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YIELD STABILITY OF COTTON GENOTYPES AT THREE DIVERSE AGRO-ECOLOGIES OF UGANDA

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A B S T R A C T

Yield and fibre qualities are economically important parameters considered by the majority of stakeholders engaged in the cotton value chain in Uganda. The study objective was to determine the stability and adaptability of advanced cotton lines in diverse agro-ecological zones. Yield potential and fibre traits of cotton genotypes were evaluated in cotton growing agro-ecologies of Uganda. Sixteen genotypes were evaluated for two-year cycles of 2013/2014 and 2014/2015 in Arua, Lira and Serere districts. Additive main effects and multiplicative interaction (AMMI) and genotype main effects and genotype by environment interaction (GGE) biplots determined the stability of genotypes for seed cotton yield in different environments. Significant differences were observed among genotype performances for all the traits assessed with exception of ginning out turn. Some genotypes showed good fibre traits and high seed cotton yield across sites in the two-year cycles. The mean yield across sites and years ranged from 1422 to 1883kg/ha with eight genotypes including the check (BPA2002), attained yield above the overall mean of 1729kg/ha. Five genotypes BTAM(13)MO.2 (1883kg/ha), MS(13)MO.1 (1838kg/ha), EZAMMAR(13)MO.1 (1839kg/ha), BTAM(13)MO.3 (1824kg/ha) and BHG(13)MO.2 (1818kg) had higher yield than the check (1777kg/ha). Using AMMI model, the genotype and environment effects revealed significant differences for yield. Genotype by environment interactions was significant, indicating that there is genetic variability among genotypes for yield in the changing environments. The relationships observed among test locations using GGE biplot revealed three mega-environments. This indicated that classifying genotypes into mega-environments implied higher heritability and faster progress for plant breeders and higher yields for growers. AMMI analysis revealed six stable genotypes G11(BPA2002), G15 [BHG(13)MO.2], G7 [BTAM(13)MO.3], G14 [EZAMMAR(13)MO.1], G9 [BPAN(13)MO.2] and G16 [BPAN(02)14] which contributed to relatively lowest interaction. Generally, these results showed that genotypes with above average means of seed cotton yield, good fibre traits and stability were considered for further evaluation in national performance trials prior to release.

Keywords: AMM1, cotton, fibre traits, genotype, GGE, stability.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is an essential crop required in the production of industrial fibre materials, edible oil and livestock feed utilized in many countries of the world. The cotton crop is commercially cultivated in both developed and developing countries by small-scale and large scale farmers. It is envisaged that for proper development and productivity of cotton crop, it requires well drained sandy loam or volcanic soils, good climate with fairly warm and optimal rainfall. Significant efforts in research are undertaken to enhance the capacity of increasing production in order to meet the increasing demand of the population (Baloch *et al*., 2015; Mukoyi *et al*., 2015). This can be possible when cotton varieties developed exhibit good yielding potential, stability and adaptability. Global statistics show that cotton production is on the increase with the world top ten most producing countries taking the lead namely China, India, USA, Pakistan, Brazil, Uzbekistan, Australia, Turkey, Turkmenistan and Greece producing over million metric tons, respectively (ICAC, 2013). For Uganda, cotton production and productivity is still trending below the world production and has stagnated

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for over the years (Baffes, 2009).

In Uganda, cotton is one of the major agricultural cash crops cherished by the government after coffee and tea. It provides livelihood to millions of people and contributes income of 10% of the country's population of over 2.5 million people in the rural areas of the east, north and west engaged in the cotton value chain (Baffes, 2009). The cotton produced in the country contributes about 5.5% to the gross domestic product (GDP) of the economy of Uganda and fetches over $48 million in export earnings (Red pepper, 2015). Its position in farming systems contributes significantly towards food security by leaving a clean seedbed for the next crop in rotation especially cereal crops like finger-millet, sorghum and maize. Cotton can be intercropped with legume crops such as beans, cowpeas, groundnuts, green grams, soybean, and pigeon pea thus ensuring nutritional diet as the farmer produces both food and cotton on the same piece of land which is eventually sold as a cash crop.

The government of Uganda has put good policies and regulations in place such that proper extension services are provided to the cotton farmers, monitoring the production, overseeing the processing and marketing of cotton, availing high quality planting of cotton seed, fertilizers and pesticides at affordable prices to farmers on time. These have relatively contributed to increased yield of cotton thus boosting the cotton sector through addressing key issues of seed quality, reorganizing ginning industry, increased cotton production in traditional cotton segregated areas, financial research and training of researchers in various disciplines. The partnership with National Agricultural Research Organization (NARO) and Cotton Development Organization (CDO) led to first releases of cotton varieties in the past which included BPA 97, BPA 99, BPA 2000 and the BPA 2002 with good performance. These varieties had good potential for various aspects, but along the way, some were stopped from being cultivated because of their proneness to biotic and abiotic stresses. In this regard, the government found it prudent to retain one variety to be produced all over the country to avoid mixing with other varieties when grown by farmers that would compromise with fibre qualities. The release of BPA 2002 was brought on board in production throughout the country because of its excellent performance. The BPA 2002 has been in production giving over 250,000 bales of cotton lint since 2004. However, production gradually fluctuated in the subsequent years thus requiring replacement with potential variety. Low cotton production in bales has been registered as a result of a reduction in area under cropping. This has been observed in the deterioration of BPA 2002 in genetic purity and yield resulting from inbreeding depression and being susceptible to emerging insect pests and diseases, proneness to drought and declining soil fertility.

