

# Progress Breeding CIP HQ Hybrid Breeding & SPVD markers

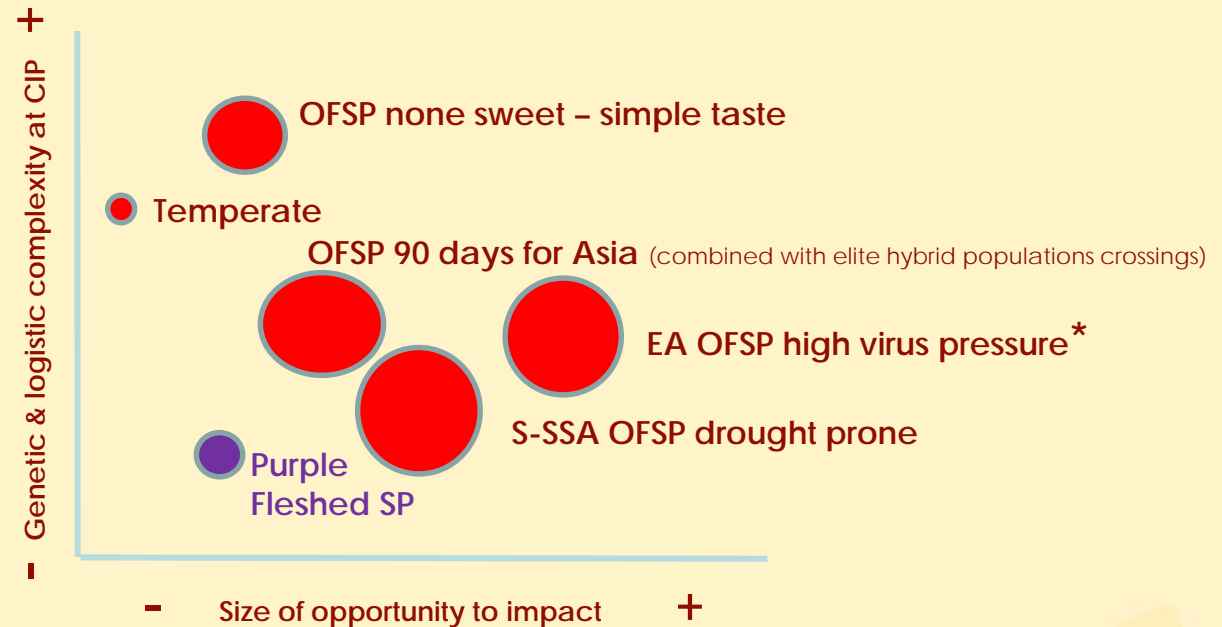
**Grüneberg W.J., R. Mwanga, F. Diaz, R. Eyzaguirre, and David M.**

**Building Resilient Food Systems with  
Sweetpotato**

*17<sup>th</sup> Sweetpotato SpeedBreeders and Genomics  
Community of Practice Meeting, Nairobi, Kenya  
05-08 June 2018*

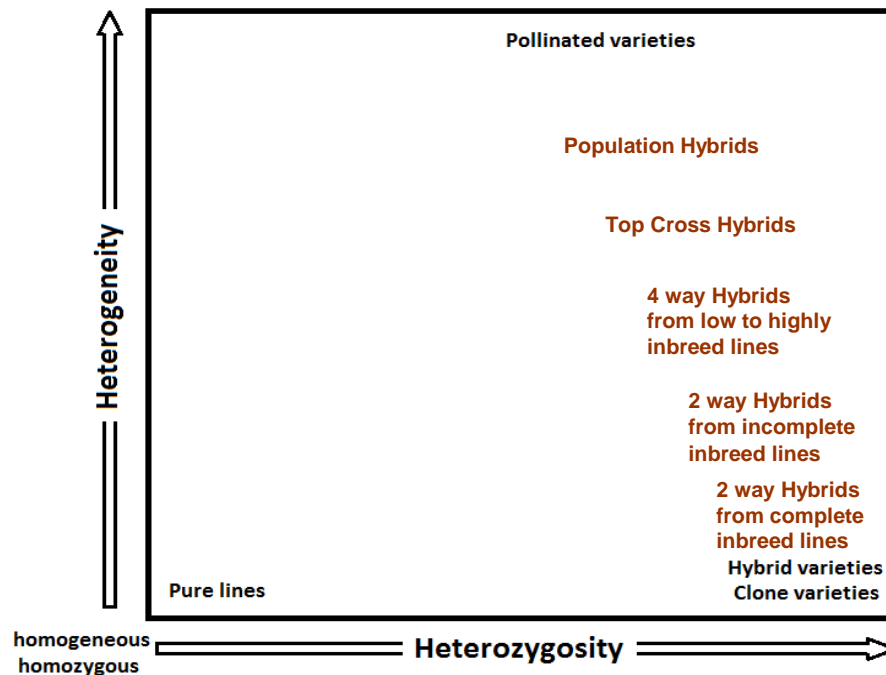
SWEETPOTATO ACTION FOR SECURITY AND HEALTH IN AFRICA

# CIP product concepts – relative global effort



\*: Size of each circle reflects current breeding efforts

# Methods and categories of plant breeding



Schnell F.W. 1982: A synoptic study of the methods and categories of plant breeding.  
Plant Breeding 89:1-18.

## Formation of 2 OFSP populations: “Jewel” (PJ) and “Zapallo (PZ)”

The PJ generated end of 1990s at CIP in Peru / open pollination among 98 clones using “desert type” OFSP and sweetpotato germplasm from different regions.

