

HERITABILITY AND EXPECTED GAIN FROM SELECTION FOR YIELD, WEIGHT LOSS IN STORAGE AND SPROUTING IN FIELD BED OF SWEET POTATO

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ABSTRACT

True seeds of sweet potato were collected from a sample of genotypes entered in the Master Polycross Nursery at Louisiana State University, grown into seedlings and vegetatively propagated. Frequency distribution and heritability estimates were prepared for yield, weight loss in storage and sprouting in field bed. In general, for all the maternal parents, the distribution of the individual progeny seedlings was skewed to the lower yielding classes. Heritability estimate for yield was low, but with a magnitude of 0.241 which indicates the possibility of selecting (by culling) for yield at a relatively early stage of the screening process. While seedling genotypes within each maternal parent differed (i.e., some had no appreciable weight loss), the genetic variance was negative, thus heritability was negative or zero. Sprouting in field bed also had low genetic variance and, subsequently, low heritability. These low heritability values indicate that either the population under study has already attained its potential limit for these two traits or that these traits are largely influenced by the environment.

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KEY WORDS: Sweet potato. Plant breeding. Genetic variance. Heritability. Selection. Polycross. Weight loss. Sprout production. Field bed. Louisiana.

INTRODUCTION

All viable breeding projects undergo at least three major stages: (1) assembly or creation of a pool of variable germplasm; (2) selection of individuals from the pool; and (3) utilization of the selected individuals to create a superior variety (Dudley and Moll, 1969). To effectively carry out activities related to these three stages, the plant breeder must have information about the plant materials he is handling. In choosing appropriate selection strategies, he must have information on genetic variance, heritability, and expected gains from selecting some quantitative traits. Since heritability and related types of data are highly population-specific, these must be gathered by the plant breeder himself. Every population that a breeder handles needs to have its own heritability estimate. A heritability estimate for any particular trait of a crop plant applies only to a particular population under study (Hanson, 1963; Jones *et al.* 1969; Robinson, 1963).

This study presents estimates of genetic variance, heritability and expected gain from selecting some quantitative traits of 53 sweet potato genotypes that were entered in the Master Polycross Nursery, Louisiana State University (LSU) in 1978-1979.

MATERIALS AND METHODS

Handling of Seedling. — True seeds collected from the Master Polycross

Nursery, Baton Rouge, Louisiana from September to November 1978 were treated for 20 min with concentrated sulfuric acid (H_2SO_4), washed with tap water and dried. The seeds were then sent to the Sweet Potato Research Center, Chase, Louisiana for seeding in the greenhouse. When most of the seedlings had formed thumb-sized fleshy roots, they were pulled and, whenever possible, 250 seedlings were randomly selected from each maternal parent and brought to LSU.

Basal portions of the vine, about 20 cm long, were used as planting materials at the Hill Farm, LSU on May 17, 1979. The field was fertilized at the recommended rates of 30.7 kg N, 56.1 kg P_2O_5 and 30.7 kg K_2O per hectare, rotavated and ridges formed. Planting was done on top of the ridges at a depth of 5 cm with a distance of 61 cm between hills and 122 cm between rows. This simulated the first vegetative propagation practiced at LSU in handling the 60,000 to 100,000 true seeds produced in the polycross breeding system each year. However, the major difference between this test and the normal handling of polycross seedlings was that no selection pressure was practiced.

The field was kept weed-free both by mechanical and hand cultivation.

Estimating Genetic Variance and Heritability. — The population of sweet potatoes served as the reference population in this test. The fol-

lowing assumptions were considered: population in random mating, not inbred and in normal diploid inheritance; progenies not inbred and can be considered random members of non-inbred population; and population in linkage equilibrium.

A polycross or a one-factor mating design was used. Analysis of data involved two steps: (1) total phenotypic variance was partitioned into its components by using the analysis of variance (ANOVA); and, (2) the component of variance of the ANOVA was interpreted genetically by translating them into covariance of relatives.

