Vol. 12(3), pp. 246-257, July-September 2020
DOI: 10.5897/JPBCS2020.0905
Article Number: C70E77564876
ISSN 2006-9758

http://www.academicjournals.org/JPBCS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Evaluation of the performance of advanced generation soybean [*Glycine max* (L.) Merr.] genotypes using GGE biplot

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Received 27 May, 2020; Accepted 3 August, 2020

Soybean is an important food and cash crop in Uganda. Despite the importance of soybean in Uganda's economy, its performance is highly affected by genotype × environment interaction making it difficult to select and recommend new superior soybean genotypes for diverse growing environments. The objectives of this study were to examine the nature of G × E interaction for soybean grain yield, to identify stable and high yielding soybean genotypes with desirable percentage protein and oil content for production in diverse environments and to determine ideal test location for future soybean breeding activities in Uganda. The experiment was conducted at six locations for two consecutive seasons of year 2018 (2018A and 2018B). Twenty-three newly advanced generation soybean lines and two commercial varieties were evaluated in a randomized complete block design replicated three times. Combined analysis of variance over locations and seasons was carried out for grain yield, protein and oil (%) content. The results for grain yield showed significant ($p<0.05$) differences for all the sources of variation except genotypes × season interaction. Percentage protein and oil content showed non-significant ($p>0.05$) for all the sources of variation except location. The genotype main effect plus G × E interaction biplot explained 65.74% of the total interaction sum of squares for grain yield and showed that the advanced generation soybean lines BSPS 48A-28; Mak 3N × 1N and NGDT 8.11×3N-2 were high yielding and stable and had other desirable agronomic traits. Nakabango was the most discriminating and representative test location.

Key words: Soybean, stability, GGE, ideal testing location, mega-environment.

INTRODUCTION

Soybean (*Glycine max* L.) is an important food and cash crop in Uganda (Ibanda et al., 2018; Gebremedhn et al.,

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2018). Due to its nutritional superiority, soybean flour is often blended with cereal flours such as maize to boost their nutritional value. In Uganda, Makerere University Soybean Improvement Centre is developing soybean varieties ideal for food and industrial purposes (Tukamuhabwa et al., 2016). Generally, majority of farmers like high-yielding, minimal stem lodging and non-shattering soybean varieties that are less susceptible to common diseases such as soybean rust and red-leaf blotch (Tukamuhabwa and Obua, 2015) and pests such as groundnut leaf miner (Ibanda et al., 2018) and bruchids (Msiska et al., 2018). Food processors also want soybean varieties with high protein and oil content. Farmers and food processors normally would want all these traits incorporated in one variety (Whaley and Eskandari, 2019). In most cases, the agronomic traits are highly heritable and can be easily selected with accuracy at early generation testing. However, the expression of quantitative traits such as seed yield, protein and oil content is highly influenced by genotype × environment interaction, hence complicates the identification and selection of superior genotypes (Gurmu et al., 2009; Hampango et al., 2017) and therefore multi-environment trials (MET) are recommended for evaluation of promising lines (Nyombayire et al., 2018).

Uganda's agro-ecological regions are highly diverse with variable climatic conditions accelerated by global climatic changes that influence mean annual rainfall (510-2160 mm), temperature (23-28°C) and varied soils influenced by soil depth, texture, acidity and organic matter (Agoyi et al., 2017; Tukamuhabwa et al., 2012). Due to the variability of abiotic and biotic factors from location to location, soybean performance remains exposed to the influence of huge genotype × environment interactions, leading to inconsistent genotypic responses (Bhartiya et al., 2017); therefore, the development of stable varieties will be the only sustainable way to cope with the ever-changing biotic stresses like the outbreak of groundnut leaf miner (Ibanda et al., 2018) and soybean rust (Maphosa et al., 2013; Gebremedhn et al., 2018) and abiotic stresses; like extreme temperature and rainfall changes (Tukamuhabwa et al., 2016). The presence of significant G × E interaction for grain yield, percentage protein and oil content in soybean has been reported by several researchers (Gurmu et al., 2009; Nascimento et al., 2010; Chaudhary and Wu, 2012; Atnaf et al., 2013; Hampango et al., 2017; Bhartiya et al., 2017) which could lead to the failure of genotypes to achieve the same relative performance in different environments (Noëlle et al., 2018; Thungo et al., 2019).

The differential performance of genotypes across several unrelated environments reduces responses to selection and subsequently progress in plant breeding programs (Crossa et al., 2002; Yan and Kang, 2002). Furthermore, the presence of significant crossover G × E interaction complicates the recommendation of new varieties from MET and the identification of ideal genotypes (Bernardo, 2002; Yan and Kang, 2002) which should be either specific or widely adapted across different agro-ecological zones. Therefore, characterizing the interaction between genotypes and environments is very important for the selection of genotypes with high adaptability to specific environments or with high stability across different environments (Yan et al., 2000; Yan et al., 2019). In this regard, Yan and Tinker (2006) presented some objectives of MET analysis that included mega-environments delineation to minimize negative G × E interaction, as well as identification of the most discriminating and representative testing locations within mega-environments and identification of superior genotypes. This is important in cultivar development in order to rationalize resources and confine genotype evaluation to ideal locations that are informative to facilitate a rapid response to selection (Tukamuhabwa et al., 2012).

