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Comparison and suitability of genotype by environment analysis methods for yield-related traits of pearl millet

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Abstract

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is an important food security and income crop for households living in semi-arid zones in Uganda. However, the genotype by environment interaction, in addition to the several methods used for its assessment, complicates selection of varieties adapted to such semi-arid areas. The objective of this study, therefore, was to compare common methods used to assess stability and adaptability of improved genotypes. Seventy six genotypes were planted in four environments in an alpha experimental design with two replications. Results showed that genotype by environment interactions were significant at p<0.05 for grain yield, days to 50% flowering and 50% physiological maturity, percentage of productive tillers and panicle area. Results further showed inconsistency in ranking of genotypes between methods; although Cultivar Superiority, REML, Yield Stability Index and GGE biplot were consistently correlated and identified high yielding and stable genotypes.

Key words: GGE biplot, grain yield, pearl millet, stability analysis, Uganda

Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is one of the widely grown millets with several food and non-food uses (IFAD, 1999). The crop responds positively to adverse environments that are extremely variable and often associated with erratic and low annual rainfall (Bashir *et al.*, 2014). Despite the adaptability, average productivity of about 600 kg ha^{-1} (Rai *et al.*, 1999) from farmers' fields is low much as relatively high yielding genotypes adapted to low-input and drought-prone environments have been developed (Serraj *et al.*, 2003; Vadez *et al.*, 2012). This is partly because the potential performance of the high-yielding genotypes under marginalised conditions is always obscured by the multiplicative effect of genotype by environment interaction (GEI) (Yan and Racjan, 2002).

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Accordingly, this causes inconsistent performance of genotypes (Alberts, 2004), and thus leading to false selection (Crossa, 1990; Falconer, 1990).

It is in response to these challenges that it is necessary to assess genotypes for adaptability and stability (Becker and Léon, 1988). Equally important is the need to develop appropriate statistical models that have the rigor and accuracy to support selection decisions in case significant GEI exists, and hence identification of a reliable method is important (Yau, 1991).

Several statistical analysis methods have been developed to assess GEI, notable of which are; analysis of variance (ANOVA), environmental variance (S^2i), deviation from regression (S^2_d), Restricted Maximum Likelihood (REML) (Bartlett, 1937), regression coefficient (b_i) (Finlay and Wilkinson, 1963), Wricke's ecovalence (Wi), Eberhart and Russell (1966), Best Linear Unbiased Predictions (BLUP) (Patterson and Thompson, 1971), Tai's (1971) approach, Shukla stability variance (σi^2) (Shukla, 1972), coefficient of determination (r_i^2) (Pinthus, 1973), coefficient of variation (CV) (Francis and Kannenberg, 1978), cultivar superiority (P_i) (Lin and Binns, 1988) and static stability (Becker and Léon, 1988). Some of the most frequently used methods include; Additive Main Effects and Multiplicative Interaction (AMMI) (Gauch, 1988), yield stability index (YSi) (Kang, 1993), AMMI stability value (ASVi) (Purchase, 2000), Genotype and Genotype by Environment (GGE) biplot (Yan and Hunt, 2002) and harmonic mean of the relative performance of genotypic values (MHPRVG) (Resende, 2007). However, most of the methods have deficiencies.

The ANOVA identifies sources of variation due to GEI effect and allows for estimation of variance components used to calculate trait heritability. However, it does not explore the underlying structure within the GEI; making it difficult to establish the true performance of genotypes across environments (Crossa, 1990). The regression approach is widely used (Westcott, 1986; Freeman and Perkins, 1971) but limited in functionality because genotype response to environments is largely under multivariate control; yet regression transforms it into a univariate variable (Lin *et al*., 1986). Crossa (1990) also noted that parameters of regression (mean, slope, and deviation) also make it difficult to identify superior genotypes for particular environments. The YSi has a weakness of weighing strongly on yield, yet the trait is influenced by many factors (Farshadfar *et al*., 2011). Wricke's partition of the interaction is non-orthogonal yet the test is parametric (Freeman and Perkins, 1971). The AMMI models (Gauch, 2006; Gauch *et al*., 2008) combine the ANOVA for the genotype and environment main effects with principal components analysis which helps to obtain further insight into the nature and extent of complex GEI (Alberts, 2004; Gruneberg *et al*., 2005). However, there is difficulty in interpretation of the interaction when there is limited variability accounted for by the first principal component, which could indicate false statistical stability of the genotypes and environments (Lavoranti *et al*., 2007). The AMMI and the GGE biplot combine genotype (G) and genotype by environment (GE) in mega environment evaluation, but the GGE biplot is superior to the AMMI in graphical analysis because it better explains G+GE (Yan *et al*., 2007). The inadequacy and contrasting argument about the best stability and adaptability analysis methods of GEI shows that most probably no stand-alone method exists (Kaya *et al*., 2006). Thus the objective was to assess stability analysis methods for correlation and consistency using traits of improved pearl millet genotypes.

