International Journal of Agricultural Sciences ISSN: 2167-0447 Vol. 4 (4), pp. 157-165, April, 2014. Available online at www.internationalscholarsjournals.org © International Scholars Journals

Full Length Research Paper

Adaptability and Stability studies of introduced Kenaf cultivars for fiber yield using GGE biplots in different environments of Ethiopia

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Accepted 01 November, 2013

An experiment to study adaptability and stability of introduced kenaf (*Hibiscus cannabinus*) cultivars for fiber yield was undertaken at different environments of Ethiopia in the 2011 main cropping season. Seven kenaf commercial cultivars introduced from Israeli and USA along with one local check were grown in randomized complete block design with four replicates. The combined analysis of variance over environments showed kenaf fiber yield was significantly affected by environments (E), genotypes (G) and genotype x environment (GE) interactions. The first two principal components (PC1 and PC2) of the GGE explained 88.3% of the sum of squares using environment standardized model. GG-2 from Israeli and the local check had the highest mean fiber yield in that order. However, the local check was relatively most unstable compared with the rest of the genotypes. GG-2 showed both highest kenaf fiber mean yield and stability performance and also was the winner in four of the five test environments. Hence, it could be considered as most adaptable and stable cultivar. Test environments, Pawe and Awassa were the most discriminating of the genotypes and representative of all other test environments.

Key words: Fiber yield, GGE biplot, Hibiscus cannabinus, stability, Ethiopia.

INTRODUCTION

Kenaf (Hibiscus cannabinus) is an annual herbaceous plant grown for the soft and quality fiber found in its stem. It is a fast growing plant which grows to a height of 2-4 meters, depending on the type of variety, environmental factors and management practices in general (Danalatos and Archontoulis, 2010). It is native of east central Africa where it has been grown for several thousand years (Liu and Labuschagne, 2009).

The importance of Kenaf fiber in Ethiopia was realized on several occasions since 1976 when the National Fiber Works Corporation organized a workshop in Addis Ababa for the first time and created a forum for Researchers, development workers and Processors to come together and deliberate in depth regarding increased production of Kenaf in Ethiopia.

Ahead of this time till now, however, farmers in the north western part of the country especially in Metekel area where different wild forms of the crop is still abundant, have been using kenaf fiber for traditional materials like rope and different packaging materials. Presently, there is only one company (G-Seven Trading and Industry PLC) who is the sole producer of different natural fiber products in the country. The company owned two factories and these factories use Jute, Sisal and Enset (Domestic sources) fiber as a raw material for the manufacturing of sacks, ropes, twines and other packaging materials and at the moment more than 90% of the raw material is being imported from abroad (Personal communication, the company). The ever increasing demand of the company's product by its customers forced the company to increase its production capacity, efficiency and market competency to a level that meets the customers demand. To this effect, the company assessed the different options and realized that the country's kenaf production potential as one sound option.

Thus, the company presented an official request to the research system of the country to access improved and adaptable cultivars of kenaf to different potential growing

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environments of the country. Although research on Kenaf in Ethiopia was embarked in the early 1980's, at Werer agricultural research center and the efforts to evaluate and release improved varieties were continued until some years back. No single improved variety of kenaf has been officially registered and/or released in the country. In addition, the local cultivar is a low yielder and most importantly unstable across growing environments in the country. This scenario urged both the company and the research system to bring short term viable solution and so agreed to import commercial kenaf cultivars from Israeli and USA and see their stability and adaptability under Ethiopian condition.Crop yield fluctuates due to suitability of varieties to different growing seasons or conditions. A specific genotype does not always exhibit the same phenotypic characteristics under all environments and different genotypes respond differently to a specific environment. This is attributed to Genotype x Environment Interaction (GE). Understanding GE is necessary to accurately determine stability of genotypes (Sabaghnia et al., 2008). The GE structure is an important aspect of both plant breeding programs and the introduction of new improved crop cultivars as yield stability analysis (Neacşu, 2011). Generally, adaptable varieties are those cultivars that can express stable genetic potential across different growing environments.