Testing of developed cotton genotypes in wide agro-ecologies in the country is paramount as this can enable to determine their stability and adaptability for yield and other desirable traits. Cotton genotypes need to be subjected to varied conditions so as to sustain stability and production. The changing environmental conditions are known to affect the performance of cotton genotypes which require cotton researchers to consider the need to evaluate such genotypes in numerous cotton growing agro-ecological zones for stability and adaptability (Baloch *et al*., 2015). Studies indicated that evaluation of the test locations for genotypes suitability in multi-environment variety trials is critical relevance because it checks the extent to which test locations which used to be selected are representative of the whole target region (Baxevanos *et al*., 2008). This helps to improve breeding effectiveness and reduce costs if only those locations that have a proper capability to discriminate between genotypes under selection are used in the variety trials (Blanche and Myers, 2006; Yan *et al*., 2007). Cotton breeders strive to develop genotypes with superior yield, fibre qualities and other desirable characteristics over a wide range of environmental conditions. The genotype by environment interaction tend to limit in the selection and subsequently the progress in plant breeding programme for genetic improvement, especially for quantitative traits such as yield because it complicates the interpretation of trials involving many environments (Kaya *et al*., 2002; Zeng *et al*., 2014). Zeng *et al*. (2014) further explained that significant genotype by environment (G x E) component necessitates multiple locations for performance tests in breeding programmes, whereas the extent of genotypic effect relative to G x E component might reduce the number of environments necessary for performance tests. In a situation where environmental differences are great, the interaction of genotypes with the environment is also expected to be great and as a result, one genotype may have the highest yield in one environment, while the

other genotype may excel in another environment (Anley *et al*., 2013). In determining the pattern of genotype response to environment and prioritise genotypes for use in the breeding programme, quantification of genotype by environment interaction is necessary (Gauch, 2006). This is considered important especially when dealing with advanced generations of genotypes which not yet tested in the different growing agro-ecologies for stability and adaptability (Tukamuhabwa *et al*., 2012).

The pattern of genotype response allows partitioning of test locations into mega-environments and ideal environments based on their discriminating ability such that test locations within a mega-environment are homogenous, whereas the variation among groups is maximized (Yan and Kang, 2003; Yan *et al*., 2007). Breeding for genotype stability is accomplished with repetitive field testing, trait evaluation and selection of genotypes that rank at or near the top of a series of individual field trials conducted across a range of environments and years (Campbell and Jones, 2005). The term mega-environment describes the separation of a crop growing area into different target zones (Gauch and Zobel, 1997). Crops that are subdivided into their growing regions into mega-environments imply higher heritability and faster progress for plant breeders and subsequently higher yields for the growers. In crop breeding, classifying environments into small groups or mega-environments can be used mainly by numerous statistical methods developed to analyze the stability and adaptability performance of genotypes across test locations (Moreno-Gonzalez *et al*., 2003). A number of statistical methods for analysis of multi-environment trials have been developed but the additive main effects and multiplicative interactions (AMMI) and genotype main effects plus genotype by environment interaction (GGE) are extensively applied to assess stability and adaptability of genotypes (Kang, 1993; Yan, 2001; Yan and Kang, 2003). AMMI uses the analysis of variance and principal component analysis to study G x E interactions (Gauch 2006; Ntawuruhunga *et al*., 2001). Accordingly, Yan *et al*. (2007) pointed out that GGE biplot was the most appropriate type for mega-environment investigation, genotype evaluation and test location evaluation; all these are summed up to help breeders appreciate the importance of the methods when making decisions on the stability and adaptation of breeding genotypes in several locations. Generally, breeding programmes are planned to satisfy the needs of various stakeholders in the cotton value chain. In this way, the farmers demand varieties that are high yielding while the ginners and spinners require high lint yield with good fibre quality characteristics at their interface. Developing and selecting cotton varieties with its production environment is often a challenge to the breeders by the occurrence of significant genotype by environment interaction in the genotypes development breeding programme. Therefore, the study was conducted to determine the stability and adaptability of 16 advanced cotton lines in diverse agro-ecological zones of Uganda.

MATERIALS AND METHODS

Fifteen advanced cotton lines developed from National Semi-Arid Resources Research Institute (NaSARRI) in Uganda and one commercial cotton variety (used as check), were evaluated in three different locations with diverse agro-ecologies namely; Arua (Northwest Nile), Lira (northern) and Serere (eastern) during two year cycles of 2013/2014 and 2014/2015. The location of Arua has latitude of $3^0$2'N/$30^0$54'E, altitude of 3923 feet above sea level (f.a.s.l), temperature range from 20^0C minimum to 31^0C maximum and annual rainfall of 1204 mm; Lira has latitude of $2^0$12'N/$32^0$55'E, altitude of 3604 f.a.s.l, temperature range from 23^0C minimum to 32^0C maximum and annual rainfall of 1400mm, and Serere has latitude of $4^0$12'N/$35^0$0'E, altitude of 3560f.a.s.l, temperature range from 23^0C minimum to 28^0C maximum and annual rainfall of 1250 mm. These locations represent the major cotton growing areas and are of different agro-ecologies in Uganda. Each location and year cycle constituted an environment, thus resulting in six environments over two year cycles. Each cotton genotype was planted with three seeds per hill in a plot size of 18m^2 (1.5 m x 12 m) and spacing was 75 cm between rows and 30 cm between plants in a randomized complete block design with four replications and later thinned to two plants in the respective locations. All the agronomic field management practices (weeding, fertilizer application and pesticide application) were done as required.

