Measuring genetic gains in applied sweetpotato breeding programs: more than one way to peel a Sweetpotato

By

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Genetic gains:meaning & implications

- The predicted change in the mean value of a trait within a population that **OCCURS WITH SELECTION**

- A breeder makes genetic gain **when the selected individual(s) has a better combination of genes that control the traits of interest than the unselected individual(s)**
- Measure of Genetic gain allow critical **analysis of efficiency of a particular breeding approach** and to plan new actions and strategies
- **Allow wise allocation of resources**

Estimating the genetic gains

Genetic gain (ΔG) =response to selection minus original population mean

The expected genetic gain, (ΔG) is given by the formula:

$$\Delta G = h^2 \times (\text{Selection Differential})$$

Heritability h^2 is the general term that describes the proportion of the genetic variance to the total variance

Selection differential=New mean of the selected population minus mean of the original population

Heritability

Two types of heritability:

- The narrow-sense heritability: the ratio of additive genetic variance to the total phenotypic variance: $h^2 = V_A/V_P$
- The broad-sense heritability is the ratio of total genetic variance to total phenotypic variance: $H^2 = V_G/V_P$

Estimating genetic gain

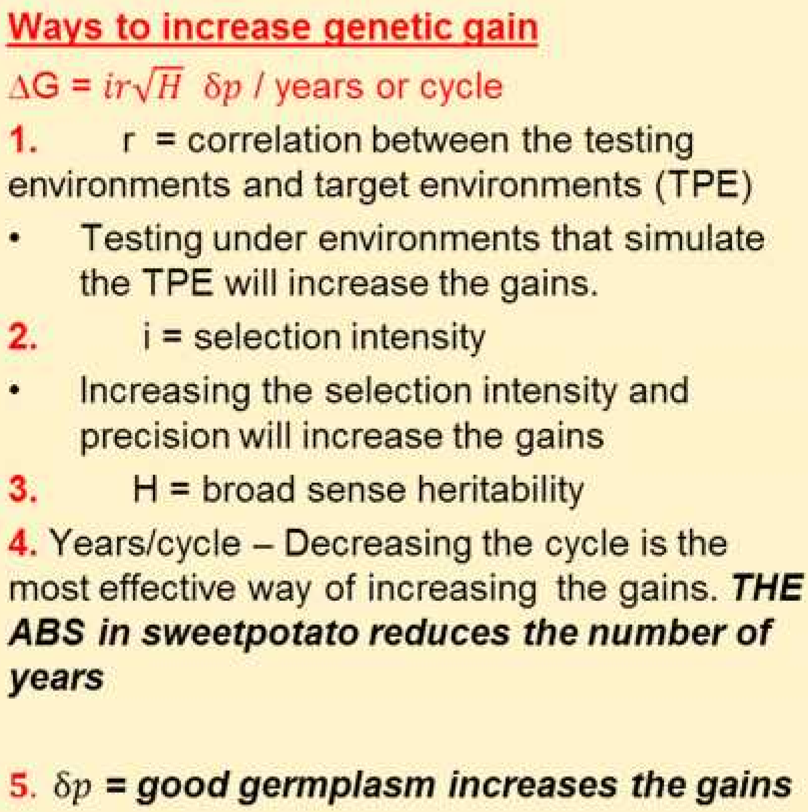
- Both generations **must be evaluated in the same environment** so that environmental effects do not cause a bias

- The same formula can be used to **estimate heritability** after several generations of selection have been completed

- The estimated genetic gain must be **divided by the number of generations of selection** so that the genetic gain is the average gain per generation of selection

- The value of the selection differential **is the average value across the multiple generations** of selection

Ways to increase the genetic gains



Ways to increase genetic gain

$\Delta G = ir\sqrt{H} \; \delta p$ / years or cycle

1. r = correlation between the testing environments and target environments (TPE)
   - Testing under environments that simulate the TPE will increase the gains.
2. i = selection intensity
   - Increasing the selection intensity and precision will increase the gains
3. H = broad sense heritability
4. Years/cycle – Decreasing the cycle is the most effective way of increasing the gains. ***THE ABS in sweetpotato reduces the number of years***

5. δp = ***good germplasm increases the gains***

- A breeder can increase **the expected genetic gain** either by increasing the heritability or by increasing the **selection differential (new mean of selected pop minus original pop mean).**
- One approach to increasing heritability is reducing the environmental variance
- Another approach to increasing heritability is to choose or create **a population that is extremely variable** (*i.e.*, large genetic variance).
- A breeder can increase **the selection differential** by selecting fewer individuals

Selection – the basis of genetic gains

Selection can be done on:

1) **Early breeding** cycles of clonally propagated crops (**ABS** adopted in sweetpotato)
2) **Later in the breeding** cycle – have an effect on ΔG
3) **Parents** to develop new populations