Several statistical methods for analyzing G × E interaction have been reviewed (Westcott, 1986). However, not all ways of exploiting G × E interaction involve trying to reduce it (Bernardo, 2002). Some methods, like analysis of variance (ANOVA), are good at detecting G × E interaction but cannot reveal the pattern of the interactions (Gasura et al., 2015). Regression-based methods (Eberhart and Russell, 1966) use environmental scores, which have less to do with genotype plus G × E interaction and explains only a small part of genotype main effect plus genotype × environment interaction (GGE) (Yan et al., 2007). In the recent past, statistically effective multivariate techniques, such as biplots based on Singular Value Decomposition (SVD) and Principal Component Analysis (PCA) have been developed for G × E interaction analysis (Gauch, 2006; Yan and Tinker, 2006). Approaches such as the genotype main effect plus G × E interaction (GGE) biplot (Yan, 2001;Yan and Tinker, 2006) and the Additive Main effect and Multiplicative Interaction biplot (AMMI) (Gauch, 2006, 2013; Gauch et al., 2008) have been widely used to exploit significant G × E interaction in soybean MET data as they effectively capture the additive (linear) and multiplicative (bilinear) components of G × E interaction and provide meaningful display and interpretation of multi-environment data set in breeding programs.

The biplot model that is fitted to residuals after the exclusion of the environment-centered data is called a GGE biplot (Yang et al., 2009). The GGE biplot is a graphical display of G × E interaction data into a two-way table for simplicity visualization of the interrelationship and it can be subjected to several ways of singular value decomposition (SVD) (Yan and Tinker, 2006). Yan and Hunt (2001) suggested that, for cultivar evaluation and recommendation, genotype and G × E interaction are the only two sources of variation that are crucial and must be considered simultaneously for appropriate genotype and test environment evaluation. Using a site's regression model (SREG) Yan et al. (2000) combined genotype

Table 1. Experimental sites used in the study during season 2018A and 2018B.

Site	Coordinates	Altitude (m)	Mean annual temperature (°C)	Mean annual rainfall (mm)	Soil type
Nakabango	00° 31'N 33°12'E	1178	26	1400	Crysalline basic
Iki-Iki	01° 06'N 34° 00'E	1156	28	1200	Sandy
Kabanyolo	00° 28'N 32° 37'E	1300	22	1255	Sand-clay loam
Bulindi	01° 28'N 31° 28'E	1230	23	1700	Sandy loam
Ngetta	02° 17'N 32° 56'E	1085	29	1483	Sandy loam
Abi	03° 5'N 30° 56E	1140	24	1250	Sandy-clay loam

Source: NARO Ngetta-Zardi (2018).

main effect and genotype × environment interaction, denoted as G + G × E interaction or GGE and repartitioned this into crossover and non-crossover G × E interaction. For exploiting G × E interaction in MET data, the strengths of the GGE and AMMI biplots have been debated unequivocally (Gauch, 2006; Yan et al., 2007; Gauch et al., 2008; Yang et al., 2009). In MET data, the GGE biplot is crucial in assessing the genotype main effects plus the G × E interaction (Yan and Tinker, 2006). This multivariate analysis technique has been widely used for delineating soybean production mega-environments and soybean variety recommendations (Bhartiya et al., 2017; Hunde et al., 2019). The objectives of this study were to examine the nature of G × E interaction for soybean grain yield, to identify stable and high yielding soybean genotypes with desirable percentage protein and oil content for production in diverse environments and to determine ideal test location for future soybean breeding activities in Uganda.

MATERIALS AND METHODS

Materials and testing environments

The study was carried out at six locations namely; Kabanyolo, Iki-Iki, Nakabango, Ngetta, Abi and Bulindi that are located in different agro-ecological regions of Uganda (Table 1). These locations have different climatic conditions, and therefore may influence the expression of soybean grain yield, protein, oil content and agronomic traits differently. Furthermore, these locations represent major soybean growing areas of Uganda. Twenty-five soybean genotypes were used in this study. Among the genotypes used, 23 were advanced generation lines and two were commercial varieties used as checks (Table 2).

Experimental design

A randomized complete block design (RCBD) with three replications was used. Each entry was represented by three rows measuring 5 m long with an inter-row and in-row spacing of 60 cm and 5 cm respectively. The study was carried out for two consecutive seasons; first rains of 2018 (2018 A), and second rains of 2018 (2018 B). The trials were kept weed free by constant weeding.

Data collection

Data was collected on soybean rust, a major soybean disease in Uganda using a scale of 1-5 (Miles et al., 2006) where 1= no visible lesion, 2= few scattered lesions present, 3= moderate number of lesions on at least part of the leaf, 4= abundant number of lesions on at least part of leaf, and 5= prolific lesion development on most of the leaf. Days to 50% flowering and plant height were recorded as described by Obua (2013). The groundnut leaf miner (GLM) severity was scored using the standard scale of 1-5 as described by Ibanda et al. (2018). The number of pods per plant was recorded at harvest. Furthermore, at harvest the genotypes were threshed, and 100 seed weight and yield per plot were determined and later corrected to 12% moisture content before determining yield per hectare (Tukamuhabwa et al., 2012). Protein and oil content (%) were quantified using the data from first and second replications of selected four locations of Nakabango, Iki-Iki, Abi and Bulindi. The locations were selected based on their previous informative study of Tukamuhabwa et al. (2012). The analysis described by Owusu-Apenten (2002) was used to quantify the protein content, whereas, the oil content was determined using Near infrared spectroscopic analysis as described by Sato (2010).

Data analysis

Analysis of variance (ANOVA) was performed initially for each environment to determine the performance of the genotypes in different environments. Combined analysis of variance over locations and seasons was conducted using mixed model as suggested by Moore and Dixon (2015) (where genotypes and locations were fixed, whereas seasons, all the interactions involving seasons, replications and error were considered random) in Genstat software version 18 (Genstat, 2016). To determine the performance of different genotypes across seasons and locations, the following model for combined analysis of variance was used as described by Gasura et al. (2015);

$$Y_{ijkl} = \mu + r_1(pt)_{jk} + g_i + p_j + t_k + (gp)_{ij} + (gt)_{ik} + (pt)_{jk} + (gpt)_{ijk} + e_{ijkl}$$

Where, $Y_{ijkm(l)}$ is observed value of *i*th genotype in the *j*th location and the *k*th season in the *l*th replication, μ is the grand mean, $r_1(pt)_{jk}$ is the effect of the *l*th replication within locations and seasons, g_i, p_j and t_k are the main effects of the genotype, locations and seasons, $(gp)_{ij}$, $(gt)_{ik}$, $(pt)_{jk}$ are the first order interactions and $(gpt)_{ijk}$ is the second-order interaction, and finally e_{ijkl} is the pooled error term.