Data on seed cotton yield, boll weight, lint index, 100-seed weight, ginning out turn and fibre traits (such as micronaire, fibre length and fibre strength) were collected. The total seed cotton yield for each cotton genotype from each plot was weighed in kilogram after picking all the split bolls and converted into kilogram

per hectare. The total yield was computed from the sum of the weight of boll samples together with the seed cotton weights at different pickings. The boll weight was considered by randomly selecting 10 plants per plot. From each plant, one good looking fully split boll ready for picking was done and the same procedure was done to the others from a selection of 10 plants. The total 10 bolls were weighed and averaged in grams to determine the cotton genotypes with heaviest boll size. Ginning of 10 boll samples was done on a 12-inch roller gin, while bulk samples for the derivation of fibre traits were ginned on a 40-inch double roller gin. Lint index was determined by weighing fibre in grams produced from any given sample of seed cotton after removing the seeds. The ginning out turn percentage (% GOT), was calculated as a percentage of lint obtained from 10 boll samples from each plot after ginning divided by the total weight of the seed together with the lint after ginning. The fibre traits (micronaire, fibre length (mm) and fibre strength (g/tex) were determined by HVI fibre testing machine. The analysis of data for all the parameters assessed was carried out using Genstat 15th Edition. The seed cotton yield across sites and year cycles was analysed using the application of the additive main effect and multiplicative interaction (AMMI) model and genetic and genetic by environment (GGE) biplots. The genotype by environment interaction (GEI) required the use of AMMI model and principal component analysis. For the suitability and stability analysis for each genotype in respective environment required the use of GGE biplot (Blanche *et al*., 2007; Yan, 2001). Moreover, the GGE biplot is generally considered the type of biplots for mega-environment investigation, genotype and test location evaluation, thus performs data by graphic approach (Xu *et al*., 2013; Zeng *et al*., 2014). The GGE biplot was constructed by considering the principal components (PC1 and PC2).

RESULTS AND DISCUSSION

Combined analysis of yield components and fiber traits: The combined analysis of variance for boll weight, lint index, seed weight and fibre traits across locations and averaged over the two year cycles (from 2013/2014 to 2014/2015) are presented in Table 1. There were significant differences ($P<0.05$) observed among the cotton genotypes evaluated for performances of all the traits considered in this study with the exception of ginning out turn percentage (% GOT). The results showed that seven cotton genotypes had high boll weights above the overall mean of 59.8 with cotton genotype MS(13)MO.1 being the best, while BHGTAMH(02)1 was the least. Lint index is one of the important traits in cotton and results showed that six cotton genotypes had high values above the overall mean of 7.2 and the least was recorded on BPAN(13)MO.1 with poor lint index. The micronaire is one of the good fibre characteristics considered when classifying genotypes that fall within the premium range of 3.7-4.2. Three genotypes MS(13)MO.2, MS(13)MO.1 and BPA 2002 were identified with good performance micronaire. The ability of genotypes to have long fibre when stretched is considered very important and the results showed that two genotypes BPAN(13)MO.3 and MS(13)MO.1 had the longest fibres. The results further showed that genotypes MS(13)MO.2, BPAN(13)MO.3, MS(13)MO.1 and BHGTAMH(02)1 had good fibre strength compared to the other genotypes. The high percentage ginning out turn (%GOT) is very much cherished by many cotton ginners and this was recorded in MS(13)MO.2, MS(13)MO.1 and BHGTAMH(02)1, while BPA 2002 and BHG(13)MO.2 had the lowest %GOT. However, there were slight differences observed for seed weights among the genotypes with most of them attaining weights above the overall mean. The genotypes BTAM(13)MO.2, MS(13)MO.1 and EZAMMAR(13)MO.1 had the highest seed weights and lowest was on BPAN(13)MO.1and BPAN(02)14. The crop productive parts of cotton are important contributors to the selection of promising genotypes associated with seed cotton yield and fibre characteristics. Of significance is the expression of a crop to properly form the yield components and fibre traits. Cultivation of high quality cotton varieties is characterized to provide strong development of vegetative parts with a longer period of forming fruiting parts and numerous vegetative branches (Zhu *et al*., 2002; Zhang and Ni, 2006). The results further demonstrated that cotton genotypes with non-significance for percentage ginning out turn (%GOT) suggests the genes controlling this trait are linked together and similar but selection could be done with high %GOT with other economic traits such as seed cotton yield and fibre quality characters (Singh and Narkhede, 2010). Boll weight is a very important trait for the breeders when developing high yielding cotton genotypes due to its positive linkage with seed index (100-seed weight) and seed cotton yield. Tyagi *et al*.

(1988) observed that boll weight contributes directly towards seed cotton yield and this was used for selection of high yielding genotypes. Improvement of different characters in cotton depends on the existence of heritable variation, and heritability is considered as a measure of the degree of genetic determination of traits which facilitates the selection process (Rasheed *et al*., 2009). The goodness of the productive and fibre traits represents the true genetic association and presence of some common genes that play a big role in these traits. Similarly, selection based on these traits would be helpful for producing high yielding cotton varieties which have positive associations observed between seed cotton yield and fibre quality traits. The yield components and fibre traits have a direct effect on seed cotton yield, indicating that selection of genotypes based on these traits would increase the production and productivity, thus enhance the livelihoods of farming communities (Iqbal *et al*., 2003; Rauf *et al*., 2004). The results also show that increase in boll size increases seed cotton yield, micronaire and fibre strength which are genetically determined.

Table 1. Mean performance of cotton genotypes for yield components and fiber traits* evaluated across locations and averaged over two year cycles from 2013/2014 to 2014/2015.

