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Yield Performance and Stability Analysis of Promising Soybean Genotypes under Contrasting Environments in the Semi-arid Zone of Sudan

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ABSTRACT

Background: The challenge to food security posed by climate change and coupled with the substantial rise in the global population, necessitate a shift in crop improvement programmes towards developing crop cultivars with stable and high yield potentials across a wide range of agro-ecological conditions.

Methods: New high yielding crop varieties with stable performance across environments are enabling the expansion of their production area into non-traditional environments with semi-arid climates. Soybean (*Glycine max* L.), a tropical leguminous crop, has received significant attention as a target crop in breeding programmes for adaptation to semi-arid environments, due to its low water content, high nutritive value and the capacity to produce a variety of products. The objective of this study was to asses yield performance and stability of promising soybean genotypes under contrasting environments in the semi-arid zone of Sudan. We evaluated five soybean genotypes using a split plot design with environment as the main plot and genotype as the subplot.

Result: Combined ANOVA showed significant differences among the genotypes, environment and genotype x environment interaction. Moreover, significant positive relationships were observed between seed yield and number of days to 95% flowering, 100-seed weight, leaf area and number of pods per plant. AMMI stability values revealed significant differences among the genotypes and genotype-by-environment main effects for seed yield. Similarly, results of GGE biplot showed significant contributions of genotypes and genotype-by-environment main effects. The stability models enabled us to identify genotypes with superior performance to specific environments. TGX 1904-6F, was found to be the most stable genotype with appreciable seed yield and adaptability across all environments that can be recommended for release to farmers in semi-arid Sudan.

Key words: AMMI, GGE biplot, *Glycine max*.

INTRODUCTION

Stable performance of genotypes across different environments for high yield and quality traits is an important goal of many plant breeding programmes. However, achieving this goal is challenging due to differential responses resulting from interaction of the genetic background of individual plants with their surrounding environments, which often lead to inconsistency in expression of traits (Crossa and Cornelius, 1997; Asfaw *et al*., 2008; Jeromela *et al*., 2011). Moreover, developing varieties with a broad range of adaptation requires the resource-demanding approach of manipulating genetic backgrounds and screening of large germplasm accessions across different environments contrasting in biotic and abiotic factors. However, the ability of some genotypes to inherently exhibit stability over a wide range of environments is a promising indication for adaptation breeding (Ojo *et al*., 2006; Kumar *et al*., 2020). Kumar *et al*. (2020) successfully used AMMI model to rank 40 promising chickpea genotypes tested in seven diverse environments in India. Breeding for adaptive traits is not only essential for attaining yield stability across different agro-ecological environments (Meseka *et al*., 2003), but will also ensure expansion of crop production into non-traditional agricultural areas.

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Soybean [*Glycine max* (L). Merrill], a legume grown mainly in tropical, subtropical and temperate regions, is one of the crops being targeted for introduction into environments, with arid and semi-arid climates, through both conventional and modern breeding approaches (Faisal, 1986;

Ngalamu *et al*., 2009). In addition to providing an inexpensive source of protein and fats and natural nitrogen fertilisation for the soil (Ngalamu *et al*., 2012; Foyer *et al*., 2016), soybean is also an important crop from which industrial products such as edible oils, wax, paints, dyes and fibre are derived (Rezaei *et al*., 2002; Raghuvanshi and Bisht, 2010). Moreover, meat substitutes based on soybean are extensively used by vegan and vegetarian consumers (Messina and Messina, 2010; Raghuvanshi and Bisht, 2010). Soybean has established its potential as an industrially vital and viable oil seed crop in Sudan. Expansion of soybean into its non-traditional areas of production requires an understanding of the influence of genotype × environment interaction on seed yield and the relationships between yield and some yield components (Ngalamu *et al*., 2020). The objective of this study was to analyse genotype × environment interaction of soybean grain yield under contrasting environments in the semi-arid zone of Sudan.