The proper F-test for a mixed model in which genotypes and locations were considered fixed effects and seasons treated as random effects was applied as suggested by McIntosh (1983) and recently by Moore and Dixon (2015). The assumption of sum to zero the effects of random interactions across each level of a fixed

Table 2. Names and codes of the soybean genotypes used in the study.

Code	Genotype name	Status
G1	Duiker × 3N-5	Advanced line
G2	GC × 2N-1	Advanced line
G3	BSPS 48A-27-1	Advanced line
G4	BSPSS 48A-28-1	Advanced line
G5	NGDT8.11×14.16B	Advanced line
G6	NII × GC 13.2	Advanced line
G7	BSPS 48A-25-1	Advanced line
G8	Nam II GC 17.3	Advanced line
G9	NII × GC 35.3-2	Advanced line
G10	NG 14.1 × UG5	Advanced line
G11	Nam 4M × 2N-2	Advanced line
G12	NII × 35.3-3	Advanced line
G13	G8586 × UG5	Advanced line
G14	NGDT 8.11× 3N-1	Advanced line
G15	BSPS 48A-28	Advanced line
G16	Bulindi 18.4B	Advanced line
G17	Maksoy 4N	Standard check
G18	BSPS 48A-24-1	Advanced line
G19	Bulindi 24.1A	Advanced line
G20	NII × GC 35.3-1	Advanced line
G21	NDGT 8.11×3N-2	Advanced line
G22	2N × GC	Advanced line
G23	Mak 3N × 1N	Advanced line
G24	NG 14.1 × NII-1	Advanced line
G25	Maksoy 3N	Standard check

factor for combined experiments was used as described by Moore and Dixon (2015). In brief, the mean squares for genotypes, genotypes × locations, genotypes × seasons and genotypes × locations × seasons were tested against the pooled error mean square, while locations, seasons and locations × seasons were tested against the mean square of replications within locations and seasons (Mclntosh, 1983). The variance components due to genotypes (δ^2g), genotypes × location (δ^2gl), genotypes × seasons (δ^2gs), genotypes × locations × seasons (δ^2gls) and random error (δ^2error) were obtained by solving the equations formed by equating the mean squares to their respective expected mean squares (Moore and Dixon, 2015). The variance components due to environments (location × seasons combinations) were estimated by summation of δ^2l, δ^2s and δ^2ls, whereas the variance component attributed to genotype × environment (δ^2ge) was estimated by adding up δ^2gl, δ^2gs and δ^2gls (Mclntosh, 1983). The broad sense coefficients of genetic determination (BSCGD) (broad sense heritability based on fixed genotypes) on a single plot basis, single environment basis and across environments basis were obtained by solving the following equations as; $\delta^2g/(\delta^2g + \delta^2gl + \delta^2gs + \delta^2gls + \delta^2error)$; $\delta^2g/ (\delta^2g + \delta^2gl + \delta^2gs + \delta^2gls + \delta^2error/ nr)$ and $\delta^2g/(\delta^2g + \delta^2gl/nl + \delta^2gs/ns + \delta^2gls/nls + \delta^2error/ nslr)$, respectively, where nr = number of replications, nl = number of locations, ns = number of seasons, nls = number of location × seasons combinations and nslr is the number of seasons × location × replications (Moore and Dixon, 2015).

Yield data was further subjected to GGE biplot (Yan and Tinker, 2006) analysis for identification of high yielding and stable soybean genotypes. The GGE biplot analysis was performed to determine the mega-environments and visualize the "which-won-where" pattern following the model for GGE biplot based on singular value decomposition (SVD) of *t* principal components as described by Yan and Tinker (2006).

GGE model: $Y_{ij} - \mu_i - \beta_j = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$

Where, Y_{ij} is the performance of genotype *i* in environment *j*, μ is the grand mean, *j* b is the main effect of environment *j*, *k* is the number of principal components (PC); λ_k is singular value of the k^{th} PC; and α_{ik} and γ_{jk} are the scores of i^{th} genotype and j^{th} environment, respectively for PC_k; ε_{ij} is the residual associated with genotype *i* in environment *j*.

For mega-environment delineation of test locations, the which-won-where scatter plot was generated by a polygon drawn by connecting genotypes that are furthest away from the biplot such that the polygon contained all other genotypes (Yan, 2002). Then the polygon was further divided by perpendicular lines drawn to the polygon sides and running from the biplot origin (Yan and Tinker, 2006). The genotype focused comparison biplot for visualization and comparing genotypes based on mean yield and stability was determined by representing an average environment by an arrow. A straight line that dissecting the biplot origin to the average environment coordinate (average genotype axis) was drawn followed by a perpendicular line that passes through the biplot origin using the appropriate singular value partitioning (SVP) methods (Yan and Tinker, 2006). For the analysis of test locations, location comparison biplot was used for identification of ideal testing site (the most discriminating and representative locations) (Gasura et al., 2015). The environment vectors were drawn from the location comparison biplot origin to the markers of the environment (Yan and Tinker, 2006).

RESULTS

Combined ANOVA and broad sense heritability estimates

Combined analysis of variance for grain yield showed significant ($p<0.05$) differences for all components except genotypes × season interaction. The broad sense coefficient of genetic determination for grain yield (BSCGD) (equivalent to broad sense heritability of fixed genotypes) on single plot basis, single environment basis and across environment basis were 3, 6 and 40% respectively (Table 3). Percentage protein and oil content results showed non-significance ($p>0.05$) for genotype, seasons, genotype × location interaction, genotype × season interaction and genotype × location × season interaction except location which was significant ($p<0.05$) (Table 4).

