Heritability estimates for an Accelerated Breeding Scheme (ABS) in clonally propagated crops - using sweetpotato as a model

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Abstract

Breeding of clonally propagated crops usually requires five or more years to produce outputs. An accelerated breeding scheme (ABS) can be designed in clonally propagated crops provided that the genotype by year interaction is low for the considered crop. The objectives of this study were to describe an ABS for clonally propagated crops and to investigate the efficiency of this breeding scheme on the basis of variance components, heritability estimations and model calculations for sweetpotato. In total 4243 clones from a seed nursery were planted nearly simultaneously at three locations in 1m row plots. The observed traits were storage root yield, upper biomass, dry matter, total carotenoids, iron and zinc contents of storage roots. Model calculations were carried out with a test capacity 12000 and 8000 field plots and a laboratory capacity of 8000 and 4000 samples. The ABS proposed reduces the time needed for one recurrent selection cycle in population improvement of sweetpotato form four to two years (the time needed for variety development is reduced from 7 to 4 years). The heritability estimates in the proposed ABS were within the range of 0.5 and 0.6 for storage root yield and upper biomass, 0.6 to 0.7 for iron and zinc and > 0.8 for dry matter and total carotenoids. For storage root yield the optimum resource allocation of 4000 and 12000 field plots was to plant 2000 or 4000 genotypes, at two and three locations, respectively. For low laboratory capacity the best allocation was to evaluate all genotypes at one location. For high laboratory capacity the best allocation was to use one or two locations. We conclude that our proposed ABS might be a very attractive breeding scheme for sweetpotato and other clonally propagated crops.

Keywords: Breeding scheme – clonally propagated crops - allocation of breeding resources – *Ipomoea batatas* – G x E interactions – variance components – heritability.

Introduction

Most breeding programs of clonally propagated crops follow a breeding scheme starting with population development until variety release that takes on average of 7-8 years in root and tuber crops. The long duration of this process often frustrates breeders and their clients. The definition of a clonally propagated crop is that the material to cultivate and maintain a variety is obtained by asexual reproduction. Usually the materials to propagate the crop are tubers, roots, stem cuttings or corms. It should be noted that clonally propagated crops are comprising also many forage crops, nearly all types of fruit and wooden ornamentals, many cut flowers and pot plants, as well as forest trees. Owing to the long crop duration of many fruits, wooden ornamentals and forest trees the time factor in breeding these plants becomes much more important compared to root and tuber crops. Apart from the crop duration the time needed to develop a better genotype is determined by the breeding scheme and high through put screening methods – both together determine the breeding efficiency. High through put screening methods are presented elsewhere at this symposium.

The essential components of a breeding scheme are: (1) definition of breeding objectives (we need to know what is needed), (2) generation of genetic variation for breeding objectives (we need a population in which its merits to select individuals), and (3) selection of individuals within the population, which match or are more close to our objectives compared to others. The breeding objectives can be grouped into yield, quality, and stress resistances. Usually several traits have to be considered by the breeder and the value of a genotype is determined by a good performance overall traits. Here we will consider yield as the most relevant trait together with several nutritional quality traits. Resistances to stresses are not considered, although this group of traits

often exhibit lowest acceptable values at which genotypes become useless. The generation of genetic variation is one of the most difficult components of a breeding scheme, because the genetic gain by selection depends not only on the genetic variation of a population. The population mean and its improvement from generation cycle to generation cycle (recurrent selection cycles) are at least as important as the variation of a population. Especially this component of breeding schemes for clonally propagated crops might be much more difficult to manage compared to other crops. The reason is that clonally propagated crops are highly heterozygotes hybrids and usually autopolyploid. This makes it easy to generate populations with a large genetic variation (provided the clonally propagated crop can be crossed), but it makes it very difficult to improve the population mean. Here we want to leave the first and second component a breeding scheme to focus on the third component: "selection of individuals within the population".

The third component in a breeding scheme – the selection of individuals within a population - bears in clonally propagated crops easily achievable improvements of the breeding efficiency. The basis is that each genotype in a population of clonally propagated crops is fixed. No genetic changes among genotypes occur after the generation of a population until genotypes are recombined for the next recurrent selection cycle. Hence a clone variety can be identified as soon as possible within a population provided that the heritability is not low.