MATERIALS AND METHODS

Plant material

Fifteen soybean genotypes, introduced from diverse agricultural institutions, were subjected to a preliminary screening for agronomic performance in a greenhouse initially. In order to select the top five genotypes, the 15 genotype were subjected to a base index that uses economic weight for each trait developed and used by maize breeders at the International Institute of Tropical Agriculture (IITA) (Meseka *et al*., 2011). The base index used for selecting promising soybean for this study combined seed yield, number of days to 95% maturity, number of productive branches per plant, number of pods per plant, number of seeds per pod, pod length and 100-seed weight for each of the genotypes. Because each parameter was standardized with mean "0" and standard deviation of "1" to minimise the effects of different scales, a positive value was considered an indicator of good agronomic performance, whereas a negative value indicates poor performance. Five genotypes combining high seed yield with other desirable agronomic traits (100-seed weight, number seeds per pod and number of pods per plant), were selected for further evaluation.

The sources of five selected genotypes originated from the International Institute of Tropical Agriculture (IITA), Nigeria and ORNAS Company in Sudan (Table 1). The experiment was conducted during 2009 and 2010 minor cropping seasons at El Gantra in the Range and Pasture Farm, Sennar State in Sudan. The yield performances of these soybean genotypes were evaluated under ten different sowing dates.

Experimental procedures

The experimental site was El Gantra farm, located in Sennar State, Sudan (latitude 14°C 24′N and longitude 33°C 29′E with an altitude of 127.41 m above sea level). Sennar State, one of the semi-arid agro-ecological zones of the Sudan, is characterized by erratic rainfall and temperature variability (Table 2). The soil was 60% clay, with pH 8.2; and low organic (0.5%) and nitrogen (0.05%) content; and available phosphorus (2.8 mg kg^{-1}).

Field preparation included ploughing, harrowing and ridging were done before sowing. The experiment was arranged in a split-plot design with three replications. Each plot size was 2.4 m × 5 m, consisting of 4 rows 5 m-long. The plots were pre-irrigated three days before sowing, to ensure sufficient moisture in the soil during planting. Two seeds were planted per hill on ridges, spaced 60 cm apart and 10 cm between hills. The seeds were inoculated with *Rhizobium japonicum* strain to ensure the process of nodulation. The experiment was implemented using five sowing dates during each of the cropping seasons of 2009 and 2010. Each sowing date was considered an environment as they differed in weather patterns of temperatures and precipitations (Table 2).

Inoculation of seeds with the nitrogen-fixing bacteria strain was carried out once in the 2009 season not as a treatment and the 2010 trial was also planted in the same field with the residual inoculum effect in the soil. Standard cultural practices recommended for soybean production, such as plant population, row planting, planting date and insect scouting were applied uniformly to all the plots to monitor pests and disease build up. In cases of poor germination, re-sowing was done seven days after planting, followed by the second irrigation. Seedlings were thinned to one seedling per hill at three weeks after planting. Plots were manually kept weed-free throughout the season. The chemical-based insecticide Malathion was used for control of pest such as aphid, bean leaf beetle and green clover worm whenever necessary. To avoid drought stress, the field was irrigated twice a week using gravity flow irrigation system.

Data collection

Field data were collected in accordance with the International Plant Genetic Resources soybean descriptors (IBPGR, 1983). The agronomic traits in this study were recorded on plot basis. Plant height was measured three weeks after 50% flowering, from the ground surface to the base of primary stem of the mother plant, for 10 randomly selected plants. Number of branches was recorded as mean count of branches of randomly selected plants with 3-week-old pods. Leaf area was computed following the empirical relations determined by Iamauti (1991). First pod height (cm) was measured 7 days after pod formation. Lodging, number of pods per plant and number of seeds per pod were recorded at physiological maturity when the seed or pod was completely yellow. A hundred seed weight was determined by randomly counting 100 seeds from a bulked seed for each plot and weighed using a digital weighing-scale. Seed yield (kg ha^{-1}) was measured on plot bases after harvest.