The PZ generated in a factorial cross design (13 male x 120 female parents). Male parents from South America or Africa with light to medium orange or cream fleshed storage root color

PJ 2005, selection, recombination, multiplication to PJ 2007 in field trials 2007 (PJ05, PJ07)

PZ 2006, selection, recombination, multiplication to PZ 2008 in field trials 2008 (PZ06, PZ08)

### Published two studies on heterosis increments without genepool separation:

- 2007/2008 at CIP in Peru / Grüneberg et al. (2015) mid-parent and mid-offspring yield 48 families (4 x 12 factorial cross) **heterosis yield increments -34% to 58%.**
- 2010/11 at KARI in Kenya / Kivuva et al. (2015) F1 and parental means (6 parents, 15 families); mid-parent – mid-offspring **heterosis yield increments under no drought -43% to 92% and -54% to 82% under drought stress**

### Published - Genepool separation with Heterosis and Hybrid breeding in sweetpotato

- 20010/2011 at CIP in Uganda / David al. (2018) Gene Pool Subdivision of East African Sweetpotato Parental Material. Crop Science in press

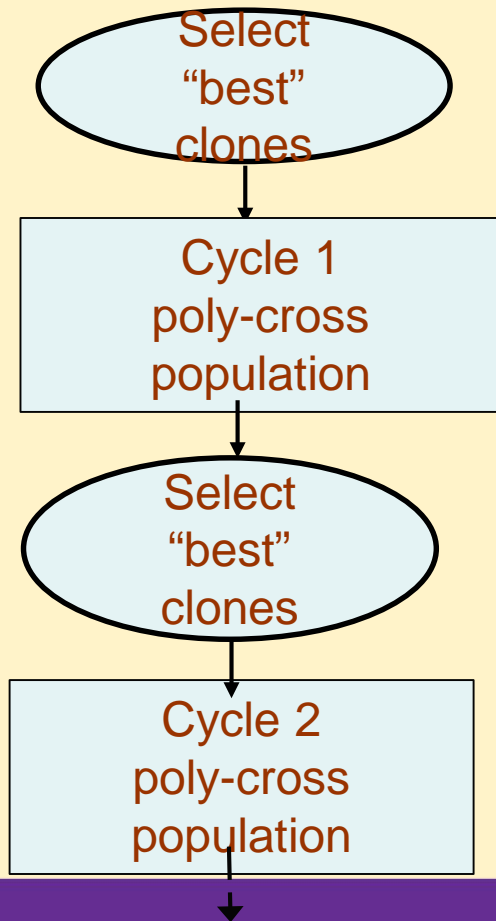
CIP 2018

- mid-parent and mid-offspring yield 48 families (4 x 12 factorial cross) **heterosis yield increments -34% to 58%**

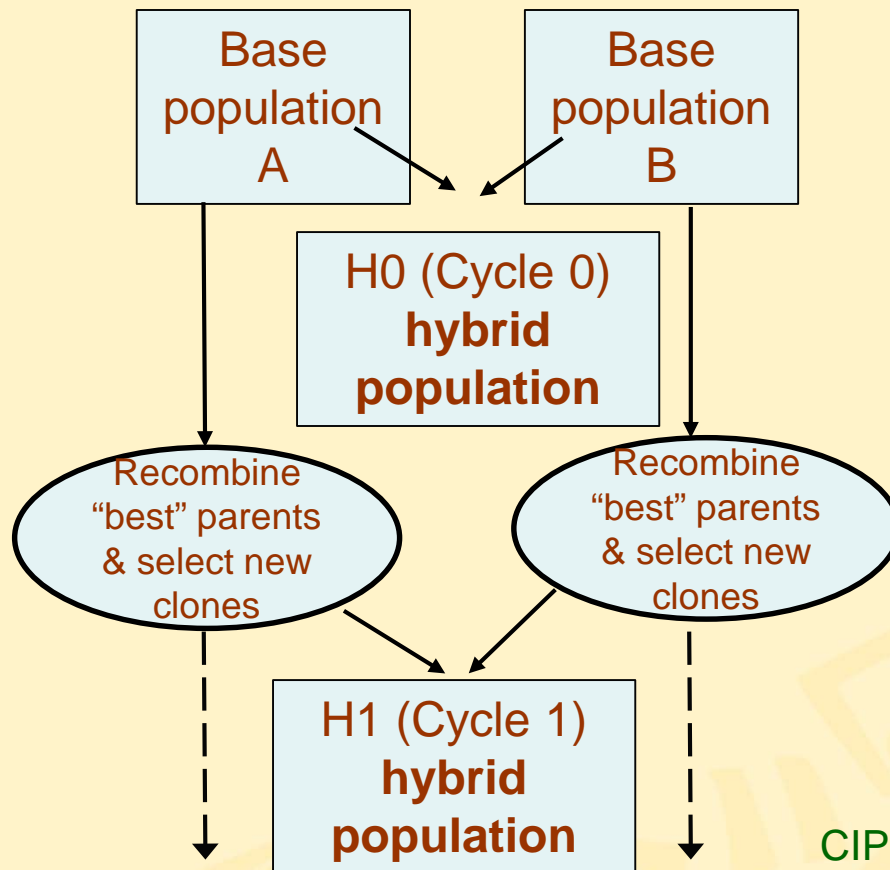
## At CIP we improve populations through:

- (i) Polycrosses with parental selection on clone performance *per se*
- (ii) Reciprocal Recurrent Selection & Offspring Parent analysis

