Genetic Gains using the Heterosis Exploiting Breeding Scheme

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SWEETPOTATO ACTION FOR SECURITY AND HEALTH IN AFRICA

Why hybrid breeding in sweetpotato?

Each sweetpotato clone is a highly heterozygous hybrid – so let us do better clone hybrid breeding

Hypothesis: The crop should be bred by the principals of hybrid breeding [heterosis exploiting breeding schemes (HEBS) and reciprocal recurrent selection (RRS)]

Advantages of hybrids / hybrid breeding

- **Hybrids show high commercial heterosis** (storage root yields, number of commercial roots, foliage yield / animal feed, seed production)

- **Ease to stack simple inherited traits** [resistances and quality such as sweetpotato virus disease (SPVD) resistance, none sweet after cooking etc.]

- **Hybrids are more yield stable than traditionally developed breeding lines** (biotic stress resistances such as short crop duration, drought etc.)

From my point of view also: (i) Clear breeding cycles & shorter turn-over of most suitable parents, (ii) offspring-parent analysis and better statistics (iii) clear monitoring the genetic gains per breeding cycle, (iv) opens the opportunity of high value true seed dissemination with elite crosses (super-parents), as well as (v) linking elite crosses with in-vitro germination and genome wide prediction
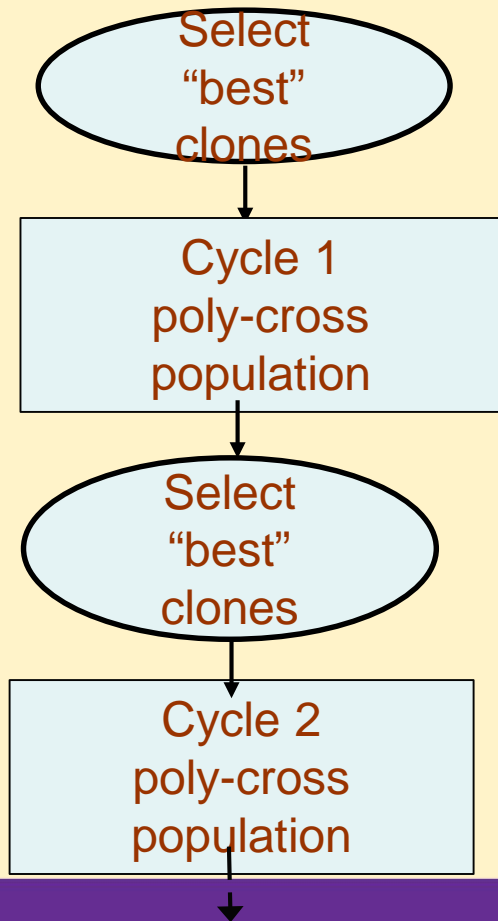
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Heterosis / Heterosis Increment
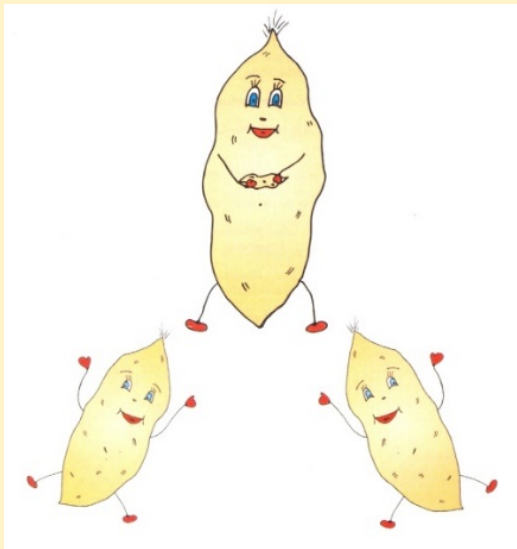
I'm a highly heterozygous hybrid developed from two mutually heterotic parents (from two genepools)