- Follow **the index selection** to have parents with multiple traits

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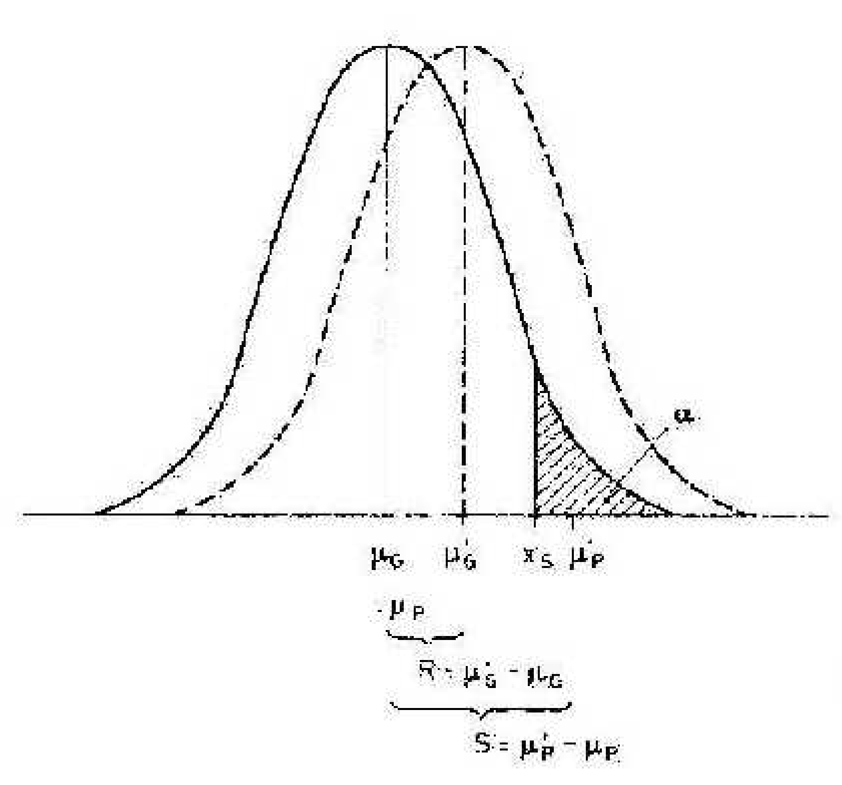


Fig 2: Genetic gains or response to selection

Breeding Methods - Selection

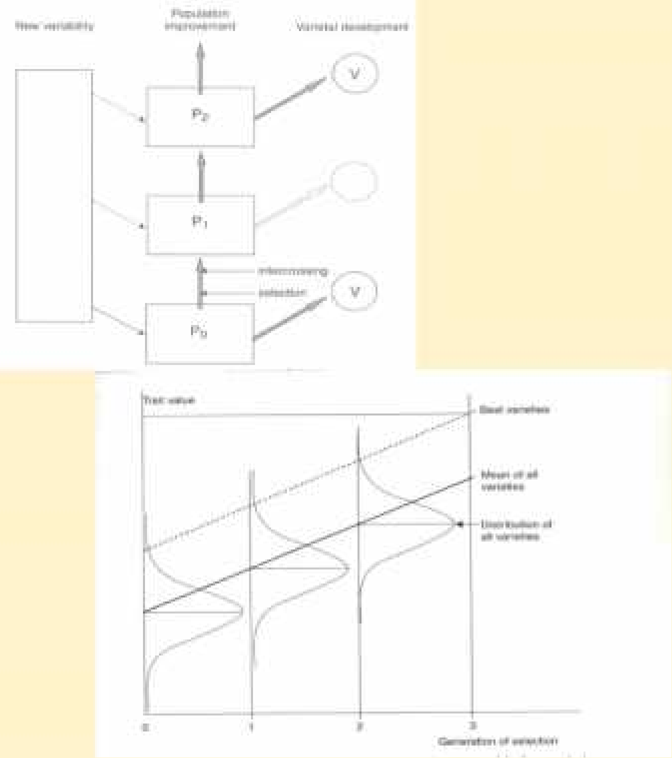
Selection for Varieties

1. **Later Breeding stages** (quite well investigated: (e.g. Cochran 1951; Hanson and Brim 1963; Finney 1966; Utz 1969, 1984, Grüneberg et al. 2004; Mi et al. 2014) – note: a dozen of PhD students have been working on this by model calculations
2. **Early breeding stages clonally propagated crops – (ABS)** (Grüneberg et al. 2009) – note: extreme rapid adoption (fostered by SASHA & AGRA funds)

Selection of Parents for new Populations

(here we have the importance of index selection – Pesek Baker 1969, not new but …)