Numerous methodologies have been proposed and used to consider genotype by environment interaction and its relationship with adaptability and stability. In the recent literatures, the use of AMMI (Additive main effect and multiplicative interaction) (Gauch, 2006; Gauch and Zobel, 1988; Zobel et al., 1988) and GGE (Genotype plus Genotype x Environment interaction) proposed by (Yan et al., 2000) models have been emphasized for multi environment trial data. However, GGE best fits for mega-environment analysis (like 'Which-won-where' pattern), genotype evaluation (mean versus stability) and test environment evaluation which provide discriminating power versus representativeness (Yan et al., 2007). GGE has been recognized and implemented as useful method to analyse and visualize the pattern of genotype x environment interaction in multi environment cultivar evaluation of different crops including wheat, maize, soybean and oilseeds (Asfaw et al., 2009; Brar et al., 2010; Fan et al.,2007; Yan et al., 2000)

The aims of this study were to evaluate the adaptability and stability of introduced kenaf cultivars under different growing environments of Ethiopia and examine the relationship among test environments in genotype discrimination of kenaf.

MATERIALS AND METHODS

The experiment was conducted at five locations with different environments in Ethiopia: Pawe, Assosa, Merawi, Awassa, and Werer (Table 1) in 2011 main growing season. Seven introduced cultivars, four from Israeli and three from Mississippi, USA along with one local check (Table 2), were grown in randomized complete block design with four replicates. A plot with 6m long and 4.5m width was used. Spacing between plants and rows were 10 and 90 cm, respectively. Standard agronomic and plant protection treatments were used uniformly across the plots for the duration of the experiment.

Fiber yield was recorded on 30 randomly selected plants taken from three central rows (10 plants from each row) to avoid boarder effects. It was measured after the stocks have cut above the ground, defoliated and sun dried, and stayed in a retting tank for about 15 days, and finally the fiber was easily taken off from the core, washed and sun dried.

The data were subjected to combined analysis of variance using SAS GLM (SAS, 2004) to examine the effects of environment (E), genotype (G), and their interaction (GE) variances, and existence of significant interaction variance (GE) justify further partitioning of this variance component. Further partitioning and analysis of GE was computed using the GGE model (Yan, 2001). The GGE biplot was constructed using the first two principal components (PC1 and PC2) derived from subjecting environment centered yield data (Yan et al., 2000). The GGE model used was:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \qquad [1]$$

Where Y_{ij} is measured mean (DBH) of genotype $i(=1,2,\ldots.,n)$ in environment $j(=1,2\ldots,m)$, μ is the grand mean, β_j is the main effect of environment j, $\mu + \beta_j$ being the mean yield across all genotypes in environment j, λ_1 and λ_2 are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively, ξ_{i1} and ξ_{i2} are eigenvectors of genotype I for PC1 and PC2, respectively, η_{1j} and η_{2j} are eigenvectors of environment j for PC1 and PC2, respectively, ε_{ij} is the residual associated with genotype i in environment j.

PC1 and PC2 eigenvectors cannot be plotted directly to construct a meaningful biplot before the singular values are partitioned in to the genotype and environment eigenvectors. Singular value partitioning was implemented by,

$$g_{i1} = \lambda_1^{f_1} \xi_{i1} \; and \; e_{ij} = \lambda_1^{1-f_1} \eta_{ij} \qquad [2]$$

Where f_1 is the portion factor for PC_1. The f_1 can range between 0 and 1. To visualize relationship among genotypes, the GGE biplot based on genotype metric (that is f=1; S.V.P=1) is appropriate and environment metric (f=0; S.V.P=2) GGE biplot is important to visualize relationship among environments. So the following formula from equation [1] was formulated to generate the GGE biplot:

$$Y_{ij} - \mu - \beta_j = g_{i1} e_{1j} + g_{12} e_{2j} + \varepsilon_{ij} \qquad [3]$$

Table 1. Description of test locations.

