Available Online at ESci Journals
Journal of Plant Breeding and Genetics
ISSN: 2305-297X (Online), 2308-121X (Print)
http://www.escijournals.net/JPBG

GENOTYPIC VARIABILITY ESTIMATES OF AGRONOMIC TRAITS FOR SELECTION IN A SWEETPOTATO (*IPOMOEA BATATAS*) POLYCROSS POPULATION IN PAPUA NEW GUINEA

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A B S T R A C T

Successful crop breeding program incorporating agronomic and consumer preferred traits can be achieved by recognizing the existence and degree of variability among sweetpotato (*Ipomoea batatas*, (L.) Lam.) genotypes. Understanding genetic variability, genotypic and phenotypic correlation and inheritance among agronomic traits is fundamental to improvement of any crop. The study was carried out with the objective to estimate the genotypic variability and other yield related traits of highlands sweetpotato in Papua New Guinea in a polycross population. A total of 8 genotypes of sweetpotato derived from the polycross were considered in two cycles of replicated field experiments. Analysis of Variance was computed to contrast the variability within the selected genotypes based on high yielding β-carotene rich orange-fleshed sweetpotato. The results revealed significant differences among the genotypes. Genotypic coefficient of variation (GCV %) was lower than phenotypic coefficient of variation (PCV %) for all traits studied. Relatively high genetic variance, along with high heritability and expected genetic advances were observed in NMTN and ABYield. Harvest index (HI), scab and gall mite damage scores had heritability of 67%, 66% and 37% respectively. Marketable tuber yield (MTYield) and total tuber yield (TTYield) had lower genetic variance, low heritability and low genetic advance. There is need to investigate correlated inheritance among these traits. Selecting directly for yield improvement in polycross population may not be very efficient as indicated by the results. Therefore, it can be conclude that the variability within sweetpotato genotypes collected from polycross population in Aiyura Research Station for tuber yield is low and the extent of its yield improvement is narrow.

Keywords: Sweetpotato, genetic variability, genetic advance, heritability, polycross.

INTRODUCTION

Sweetpotato (*Ipomoea batatas*, (L.) LAM.), being under the *Convolvulaceae* family, is a root crop that is widely cultivated in tropical and subtropical regions of the world. It is a globally important crop, ranked second most important tropical staple root crop in area and production after cassava (FAOSTAT, 2014). In Papua New Guinea (PNG), although reliable statistical information on the distribution and production of sweetpotato and breeding effort is lacking (Gibson, 2000; FAOSTAT, 2014), the crop has been cultivated widely in many areas of the country with relatively low yields (Hartemink *et al.,* 2000; Bryan *et al.,* 2003).

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Present farmer production is also affected by production constraints such as declining soil fertility, insufficient knowledge of the suitability of varieties at different altitudes, sweetpotato pests, diseases, non-adoption by farmers of elite lines and post-harvest losses, limited processing and production utilization, high labour costs and production losses arising under moisture extremes (Bang and Kanua, 2000; Lutulele, 2000) and viruses (Bryan *et al.,* 2003). Most research up to present have been aimed at addressing production constraints and as such, the country has not witnessed commercial yield increase from plant breeding efforts (Guaf and Demerua, 2001; Wijmeersch, 2000). There have been minimal genetic studies on sweetpotato due to its self-incompatibility and high level of cross incompatibility, polyploidy level (hexaploid), and large chromosome

number (2n=6X=90) (Mulualem and Mohammed, 2012). Genetic variability is the principal foundation of any breeding programme. Determining the level of variation and identifying the variants within the collected species is invaluable for genetic improvement and conservation of the crop (Lin *et al.,* 2007; Clark and Hoy, 2006). However in PNG, where sweetpotato is an important food security crop (Gibson, 2000), there has been little scientific effort to understand the magnitude of genotypic variation, heritability, genetic advance and correlation of yield contributing traits among the collected accessions of this crop especially in a polycross populations (Bang, 1987). Such genetic analysis reveals the genetic nature of the inheritance of tuber yield and yield components which is required to design efficient sweetpotato improvement breeding strategy.

The present study, therefore, intended to assess the nature and extent of genetic variability of sweetpotato in PNG from a polycross population derived from a breeding programme initiated by the National Agriculture Research Institute (NARI) at Aiyura.