1. **Poly-Cross versus Controlled Cross Breeding**
2. **Selection of parents on off-spring performance – Heterosis**



Figures: From Gallais (2003) part III: ‘Population improvement and varietal development’ to illustrate the relevance of variety development and populations improvement

Recurrent selection in ABS adapted in Mozambique

SASHA
Sweetpotato Action for Security and Health in Africa

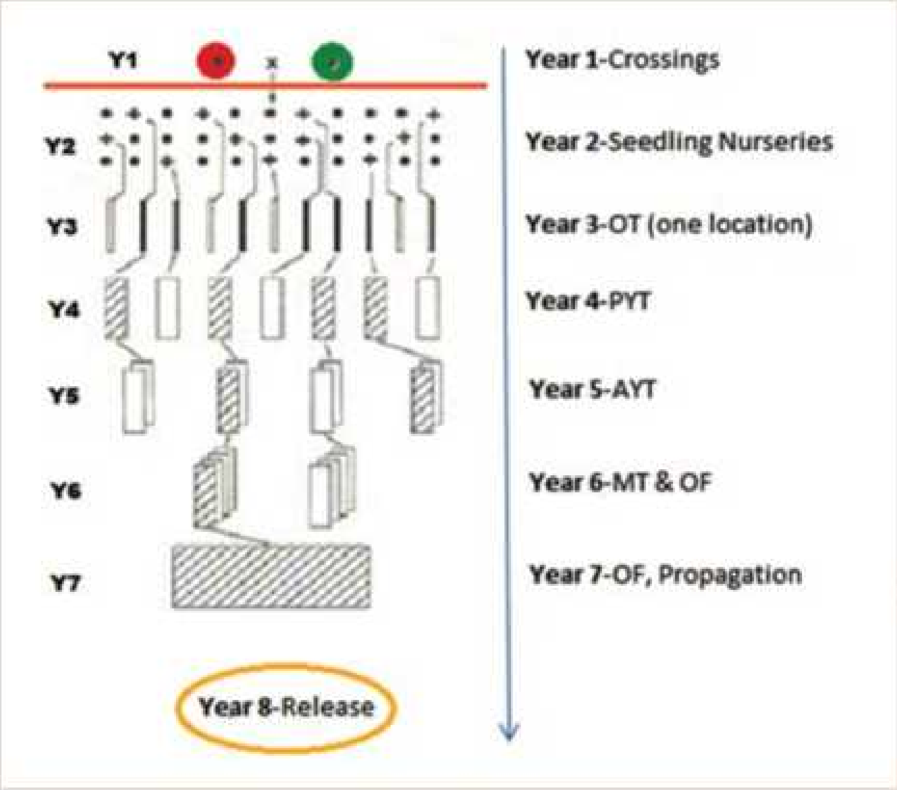


Fig. 1. Conventional breeding scheme for sweetpotato

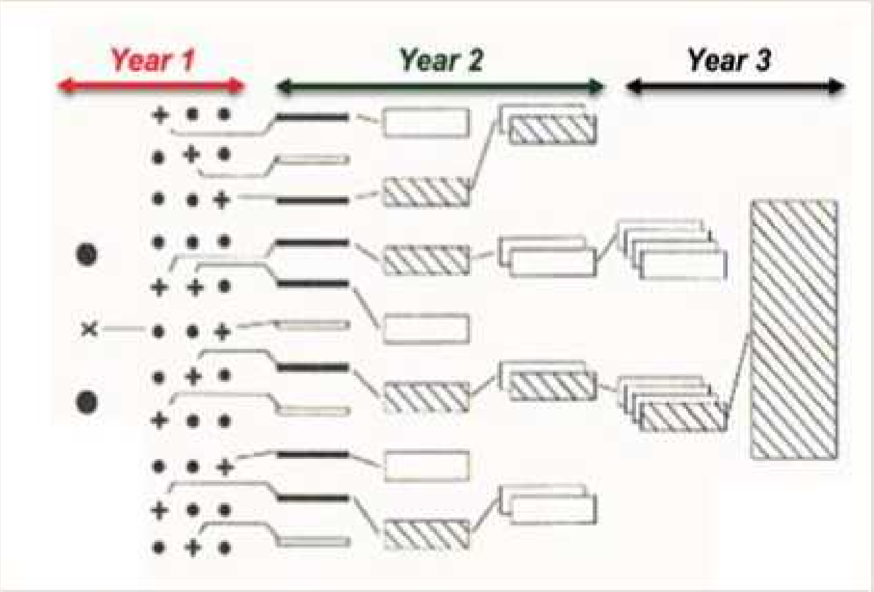


Fig. 2. Accelerated Breeding Scheme (ABS) for sweetpotato

Achievements – the case of Mozambique
Variety releases

Trait	Farmer varieties	1st release	Gain (%)	2nd release	Gain (%)	3rd release	Gain (%)
	1999	2000		2011		2015	
Total root yield (dry weight, t/ha)	1.9	3.5	84	5.6	60	5.75	2.7
Variation in total root yield	2.1 - 12.6	13.6 -16.1		14.9 -27.1		14.4 - 29.0	
Dry matter content (%)	33.0	23.5		27.6	17	30.2	9
Variation in dry matter content				23.6 -33.5		24.6 -36.6	
Beta-carotene (mg/100g/DW)				21.3		24.8	16
Variation in BC				16.4 -42.9		17.2-36.3	
Iron content (mg/100g/DW)				1.8		1.9	6
Variation in Fe				1.4 -1.9		1.67-2.44	
Zinc content (mg/100g/DW)				1.1		1.3	18
Variation in Zn				0.95 -1.2		1.12-1.75	

Several approaches taken at our Platforms in Mozambique, Uganda, Ghana, and CIP HQ to predict and measure genetic gains for key attributes in breeding

- Key attributes include **yield - through approaches of ABS and exploitation of heterosis,** virus disease **(SPVD) resistance, drought tolerance, BC, iron and zinc, and reduced sweetness, perishability**

Large genetic variation and expected genetic gains for yield, drought, BC, and sweetness exhibited. Iron and zinc appeared to exhibit **low genetic variation.** SPVD resistance tricky trait, due to its **GXE and mode of inheritance**

Also another approach by **comparison of means of selected clones with parents,** comparison of **means in sets of variety release trials and demonstration trials including new and old varieties,** or comparison of **means of selected clones to those of standard checks**

- Yield increases were high (convincingly in the heterosis in HQ)
- Gains for DM, BC and RS were high
- Gains for iron and zinc were low
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Genetic gain – under farm practice

Series of multi-environmental trials (METs) usually over 2 to 3 years

For example **5 years** SASHA I then **3 MET sets are possible** – these can serve a) **variance component estimations** in later breeding stages b) the genetic gains (development of the mean in these METs) during these time period Comment: this is still a small section of the long term genetic gain – 10 or 20 years)

In practice 10 to 20 years of METs from variety release time using 8 to 18 METs allows to estimate long term yield trends and changes in long term yield trends (by some kind of regression analysis or plots of year and/or genotype means against time - assess time trends) including gain components due to better practice