Materials and methods

Test environments and materials

The study was conducted for two rainy seasons which coincided with the second rains of 2012 and first rains of 2013. The evaluation was done in two locations (Kitgum and Serere) and this resulted in four environments. The Kitgum environments (E1 and E2) are located at 03°132 N, 032°472 E, 969 m.a.s.l while the Serere (E3 and E4) environments are located at 01°32'N, 033°27'E, 1140 m.a.s.l. E1 received 391 mm of rainfall in 2012; while E2 received 817 mm of rainfall in 2013. E3 received 499.3 mm of rainfall in 2012; while E4 received 589 mm of rainfall in 2013). The environments were characterised as hot spots for rust disease (Lubadde *et al*., 2014), sandy soils and being semi-arid.

The 76 improved pearl millet genotypes evaluated were replicated twice in a 4 x 19 alpha experimental design. The materials were planted in 8 m x 5 m plots at a spacing of 60 cm x 30 cm. A soil fertility regime recommended for seed production under rain fed conditions was adopted and standard agronomic practices for crop management were used (Khairwal *et al*., 2007).

Data collection and analysis

Data were collected on at least 36 randomly selected plants per plot, using the 'Descriptors of Pearl Millet' (IBPGR and ICRISAT, 1993). The panicle area (PAR) was calculated as 3.14 x L x W; where L and W were panicle length and width, respectively. Data were also collected on: grain yield (GY in kg ha^{-1}) at 50% physiological maturity after threshing, days to 50% flowering (FLO_{50}) at plot level when 50% of the plants have developed stigmas, days to 50% physiological maturity (PSM_{50}) and percentage of productive tillers (PRO) at plot level. Data analysis was conducted using the Integrated Breeding Platform for Breeding Management System version 3.0.8 (IBP-BMS, 2014) and GenStat 15th Edition (Payne *et al*., 2012). The performance and ranking of genotypes was used to compare the consistency of the GEI methods. The models and computations for ANOVA, REML and AMMI indices for calculating ASVi were computed using GenStat 15 while the YSi, Wricke's ecovalence, Finlay and Wilkinson, static stability, cultivar superiority and were computed using IBP-BMS 3.0.8.

Results

Assessing GEI effect using stability indices
The ANOVA showed that the main effects of environments were significant ($p< 0.05$) on GY and PSM_{50} and highly significant ($p<0.001$) for FLO50, PAR and PRO. The main effects of the genotypes were also significantly ($p<0.05$) important for the yield-related traits except PAR. In addition, (GEI) was significant ($p<0.05$) for all the test traits.

Results for stability and GEI assessment for twenty most stable genotypes are shown in Tables 1- 8. Generally, Cultivar superiority, REML, Yield stability index (YSi) and GGE biplot identified highly performing genotypes, as being stable with a significant positive correlation observed for most traits (Table 1) and among the methods (Table 2). A

Table 1. Correlation between highly correlated stability methods and traits

Traits	Pi+REML	Pi+GGEbiplot	Pi+YSi	REML+YSi
GY	0.9**	0.5*	0.5*	0.5*
FLO_{50}	-0.8**	0.5*	-0.5*	0.5*
PSM_{50}	-0.9**	0.5*	-0.6*	0.6**
PRO	0.9**	-0.0ns	0.8**	0.7**
PAR	0.6*	-0.0ns	0.1ns	-0.1ns

Traits: GY = Grain yield, FLO_{50} = Days to 50% flowering, PSM_{50} = Days to 50% physiological maturity, PRO = Percentage of productive tillers, PAR = Panicle area
Methods: Pi = Cultivar superiority, REML = Restricted maximum likelihood, YSi = Yield stability index

Table 2. Correlation among stability analysis methods for grain yield

Methods	Wi	Static stability	Pi	REML	ASVi	GGE biplot	YSi
bi	-0.1	0.3	-0.1	-0.0	-0.2	0.2	-0.2
Wi	1.0	-0.0	0.0	0.1	-0.2	0.5*	-0.2
Static stability		1.0	-0.5*	-0.6*	0.3	-0.4	-0.6*
Pi			1.0	0.9**	0.1	0.5*	0.5*
REML				1.0	-0.0	0.5*	0.5*
ASVi					1.0	0.0	-0.3
GGE biplot						1.0	0.1

Methods: bi = Finlay and Wilkinson, Wi = Wricke's ecovalence, Pi = Cultivar superiority, REML = Restricted maximum likelihood, ASVi = Ammi stability value, YSi = Yield stability index

high correlation was observed between Cultivar superiority and REML, Cultivar superiority and GGE biplot, Cultivar Superiority and YSi, REML and YSi and Finley and Wilkenson and Static stability for all the traits. However, significant negative correlation was observed between Finley and Wilkenson and Static stability for most traits except grain yield.

