Heritability Studies of Some Cassava Genotypes

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Abstract

Three traits, namely root number (RTNO), root weight (RTWT), and fresh yield (FYLD) of some cassava genotypes were scored and analyzed for heritability. The genotypes differed significantly for each of the three traits. Generally, heritability per replicate was above 50% indicating that the additive portion of the genetic variance might be high. Heritability per plot ranged between 69% and 86% which might indicate that non-additive effect of the genotypic variance might be small. Phenotypic and genotypic variances differed significantly, which reflects an environmental influence on the genotypes. By assuming a 5% differential selection of the top population, an advance of 46.5%, 41.5% and 33.5% can be arrived at for RTNO, RTWT and FYLD, respectively, over their population means. Correlation between the three traits was highly significant and positive.

Introduction

Estimates of genetic variance and heritability are of great importance in plant breeding programmes. Plant breeders have made efforts to use heritability estimates as an indication of selection pressure to a segregating population (Burton & Devane, 1955). High genetic variation in germplasm pool is a strong indication of significant genetic variability. The range or magnitude of this genetic variability within the germplasm can be quantified by broad sense heritability estimate among other genetic parameters (Dudley & Mall, 1969). The broad sense estimate, however, has some environmental component. Some breeders estimate the environmental component of the total population variance by using non-segregating population since variation in such populations is environmental. Kalton *et al.*(1952) and McDonald *et al.* (1952) assessed the variances between propagules of a clone (V_{SO}) as a measure of the ratio of the difference between the variance of the S_1 population (V_{S1}) and the environmental variance to the S_1 population variance expressed as a percentage by the formula:

$$[(V_{S1} - V_{SO}) \times 100]/V_{S1}$$

Burton (1951) used the variance of the F_1 generation in pearl millet to measure environmental variance. Working with soybeans, Mahmud & Kramer (1951) estimated environmental variance by the formula:

$$(VP_1 + VP_2 + VF_1)^{1/2}$$

where VP_1 and VP_2 are variances for the two parents and VF_1 is the F_1 variance. Weber (1950) reported that the best estimate of environmental variance for calculating heritability for characters in interspecific cross of soybeans was the formula:

$$(VP_1 \times VP_2 \times F_1)^{1/3}$$

where VP_1 and VP_2 are variances for the two parents and VF_1 is the F_1 variance.

Realistic choices among selection approaches must be based on gain per unit input of time and cost. For particular populations, relative gain from different selection procedures can be predicted if

precise estimate of genetic and environmental variances are available (Dudley & Moll, 1969). Heritability is the critical component of the prediction formula for computing expected response to selection since it is based on the phenotypic variance.

It is important to use more than 1 year at one location to estimate the component of variance for heritability studies if the genotype × year, genotype × location, or genotype × year × location interaction are of importance. Heritability value should also be computed based on the type of selection unit which will be used in the selection programme for which advance is being predicted. Selection unit includes numbers of replications, time period, locations, types of progenies, and plots (Dudley & Moll, 1968). For purposes of heritability estimation, it would be necessary for the breeder of a particular species to standardize his selection units. The type of selection to be practised and the type of variety would determine the type of genetic variance to be included in the numerator of a heritability estimate (Hanson, 1963). Selection should be based on total genetic variance in the following three situations:

1. selection among clones for a superior clone to be used for a vegetatively propagated variety,
2. selection among F_1 hybrids for a particular hybrid to be used directly, and
3. selection among homozygous lines for a pure line to be used as a variety (Hanson, 1963).

However, among homozygous lines the total genetic variance includes only the additive genetic variance and additive × additive types of epistatic variance, where all types of genetic variance are included in other two situations. Therefore, the numerator of heritability estimate should include only additive types of genetic variance in the case of pure lines and the total genetic variance in the other cases.

