

GENETIC VARIATION IN A WIDE GENE BASE POPULATION OF SWEET POTATO [*Ipomoea batatas* (L) Lam]

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ABSTRACT

Design I mating system was used to estimate the components of genetic variation of sweet potato base population. Characters studied were total root yield, weight and number of marketable roots, total number of roots, fresh weight of vines, harvest index, scab rating and dry matter content of roots. Significant additive and dominance genotypic variances were observed in the population with high magnitude of the latter in all characters except in scab rating. The moderately high magnitudes of additive genetic variance for scab rating and dry matter content obtained suggest that the population may be improved using any available intrapopulation selection procedure like mass selection and full-sib family selection for the characters mentioned. Selected individuals or full-sib families can be intercrossed to utilize the high dominance variation in the population. Dry matter content of the roots with its very low coefficient of variability, is considered the most reliable basis for selection in this population.

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KEY WORDS: Sweet potato. *Ipomoea batatas*. Genetic variation. Wide gene base population. Mass selection. Full-sib family selection. Design I mating system. Root yield.

INTRODUCTION

Sweet potato [*Ipomoea batatas* (L) Lam] is dubbed as the "people's root", and is considered an important food in many areas in the Philippines and in many tropical and sub-tropical countries (Wang, 1965). Its production has been accelerated because its potential for food, feed and industry has gained national interest.

A sound breeding program provides the opportunity to produce improved high yielding and acceptable varieties. However, the development of an intensive breeding and improvement program needs detailed biological information and an understanding of genetic variation in yield and its components. Furthermore, Gardner (1963) stressed that information on variation attributable to genetic differences and also on the relationship among various quantitative traits is fundamentally significant in a breeding program. There must also be a thorough knowledge of the existence of genetic variability, the mode of inheritance of economic character, the kind of gene action, and the relative magnitude of additive, dominance, total genetic and phenotypic variances of the base population. Components of genetic variances are usually estimated using an appropriate genetic design.

This study utilized an introduced sweet potato population from the United States Department of Agriculture (USDA) to determine the genetic variability of the population and the appropriate breeding procedure for the sweet potato variety under study.

MATERIALS AND METHODS

The experiment utilized the introduced base population (J/3) of sweet potato from USDA. The test progenies were developed using the North Carolina Design I mating design (Comstock and Robinson, 1948; 1955). A total of 300 sweet potato plant population was established from 600 sown seeds of the base population. Individual plants were planted in clay pots (30 cm dia.) in an open field. A total of 60 randomly chosen plants were designated as male parents and each was mated to four randomly chosen plants designated as female seed parents.

Hybridization commenced when both male and female plants bore considerable flowers. Emasculation was done every afternoon, 2 to 3 hours before sunset, while pollination was done at early morning (7:00 to 9:00 a.m.) of the following day. Seeds developed in each female plant represented a full-sib family since they had two common parents. Each group of four crosses with common male parents but different female parents represented a half-sib family. Due to some constraints in successful pollination work, only 40 half-sib groups out of a total of 160 full-sib families were obtained.

The hybrid progenies were sown and allowed to multiply vegetatively for field evaluation. The field trial for the different sib progenies was originally done at the UPLB Central Experiment Station. However due to heavy rains caused by successive typhoons

during the critical growing period, the evaluation was not successful. Thus, the final evaluation of the different sib progenies was done at the Visayas State College of Agriculture experimental field in Baybay, Leyte using the same set-up as in UPLB. Entries were laid out using the randomized complete block design with four replications. Each replication had 160 entries representing full-sib crosses which were further subdivided into eight sets of 20 entries each. Each set is composed of five half-sib groups with four full-sib families per group. Fresh terminal cuttings of about 25-30 cm from every hybrid plant were prepared and planted in the field at a distance of 1 meter between ridges and 30 cm between hills at the rate of one cutting per hill. Ten plants per entry occupied a single 3 meter row. The roots were harvested at 130 days after planting.

