

Practical approaches to the systematic exploitation of heterosis in sweetpotato breeding: How far?

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6th Annual SPHI Technical and Steering Committee Meeting, Kigali, Rwanda,

29 Sept – 2 Oct 2015







Heterosis & Heterosis increments

- Heterosis increments (heterotic gains) -Offspring is superior to mid-parent performance $\overline{F1} > \frac{(P1)}{P1}$
- \overline{F} offspring is the family from a cross
- In clone breeding the F1s are segregating, need to estimate the mean across all clones of the family without selection!
- In heterotic cross combinations/families, we can still select for "the best" clone
- Why? For better population improvement (or to increase frequencies of "good" crosses) Not to develop hybrid varieties (a clone is already a hybrid variety)

Target: Generate and select systematically from better/"fortified" populations via the advantages of heterosis exploiting breeding schemes



Fig 1. Heterosis [Parental performance (P1, P2), & F1 offspring]

What do we have for sweetpotato?

- A) Comments / publications from heterosis gurus: (Hull 1945, Melchinger 1998)
- B) Heterosis increment studies in sweetpotato:
- Mega-clones (important clones across regions) 4 x 12 crosses (48 families) – no separation of genepools, no selection of recombining ability, no inbreeding (up 60% heterosis increment)
- 2) PJ1 x PZ1 population (two populations at CIP developed independently since 2004) 231 families (49 PJ parents and 31 PZ parents) no separation of genepools, no selection of recombining ability, no inbreeding (up to 80% heterosis increment.)
- 3) A x B population with 8 x 8 parents (64 families, 20 genotypes per family) from Namulonge tested at Namulonge) genepools separated, no selection of recombining ability, no inbreeding (>100% heterosis increment; across all crosses still quite small).



Fig 2. Illustration of what we want – this is efficiently generating better populations !!!

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

What do we have for sweetpotato?

B) Heterosis increment studies in sweetpotato:

- 1) A x B population with 8 x 8 parents (64 families) from Namulonge tested at Umbelusi / Mozambique) genepools separated, no selection of recombining ability, no inbreeding (>100% heterosis increment, across all crosses still quite small). => A and B are not much mutually heterotic, but this can developed)
- 2) PJ and PZ populations (tracing back to 49 PJ parents and 31 PZ parents genepools separated, selection of recombining ability, with inbreeding, and now in cross " PJ x PZ" to determine gains after one complete reciprocal recurrent selection cycle for various purposes (WA & EA, Non-sweet (NS), high iron (HI), wide adaptation & earliness) => three hybrid populations)



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

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

Table 1. Storage root yield (t/ha) of 4 male and 12 female (only 6 shown) sweetpotato parents (underlined), their offspring means and heterosis increments of offspring based on mid-parent – mid-offspring estimates (percentage) evaluated at 2 locations, San Ramon and La Molina, in Peru.

Yes	Parents		INIA100		Zapallo		Wagabolige		Tanzania	
That was the go			<u>(25.2)</u>		<u>(22.0)</u>		<u>(10.9)</u>		<u>(23.3)</u>	
decision to estimate	SR02.132	<u>(33.5)</u>	26.8	(-8.5%)	21.5	(-22.5%)	17.3	(-21.9%)	28.4	(-0.1%)
with parents in applied breeding material by	LM02.082	<u>(18.4)</u>	19.4	(-11.2%)	23.9	(18.3%)	16.6	(13.4%)	23.3	(11.5%)
	SR02.174	<u>(22.7)</u>	27.4	(14.7%)	28.8	(28.9%)	26.6	(58.7%)	28.2	(22.6%)
	SR02.177	<u>(41.3)</u>	23.2	(-30.3%)	22.9	(-27.8%)	17.3	(-33.7%)	25.2	(-22.0%)
PJ05 x PZ06	SR90.021	<u>(4.6)</u>	14.6	(-1.8%)	11.5	(-13.9%)	11.1	(43.5%)	13.1	(-6.6%)
	SR01.002	(32.1)	24.5	(-14.5%)	19.1	(-29.6%)	18.3	(-15.1%)	20.3	(-26.7%)

Examples of heterosis increments in the crosses:

Wagabolige x SR02.174 (58.7%) !! or Zapallo x SR02.174 (28.9%) !!!