Note: Heterosis H = F1 / [(P1 + P2) / 2], where F1 is the offspring and P1 and P2 are the parents, is defined on the homozygous basis of P1 and P2 –> therefore the term heterosis increment is used as a parameter to determine the magnitude of superiority of an entire offspring (family) compared to heterozygous (only partially inbred) parents
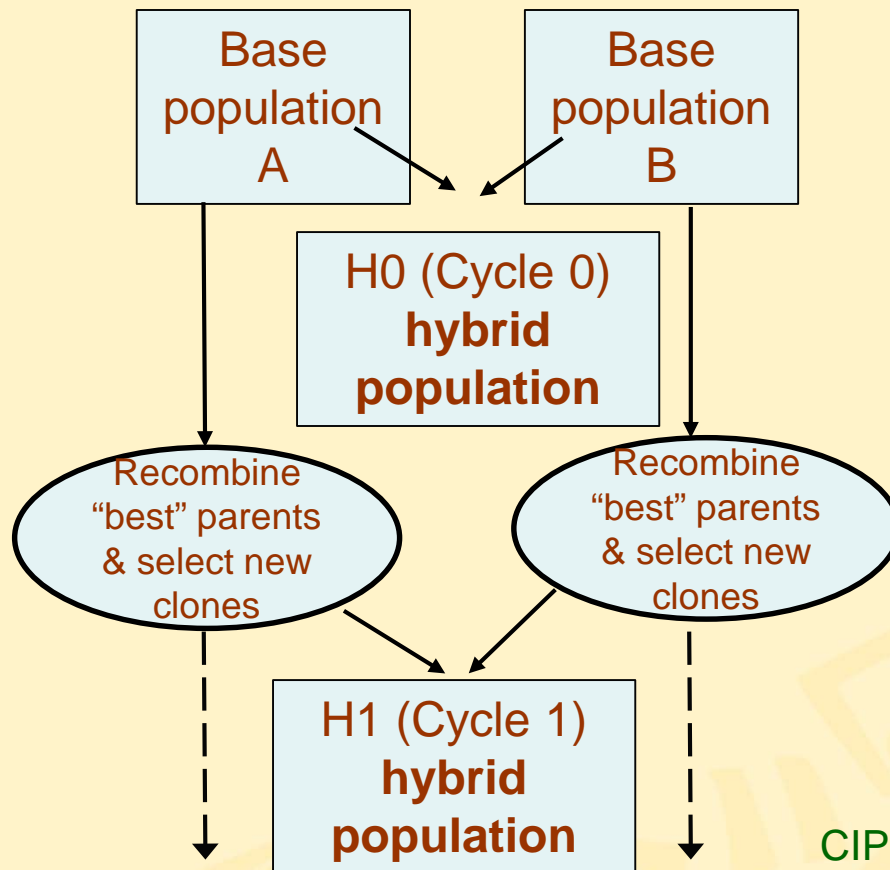
The breeding schemes at CIP to improve populations:
(i) Polycrosses with parental selection on clone performance *per se*
(ii) Reciprocal Recurrent Selection & Offspring Parent analysis

Poly-cross breeding

```
Select "best" clones
        │
        ▼
Cycle 1 poly-cross population
        │
        ▼
Select "best" clones
        │
        ▼
Cycle 2 poly-cross population
        │
        ▼
```

Reciprocal recurrent selection

```
Base population A        Base population B
        │        ╲    ╱        │
        │         ╲  ╱         │
        │      H0 (Cycle 0)    │
        │      hybrid          │
        │      population      │
        ▼                      ▼
Recombine "best"        Recombine "best"
parents & select        parents & select
new clones              new clones
        ╲                    ╱
         ╲                  ╱
        H1 (Cycle 1)
        hybrid
        population
```

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Don't tell me – show me! (PJ & PZ 1 at CIP-HQ)