The heritability for fixed genotypes (also called the broad sense heritability) is defined as:

$$h^2 = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_{GxL}^2}{l} + \frac{\sigma_{GxY}^2}{y} + \frac{\sigma_{GxLxY}^2}{ly} + \frac{\sigma_\varepsilon^2}{lyr}},$$

where: σ_G^2, σ_{GxL}^2, σ_{GxY}^2, σ_{GxLxY}^2, and σ_ε^2, are the variance components due to the effect of genotype, genotype by location interaction, genotype by year interaction, genotype by location by year interaction, and plot error, respectively; and where: l, y, and r, are number of locations, years and plot replications, respectively. Obviously the heritability is not set into concrete even if the magnitude of σ_G^2 is constant. The heritability depends largely on σ_{GxL}^2, σ_{GxY}^2, σ_{GxLxY}^2, and σ_ε^2 as well as the test precision determined by l, y, and r (Patterson 1997). Even in the case where the σ_G^2 is very small the breeder can gradually increase the heritability very close to 1, provided he could make huge amounts of investments in numbers of locations, years and replications. From the above formula it can also easily been seen that in the case of no or very small σ_{GxY}^2, the breeder can gradually increase the heritability close to 1 by making no investments into years (in other word by using only one year) and allocate all resources into locations. Furthermore, it can be seen that the number locations are much more important than replications for increasing the heritability. Above it was mentioned that this is the definition of the so called broad sense heritability. The narrow sense heritability takes into account that not all the genetic variation can be used in improving the population mean (see above the 2nd component of a breeding scheme). The narrow sense heritability is not relevant for the third component of a breeding scheme in clonally propagated crops (Wricke and Weber 1986).

There were three objectives in this study. First to present an accelerated breeding scheme (ABS) for clonally propagated crops in which temporal variation of test environments is spatial variation of test environments in early stages of a breeding program. The second objective was to estimate variance components and heritabilities for the proposed ABS in early breeding stages by using sweetpotato as a model to provide information which traits merits selection in ABS. Sweetpotato is a quite suitable crop for such a study because it has a high propagation coefficient (30 and more cuttings of a genotype in a seedling nursery can be easily obtained within 4 months). The third objective was to allocate for sweetpotato the optimum of the resource allocation in ABS.

Material and methods

Accelerated Breeding Scheme (ABS)

The ABS is building out on the general principle of breeding clonally propagated crops. This principle is to break normal clonal propagation by introducing a crossing step which culminates in sexual seed production. After the genetic recombination, all subsequent propagation steps are asexual in nature, i.e. clonal propagation. The population developed from seeds consists of very different and heterozygous genotypes, which do not exchange genetic material. Each of these seed plants grown in the so-called seedling nursery can be considered a potential new variety. This is the base population for selection. This selection in breeding clonally propagated crops is described most often in plant breeding textbooks as a process conducted in several steps and years (Figure 1).

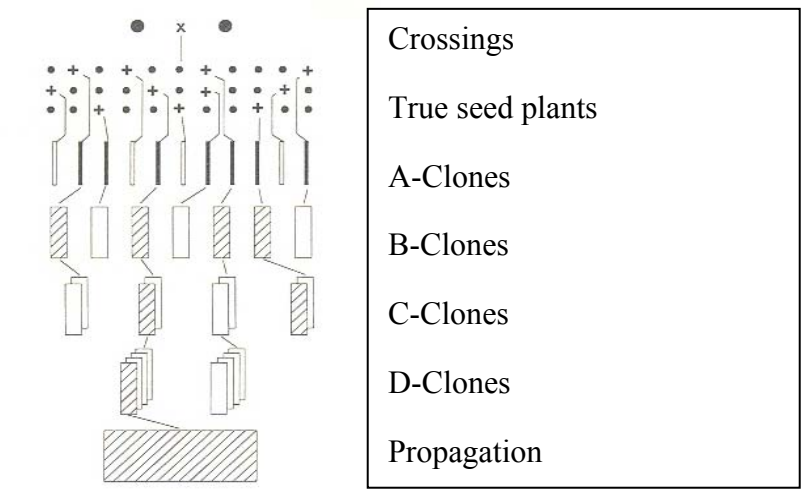

Figure 1. General scheme of breeding clonally propagated crops (Becker 1993)