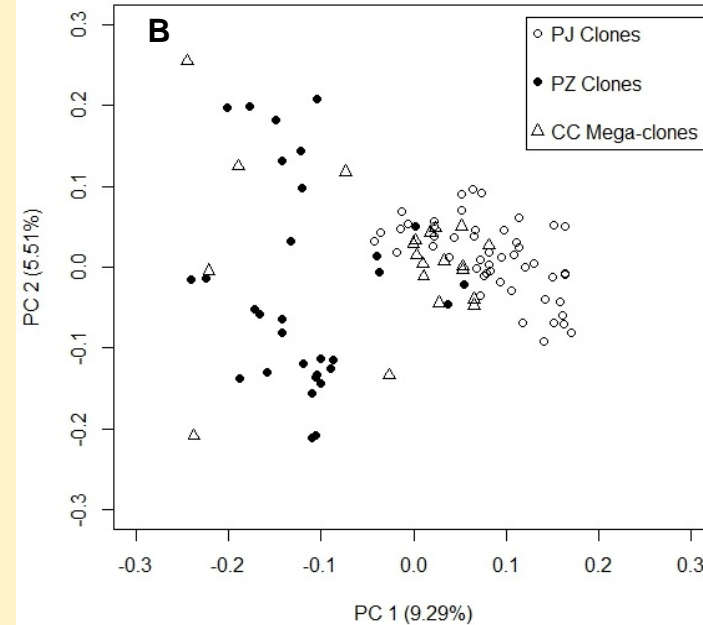
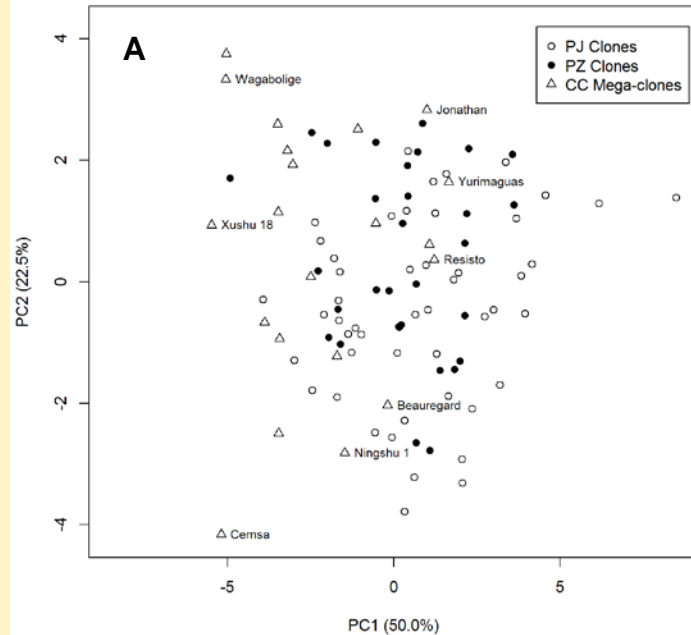
### Poly-cross breeding



### Reciprocal recurrent selection



# PJ and PZ population at CIP-HQ relative to Mega-Clones

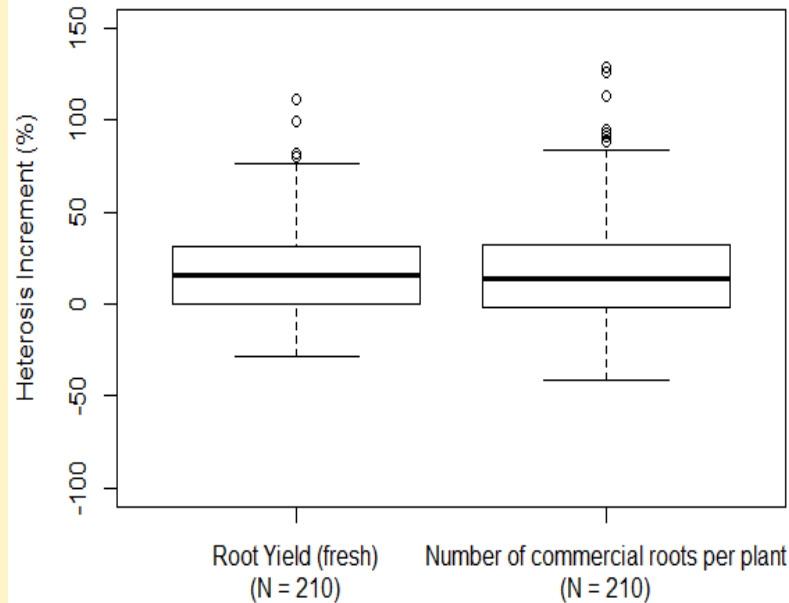


**Fig. 1.** First (PC1) and second (PC2) principal component scores of the principal component analyses of 49 PJ 31 PZ, and 21 mega clones on agronomic yield and quality traits (A); First (PC1) and second (PC2) principal component scores of the principal component analyses of 49 PJ 31 PZ, and 21 mega clones on 66 SSR marker data (B).