(A) H0, PJ, PZ – normal harvest (120dys)
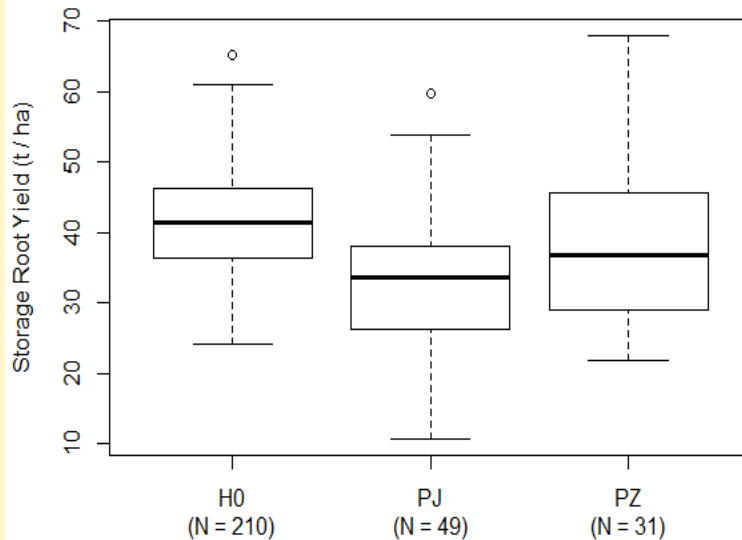
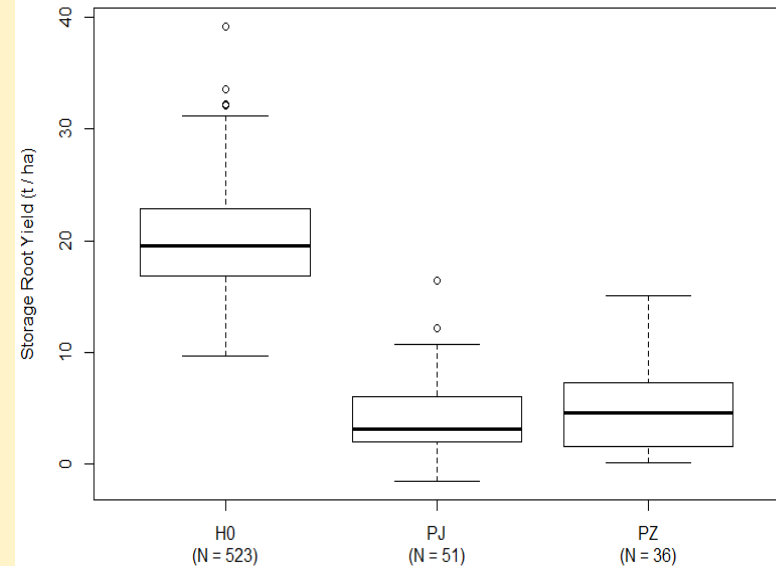**(B) H0, PJ, PZ – stress harvest (100dys)**

Fig. 1. Storage root yields in H0 hybrid families from PJ05 and PZ06 parents with normal harvest (120 days) across two environments developed under SASHA I (A) and in H0 hybrid families from PJ05, PJ07, PZ06, and PZ08 parents under early / stress harvest (100 days) across two environments developed under USAID).

⇒ **PJ and PZ genepools (global program) are mutually heterotic for root yield**
⇒ **Heterosis increments of PJ and PZ are more pronounced under stress**