The statistical model for the ANOVA was:

$$Y_{ij} = \mu + \alpha_i + \epsilon_{ij}$$

where Y_{ij} = j th observation within i th group; μ = overall mean; α_i = effect of i th group; and ϵ_{ij} = residual or error. Table 1 shows the degrees of freedom and expectation mean squares for the ANOVA. The component of variance due to differences between parental group

(σ^2_g) was estimated as:

$$\sigma^2_g = \frac{MS_g - MS_w}{K}$$

where σ^2_g = component of variance due to differences among parental groups; MS_g and MS_w are from the ANOVA referring to the mean square between parental group and mean square within parental group, respectively.

Since the relationship between progenies in this mating design was half-sibs, then σ^2_g = covariance of half-sibs, cov_{hs} . The genetic interpretation for the variance component then was:

$$\sigma^2_g = COV_{hs} = \frac{1}{4}V_a$$

where V_a = the additive genetic variance.

Heritability (h^2) was estimated as follows:

$$h^2 = \frac{4V_a}{\sigma^2_w + \sigma^2_g}$$

Table 1. Analysis of variance with expectation mean squares.

Source of variance	Degrees of freedom	Mean square	Expectation mean square
Total	$\sum n_i - 1$		
Between parental group	$q - 1$	MS_g	$\sigma^2_{\epsilon} + \sigma^2_g$
Within group	$\sum n_i - q$	MS_w	σ^2_{ϵ}

Note: $\sum n_i$ = number of all i ; 1 = number of parent groups; σ^2_g = component of variance due to differences among parent groups; σ^2_w = compound of variance due to within groups or error; and k = coefficient, approximately the average number of progeny per parent group.

Expected gain or response (R) from selection was estimated as:

$$R = \frac{iVah^2}{\bar{Y}} \times 100$$

where i = intensity of selection and assuming a selection of the top 5% of the population, $i = 2.06$; \bar{y} = the observed mean; and Va and h^2 are as defined above.

RESULTS AND DISCUSSION

Yield.

The frequency and percentage distribution, progeny mean, and coefficient of variation for total fleshy root yield of polycross progenies of five maternal parents are shown in Table 2. In general, the distributions were skewed to the

lower yielding classes, indicating that the chances of selecting high-yielding seedlings from polycross parents are relatively low. Differences between parental groups were observed. 'Centennial,' 'LO-323' and 'L9-163' had progenies that fell on the classes for high yield, while 'L4-312' and 'L8-343' had no progenies falling on the highest or the next highest yield classes.

If selection for parents were based on progeny performance (i.e., progeny means), as is usually done in progeny tests, 'Centennial' and 'LO-323' would be candidates for selection. If selection were on the progenies themselves to determine which would be advanced for the next generation of polycrosses, heritability estimates would be used as guide. The estimate of heritability for total fleshy root yield (weight) was 0.241 (Table 5). This heritability

Table 2. Frequency and percentage¹ distribution of total fleshy root weight of polycross seedling progenies of some sweet potato maternal parents.

Maternal Parent	Total Progeny	Class ²					Progeny mean ³ (kg)	CV ⁴
		0	0.05-1.36	1.41-2.72	2.77-4.08	4.13-above		
Centennial	150	7 (4.7)	108 (72.0)	31 (20.7)	3 (2.0)	1 (0.7)	0.898	88.6
L0-323	182	15 (8.2)	135 (74.2)	24 (13.2)	6 (3.3)	2 (1.1)	0.866	94.7
L9-163	159	24 (15.1)	113 (71.1)	20 (12.6)	1 (0.6)	1 (0.6)	0.685	103.1
L4-312	129	21 (16.3)	99 (76.7)	11 (8.4)	0	0	0.540	93.4
L8-343	36	7 (19.4)	29 (80.6)	0	0	0	0.313	95.6

¹Percentage values are enclosed in parenthesis.

²Class ranges and intervals are in kg fleshy root per hill.

³LSD .05 = 0.272; LSD .01 = 0.349 for progeny means.

⁴CV = coefficient of variation.

Table 3. Frequency and percentage¹ distribution of weight loss in storage of polycross seedling progenies of sweet potato maternal parents.