Genotypes evaluation based on GGE biplots

The which-won-where biplot showed different winning genotypes in different environments (Figure 1). The biplot accounted for 65.74% of the genotype main effect and G × E interaction for grain yield of the genotypes. The biplot was dissected into eight sectors and four mega-

Table 3. Mean squares for grain yield of 25 soybean genotypes evaluated over locations and seasons .

Source of variation		GY (kg/ha)
	Df	MS
Season	1	161551161***
Location	5	60563205***
Season. Location	5	10263901**
Replication. Season. Location	24	2274739***
Genotype	24	320102***
Genotype × Location	120	195916**
Genotype × Season	24	152514^{ns}
Genotype ×Location × Season	120	193393*
Pooled Error	576	142233
LSD		770.1
CV (%)		23.4
δ^2g		4940.81
δ^2gl		8947.17
δ^2gs		571.17
δ^2gls		17053.33
δ^2error		142233
H2 on single plot basis		0.03
H2 individual environment basis		0.06
H2 on across environment basis		0.41

***=p<0.001; **=p<0.01; *=p<0.05; ns=not significant; GY= grain yield; G= genotype; H2= broad sense heritability; δ^2g= variance component due to genotype; δ^2gl= variance component due to genotype × location; δ^2gs= variance component due to genotype × season; δ^2gls= variance component due to genotype × location × season.

environments and showed six vertex genotypes. The biplot identified winning genotypes in each mega-environment as follows; BSPS 48A-28 (G15) for mega-environment I (Bulindi, Nakabango and Kabanyolo), BSPS 48A-28-1 (G4) for mega-environment II (Iki-Iki), Bulindi 18.4B (G16) for mega-environment III (Ngetta) and BSPS 48A-24-1 (G18) for mega-environment IV (Abi). Genotypes within the polygon were less responsive than the vertex genotypes.

The ranking plot (Figure 3) and genotype focused comparison biplot (Figure 2) ranked genotypes based on both mean grain yield and stability performance in order to identify the highest yielding and stable genotypes. Based on mean yield performance and stability, the biplots ranked G15>G16>G22>G17>G21, as ideal genotypes followed by a check variety Maksoy 3N and the rest of the advanced generation lines.

Test location evaluation based on GGE biplots

The environment vector plot showed that Abi, Nakabango and Bulindi had the longest vectors from the biplot origin. The angle between Abi and Bulindi was almost right angle and locations Ngetta and Iki-Iki had the shortest vectors from the biplot origin as well as a small angle between them. Abi, Nakabango and Bulindi were the most discriminating locations, while Ngetta and Iki-Iki were the least discriminating test locations (Figure 4).

The environment focused comparison showed the ideal test location was Nakabango which was located near the center of the concentric circles as the most representative testing location, while other test locations, Bulindi, Kabanyolo, Ngetta, Iki-Iki and Abi were not representative (Figure 5).

Genotypes mean performance for yield, protein, oil content and agronomic traits

The mean performance of 25 soybean genotypes evaluated for two seasons across six locations are summarized in Table 4. Genotype BSPS 48A-28 had the highest yield of 1767 kg/ha followed by Maksoy 3N and Mak 3N × 1N both with average grain yield of 1725 kg/ha; these genotypes had the longest days to 50% flowering as well as lowest groundnut leaf miner damage and rust scores (Table 4). The results of mean percentage protein content are shown in Table 4. The results showed that the overall mean for percentage protein content across

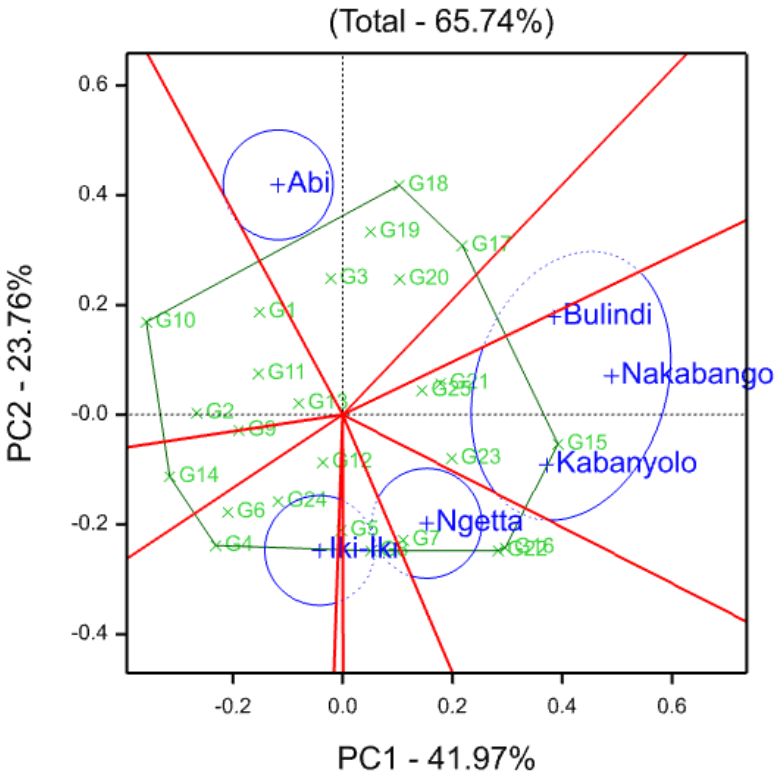

Figure 1. The which-won-where and mega-environment delineation biplot for yield of 25 soybean genotypes evaluated in six locations for two seasons (2018A and 2018B)