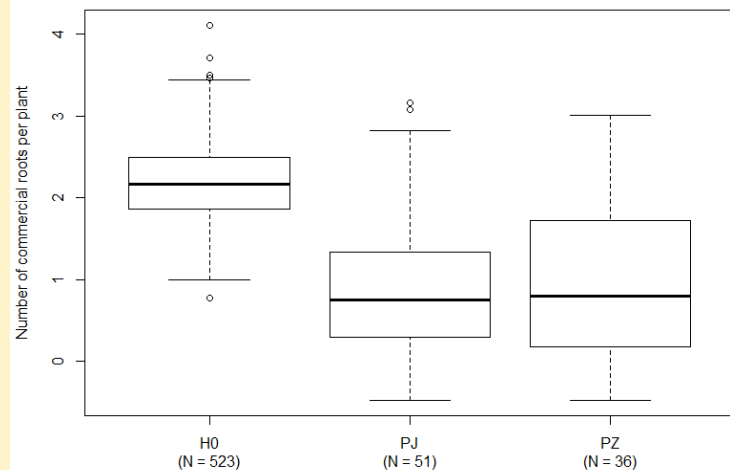
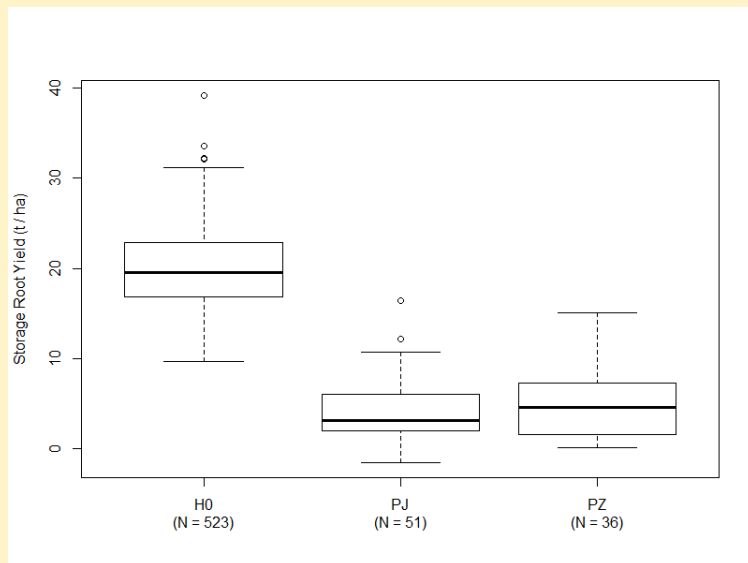
# CIP 2009-2013 / SASHA phase 1 – H0 population PH10

## PJ and PZ populations are mutually heterotic



**Fig 2.** Heterosis increments in percentage for yield and number of commercial roots per plant in H0 PJxPZ cross combinations (N=210) across experimental sites [zero is parental basis (PJ parent + PZ parent) / 2, PJ parents (N=49), and PZ parents (N=31) across experimental sites (Huaral, San Ramon) and replications (n=2)]

# Another H0 population on basis of PJ05, PJ07 and PZ06, PZ08 parents funded by USAID for 100 days OFSP H0 hybrid population PH15)

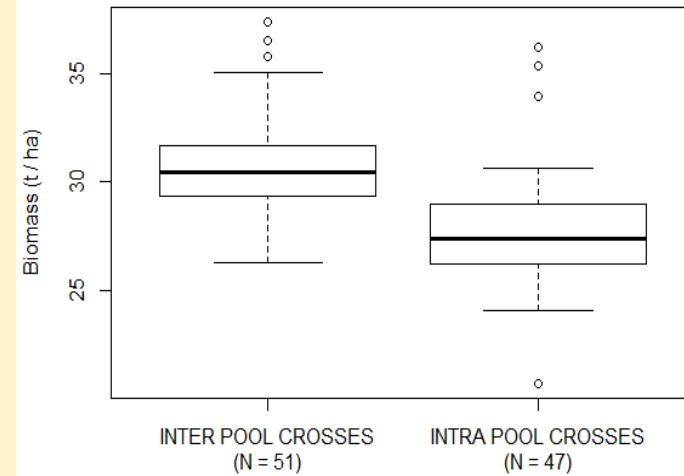
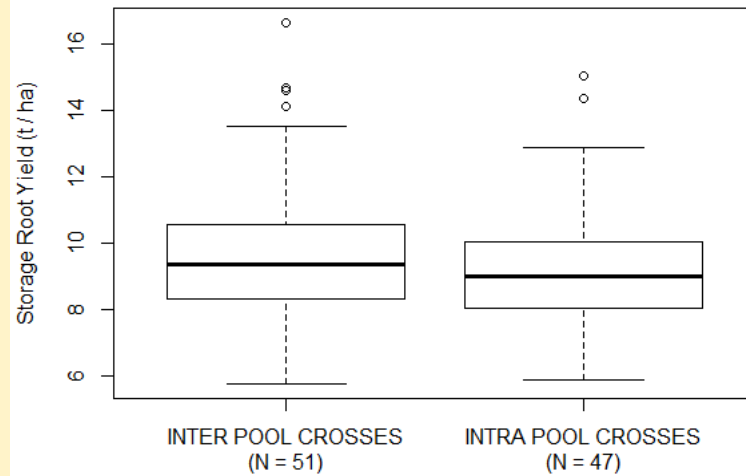


**Fig. 3.** Storage root yields (A) and number of commercial storage roots per plant (B) for H0 cross combinations (N=523 cross combinations) with PJ and PZ parents across experimental sites (Ica, Satipo).

**Note:** This hybrid population was “stressed” due to 100 days harvest / many parents were already PJ07 and PZ08 parents.