Data analysis

Correlation coefficients were computed to determine the relationships between seed yield and yield components

using SAS ver. 8 [SAS Institute Inc, (2000) Cary, North Carolina, USA]. Combined analysis was performed for seed yield to determine variability among the soybean genotypes and the effect of GEI across the 10 environments. For stability analyses, Additive Main Effect and Multiplicative Interaction (AMMI) and Genotype and Genotype × Environment (GGE) biplot analyses using GEA-R ver. 4.1 (Pacheco *et al*., 2015), were used to determine the effects of genotype × environment interaction (GEI) on seed yield across the environments. To generate a visual AMMI biplot, the following statistical model equation was used:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma\lambda_n y_{gn}\delta_{en} + p_{ge} + \in_{ger}$$

Where,

Y_{ger} = Trait rating of genotype *g* in environment *e* for replicate *r*.

μ = Grand mean.

α_g = Mean deviation of genotype *g* (genotype means minus grand mean).

β_e = Mean deviation of the environment e.

n = Number of PCA axes retained in the model.

λ_n = Singular value for PCA axis *n*.

y_{gn} = Genotype g eigenvector value for PCA axis *n*.

δ_{en} = Environment e eigenvector values for PCA axis *n*.

p_{ge} = AMMI residuals.

$\in_{ger}$ = Residual error.

The eigenvectors are scaled as units of error and are unit less, whereas λ has the units of yield. To generate a GGE biplot for visual analysis of the multi-environment trial (MET) data, the singular value decompositions (SVDs) were portioned into genotype and environment eigenvector of the model as follows:

$$Y_{ij} - \mu - \beta_j = \sum_{i=1}^{k} g_{il}e_{li} + \in_{ij}$$

Where,

g_{il} and e_{ij} are called PC1 scores for genotype *i* and environment *j*, respectively. Genotype *i* was displayed as a point defined by all g_{il} values and environment *j* was equally shown as a point defined by all $\in_{ij}$ values.

RESULTS

Combined ANOVA

The combined ANOVA for seed yield is shown in Table 3. Significant differences ($p<0.01$) were found among genotypes, environments as well as genotype-by-environment interaction for seed yield. Similarly, the interactions between genotype and test environment were highly significant ($p<0.01$) for seed yield. Because genotype-by-environment interaction for seed yield was significant, the data were subjected to further analyses using AMMI and GGE biplot to identify genotypes combining stability with high seed yield. The correlations between seed yield and other agronomic traits were also computed to determine traits which were strongly correlated with the primary trait of interest (seed yield).

AMMI stability analysis

Based on the AMMI analysis, seed yield was significantly ($p<0.001$) influenced by genotypic background and test environments (Table 4). Also, genotype-by-environment interaction had significant effect on seed yield. The environment, genotype and genotype-by-environment interactions accounted for 59.67, 64.65 and 100.00%, respectively, of the total sum of squares (Table 4 and 5). The first three principal components (PC1, PC2 and PC3) accounted for 94% of the total variability for seed yield

Table 1: Photoperiod neutral genotypes of soybean used in the study.

Genotype	Origin	Source	Code	Year of introduction
NA 5009 RG	Argentina	ORNAS	G1	2008
TGX 1740-2F	Nigeria	IITA	G2	2009
SOJA	Argentina	ORNAS	G3	2009
TGX 1937-1F	Nigeria	IITA	G4	2009
TGX 1904-6F	Nigeria	IITA	G5	2009

Table 2: Test environment at range and pasture farm, El gantra, Sennar State.

Month	T_{max}		T_{min}		T_{mean}		Rainfall (mm)		Environment	
	2009	2010	2009	2010	2009	2010	2009	2010		
Jun	40.6	37.7	26.3	36.0	33.45	36.85	26.1	31.2	Env 1	Env 6
Jul	35.0	32.5	22.8	23.5	28.9	28.0	198.5	59.9	Env 2	Env 7
Aug	35.4	32.1	23.3	23.2	29.35	27.55	33.9	116.5	Env 3	Env 8
Sep	37.5	33.6	23.8	23.0	30.65	28.3	23.6	125.5	Env 4	Env 9
Oct	38.8	37.6	21.5	27.5	30.15	32.55	128.0	45.7	Env 5	Env 10
Nov	34.7	37.7	18.3	18.1	26.5	27.9	N/A	N/A		

T_{max} = Maximum temperature (°C); T_{min} = Minimum temperature (°C); T_{mean} = Mean temperature (°C).

