon and La Molina, in Peru.

Parents		**INIA100** **(25.2)**		**Zapallo** **(22.0)**		**Wagabolige** **(10.9)**		**Tanzania** **(23.3)**	
SR02.132	(33.5)	26.8	(-8.5%)	21.5	(-22.5%)	17.3	(-21.9%)	28.4	(-0.1%)
SR01.024	(11.7)	19.5	(5.6%)	20.8	(23.3%)	16.8	(48.9%)	22.5	(28.5%)
SR01.022	(12.7)	16.6	(-12.4%)	19.1	(9.9%)	14.2	(20.6%)	22.7	(26.0%)
LM02.082	(18.4)	19.4	(-11.2%)	23.9	(18.3%)	16.6	(13.4%)	23.3	(11.5%)
SR02.174	(22.7)	27.4	(14.7%)	**28.8**	**(28.9%)**	**26.6**	**(58.7%)**	28.2	(22.6%)
SR02.177	(41.3)	23.2	(-30.3%)	22.9	(-27.8%)	17.3	(-33.7%)	25.2	(-22.0%)
LM02.032	(23.1)	20.3	(-16.1%)	19.2	(-15.1%)	15.6	(-8.0%)	21.5	(-7.4%)
LM02.035	(13.7)	18.2	(-6.4%)	18.9	(5.8%)	15.1	(23.2%)	17.9	(-3.0%)
SR90.021	(4.6)	14.6	(-1.8%)	11.5	(-13.9%)	11.1	(43.5%)	13.1	(-6.6%)
SR01.029	(8.6)	15.0	(-11.3%)	13.8	(-10.1%)	10.9	(12.1%)	14.6	(-8.5%)
SR01.005	(11.5	15.1	(-17.7%)	12.9	(-23.0%)	8.0	(-28.7%)	12.7	(-27.0%)
SR01.002	(32.1)	24.5	(-14.5%)	19.1	(-29.6%)	18.3	(-15.1%)	20.3	(-26.7%)

Mid-parent to mid-offspring correlation r = 0.705, Pearson's correlation coefficient, N = 48.

Examples for heterosis increments we find in the crosses:

!! Wagabolige x SR02.174 (58.7%) !! or

!!! Zapallo x SR02.174 (28.9%) !!!

Heterosis increments in a hybrid population derived by crossing two mutually heterotic genepools

PJ05 & PZ06 are two mutually heterotic genepools so far without selection on combining ability