Genotype	Boll weight (gm)	Lint index	Micronaire	Fibre length (mm)	Fibre strength (g/tex)	%GOT	100-Seed weight(gm)
BHGMAR6(13)MO.1	58.5	7.1	3.4	28.9	31.1	38.9	10.6
BPAN(13)MO.1	56.7	6.6	3.5	28.9	30.6	38.5	10.5
MS(13)MO.1	65.1	7.8	3.9	30.4	31.5	39.6	11.5
MS(13)MO.2	60.0	7.5	4.0	28.8	31.6	39.7	11.2
BPMAR6(13)MO.1	61.3	7.3	3.6	28.4	28.9	39.2	11.3
BTAM(13)MO.1	61.4	6.9	3.4	28.7	30.5	38.5	11.1
BTAM(13)MO.3	57.8	7.1	3.4	28.6	30.5	39.3	11.0
BTAM(13)MO.2	61.5	7.2	3.6	29.1	30.6	38.4	11.7
BPAN(13)MO.2	57.9	7.1	3.3	28.4	30.5	39.4	11.0
BPAN(13)MO.3	63.4	6.9	3.4	31.2	31.6	38.5	11.1
RASMAR(13)MO.3	57.3	6.8	3.4	29.0	31.3	38.7	10.9
BHGTAMH(02)1	55.7	8.5	3.3	28.7	31.5	39.5	11.0
EZAMMAR(13)MO.1	62.0	8.2	3.3	28.7	31.4	39.0	11.5
BHG(13)MO.2	59.4	7.3	3.6	29.1	27.2	38.1	11.2
BPAN(02)14	59.4	6.7	3.5	28.7	30.3	38.8	10.5
BPA2002 (check)	59.4	6.7	3.7	28.5	31.3	38.1	11.0
Mean	58.4	7.2	3.5	29.0	30.7	41.1	11.1
$LSD_{0.05}$	6.9	1.1	0.23	0.95	1.7	2.0	0.9
CV%	8.2	10.7	6.7	3.2	5.6	3.6	5.7

*Values for fibre attributes were directly computed in standard deviation, %GOT = percentage ginning out turn

AMMI analysis: The AMMI analysis showed that treatments (genotypes and environments) were significantly high (P<0.000001) indicating the different responses of the genotypes to varying environments under the study (Table 2). Using the AMMI analysis, it provided the partitioning of the main treatment effects into genotypes, environments and interactions (genotype x environment, G x E), and all these showed high significance (P<0.000001). The verification of the model indicated that both principal component axes were considered as important. The principal component axes (IPCA 1 and IPCA 2) were significant at P<0.000001 and P<0.001, respectively. The partitioning of the sum of squares indicated the contribution of genotypes and environments to be 1.85% and 69.34% of the total variation, respectively. The genotype by environment interactions accounted for 9.02% which was bigger than the variation resulting from the genotypic effects. The principal component axes (IPCA 1 and IPCA 2) explained only 54.98% and 24.8% of the interaction, respectively.

This explains that the large sum of squares of environment revealed great influence on the performance of cotton genotypes for seed cotton yield across the locations averaged over the two year cycles. The large proportion of genotype by environment interaction was about five times when compared with the genotypic effects and is considered to result into important consequence. The highly significant genotype by environment interaction clearly indicated that there were variations in the performance of the genotypes across the environments.

The AMMI analysis showed that there was a strong significant difference among genotypes, environments and genotype by environment interactions, indicating the need to evaluate the stability of the genotypes in several environments. The presence of significant differences indicated that the performance of the genotypes was affected by genotype by environment interactions and this resulted in varied seed cotton yield across environments. This further revealed that environment effect was responsible for the bigger part of the variation. This large proportion explained by environments indicated that they were highly diverse and discriminating on the basis of the environment means (Mukoyi *et al*., 2015). These results conform to the findings of Anley *et al*. (2013) that environmental effects are responsible for affecting the genotype performance and are likely to cause consequences in yield performance across locations. Similar studies have been reported to have effects on maize yield (Kaya *et al*., 2002). The presence of this effect is considered a common phenomenon among quantitative traits such as yield that occur in many crops and tends to complicate breeding efforts by plant breeders.

Table 2. AMMI analysis of variance of 16 cotton genotypes in three environments during two cropping year cycles from 2013/2014 to 2014/2015.

Source	Degree of freedom	Sum of square	Mean square	F-ratio	F-prob
Total	383	269341629	703242		
Treatments	95	216027164	2273970	16.01	0.00000
Genotypes	15	4980199	332013	2.34	0.00368
Environments	5	186751104	37350221	44.89	0.00000
Block	18	14975859	831992	5.86	0.00000
Interactions	75	24295860	323945	2.28	0.00000
IPCA 1	19	13357406	703021	4.95	0.00000
IPCA 2	17	6024228	354366	2.50	0.00111
Residuals	39	4914227	126006	0.89	0.66427
Error	270	38338606	141995		

The combined analysis of variance indicated that several genotypes were highly interactive as observed over the two year cycles (Table 3). The yielding potential of cotton genotypes during the two year cycles across the different sites was BTAM(13)MO.2, EZAMMAR(13)MO.1, MS(13)MO.1, BTAM(13)MO.3 and BHG(13)MO.2, and the lowest were on BPMAR6(13)MO.1 and MS(13)MO.2. Using the IPCA 1, the most interactive genotype was MS(13)MO.2 and the least interactive genotype was the commercial check (BPA2002). Considering the IPCA 1 scores, it revealed that the genotypes MS(13)MO.2, BTAM(13)MO.1, MS(13)MO.1, BPMAR6(13)MO.1 and BPAN(13)MO.3 were unstable to all environments. However, genotypes MS(13)MO.1 and BTAM(13)MO.1were relatively adapted to high yielding favourable environments. The genotypes adapted to relatively low yielding environments and stable when IPCA 1 scores were considered included BPAN(13)MO.2 and BPAN(02)14. The results also indicated that MS(13)MO.2 and BPMAR6(13)MO.1 were adapted to low yielding environments but unstable. Using the IPCA 1 scores, the relatively stable and high yielding genotypes were BPA 2002 and BHG(13)MO.2. Yan and Rajcan (2002) have reported similar findings on other crops like soybean. These results show that principal components (IPAC 1 and IPAC 2) can be used to predict the accuracy of the AMMI model and therefore, were considered for explaining the results.