Maternal parent	Total progeny	Class ²					Progeny mean ³ (%)	CV ⁴
		1	2	3	4	5		
L3-77	40	3 (7.5)	28 (70.0)	7 (17.5)	1 (2.5)	1 (2.5)	18.3	94.6
L0-323	40	2 (5.0)	26 (65.0)	9 (20.5)	3 (7.5)	0	21.2	79.4
L9-163	40	7 (17.5)	26 (65.0)	7 (17.5)	0	0	16.8	80.6
L4-312	40	7 (17.5)	21 (52.5)	8 (20.0)	3 (7.5)	1 (2.5)	22.6	97.1

¹Percentage values are in parenthesis.

²The classes represent percent weight loss in storage as follows:

- 1 - no weight loss
- 2 - 0.1 to 25% weight loss
- 3 - 25.1 to 50% weight loss
- 4 - 50.1 to 75% weight loss
- 5 - 75.1 to 100% weight loss

³ANOV shows no significant differences between progeny means.

⁴CV = coefficient of variation.

value, although low, is greater than 0.20, thus selection by culling the low-yielding genotypes could be practiced at the first vegetative propagation of the polycross seedlings. The expected gain from selection, assuming that total potential will be realized, is 19.31% of the population under study (Table 5).

Weight Loss in Storage and Sprouting in Field Bed.

Of the 40 seedlings randomly selected from the 'Centennial' parent, 7.5% did not have any measurable weight loss and 70% had lower than 25% weight loss (Table 3). Of the 'L0-323' progeny, 5% of the seedlings had no appreciable weight loss while 65% had weight loss lower than 25%. In terms of

progeny means, 'L9-163' seedlings had the lowest weight loss and 'L4-312' progenies had the highest. The estimated genetic variance was negative (Table 5) which shows that variations in weight loss were largely influenced by the environment rather than the genes.

The test of sprout production shows that 25.0% of 'Centennial', 32.5% of 'L0-323', 35.0% of 'L9-163' and 30.0% of 'L4-312' progeny did not produce any sprout in the field bed (Table 4). The progeny mean for number of sprouts was highest for 'L0-323', followed by 'L4-312', while that of 'Centennial' was the lowest. The genetic variance, heritability, and expected gain from selection for this trait were very low (Table 5) which again indicates environmental influence rather than genetic influence.

Table 4. Frequency and percentage¹ distribution of number of sprouts per root of polycross seedling progenies of four sweet potato maternal parents.

Maternal parent	Total progeny	Class ²					Progeny mean ³ (No.)	CV ⁴
		1	2	3	4	5		
L3-77	40	10 (25.0)	24 (60.0)	5 (12.5)	0	1 (2.5)	4.65	115.2
L0-323	40	13 (32.5)	15 (37.5)	8 (20.0)	1 (2.5)	3 (7.5)	6.38	124.4
L9-163	40	14 (35.0)	14 (35.0)	10 (25.0)	2 (5.0)	0	4.94	119.1
L4-312	40	12 (30.0)	13 (32.5)	11 (27.5)	4 (10.0)	0	5.99	102.9

¹Percentage values are enclosed in parenthesis.

²Classes denote the following:

1 = No sprout produced

2 = 0.1 to 8 plants per root

3 = 8.1 to 16 plants per root

4 = 16.1 to 24 plants per root

5 = 24.1 to 32 plants per root

³ANOV shows no significant difference between progeny means.

⁴CV = coefficient of variation.

Table 5. Mean, genetic variance, genetic coefficient of variation (CV), heritability, and expected gain from selection for some root characters in sweet potato.

Characters	Mean	Genetic variance	Genetic CV	Heritability	Expected gain from selection *
Weight of total fleshy roots	1.620	0.397	38.89	0.241	19.31
Weight loss in storage (%)	19.750	-3.089	—	0.000	0.00
Sprouting in field bed	5.496	0.604	14.14	0.057	0.81

* Expected gain from selection is presented as percent of the mean and calculated based on an assumed selection of the top 5% of the population following the method of Burton and Devane (1953).

There are two possible reasons for low heritability of weight loss in storage and sprouting in field bed: (1) these traits had already attained their maximum potential in this population, or (2) these are controlled by a large number of genes

with very little effects. The latter may explain the observation earlier made. Thus, there is a need to conduct the screening and selection for weight loss in storage and for sprout production in field bed using advanced replicated tests.

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