Genetic Analysis for Yield and Yield Components in Grain Sorghum
Sorghum bicolor L.

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ABSTRACT

Proper choice of source populations contributes to the ultimate success of selection for genetic improvement. The source population should possess the most desirable alleles at as many loci as possible for intrapopulation improvement. Significant differences among selfed progenies within SPV-104 x S-512 were observed for all traits, while significant differences among selfed progenies within SPV-126 were noted for grain yield per plant, panicle length, 100-grain weight and days to flowering. Progenies developed from SPV-104 x S-512 population had higher estimates of σ^2_G for number of branches per panicle, plant height and days to flowering, showing that selection to improve these traits would be more effective in progenies of SPV-104 x S-512. On the other hand, progenies developed from SPV-126 population had higher estimates of σ^2_G for panicle length, indicating that progenies from this population would have better genetic gain for this trait. Comparable estimates of genetic variance were found for grain yield per plant and 100-grain weight, indicating that genetic improvement of the source populations is expected to produce similar genetic gains for these two traits. Therefore, selfed progenies developed from both source populations could be used to develop superior genotypes for immediate use in the production system.

Keywords: Genetics, Variability, Response to selection, *Sorghum bicolor* L.

INTRODUCTION

In plant breeding programmes, success of selection for genetic improvement is partly determined by proper choice of source populations. The source populations used by breeders for genetic improvement include local or exotic germplasms so that the source populations possess the most desirable alleles at as many loci as possible to undertake selection. Such desirable alleles can be intensified in the target source populations through introgression of exotic germplasms into locally adapted ones (Russell, 1991). Exotic germplasms from similar environmental conditions would be most useful, provided that they possess favorable alleles that could complement those possessed by the adapted materials. The source populations developed in this way can be improved through recurrent selection.

Recurrent Selection (RS) is a process of cyclical selection in a breeding population to increase the frequency of favorable alleles and thus improve mean performance. Selfed progeny selection is considered to be superior to other methods of recurrent selection for improvement of population *per se* (Lamkey, 1992). In this selection scheme, alleles are fixed rapidly, where deleterious homozygous alleles are exposed and eliminated early in selection (Azanza *et al.*, 1996; Weyhrich *et al.*, 1998; Saleh *et al.,* 2003; Nigussie and Saleh, 2005).

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The main emphasis in the sorghum improvement programme in tropical regions is to select short types with high grain potential for combine harvesting and tall to medium types for dual purposes of grain and forage. To meet this diverse requirement, adequate information of grain yield and associated developmental traits is required. The knowledge of the nature of gene actions for yield and its components will provide further basis for the reappraisal of breeding methods, since advance from selection usually depends on additive genes (Saleh *et al.,* 2003*).*

Many efforts had been done and are still underway to examine and exploit the potential of exotic and local germplasms crosses for the improvement of sorghum genotypes in tropical countries. Liang and Walter (1968) estimated gene effects by generation means based on F_1, F_2 generations and their progenies. They announced that additive gene effects seemed to have a minor contribution to the inheritance for grain yield, head weight, kernel weight and kernel number. However, the additive x additive interaction effects formed a major component. The dominance x dominance gene effects were also of considerable magnitude. Gene effects for quantitative traits in grain sorghum hybrids were studied by Dangi and Paroda (1978) who reported that among all the variance components, additive, dominance and both types of non-allelic interaction played a significant role in the expression of these traits, additive gene action was found to be predominant for days to flowering, plant height and stem thickness. Height and maturity genes have considerable effects on yield in sorghum. Role of height and maturity genes in growth control has been explained in detail by Tripathi (2006). He reported two dominant and eleven recessive alleles at the Ma_1 locus; twelve dominant and two recessive alleles at the Ma_2 locus, nine dominant and seven recessive alleles at the Ma_3 locus and eleven dominant and one recessive allele

at the Ma_4 locus. Combinations of dominants and recessives at the four loci resulted in flowering periods ranging from 40 to over 100 days. Tropical varieties were always dominant at the first maturity and were usually dominant at the other three loci. Temperate varieties with very few exceptions were recessive at the first maturity locus.

The objectives of this study were to compare selfed progenies by estimating the genetic variability within two grain sorghum populations, to estimate heritability of the traits and to predict gains from selection in each population.

