CONVENTIONAL BREEDING STRATEGIES

ABS - Polycross versus Controlled cross - Heterosis

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SP-breeding – Malawi - 20/06/2014

Polyploidy and Genetics of SP

- **Heterozgous genotypes occur at much larger frequencies in 6x** than in 2x (see Fig. 1a) => heterosis much more important in 6x than in 2x – for quantitative traits (yield, yield stability, earliness & vigor = drought resistance etc.
- **Recessive inherited traits are much more difficult to fix** (see Fig. 1b) – inbreeding much more difficult to achieve in 6x than 2x – for some traits we want strong inbreeding such as SPVD (and quality traits)

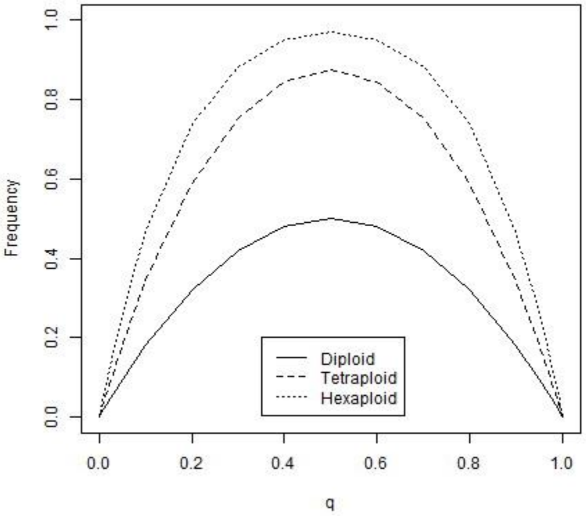


Fig 1a. Effect of ploidy level on the frequency of heterozygous genotypes (modified from Gallais 2003 by introducing to 6x curve

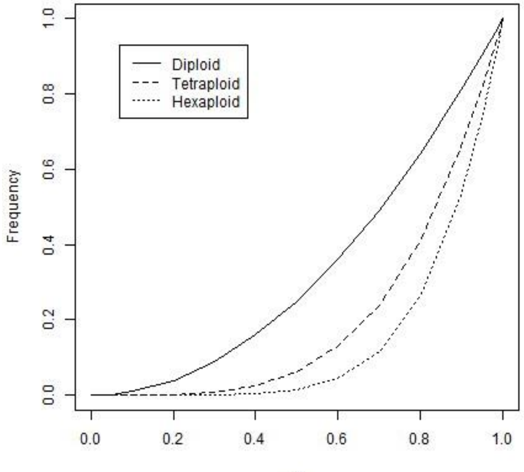


Fig 1b. Effect of ploidy level on the frequency of phenotypes expressing a one locus recessive inherited trait as a function of the allele frequency of the recessive allele.

ABS – Accelerated Breeding Scheme

Plot size: 1m row plot in early breeding stages not more not less and no plot replications !!!

ABS – Accelerated Breeding Scheme

Table 1. Variance components and operative heritability for observed traits[†] in early breeding stages of the population ‘Jewel 2005’ planted at three locations (Loc) in Peru (San Ramon, La Molina and Cañete) without replications in 1-m row plots.

Traits	σ^2_G	σ^2_{GxE}	σ^2_E	N clones	N Loc	h^2
Storage root yield, t^2/ha	47.7	23.2	98.0	4175	3	**0.59**
Foliage yield, t^2/ha	237.0	52.1	349.0	4167	2	**0.58**
Dry matter content of roots, % FM[§]	13.94	8.18	6.22	2709	2	**0.82**
Carotene content of roots, ppm DM[§§]	33651	3453	9539	2709	2	**0.88**
Iron content of roots, ppm DM[§§]	7.41	5.79	7.61	2709	2	**0.66**
Zinc content of roots, ppm DM[§§]	**3.10**	**4.63**	**2.92**	**2709**	**2**	**0.68**

† Variance components: σ^2_G = genotypes, σ^2_E = environments, σ^2_{GxE} = genotype by environment interactions; h^2= operational broad-sense heritability.

§ FM = fresh matter; §§ DM = dry matter.

ABS – Accelerated Breeding Scheme

Table 2. Variance component estimations on basis of 2 environments and 2 replications for observed traits for populations generated in different ways from a similar set of parents (22 parents).