Some consistency in genotype ranking was observed between Finley and Wilkinson and Static stability then Wricke's ecovalence, static stability and ASVi for all the traits while a similar pattern was observed between Cultivar superiority and REML for grain yield, panicle area and percentage of productive tillers. Similarity was also observed between Wricke's ecovalence and GGE biplot for days to 50% physiological maturity and percentage of productive tillers.

Grain yield (GY)

Results of ranking of the twenty most stable genotypes for grain yield are shown in Table 3. Generally, differences in the ranking of the genotypes existed for all the seven stability analysis methods with Finley and Wilkinson, Wrike's ecovalence, static stability and ASVi identifying low

Table 3. Genotype by environment analysis for grain yield (kg ha^{-1})

Rank	Finley and Wilkenson		Wricke's ecovalence		Static stability		Cultivar superiority		REML		ASVi		GGE biplot		Yield stability index	
	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means
1	1x8	1820	2	1812	2x12	1482	6x10	2506	6x10	2324	2	1812	5x12	2322	3x11	2413
2	1x16	1585	8	2005	6x16	1306	3x11	2413	3x11	2258	6x16	1306	6x8	2387	3x12	2257
3	1x9	1977	6	2054	1x16	1585	4x16	2344	6x8	2210	1x11	1427	1x14	2355	6	2054
4	4x12	1712	9	2027	4x12	1712	6x8	2387	5x12	2183	3x11	2413	5x8	2187	8	2005
5	6x16	1306	12	1878	1x11	1427	3x12	2257	1x14	2173	8	2005	6x7	2149	9	2027
6	2x12	1482	3x9	1797	1x12	1518	1x14	2355	6x9	2172	6	2054	4x11	2100	6x10	2506
7	2x15	2169	4x7	1903	16	1799	5x15	2230	4x16	2171	2x12	1482	4x14	2054	4	1952
8	4x13	2026	4	1952	5x16	1621	5x12	2322	3x12	2154	3x9	1797	5x13	2210	4x16	2344
9	1x7	1671	3x7	1784	1	1787	6x9	2371	5x13	2102	4x10	1680	6x11	2030	6x8	2387
10	1x13	1906	4x10	1680	3x14	1642	6x7	2149	5x8	2076	12	1878	2x11	1971	6x7	2149
11	2x7	1723	13	1907	4x7	1903	2x15	2169	1x15	2071	4x7	1903	4x8	2003	4x7	1903
12	3x16	1923	16	1799	4x10	1680	4x11	2100	6x12	2057	3x12	2257	6x12	2229	2	1812
13	6x14	2003	2x9	1822	7	1869	5x8	2187	5x15	2046	9	2027	3x11	2413	12	1878
14	3x14	1642	3	1864	4	1952	6	2054	4x11	2041	4	1952	1x16	1585	5	1993
15	4x15	1821	3x12	2257	4x15	1821	9	2027	6x7	2023	3x7	1784	6x10	2506	1x15	2027
16	5x15	2230	1	1787	2	1812	6x14	2003	2x15	2011	3x13	1572	5x10	1938	15	1965
17	1x12	1518	10	1855	14	1922	8	2005	5x9	2002	16	1799	11	1929	13	1907
18	6x13	1914	7	1869	3x13	1572	4x14	2054	6	1992	3x10	1463	4x9	1904	5x12	2322
19	1x11	1427	14	1922	3x10	1463	15	1965	4x14	1988	1x12	1518	5	1984	4x11	2100
20	5x16	1621	15	1965	3x9	1797	5x13	2210	4x8	1976	1	1787	14	1917	14	1922

1 = ICMV3771, 2 = Manganara, 3 = Okashana2, 4 = ITMV8001, 5 = SDMV94001, 6 = Shibe, 7 = Exbornu, 8 = CIVT9206, 9 = GGB8735, 10 = ICMV221, 11 = ICMV221white, 12 = KatPM1, 13 = Okoa, 14 = SDMV96053, 15 = Sosank, 16 = Okollo