MATERIALS AND METHODS
Formation of Base Populations

In a previous breeding programme in All India Co-ordinated Sorghum Improvement Project (AICSIP), Hyderabad in India, four (two local and two introduced) grain sorghum *sorghum bicolor* L. populations were selected as parents in making crosses. The four populations were SPV–102, SPV–104, S–512 and S–53, SPV–102 and SPV–104 were locally advanced materials with relatively high grain yield, tall stature, late in maturity and well adapted to local conditions. On the other hand, the two introduced populations (S-512 and S-53) had high grain yield, relatively high 100 – grain weight, long panicles, moderately high number of branches per panicle and were earlier maturing than the local populations. Crosses were made among the four source populations at (AICSIP) farm which was characterized by tropical climate with moderate rain-fall during the growing period of the crop. As a result, four sets of crosses were obtained. The four crosses were evaluated. SPV–104xS–512, which was a product of a cross between local and exotic germplasms, had superior overall performance for most traits. SPV–126 also had comparable grain yield with SPV–104 x S-512. As a

result, these two populations were selected as source populations to undertake selection. The F_1 seeds of the selected population cross, SPV–104 x S–512, were planted in isolation for intermating. The intermated population was used as a base population to generate selfed progenies.

Population SPV–126 (SPV–104 x S–53) was obtained from previous breeding efforts in the AICSIP. This second base population was also selected as a parent based on performance *per se* and its adaptation to the local environmental conditions.

Formation of Selfed Progenies

The two base populations were planted, following the recommended cultural practices. Within each of the two populations, 200 to 300 plants were self–pollinated at (AICSIP) Hyderabad India farm. Self – pollinated heads were individually harvested and dried. Each head was then shelled in a separate bag and seeds were put in cold storage.

Evaluation of Selfed Progenies

Of the selfed progenies developed from each population in the previous breeding efforts in the (AICSIP), seeds of 100 progenies were taken for evaluation at the Faculty of Agriculture, University of Putra, Malaysia located at west Malaysia, characterized by tropical climate. The experiment was carried out at the farm using a 10x10 simple lattice design. Each progeny was planted in a 5 m long row, using 0.75m x 0.25m between and within row spacing in 10 rows per plot with three plots per treatment arranged in three replications in 2007. Recommended rates of fertilizers and other cultural practices were followed.

Data Collection

Data were collected for grain yield per plant (g), 100– grain weight (g), number of branches per panicle, panicle length (cm), plant height (cm) and days to flowering (number of days from emergence to the day when the flowers of panicles appeared in 50% of the plot).

Data Analysis

Analysis of variance (ANOVA) was employed and mean comparisons were made using the Statistical Analysis System (SAS) Software Version 8.2 developed by SAS Institute Inc. (2001). ANOVA was used to detect the effects of progenies, blocks and replications. Phenotypic, genotypic and environmental components of variance were estimated using the observed mean squares, based on the expected mean squares from each population from the ANOVA table as suggested by Kang (1995). Variation among selfed progenies (σ^2_G) has the expected additive genetic variance of 1/4 σ^2_A and dominance genetic variance of 1/16 σ^2_D, assuming no epistasis and allelic frequencies of one-half (P=q= 0.5) for segregating alleles.

Broad–sense heritability (h^2_B) was calculated using the variance components method, as suggested by Becker (1984), as follows:

$$h^2_B = \frac{\sigma^2_G}{\sigma^2_P}$$

$$\text{where: } \sigma^2_G = \frac{(\sigma^2_e + \sigma^2_G) - \sigma^2_e}{r}$$

$$= \frac{(MS_G - MS_e)}{r},$$

$$\text{where: } \sigma^2_P = \sigma^2_G + \sigma^2_e ,$$

$$= \frac{(MS_G)}{r},$$

(h^2_B) = broad–sense heritability,

σ^2_G = genotypic variance,

σ^2_P = phenotypic variance,

σ^2_e = environmental variance,

MS_G = mean squares due to genotype,

MS_e = error mean squares and

r = number of replications.

Predicted responses to selection (R) were computed using the formula suggested by Falconer and Mackay (1996) as follows:

$$R = i\sigma_P h^2$$

where, i is the standardized selection differential, σ_P is the phenotypic standard deviation and h^2 is the estimate of heritability on a selfed progeny mean basis.

RESULTS AND DISCUSSION

The overall mean values and ranges for selfed progenies developed from SPV–104 x S–512 and SPV–126 populations are shown in Table 1. Significant differences among selfed progenies of SPV–104 x S–512 were found for all the studied traits, whereas significant differences among selfed progenies of SPV–126 were observed for grain yield per plant, 100–gram weight, panicle length and days to flowering. Selfed progenies developed from SPV–126 had wider ranges for grain yield per plant and number of days to flowering, than selfed progenies developed from SPV–104 x S–512. On the other hand, selfed progenies developed from SPV–104 x S–512 had wider ranges for number of branches per panicle and plant height than progenies developed from SPV–126, suggesting that greater variability exists in SPV–104 x S–512 population for these traits. Such genetic variability in SPV–104 x S–512 population could be exploited through selection.