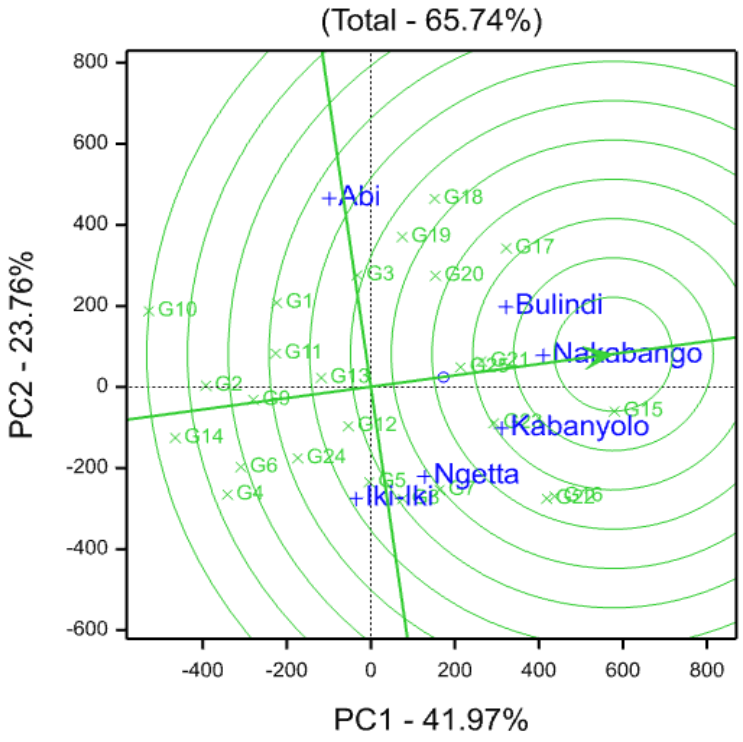

Figure 2. Genotype focused comparison biplot for yield showing the best genotypes based on mean performance and stability

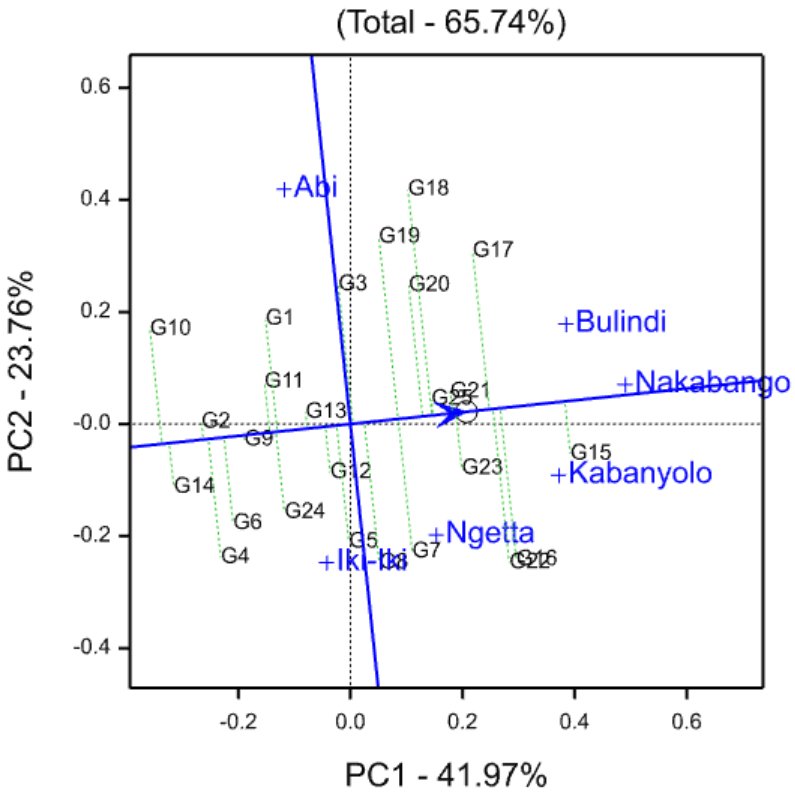

Figure 3. Ranking plot for yield showing the best genotypes based on mean performance and stability.

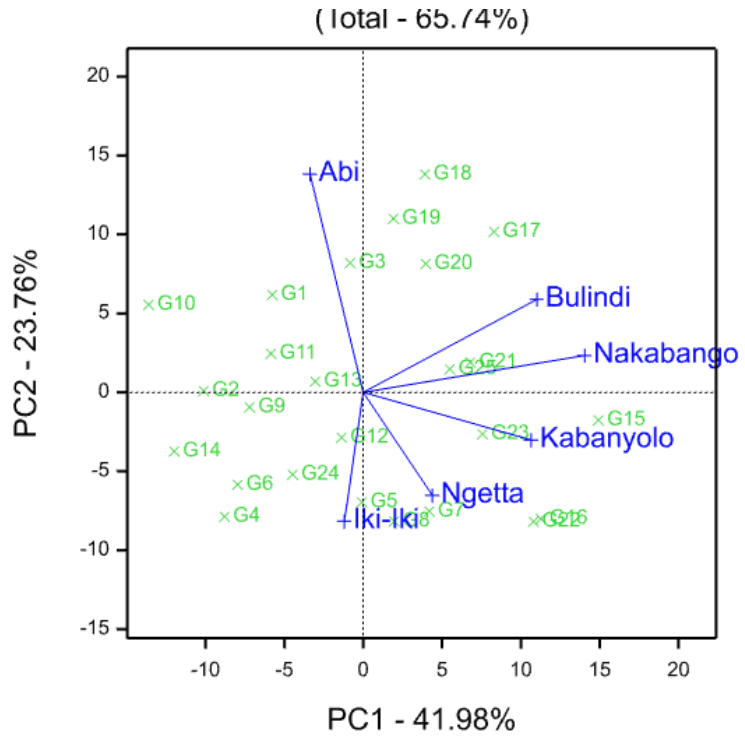

Figure 4. Environment vector plot showing discriminating ability of test locations based on yield