The breeding scheme illustrated in Figure 1 is straightforward and is most often interpreted as requiring selection sequentially in several steps over several years. The diagram implies that there are two parents crossed, followed by 5 subsequent selection steps in time. This is very misleading. First, parental selection is a very difficult task and the breeder must work with many parents (the correlation between parental performance and offspring performance can be very weak in clonally propagated crops). Second, there is no further genetic development as one moves between selection steps. In other word, the selected D-clone in figure 1 is absolutely genetically identical with the true seed plant the selected D-clone is tracing back to. Theoretically, the breeding scheme illustrated in figure 1 could be rotated and all selection work done in one year. To which this can be done practically depends on the crop duration, the propagation rate and the genotype by year interaction (no or small σ^2_{GxY}) and the result is the ABS. The principle of the ABS for clonally propagated crops is to do as much as possible simultaneously, what is done in the general breeding scheme in Figure 1 sequentially in several steps over several years..

In the ABS all genotypes developed from seeds are planted simultaneously in several environments in small plots (in our experimental study 3 plants per row) without replications. It should be noted that development of new genotypes (crossings) raising seed plants and multiplication of planting material for multi-location field trials requires in sweetpotato not more than 1 year. The first multi-location field trials in ABS for sweetpotato starts at the beginning of year 2 and this first series of trials are completed within 4 to 5 months. The ABS applied for sweetpotato requires 1 year for crossings and multiplication of planting material. In the second year, a very large number of clones are planted in at least two environments (this can be managed by 1 assistant, 3 technicians and casual laborers). A visual agronomic evaluation (sufficient storage root formation, acceptable storage root size shape and form) can be conducted (at least at one environment preferable at a stress environment for example drought) to allocate work to genotypes which merit data recording – this can be linked to a farmer participatory breeding approach (Grüneberg et al. in press). All genotypes (or all selected

clones on basis of the agronomic evaluation) are measure across environments for storage root yield, upper biomass yields and storage root quality traits. In the case all clones are evaluated across environments this is a one stage selection process (traits can be aggregated into an index). In case only selected clones on basis of the visual agronomic evaluation are measured across environments the ABS becomes two stage selection process (further modifications to a three stage selection process to measure virus diseases are straight forward). This accelerated breeding scheme can be visualized as a rotated general breeding scheme for clonally propagated crosses and is illustrated in figure 2.

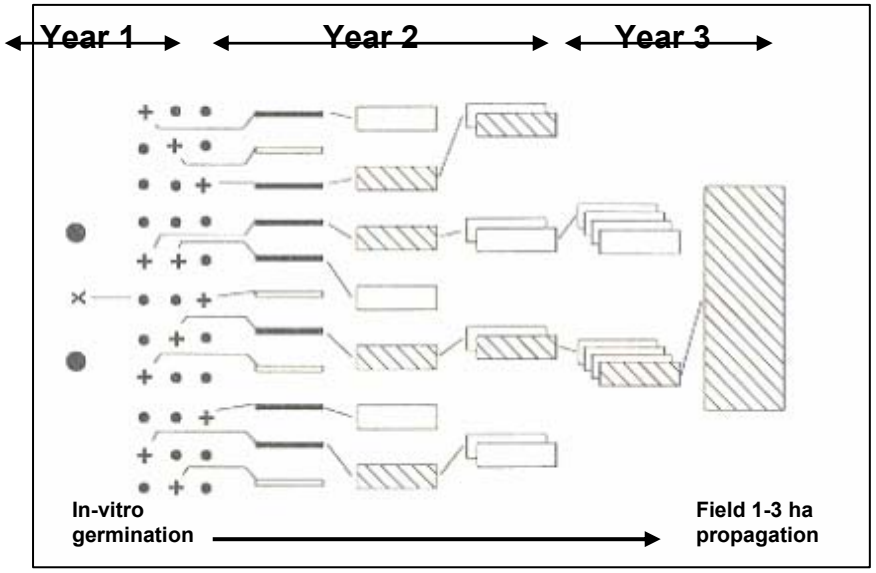

Figure 2. Accelerated breeding scheme (ABS) for clonally propagated crops, illustrated here with an in-vitro germination to keep clones virus free.