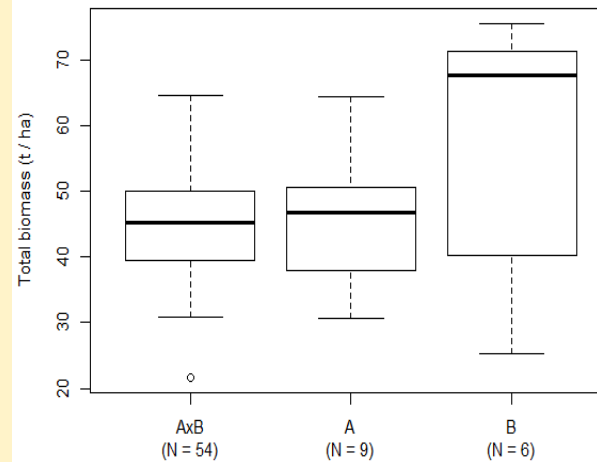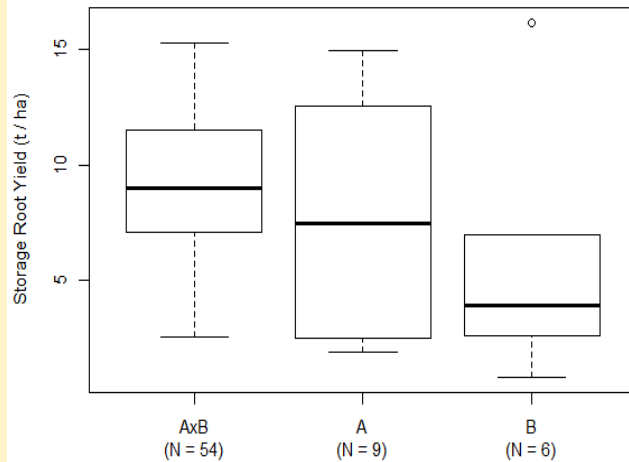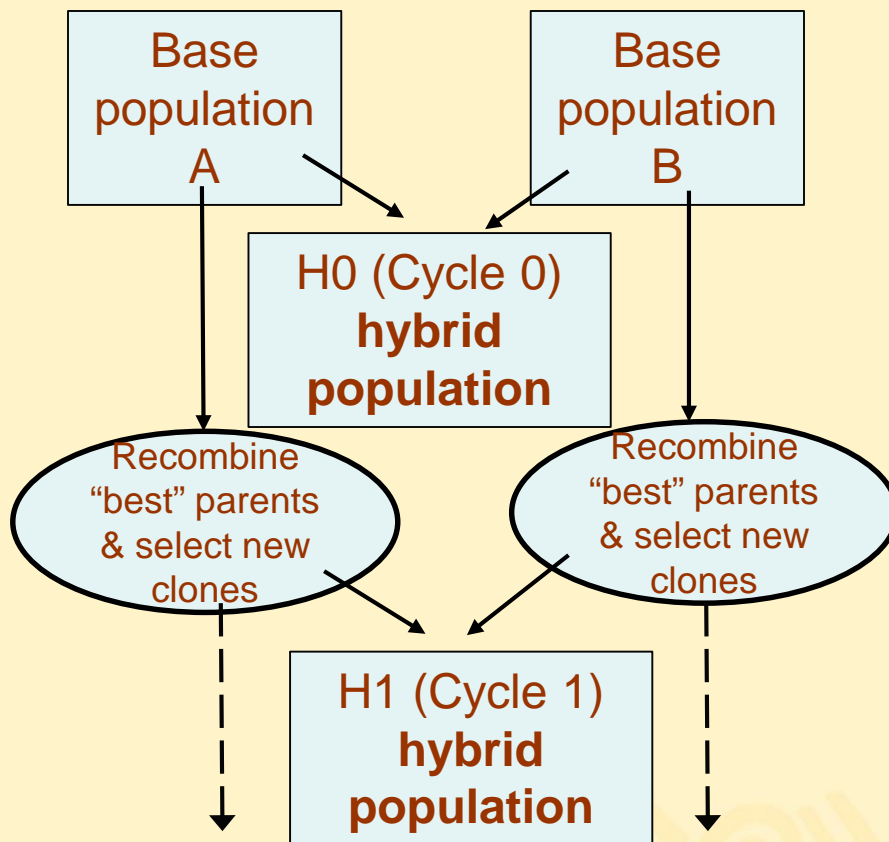# Don't tell me – show me! (A & B at CIP-Uganda)

Fig. 2. Storage root yields (A) and biomass yields (B) for A x B genepool cross combinations (N = 54), A parents (N = 9), and B parents (N = 6) across four experimental sites in Uganda.

⇒ **A and B genepools at the East African platform are most likely mutually heterotic for storage root yield as well as biomass production**
[AxB are superior to AxA and BxB crosses tested in Uganda & Mozambique (irr. – no irr.]