Table (1): Mean values and ranges of six traits measured on selfed progenies developed from two grain sorghum populations.

	Population			
	SPV–126		SPV–104xS–512	
Trait	Mean	Range	Mean	Range
Grain yield per plant(g)	68.0*	66.6 to 69.1	62.0*	61.0 to 62.9
100-grain weight (g)	2.4*	1.8 to 3.0	2.6*	2.0 to 2.9
No. of branches per panicle	80.7[ns]	78 to 83.7	86.9*	79.9 to 88.9
Panicle length (cm)	33.3*	30.2 to 37.8	35.0*	30 to 37.5
Plant height (cm)	183.9[ns]	151.7 to 220.9	189.1*	153 to 228.4
Days to flowering	68.1*	59.3 to 73.8	76.2*	72.2 to 82.0

[*] Significant at 5%.
ns= not significant.

Diversity among genotypes, performance *per se* and combing ability determine the choice of parents to achieve appropriate breeding objectives. Most of the tropical cultivars are excessively tall, late and low in productivity due to inefficient translocation and injudicious dry matter distribution in stalk and ear-head. But dominant genes for yield are present in tropical varieties (Venkataswarlu, 2002). On the other hand, temperate sorghums represent sources of dwarfing genes, earliness, population performance and disease

resistance (Jotwani, 2000). Thus hybridization between tropical x temperate sorghums form the basis of yield improvement in all the sorghum producing countries. The parents involved in this study are the derivatives of temperate x tropical crosses. They are genetically different in performance *per se* and general combining ability for yield and its components.

Estimates of phenotypic variance (σ^2_P), genotypic variance (σ^2_G) and heritability (h^2) in selfed progenies within each of the two populations are shown in Table 2. Estimates of genetic components of variance (σ^2_G) were positive ($\sigma^2_G>0$) for all traits measured in selfed progenies of SPV–104 x S–512, while SPV–126 progenies had positive estimates for grain yield per plant, 100-grain weight, panicle length and days to flowering. When selfed progenies developed from the two source populations were compared, higher estimates of components of genetic variance (σ^2_G) for panicle length were obtained from SPV–126 progenies than those obtained from SPV–104 x S–512, while SPV–104 x S–512 progenies had higher estimates for number of branches per panicle, plant height and days to flowering, compared to SPV–126 progenies. Falconer and Mackay (1996) suggested that such genetic variance is dependent on the allelic frequencies within the populations and that genetic variances of this sort could provide the opportunity to increase the allelic frequency towards the desirable direction.

Table (2): Estimates of phenotypic variance (σ^2_P), genotypic variance (σ^2_G)
and heritahlity (h^2) for 100 selfed progenies of two grain sorghum populations.

Trait	Population					
	SPV–126			SPV–104xS–512		
	σ^2_P	σ^2_G	h^2	σ^2_P	σ^2_G	h^2
Grain yield per plant (g)	0.07	0.04	57.1	0.05	0.02	40.00
100-grain weight (g)	1.44	0.31	21.4	1.56	0.39	25.00
No. of branches/panicle	0.58	−0.03	na	0.92	0.50	53.8
Panicle length (cm)	1.82	1.21	66.7	2.40	0.88	36.5
Plant height (cm)	197.68	-25.78	na	199.66	104.42	52.3
Days to flowering	5.52	1.85	33.5	8.76	4.46	50.9

na= estimate not available because of negative variance estimate.

The higher estimates of σ^2_G for panicle length in progenies of SPV–126 population suggest that progenies developed from this population could have better genetic gains for this trait than progenies from SPV–104 x S 512. On the other hand, SPV–104 x S–512 population had higher σ^2_G estimates for number of branches per panicle, plant height and days to flowering, showing that there is a greater potential to improve these traits in selfed progenies of SPV–104 x S–512. Similar results of genetic variance for such traits were reported by Azanza et al. (1996) upon studying variation in grain sorghum head

characteristics after introgression of exotic germplasms to local populations.

Progenies from both source populations revealed comparable estimates of components of genetic variance for grain yield and 100-grain weight. Higher estimates of components of genetic variance were expected in SPV–104 x S–512 (a cross between local and exotic germplasms) progenies as it was a cross between parents of divergent growth habits. Linkage Disequilibrium (LD): under recurrent self–fertilization, the level of heterozygosity decays at the rate of one-half per locus, per generation. Thus, within a few generations the low genetic variance for panicle length in SPV–104 x S–512 could be due to linkage disequilibrium present in the SPV–104xS–512 populations which could have hindered the release of some genetic variation (Nigussie and Saleh, 2005). The other reason for higher genetic variance in SPV–126 population for this trait than that in SPV–104 x S–512 could be that SPV–126 had undergone two cycles of mass selection and hence, the frequency of favorable alleles would be expected to be higher for this trait.