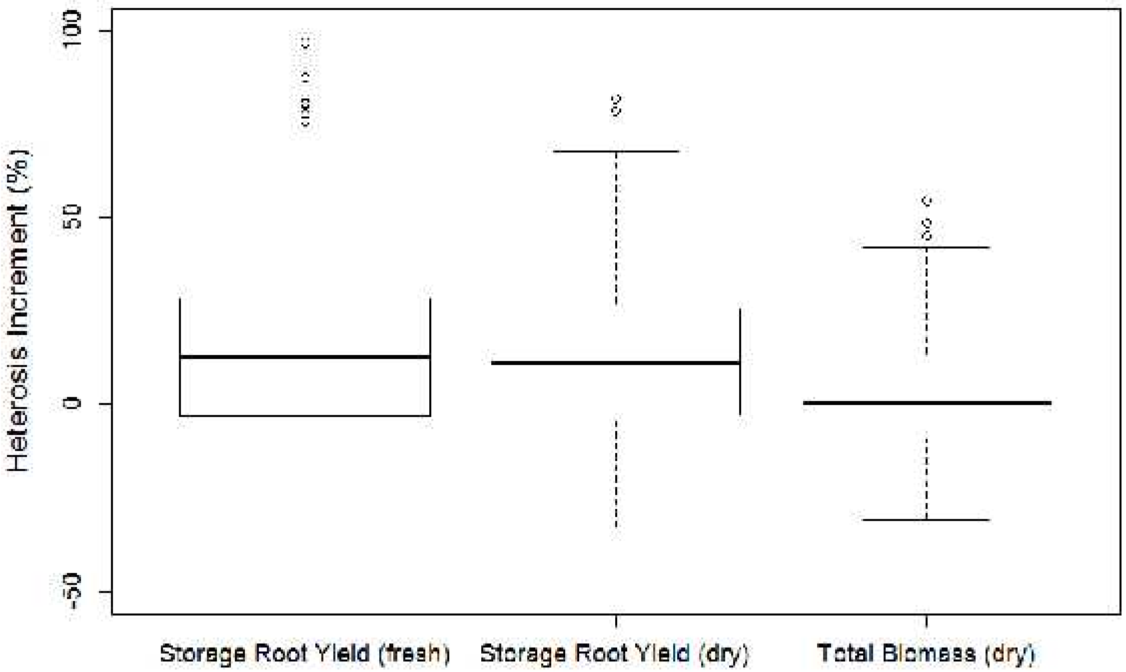
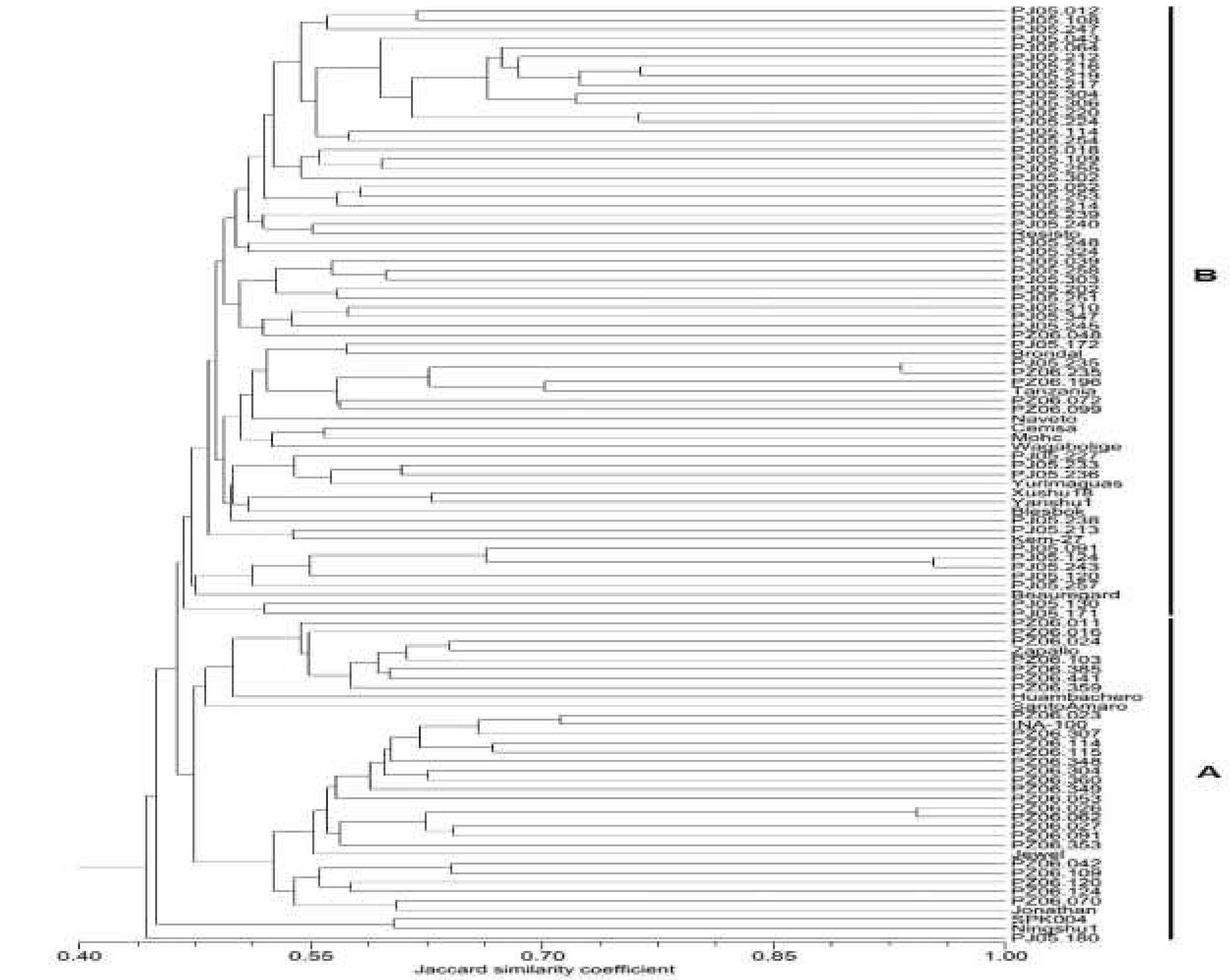