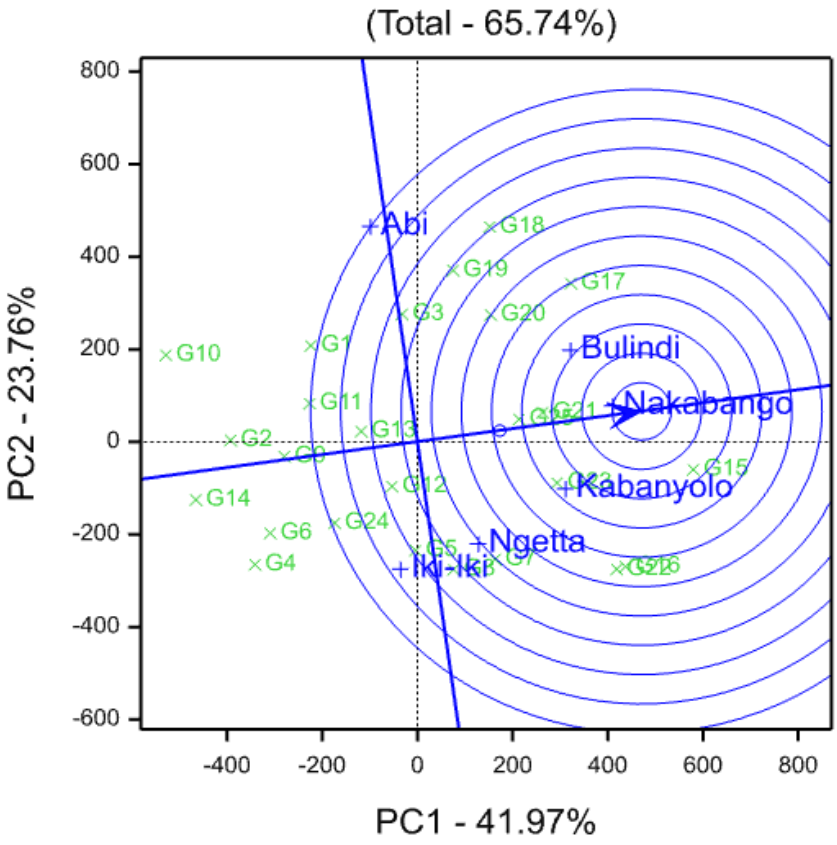

Figure 5. Environment focused comparison biplot showing the ideal testing location for soybean yield among the locations used in evaluations.

seasons and selected locations was 33.54%, with genotypes 2N × GC, G8586 × UG5 and Bulindi 24.1A had the highest percentage protein content of 34.67, 34.62 and 34.45, respectively. The results of mean percentage oil content analysis are presented in Table 4. The overall mean for oil content across seasons and selected locations was 16.01%, with genotypes Duiker × 3N-5, NDGT 8.11× 3N-1 and NGDT 8.11 × 14.16B, were ranked the best three with percentage oil content of 17.26, 16.62 and 16.55, respectively (Table 4).

For locations, Bulindi had the highest mean yield (2650 kg/ha) followed by Abi (1845 kg/ha), Nakabango (1698 kg/ha), Ngetta (1567 kg/ha) and Kabanyolo (1017 kg/ha) while Iki-Iki had the lowest mean yield of 889 kg/ha (Table 5). The overall mean yield performance for the genotypes across locations and seasons was 1611kg/ha.

DISCUSSION

Nature of the G × E interaction, variance components and heritability estimates

The presence of significant genotype main effect as well as G × E interaction for grain yield suggested differential responses of soybean genotypes across tested environments and implied the need to identify high-yielding and stable genotypes across the test environments. Similar results have been reported by several researchers (Gurmu et al., 2009; Atnaf et al., 2013; Kumar et al., 2014; Bhartiya et al., 2017). The large variance component attributed to locations alone justified the need to use genotype main effect plus G × E interaction (GGE) biplots, in which the GGE biplot captured much of the variation due to genotype plus G × E interaction as a fraction of the total sum of squares (G + E + GE) (Yan et al., 2007). The large variance component due to locations and seasons depicted that the locations used in the present study were very diverse across seasons. Indeed, Uganda has diverse agro-ecological zones with highly variable mean annual rainfall of 510-2160 mm, also varied with soil depth, texture, acidity and organic matter (Agoyi et al., 2017). The huge variability of these predictable factors (soil characteristics) and unpredictable factors (temperature and rainfall) (Table 1) from location to location leading into inconsistent genotypic performances (Obua, 2013) and therefore, widely adapted soybean genotypes with dynamic yield stability are recommended to strengthen soybean production country wide (Tukamuhabwa et al.,

Table 4. Grain yield, protein, oil content and agronomic performance of 25 soybean genotypes evaluated across two seasons in Uganda (2018A and 2018B).