Source: Agricultural Research Station Sennar, Republic of Sudan.

observed among the genotypes across the test environments.

GGE biplot analysis

The results of GGE biplot analysis are shown in Fig 1. The first two principal components (PC1 and PC2) explained 84% of the total variation for seed yield observed among the genotypes across the test environments. The genotypes on the vertex of the polygon were G1 (NA 5009 RG), G3 (SOJA), G4 (TGX 1937-1F) and G5 (TGX 1904-6F). Genotypes G1 (NA 5009 RG) and G2 (TGX 1740-2F) were less responsive and were low yielding compared to G5 (TGX 1904-6F), which was the most stable and high yielding.

The discriminating ability among the five genotypes tested under diverse environments was determined by the average tester axis (ATA) in GGE biplot with stability lines connecting genotypes and grouping them into a specific environment based on their responsiveness. A longer projection from a genotype onto the stability line determines its stability and the short projection indicate instability of the genotype to test environments. In Fig 2, environments (hereafter referred to as Env) 1 and 2, had long vectors and more discriminating than those with short vectors (Fig 2). The discrimination pattern of the genotypes and environmental representativeness of the five genotypes indicated that Env 1 and 2 were more representative environments with a short projection onto the stability line and clustered on or near the ATA .

The GGE Biplot also computes a stability statistic for each genotype, which is interpreted such that genotypes with greater absolute values are less stable and those with lesser absolute values closer to zero are highly stable. Our results showed that genotype G2 was less responsive across the test environments indicating its stability. The position of G5 closer to ATA line in Fig 2 indicated that it was relatively stable and had consistent performance across environments compared to the other genotypes with greater distance from ATA.

Correlation analysis

The number of pods per plant was positively correlated ($p<0.01$) with seed yield and leaf area (Table 6). Seed yield was also strongly associated ($p<0.001$) with 100-seed (Table 6).

Table 3: Combined ANOVA for seed yield of soybean genotypes across 10 test environments.

ANOVA	Df	Mean squares
Replication (R)	22	0.30^{NS}
Environment (Env)	99	1.89***
Genotype (Gen)	44	0.35*
Gen × Env	3636	0.28**
Pooled error	9898	0.15

*, **, ***Significant at 0.05, 0.01 and 0.001 levels of probability, respectively, ^{NS} = Not significant.

Table 4: AMMI for seed yield of soybean genotypes across test environments in Sudan.

SOV	DF	SS	MS	Sum of squares explained		
				% Total	%G × E	%G × E cumulative
Env	9	16.97	1.89***	59.67		
Gen	4	1.42	0.35*	64.65		
Env*Gen	36	10.06	0.28***	100.00		
PC1	12	5.41	0.45***	53.75	53.75	53.75
PC2	10	2.83	0.28*	28.15	28.15	81.90
PC3	8	1.18	0.15^{NS}	11.71	11.71	93.61
PC4	6	0.64	0.11^{NS}	6.39	6.39	100.00
Residuals	96	15.16	0.15			

*, **, ***Significantly different at 0.05, 0.01 and 0.001 levels of probability, respectively, ^{NS} = Not significant; SOV = Source of variation; Gen = Genotype; Env = Environment; MS = Mean square, SS = Sum of squares, G×E = Genotype-by-environment interaction and DF = Degree of freedom.

Table 5: ANOVA for AMMI model and Gollob's *F*-test and average root mean square predictive difference.