Technology revolution – use of molecular markers to enhance genetic gains

- The study in Peru appears that **molecular markers are useful to identify heterotic gene pools in sweetpotato,** but that the identification of best combiners among genepools (prediction of heterosis on basis of molecular distances) is not possible or is associated with a very large error in sweetpotato.
- Markers defined **population structure in Uganda sweetpotato:** two distinct Uganda populations (A & B)
- Utilised in heterosis studies (1). **for SPDV resistance in Uganda** (2). **drought tolerance in Mozambique**
- Three populations were generated; intra-gene population A, intra-gene population B and inter-gene population A x B.
- Molecular markers accelerate and improve efficiency of selection: **Development of SPDV markers and validation in the VZ08 population**

Heterosis in Mozammbique

From the preliminary results;

- the inter_ A x B population had higher root yield than intra_A population under the two treatments

- The inter_A x B population had some clones which had higher root yield under drought than highest yield clones from intra_B and A populations

Results for Proof of Concept for Heterosis

- The observed mid parent – mid offspring heterosis for fresh storage root yield, DM storage root yield and total DM biomass yield were 115.3%, 122.9%, and 107.9%

- This is a clear proof of the presence of heterosis in

- Observed on average a hybrid storage root yield advantage of 15.3% on fresh weight basis and 22.9% on dry weight basis.

- On average we observed that the best offspring clone within each family has a storage root yield advantage of 119.8% on fresh weight basis and 136.6% on dry weight basis compared to his parents
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- Yield advantages in offsprings and heterotic effects of 2 to 4 times higher than the parental mean are not rare events . We think this is a reflection of the contribution of heterosis to yield performance in sweetpotato.

Conclusions and perspectives

Use of molecular markers can increase genetic gains

Scientific and institutional capacity play a role in genetic gains – need strengthening

Simulating TPE (testing enviroments and target environment) is important during experiments

Continue to refine approaches for tracking progress in our breeding programs in the coming years

Emphasis will be given on the use of **demonstration trials comparing newly-released and older varieties over years** as well as the use of data from national variety release trials to monitor genetic gains in released varieties over time

Conclusions and perspectives

- **Disaggregate genetic gains from cultural practices**
- Continue **to monitor observed genetic gains and genetic variability in breeding populations**, particularly in partially inbred and mutually heterotic populations to aggressively improve specific attributes, including SPVD, micronutrient mineral content, earliness, quality attributes and reduced perishability

Thank-you for your Attention