Genotypes	Yield(kg/ha)	Protein (%)	Oil (%)	100SWT	DT50%F	GLM	NPODS	PH	RUST
BSPS 48A-28	1767	32.9	15.8	17.0	44	1.1	32	74.3	1.1
Mak 3N × 1N	1725	33.8	16.2	16.7	44	1.1	29	65.8	1.2
Maksoy 3N	1725	33.3	15.9	17.3	41	1.2	31	66.7	1.1
2N × GC	1710	34.7	16.0	15.2	43	1.2	33	67.4	1.6
NGDT 8.11× 3N-2	1702	33.7	16.3	15.8	44	1.3	24	61.3	1.3
BSPS 48A-27-1	1681	34.1	15.6	17.0	43	1.2	28	70.7	1.2
BSPS 48A-25-1	1678	33.4	15.8	16.8	43	1.3	31	75.8	1.3
BSPS 48A-24-1	1672	33.1	15.7	15.4	44	1.2	29	71.6	1.4
Maksoy 4N	1671	32.9	16.1	16.9	44	1.1	30	72.5	1.3
NGDT8.11×14.16B	1652	33.3	16.6	16.9	40	1.2	29	65.0	1.3
Bulindi 18.4B	1648	33.3	16.0	15.2	42	1.4	28	62.2	1.2
NII × GC 35.3-1	1633	33.1	16.1	15.0	44	1.2	30	74.8	1.6
Nam II GC 17.3	1624	33.9	16.4	15.8	44	1.2	27	48.3	1.3
Duiker × 3N-5	1609	34.3	17.3	17.4	43	1.1	33	85.0	1.6
G8586 × UG5	1606	34.6	16.3	15.3	43	1.5	29	52.9	1.6
NII × 35.3-3	1590	33.9	15.0	14.8	43	1.3	30	74.4	1.8
NII × GC 35.3-2	1585	33.5	15.8	15.0	43	1.2	30	73.3	1.5
Bulindi 24.1A	1572	34.5	15.5	16.0	43	1.2	31	81.0	1.8
Nam 4M × 2N-2	1543	32.8	15.6	15.8	42	1.2	30	67.0	1.7
BSPS 48A-28-1	1539	34.4	15.7	16.3	42	1.2	32	64.3	1.6
NG 14.1 × NII-1	1531	33.8	15.8	18.1	42	1.2	24	66.8	1.4
NG 14.1 × UG5	1491	33.8	15.3	16.2	45	1.2	31	80.5	1.4
GC × 2N-1	1469	33.2	16.4	15.5	42	1.2	27	71.6	1.5
NII × GC 13.2	1469	32.1	16.5	16.6	43	1.3	35	68.7	1.6
NDGT 8.11× 3N-1	1385	32.3	16.6	18.1	42	1.1	23	68.4	1.4
Mean	1611	33.5	16.0	16.3	42	1.2	29	69.2	1.5
LSD	174.6	5.4	4.4	2.5	2.5	0.4	14.6	14.3	0.7
CV (%)	23.4	8.3	13.4	9.0	3.1	19.7	27.7	11.1	29.8
F probability	<.001	NS	NS	<.001	<.001	<.001	<.001	<.001	<.001
Genotype × Location	0.009	NS	NS	<.001	NS	<.001	<.001	<.001	<.001
Genotype × Location × Season	0.012	NS	NS	NS	NS	NS	NS	NS	NS

100SWT=100 seed weight (gm); GLM=groundnut leafminner (scores); NPODS= number of pods; PH= plant height (cm); DT50%F= days to 50% flowering, Rust (scores); NS= non-significant.

2012).

The large G × E interaction and error variance components found in the present study could reduce selection progress by complicating the identification and recommendation of superior genotypes for a target environment (Nyombayire et al., 2018; Hunde et al., 2019). The results observed in this study, however, were of a lesser magnitude than that reported by Bhartiya et al. (2017) on 36 soybean genotypes evaluated in 3 environments in India, where G × E interaction almost doubled the genotypic main effects and five times larger than environmental effects. Large G × E interaction and residuals observed in multi-environment trials (MET) affect the repeatability of the experiment (Simion et al., 2018) could have contributed to the low broad sense coefficient of genetic determination (which is equivalent to broad sense heritability based on fixed genotypes) of 3% on a single plot basis and 41% on across environments which has improved as the number of locations and seasons increased. Similar results were reported by Gasura et al. (2015) in sorghum where broad sense heritability increased from 2.8% on single plot basis to 31.8% on across environments basis. Gasura et al. (2015) and Sousa et al. (2018) suggested that large G × E interaction and error variance components increase the cost of variety evaluation due to increase in numbers of replications, locations and seasons needed to improve broad sense coefficient of genetic determination, and hence the selection efficiency. Since crop growing locations have no precisely stated demarcations and most farmers tend to influence each other in the choice of variety that is grown (Gasura et al., 2015), the

Table 5. Grain yield performance in kg/ha of 25 soybean genotypes evaluated across 12 locations.

Genotype	Location							
	Abi	Bulindi	Iki-Iki	Kabanyolo	Nakabango	Ngetta	Mean yield	Rank
BSPS 48A-28	1683	3006	843	1165	2069	1836	1767	1
Mak 3N × 1N	1809	2773	1073	1317	1841	1538	1725	2
Maksoy 3N	2001	2642	817	1041	1937	1912	1725	3
2N × GC	1578	2739	988	1346	1932	1678	1710	4
NDGT 8.11 × 3N-2	1942	2592	850	1189	2021	1621	1702	5
BSPS 48A-27-1	2139	2844	1092	924	1717	1369	1681	6
BSPS 48A-25-1	1696	2686	1027	1181	1709	1766	1678	7
BSPS 48A-24-1	2194	2729	747	1038	2002	1321	1672	8
Maksoy 4N	1926	3036	630	983	1926	1526	1671	9
NGDT 8.11×14.16B	1805	2540	986	1143	1598	1838	1652	10
Bulindi 18.4B	1380	2938	926	1260	1867	1515	1648	11
NII × GC 35.3-1	1915	3030	674	1064	1623	1492	1633	12
Nam II GC 17.3	1694	2376	1014	1189	1861	1610	1624	13
Duiker × 3N-5	2112	2712	937	883	1491	1519	1609	14
G8586 × UG5	1928	2578	978	861	1716	1578	1606	15
NII × 35.3-3	1757	2652	963	973	1635	1563	1590	16
NII × GC 35.3-2	1978	2578	943	1064	1303	1643	1585	17
Bulindi 24.1A	2016	2631	446	1040	1851	1448	1572	18
Nam 4M × 2N-2	1935	2617	799	1111	1359	1438	1543	19
BSPS 48A-28-1	1790	2313	1034	849	1513	1735	1539	20
NG 14.1 × NII-1	1648	2561	1049	793	1670	1464	1531	21
NG 14.1 × UG5	2121	2362	869	733	1440	1419	1491	22
GC × 2N-1	1861	2392	802	865	1447	1447	1469	23
NII × GC 13.2	1616	2520	876	759	1462	1579	1469	24
NDGT 8.11× 3N-1	1603	2417	858	662	1453	1319	1385	25
Mean	1845	2650	889	1017	1698	1567	1611	
CV (%)	25.4	20.5	26.8	31.4	19.1	17.6		
LSD	538	621.5	272.6	365.8	371.1	316		

development of soybean varieties adapted to a broad range of environments is strongly recommended, rather than environment-specific varieties (Bhartiya et al., 2017).