SOV	DF	SS	MS	F
ENV	9	17.00	1.89***	12.44
GEN	4	1.42	0.35^{NS}	2.34
ENV*GEN	36	10.06	0.28**	1.84
PC1	12	5.41	0.45**	3.03
PC2	10	2.83	0.28^{NS}	1.91
PC3	8	1.18	0.15^{NS}	0.99
PC4	6	0.64	0.11^{NS}	0.72
PC5	4	0	0^{NS}	0
Residuals	100	15.16	0.15	NA

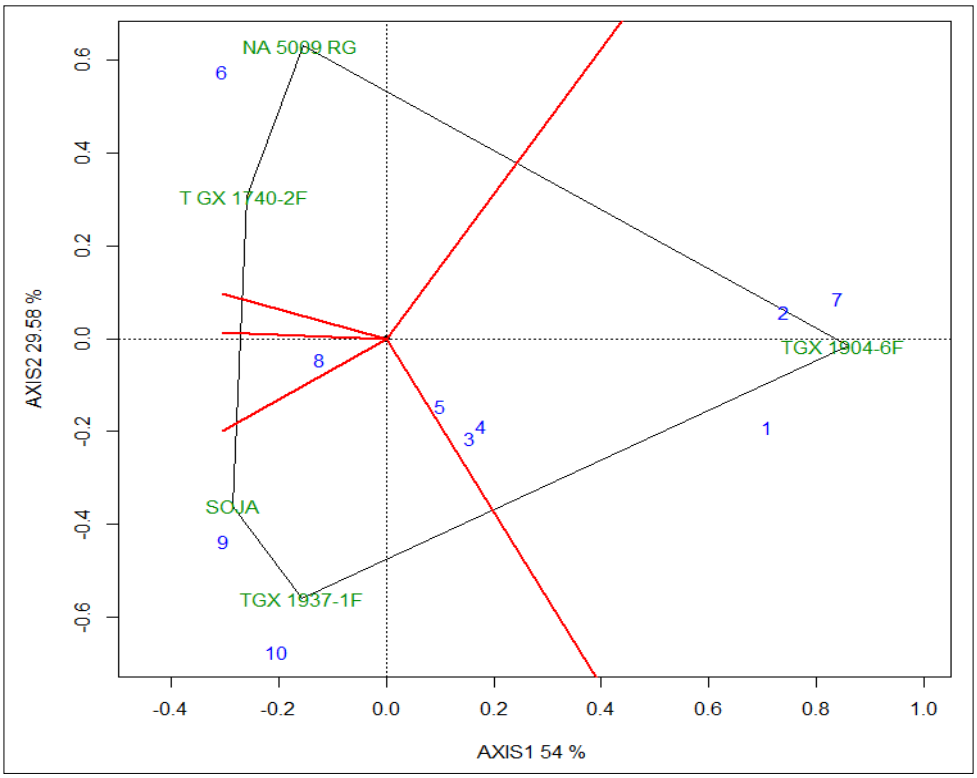


Fig 1: Polygon view of genotype by environment interaction of soybean genotypes.