MATERIALS AND METHODS

Description of the Study Area and Experimental

Design: The experiment was conducted at NARI Highlands Regional Centre research station at Aiyura from the year 2012 to 2013 cropping season. The center is located at latitude 06^0 20' S'' and longitude 145^o 54' E at an altitude of 1660 m.a.s.l. The area receives mean annual rainfall of 1926 mm with maximum and minimum mean air temperature of 23.7 ^{o}C and of 12.9 ^{o}C respectively. The soil is generally classified as Rankers dystric Cambisols (black), mostly loamy with well drained texture.

A total of 576 genotypes of sweetpotato were derived from the polycross with mix parentage from progenies in the first polycross recurrent cycle and selected locally available yellow to orange-fleshed varieties maintained in NARI national sweetpotato gene bank. Seven elite orange-fleshed sweetpotato (OFSP) genotypes and one standard check (Beauregard) were considered in this study for two consecutive cycles from the year 2012 to 2013.

The trials were laid out in randomized complete block design (RCBD) with four replications. Plot size was 4m x 4m with spacing of 1m x 1m between plants and within the rows. Four plants from the two inner rows (2m x 2m) were used as net plot for data collection. The trials were maintained using local cultural practices under rainfed condition. The trials were harvested around 120 days after planting (DAP) using destructive harvest method.

Data Collection: Data were recorded on four plants from the net of each experimental plot and expressed on per plant basis for each trait under study. The mean of four plants was used for statistical analysis. The following attributes were measured according to Kapila *et al.* (2010), during the course of this study: fresh aerial biomass (kg), marketable tuber number per plant, non-marketable tuber number per plant, marketable tuber yield (t/ha), total tuber yield (t/ha), tuber dry matter content (%), harvest index (%), scab disease and gall mite.

Statistical Analysis: All data were standardized and subjected to analysis of variance for all the characters using Statistical Analysis Procedures (GenStat Discovery Edition 4). The phenotypic and genotypic coefficients of variation were computed by Mulualem and Mohammed (2012), considering genotypes as random effects using Genstat (Edition 17) and R statistical packages (R 3.1.1. (2014)). The Genotype by Environment (GxE) model was used.

GxE Model

$y_{ij} = \mu + g_i + e_i + (ge)_{ij} + error$

Where y_{ij} is the observed trait measured, μ is the grand mean of the trait, g_i is the genotypic effect, e_i is the environmental effect which is the two evaluation cycles and $(ge)_{ij}$ is the GxE interaction effect according to DeLacy et al. (1996).

GxE Phenotypic Variance Component Model

$$\sigma_P^2 = \sigma_G^2 + \sigma^2_{\frac{GE}{ne}} + \sigma^2_{\frac{e}{ne.nr}}$$

Where σ_P^2 is the total phenotypic variance, σ_G^2 is the Genotypic variance component, $\sigma^2_{\frac{GE}{ne}}$ being the GxE variance component and $\sigma^2_{\frac{e}{ne.nr}}$ being the Error variance component. The subscripts *ne* and *nr* represent number of environments (or cycles in this experiment) and number of replications respectively.

Genotypic variance component

$\sigma^2_g = (MS_g - MS_{ge} - MS_e)/nr.ne$

Where MS_g is genotypic mean square, MS_{ge} is the genotype by environment mean square, MS_e is error mean square.

Genotype by Environment variance component

$\sigma^2_{ge} = (MS_{ge} - MS_e)/nr$

Environmental variance component

$\sigma^2_e = MS_e$

Genotypic and phenotypic coefficients of variation were calculated according to the method suggested by Mulualem and Mohammed (2012) as:

Genotypic coefficients of variation (GCV)

$GCV = \frac{\sqrt{\sigma^2_g} * 100}{\mu}$

Phenotypic coefficients of variation (PCV)

$PCV = \frac{\sqrt{\sigma^2_p} * 100}{\mu}$

Where $\mu$is the grand mean value of the trait

Broad sense heritability (H^2) in percentage was estimated in each character using variance components as described by DeLacy *et al.* (1996).

$$H^2 = \sigma_G^2/(\sigma_G^2 + \sigma^2_{\frac{GE}{ne}} + \sigma^2_{\frac{e}{ne.nr}})$$

The expected gain or genetic advance with one cycle of selection, assuming the selection intensity of 5%, was predicted as suggested by Galwey (2006).