Table 3. Mean seed cotton yield and interaction scores of 16 cotton genotypes across two year cycles of 2013/2014 and 2014/2015.

Genotype	Seed cotton yield (kg/ha)	IPCA 1	IPCA 2
BHGMAR6(13)MO.1	1765	8.87362	5.33842
BPAN(13)MO.1	1704	-7.62151	16.79993
MS(13)MO.1	1838	-15.52944	-22.26861
MS(13)MO.2	1567	-24.230361	7.69511
BPMAR6(13)MO.1	1422	-14.18027	-0.96739
BTAM(13)MO.1	1794	18.38375	-5.73576
BTAM(13)MO.3	1824	3.54794	-7.78169
BTAM(13)MO.2	1883	8.80387	3.19490
BPAN(13)MO.2	1636	1.37857	0.68074
BPAN(13)MO.3	1679	11.87557	-0.15882
RASMAR(13)MO.3	1738	-5.271563	6.34911
BHGTAMH(02)1	1685	6.13067	9.42341
EZAMMAR(13)MO.1	1839	4.21563	-2.56920
BHG(13)MO.2	1818	1.06511	0.68251
BPAN(02)14	1702	2.43100	0.27335
BPA2002 (check)	1777	0.12765	-10.95601

The results showed that some of the environments were highly interactive with Serere in the first year cycle (Serere-1) with the highest IPCA 1 score of 38.1 (Table 4). The least interactive environment was observed with Serere (Serere-2) in the second year cycle with IPCA 1 score of 0.3. The highest seed cotton yield across the genotypes was at Serere and Lira during the second year cycle. The lowest seed cotton yield was observed at Arua during both first and second year cycles.

Table 4. Environment means of seed cotton yields, IPCA 1 and IPCA 2 scores across cotton genotypes.

Environment	Seed cotton yield (kg/ha)	Site mean (kg/ha)	IPCA 1	IPCA 2
Arua-1	836	925	-8.27861	5.42852
Arua-2	1014		-9.65991	5.93594
Lira-1	1346	1847	-9.82011	19.53924
Lira-2	2348		-10.67093	-10.44895
Serere-1	2159	2417	38.14651	4.97706
Serere-2	2675		0.28305	-25.43182

Suffixes 1 and 2 represents year cycles 2013/2014 and 2014/2015, respectively.

The results of the average seed cotton yields for the 16 cotton genotypes at the different sites showed significant ($P<0.001$) variation across sites averaged over the two year cycles (Table 5). Arua attained the lowest overall seed cotton yield, while Serere attained the highest overall seed cotton yield. There was also significant ($P<0.001$) differences observed among the genotypes across sites averaged over years, with six genotypes yielding higher than the check. The mean seed cotton yield for all the genotypes was highest at Serere located in the eastern region of Uganda averaged over the two year cycles. Serere showed high positive interaction based on IPAC 1 during the first year period but a low interaction during the second year period. This is due to lack of consistency of some genotypes in performance in this location during the two year periods, indicating relatively unstable in spite of high yielding potential. This may probably indicate that performance of the genotypes is influenced by the amount of rainfall received in the location, and yet flowering and boll formation are critical stages requiring sufficient rainfall. Similar observations were made in

other locations where the second year period gave good yield performance compared to the first year period. Variations in yield in the two year periods could also be attributed to other factors such as cropping system, soil fertility gradient, temperature, pest and disease pressure. Similar findings have been documented on soybean and pigeon-pea seed yield as being sensitive to environmental differences and attributed this to variations in climatic factors and cropping pattern (Sudaric *et al*., 2006; Wamatu and Thomas, 2002). The low seed cotton yield obtained at Arua could be attributed to relatively erratic weather pattern compared to the other locations, thus affecting flowering and maturing stages of the crop. The cotton genotypes BTAM(13)MO.2, EZAMMAR(13)MO.1, MS(13)MO.1 and BTAM(13)MO.3 tested showed good potential compared to the check (BPA 2002). Most genotypes tested were unstable except (BHG(13)MO.2, BTAM(13)MO.3, EZAMMAR(13)MO.1, BPAN(13)MO.2 and BPAN(02)14) which were relatively stable. These could be selected for further evaluation before considering for DUS testing, and consequently for release for farming communities in Uganda.

Table 5. Mean seed cotton yield of cotton genotypes at three locations averaged over two year cycles from 2013/2014 to 2014/2015.

Genotype	Mean seed cotton yield (kg/ha)			Genotype mean
	Arua	Lira	Serere	
BHGMAR6(13)MO.1	943	1815	2537	1765
BPAN(13)MO.1	980	2038	2095	1704
MS(13)MO.1	954	2102	2458	1838
MS(13)MO.2	1173	1855	1673	1567
BPMAR6(13)MO.1	828	1553	1884	1422
BTAM(13)MO.1	880	1593	2910	1794
BTAM(13)MO.3	957	1926	2589	1824
BTAM(13)MO.2	1001	1929	2719	1883
BPAN(13)MO.2	747	1751	2409	1636
BPAN(13)MO.3	849	1570	2619	1679
RASMAR(13)MO.3	933	2001	2282	1738
BHGTAMH(02)1	911	1856	2288	1685
EZAMMAR(13)MO.1	899	1916	2702	1839
BHG(13)MO.2	847	2093	2513	1818
BPAN(02)14	894	1737	2476	1702
BPA2002 (check)	1004	1811	2516	1777
Site mean	925	1847	2417	1729
$LSD_{0.05}$	591.6			
CV%	24.6			