Evaluation of soybean genotypes across environments

The significant difference for grain yield and yield related traits observed among genotypes across environments indicated the presence of genetic and environmental causes of variation. The significant G × E interaction observed in this study also showed the significance of environmental effects in the expression of soybean grain yield. These results are consistent with the findings of other researchers (Chaudhary and Wu, 2012; Atnaf et al., 2013; Krisnawati and Adie, 2018; Hunde et al., 2019). The absence of significant genotype, G × E interaction for protein and oil content observed in this study was inconsistent with previous studies (Gurmu et al., 2009; Nascimento et al., 2010; Chaudhary and Wu, 2012; Hampango et al., 2017) who reported the presence of significance genotype, G × E interaction for protein and oil content. The results obtained from this study showed that there was limited genetic variation among the tested genotypes for protein and oil content and therefore there is no need to advance this set of genotypes targeting commercial improvement of these two traits.

Based on scatter biplot for mega-environments delineation, only four mega-environments with their winning genotypes located at the vertices of the polygon were identified. Locations Kabanyolo, Bulindi and Nakabango were classified on mega-environment I, in which BSPS 48A-28 was the winning genotype. Mega-environment II had Iki-Iki with BSPS 48A-28-1 as the winning genotype, Ngetta was classified on mega-environment III where genotype Bulindi 18.4B was the most adapted. Mega-environment IV had Abi found in the West Nile region where BSPS 48A-24-1 was the winning genotype, indicating that Uganda had broad agro-

ecological regions with unique environmental characteristics with specific suited high yielding genotypes. Location Bulindi had the highest mean yield of 2650 kg/ha, while Iki-Iki had the lowest mean yield of 889 kg/ha. The reason is Bulindi received high rainfall (1700 mm/ annum) and the site has good soil types, with good nutritional status and water holding capacity (Table 1). The reason for low yielding in Iki-Iki might be the gradual changes in biotic and abiotic factors from season to season. On the other hand, Iki-Iki is characterized by poor sandy soils, with low water holding capacity (Tukamuhabwa et al., 2012). Also Iki-Iki is a hot spot for groundnut leaf miner, a new soybean pest which is devastating soybean in Uganda (Ibanda et al., 2018). Despite the relatively low yield potential for soybean in Iki-Iki, genotype BSPS 48A-28 managed to maintain its average performance implying that this genotype had good dynamic stability. This is a good attribute for any commercial variety given the unpredictable patterns of biotic and abiotic factors in most parts of the country (Obua, 2013). The existence of crossover G × E interaction in this study indicated that genotypes evaluation and recommendation typically based on any single location was unreliable because there is differential response of genotypes across locations (Mare et al., 2017). The presence of crossover interactions indicated genotype evaluation should be based on mean performance and stability (Yan and Kang, 2002).

The genotype focused comparison biplot indicated that the most stable and high-yielding genotype was BSPS 48A-28 probably due to having lowest groundnut leaf miner damage, rust scores, high number of pods and, is late maturing advanced line (Table 4). Based on mean yield and stability, the genotype maintained its above average performance in most of the environments. Genotype Mak 3N × 1N was comparable in yield performance to the commercial variety Maksoy 3N which was one of its parents. Meanwhile, a commercial variety Maksoy 4N performed well based on mean yield and stability, although it was ranked fourth (Figure 3) outperformed by three experimental genotypes and Maksoy 3N a commercial variety. Based on ranking plot for mean yield performance and stability (Figure 3), genotypes BSPS 48A-28; Mak 3N × 1N and NGDT 8.11×3N-2 are potential candidates for release since the variety release condition in Uganda advocate for broad instead of specific adaptation.

Evaluation of the test environments

The presence of G × E interaction for soybean yield justifies undertaking MET during cultivar selection and recommendations (Krisnawati and Adie, 2018). Based on test location biplot, the vector length of the biplot approximates the standard deviation within each location and a measure of the discriminating ability of the location (Yan and Tinker, 2006). Nakabango, Bulindi and Abi locations, which had the longest vectors from the biplot origin, were the most discriminating testing locations and, therefore these three testing locations could be used jointly as discriminating locations for testing early generation breeding materials (Yan et al., 2007; Yan and Tinker, 2006). Bulindi and Abi were discriminating genotypes but not representative and therefore, these two sites could be used together as “culling environments” for easily selecting against unstable genotypes during the breeding process (Yan and Kang, 2002). Nakabango was both discriminating and representative. Discriminating and representative test locations are useful for selecting superior genotypes while eliminating inferior ones (Atnaf et al., 2013).

CONCLUSION AND RECOMMENDATIONS

There was crossover G × E interaction for soybean grain yield which was twice larger than the effect of genotypes. Non-significant G × E interaction for percentage protein and oil content observed in the present study, hence no need to advance this same set of genotypes targeting commercial improvement of these two characters. We recommend BSPS 48A-28; Mak 3N × 1N and NGDT 8.11×3N-2 as widely adapted and higher yielding genotypes that could be advanced to the national performance trials before commercialization in Uganda. These three genotypes had lowest groundnut leaf miner damage, rust scores, high number of pods and, are late maturing advanced lines. They have almost all desirable attributes of a good soybean cultivar. Location Nakabango was both discriminating and representative, hence testing soybean genotypes at this location is ideal; it can save time and resources.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

This research was implemented with funding from Intra-ACP Academic mobility for Crop Scientists for Africa Agriculture (CSAA) project. The authors also thank the Makerere University Soybean Improvement Centre and RUFORUM for partial financial support.

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