Table 4. Genotype by environment analysis for days to 50% flowering

Rank	Finley and Wilkenson		Wricke's ecovalence		Static stability		Cultivar superiority		REML		ASVi		GGE biplot		Yield stability index	
	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means
1	5x13	57.5	12	56.4	4x14	55.9	5x7	62.8	2x11	53.1	2x14	54.6	6x8	59.9	2x14	54.6
2	4x14	55.9	10	57.7	13	57.3	4x15	61.4	1x9	53.6	2x16	56.5	4x13	60.3	11	55.8
3	1x13	58.0	11	55.8	5x10	58.3	3x16	60.4	1x11	54.6	12	56.4	4x16	59.9	2x10	55.6
4	2x12	55.5	1x7	56.3	4x12	59.4	4x8	60.9	3x12	54.6	1x7	56.3	4x10	60.6	1x7	56.3
5	4x10	60.6	6	57.5	6x14	55.6	6x8	59.9	2x12	54.9	4x11	57.5	4x8	60.9	1x10	54.8
6	3x10	56.3	4	58.6	2x7	58.6	4x10	60.6	2x14	54.9	10	57.7	1x16	60.0	12	56.4
7	5x9	55.8	4x11	57.5	10	57.7	4x13	60.3	6x13	55.0	13	57.3	1x14	58.4	2x16	56.5
8	4x12	59.4	2x16	56.5	5x9	55.8	2x15	59.1	1x10	55.1	8	57.5	6x10	58.4	6x14	55.6
9	3x11	56.1	7	58.2	12	56.4	1x16	60.0	2x9	55.6	11	55.8	5x16	57.9	5x12	55.9
10	5x10	58.3	6x16	57.6	3x7	56.5	6x15	59.8	3x8	55.7	4	58.6	11	55.3	6x12	56.6
11	3x13	55.9	1	57.8	3x14	58.9	3x14	58.9	2x10	55.8	6x12	56.6	1x15	58.0	13	57.3
12	5x7	62.8	8	57.5	1x10	54.8	1x12	58.6	6x14	55.8	6	57.5	2x15	57.5	4x11	57.5
13	1x12	58.6	16	58.5	11	55.8	4x16	59.9	5x8	56.0	1x16	60.0	1x12	58.6	2x9	54.8
14	13	57.3	2x10	55.6	9	57.2	4x12	59.4	6x11	56.0	2x10	55.6	5x13	57.5	3	56.3
15	5x11	56.1	1x10	54.8	1	57.8	3x9	57.9	11	56.0	16	58.5	6x9	57.6	3x12	54.1
16	4x13	60.3	13	57.3	5x11	56.1	2x7	58.6	4x14	56.0	6x16	57.6	16	58.7	5x8	55.4
17	4x15	61.4	5x12	55.9	6x9	57.6	6x10	58.4	5x12	56.1	2x7	58.6	3x14	58.9	6	57.5
18	6x13	56.4	6x14	55.6	3x13	55.9	4x7	60.9	3x7	56.2	7	58.2	14	56.6	8	57.5
19	3x7	56.5	6x11	56.5	6x16	57.6	16	58.5	1x13	56.2	1	57.8	1x8	57.4	4x14	55.9
20	6x14	55.6	1x15	58.0	3x11	56.1	15	58.3	1x7	56.2	6x14	55.6	2x11	51.6	4x9	56.1

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Table 5. Genotype by environment analysis for days to 50% physiological maturity