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

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

Heterosis increments on average across all PJ05 & PZ06 crosses show us that these pop. are two mutually heterotic genepools and so far without the push of selection on combining ability (NB: the pops have a different gen. background)



Fig 3. 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

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 based on molecular

 characterization by SSR markers and they are mutually heterotic!!

Fig. 4. 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 platform (David 2012)

Populations in Uganda



Fig. 5. Separation of 150 polycross parents into 2 genepools. Similar studies EA germplasm (Tumwegamire et al. 2011); Parental material EA breeding platform (David 2012)

Populations in Uganda

2.b



Genepool B East African material

What was done 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 were tested in 2014/15 in Uganda and Mozambique

Fig. 6. Genepool B East African material. Similar studies EA germplasma (Tumwegamire et al. 2011); Parental material EA breeding platform (David 2012)

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

= 7.6 % overall

NB: 3 parents performed extremely well and only 16 (2 x 8) parents used Important 8 x 8 table for these results including parental yield to get a better overview of what is happening here

Quatiles	Percent				
Level	Min	Median	Max		
AxA	0.8	5.9	9.6		
BxA	1.8	5.5	9.4		
BxB	1.4	4.7	9.0		
PA	1.4	4.1	14.8		
PB	0.3	2.9	12.5		

Level	No	Mean	Std	Std Err	Lower	Upper	
			Dev	Mean	95%	95%	
AxA	28	5.971	2.145	0.4054	5.1397	6.803	
BxA	64	5.661	1.98	0.2475	5.1664	6.155	
BxB	28	5.014	2.105	0.3979	4.1979	5.831	
PA	8	6.55	5.575	1.9711	1.889	11.21	
PB	8	3.888	3.867	1.3671	0.6547	7.12	

AxB population from Uganda in Uganda

8Ax8B parents



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)

Quantiles	Percent							
Level	Min	10	25	Median	75	90	Мах	
Biomass	-58.3	-47.55	-37.6	-23.15	-6.575	27.85	73.7	
Root	-67.6	-44.3	-21.3	2.85	103.08	253.3	551.1	
Vine	-62.7	-54.3	-43.9	-26.4	-8.175	20.95	134.3	

_AxB Population from Uganda in Mozambique

Boxplot of family means for root yield (tn/ha)



Next steps for heterosis exploiting breeding schemes

GW(5

How to get heterosis exploiting breeding schemes into practice in clone breeding

- I) First look to other crops especially maize:
- 1) We with sweetpotato do not have the driving factor, "hybrid seed"

2) **Seed** was not the only factor driving **maize hybrid breeding/varieties**, especially the adoption – that was **drought** in the **mid 1930s** in the US (before the drought all were open pollinated varieties in the mid-west after the drought nearly all used hybrid varieties)

3) After this step there was **tremendous genetic gains due to inbreeding** (quality and resistances)

- without sacrificing yield and yield stability due to outbreeding and the yield jumps from heterosis and heterosis increments
- and the economic gains from the seed industry to invest more in breeding (there was no homogenous hybrid varieties at first all were 4 way crosses, and many crops later even started with population hybrids such as rye)

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Next steps for heterosis exploiting breeding

GW(7

II) Which strategy do we follow to get heterosis exploiting breeding schemes in to practice?

- At the point where we need much more inbreeding for quality (nonsweet) and high iron) – Lima – with the secret hope to get a spill over to potato and the potato breeding industry in the US
- 2) At the point where we need much more inbreeding for resistance (SPVD) – Namulonge – this devil is dominating and resistance is recessive => you need rrrrr in sweetpotato)
- 3) Do it right (especially for the time being) recombine many parents to get all bad family makers out of the populations (we have about 150 parents at Namulonge) Jan we need staff to cross and in three years our hybrid population will have much higher SPVD resistance + good yields (the quality we already have with respect to dry matter & BC)

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Thank-you for your Attention