IPBO Summer Course 2012

Advanced Breeding Methodologies for Sweetpotato / Clonally Propagated Crops

CIP Breeding
20th to 31th of August 2012

Content

1. Clonally Propagated Crops
2. Breeding Objectives (examples for sweetpotatoes)
3. Selection by Accelerated Breeding and Developing Varieties in 4 to 5 Years
4. Some Population Genetics for Autopolyploids (recessive inheritance and inbreeding)
5. Heterosis Exploitation and Achieving a Yield Jump of 20%, 40%, and more for Sweetpotato and other RTB Crops

1. Clonally Propagated Crops

What are clonally propagated crops?

All important root and tuber crops
Many forage crops
Nearly all types of fruits and wooden ornamentals
Many cut flowers and pot plants
Forest trees.

Definition for a clonally propagated crop:
The <u>material to cultivate and maintain</u> a variety is <u>by asexual reproduction</u>
e.g. tubers, roots, stem cuttings, corms ... asexual developed seeds (apomixis)

Important note:
Maize (breed as open-pollinated or hybrid crop) or beans (breed as cross-fertilizing, self-fertilizing or hybrid crop) or rice (self-fertilizing or hybrid crop) if multiplied by cuttings or apomixtic seed => these would become clonally propagated crop

Overview clonally propagated Crops

Note:

Root and tuber, fruit and tree plant species are very old as food plants they were used by humans before agriculture

Species	Planting material	World Production	Polyploidy
Potato (*Solanum tuberosum*)	Sprout tubers	315 Mio t	2x, 3x, 4x, 5x
Cassava (*Manihot esculenta*)	Wood cuttings	226 Mio t	2x
Sweet Potato (*Ipomoea batatas*)	Sprout cuttings	124 Mio t	6x
Yam (*Dioscorea ssp.*)	Root tubers	51 Mio t	3x – 10x
Taro (*Colocasia esculenta*)	Corms	12 Mio t	4x
Sugarcane (*Saccharum officinarum*)	Sprout parts	194 Mio t sucrose	8x
Banana (*Musa x paradisiaca*)	Corms	105 Mio t	3x
Citrus fruit (*Citrus spp.*)		89 Mio t	2x, 3x+1, 4x-3
Grapes (*Vitis vinifera*)		69 Mio t	6x
Apple (*Malus pumila*)		64 Mio t	2x, 3x

The Three Major Components of Breeding

What is the principle to breed clonally propagated crops?

1. **Determine Breeding Objectives - can be grouped into (i) yield and yield stability, (ii) quality for food and industry and (iii) resistance to pest and diseases**
=> only one objective and this is the better variety with good performance over all traits (Röbbelen 1985)

2. **Formation of Variation in Base Material (collect in existing variation or generate by crossings)**
=> those who want to find a better potato adapted to their fields simply have to collect and raise plants from true seed
=> selection of parents is the most difficult part of breeding especially when parent offspring correlations are low (true for most clonally propagated crops due to complex polyploid genetics)

3. **Selection of Types most similar to Breeding Objectives over all traits (selection for several / many traits !!!)**
=> the need to know the "true needs" of clients / farmer participatory and allocation of breeding resources determines who comes (first) and serves (first)
=> selection can be made very fast in many clonally propagated crops especially sweetpotato (short growing cycle and high propagation coefficient in sweetpotato)

What is the principle to breed clonally propagated crops?

Principal to breed clone crops appears simple:

- Simply break normal clone propagation by a crossing step and to develop sexual seeds = genetic variation

- *Genetic variation & select new clones* (all propagation steps from the first to the last selection step are again by "normal" asexual reproduction)

The finally selected clone is genetically absolutely identical with the original seed plant

$\Rightarrow$ *!!! Each seed plant is a potential variety !!!*

Breeding Objectives in Sweetpotato

30g†
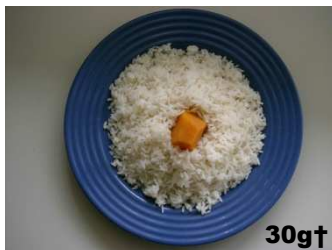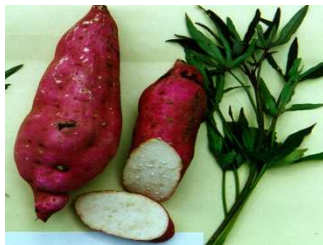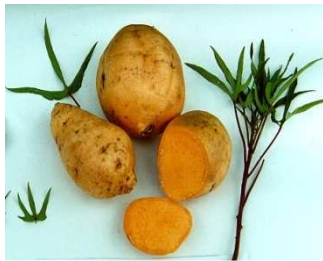
A piece of OFSP served to rice dominated dishes ....