$G_A = (k)\ (\sigma_p)\ (H^2)$

Genetic advance in percentage of the mean (GAM) was calculated to compare the extent of predicted genetic advance of different traits under selection, using the following formula:

GAM = (GA /) x100

RESULTS AND DISCUSSION

The analysis of variance for traits (Table 1) showed significant difference between genotypes for traits NMTN, ABYield, TBYield, HI, TDM, scab and GM. All the tuber yield components MTN, MTYield and TTYield showed highly significant environmental differences with no genotypic difference. As such the significant GxE interaction effect is clearly explained as an effect of the Genotype or Environmental influence. The significant GxE interaction for MTN can be attributed to environment, whilst the significant GxE interactions in ABYield, TDM and GM can be attributed to the genotypic differences. The traits TBYield, HI and scab are both influenced by environment and genotype. Analyzed data indicated the existence of variability in the selected genotypes.

The extent of this variability was assessed in terms of broad sense heritability (H^2), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) and Genetic Advance (GA) as shown in Table 2.

Phenotypic variance for all the traits was partitioned into genotypic variance, GxE variance and error variance. Only genotypic variance was compared with total phenotypic variance to understand the magnitude of genotype contribution to sweetpotato improvement in the open pollinated sweetpotato breeding program.

Moderate genotypic variance was observed on traits such as non-marketable tuber number (NMTN) which had 16.6% GCV, aerial biomass yield (ABYield) (18.4% GCV) and scab which had GCV of 26.3%. PCV represents total variability whilst GCV represents heritable variability. Only harvest index (HI) and scab assessment had a high heritability of 67% and 66% respectively, followed by non-marketable tuber number (NMTN) which had a moderate heritability of 50%. Given the present breeding strategy, this low heritable variation pattern in the traits measured indicates an interesting pattern in predicting future improvement as calculated by percentage genetic advance of the mean trait (GAM).

Current selection pressure seems to favour scab assessment with highest 44% genetic advance, followed by GM with 24.6% and NMTN with 24.5%. The tuber yield and other traits have the lowest genetic gains in predicted percent improvement.

It is notable that marketable tuber yield (MTYield) under present selection pressure is predicted to be improved by 1.2 tonnes/ha or 10.4%. However there are other sweetpotato programs in the world that have achieved higher yield improvements (AVRDC, 1992).

Phenotypic coefficient of variation (PCV %) was found to be higher than the genotypic coefficient of variation (GCV %) for all the characters. High GCV along with high heritability and high genetic advance gives good information in terms of selection advance than each parameter alone (Lynch and Walsh, 1998). Thus, in this study, number of non-marketable tubers (23.79), aerial biomass yield (24.4), harvest index (0.59), scab (2.29) and GM (2.46) showed relatively high genotypic coefficients of variation, heritability and genetic advance expressed as percent of means. This suggests the occurrence of additive gene action with low environmental influence for the determination of these traits, compared to tuber yield traits and could be valuable in phenotypic selection of sweetpotato through devising appropriate correlated inheritance breeding strategies.

Heritability estimates varied from -0.375% for total tuber yield (TTYield) to 66.3% for scab assessment (Table 2). It was observed that the maximum heritability was influenced by high estimate of genotypic coefficients of variation. Genetic advance indicates the degree of gain in a character obtained under a particular selection and helps the breeder to predict the rate of improvement that can be achieved in different characters.

Table 1. Genotype, Environment and GxE mean squares for yield traits in selected population.

Source of Variation	Degrees of freedom	Mean Squares									
		MTN	NMTN	MTYield	TTYield	ABYield	TBYield	HI	TDM	Scab	GM
Environment (E)	1	850.08**	768 *	190.84***	267.25***	1.84	224.81**	0.08755***	7.68	16.3333***	0.0833
Rep within Environ.	6	8.03	64.93	3.78	6.35	3.6	12.29	0.00156	4.982*	0.3194	0.3056
Genotypes (G)	5	21.58	299.08***	36.88	34.8	143.2***	263.28***	0.08444***	20.561***	4.6333***	5.0333***
GxE	5	84.18*	123.5	13.85	24.31	107 ***	215.23***	0.02741***	15.32***	1.4833***	3.0333***
Error	30	24.56	50.78	15.45	17.12	7	37.99	0.00225	1.904	0.2361	0.1889

***Significant level at P<0.001,* significant at 0.01, ns = Not Significant; marketable tuber no (**MTN**); non marketable tuber number (**NMTN**); marketable tuber yield in tonnes per hectare (**MTYield**); total tuber yield in tonnes per hectare (**TTYield**); aerial biomass yield in tonnes per hectare (**ABYield**); total biomass yield tonnes per hectare (**TBYield**); harvest index in percentage (**HI**); total dry matter in percentage (**TDM**); scab damage at harvest in percentage (**scab**); gall mite damage at harvest in percentage (**GM**).*

Table 2. Estimation of Means, Ranges, Variance Components, PCV, GCV, Broad sense Heritability (%) (H^2), Genetic advance (GA), and Genetic advance as Percent of the Mean (GAM) for 10 traits of sweetpotato grown at Aiyura in 2012-13.