Location	**Altitude (masl*)**	**Latitude**	**Longitude**	**Annual RF(mm)****	**Mean min T (0^c)**	**Mean max T (0^c)**	**Soil Type**	**Region**
Pawe	1123	11^o09'N	36^o03'E	1588	16.7	32.7	Nitosols	Benishangul Gumuz
Awassa	1720	07^o04'N	38^o04'E	1100	12.4	27.1	clay loam	SNNP
Assosa	1548	10^o02'N	34^o34'E	1130	15.9	29.0	Nitosols	Benishangul Gumuz
Merawi	1960	11^o42'N	37^o17'E	NA	7.75	25.77	NA	Amhara
Werere	740	9^o60'N	40^o9'E	540	19.6	34.4	Vertisol	Afar

masl* = meters above sea level; RF (mm) = Rain fall in millimetre; min T(0^c) = Minimum Temperature in degree Celsius; max T(0^c) = Maximum Temperature in degree Celsius; SNNP = South Nations Nationalities People; NA=Not available.

Table 2. Description of kenaf cultivars used for the experiment.

Cultivar		**Source**
Name	**Code**	
GG-2	G1	Israeli
s-14	G2	Israeli
Whitten	G3	Mississippi, USA
Local	G4	Ethiopia
E-1	G5	Israeli
Everglades-41	G6	Mississippi, USA
TainunGG-2	G7	Mississippi, USA
GG-1	G8	Israeli

If the data were environment-standardized, the common formula to generate the GGE biplot was as follows:

$$\frac{Y_{ij}-\mu-\beta_j}{s_j} = \sum\nolimits_{i=1}^{k} g_{i1}\, e_{1j} + \varepsilon_{ij} \qquad [4]$$

Where s_j is the standard deviation in environment j, $i=1,2,\ldots,k$, g_{i1} and e_{1j} are PC_1 scores for genotype i and environment j, respectively.

In the present study we used environment standardized model, [4].

RESULTS AND DISCUSSION

Combined Analysis of Variance

The combined analysis of variance over environments showed kenaf fiber yield was significantly ($p<0.01$) affected by environments (E), genotypes (G) and genotype x environment (GE) interactions (Table 3). Environment significantly explained about 70.2% of the total sum of the square. This indicated that the environments were diverse. Environment mean fiber yield

Table 3. Summary of the analysis of variance for fiber yield (kgha^{-1}) of 8 kenaf cultivars grown at five environments of Ethiopia in 2011.

Sources of variation	DF	SS	MS	F value	Probability	Explained % of SS
Genotype (G)	7	16808705.2	2401243.6	50.77	<0.0001	15.4
Environment (E)	4	76640067.0	19160016.8	405.1	<0.0001	70.2
Replication (E)	15	1525395.7	101693.0	2.2	0.01	
GE	28	15726188.7	561649	11.9	<0.0001	14.4
Error	105	4966187.4	47297.0			
Total	159	115666544.0				

GE= Genotype x Environment interaction; DF= Degrees of freedom; SS= Sums of square; MS= Means square.

Table 4. Mean fiber yield (kgha^{-1}) of kenaf cultivars tested at five environments of Ethiopia in 2011.

	Environments					
Cultivars	**Pawe**	**Awassa**	**Assosa**	**Merawi**	**Werer**	**Mean**
G1(GG-2)	3988.00	336.94	1501.90	1437.50	658.75	1584.59a
G2(s-14)	1614.80	220.56	701.90	769.90	167.00	694.83d
G3(Whitten)	2184.30	321.53	1043.50	1006.60	205.25	952.24bc
G4(Local)	2849.10	314.75	1004.60	745.10	**736.75**	1130.06b
G5(E-1)	1888.00	251.87	1209.30	716.60	317.75	876.70cd
G6(Everglades-41)	2259.30	329.40	1223.10	516.90	357.25	937.20bc
G7(Tainungg-2)	2073.10	214.68	1025.90	687.10	271.50	854.47cd
G8(GG-1)	688.90	158.26	534.30	360.20	135.00	375.32e
Mean	2193.17ᵃ	268.50d	1030.56b	780.00c	356.16d	925.68

[a]Means with the same letter are not significantly different at the 0.05 probability level based on Tukey's Studentized Range Test; [b]Bolded values are highest fiber yield at each test environments.

ranged from 2193.17 kgha^{-1} at Pawe to 268.50 kgha^{-1} at Awassa (Table 4). As compared to the environment, small portion which is, 15.4% of the total sum of squares was attributed to genotypic effects. Genotype mean fiber yield ranged from 1584.59 kgha^{-1} (GG-2) to 375.32 kgha^{-1} (GG-1) (Table 4). The significance of the interaction component which explained 14.4% of the total sum of the square indicated the best cultivars in one environment are not necessarily the best in another. This justifies the need to consider adaptability and stability into account while recommending promising kenaf cultivars to an environment.