To improve performance of a random-mating population only the additive and additive × additive types of genetic variance can be used and should be included in the numerator of the heritability. In mass selection, the selection unit is the individual plants, and genetic variance among the individual plant is the total genetic variance.

Experimental designs aimed at estimating variance components for heritabiltiy study must be designed in such a way that the estimate of genotype-environment(G×E) interaction variance and also the appropriate proportions of the various G×E interaction components can be included in the estimate of phenotypic variance.

Cassava breeding is at a less advanced stage relatively, with regard to active studies of heritability. This paper aims at generating insight into the genetics of cassava in terms of heritability estimation.

Materials and methods

Yield trials were conducted for 2 years (1991 and 1992) using 10 cassava genotypes developed at the International Institute of Tropical Agriculture (IITA) at nine locations in three West African countries: Nigeria (Abuja, Agbarho, Calabar, Ibadan, Ilorin, Onne and Ubiaja); Ghana (Fumesua) and Benin (Seko). The genotypes were 30555, 30572,4(2)1425,50395,81/00110,81/01635, 82/00058,82/00661,82/00942 and 900942. These genotypes were grown under rainfed conditions in a randomized complete design with four replicates (Fig. 1). No fertilizers or any other agrochemicals were applied to the experimental plots. Plants were planted

on 4-row plots consisting of 40 plants per plot; spacing was 1 m × 1 m between plants. Plants were harvested 12 months after planting. Results on a plot based on the two inner rows were taken for each genotype on root number (RTNO), root weight (RTWT) and fresh yield (FYLD) measured in tons per hectare.

Analysis of variance was carried out for the three traits (SAS, 1989). The form of analysis of variance and the expected mean square (MS) involving genotypes are presented in Table 1. Variance components were calculated from linear functions of the MS as follows:

$\sigma^2_e = M_e$; $\sigma^2_{gly} = (M_{gly} - M_e)/r$; $\sigma^2_{gl} = (M_{gl} - M_{gly})/ry$

$\sigma^2_{gy} = (M_{gy} - M_{gly})/rl$; and $\sigma^2_g = (M_g - M_{gy} + M_{gyl})/rly$

where

g = number of genotypes
l = number of locations
r = number of replicates
y = number of years
σ^2_e = environmental variance component
σ^2_g = genotypic variance component
σ^2_{gly} = variance component associated with g × l × y
σ^2_{gl} = variance component associated with g × l
σ^2_{gy} = variance component associated with g × y

Broadsense heritability was defined as the proportion of the total variance due to genetic effects and represented symbolically as follows:

$$H^2 = \sigma^2_g/\sigma^2_p$$

where

σ^2_p is the phenotypic variance component which is equal to $\sigma^2_e/rly+\sigma^2_{gly}/ly+\sigma^2_{gy}/l+\sigma^2_{gl}/y + \sigma^2_g$. This is heritability per replicate. Heritability per plot was calculated by dividing the environmental variance component by the product of number of locations and the number of years as follows:

$$\sigma^2_e/l \times y$$

The genetic coefficient of variation was calculated as the square of the genetic variance component expressed as a percent of the mean as follows:

$$(\sigma^2_g \times 100)/X$$

where X is the phenotypic mean.
Phenotypic variance was calculated as shown below:

$$(\sigma^2_p \times 100)/X$$

Results and Discussions

Table 2 shows the mean squares from analysis of variance for the three traits. F

TABLE 1

Form of the analysis of variance for obtaining estimates of variance from variance test

Source	*df*	*MS*	*Expected mean squares*
Loc.	l-1	M_l	$\sigma^2_e+r\sigma^2_{gly}+ry\sigma^2_{ly}+rl\sigma^2_{ly}+rly\sigma^2_l$
Gen.	g-1	M_g	$\sigma^2_e+r\sigma^2_{gly}+ry\sigma^2_{gy}+rl\sigma^2_{gy}+rly\sigma^2_g$
Gen.*loc.	(g-1)(l-1)	M_{gr}	$\sigma^2_e+r\sigma^2_{gly}+ry\sigma^2_{gl}$
Gen.*Yr.	(g-1)(y-1)	M_{gy}	$\sigma^2_e+r\sigma^2_{gly}+rl\sigma^2_{gy}$
Gen.*loc*Yr.	(g-1)(l-1)(y-1)	M_{gry}	$\sigma^2_e+r\sigma^2$gly
Error	ly(g-1)(r-1)	M_e	σ^2_e

Where g, y, l and r are numbers of genotypes, years, locations and replicates, respectively.