How to estimate genetic gains in a complete reciprocal recurrent selection cycle? Baseline (foundation), new selected parents, and H1 offspring cross environments

Reciprocal recurrent selection

Base population A

Base population B

H0 (Cycle 0) **hybrid population**

Recombine "best" parents & select new clones

Recombine "best" parents & select new clones

H1 (Cycle 1) **hybrid population**

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Objective: Genetic gains (GG) for 1 complete reciprocal recurrent selection (RRS) cycle using HEBS

Genepool separation (Confirmed genetic distance between PJ and PZ)

*Crossings for H0 population (**49 PJ05 x 31 PZ06; in total 80 parents base line**)*

H0 population field evaluation (231 families / 210 cross combinations, 6898 offspring clones)

Crossings for partial inbreed populations (23x23 PJ, 17x17 PZ for WAEA; 5x5 PJ05, 5x5 PZ06 for HIFE and 5x5 PJ05, 5x5 PZ06 NSSP)

Partially inbreed populations field evaluation (9324 PJ', 2152 PZ' for WAEA; 1006 PJ', 711 PZ' for HIFE and 702 PJ', 379 PZ' for NSSP)

Crossings for H1 population (**42 PJ' x 42 PZ' WAEA, 25 PJ' x PZ' 28 NSSP , 23 PJ' x 23 PZ' HIFE**)

H1 population field evaluation / H1 families 742 (**9881 H1 hybrid clones**), 336 (**3742 H1 hybrid clones**), and 272 (**3292 H1 hybrid clones**) for WAEA, NSSP, HIFE (Canete, Satipo)

Three objectives / three studies across two environments:

(A) WAEA wide adaptation & earliness (normal selection intensity / normal no. parents)

(B) NSSP less sweet (very high selection intensity / few parents / inbreeding),

(C) HIFE high Fe and Zn (very high selection intensity / few parents / inbreeding).

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)
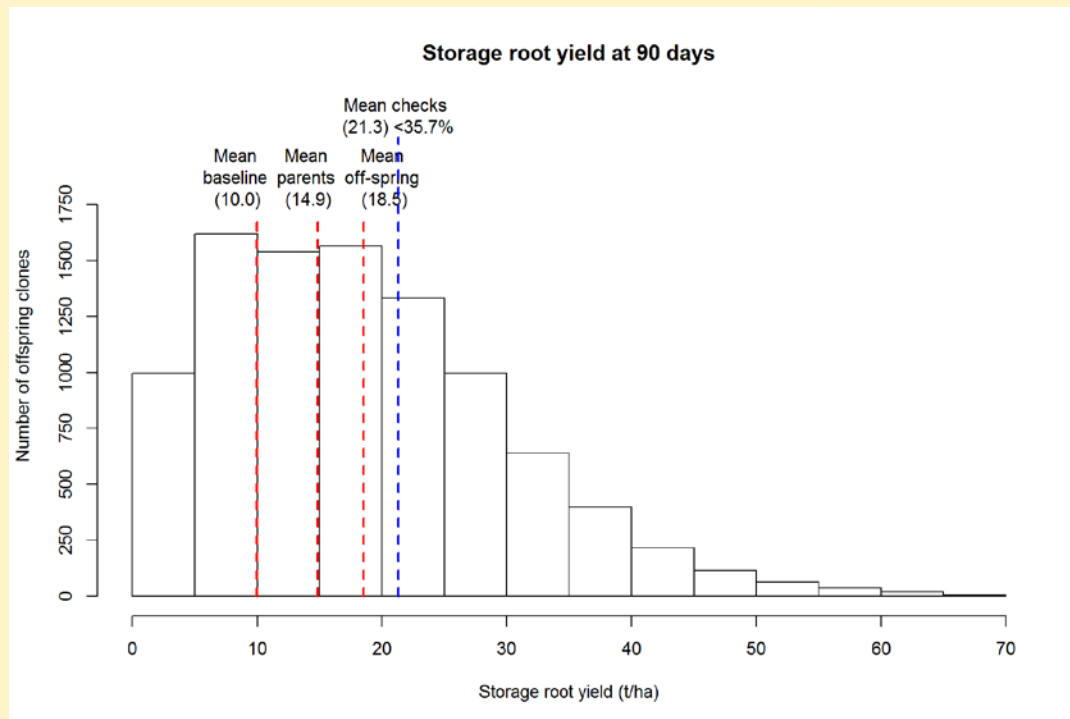
Fig. 3a. Genetic gain (GG) for storage root yield by genepool separation and one complete reciprocal recurrent selection cycle estimated in population WAEA 90 days harvest at two locations in Peru / Canete – arid pacific coast / Satipo – humid tropics [[Mean baseline (10.9 t/ha), 80 clones each clone 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%].