# Uganda Parents Inter AxB - Intra pool crosses (AxA & BxB)

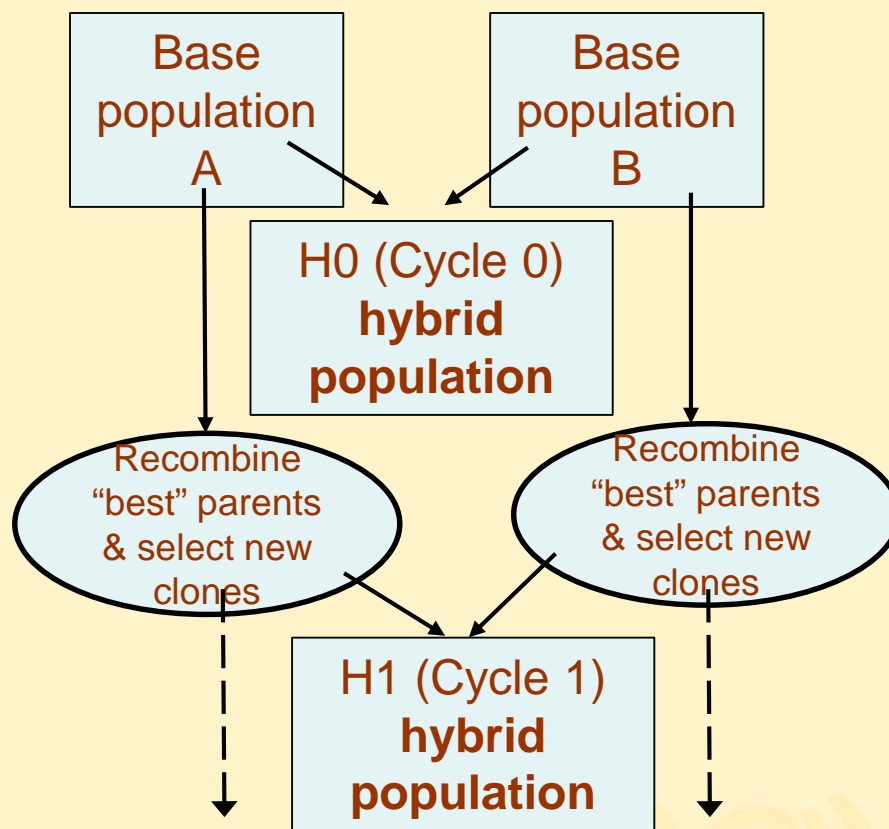


**Fig. 4** Storage root yields (A) and total biomass production (B) for interpool (AxB) and intrapool (AxA and BxB) crosses across environments (irrigated in 2015 and 2016, not irrigated in 2015 and 2016).

# The hybrid breeding scheme for three big experiments

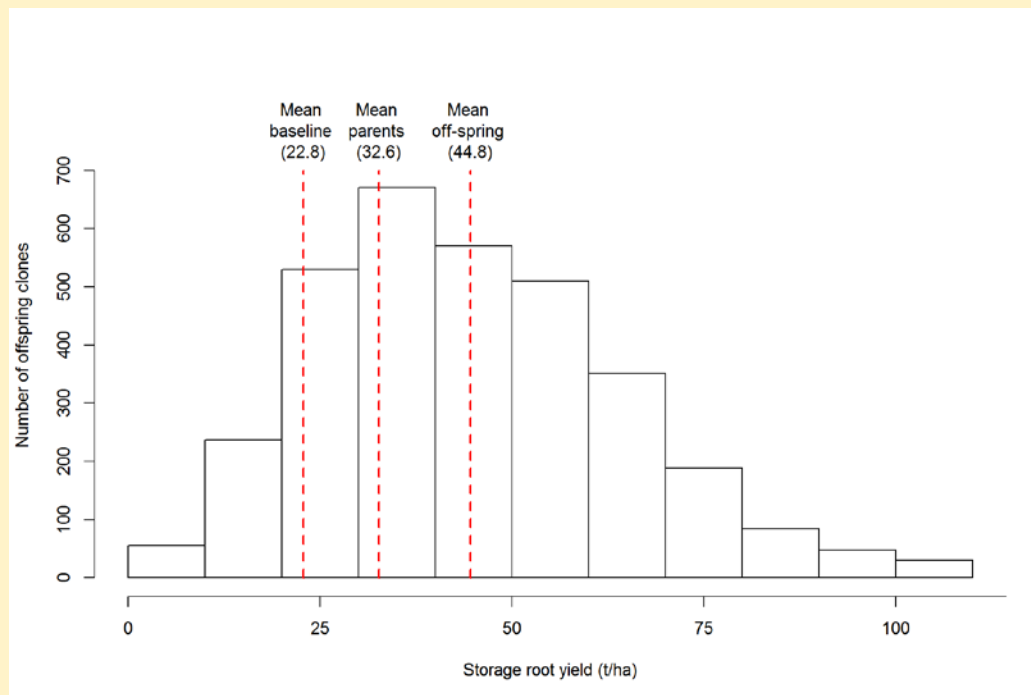
1) High iron, 2) None sweet, 3) wide adaptation and earliness