GGE Biplot Analysis

The GGE refers to the genotype main effect (G) and the genotype x environment interaction (GE), which are the two most important sources of variation for cultivar evaluation in a multi environment trials (Yan et al., 2007). A GGE biplot is a biplot that displays the genotypic main effect (G) and genotype by environment interaction (GE) of a genotype-by-environment dataset (Yan et al., 2000). This biplot is specially and perfectly used for mega-environment analysis based on genetic correlation between environment and the which-won-where pattern; test environment evaluation based on their discriminating ability and representativeness; and genotype evaluation based on their mean performance and stability across a mega-environment. The present data set showed 0.996 correlations between the primary effects and the genotypic main effect which is a near perfect correlation that justifies the use of GGE biplot (Crossa et al., 2002; Yan et al., 2000). The first two principal components (PC1 and PC2) of the GGE explained 88.3% of the sum of square with PC1=76.3% and PC2=12% of the GGE sum

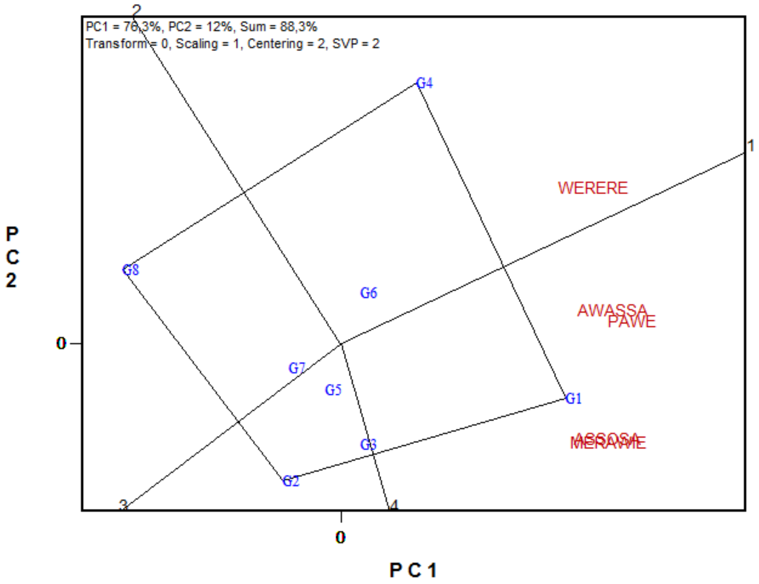

Figure 1. Polygon view of the GGE biplot to show which kenaf cultivar wins where. Vertex genotypes on the polygon are the best at environments whose markers fall in to the respective sector. G1-G8 is codes for kenaf introduced cultivars, while G4 is local check.

of square using environment standardized model.

Mega-environment Analysis

GGE biplot produces best polygons to view or visualize the genotype x environment interaction pattern (Yan and Kang, 2003). Visualization of the 'Which-won-where' pattern in the polygon view is helpful to estimate possible existence of different mega-environments in the target environment (Yan and Rajcan, 2002; Yan et al., 2000; Yan and Tinker, 2006). Figure 1 presents a polygon view of seven introduced and one (G4) local check kenaf cultivars multi environment trial data. With this biplot, a polygon was constructed by connecting the vertex genotypes (located farthest away from the biplot origin in various directions) with straight lines and as a result, the rest of the genotypes placed inside the polygon. PC1 and PC2 together explained 88.3% of the total GGE sum of squares with 76.3% accounted by PC1 and 12% by PC2. Genotypes, G1, G2, G4 and G8 were vertexes of the polygon. These are either best or poorest genotypes in some or all of the test environments as they are located farthest from the origin (Yan and Kang, 2003). From the polygon view of this biplot, genotypes fell in to four sectors and the test environments in to two. The section which contains four out of five test environments had only one genotype (G1) which is also the winner. The second section contains only one test environment (Werer) with two genotypes (G4 and G6) where G4 was the best yielder. The other five genotypes were fall in two different sections where G3, G2 and G5 in one section and G7 and G8 in another, both without test environments. Among the vertex genotypes, G1 and G4 were the winners in which the former won in four and the later in one of the five test environments.