Rank	Finley and Wilkenson		Wricke's ecovalence		Static stability		Cultivar superiority		REML		ASVi		GGE biplot		Yield stability index	
	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means
1	1x13	84.3	12	86.2	4x14	86.3	4x16	95.3	2x11	82.0	13	87.7	4x10	91.3	2x9	81.6
2	5x13	88.6	4x11	87.1	3x7	87.4	4x7	94.5	2x9	82.2	12	86.2	4	90.9	1x10	83.5
3	5x10	89.5	6	87.5	6x15	89.6	4x15	92.8	3x12	82.8	6	87.5	3	87.2	6x14	83.4
4	3x14	89.8	11	85.2	1x10	83.5	3x16	91.5	1x9	83.0	4x11	87.1	2x12	84.4	11	85.2
5	4x14	86.3	5x11	83.5	5x10	89.5	5x7	93.0	1x13	83.0	11	85.2	4x12	91.0	12	86.2
6	6x16	87.4	15	88.2	6x14	83.4	4x12	91.0	6x14	83.2	3x8	86.6	5x12	84.9	5x11	83.5
7	6x9	88.0	16	90.1	6x16	87.4	4x8	91.9	1x11	83.3	8	88.0	12	86.8	2x11	81.5
8	3x7	87.4	1	87.7	6x9	88.0	4x10	91.3	5x11	83.4	1x10	83.5	11	84.3	3x8	86.6
9	6x15	89.6	10	87.9	10	87.9	6x8	91.5	1x10	83.5	1x16	90.4	3x12	83.0	2x10	85.0
10	1x10	83.5	4x12	91.0	13	87.7	4x13	91.5	2x12	83.5	2x7	88.4	3x14	89.8	4x11	87.1
11	5x7	93.0	2x16	88.3	3x11	84.3	16	90.1	3x11	84.0	6x14	83.4	16	90.3	4x14	86.3
12	2x12	84.4	6x12	86.5	9	88.0	1x16	90.4	5x8	84.3	2x9	81.6	4x11	87.1	6	87.5
13	5x9	89.5	4	90.0	1x13	84.3	4	90.0	2x10	84.4	1x15	87.6	6	87.6	2x14	84.1
14	6x14	83.4	6x10	88.4	2x12	84.4	6x15	89.6	2x14	84.7	1x14	89.6	4x9	87.3	13	87.7
15	1x14	89.6	13	87.69	5x11	83.5	1x12	90.3	11	84.9	10	87.9	3x15	88.4	6x12	86.5
16	4x15	92.8	7	89.0	1	87.7	7	89.0	5x12	84.9	5x11	83.5	9	86.4	3x11	84.3
17	4x16	95.3	5x12	84.9	3x13	85.1	5x10	89.5	3x13	85.0	15	88.2	15	89.0	5x12	84.9
18	3x11	84.3	6x14	83.4	6	87.5	1x8	90.3	4x14	85.8	4x14	86.3	5x11	83.5	2x8	87.0
19	13	87.7	3	86.5	3x14	89.8	3x14	89.8	6x7	85.9	2x10	85.0	5x8	83.6	8	88.0
20	1x12	90.3	2	86.7	14	87.5	5x9	89.5	2x8	85.9	2x8	87.0	2x11	81.5	5x15	87.0

1 = ICMV3771, 2 = Manganara, 3 = Okashana2, 4 = ITMV8001, 5 = SDMV94001, 6 = Shibe, 7 = Exbornu, 8 = CIVT9206, 9 = GGB8735, 10 = ICMV221, 11 = ICMV221white, 12 = KatPM1, 13 = Okoa, 14 = SDMV96053, 15 = Sosank, 16 = Okollo

Table 6. Genotype by environment analysis for percentage of productive tillers

Rank	Finley and Wilkenson		Wricke's ecovalence		Static stability		Cultivar superiority		REML		ASVi		GGE biplot		Yield stability index	
	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means	Geno-type	Means
1	2x15	71.04	1	82.35	1x9	92.49	1x9	92.49	1x9	92.16	11	85.61	3	82.22	1x9	92.49
2	1x14	68.5	14	82.68	5x8	91.24	5x12	91.92	6x7	91.28	1	82.35	4x13	86.76	1x13	89.46
3	6x10	86.24	5	83.53	5x12	91.92	2x11	91.23	5x8	91.16	3x12	86.35	2	82.15	4x7	89.94
4	6x11	88.51	2	81.69	2x11	91.23	6x7	92.17	5x12	90.98	14	82.68	6	84.21	4x10	90.56
5	5x9	78.96	13	87.24	5x10	81.55	5x8	91.24	2x11	90.84	6x15	73.77	15	76.61	4x9	88.91
6	6x12	84.27	6	82.65	9	82.26	4x9	88.91	4x10	90.8	5	83.53	1x10	85.93	4x14	89.79
7	5x10	81.55	11	85.61	6	82.65	4x7	89.94	1x13	89.72	7	85.19	10	84.64	11	85.61
8	1x9	92.49	10	82.99	6x15	73.77	4x14	89.79	4x11	89.36	2	81.69	5x13	84.82	7	85.19
9	3x13	86.57	4	85.5	2x16	82.53	13	87.24	5x7	89.3	10	82.99	3x13	86.58	1x10	85.93
10	5x12	91.92	9	82.26	5	83.53	6x14	87.72	4x7	89.24	13	87.24	2x15	81.48	4x11	89.19
11	1x16	86.13	4x16	78.88	1	82.35	1x13	89.46	4x14	88.46	5x8	91.24	5x16	76.6	1x16	86.13
12	5x8	91.24	2x11	91.23	12	82.5	2x13	87.98	4x9	88.41	6	82.65	2x16	83.39	4x13	86.75
13	4x14	89.79	2x16	82.53	3x12	86.35	3x12	86.35	2x14	87.54	4x7	89.94	12	82.1	10	82.99
14	4x15	74.8	7	85.19	5x9	78.96	6x11	88.52	3x11	87.53	1x11	84.23	6x12	84.27	2x11	91.23
15	3x12	86.35	4x9	88.91	4x9	88.91	11	85.61	6x8	87.38	4	85.5	9	85.03	4	85.5
16	6x14	87.72	12	82.5	10	82.99	4x11	89.19	5x14	87.18	9	82.26	2x8	81.38	2x13	87.98
17	2x13	87.98	1x13	89.46	14	82.68	1x16	86.13	13	87.15	2x11	91.23	5x15	84.62	9	82.26
18	2x12	75.51	2x9	81.66	6x14	87.72	4x13	86.75	6x11	87.08	4x16	78.88	6x16	77.71	1x11	84.23
19	6x15	73.77	3	82.97	6x7	92.17	4	85.5	4x13	87.08	4x9	88.91	3x10	81.81	1	82.35
20	5x11	75.14	6x7	92.17	6x11	88.52	2x14	86.97	6x14	86.85	2x16	82.53	2x9	81.66	2x14	86.97

