Kernel Yield Stability Analysis in Groundnut (*Arachis hypogea* L.)

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Abstract: Multiple-environment trials identify genotypes that thrive in different environments since the occurrence of genotype x environment interaction (GEI) produces stable performance of genotypes. This research was conducted to determine the effect of GEI on the stability of groundnut genotypes for kernel yield. The field experiment was conducted for 16 groundnut genotypes evaluated for kernel yield in a Randomized Complete Block Design (RCBD) across six locations in Ethiopia. The additive main effect and multiplicative interaction (AMMI) Model analysis of variance (ANOVA) revealed that the largest proportion of the observed kernel yield variation was due to GEI (41.5%) and G (38.5%) rather than environment (19%). The mean yield, stability parameters from linear regression, AMMI and genotype main effect and genotype x environment (GGE) biplot models selected Bahagudo as the best genotype in across environments and Tole-1, Werer-962 and Manipeter genotypes with second to fourth highest kernel yield identified as best in favorable, representative and unfavorable environments, respectively. The GGE biplot has shown that the six environments fell into two sectors with different winning genotypes. Babile and Guba were identified as representative and discriminating environments, respectively. Therefore, it is necessary to grow groundnut genotypes in the environments where they performed best and testing genotypes in most discriminating environments to reduce the cost related to testing genotypes over locations.

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INTRODUCTION

The presence of Genotype and Environment Interactions (GEI) affects performance of genotypes across locations in which similar sets of genotypes are undergoing different performance rankings in different environments[1]. Therefore, targeting of genotypes to specific location is difficult when GEI is present, since,

yield is less predictable and cannot be due to the additive the genotype (G) and environment (E) means only. In such situations, the ultimate goal of crop breeders is to identify ideal genotypes that combine high mean yield and low degree of fluctuations when grown over diverse environments[2]. Therefore, it is necessary to conduct multi-environment trials to identify stable and high performing groundnut genotypes. This is because GEI complicates the selection of genotypes due to the fact that the best genotype in one environment may exhibit a poor performance in another environment[3]. Multi-environment trials not only allow to test genotypes consistency in performance over the locations but also allow us to estimate the magnitude of genotype, environment and GEI effects on the trait of interest, thus, helping the breeders to design appropriate breeding strategies[4].

The breeders employ statistical methods to analyze data generated from multiple-environment trials so as to understand the effect of GEI and increasing the accuracy of breeding experiments. In Ethiopia, Kebede and Tana[5] have conducted GEI for pod yield in groundnut genotypes across two locations. However, no studies are found for the influence of GEI on kernel yield trait among groundnut genotypes grown in the country. Therefore, this research was planned to study effect of genotype x environment interaction on kernel yield so as to identify particular genotypes having high performance across locations.

MATERIALS AND METHODS

The experimental materials involved 16 groundnut genotypes assessed for kernel yield (kg/ha) across six locations in three replications during 2015/16 growing seasons in Ethiopia. The stability analysis for kernel yield was done based on linear regression of genotype mean yield on an environmental index derived from the average performance of all genotypes in each environment according to Eberhart and Russell[6] and AMMI[7] and GGE biplot models[8].

The AMMI analysis developed by Gabriel[9] and Gollob[10] a statistical Model which combines features of additive ANOVA and non-additive factor analytic techniques. Among the various methods of genotype environment data (GED) analysis, the Additive Main Effects and Multiplicative Interaction (AMMI) model can help in the identification of genotypes that have high productivity and are well adapted to agronomic zones, with the aim of regionalized recommendation and selection of test sites[11, 4]. This model is defined by: The AMMI stability value (ASV)[12] measure was computed in order to quantify and rank genotypes according to their yield stability.

The AMMI stability value (ASV) was calculated as follows:

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1)^2 + (IPCA2)^2}$$

Where:
ASV = AMMI's stability value
SS = Sum of squares
IPCA1 = Interaction principal component axis 1
IPCA2 = Interaction principal component axis 2

The sites Regression Analysis (SREG/GGE Biplot) is a model in which the main effects of genotype (G) plus the GE interaction were absorbed into the bilinear terms[13, 14]. The GED analysis for kernel yield and were conducted using VSN International[15], GENES software[16] and GEA-R[17].

RESULTS AND DISCUSSION

Linear regression based on Eberhart and Russell's model: Eberhart and Russell's model (Table 1), that partitions total variation into Genotype, environment (linear), GEI (linear) effects, sum of squares due to regression and unexplained deviation from linear regression (pooled deviation mean squares), indicated that all effects were significant (p<0.01) which indicated contrasts between the environments and the occurrence of differential response of genotypes across environments. The significant GEI (linear) indicated that the stability parameter estimated by linear response of genotypes to change in environment and the result indicated the response of genotypes across six environments was not the same and the variability of genotypes for performance was partially unpredictable. However, the linear regression method captures a small part of sum of squares of GEI and confuses GEI and main effects (Table 1). Nachit *et al.*[18] also suggested regression technique is unable to predict non-linear genotypic response to environment.