† provides 50% of pro-vitamin A RDA

Yield, Stability & Adaptation – wide and specifically adapted genotypes can be selected; Important to know: (i) genotypes well adapted to drought can be found determined by vine survival, harvest index stability and most likely etc. (ii) certainly genotypes extremely adapted to saline soils can be found, (iii) it is assumed that genotypes extremely adapted to heat can be found

Taste - two major types were distinguished in the past: (i) the orange fleshed, sweet, moist, low dry matter (DM) - (ii) the white or pale yellow fleshed, high DM, low-sweet or bland type (Brasil and Africa) - note the taste in sweetpotato can be very differ - new directions: (iiii) non-sweet sweetpotato or "sweetpotato with simple taste", (iv) purple fleshed and (v) high starch sweetpotato & biofuel

Biotic Stress / Pest & Diseases: (i) Across regions sweetpotato virus disease (SPVD) - the story of Jonathan and Humbachero - SP clorotic stunt virus (SPCSV) is the important component of SPVD (generally SP is very resistant to virus but ...... ; (ii) weevil damage - all drought prone regions (Central and South America, SSA and SWCA) - storage roots deep in the soil and clearly tapering at top (Malawi & Mozambique) - latex in storage root skin / varieties like "Santo Amaro" from Brazil, New Kawogo (Stevenson et al. 2009) from Uganda, and PZ06.120 from Peru are clearly less affected than other clones – it can be discussed if there is "no resistance to weevil" in sweetpotato
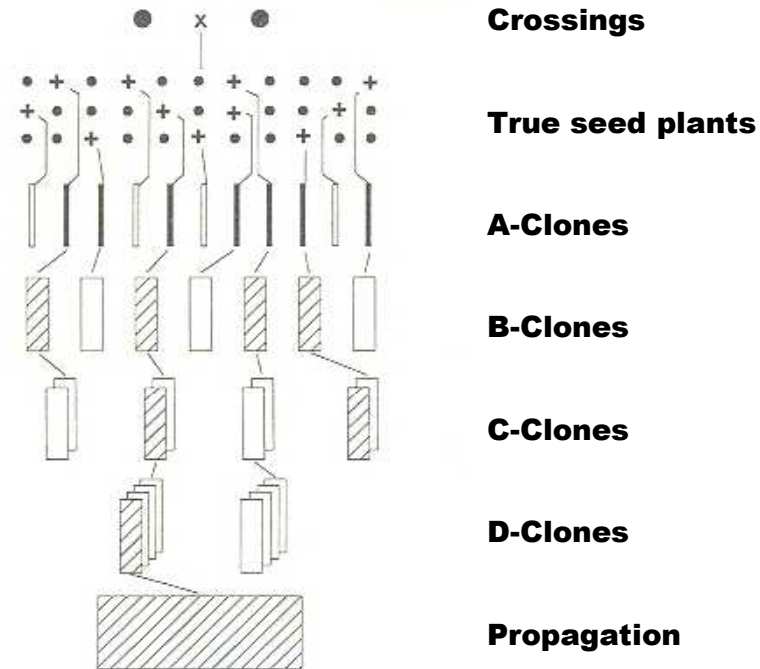
The general breeding scheme for clonally propagated crops

Selection

The long way to a new variety

Selected potatoes derived from crosses between S. phureja and S. tuberous

Crossings

True seed plants

A-Clones

B-Clones

C-Clones

D-Clones

Propagation

This figure "The general breeding scheme of clonally propagated crops" is from Becker (1992)

Similar scheme can found in many other textbooks – unfortunately !!!