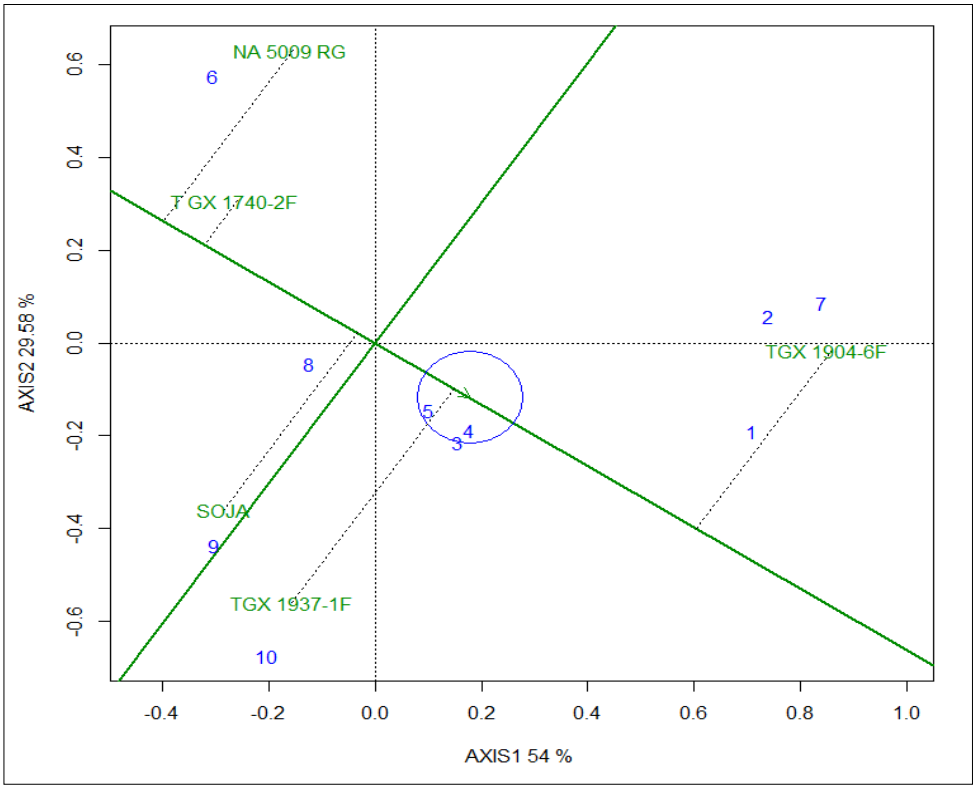


Fig 2: Mean *vs* stability view of main and GEI effects.

Additionally, the number of branches per plant and number of days to 50% flowering were moderately correlated ($p<0.05$) with seed yield, whereas no significant associations were observed between seed yield with plant height and first pod height. Finally, increasing number of pods per plant had positive effects on seed weight per plant and seed yield.

DISCUSSION

Genetic and environmental responsiveness

Our result showed that both the genotypes and environmental conditions had significant influence on the yield and yield components of the soybean across the test environment (Table 3, Fig 1). This has confirmed that introduction and evaluation of new sources of genetic variation that aids the development of improved varieties through selection of parents based on both agronomic value and genetic dissimilarity (Ghosh *et al*., 2014). The significant GEI detected in combined ANOVA of seed yield implies that these genotypes respond differently to the test environments. Such differences may partially be attributed to differences in the genetic backgrounds of the genotypes used in this study. Furthermore, environments tend to influence seed yield of the genotypes, suggesting that environments affected the yielding ability and stability of the five soybean genotypes. Our results corroborate previous findings (Temesgen *et al*., 2015; Sharifi *et al*., 2017; Dia *et al*., 2018), whereby it was observed that the extent of genotype by environmental interaction on yield and stability are higher where there is a wide-ranging variation between environments in incidence of the same climate, soil, biotic and management factors.

AMMI stability analysis

The newly introduced varieties were evaluated and assessed for stability in order to recommend the best performer for possible release to farmers. We found that environment accounted for 60% of the total variability (Table 4), suggesting significant role of environment in genotype adaptation and yield performance of the soybean genotypes evaluated across the contrasting test environments. Our finding are in agreement with those of Rashidi *et al*. (2013) who reported slightly higher value of 81.2% total variability accounted for by the environment. Similarly, Singh *et al*. (2018) found that environment accounted for 50-80% of the total variation in multi-environment data. Using AMMI analysis for the five promising soybean entries, we found that G5 (TGX 1904-6F) was the most adaptable and high yielding genotype across the test environments.