Data Gathered. The number and weight of marketable roots, total number and weight of roots, harvest index, fresh weight of vines, scab rating and dry matter content of the roots were taken from all sweet potato plants in each row. All parameters measured were subjected to analysis of variance.

Estimates of Genetic Parameters. Genetic parameters were estimated from the components of variance as follows:

1. Additive genetic variance, $V_A = 4 V_M$
2. Dominance variance, $V_D = 4 (V_{F/M} - V_M)$
3. Narrow sense heritabilities under mass and full-sib family selection

$$h^2 M = \frac{\frac{1}{2} V_A}{V_A + V_D + n V_e}$$

$$h^2 FS = \frac{\frac{1}{2} V_A}{\frac{1}{2} V_A + \frac{1}{4} V_D + \frac{V_e}{r}}$$

4. Expected genetic advance for mass selection and full-sib family selection based on the procedure of Hallauer and Miranda (1981)

$$\Delta G (ms) = \frac{K (\frac{1}{2}) V_A}{V_A + V_D + n V_e}$$

$$\Delta G (Fs) = \frac{K (\frac{1}{2}) V_A}{\frac{1}{2} V_A + \frac{1}{4} V_D + \frac{V_e}{r}}$$

Where K = selection differential in standard unit

r = number of replications

n = number of plants per plant

V_A = additive genetic variance

V_D = dominance genetic variance

V_e = error variance

RESULTS AND DISCUSSION

Estimates of Variance Components

The analysis of variance presented in Table 1 was used to analyze all characters measured and to obtain estimates of variance due to male effect and effect of female mated to the same male, additive genetic variance, dominance variance, pheno-

Table 1. Analysis of variance of (characters) a wide gene base population of sweet potato.

S.V.	d.f.	MS	EMS
Sets	(S-1)		
Replication/Sets	S (r-1)		
Males/Sets	S (m-1)	M ₁	$V_e + r V_{F/M} + rf V_M$
Females/Males/S	Sm (f-1)	M ₂	$V_e + r V_{F/M}$
Pooled error	S (mf-1) (r-1)	M ₃	V_e

where:

- S = number of sets
 r = number of replications
 f = number of females in each male
 m = number of males in each set
 V_e = experimental error
 $V_{F/M}$ = variance due to differences among females mated to the same male
 $= \text{cov}(FS) - \text{cov}(HS) = \frac{1}{4} V_A + \frac{1}{4} V_D$
 V_M = Variance due to differences among males
 $= \text{cov}(HS) = \frac{1}{4} V_A$

typic variance, heritability and expected gain in selection.

Results revealed significant male effects on number of marketable roots, total number of roots, fresh weight of vines, scab rating and dry matter content (Table 2). All parameters have highly significant variance due to females. The amount of variance due to females was greater than the variance due to males for all characters except scab rating. This indicates that the variation in the population under investigation is more of dominance than additive in nature. However, estimates of female within male effects may be biased upward by genotype-environment interaction, which could not be estimated in this study.

Estimates of Additive Genetic Variance

The additive genetic variance estimates for all characters were derived using the procedure of Comstock and Robinson (1948) and Robinson et al. (1949).

A moderate amount of additive genetic variance existed in the reference population of sweet potato (Table 3). Significant additive variances were observed in number of marketable roots, total number of roots, fresh weight of vines, scab rating and dry matter content of the roots. Additive genetic variance for marketable and total root yield was not evident in the population studied. This observation disagrees with the

Table 2. Estimates of variance of different characters of sweet potato hybrid progenies from design I mating system.