Figure: Mid parent – mid offspring heterosis increments in 231 families (means) for fresh storage root yield, dry matter storage root yield, and dry matter biomass yield – Note each boxplot shows the distribution of 231 family means - In total 6898 offspring clones tracing back to 31 PZ and 49 PJ parents recombined in 231 cross combinations / families tested at two locations and two plot replications

The Populations PJ and PZ in Lima



PJ clones belong to the Breeding Population Jewel

PZ clones belong to the Breeding Population Zapallo-SPKI

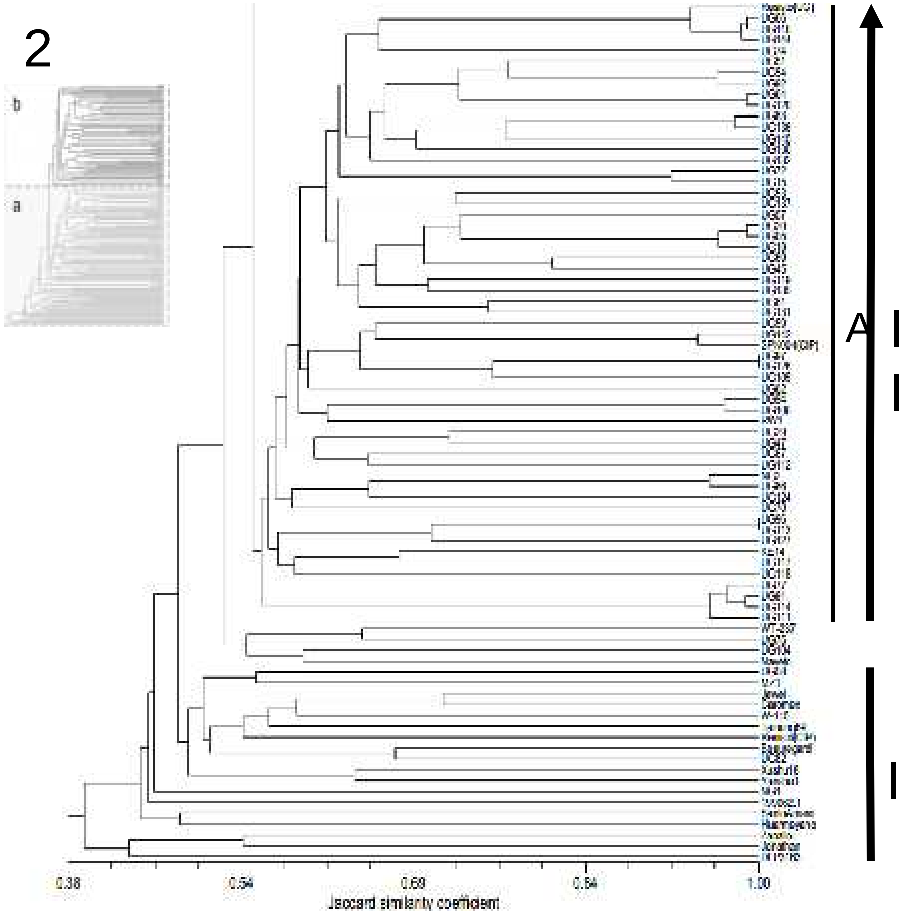
Clones with names are 22 Mega Clones (important clones in different regions of the world

The heterotic breeding populations in Lima are clearly two genepools on basis of molecular characterization by SSR markers and they are mutually heterotic!!