GGE biplot analysis of genotype, genotype-by-environment interaction

In the GGE biplot analysis, environment had a significant contribution to the variability in seed yield among the soybean genotypes that was also detected by AMMI analysis (Table 5), confirming the implication of test environments on yield stability. We observed some genotypes with relatively high seed yields, but did not fall in specific environments or group of environments; suggesting that they were not adapted to any of the test environments. Most of the soybean genotypes evaluated in the present study were less responsive to the test environments, indicating their poor performance and lack of adaptability, largely due to environment and GEI effects. None of the genotypes had a broad adaptation across the test environments. G5 (TGX 1904-6F) was the only genotype that adapted to two test environments, Env 1 and 2, demonstrating its suitability for production in these contrasting environments. Our results corroborate with the findings of Simion (2018), who reported significant differences among genotypes, environment and GEI effect on grain yield. This is the first study to attempt to classify soybean production into mega environments and assess discriminating ability of test environments based on grain yield of soybean genotypes in Sennar State in Sudan. Such an attempt is important as it may reduce costs when conducting multi-locational trials for soybean grain yield.

In the polygon view of the discriminating environments, Env 1 (1), Env 2 (2), Env 6 (6), Env 7 (7), Env 8 (8), Env 9 (9) and Env 10 (10) were strongly correlated and most discriminatory (Fig 2). Environments Env 3, 4 and 5 were non-discriminatory and tended to cluster together, making them unsuitable for selection of stable high yielding soybean genotypes. Thus, removing one of the locations as testing environments would not lead to any loss of information. This reduction could cut down on resources that could be put to better use in other locations (Meseka *et al*., 2016). Our findings confirm the results obtained by Yan and Tinker (2005), who suggested that test environments that are none discriminating provide no information on the genotypes and therefore should not be used as test environments.

Correlation analysis

Though some yield components showed weak relationships with seed yield (Table 6), the trend was still in positive direction, suggesting an appreciable level of contributions to seed yield. The result indicates that these traits could be simultaneously improved based on phenotypic selection; thus improving seed yield components. The strong association between these traits with seed yield suggest that they could be used for indirect selection of high yielding

Table 6: Correlation coefficients between seed yield and yield components of soybean genotypes across 10 environments in Sudan.

Traits	Seed yield (kg/ha)
Plant height (cm)	0.46^{NS}
First pod height (cm)	0.43^{NS}
Number of branches per plant	0.55*
Number of pods per plant	0.58**
Leaf area (cm^2)	0.69**
Number of days to 50% flowering	0.50*
100 seed weight (g)	0.98***

*, **, *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively, ^{NS} = Not significant.

soybean genotypes. These findings agree with previous reports on strong associations between seed yield and plant height in soybean (Jagtap and Choudhary, 1993; Oz *et al*., 2002; Malik *et al*., 2006).

Increase in days to 50% flowering indicates that late maturing genotypes would have a greater number of pods, given opportunity to mature late resulting in high seed yield. Adugna and Labuschgne (2003) also reported significant variations among locations for days to 50% flowering in linseed. However, temperatures do play dominant roles in early flowering in some genotypes. Ngalamu *et al*., (2012) reported that during flowering and pod setting, temperatures as high as 30°C favoured greater pod set; while temperatures above 40°C severely limited pod formation. We also observed that seed yield potential was strongly associated with leaf area, suggesting that genotypes with larger leaf area had a greater chance of interception and efficient utilisation of solar radiation for photosynthesis leading to improved seed yields. Thus, breeders could use leaf area and leaf duration as traits for indirect seed yield improvement in soybean.

CONCLUSION

This study demonstrates that some yield components, including 100 seed weight, leaf area, number of pods and branches per plant as well as days to 50% flowering have significant contributions to soybean seed yield under semi-arid agro-ecological environments. Genotype and environment main effects and genotype by environment interaction effects were significant for seed yield of the five soybean genotypes evaluated in this study. G5 (TGX 1904-6F) was found to be the best genotype with stable high seed yield across two test environments (Env 1 and Env 2). This genotype can further be evaluated for seed yield and other desirable agronomic traits to confirm the consistency of its performance for possible release. Env 1, the first planting date (second week July) gave the highest seed yield followed by Env 2, the second planting date (third week July). These results suggested that farmers in the Sudan's semi-arid environments should plant their soybean in July; any planting later than this month will result in low seed yield.

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