Character	V_M	$V_{F/M}$	V_e
Total yield (kg/row)	0.066 ± 0.0338	0.421** ± 0.0611	0.219 ± 0.0145
Number of marketable roots/row	0.069* ± 0.0540	0.466** ± 0.0730	0.393 ± 0.0260
Weight of marketable roots (kg/row)	0.004 ± 0.0164	0.384** ± 0.0557	0.198 ± 0.0131
Total number of roots/row	0.021** ± 0.0110	0.066** ± 0.0720	0.127 ± 0.0010
Fresh weight of vines (kg/row)	0.241** ± 0.1601	1.340** ± 0.1975	0.819 ± 0.0541
Harvest index	0.001 ± 0.0002	0.008** ± 0.0012	0.006 ± 0.0004
Scab rating	0.052** ± 0.0160	0.049** ± 0.0080	0.046 ± 0.0030
Dry matter content (%)	8.195** ± 3.4312	19.641** ± 2.5325	0.555 ± 0.0367

* Significant at 5% level

** Significant at 1% level

Table 3. Estimates of additive genetic variance (V_A) obtained from biparental crosses of sweet potato.

Character	V_A
Total yield (kg/row)	0.024 ± 0.135
Number of marketable roots/row	0.274* ± 0.216
Weight of marketable roots (kg/row)	0.016 ± 0.065
Total number of roots/row	0.082** ± 0.045
Fresh weight of vines (kg/row)	0.964* ± 0.640
Harvest index	0.004 ± 0.001
Scab rating	0.206** ± 0.014
Dry matter content (%)	32.779** ± 13.725

* Significant at 5% level

** Significant at 1% level

findings of Li (1975) that additive variance for root yield¹ in sweet potato is considerable. The deviation was probably due to the large experimental error for root yield and the possible effect of genotype-environment interaction which could not be assessed since only one location was used in the evaluation.

Estimates of Dominance Genetic Variance

The dominance genetic variance was prevalent in the reference population (Table 4). Statistical significance was obtained in all characters except for scab rating which showed negative value. Although theoretically there is no negative variance, negative estimates of V_D were observed not only in this experiment but also in many other experiments as reported by Robinson et al. (1949) and Lindsey et al. (1962).

In this study, the dominance variances of majority of the characters measured were higher in magnitude than their respective additive genetic variances. This differs from the findings of Li (1975) that non-additive variance is not as important as additive genetic variance in sweet potato. Robinson et al. (1949) explained the presence of large dominance variation to be most likely affected by genotype-environment interaction. The absence of estimates of genotype and environment interaction leads to an over-estimation of the dominance variance relative to the additive genetic variance.

Estimates of Heritabilities and Expected Genetic Advance

Narrow sense heritability estimates were determined using two selection schemes; namely, mass selection and full-sib family selection. Half-sib fami-

Table 4. Estimates of dominance genetic variance V_D obtained from biparental crosses of sweet potato.

Character	V_D
Total yield (kg/row)	1.662** \pm 0.203
Number of marketable roots/row	1.589** \pm 0.049
Weight of marketable roots (kg/row)	1.520** \pm 0.213
Total number of roots/row	0.184** \pm 0.285
Fresh weight of vines (kg/row)	4.396** \pm 0.463
Harvest index	0.028** \pm 0.004
Scab rating	-0.010 \pm 0.014
Dry matter content (%)	45.785** \pm 0.926

** Significant at 1% level

ly selection was not included because female effects were more pronounced than male effects indicating that more attention should be given to full-sib families. Results revealed that heritability estimates among full-sib families were generally higher than among individual plants (Table 5). This was because the phenotypic variance among full-sib families was lower than the phenotypic variance among individuals. Total root yield had very low heritability in both schemes (0.3% for mass selection and 1.2% for full-sib family selection). Very low heritability values for root yield in sweet potato were also obtained by Thibodeaux (1972) and Jones (1977) and this was attributed primarily to small additive genetic variance. Among the characters measured, the dry matter content of the roots had the highest estimate of heritability in both selection schemes. This suggests that this character can be

subsequently improved effectively through either mass selection or full-sib family selection scheme.