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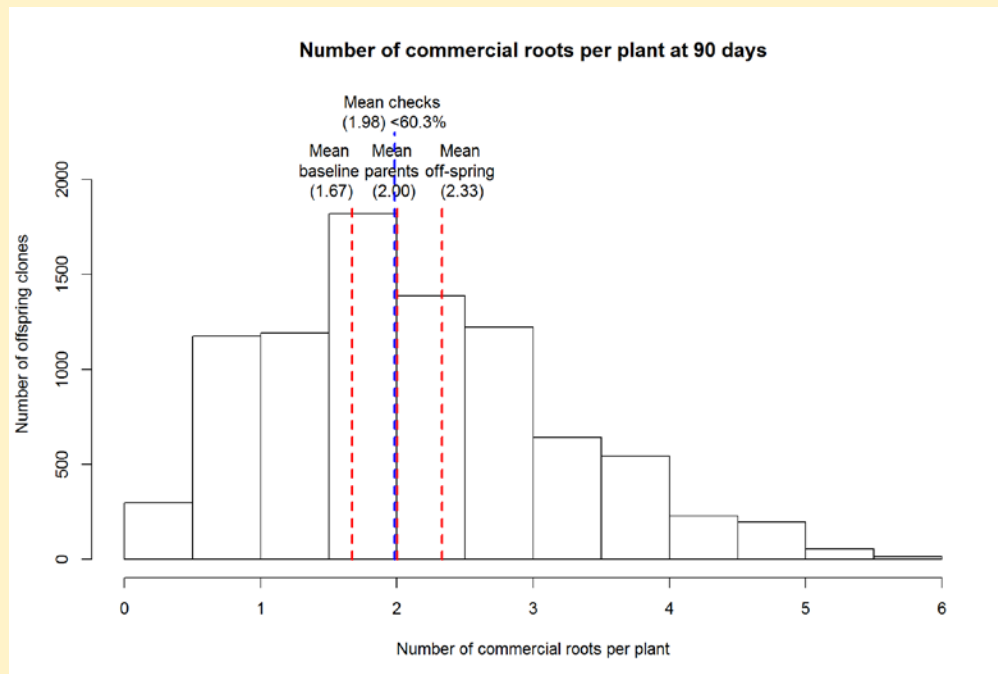**Number of commercial roots per plant at 90 days**