## Reciprocal recurrent selection



# CIP 2014-2019 / SASHA phase 2

## Genetic Grains & Heterosis increments in high iron hybrid H1 population



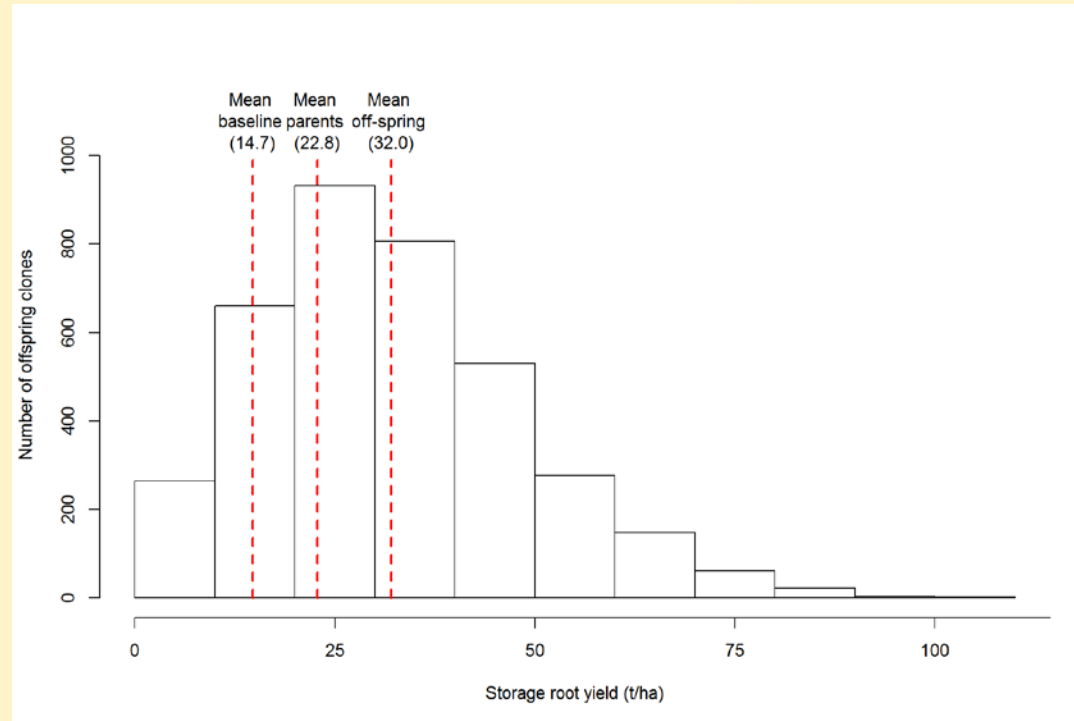
**Fig. 5. Genetic gain (GG) for storage root yield by genepool separation and one complete reciprocal recurrent selection cycle estimated in population HIFE at two locations in Peru / Canete – arid pacific coast / Satipo – humid tropics** [Mean baseline (22.8 t/ha), 80 clones each clone in 8 one-meter row plot replications, selected fraction in baseline PJ = 0.10 and PZ = 0.16; mean parents (32.6 t/ha), 46 clones each clone in 8 one-meter row plot replications; mean offsprings (44.8 t/ha), 3292 H1 hybrid clones; total GG: 96.2%; heterosis increment in H1: 36.4%, estimated gain by one reciprocal recurrent selection cycle: 43.8%].



Iron and zinc H1 population (about 4000 genotypes / 2 locations with checks and with parents are evaluated by NIRS – about 15 USD per sample plus selected fraction by XRF (14 USD per sample)

# CIP 2014-2019 / SASHA phase 2

## Genetic Grains & Heterosis increments in none sweet hybrid H1 population



**Fig. 6. Genetic gain (GG) for storage root yield by genepool separation and one complete reciprocal recurrent selection cycle estimated in population NSSP at two locations in Peru / Canete – arid pacific coast / Satipo – humid tropics** [Mean baseline (14.7 t/ha), 80 clones each clone in 8 one-meter row plot replications, selected fraction in baseline PJ = 0.10 and PZ = 0.16; mean parents (22.8 t/ha), 53 clones each clone in 8 one-meter row plot replications; mean offsprings (32.0 t/ha), 3742 H1 hybrid clones; total GG: 117.7%; heterosis increment in H1: 40.4%, estimated gain by one reciprocal recurrent selection cycle: 55.1%].

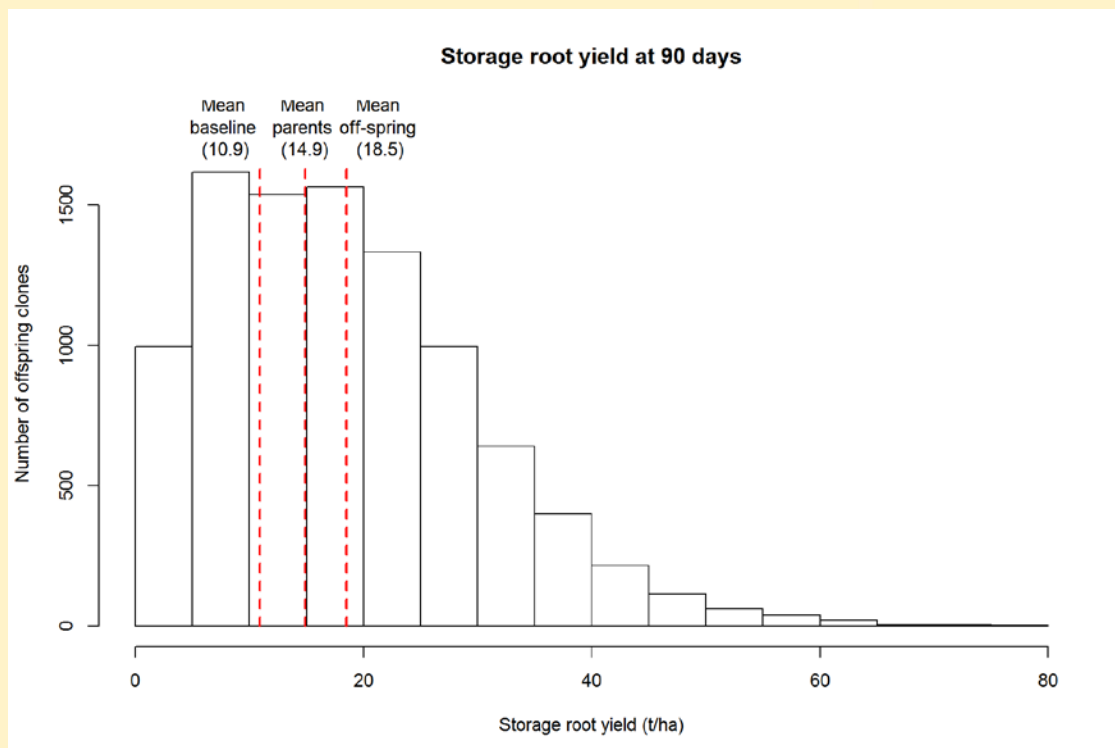


Sensorial evaluation for low sugar H1 hybrid population (about 5000 genotypes) –  
note: sugar contents before and after cooking can be extremely different



# CIP 2014-2019 / SASHA phase 2

## Genetic Grains & Heterosis increments in wide adaptation & earliness hybrid 1 population



**Fig. 7. Genetic gain (GG) for storage root yield by genepool separation and one complete reciprocal recurrent selection cycle estimated in population WAEA 90 days harvest at two locations in Peru / Canete – arid pacific coast / Satipo – humid tropics** [Mean baseline (10.9 t/ha), 80 clones each clone in 8 one-meter row plot replications, selected fraction in baseline PJ = 0.56 and PZ = 0.55; mean parents (14.9 t/ha), 84 clones each clone in 8 one-meter row plot replications; mean offsprings (18.5 t/ha), 9881 H1 hybrid clones; total GG: 69.7%; heterosis increment in H1: 27.6%, estimated gain by one reciprocal recurrent selection cycle: 36.7%].