Figure: Molecular characterization of the heterotic genepools PJ and PZ by 60 SSR marker (Diaz manuscript) Similar studies EA germplasma (Tumwegamire et al. 2011); Parental material EA breeding plat form (David 2012)

The Populations in Uganda

2



Seperation of 150 polycross parents into

II) Genepool A East African material

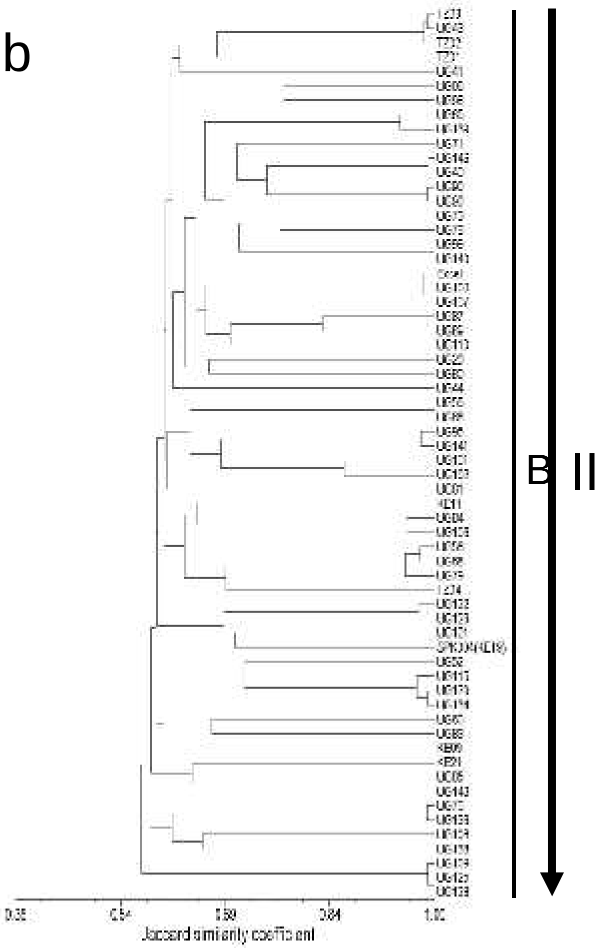
I) And material mainly from other parts of the world

Figure:

Similar studies EA germplasma (Tumwegamire et al. 2011); Parental material EA breeding plat form (David 2012)

The Populations in Uganda

2.b



Genepool B East African material

What was made with Genepool A and B? 16 clones were selected (8 from each pool) – criteria would have been crossed anyway