AMMI biplot was constructed to determine the stability of the 16 cotton genotypes evaluated in six environments as presented in Figure 1. In constructing a plot of genotypes and environment on the same graph, it revealed that the greater the IPCA scores (positive or negative), the more specifically adapted genotype or genotypes is to particular environments. The genotypes G11=BPA2002, G9=BPAN(13)MO.2, G15=BHG(13)MO.2, G16=BPAN(02)14 and G7=BTAM(13)MO.3 showed the lowest genotype by environment interaction as there were low IPCA 1 scores, thus were considered stable genotypes. The genotypes G4=MS(13)MO.2, G6=BTAM(13)MO.1, G3=MS(13)MO.1 and G5=BPMAR6(13) were highly interactive across the two year cycles and IPCA 1 scores were -24.2, 18.4, -15.5 and -14.2, respectively which showed environment specific. The results also indicated that the environments making the greatest contributions were Serere-1 and Lira-2 which had very high positive and negative values and were highly interactive

environments. The less interactive environments were observed with Arua-1, Arua-2 and Lira-1, which provided mean yields relatively below those of other environments. The most favourable environments were Serere-2 and Lira-2 and had positive values. The environment of Lira-2 showed positive interaction with genotype G3=MS(13)MO.1 and negative interaction with G4=MS(13)MO.2, while Serere-2 showed positive interaction with G8=BTAM(13)MO.2, G14=EZA MMAR(13)MO.1 and G7=BTAM(13)MO.3 which were high yielding averaged over the two year cycles. The genotypes G11=BPA2002, G15=BHG(13) MO.2 and G9=BPAN(13)MO.2 revealed minimal sensitivity to environmental and interactive forces. The genotypes that are close to each other perform similarly, while those that are close to the environment shows their good adaptation to that particular environment. For instance, the genotypes G11=BPA2002, G15=BHG(13)MO.2, G9=BPAN(13)MO.2, G16=BPAN (02)14, G7=BTAM(13)MO.3and G14=EZAM MAR(13) MO.1 indicated the same performance as they are close to each other.

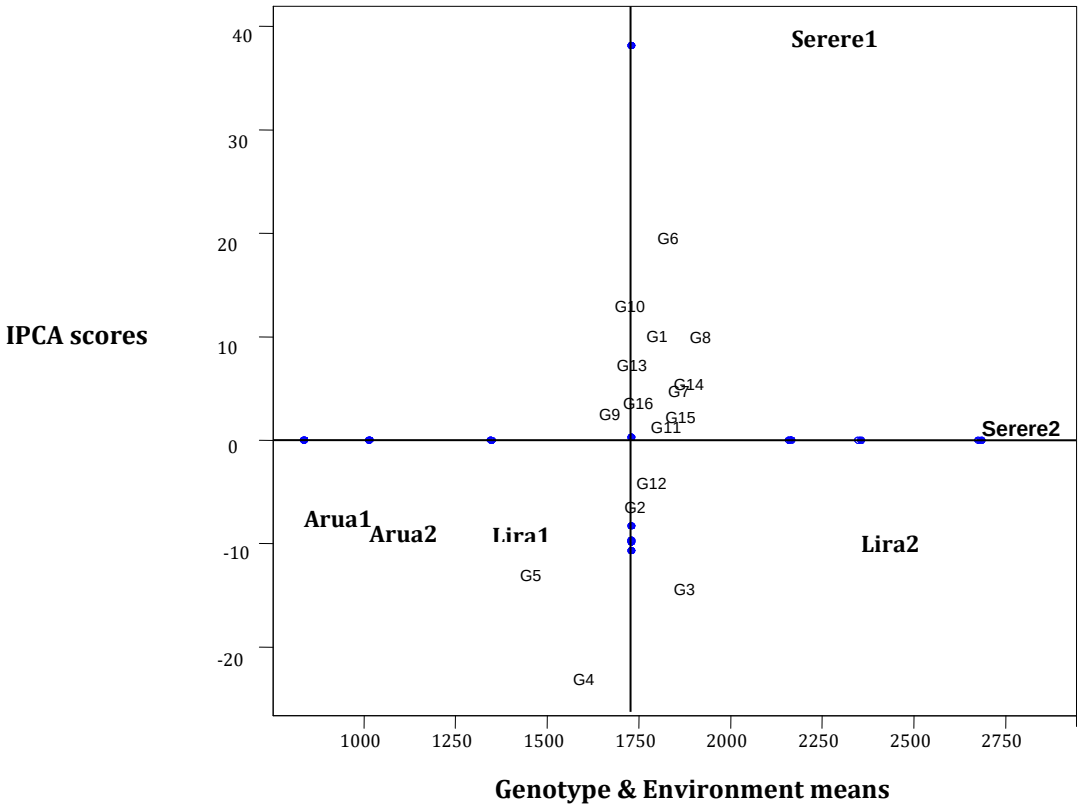

Figure 1. AMMI biplot for seed cotton yield showing IPCA 1 scores plotted against genotype and environment during 2013/2014 and 2014/2015 year cycles. Where: G1= BHGMAR6(13)MO.1, G2= BPAN(13)MO.1, G3= MS(13)MO.1, G4= MS(13)MO.2, G5= BPMAR6(13)MO.1, G6= BTAM(13)MO.1, G7= BTAM(13)MO.3, G8= BTAM(13)MO.2, G9= BPAN(13) MO.2, G10= BPAN(13)MO.3, G11= BPA2002, G12= RASMAR(13)MO.3, G13= BHGTAMH(02)1, G14= EZAMMAR(13) MO.1, G15= BHG(13)MO.2, G16= BPAN(02)14.