	Var comp	Root yield (t^2/ha^2)	Upper biomass (t^2/ha^2)	Harvest index (%^{2})	Storage root dry matter (%^{2} fwb[§])	Starch (%^{2} dwb[§§])	b-carotene NIRS (mg^2 / 100g^2 fwb[§])	Fe (ppm^2 dwb[§§]
Pop – Poly-cross ws[†] (N=1021)	G	10.7	163.3	105.9	17.3	51.4	25.3	8.9
	GxE	48.8	50.9	48.4	1.7	7.7	0.9	1.8
	Error	189.2	572.6	226.1	8.1	43.8	5.1	8.1
Pop – Poly-cross (N=1015)	G	21.4	178.2	124.2	21.3	61.9	21.2	9.0
	GxE	31.8	48.7	57.1	2.0	4.3	1.5	2.9
	Error	98.9	498.2	149.6	9.1	14.1	3.0	7.5
Pop – Diallele (N=1041)	G	31.5	153.4	144.8	21.5	51.4	14.6	8.4
	GxE	26.1	30.7	45.0	1.4	3.2	1.6	0.3
	Error	148.4	623.6	187.4	8.8	16.0	3.7	6.9
Pop – Factorial (N=1042)	G	15.7	238.5	146.4	23.7	83.4	18.6	13.2
	GxE	38.6	107.8	20.8	2.7	5.4	3.0	2.0
	Error	119.0	761	163.6	7.8	13.1	2.7	6.3

[†] poly-cross with initial single plant selection (reduction of 5349 clones to 1021 clones by single plant selection)
[‡] CC, color charts. [§] fwb, fresh weight basis. [§§] dwb, dry weight basis.

=> These variance component estimations are further indications that ABS works !!!

Three levels to investigate the efficiency of ABS (see APA paper)

=> **Estimate heritabilities** when you apply ABS in early breeding stages (4 times in applied breeding material at CIP Lima all with consistent results – when study do not apply perivous selection !!

$h^2 = \sigma^2_G / [\sigma^2_G + \sigma^2_{GL}/L]$

=> **Estimate heritabilities** when you apply ABS in early breeding stages with a check clone and **plant the selected fraction again with the check** for one further breeding stage to estimate the observed response to selection [3 studies in SSA (Ghana, Uganda and Mozambique) in process]

$h^2 = \sigma^2_G / [\sigma^2_G + \sigma^2_{GL}/L]$

R_{obs} = mean across sel fraction rel. to check in year 2 – mean all clones rel to check in year 1