This scheme is misleading:

1) a breeder makes more than 1 cross (he makes hundreds of crosses)
2) different selection steps must not be in different years in clonally propagated crops – remember the finally selected D-clone is genetically absolutely identical with the true seed plant the D-clone is tracing back to

Clonally Propagated Crops 06

Modification of the general breeding scheme => the accelerated breeding scheme (ABS) for clonally propagated crops

Selection by ABS

Save time no one is waiting for you 7 to 10 years

Year 1   Year 2   Year 3   Year 4   Multiplication
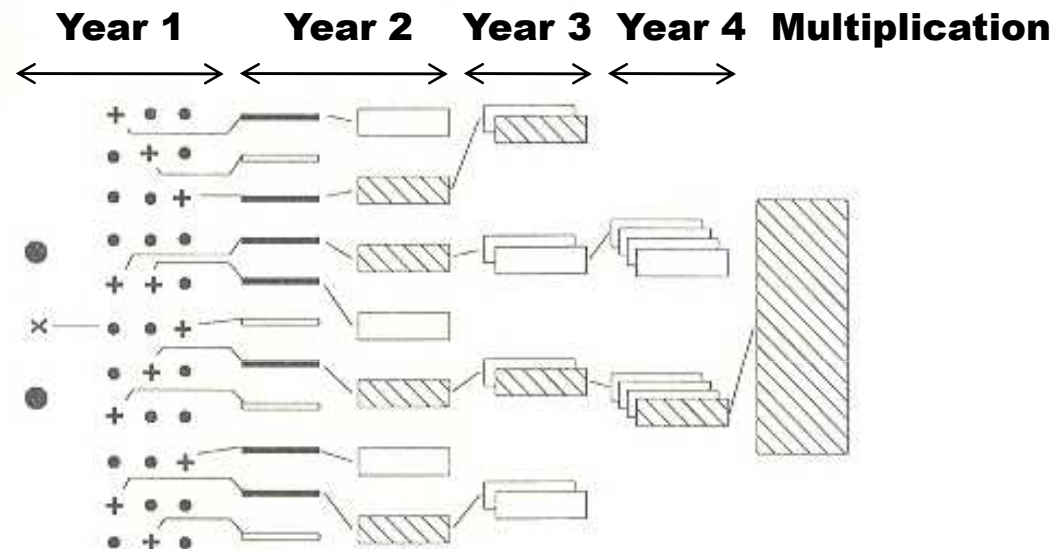
Rules:

1) the seed plant is already the final genotype = variety selection is relatively easy in clonally propagated crops

2) early breeding stages: 1m row plots (8000 – 12000 clones) - everything what can be made simultaneously is made simultaneously – 2 to 4 locations no replications

3) later breeding stages: 4-5 row plots - 1st selection step: 300 clones, 3 locations, 2 replications - 2nd selection step: 40 clones, 6-12 locations, 2 replications

Plot size: 1m

If ABS works depends on the heritability (h²)

⇒ **if h is low (h < 0.3) clear " no go" decision for ABS**

⇒ **if h is medium to high (h > 0.5) " go" decision for ABS**

- h: √heritability – in case of ABS only the broad sense heritability is used, because there is no need to devide the **variance components due to genotypes (σ^2_G)**

- Heritability - a genetic parameter between 0 and 1 and it should be noted that it is an operational parameter, because it depends on size and numbers of test units (i.e. plot size, number of test locations and number of years:

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

  with σ^2_G, σ^2_{GY} , σ^2_{GL}, σ^2_{GLY} , and σ^2_e the variance components due to genotypes, genotype x year interaction, genotype x location interaction, genotype x location x year interaction and the plot error, respectively; Y, L, and R the number of locations, years, and replications, respectively.

Critical is the genotype by year interaction or σ^2_{GY} in ABS

$\Rightarrow$ if σ^2_{GY} is extremely large " no go" decision for ABS (what is extremely large?)

$\Rightarrow$ if σ^2_{GY} is medium to low " go" decision for ABS

■ Note in case years are replaced completly by locations with no plot replications the operational broad sense heritability becomes:

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

■ Note in case variance component are estimated only from multi-environmental trails in which years are replaced completly by locations with no plot replications the operational broad sense heritability becomes:

■

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

with σ^2_G, σ^2_{GY}, σ^2_{GL}, σ^2_{GLY}, and σ^2_e the variance components due to genotypes, genotype x year interaction, genotype x location interaction, genotype x location x year interaction and the plot error, respectively; L the number of locations

Clonally Propagated Crops 10

Variance component and heritability estimates for observed traits (ratio $\sigma^2_G : \sigma^2_{GL}$ in brackets) for two groups of clones divided on basis of agronomical scores.