Traits	Mean±SE	Range	s^2_g	s^2_p	PCV	GCV	Heritability (%)	Genetic advance	GAM (%)
MTN	17.54±2.48	5-35	0.0	10.52	18.5	0.0	0.00	0.0	0.00
NMTN	23.79 ±3.56	2-48	15.6	31.04	23.4	16.6	0.50	5.8	24.48
MTYield	11.57 ±1.97	3.53-22.66	0.9	2.68	14.1	8.4	0.35	1.2	10.41
TTYield	14.08±2.07	4.98-26.80	-0.8	2.21	10.6	-6.5	-0.38	-1.2	-8.24
ABYield	24.48±1.32	1.25-22.55	3.7	17.03	39.7	18.4	0.21	1.8	17.69
TBYield	24.48±3.08	9.46-49.05	1.3	28.16	21.7	4.6	0.04	0.5	2.01
HI	0.59±0.02	0.35-0.88	0.0	0.01	17.0	13.9	0.67	0.1	23.58
TDM	21.63±0.69	13.6-27.80	0.4	2.33	7.1	3.0	0.18	0.6	2.63
Scab	2.29±0.24	1-4	0.4	0.55	32.4	26.3	0.66	1.0	44.59
GM	2.46±0.22	1-5	0.2	0.61	31.7	19.4	0.37	0.6	24.62

High heritability together with high genetic advance is vital tool for selection of the best individuals and for successful genetic improvement. Estimates of genetic advance as percent of mean varied from -8.2% for total yield (tonnes/ha) to 44.6% for scab assessment. It was indicated that scab resistance per plant with high heritability (66%) had the genetic advance of 1. Harvest index (HI) and non-marketable tuber number (NMTN) showed similar tendency in heritability and genetic advance. The genetic advance as percent of mean was also moderate for marketable tuber yield (10.4%) but negative for total tuber yield (-8.2%) which is consistent with their respective heritabilities (Table 2).

This indicates that under present selection pressure, the selection for the traits like NMTN and ABYield, HI, scab and GM is easier than selection for other characters. Moderate genetic advance together with moderate heritability noticed for marketable tuber yield indicated the presence of intra and inter allelic interactions in the appearance of these characters (Falconer and Mackay, 1996).

There is need for genotypic and phenotypic correlation analysis among these traits to understand correlated inheritance.

It is evident from low genotypic variance and heritability for tuber yield traits that its improvement might be more efficient selecting for other positively correlated non-tuber yield traits.

CONCLUSION

The range and mean performance of the character showed substantial amount of variability among the genotypes. For instance, marketable tuber yield ranged from 3.53 to 22.6 tonnes/ha, number of marketable tuber varied from 5 to 35, non-marketable tuber number varied from 2 to 48 and scab and GM ratings varied from 1 to 4 and 1 to 5 respectively. The estimate of heritability ranged from -37% for total tuber yield to 66.3% for harvest index (HI) and scab ratings. Values of genetic advance expected from selection of the superior 5% of the genotypes and expressed relative to the means ranged from -8.24 for total tuber yield to 44.59 for scab assessment. PCV was higher than GCV for all the traits though the rating percentages such as HI, scab and GM seem to have higher heritability. This may be nothing entirely non inheritable and may be a result of the non-continuous nature of percentages. There is a need to test genotypic and phenotypic correlations of all the other traits with tuber yield. It can be concluded that genetic variability within the selected elite varieties from the open pollinated nurseries is low for marketable tuber yield and yield components.

AKNOWLEDGEMENTS

The Authors would like to acknowledge the management and staff of NARI Highlands Regional Centre at Aiyura particularly Kuia Pirao, Willie Sai and Gena Kawale who were engaged in the Crop Breeding Programme. Authors are also grateful to Rakesh Kapila for providing invaluable comments on the manuscripts.

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