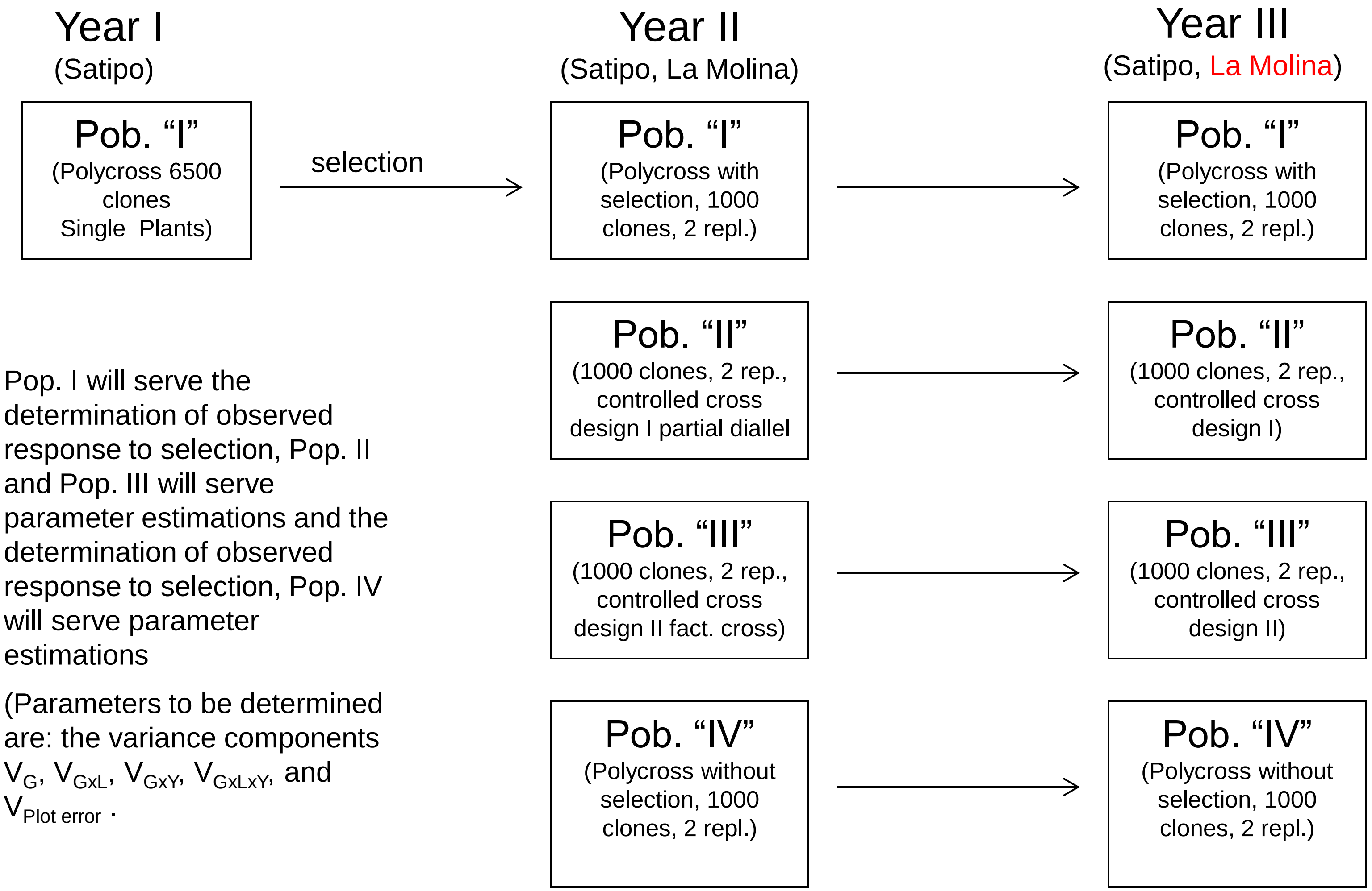
=> **Estimate heritabilities when you apply ABS** in early breeding stages with a plot replication (2 plots per location) and **replant all clones in year 2 without selection** at same locations and same replication numbers and estimate the observed R and predicted R with models / testing different breeding senarios [study at CIP Lima in the frame of the poly versus controlled cross breeding study]

$h^2 = \sigma^2_G / [\sigma^2_G + \sigma^2_{GY} + \sigma^2_{GL}/L + \sigma^2_{GLY}/L + \sigma^2_e/L]$

R_{obs} = mean across sel fraction rel to check in year 2 – mean all clones rel to check in year 1

R_{pre} = standard models of selection theory

PvC – Polycross versus controlled cross breeding study with 22 mega-clones as parents - Overview



Year I
(Satipo)

Year II
(Satipo, La Molina)

Year III
(Satipo, La Molina)

Pob. “I”
(Polycross 6500 clones
Single Plants)

selection

Pob. “I”
(Polycross with selection, 1000 clones, 2 repl.)

Pob. “I”
(Polycross with selection, 1000 clones, 2 repl.)

Pob. “II”
(1000 clones, 2 rep., controlled cross design I partial diallel

Pob. “II”
(1000 clones, 2 rep., controlled cross design I)

Pob. “III”
(1000 clones, 2 rep., controlled cross design II fact. cross)

Pob. “III”
(1000 clones, 2 rep., controlled cross design II)

Pob. “IV”
(Polycross without selection, 1000 clones, 2 repl.)

Pob. “IV”
(Polycross without selection, 1000 clones, 2 repl.)

Pop. I will serve the determination of observed response to selection, Pop. II and Pop. III will serve parameter estimations and the determination of observed response to selection, Pop. IV will serve parameter estimations

(Parameters to be determined are: the variance components V_G, V_{GxL}, V_{GxY}, V_{GxLxY}, and $V_{\text{Plot error}}$.

Note: Check clones included in each population are Tanzania, Jonathan, and Resisto.

PvC – Polycross versus controlled cross breeding

Table 3. Genetic gains (R) for storage root yield for polycross versus controlled cross breeding.