Planting material and field experiments

In total 4243 sweetpotato genotypes were planted at three environments, namely La Molina (LM), San Ramon (SR), San Ramon without fertilizer treatment [SRWF (an area at the station without fertilizer application)] in 1 m row plots (comprising 3 plants, 0.25m distance between plants and 0.25m distance to the next plot) and 0.9 m distance between rows (total size of the experiment at each environment about 0.45 hectares). The planting date at LM, SR, and SRWF was 13.01.2006, 20.01.2006, and 21.01.2006, respectively. The harvest date at LM, SR, and SRWF was 30.05.2006, 06.06.2006, and 08.06.2006, respectively. The breeding population was tracing back to a polycross with 128 clones (comprising CIP-Numbers: YM89., SR90., and SR93.) aiming at the development of an orange fleshed breeding population at CIP. This population was designated as "Jewel".

Data analysis

Storage root yield (RYLD in kg/m^2), upper biomass yield (FYLD in kg/m^2), agronomic score (AGRO from 1 to 5), storage root dry matter (DM in %), total carotene (TcDM in ppm), iron (FeDM in ppm) and zinc (ZnDM in ppm) concentrations of storage roots were recorded. TcDM, FeDM, and ZnDM were recorded on storage root dry matter basis using Near Infrared Spectroscopy calibrations (Zum Felde et al. at this symposium). All traits were recorded at LM and SR; however, at SRWF only RYLD and AGRO (1 – 5) were recorded. The analysis of variance was carried out using SAS6.12 (SAS Institute Inc. 1988, SAS Institute Inc. 1997) specially using the procedure MIXED and the method REML (Patterson 1997). The variance components σ_G^2, σ_E^2 and σ_{GxE}^2 were estimated, where: σ_G^2, σ_E^2, and σ_{GxE}^2 are the variance components due to the effect of genotype, location and genotype by environment interaction, respectively. The corresponding model in the analysis is $y = \mu + g + e + gxe$. The

heritability was calculated by $h^2 = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_{GxE}^2}{l}}$, where: l the number of environments. The correlation between RYLD and AGRO was determined by Spearman rank correlation for each environment using the SAS procedure CORR.

The estimated variance components ratios $\sigma_G^2 : \sigma_{GxE}^2$ and a total test capacity of 12000 and 4000 plots for RYLD were used to calculate the optimal allocation of resources for the response to selection (Wricke and Weber 1986) for the 300 best clones (selection of 300 clones to be tested in advanced and elite trials). The same was done for quality traits (storage root dry matter, total carotenoids, iron and zinc) with a laboratory capacity of 8000 and 4000 samples. The response to selection R was given in standardized units $R_s = \frac{R}{\sqrt{\sigma_G^2}}$. Self written programs, in SAS IML programming language were used.

Results

The RYLD across genotypes in the breeding population Jewel were clearly differed among environments and ranged from 1.1 kg/m^2 to 2.1 kg/m^2 (Table 1). SRWF appeared to be a low yielding selection environment in which more clones obtained lower AGO scores values compared to LM and SR. At environments LM and SR two and six observations, respectively, appeared to have unrealistic RYLD and FYLD values. This resulted in maximum RYLD values of 14.9 kg/m^2 in LM and SR and maximum FYLD values of 14.9 kg/m^2 and 20.0 kg/m^2, respectively. For LM a lower DM mean value was observed compared to SR. For the remaining quality traits, namely TcDM, FeDM and ZnDM, a higher mean at LM was observed compared to SR. Quality traits appeared to be within the range reported in the literature (Woolfe 1992). Correlations between RYLD and AGRO scores were 0.558, 0.452 and 0.593 for LM, SR and SRWF, respectively (results not presented).