Test Environment Evaluation

Relationship among Test Environments

The GGE biplot of kenaf fiber yield showing relationship among the test environments is presented in figure 2. Lines that connect the biplot origin with environment markers are known as environment vectors and the angle between the vectors of two environments is related to the correlation coefficient between them which is approximated by the cosine of that angle (Yan, 2002). Acute angles indicate a positive correlation, obtuse and right angles show negative and no correlation, respectively (Yan and Kang, 2003). In the biplot, Pawe and Awassa were separated very close together as a group and more similarly, Assosa and Merawi were very close together showing maximum correlation. Werer was a little bit separated alone in relation with others; however, the angle between it and Awassa and/or Pawe is still acute showing positive correlation between them. Generally, in the present study the correlation among all environments was positive as the angle between any two environments is acute.

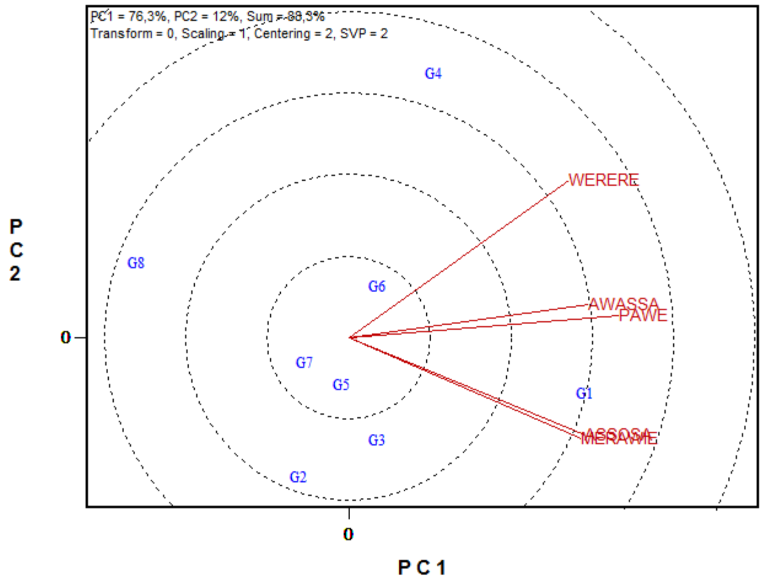

Figure 1. GGE biplot showing relationship among test environments. G1-G8 is codes for kenaf introduced cultivars, while G4 is local check.