	Number of genotypes	Number of locations	Rep	Selected genotypes	Mean Root yield (t/ha) [‡‡]	R standard ized	R (t/ha)	Root yield (t/ha)
Pop – Poly-cross	6000[†]	2	1	100	15.0 (14.5-15.5)	1.235	5.714	20.7
Pop – Poly-cross	6000 =>1000[††]	1 =>2	1	100	15.0 (14.5-15.5)	1.350	6.243	21.2
Pop – Diallel	1000[‡]	2	1	100	18.4 (17.8-18.9)	0.904	5.073	23.5
Pop – Factorial	1000[‡]	2	1	100	14.6 (14.1-15.1)	0.715	2.834	17.4

[†] Test capacity 12000 1m row plots; [††] Test capacity 8000 1m row plots; [‡] Test capacity 2000 1m row plots; [‡‡]Confidence interval 95% in bracket

=> Controlled cross partial diallel (4x22) > Polycross 2 step selection > Polycross 1 step selection > Controlled cross factorial [the best with the rest (5 x 17)]

Heterosis

Offspring is superior to the mid-parent performance
=> mid-parent or mid-offspring heterosis increment

F1 > (P1 + P2) /2 - where F1 is the family mean and P1 and P2 is the parental performance

What is offspring in a clonally propagated crops? The family derived from a cross – note in a heterotic cross combinations / families you still can select for "the best" clone !

Experiments - (design and results see APA paper)

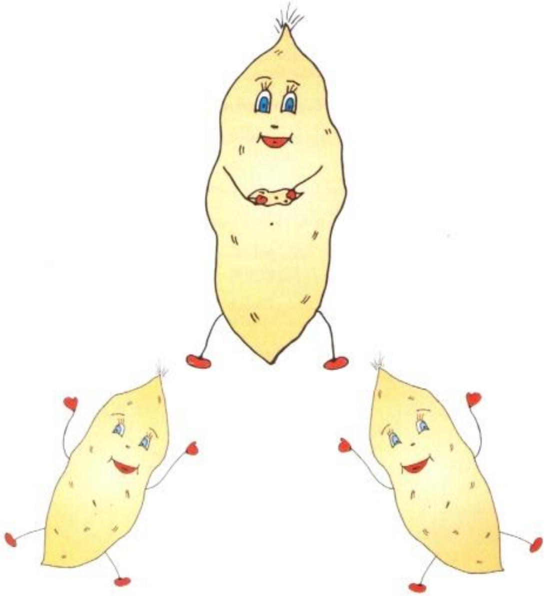


Fig. Illustration of Heterosis

Heterosis in sweetpotato (mid-parent – mid-offspring heterosis)

Table 4. 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%)

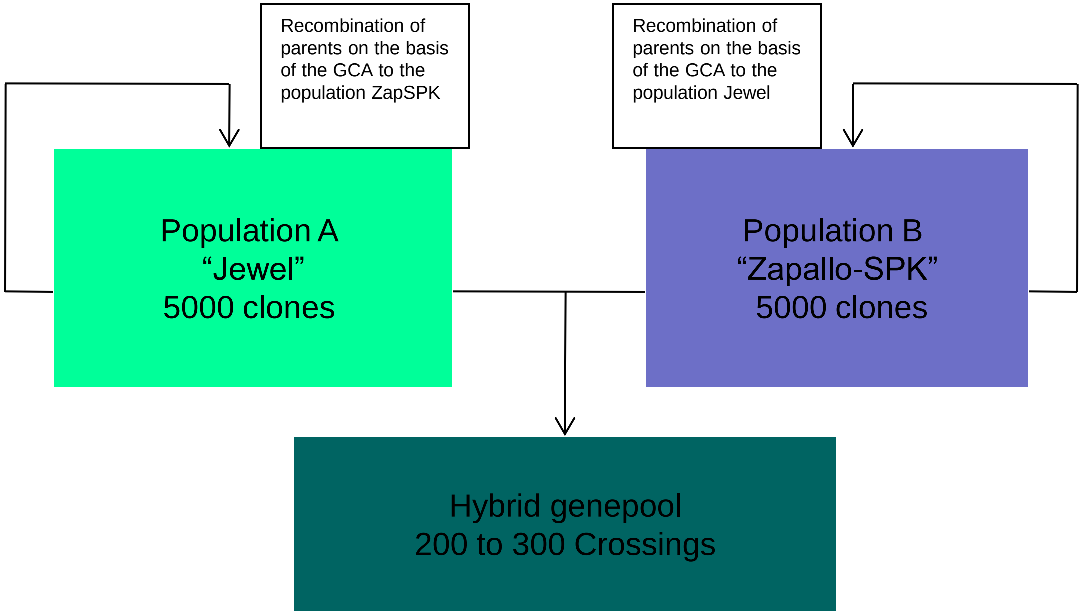
⇒ **Heterosis increments of up to 58.7% (Wagabolige × SR02.174)**