Fig. 3b. Genetic gain (GG) for commercial storage roots per plant 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.
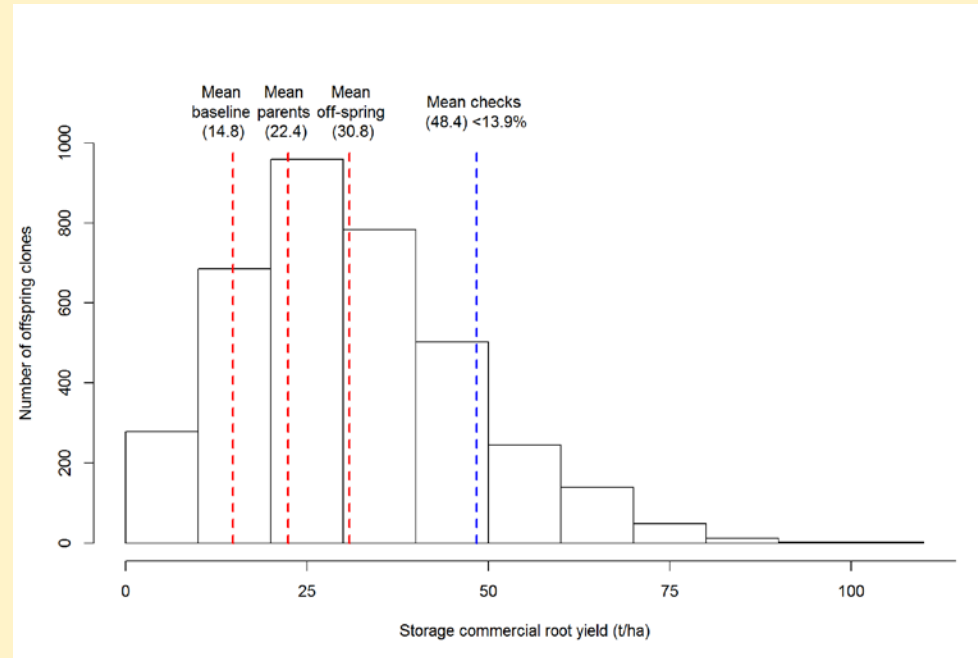
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Fig.4. Genetic gain (GG) for storage root yield by genepool separation and one complete reciprocal recurrent selection cycle estimated in population NSSP at two locations in Peru / Canete – arid pacific coast / Satipo – humid tropics [Mean baseline (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%].
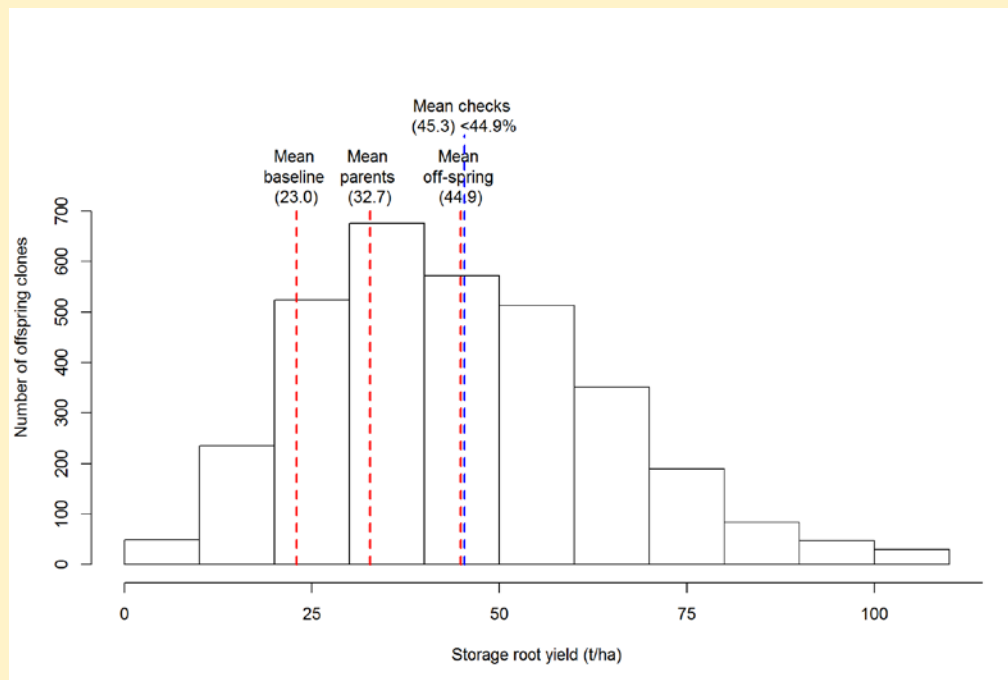
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Fig.5. Genetic gain (GG) for storage root yield by genepool separation and one complete reciprocal recurrent selection cycle estimated in population HIFE at two locations in Peru / Canete – arid pacific coast / Satipo – humid tropics [Mean baseline (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%].