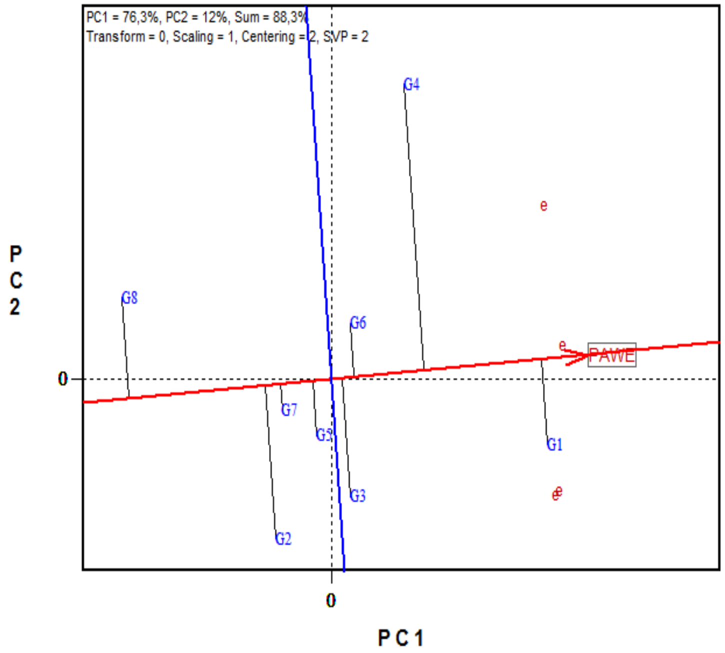

Figure 2. Ranking genotypes relative to Pawe, which is the highest kenaf fiber yielding environment. G1-G8 is codes for introduced kenaf cultivars, while G4 is local check.

Ranking Genotypes Relative to Highest Yielding Environment

The highest yielding environment, Pawe, was used to evaluate the genotypes and ranking of genotypes relative to Pawe is presented in figure 3. A line that passes through the biplot origin and Pawe marker was drawn to make Pawe-axis. A perpendicular line from each genotype towards this axis was also drawn and used to compare the relative yield of the genotypes. The genotypes were ranked based on length of their projections onto Pawe-axis.

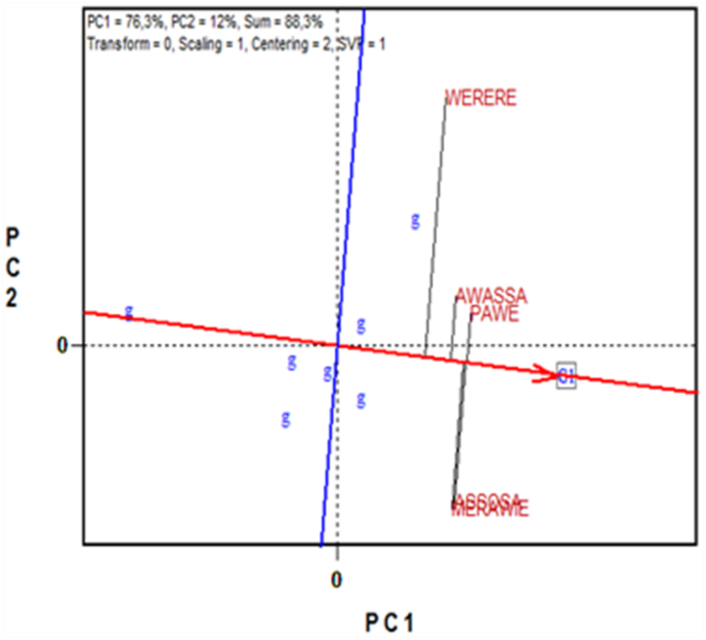

Figure 3. Examining the performance of test environments relative to the highest yielding genotype (G1). G1-G8 is codes for introduced kenaf cultivars, while G4 is local check.

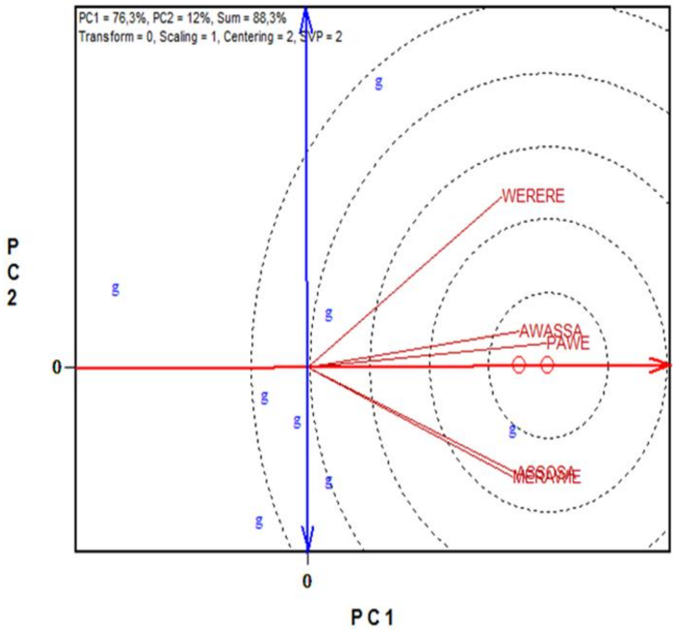

Figure 4. Ranking environments based on both discriminating ability and representativeness of the test environments.