⇒ **high-yielding parental combinations with heterosis increments (i.e. Zapallo × SR02.174)**

⇒ **Interest to generate more crosses like Zapallo × SR02.174**

Selection of Parents and Heterosis Exploitation

Selection for new crosses / parents – best family makes



Recombination of parents on the basis of the GCA to the population ZapSPK

Recombination of parents on the basis of the GCA to the population Jewel

Population A
"Jewel"
5000 clones

Population B
"Zapallo-SPK"
5000 clones

Hybrid genepool
200 to 300 Crossings

A potential heterosis exploiting breeding scheme (HEBS) - ! inbreeding by selfings not required !.

Note 1: Population A and B and the hybrid genepool can be used to select clonally propagated varieties.

Such a scheme was already proposed by Hull for clonally propagated crops using sugercane as an example – (Hull, F.H. 1945 Recurrent selection for specific combining ability in corn. J. Am.Soc. Agron. 37: 134-145)

Dry Matter Storage Root Yield – Heterosis Experiment

49 PJ & 31 PZ => 231 cross combinations / offsprings

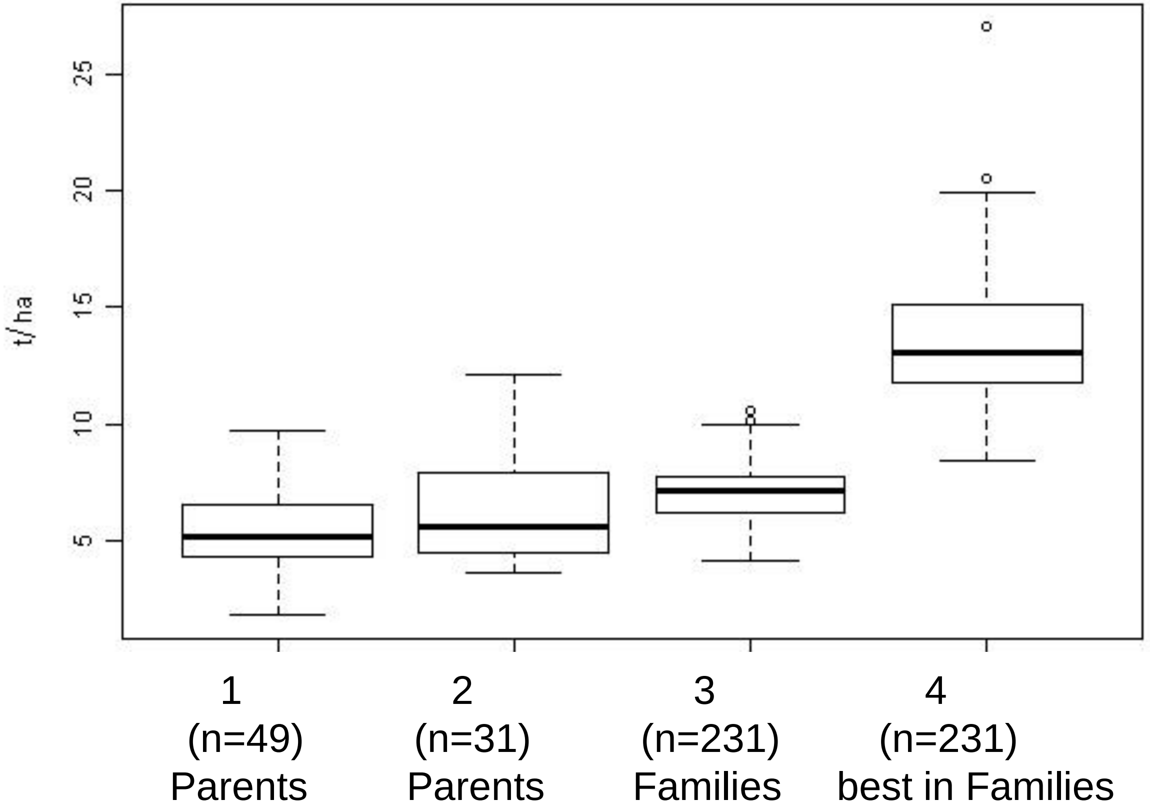
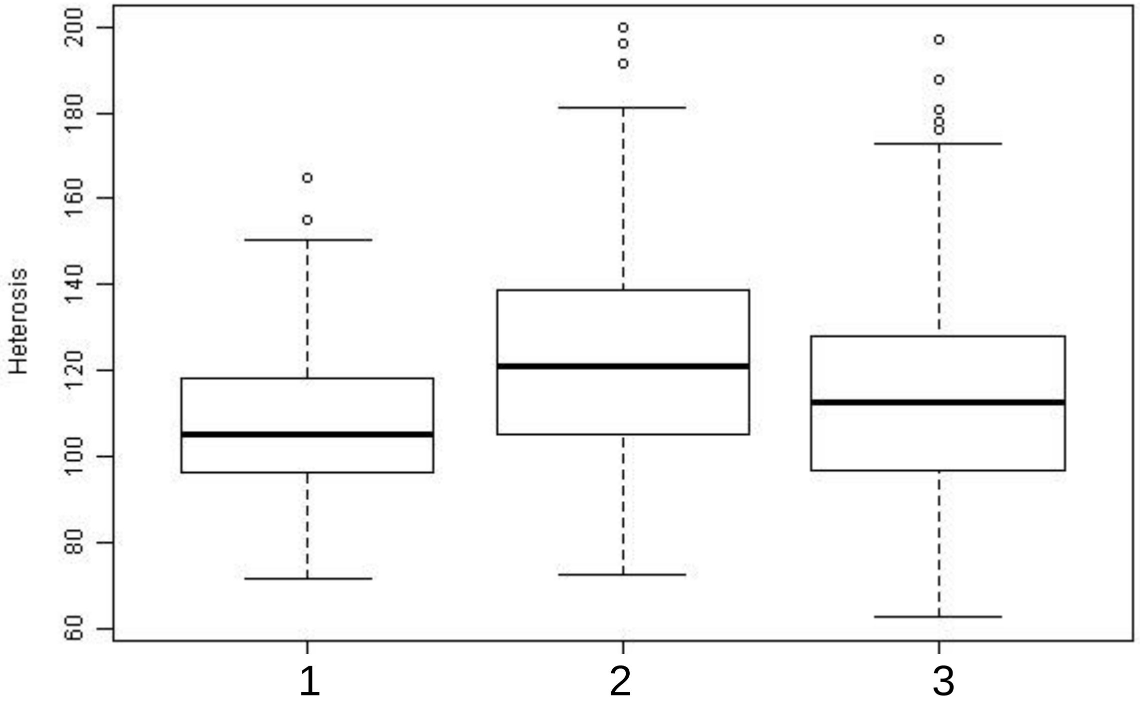


Figure 4. Dry matter storage root yield for parents PJ (1), PZ (2), hybrid family means (3), and best clone with each family (4) determined across two locations and two plot replications (in total 6898 offspring clones tracing back to 31 PZ and 49 PJ parents)