TABLE 2

Mean squares from analysis of variance for data collected over at 9 locations for 2 years

Source	*Df*	*RTNO*	*RTWT*	*FYLD*
Loc.	8	46271.75***	19515.74***	4878.94***
Gen.	9	11841.39***	2076.26**	519.06**
Gen.*Yr.	9	664.63	148.12	37.03
Gen.*Loc.	72	1131.77	350.50**	87.62**
Gen.*Loc.*Yr	72	796.48**	329.59**	82.40**
Error	486	448.30	268.45	67.11

ratios for the genotypes were highly significant at the 1 per cent level of probability in all traits. This suggests that some of the genotypes were evidently superior to others in these cassava traits.

Genetic characterization constants for the traits are presented in Table 3. From the results, differences between phenotypic and genotypic coefficients for RTNO, RTWT and FYLD were 2.40, 0.73 and 1.93 t/ha, respectively.

Genetic coefficient of variation is much greater for RTNO than for the two other traits relatively. Therefore, the potential advance in root number would be the highest of the three traits.

Heritability per replicate in all traits was above 50 per cent (Table 4). It is quite possible that the additive portion of the genetic variance for these characters might be high. Therefore, the genotypes of these traits can be passed on to their progenies.

Heritability per replicate (54-65 per cent) was lower than heritability per plot (69-86 per cent). This indicates that the non-additive effect of the genotypic variance

TABLE 3

Variance components for cassava traits

Traits	σ^2_g	σ^2_{gy}	σ^2_{gl}	σ^2_{gly}	σ^2_e
RTNO	135.52	0	41.91	87.04	448.30
RTWT	26.49	0	2.61	3.40	268.45
FYLD	6.62	0	0.65	3.82	67.11

TABLE 4

Genetic constants for measurements on traits

Trait	*Mean*	*Genetic variance*	*Phenotypic CV (percent)*		*Genetic CV (percent) per plot*		*Heritability per rep.*
RTNO	89.21	135.52	189.92	13.00	15.40	0.71	0.65
RTWT	53.24	26.49	30.70	9.67	10.40	0.86	0.63
FYLD	26.62	6.62	9.54	9.67	11.60	0.69	0.54

might be higher on plot basis than for replicate basis.

Many breeders normally think of advance per cent of the mean of a population which is the expected gain in per cent of the mean. This was calculated as follows:

$$100s\sqrt{\overline{V}_G}\ V_G/\overline{X}V_P$$

(Dodley & oll, 1969), where s is assumed selection differential, V_G = genetic variance, V_P phenotypic variance and X = mean.

By this formula, RTNO, RTNT and FLYD showed that an advance of 46.5 per cent, 41.5 per cent and 33.5 per cent, respectively, over the population mean could be arrived at, assuming a 5 per cent differential selection of the top population. Since cassava is a cross-pollinated plant, these advances could be realized by heterosis in the F_1 generation. The superior F_1 clones could be selected and multiplied since cassava is vegetatively propagated.

Generally, the results indicate that high RTNO, RTWT and FYLD are under genetic control and that selection for these traits in the cassava genotypes studied will be possible. Correlation coefficients were calculated for these three traits. Highly significant correlation coefficient values ranging from 0.73 to 1.00 were estimated. Therefore, any one of these traits can reasonably evaluate yield in these cassava cultivars at the trial sites.

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