Assessing GGE Biplot analysis: The GGE biplots were conducted for the mega-environments and this was compared across the year cycles. The principal components of PC1 and PC2 when plotted, contributed 74.89% of the total variations of GGE for the seed cotton yield across the year cycles of 2013/2014 and 2014/2015 (Figure 2). The six environments were grouped into three mega-environments in which Serere-1 was in one environment and the winning genotype was G6=BTAM(13)MO.1, Serere-2 and Lira-2 shared the

same environment and the winning genotype was G3=MS(13)MO.1 while the other environments that constituted Arua-1, Arua-2 and Lira-1had the winning genotypes G2=BPAN(13)MO.1 and G4=MS(13)MO.2. The environments that tend to be close to the centre are considered as ideal test environments. The environment represented by Serere-2 was identified as ideal test environment as it falls in the innermost concentric rings (Figure 3), while Lira-2 and Serere-1 are fairly good ideal test environments. However, the environments Lira-1 and Serere-1 that are away from the centre are considered as diverse environments because they are far from each other (Figure 3). It was considered that the environments Serere-2, Serere-1 and Lira-2 are ideal test environments in discriminating and representativeness manner. In developing adapted cotton varieties, the concept of mega-environment has been proposed and using the GGE biplot, resulted in identifying three distinct mega-environments where cotton trials were evaluated during the two year periods. The use of GGE in explaining the principal components of PC1 and PC2 clearly provided an indication of their suitability for analysis of environments in the trials. The identification of distinct mega-environments showed that the main mega-environment and second mega-environment still shared the same niche and weather pattern, while the small mega-environment varied with other mega-environment because of the differences in the climatic conditions and soil types which is likely to affect seed cotton yield performance. The GGE biplot provides an effective statistical analysis approach for analysing the effects of genotype by environment interaction in crop test locations (Yan *et al*., 2000; 2001). However, test environments are dynamic factors that fluctuate considerably between years (Yan, 2015). When using GGE biplot for genotype by environment interaction and define ecological locations for planting genotypes, it is necessary to perform analysis based on test data from multi-years and locations (Yan, 2015). The ideal test locations demonstrate high efficiency in selecting genotypes with a wide adaptability and genotypes selected from ideal environments have an outstanding average performance with wide adaptation.

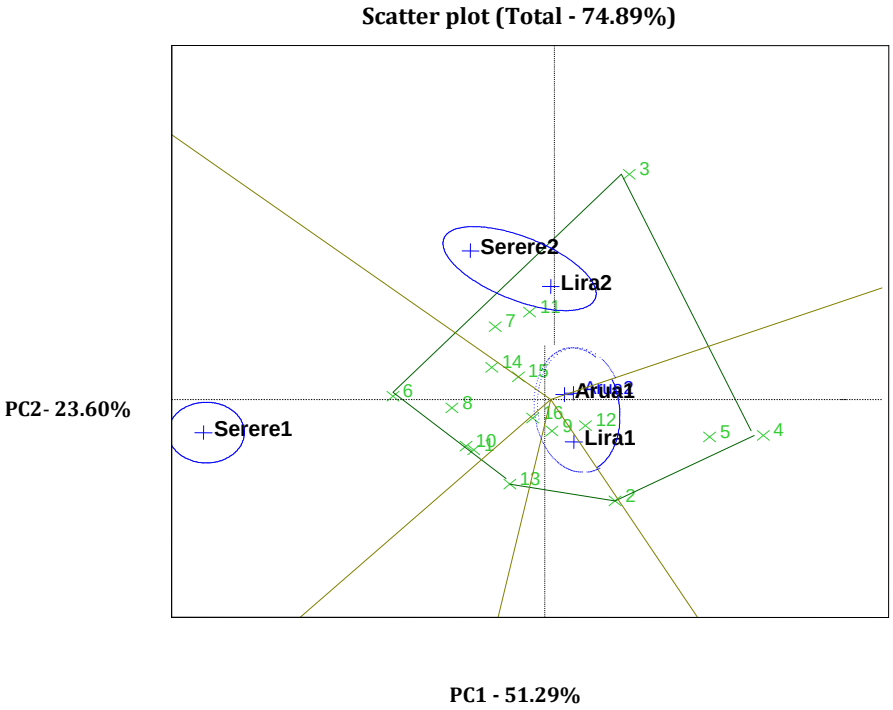

Figure 2. GGE biplots based on environment focused showing "winning genotypes" for three mega-environments for seed cotton yield at six environments tested during the two year cycles of 2013/2014 and 2014/2015 in cotton growing zones in Uganda.