Design of 8x8 heterosis experiment

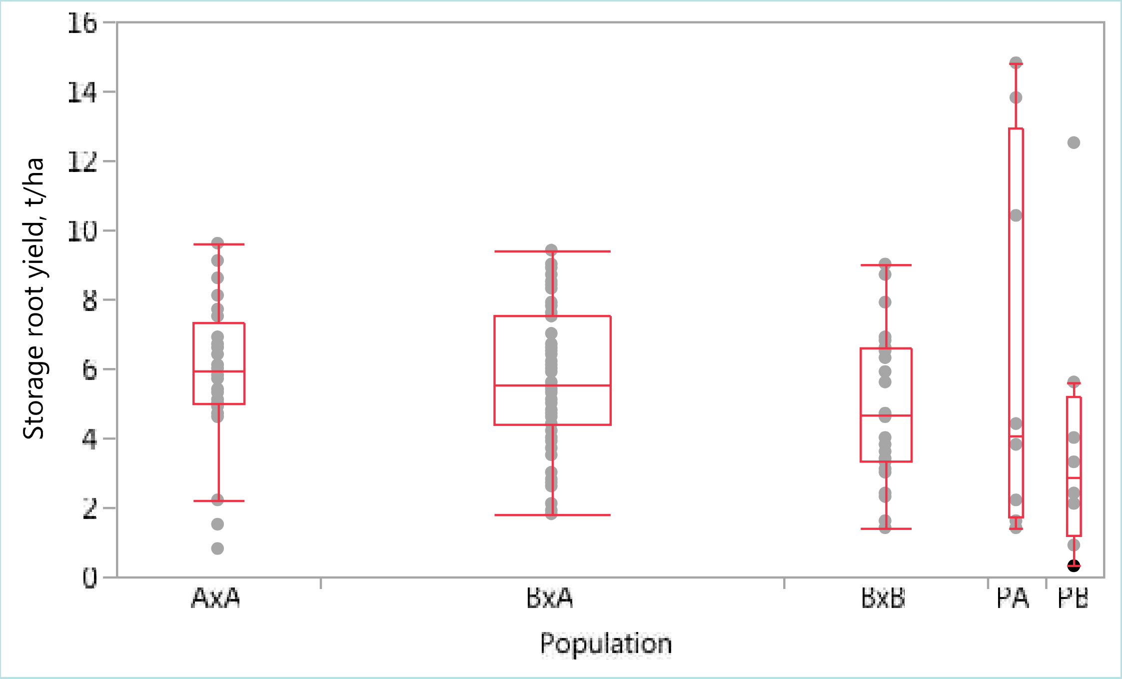
Recombination of 8 parents of genepool A with 8 parents of genepool B (64 families)

20 clones of each cross combination are tested in 2014/15 in Uganda and Mozambique

Figure:

Similar studies EA germplasma (Tumwegamire et al. 2011); Parental material EA breeding platform (David 2012)

The Populations and parents in Uganda



Overall Heterosis increment for AxB population

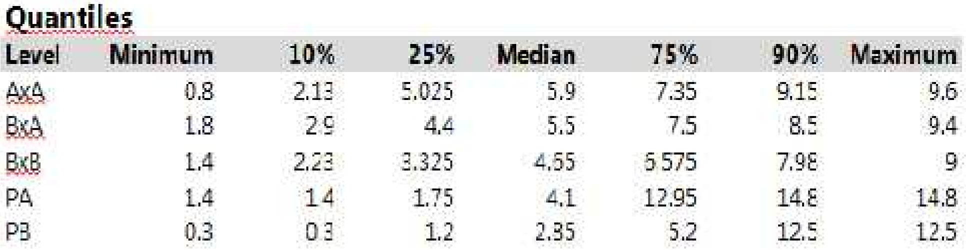
H = 5.7 – (6.6 + 3.9) / 2 / (6.6 + 3.9)/2 *100

= (5.7 - 5.3) / 5.3 * 100

= 7.6 % overall

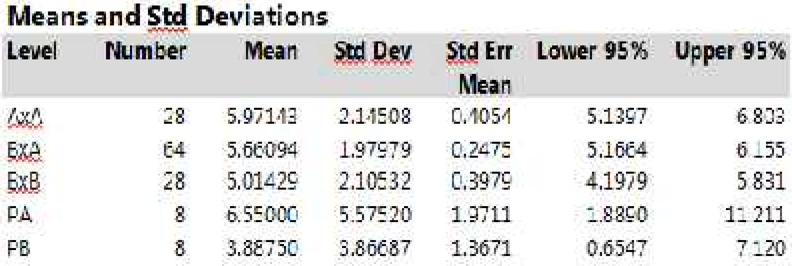
Please note there were 3 parents in this experiment performing extremely well in this experiment and only 2 x 8 parents

Important 8 x 8 table for these results including parental yield to get a better overview what is happening here