Traits	σ^2_G	σ^2_L	σ^2_{GxL}	N Obs	N Loc	Heritability
Observations with Agronomic Scores 1 to 5						
RYLD (t^2/ha^2)	47.7 (1	23.2	98 2.05)	12093	3	0.59
FYLD (t2/ha2)	237 (1	52.1	349 1.47)	8066	2	0.58
DM ($\%^2$)	13.94 (1	8.18	6.22 0.45)	3875	2	0.82
TcDM (ppm^2)	33651 (1	3453	9539 0.28)	3865	2	0.88
FeDM (ppm^2)	7.41 (1	5.79	7.61 1.03)	3874	2	0.66
ZnDM (ppm^2)	3.1 (1	4.63	2.92 0.95)	3872	2	0.68
Observations with Agronomic Scores 3 to 5						
RYLD (t^2/ha^2)	36.2 (1	23	110.4 3.05)	3655	3	0.5
FYLD (t2/ha2)	202 (1	16.6	265.2 1.31)	2718	2	0.6
DM ($\%^2$)	14.13 (1	11.28	5.01 0.36)	2040	2	0.85
TcDM (ppm^2)	31518 (1	5593	11896 0.38)	2038	2	0.84
FeDM (ppm^2)	7.39 (1	7.45	7.6 1.03)	2038	2	0.66
ZnDM (ppm^2)	3.07 (1	5.28	2.88 0.94)	2038	2	0.68

Three levels to investigate the efficiency of ABS

=> Estimate heritabilities when you apply ABS in early breeding stages (4 studies in applied breeding material at CIP Lima all with consistent results

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

$\Rightarrow$ 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

$\Rightarrow$ 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
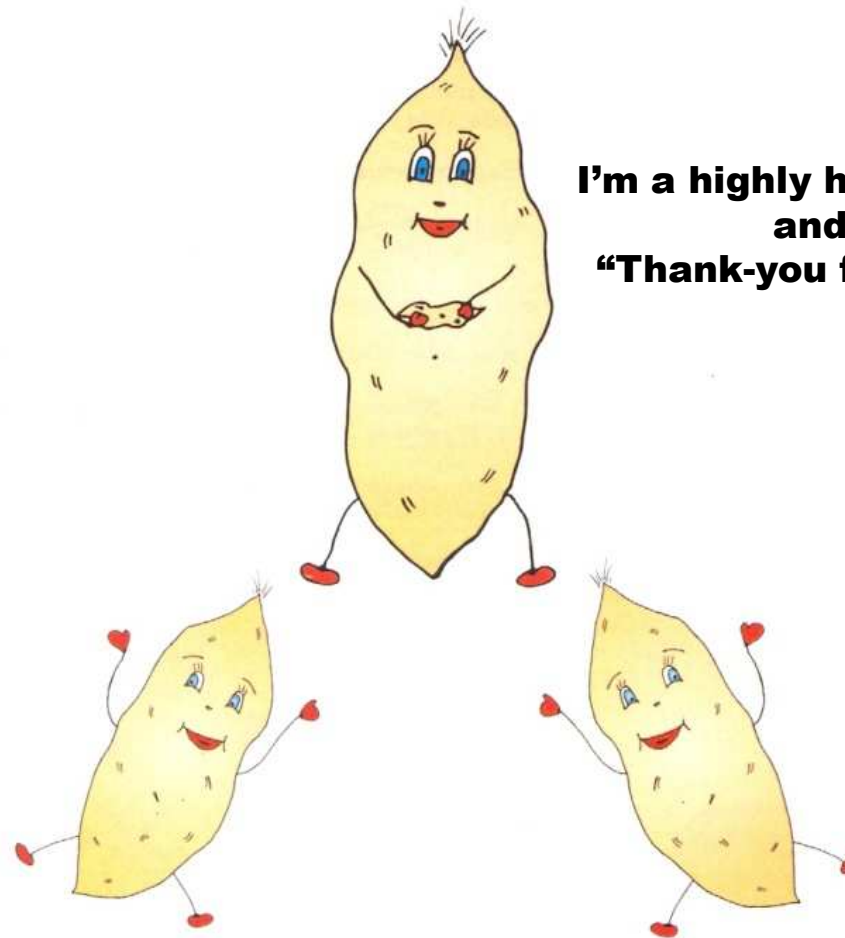
References:

Grüneberg W.J., Mwanga R., Andrade M. and Espinoza J., 2009. Selection methods Part 5: Breeding clonally propagated crops. In: S. Ceccarelli, E.P. Guimarães, E. Weltzien (eds) Plant breeding and Farmer Participation, 275 – 322. FAO, Rome.