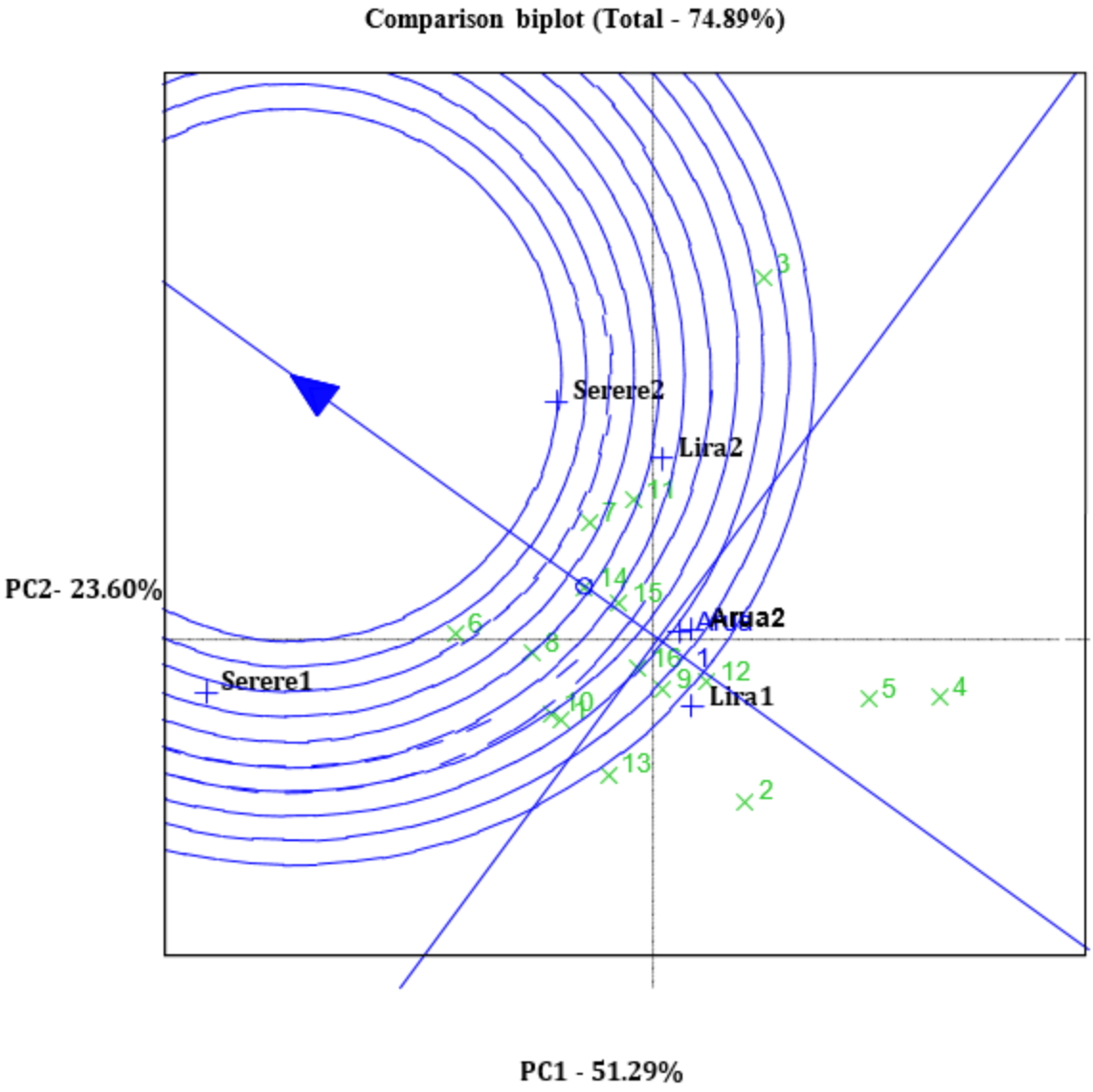

Figure 3. GGE biplots showing environment comparison of the average environment for seed cotton yield of 16 cotton genotypes (as indicated in figures) at six testing environments across two year cycles of 2013/2014 and 2014/2015.

Discriminating test environments, accurately resolve genotype differences; thus providing the necessary information for selection by plant breeders (Tukamuhabwa *et al*., 2012). Mukoyi *et al*. (2015) have shown similar findings for ideal test environment as one which could be discriminating of the genotypes and representative of the mega-environment because such sites can be used for early generation screening of the experimental lines while discriminating sites can be used for selecting specifically adapted varieties in the mega-environment. Considering the test location at Lira-1 is highly discriminating but not representative and therefore, it can be used as a culling environment to quickly eliminate unstable genotypes in regard to performance during the selection stages of evaluation (Yan and Kang, 2003). This information is relevant to plant breeders intending to evaluate the advanced experimental materials in several multi-location trials as some may give inaccurate results because of their low discriminating capability and lack of representativeness considering the costs in terms of time and resources likely to be incurred (Zeng *et al*., 2014; Mukoyi *et al*., 2015).

CONCLUSION

The productive parts associated with high boll weight, lint index and seed weight are important contributors of the cotton genotypes in the performance of seed cotton yield as well as fibre characteristics. It is important that great effort could be made to enhance the performance of the genotypes since breeders tend to base their emphasis on genotypes that show good traits. The cotton genotypes that showed good performance on the basis of these traits were MS(13)MO.1, MS(13)MO.2, EZAMMAR(13)MO.1, BPAN(13)MO.3, BHGTAMH(O2)1 and BTAM(13)MO.2. Using both the AMMI and GGE biplot among the interactive factors namely environment and genotype by environment interaction showed the greatest effect on seed cotton yield. Based on the GGE biplot, three mega-environments were identified which represented; 1) Arua-1, Arua-2 and Lira-1, 2) Serere-2 and Lira-2 and 3) Serere-1. In this study, Serere-2, Serere-1 and Lira-2 were identified as good ideal test environments for the selection of widely adaptable high yielding cotton genotypes, whereas Lira-1, Arua-1 and Arua-2 were undesirable environments because they don't provide any information about the genotype performance as they are so close to each other. Generally, Lira-1 is considered as discriminating site and can be recommended as important testing sites before a new variety is approved for release. Based on the overall results, genotypes BHG(13)MO.2, BTAM(13)MO.3, EZAMMAR(13)MO.1, BPAN(13)MO.2 and BPAN(02)14 were considered as ideal genotypes including the check (BPA 2002), and were relatively stable and adaptable across locations over the two year cycles. Five cotton genotypes produced higher seed cotton yield than the other genotypes including the check with the genotype BTAM(13)MO.3 attaining the highest seed cotton yield.

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