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

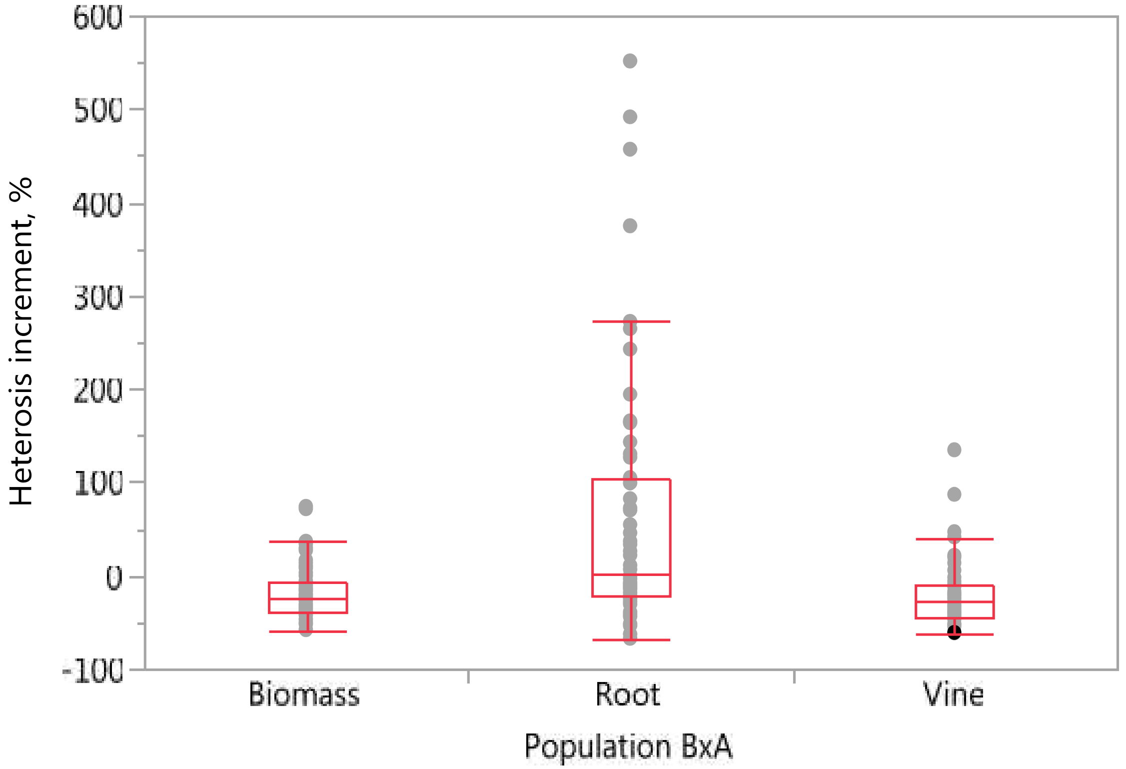


Means and Std Deviations

Level	Number	Mean	Std Dev	Std Err Mean	Lower 95%	Upper 95%
AxA	28	5.97143	2.14508	0.4054	5.1397	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