1= ICMV3771, 2 = Manganara, 3 = Okashana2, 4 = ITMV8001, 5 = SDMV94001, 6 = Shibe, 7 = Exbornu, 8 = CIVT9206, 9 = GGB8735, 10 = ICMV221, 11 = ICMV221white, 12 = KatPM1, 13 = Okoa, 14 = SDMV96053, 15 = Sosank, 16 = Okollo

Table 7. Genotype by environment analysis for percentage of productive tillers

Rank	Finley and Wilkenson		Wricke's ecovalence		Static stability		Cultivar superiority		REML		ASVi		GGE biplot		Yield stability index	
	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means
1	2x15	71.0	1	82.4	1x9	92.5	1x9	92.5	1x9	92.2	11	85.6	3	82.2	1x9	92.5
2	1x14	68.5	14	82.7	5x8	91.2	5x12	91.9	6x7	91.3	1	82.4	4x13	86.8	1x13	89.5
3	6x10	86.2	5	83.5	5x12	91.9	2x11	91.2	5x8	91.2	3x12	86.4	2	82.2	4x7	89.9
4	6x11	88.5	2	81.7	2x11	91.2	6x7	92.2	5x12	91.0	14	82.7	6	84.2	4x10	90.6
5	5x9	79.0	13	87.2	5x10	81.6	5x8	91.2	2x11	90.8	6x15	73.8	15	76.6	4x9	88.9
6	6x12	84.3	6	82.7	9	82.3	4x9	88.9	4x10	90.8	5	83.5	1x10	85.9	4x14	89.8
7	5x10	81.6	11	85.6	6	82.7	4x7	89.9	1x13	89.7	7	85.2	10	84.6	11	85.6
8	1x9	92.5	10	83.0	6x15	73.8	4x14	89.8	4x11	89.4	2	81.7	5x13	84.8	7	85.2
9	3x13	86.8	4	85.5	2x16	82.5	13	87.2	5x7	89.3	10	83.0	3x13	86.6	1x10	85.9
10	5x12	91.9	9	82.3	5	83.5	6x14	87.7	4x7	89.2	13	87.2	2x15	81.5	4x11	89.2
11	1x16	86.1	4x16	78.9	1	82.4	1x13	89.5	4x14	88.5	5x8	91.2	5x16	76.6	1x16	86.1
12	5x8	91.2	2x11	91.2	12	82.5	2x13	88.0	4x9	88.4	6	82.7	2x16	83.4	4x13	86.8
13	4x14	89.8	2x16	82.5	3x12	86.4	3x12	86.4	2x14	87.5	4x7	89.9	12	82.1	10	83.0
14	4x15	74.8	7	85.2	5x9	79.0	6x11	88.5	3x11	87.5	1x11	84.2	6x12	84.3	2x11	91.2
15	3x12	86.4	4x9	88.9	4x9	88.9	11	85.6	6x8	87.4	4	85.5	9	85.0	4	85.5
16	6x14	87.7	12	82.5	10	83.0	4x11	89.2	5x14	87.2	9	82.3	2x8	81.4	2x13	88.0
17	2x13	88.0	1x13	89.5	14	82.7	1x16	86.1	13	87.2	2x11	91.2	5x15	84.6	9	82.3
18	2x12	75.5	2x9	81.7	6x14	87.7	4x13	86.8	6x11	87.1	4x16	78.9	6x16	77.7	1x11	84.3
19	6x15	73.8	3	83.0	6x7	92.2	4	85.5	4x13	87.1	4x9	88.9	3x10	81.8	1	82.4
20	5x11	75.1	6x7	92.2	6x11	88.5	2x14	87.0	6x14	86.9	2x16	82.5	2x9	81.7	2x14	876.0

