

Let's talk about Heterosis

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- In his famous experiment on peas, Gregor Mendel analysed seven traits – one trait was quantitative trait – the length of internodes
- About the inheritance of this trait he wrote: ".. es muss bemerkt werden, dass die längere der beiden Stamm-Axen von der Hybride gewöhnlich noch übertroffen wird". Translated ".. it is remarkable, that the longer one of the two stem axes is normally surpassed by the hybrid"
- Mendel's observation is a typical example of heterosis

<u>Hybrid cultivars play an important role in</u> <u>several major crops</u>

- In more and more cross fertilizing and self fertilizing species
- Table 1. Importance of hybrid cultivars in several major cross fertilizing and self fertilizing species

Crop	Area planted with hybrids (%)	Hybrid yield advantage† (%)
Maize	65	15
Sunflower	60	50
Sorghum	48	40
Rice	12	30
Rye	5	20

† estimated in yield of hybrids over superior open pollinated cultivars at time of hybrids introduction

In all clonally propagated crops, because all are highly heterozygous hybrids or with other words a clone cultivar is and was always a hybrid.

Definitions

Mid parent - mid offspring heterosis

$$\overline{H}_i = \frac{\overline{F_i}}{\frac{(P_{i1} + P_{i2})}{2}} *100$$

where \overline{H}_i = mid-offspring heterosis, \overline{F}_i = family mean, and P_{ii} = performance of parent ij

Additionally we suggest to use in clone breeding the parameter:

Wid parent – best offspring heterosis
$$H_{\max i}$$
 $H_{\max i} = \frac{F_{\max i}}{\frac{(P_{i1} + P_{i2})}{2}} *100$

where $F_{\max i}$ = the best performing clone in each family \dot{l}

We analyzed all key yield traits for heterosis:

Storage root fresh yield, storage root dry matter yield, and dry matter biomass yield.

Why dry matter yield? To make clear that heterosis effect is not confounded with water incorporation.

We analyzed applied breeding material.

Why applied breeding material? To show that there is exploitable heterosis in our breeding material and not among some clones in a careful selected experiment.

The experimental design:

- Two locations (San Ramon and Huaral in Peru) and two plot replications.
- Plot size 1m row plot for each offspring clone and thirty 1m row plots for each parent in each replication.
- Offspring clones and parental clones were planted together in each replication.
- In total 6898 offspring clones tracing back to 31 PZ and 49 PJ parents
- The PJ and PZ population has been developed in 2004 and 2005, respectively. Both populations were undergoing two cycles of recombination and selection and were not recombined before in inter-genepool crossings.

Note: PZ and PJ are two different breeding populations and have been developed at CIP in the frame of the OFSP population development funded by HarvestPlus and AgroSalud.

Dry Matter Storage Root Yield



Figure 1. Dry matter storage root yield for parents PJ (1), PZ (2), hybrid family means (3), and best clone with each family (4).

<u>Mid parent – Mid offspring Heterosis</u>



Figure 2. Mid parent – mid offspring heterosis for fresh storage root yield (1), dry matter storage root yield (2), and dry matter biomass yield (3).

<u>Mid parent – Best offspring Heterosis</u>



Figure 2. Mid parent – best offspring heterosis for fresh storage root yield (1), dry matter storage root yield (2), and dry matter biomass yield (3).

Table 2. Significance tests and confidence limit estimations for mid parent – mid offspring and mid parent – best offspring heterosis in fresh storage root yield, dry matter storage root yield and total dry matter biomass yield.

Variable	Mean	t-value	Р	95% CL		
Fresh root yield	115.3	9.36	<0.0001	112.1 – 118.5		
Dry root yield	122.9	14.16	<0.0001	119.7 – 126.1		
Biomass	107.8	6.90	<0.0001	105.6 – 110.0		
Dry matter %	101.6	3.97	<0.0001	100.8 – 102.5		
Mid parent – best offspring heterosis						

Mid parent – mid offspring heterosis

Fresh root yield	219.8	33.64	<0.0000	212.8 – 226.8
Dry root yield	236.6	35.82	<0.0000	229.1 – 244.1
Biomass	196.5	32.89	<0.0000	190.7 – 202.3
Dry matter %	138.7	45.45	<0.0000	137.1 – 140.4

<u>Please remember</u>



We are the parents from two separate heterotic gene pools