Rank increases as one goes to the positive end (Yan et al., 2000). Hence, genotypes, G1, G4, G6 and G3 had yields above average yield, while genotypes, G5, G7, G2 and G8 yielded below the average performance.

Relative Adaptation of G1, Which is the Best Yielding Genotype

Figure 4 reveals the performance of test environments

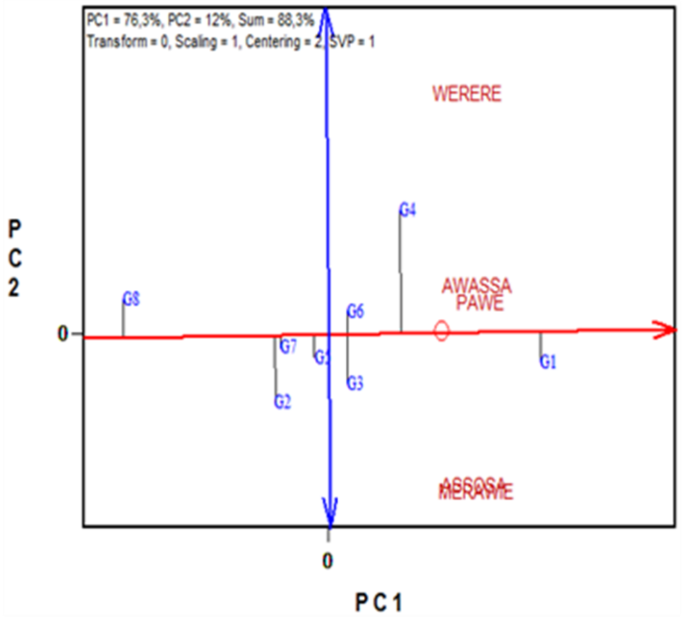

Figure 5. GGE biplot showing ranking of genotypes for both mean yield and stability performance across environments. G1-G8 is codes for introduced kenaf cultivars, while G4 is local check.

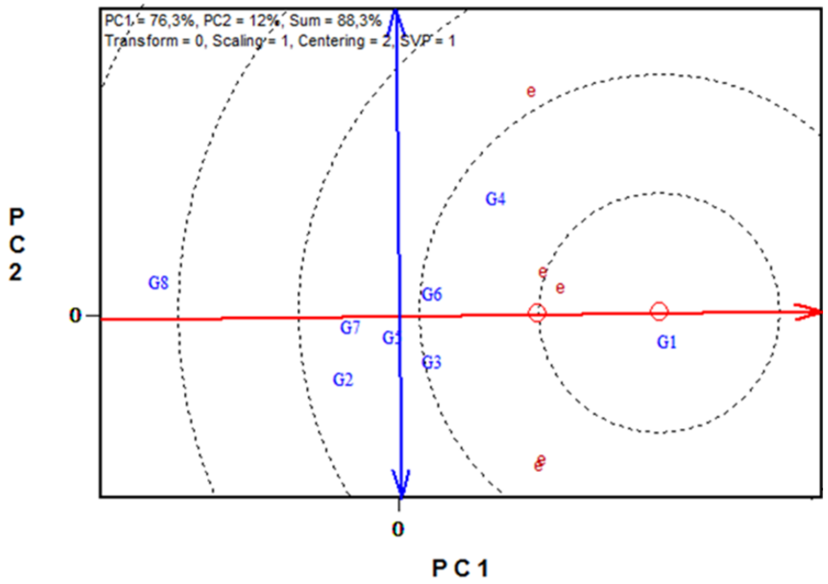

Figure 6. Ranking genotypes based on both mean and stability relative to an ideal genotype. Putting the ideal genotype at the center, concentric circles were drawn to visualize how far each genotype from the ideal genotype is.

relative to the highest yielding genotype (G1). The relative adaptation of G1 was studied by drawing a line that passed through the biplot origin and G1 marker and environments and G1 were ranked along this axis (Yan et al., 2000). The length of environment projections onto the G1 axis assessed the performance of G1 at different environments, relative to other genotypes. Thus, G1 had yields higher than the average in all of the testing environments with the following order from highest to lowest, Pawe, Assosa, Merawi, Awassa and Werer. Moreover, it performed best (the winner) in four of the five testing environments that is except at Werer.