Table 1. Mean, minimum and maximum of observed traits and number of evaluated genotypes (N) for each environment

Trait	N Genotypes	Mean	Min.	Max.
	La Molina (LM)			
RYLD (kg/m^2)	3986	1.8	0	14.9
FYLD (kg/m^2)	3985	3.9	0.1	20.0
Agro (score)	3905	2.2	1	5
DM (%)	1946	27.7	13.6	51.1
TcDM (ppm)	1940	184	0	3313
FeDM (ppm)	1940	24.0	3.6	47.7
ZnDM (ppm)	1941	13.3	6.7	31.6
	San Ramon (SR)			
RYLD (kg/m^2)	4080	2.1	0	14.9
FYLD (kg/m^2)	4081	2.8	0.1	16.0
AGRO (score)	3978	2.3	1	5
DM (%)	1929	32.0	18.2	54.0
TcDM (ppm)	1925	93	0	593
FeDM (ppm)	1931	20.5	10.5	33.1
ZnDM (ppm)	1931	10.1	4.7	18.8
	San Ramon without fertilization (SRWF)			
RYLD (kg/m^2)	4027	1.1	0	8.6
Agro (score)	4243	1.8	1	5

For all traits σ^2_G was clearly different from zero (Table 2). High σ^2_G estimates were observed for RYLD, FYLD and DM. Low to medium σ^2_G estimates were observed for FeDM and ZnDM. An extreme large σ^2_G was of observed for TcDM. The σ^2_{GxE} / σ^2_G ratio was clearly >1 for RYLD and FYLD, about 1 for FeDM and ZnDM, whereas for DM and TcDM the σ^2_{GxE} / σ^2_G ratio is clearly <1. The observed h^2 estimates were between 0.5 and 0.6 for RYLD and FYLD, between 0.5 and 0.7 for FeDM and ZnDM, and > 0.8 for DM and TcDM. A striking observation was that by discarding all data records with AGO scores < 3 the estimates and the σ^2_{GxE} / σ^2_G do not change much for FYLD, DM, TcDM, FeDM, and ZnDM, except RYLD. Obviously there was still remaining genetic variation for RYLD after a selection for AGRO and h^2 for RYLD was not low. However, by discarding all data records with AGO scores < 3 the number of observations was considerably lower.

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

Traits	σ^2_G	σ^2_E	σ^2_{GxE}	N Obs	N Loc	h^2
	Observations with Agronomic Scores 1 to 5					
RYLD (t^2/ha^2)	47.7 (1)	23.2	98.0 (2.05)	12093	3	0.59
FYLD (t^2/ha^2)	237.0 (1)	52.1	349.0 (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)	3.10 (1)	4.63	2.92 (0.95)	3872	2	0.68
	Observations with Agronomic Scores larger or equal 3					
RYLD (t^2/ha^2)	36.2 (1)	23.0	110.4 (3.05)	3655	3	0.50
FYLD (t^2/ha^2)	202.0 (1)	16.6	265.2 (1.31)	2718	2	0.60
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	7.60 (1.03)	2038	2	0.66
ZnDM (ppm^2)	3.07	5.28	2.88 (0.94)	2038	2	0.68

For RYLD the highest R_s was reach with a value 1.46 for the allocation 6000 or 4000 genotypes (12000 plots) planted at 2 or 3 locations, respectively, assuming a σ^2_{GxE} / σ^2_G = 2 (Table 3). In case σ^2_{GxE} / σ^2_G = 3 the optimum allocation of 12000 plots is moving to 4000 genotypes and 3 locations. However, if the test capacity is considerably lower (4000 plots) the optimum allocation is 2000 genotypes planted at 2 locations for a σ^2_{GxE} /

σ_G^2 of 2 or 3. However, with a test capacity of 4000 plots the response to selection is about 25% to 33% lower, compared to a test capacity of 12000 plots. For quality traits there is the general trend to find the optimum allocation if the laboratory capacity is completely used for one location. Only for a laboratory capacity of 8000 samples and a $\sigma_{GxE}^2 / \sigma_G^2 = 1$ the optimum was allocated at 8000 or 4000 genotypes at 1 or 2 locations. The differences between using one and two locations appeared not to be large as long as the laboratory capacity is large. However, if the laboratory capacity is small it appears that this capacity should completely allocated to genotypes without using different locations. The determined optimum resource allocation is close to the experimental design used in this study for the variance component estimations [for RYLD: about 12000 plots, 4000 genotypes, 3 locations; for quality traits: about 4000 quality samples, 2 locations (Table 1)]. For DM and TcDM the resource allocation in the experimental part of this study corresponds to 10% less R_s (2000 genotypes, 2 locations) compared to the optimum R_s (4000 genotypes, 1 locations). For FeDM and ZnDM this was only 5% less R_s. It should be noted that the genetic variance for DM and TcDM was extreme (Table 2), so that some reductions of R_s for TcDM and DM can be tolerated due to the high R (not standardized response to selection). The R for FeDM and ZnDM is considerable lower compared to the R of DM and TcDM. Note R values can be easily determined by $R = R_s\sqrt{\sigma_G^2}$ (results not presented).