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Table 8. Genotype by environment analysis for panicle area

Rank	Finley and Wilkenson		Wricke's ecovalence		Static stability		Cultivar superiority		REML		ASVi		GGE biplot		Yield stability index	
	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means	Genotype	Means
1	4x12	759.8	6	572.3	4x7	406.2	3x15	1065.3	2x15	1103.5	4x9	516.1	4	536.5	1x16	663.7
2	3x15	1065.3	12	608.2	4x11	379.8	2x8	754.3	4x15	1093.9	6	572.3	5x12	770.2	1x13	654.7
3	4x7	406.2	5x14	430.0	4x16	408.0	3x10	794.4	6x15	956.0	5x14	430.0	2x7	642.2	4x12	759.8
4	2x8	754.3	4x9	516.1	4	533.2	6x8	718.5	6x10	942.7	12	608.2	4x9	516.1	10	600.0
5	6x8	718.5	3x9	434.9	2x9	654.7	4x12	759.8	5x12	835.1	5x11	485.8	9	499.8	9	597.3
6	2x9	654.7	1x10	437.1	6x14	547.2	15	655.5	6x16	759.4	5x10	418.1	14	515.9	4x15	749.5
7	4x16	408.0	3x12	390.4	2x11	513.1	6x15	809.2	9	757.9	3x9	434.9	6x16	598.3	1x11	635.2
8	4x11	379.8	5x10	418.1	5x11	485.8	3	603.3	6x12	744.5	6x11	362.6	4x11	379.8	8	563.9
9	6x14	547.2	2	598.4	6x11	362.6	8	563.9	2x9	729.5	1x10	437.1	4x16	408.0	2x8	754.3
10	2x11	513.1	6x11	362.6	2x12	472.6	6x10	812.9	6x8	716.3	10	600.0	6x12	634.5	4x13	643.2
11	4	533.2	6x9	436.1	11	477.5	12	608.2	1x11	710.5	3x12	390.4	4x14	468.7	7	551.6
12	2x15	728.3	6x13	508.6	6x7	562.7	10	600.0	5x11	674.1	2	598.4	15	734.6	1x12	579.1
13	6x7	562.7	1x15	446.2	6x12	634.5	1x16	663.7	3x15	673.8	6x9	436.1	1x7	547.3	2x10	656.1
14	4x15	749.5	10	600.0	6x8	718.5	4x8	526	16	633.0	6x13	508.6	2x15	749.3	2x15	728.3
15	5x11	485.8	11	477.5	6x16	598.3	4x15	749.5	12	610.2	11	477.5	3x11	591.0	3x10	794.4
16	2x12	472.6	3x7	491.2	12	608.2	2x7	642.2	2x7	602.3	1x15	446.2	1x11	635.2	2x9	654.7
17	6x16	598.3	14	538.8	9	597.3	2	598.4	15	601.7	6x16	598.3	2x16	595.9	1x7	547.3
18	6x11	362.6	3x16	452.6	2	598.4	6x12	634.5	1x13	593.0	16	562.5	6x15	809.2	2x7	642.2
19	5x7	623.9	3x8	470.4	6x13	508.6	5x12	770.2	1x16	591.4	3x8	470.4	13	576.1	1	537.7
20	9	597.3	5	526.9	6	572.3	2x15	728.3	2	590.1	3x7	491.2	2x13	483.9	3x15	1065.3

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yielding (<2000 kg ha^{-1}) genotypes as being the most stable across environments; while Cultivar superiority, REML, GGE biplot and YSi identified high yielding genotypes as being the most stable. A significant positive correlation was also observed between Cultivar superiority, REML, GGE biplot and YSi although the correlation was stronger between Cultivar superiority and REML where both methods identified 16 genotypes as being stable but with a slight difference in ranking. The Wricke's ecovalence, static stability and ASVi identified 11 out 20 genotypes as being stable although ranked differently.

Days to 50% flowering (FLO$_{50}$)

The ranking of the genotypes by the methods was different for the trait, with similarity existing only in number of genotypes identified by each method (Table 4). The Finley and Wilkinson and Static stability had 10 genotypes in common, 6 with Cultivar superiority and REML while Wricke's ecovalence and ASVi had 16 in common, 8 with static stability and 7 with REML. Cultivar superiority also had 9 genotypes in common with GGEbiplot and no genotype in common with REML.

Days to 50% physiological maturity (PSM$_{50}$)

Variation in genotypes and ranking was also observed across the methods for days to 50% physiological maturity. In addition, the similarity level in number of genotypes commonly identified also varied (Table 5). The Finley and Wilkinson and Static stability methods had the highest number (13) of genotypes in common but ranked differently. This was followed by Wricke's ecovalence and GGE biplot (11), then Wricke's ecovalence and ASVi (9). The cultivar superiority had no genotype in common with REML while it had only one with ASVi.