The expected genetic advance for different sweet potato characters depends on the heritability estimates which help the breeder in formulating appropriate breeding methods to effectively improve a particular character. Based on the heritability data, it appears that full-sib family selection is appropriate and progress through this selection is expected to be high. For instance, the dry matter of the roots which has high heritability values of 19.5 and 58.9 percent for mass and full-sib family selections, respectively has expected gains at 10% selection intensity of 8.74 and 15.16 percent with respect to the mean (Table 6). Apparently, heritability estimates vary directly with genetic advance.

Despite biases that could not be separated from the different estimates

Table 5. Estimates of narrow sense heritability for different characters of sweet potato under mass (h^2M) and full-sib family (h^2FS) selection schemes.

Character	h^2M (%)	h^2FS (%)
Total yield (kg/row)	0.3 ± 0.034	1.2 ± 0.280
Number of marketable roots/row	2.4 ± 0.037	21.6 ± 0.405
Weight of marketable roots (kg/row)	0.2 ± 0.018	1.8 ± 0.149
Total number of roots/row	2.7 ± 0.028	34.5 ± 0.370
Fresh weight of vines (kg/row)	5.2 ± 0.069	69.4 ± 0.923
Harvest index	2.2 ± 0.008	18.6 ± 0.074
Scab rating	15.7 ± 0.101	91.9 ± 0.593
Dry matter content (%)	19.5 ± 0.163	58.9 ± 0.491

of genetic components; results revealed that in order to exploit the genetic variability of the population, mass and full-sib family selections could be used to further improve dry matter content of the roots. On the other hand, slow progress in the improvement of root yield is expected owing to its very low estimates of heritability. However, the number of marketable roots and total number of roots could be effective units for subsequent improvement of yield in the population due to their high estimates of heritability under full-sib family selection. Pasharon et al. (1976) showed that sweet potato yield was influenced by the number of roots. Thus, it is possible that improvement in number of marketable roots would correspondingly increase yield *per se*.

In general therefore, the dry matter content of the roots should be given utmost importance because it is the

only character which apparently gives reliable information on estimates of components of genetic variation. This character is also important for sweet potato whether the variety is intended for table use, feed or industrial purposes. Hence at the initial phase, breeding for high dry matter content should first be undertaken through accumulation of favorable additive genes either through mass selection or full-sib family selection, then selected individuals or full-sib families should be intercrossed to take advantage of the high dominance variance for the character.

CONCLUSIONS AND RECOMMENDATION

Results show that a wide genetic variation exists in the reference population of sweet potato. Dry matter content apparently has the best chance

Table 6. Estimates of the expected genetic advance for different characters of sweet potato hybrid progenies using mass and full-sib family selection schemes at 10% selection intensity.

Character	Mass Selection		Full-Sib Family Selection		Mean ¹
	G's/Plot	G's % of Mean	G's/Plot	G's % of Mean	
Total yield (kg/row)	0.0107	1.23	0.0214	2.46	0.87
Number of marketable roots/row	0.1002	8.08	0.3032	24.45	1.24
Weight of marketable roots (kg/row)	0.0075	1.32	0.0213	3.73	0.57
Total number of roots/row	0.0582	2.03	0.2094	7.32	2.86
Fresh weight of vines (kg/row)	0.2799	7.29	1.0180	26.52	3.84
Harvest index	0.0115	6.39	0.0330	18.86	0.18
Scab rating	0.2238	15.43	0.5416	37.35	1.45
Dry matter content (%)	3.1452	8.74	5.4530	15.16	35.98

¹ Average of 160 progenies harvested in a single row plot at 10 plants each with four replications from a nested design experiment.

for further improvement using either mass selection or full-sib family selection scheme. However, for characters showing high degree of dominance like number of marketable roots and dry matter content; intercrossing among selected individuals or full-sib families to produce varietal crosses is a good

improvement procedure. The genotype-environment effects were not fully measured in this experiment hence, the conduct of similar studies under varied environments but considering the relationship of different characters is recommended.

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