# CIP 2014-2019 / SASHA phase 2

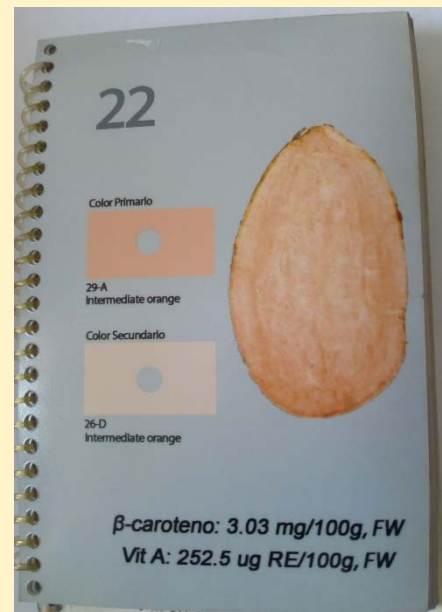
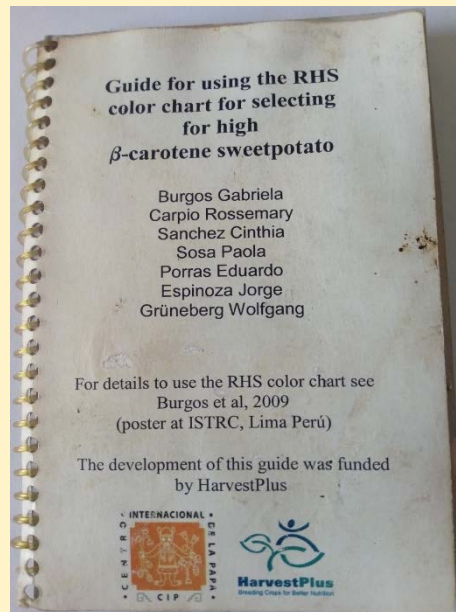
## Genetic Grains & Heterosis increments in wide adaptation & earliness hybrid 1 population



Canete / Peru 2017 (temperate arid pacific coast) – Planting of H1 for wide adaptation and earliness (N > 16,000) in double plots for early (90 days) and for normal harvest (120 days)

# CIP 2014-2019 / SASHA phase 2

## Genetic Grains & Heterosis increments in wide adaptation & earliness hybrid 1 population



Beta-carotene color charts – all clones in populations are evaluated for dry matter and by color charts in quality lab San Ramon

# Hybrid Breeding Schemes / Heterosis Exploiting Breeding resulted in production of Elite Crossings

**Table 1: Hybrid population H0 (PH15 / USAID) family Ismean estimates for “Elite OFSP Hybrid Crosses” for 100 day growing periods.**

Cross combination PJ x PZ	Number of commercial root per plant	Storage root yield (t/ha)	Foliage yield (t/ha)	Root dry matter (%)
<b>Low dry matter elite OFSP cross combinations</b>				
PJ05.124-PZ08.038	3.50	27.4	30.0	25.7
PJ05.120-PZ08.011	3.31	31.0	16.1	25.8
PJ05.130-PZ08.038	2.83	27.9	25.2	26.2
PJ05.213-PZ08.038	2.78	24.3	40.3	27.4
PJ05.213-PZ08.090	2.70	25.7	42.3	27.3
PJ07.265-PZ08.011	2.68	20.1	30.7	28.0
<b>High dry matter elite OFSP cross combinations</b>				
PJ07.061-PZ08.038	2.67	27.8	31.3	29.8
PJ07.061-PZ06.085	2.62	19.5	30.0	28.7
PJ07.690-PZ06.304	2.17	16.3	29.8	29.7
PJ07.079-PZ06.304	2.17	20.5	40.4	28.3
PJ05.213-PZ08.153	2.15	25.8	23.8	32.3
PJ05.064-PZ08.153	2.00	17.4	14.7	31.6

# UG H0 population



**Table 10.** True seed for 50 A parents x 80 B parents (No. of families with at least 6 seed = 41.2%)

[illegible]



## Additional lessons learned:

- Varcomp general combining ability (GCA) considerably much larger specific combining ability (SCA) / this makes happy breeders;
- Potential testers found => several cross combinations and high GCA (2 in H0 SASHA, 6 in H0 USAID);
- Logistics and operation required special field design – Westscott (1982) design now used (for safety reasons), clones per family within 8 -16 without rep., parents in 6-8 replications;
- SSR markers separate genepools quite well – a) PJ and PZ pools in Peru and b) UG\_A and UG\_B in Uganda;

## Future:

- Implementation of Hybrid Breeding Scheme and Heterosis Exploiting Breeding Scheme on Breeding Platform;
- Elite crossing true seed dissemination (on basis of “Super Parents”);
- Elite crossing will become our target to apply genome wide prediction + marker assisted selection – this is within the logistical and operational capacity (1000 to 2000 clones)