Estimates of heritability measured on the progenies generated from the two source populations are presented in Table 2. Heritability estimates for traits measured on the progenies generated from SPV–126 were found to be moderate for panicle length (66.7%), grain yield per plant (57.1%) and days to flowering (33.5%). Progenies generated from SPV–104 x S–512 had moderate heritability estimates for almost all the traits measured, excluding the 100-grain weight indicating that these traits were moderately influenced by the environment.

When heritability estimates of the two source populations are compared, estimates were higher for grain yield and panicle length in SPV–126 compared to SPV–104 x S–512. On the other hand, higher estimates of heritability for number of branches per panicle, plant height and days to flowering were observed in progenies generated from SPV–104 x S–512 than those from SPV–126.

Predicted response to selection (R) at 10% and 20% selection intensities are presented in Table 3. For progenies developed from SPV–126 population, (R) exceeding 5% was obtained for grain yield, panicle length and 100–grain weight. Progenies generated from SPV–104 x S–512 population had (R) higher than 5% for grain yield, panicle length, plant height, 100–grain weight and number of branches per panicle. Progenies generated from SPV–126 had higher (R) (at both 10% and 20% selection intensities) than those from SPV-104 x S–512 for grain yield and panicle length, while progenies of SPV–104 x S–512 had better (R) than those of SPV–126 for number of branches per panicle, plant height and days to flowering. Progenies generated from both populations had comparable response to selection for 100-grain weight.

Table (3): Estimates of predicted response to selection (R) for traits measured in selfed progenies of two grain sorghum populations.

Population / Trait	Mean	Standard deviation	Heritability (%)	Predicted response*(%) (R)	
				A	B
SPV–126					
Grain yield per plant (g)	68.0	0.27	57.1	25.9	20.8
100–grin weight (g)	2.4	1.2	21.4	8.5	6.7
No. of branches/panicle	80.7	0.76	na	nh	nh
Panicle length (cm)	33.3	1.35	66.7	15.8	13.4
Plant height (cm)	183.9	14.06	n	n	nh
Days to flowering	68.1	2.35	33.5	2.6	2.0
SPV–104xS–512					
Grain yield per plant (g)	62.0	0.23	40.0	14.3	11.2
100-grain weight (g)	2.6	1.25	25.0	9.1	6.2
No. of branches/panicle	86.9	0.96	53.8	7.6	5.5
Panicle length (cm)	35.0	1.55	36.5	11.4	9.8
Plant height (cm)	189.1	14.13	52.3	9.5	7.6
Days to flowering	76.2	2.96	50.9	4.5	3.6

* A = at 10% selection intensity; B= at 20% selection intensity.

nh = estimate not available because heritability estimate was not available.

na = estimate not available because of negative variance.

Therefore, SPV–126 appeared to have greater potential for improvement of grain yield and panicle length than SPV–104 x S–512, whereas SPV–104 x S–512 would be expected to have higher potential for improvement of number of branches per panicle, plant height and days to flowering than SPV–126. Comparable (R) between the two source populations could be expected for further improvements for 100–grain weight.

Comparable estimates of genetic variance were found for grain yield and 100 grain weight, indicating that genetic improvement of the two source populations could lead to similar genetic gains for gain yield and 100-grain weight.

Moderate estimates of heritability for grain yield and panicle length were obtained from progenies of SPV–126 and SPV–104 x S–512, indicating that selection for improvement of these traits would be effective in selfed progenies of the two source populations. Moreover, progenies of SPV–104 x S–512 had moderate as well as higher estimates of heritability for number of branches per panicle, plant height and days to flowering than those of SPV–126, indicating that selection for

improvement of these traits would be more effective in selfed progenies of SPV–104 x S–512 than those of SPV–126.

Among direct yield components, number of panicle branches, panicle length, plant height and days to flowering represent substantial variability. Similar results were reported by Subba Reddy (2004).

For selection to improve panicle length, SPV–126 seems to be the appropriate source population, whereas in selection to improve number of branches per panicle,

plant height and days to flowering, SPV–104 x S–512 seems to be the appropriate one. There was no clear distinction between the effectiveness of the use of progenies of SPV–126 or SPV–104 x S–512 to select for 100–grain weight, as progenies from both populations had comparable genetic variance. Therefore, selfed progenies developed from both source populations with elite progenies could be used to improve quantitative traits and thereby develop superior genotypes with desirable traits.

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