Percentage of productive tillers (PRO)

Differences in genotypes and ranking by the stability methods were observed for productive tillers (Table 7). The Cultivar superiority and REML identified 15 of the 20 genotypes in common and 9 out of 20 with Finley and Wilkinson's while Wricke's ecovalence and ASVi had 14 of 20 most stable genotypes in common but differences existed in ranking. Using static stability, 6 out of 20 genotypes were common with REML while for GGE biplot, 6 genotypes ranked in common with Wricke's ecovalence method. The ranking for all the genotypes was different in all the stability methods tested irrespective of the commonality observed.

Panicle area (PAR)

Variation in ranking of the most stable genotypes by the tested stability methods was also observed for panicle area although some similarities among the methods existed (Table 8). The Finley and Wilkinson and static stability had 14 genotypes in common of the 20 most stable; while Cultivar stability and REML methods identified 12 genotypes in common. In addition, Wricke's ecovalence and ASVi identified 17 common genotypes out of 20 most stable genotypes across environments. The GGE biplot identified 6 common genotypes as Cultivar superiority and REML while 5 common genotypes were identified by Finley and Wilkinson and Static stability.

Discussion

Across the evaluation sites, yield ranged between 1427 kg ha^{-1} to 2506 kg ha^{-1}. The ANOVA indicated significant variation among the genotypes tested and the GEI, showing that the multiplicative interaction of the genotypes and environments affected the performance of the test materials as also reported by Subi *et al.* (2013). However, as noted by Crossa (1990), ANOVA does not explore the underlying structure within the GEI and thus other methods were adapted. Significant correlation among the Cultivar superiority with REML, YSi and GGE biplot shows that a prediction of comparable results can be revealed when any of the methods is used independently with minimal variation in the ranking of the genotypes.

Significant correlation was also observed elsewhere between Cultivar superiority and YSi in cotton (Blanche Sr., 2005) and Faba bean (Temesgena *et al.*, 2015) studies. These correlated methods aid in simultaneously selecting stable and high yielding genotypes unlike the Finlay and Wilkinson, Wricke's ecovalence, ASVi and Static stability which, in this study, identified mostly low yielding genotypes as being the most stable. Except ASVi, similar observations were made by Mohammadi and Amri (2008) in studies on wheat. Wrike's method has also been reported to identify low yielding genotypes in sugar cane (Mendes de Paula *et al.*, 2014) and field pea (Fikere *et al.*, 2014) as also observed in this study.

The various analysis methods ranked genotypes differently for the same traits across the test environments. Similar observations were also made by Pabale and Pandya (2010) when they compared Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971) models in ranking of pearl millet genotypes basing on grain yield. Mustapha and Bakari (2014) reported no similarity between static and cultivar superiority; while cultivar superiority and GGE biplot identified the same genotypes as being stable, but ranked them differently in pearl millet. In this study, Cultivar superiority and GGE biplot were significantly correlated for grain yield, days to 50% flowering and days to 50% physiological maturity; with a difference in ranking of genotypes. Variation in ranking of genotypes was also reported by Parmar *et al.* (2012) when they compared nonparametric tests in rice; Mosleh *et al.* (2012) when they compared Wricke's ecovalence, Shukla stability variance, rank test, and Eberhart and Russell; and Namorato *et al.* (2009) when they compared AMMI and Eberhart and Russell methods in maize. The inconsistency in ranking was also reported by Alberts (2004) and Khosa (2012) when cultivar superiority, Finlay and Wilkinson, Wricke's ecovalence and ASVi were compared in maize. In addition, Dehghani *et al.* (2008) also observed variation in ranking Lentil genotypes, although they observed similarity between Shukla and Wricke's, cultivar superiority and Wricke's ecovalence, Finlay and Wilkinson and cultivar superiority. However, in the present study the methods had no significant correlation. The lack of significant association and differential ranking of genotypes by ASVi and GGE biplot was also observed in wheat studies by Naroui Rad *et al.* (2013). Results showed no significant association between cultivar superiority and Finlay and Wilkinson's methods as also reported by Purchase *et al.* (2000). On the contrary, Purchase *et al.* (2000) reported a significant correlation between ASVi and Wricke's ecovalence as also noted by Alberts (2004). This implies that results from the comparisons may greatly depend on the method, types of genotypes and environments being evaluated as also observed by Westcott (1986) and thus more than one method should be used to characterise and explore performance of genotypes across environments as also suggested by Lin and Binns (1988).

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