# SPVD – Frist population VJ08

- 104 OFSPs x DLP3163 (CIP420269)
  - Parental material OFSP  
4 of 104 Jewel clones were resistant to SPCSV (frequency 0.0385)
  - Offsprings – 718 clones  
40 of 718 were resistant to SPCSV (frequency 0.057)

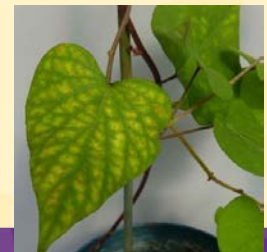
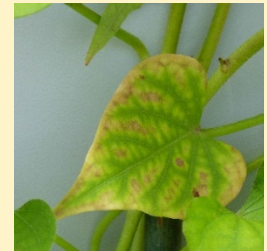
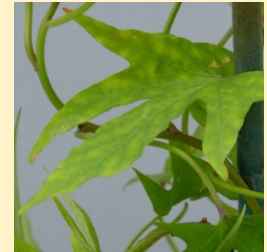
Family	Resistance frequency
PJ05.072 x DLP3163	5 of 12 (0.42)
PJ05.090 x DLP3163	3 of 6 (0.50)

• **Two small sets of clones were formed (a resistant set [VJ08.330 x VJ08.330, VJ08.330 x PJ05.064] and susceptible set of clones, each comprising 12 clones) and marker association was performed on them.**

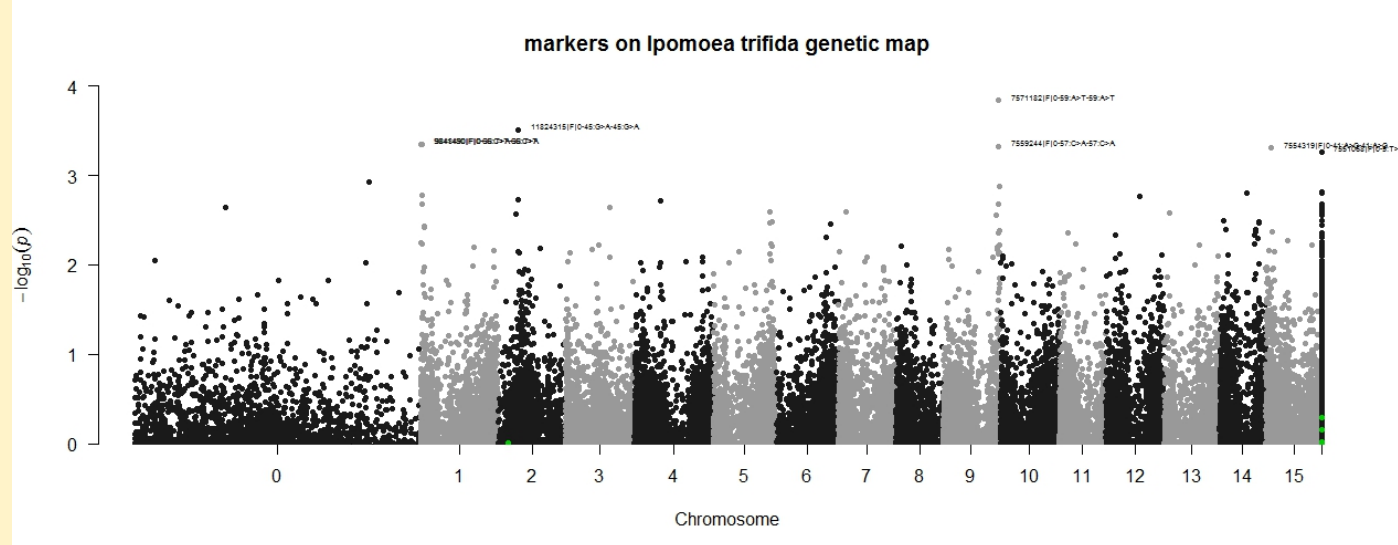
- AFLP: E44M34.533, E33M48.460, E36M34.400, E33M48.343, and E39M32.440, band absent in the resistant bulk and present in the susceptible bulk; E39M34.156, band was present in the resistant bulk and absent in the susceptible bulk.
- SSR: IBS204-172, IBS169-162, Ib-286-125, IbJ559-262, IbJ559-269, IbJ116a-229, and IBS149-225.
- DARt: 758044, 7563062, 7572542, 753123, and 7574925.

# SPVD – Second population VZ08

- Screening for resistance
  - Sweetpotato plants were grafted with *I. setosa* that carried SPFMV and SPCSV, in San Ramon greenhouse.
  - DAS and TAS Elisa tests were performed on sweetpotato clones to diagnose virus susceptibility.
  - Serological test was selected because it requires less laboratory equipment compared to other methods.



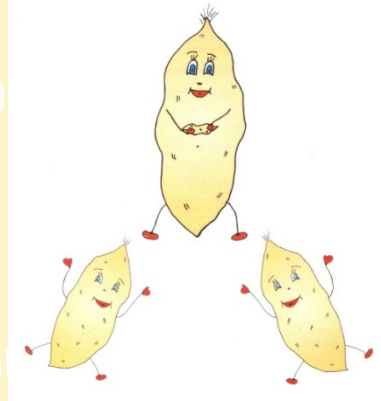
- Marker association VZ08
  - From ELISA results, we selected contrasting groups for SPCSV resistance (25 resistants and 31 susceptible).
  - We obtained DArT markers from 325 genotypes. Seven markers were identified to show correlation with SPCSV resistance.



- RESULTS
  - With DArT markers we have found in total 13 associations and only 2 in validation (both populations VJ08 and VZ08) - test these markers in a third population.
  - Currently, we have two experiments in two locations (San Ramon and Satipo) for selected clones of the VZ08 population.







**Thank-you for your Attention**