Discussion

The long duration of a breeding process often frustrates breeders and their clients. Donors are also reluctant to invest in breeding when concrete outputs (varieties) take so long to produce. Since all genotypes in clonally propagated crops are fixed (potentially varieties) it is strait forward to design an accelerated breeding scheme (ABS) for clonally propagated crops. Our proposed ABS is consequently replacing temporal variation of test environments (years) by spatial variation of test environments (locations and treatments at locations). In other word everything what can be done simultaneously is made simultaneously, but with incooperation of sequential selection steps within the same year to reduce work (i.e. the AGRO evaluation in this study). The visual agronomic evaluation in our experimental study clearly showed that this procedure is useful to discards low yielding genotypes, which do not merit further evaluations (correlations between RYLD and AGRO within the range of 0.452 and 0.593 were observed).

Our proposed ABS requires only that the clonally propagated crop can be crossed and that it can be cloned rapidly. To managed thousands of genotypes at several environments the clones are planted in small plots. The ABS reduces the selection process in early breeding stages form 4 years to 2 years. However, this is followed by yield trials in later breeding in large plots. It is important to note that this concept makes it also possible to conduct very short recurrent selection cycles. In our ABS for sweetpotato 300 clones are selected within 2 years to be used for recombination tests for the next recurrent selection cycle as well as for the yield trials in later breeding stages. Since we work with two populations in each year one population is undergoing recombination and multiplication, while the other population is in the fields (each year field and crossing capacity is fully used). It should be noted that short recurrent selection cycles is one of the two keys to improve the population mean (the second key is efficient selection of parents for their recombination ability). Moreover, the advantage of ABS is that it allows to estimate variance components and genetic correlations, which is quite important in case of negative genetic correlations for population improvement and recurrent selection.

Table 3. Response to selection in standardized units (R_s) of the 300 best genotypes for storage root yield (RYLD) and storage root quality in an ABS

Trait	$\sigma_G^2 : \sigma_{GxE}^2$	Plot capacity	N Genotypes	N Locations	R_s	Rel. R_s
RYLD	1:2	12000	12000	1	1.35	92
			6000	**2**	**1.46**	**100**
			4000	**3**	**1.46**	**100**
			3000	4	1.43	98
	1:3		12000	1	1.17	80
			6000	2	1.31	90
			4000	**3**	**1.34**	**92**
			3000	4	1.32	90
	1:2	4000	4000	1	1.09	75
			2000	**2**	**1.10**	**75**
			1333	3	1.03	71
			1000	4	0.95	65
	1:3		4000	1	0.94	64
			2000	**2**	**0.98**	**67**
			1333	3	0.94	64
			1000	4	0.88	60
Quality traits	1:1	8000	**8000**	**1**	**1.54**	**106**
(i.e. iron & zinc)			**4000**	**2**	**1.54**	**106**
			2667	3	1.47	101
			2000	4	1.39	95
	1:1	4000	**4000**	**1**	**1.33**	**91**
			2000	2	1.27	87
			1333	3	1.15	79
			1000	4	1.04	71
Quality traits	1 : 0.5	8000	**8000**	**1**	**1.78**	**123**
(i.e. dry matter & carotenoids)			4000	2	1.69	116
			2667	3	1.57	108
			2000	4	1.46	100
	1:0.5	4000	**4000**	**1**	**1.54**	**106**
			2000	2	1.39	95
			1333	3	1.23	84
			1000	4	1.09	75