AxB population from Uganda in Uganda

8Ax8B parents



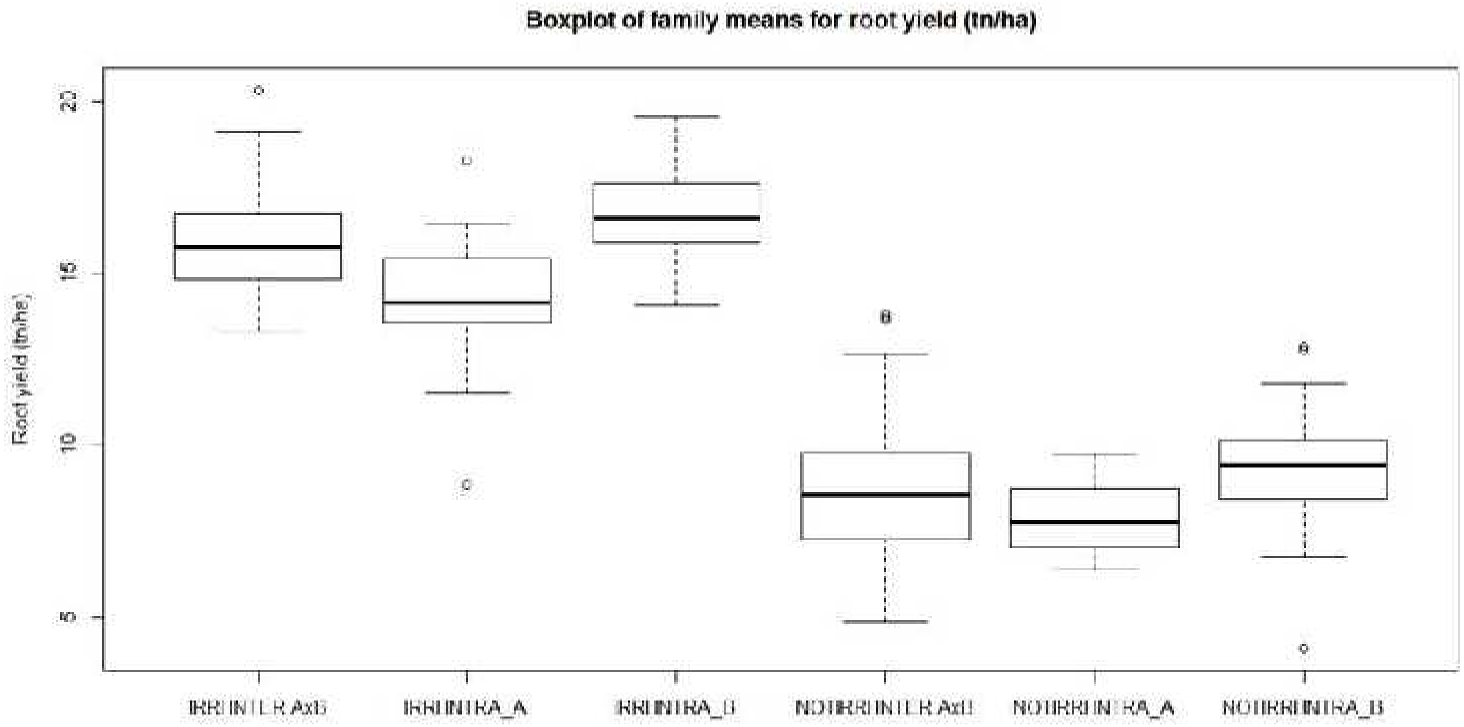
Level	Minimum	10%	25%	Median	75%	90%	Maximum
Biomass	-58.3	-47.6	-37.6	-23.2	-6.6	27.9	73.7
Root	-67.6	-44.3	-21.3	2.9	103.1	253.3	551.1
Vine	-62.7	-54.3	-43.9	-26.4	-8.2	21.0	134.3

With respect to storage root yield 16 out of 64 cross combinations were observed with heterosis increments >100%

Heterosis increments were observed up to 74, 551, and 134.3% for fresh biomass, storage root yield and vine yield, respectively; however, still further data checking required for example which cross combinations generate extreme high heterosis increments !!!

8x8 table with yield and heterosis increment values of families and parental (performance see table 1 for 4 x 12 mega clone cross)

AxB Population from Uganda in Mozambique



Next steps for heterosis exploiting breeding schemes and/or better population improvement in sweetpotato

Step 1: Intensive data checking !!

Step 2a: Publish!