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Table 1. Offspring means, heterosis increments, genetic gains relative to 49 PJ and 31 PZ baseline clones, and frequency of offspring clones superior to checks in H1 hybrid populations wide adaptation and earliness (WAE, N = 9881), none sweet sweetpotato (NSSP, N = 3742), and high iron (HIFE, N = 3292) for storage root yield and number of commercial storage roots per plant harvested evaluated at Canete (arid pacific coast) and Satipo (humid tropics) in Peru.].

H1 Population	Trait[§]	H1 offspring mean[§§]	Heterosis increment[‡] (%)	Genetic Gain (%)	Frequency of offspring clones superior to checks[‡‡] (%)
WAE 90d harvest	RYTHA	18.5 (t/ha)	24.2	85.0	35.7
	NCRP	2.33	16.5	39.5	60.3
WAE 120d harvest	RYTHA	37.8 (t/ha)	9.3	68.8	22.1
	NCRP	3.30	3.5	31.0	50.4
NSSP 120d harvest	RYTHA	32.6 (t/ha)	37.6	110.3	13.2
	NCRP	3.04	21.6	42.1	49.3
HIFE 120d harvest	RYTHA	44.9 (t/ha)	37.3	95.2	44.9
	NCRP	3.56	21.1	55.5	75.6

[§] **RYTHA, storage root yield in t / ha; NCRP, number of commercial storage roots per plant harvested.**

• [§§] **Offspring families estimates WAE (n = 742), NSSP (n = 336), and HIFE (n = 272).**

• [‡‡] **relative to 42 PJ', 42 PZ', 25 PJ'', 28 PZ'', 23 PJ''', and 23''' PZ parents for WAE, NSSP, and HIFE, respectively.**

• [‡‡] **relative to mean of check clone Dagga and Cemsa.**

Table 2. Mean of selected material for wide adaptation and earliness / 90 days harvest (N=400) and for none sweet sweetpotato under normal harvest (N=200) and check clones for observed traits evaluated at two locations in Peru (Canete and Satipo) after discarding all clones with virus symptoms.

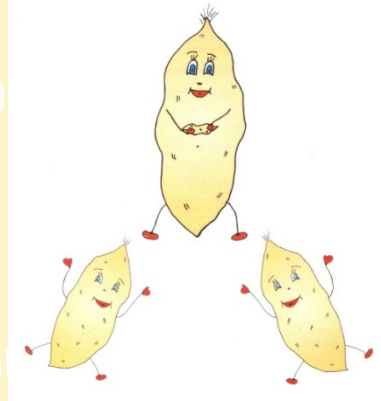| Mean H1 breeding lines & checks	Root yield (t/ha)	No. Comm. Roots per plant	Foliage yield (t/ha)	B-carotene (mg / 100 g FW)	Root dry matter (%)	Sweetness taste score§
WAE (N=400)	30.2	3.70	49.0	6.44	26.2	-
Dagga	26.8	2.44	49.1	1.16	26.4	-
Cemsa	15.9	1.53	55.5	0.08	28.4	-
NSSP (N=200)	44.4	3.69	71.6	6.2	25.2	4.1
Dagga	41.1	2.64	72.6	1.11	25.7	5.1
Cemsa	61.7	3.20	115.6	0.88	25.6	6.8

§ taste test scale from 1 = not sweet to 9 = very sweet

SASHA phase 2 / CIP-Uganda
H0 Hybrid Population to select among A and B parents for HEBS & one complete RRS cycle

Namulonge / Uganda 2018 (humid tropics, high virus pressure zone) – Field trial of H0 for SPVD resistance and root yield (N > 10,600, 987 H0 families, tracing back to 50 UG_A x 80 UG_B parents) to select UG_A and UG_B parents to enter in a reciprocal recurrent selection cycle for H1

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Thank-you for your Attention