Ranking Environments Relative to an Ideal Environment

Figure 5 illustrates environment ranking based on both discriminating ability and representativeness of the test environments. This view of the GGE biplot is useful to assess how much a test environment is, capable of providing as much information of the differences among the genotypes, representative of the mega-environment and generating unique information about the genotypes. The ideal environment, represented by small circle with an arrow pointing to it, is the most discriminating of the genotypes and representative of all other test environments. Hence, Pawe and Awassa were located very near to the ideal environment and could be considered the most ideal test environments. Moreover, Assosa and Merawi could also be considered desirable test environments for kenaf in Ethiopia.

Genotype Evaluation

Mean Yield and Stability Performance of Genotypes

Ranking of eight kenaf cultivars based on their mean yield and stability performance are presented in figure 6. The line passing through the biplot origin is called the average tester coordinate (ATC) (Yan and Kang, 2003). The double arrow line which is perpendicular to ATC and passes through the origin represents stability of genotypes. The ideal genotypes are those with both high mean yield and stability which in the biplot are close to the origin and with the shortest vector from the ATC. Hence, genotypes 1 and 4 had the highest mean fiber yield in that order and genotype 8 was the poorest. The other genotypes 2, 7 and 5 performed below the grand mean being located left of the double arrow line and genotype 3 and genotype 6 had mean fiber yield above the grand mean appeared right of the double arrow line. Genotype 4 was relatively most unstable compared with the rest of the genotypes. Genotypes 7, 5, 6, 1 and 8 were most stable. The other two (G2 and G3) were moderate in their stability. Genotype 1 showed both highest mean yield and stability performance and could be considered as most adaptable and stable cultivar to be produced by the farmers and other producers.

Genotypes Evaluation Relative to an Ideal Genotype

Ranking of kenaf cultivars based on both mean fiber yield and stability relative to an ideal genotype is presented in figure 7. An ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2003). Thus, in the biplot, an ideal genotype is located at the center of the concentric circle. It is a location with the longest vector of all the genotypes projected from abscissa ATC axis and with nears zero ordinate ATC axis projection. Perfectly, genotype 1 placed itself in the center of the concentric circle and could be considered as an ideal kenaf genotype with the highest mean fiber yield and be most stable across the test environments of Ethiopia. Other genotypes were ranked as G4>G6>G3>G5>G7>G2>G8, where those ranked last were unfavourable as they are most far from the ideal genotype.

CONCLUSION

The results revealed that kenaf fiber yield performance were significantly influenced by environment, genotype and their interaction. GGE biplots were effective enough for analyzing and visualizing the patterns of genotype x environment interaction in a multi environment trial data and hence the relationship and variations in genotypes performance across test environments was clearly examined. Thus, GG-2, a kenaf cultivar introduced from Israeli, showed both the highest mean fiber yield and stability performance across the test environments and could be characterized as an ideal cultivar. Farmers and growers are advised to grow this cultivar. Moreover, GG-2 could be considered as source parent in kenaf breeding programme. Test environments, Pawe and Awassa were the most discriminating of the genotypes and representative of all other test environments.

ACKNOWLEDGMENT

The study was financially supported by G-Seven Trading and Industry PLC. The authors appreciate Ethiopian Institute of Agricultural research and Pawe research center for overall coordination of the trial, provision of necessary research facilities and financial administration. We also highly appreciate and acknowledge the efforts made by respective research staffs at Pawe, Awassa, Assosa, Adet and Werer research centers for field management and data collection during the field trial. We are very grateful to Prof. W. Yan for his kind provision of GGE software.

Abbreviations

ANOVA, analysis of variance; ATC, average tester coordinate; GE, genotype x environment interaction; GGE, genotype and genotype x environment interaction; PC, principal component; masl, meters above sea level.

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