There is no information if it is possible to select and to obtain genetic gains in an ABS in early breeding stages for sweetpotato and to our knowledge there is no information for such a system in clonally propagated crops at all. We expected that it is possible to obtain genetic gains for quality traits in an ABS for sweetpotato. It should be noted that the untapped nutritional food quality of sweetpotato is under exploitation in many breeding programs in the world. Our results show that it is nearly certain to select and obtain significant responses to selection for quality traits in an ABS for sweetpotato. A genetic variation of about $\sigma_G^2 \approx 14\ \%^2$, $\sigma_G^2 \approx 33000\ ppm^2$, $\sigma_G^2 \approx 7.5\ ppm^2$, $\sigma_G^2 \approx 3.0\ ppm^2$, were observed for storage root dry matter, total carotenoids, iron and zinc concentrations of storage roots, respectively. It was not expected to observe considerable amounts of genetic variation for storage root yield and upper biomass yield in ABS. However, variance components of $\sigma_G^2 = 47.7\ t^{2/}/ha^2$ and $\sigma_G^2 = 237\ t^{2/}/ha^2$ for storage root yield and biomass yield, respectively, are clearly not small. We assume that it is also is possible to select and to obtain genetic gains for yield in an ABS. Moreover, it was unexpected that a visual agronomic screening (AGRO) was not reducing σ_G^2 across all observed traits, except storage root yield. Considerable amount of work can be saved by including such a visual agronomic selection step in an ABS (measuring and sampling only those genotypes with AGRO >= 3 in our study). It appears that with such an agronomic evaluation some traits are becoming more pronounced and get lower genotype environment interactions (i.e. FYLD, DM and TcDM).

A clear advantage of the ABS is that it considers the genotype by environment interaction already from the beginning of a breeding program. In the general breeding scheme for clonally propagated crops (Fig.1) the genotype by environment interaction is not considered in early breeding stages. The result is an extreme inflation and over estimation of σ_G^2 in early selection stages. Those who have ever conducted heritability estimations for yield at one location with two replications know how unrealistic large these estimates are. In other word in the general breeding scheme the genotypes in the selected fraction are over estimated, especially for yield, and often do not keep their "promise" in later breeding stages. However, this leads to a still weak aspect in our study on the ABS: the magnitude of σ_{GxY}^2. Also in our study the σ_G^2 might be overestimated depending on the genotype by year interaction. We assumed here that σ_{GxY}^2 is zero or low and then it can be neglected for an ABS study. We do not know if this is true. However, the magnitude of σ_{GxY}^2 depends extremely on regions and sub-regions. In example in Europe - with its very different soils and different weather conditions each year - the σ_{GxY}^2 is very small across crops, whereas in the great plains of the USA and Canada - with very homogenous soil conditions and differences in rainfall each year - the σ_{GxY}^2 is not small across crops. Estimates of σ_{GxY}^2 are not available for sweetpotato. However, in East Africa we estimated instead of σ_{GxY}^2 the σ_{GxS}^2 (variance component due to genotype by season interactions). For storage root yield the observed ratio $\sigma_G^2 : \sigma_{GxL}^2 : \sigma_{GxS}^2 : \sigma_{GxLxS}^2 : \sigma_\varepsilon^2$ was 1 : 1.46 : **0.96** : 1.83 : 2.62. For storage root dry matter the observed ratio $\sigma_G^2 : \sigma_{GxL}^2 : \sigma_{GxS}^2 : \sigma_{GxLxS}^2 : \sigma_\varepsilon^2$ was 1 : 0.04 : **0.0** : 0.15 : 0.63 (Grüneberg et al. 2004). This study was based on field trials comprising few genotypes and many environments, which represent later breeding stages. We expect a small σ_{GxY}^2 interaction in early breeding stages in which trials are carried out with many genotypes and few locations, but this needs to be confirmed. Currently we investigate such trial with breeding material from early breeding stages at two locations and years.

In conclusion our proposed ABS clearly reduce the time needed for breeding and it is nearly certain that it will lead to significant breeding progress for quality traits in sweetpotato and other clonally propagated crops. It might also be a very attractive breeding scheme for yields at least in sweetpotato. The allocation of resources into three environments for yield selection in ABS might be optimal or very close to the optimum. The allocation of laboratory capacity in more than two environments can not be recommended.

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