Step 2b: Complete reciprocal recurrent selection cycle and corresponding genetic gains (80 parents versus new hybrid population and selected parents)! …. The expectations are high for yield as well as quality such as Fe and Zn (inbreeding for quality without sacrificing out breeding)

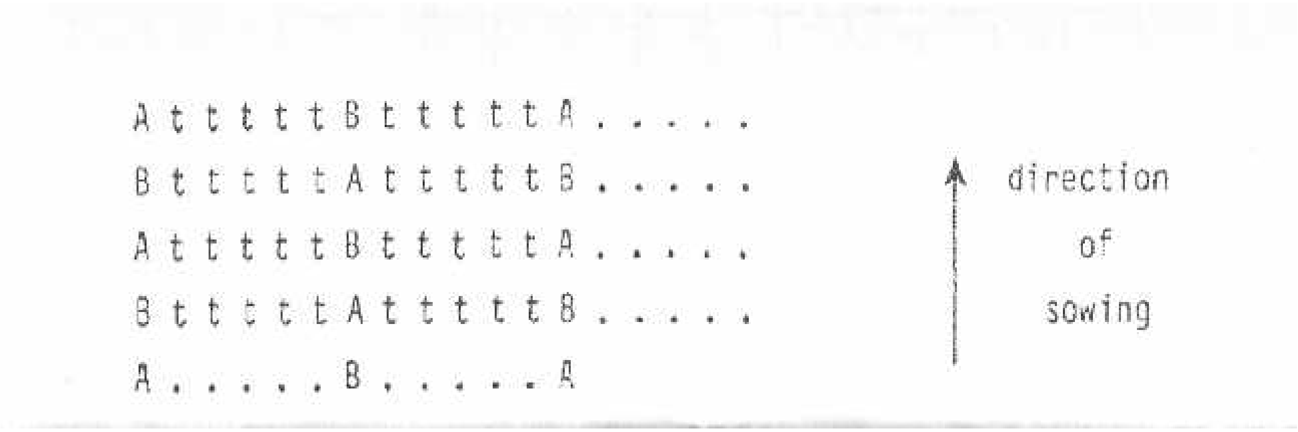
Shall we or shall we not continue?

Step 3: Make more secure experiments especially when we make large experiment (checks - Westscott and Kempton design – sacrify in experiments with > 100 genotypes 10% of the test capacity for security – 10% security tax) – my opinion 120% yes

Step 4a (suggestion): Combine yield and SPVD resistance selection in a heterosis exploiting breeding scheme at Namulonge cross 40-50 parents from each pool (huge step !!) and select 20 – 25 parents in each pool on basis of offspring performance (target high yielding breeding population+ the plus stands for 5% frequency of SPVD resistance – my opinion 80 to 90% yes – one criteria could be would we like to repeat the good cross combinations and / or would we like to select all "bad family makers" (in 8 x 8 we have 16 parents - we can't select much among parents in the 8x8 experiment with respect to family makes because these are only 16 parents)

Step 4b (suggestion): We select testers on basis of 8x8 results - 3 to 4 testers in each pool and then we cross all clones in pool A and B, respectively, against these 3 to 4 testers – my opinion 50 to 60% yes

Making trials more secure – especially the large trials > 100 clones



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A t t t t t B t t t t t A . . . . .
B t t t t t A t t t t t B . . . . .
A t t t t t B t t t t t A . . . . .
B t t t t t A t t t t t B . . . . .
A . . . . . B . . . . . A
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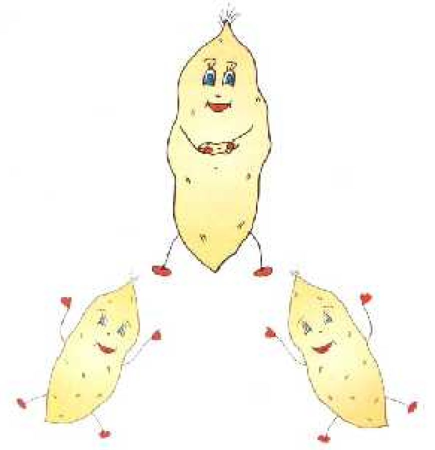
From Kempthon 1984 - see also Peters et al 1992 for company Stube – origin Westcott 1981

Check clones – Cemsa and Dagga



Thank-you for your Attention