Heterosis observations in sweetpotato – two genepools

Heterosis exploitation by establishing two genepools

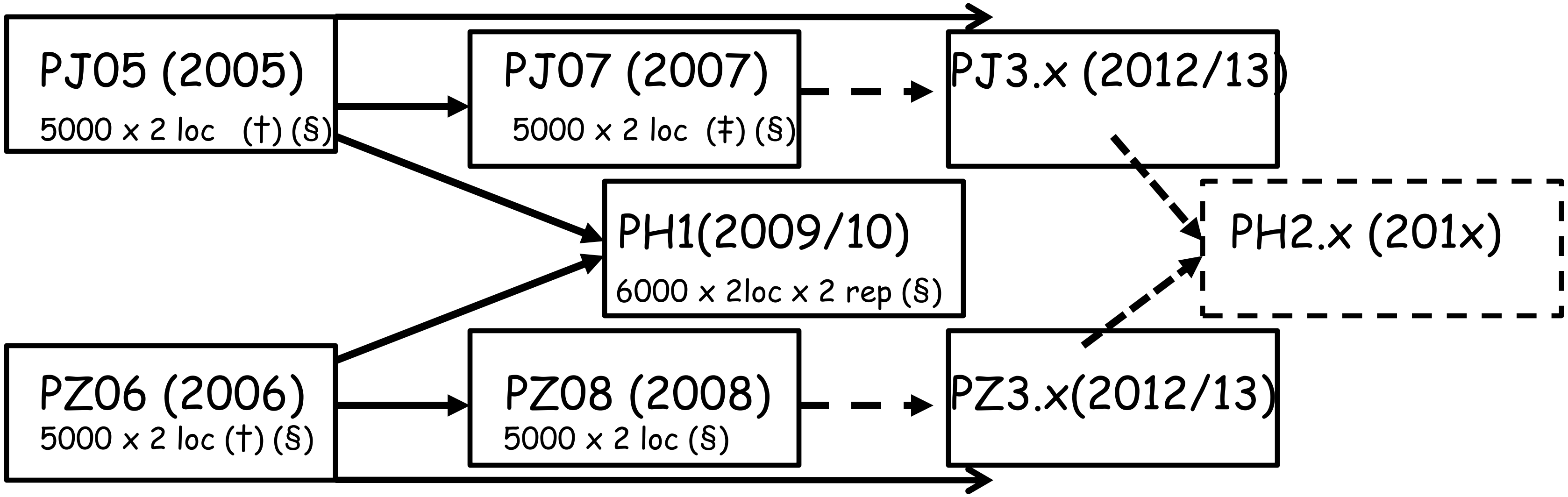


Mid parent – mid offspring heterosis increment for fresh storage root yield (1), dry matter storage root yield (2), and dry matter biomass yield (3) – Note each boxplot shows the distribution of 231 family means.

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 & PZ and Hybrid Populations PH I-III (IV)

History of the Hybrid Populations: *Population **PJ05** formed on basis of selection for orange flesh color - generated by open pollination before 2004 (phenotypically and genotypically **more similar to North American varieties** such as Jewel and Resisto). Population **PZ06** formed by factorial controlled crosses conducted in 2005 (8 male parents, namely: **Jonathan, Zapallo, Huambachero, Tanzania, Yurimaguas, Wagabolige, Xushu18, Ninshu1) x 200 OFSP** female parents, which were selected visually for agronomic performance and orange flesh color – PZ06 clones resulted in several variety releases; PJ07 and PZ08 in the pipeline for release (4 clones)*



PJ05 (2005)
5000 x 2 loc (†) (§)

PJ07 (2007)
5000 x 2 loc (‡) (§)

PJ3.x (2012/13)

PH1(2009/10)
6000 x 2loc x 2 rep (§)

PH2.x (201x)

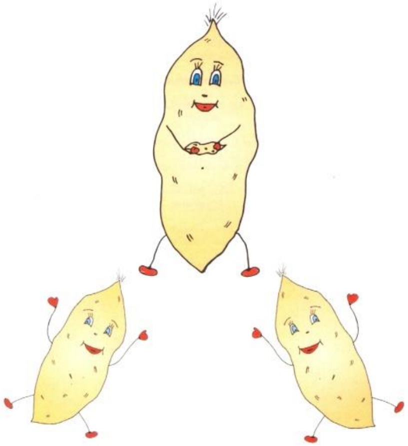
PZ06 (2006)
5000 x 2 loc (†) (§)

PZ08 (2008)
5000 x 2 loc (§)

PZ3.x(2012/13)

(†) *true seed of PJ05 and PZ06 (several thousands) were sent to Southern Africa and formed the **population Gurue** in Mozambique* , (‡) *true seed of PJ07 (several thousands)send to **India***

PJ07 100g fresh storage root mean: β-carotene: 10.2 mg, iron: 0.64 mg, zinc: 0.38 mg
PZ08 100g fresh storage root mean: β-carotene: 7.9 mg, iron: 0.56 mg, zinc: 0.34 mg
Child 1 – 3 years needs per day: β-carotene: 4.8 mg, iron: 5 mg, zinc: 4 mg



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