In the present study a linear regression coefficient (b_i = 1) (adaptable) and nonlinear = 0 (stable or predictable) (Table 2) were observed for Bulki, Oldhale, Sedi, Werer-961 and Werer-963 genotypes. All these genotypes were poorly adapted to all environments since they were associated with low mean kernel yield. Thus, there were no ideal genotype for kernel yield that is both stable and adaptable. A regression coefficient (b_i = 1) and S^2_{di} = 0 was observed for Lote, Manipeter, Shulamith, Werer-961 and Werer-962 genotypes as having average adaptability and stability. Among these genotypes Shulamith and Werer-961 were considered as desirable genotypes with general adaptability and

Table 1: ANOVA based on Eberhart and Russell's Linear regression model for kernel yield

	Kernel yield regression ANOVA			
Source	DF	SS	MS	Proportion (%)
Total	175	1.01E+09	5.70E+06	-
Gen	15	2.43E+08	1.6E+07**	38
Env+ GXE	80	3.82E+08	4.8E+06**	50
Env.Linear	1.0	1.20E+08	1.2E+08**	15
GxE linear	15	1.00E+08	6.7E+06**	13
Deviation	64	1.60E+08	2.5E+06**	21

**significant at 0.01 level

Table 2: Pooled mean kernel yield with rank, stability parameters from Eberhart and Russell's model

	Kernel yield		
Variety	b_i	S^2d_i	R^2
NC-343	-0.24**	1493782**	2.21
Behagudo	1.88*	538715.6**	76.39
Behajidu	-0.38**	1035275**	6.97
Bulki	0.60	108993.5	47.04
Fetene	1.52	465226.1**	70.45
Lote	0.68	239355.9*	43.03
Manipeter	-0.23**	697634.3**	3.85
Oldhale	0.17	-4663.46	11.68
Roba	0.44	1353120**	7.62
Sedi	1.19	-14228.8	87.47
Shulamith	2.20**	129188.6	91.77
Tole-1	2.71**	1185358**	77.55
Tole-2	2.31**	256934.5*	89.35
Werer-961	0.95	-99039.6	93.18
Werer-962	1.14	3647367**	17.55
Werer-963	1.07	178645.9	68.95

*, **significant at 0.05 and 0.01 probability levels, respectively

Table 3: ANOVA and Gollob F-test based on AMMI model for kernel yield (kg/ha)

	Kernel yield				
Source	DF	SS	MS	Proportion (%)	Cumulative
Total	287	7.06E+08	2.46E+06	-	-
Treatments	95	6.25E+08	6.57E+07**	-	-
Environment	5	1.20E+08	2.40E+07**	19	19
Blocks	12	5.80E+06	4.83E+05	0.9	19.9
Genotype	15	2.43E+08	16199246**	38.5	58.4
GEI	75	2.62E+08	3.49E+06**	41.5	99.9
IPCA1	19	8.45E+09	4.45E+08**	53.5	53.5
IPCA2	17	3.46E+09	2.03E+08**	21.9	75.4
Residuals	39	6.44E+07	1.65E+06**		
Error	180	7.59E+07	4.22E+05		

**significant at 0.01 probability level

stability, since, they are associated with a relatively high mean kernel yield. Since, the linear ANOVA captures only the additive part of variances, further models that explain the multiplicative interaction patterns due to GEI are required.

The existence of significant genotype×environment interactions for yield, yield components, physiological and quality traits in groundnut crop were also reported earlier by Patil *et al*.[19] and Reddy *et al*.[20] for days to 50% flowering, pods per plant, pod yield per plant, sound mature kernel percent, 100 kernel weight, kernel yield per plant, haulm yield per plant, oil and protein content. Despite the frequent use of the regression methods, several researchers reported deficiencies of the

method for determination of GEI patterns[8, 21]. Therefore, analysis of variance was conducted using an AMMI model.

The AMMI model analysis: The result of ANOVA from AMMI model (Table 3) revealed the significant effect of genotype (G), environment (E) and genotype x environment interaction (GEI) for kernel yield. The ANOVA results from AMMI model also revealed that the higher proportion of the yield variation among groundnut genotypes was due to GEI and G as compared to E for kernel yield. The large sum of squares for genotypes indicated that the genotypes were diverse with large differences among genotypic responses causing most of

Table 4: Pooled mean kernel yield with respective rank, stability parameters from AMMI model

| | Kernel yield | | | |
| | Mean & rank | PC1 | PC2 | ASV & rank |
Variety				
NC-343	4115.2 (11)	-14.1	-6.7	23.01(7)
Behagudo	6430.6 (1)	20.10	13.9	34.30(10)
Behajidu	4444.7 (9)	-34.4	8.5	54.40(14)
Bulki	3761.7 (12)	-0.40	-13.9	13.95((3)
Fetene	5188.2 (6)	11.0	-0.41	17.27(5)
Lote	4194.9 (10)	-3.6	-18.6	19.44(6)
Manipeter	5349.4 (4)	-26.5	-18.1	45.23(12)
Oldhale	3311.2 (15)	-15.8	-7.1	25.74(8)
Roba	4777 (7)	-21.6	-0.24	33.85(9)
Sedi	2996 (16)	4.10	-6.9	9.39(2)
Shulamith	4549.7 (8)	24.0	-2.2	37.65(11)
Tole-1	5450.5 (2)	40.9	8.8	64.59(16)
Tole-2	5280.6 (5)	28.9	1.9	45.26(13)
Werer-961	3611 (13)	-0.59	-0.6	1.10(1)
Werer-962	5407 (3)	-18.6	53.6	60.99(15)
Werer-963	3541.8 (14)	6.7	-11.8	15.79(4)
Overall mean	4525.6			

*and** significant at 0.05 and 0.01 probability level, respectively. Numbers in parenthesis indicate the rank for pooled mean yield and ASV

the variation in kernel yield which is consistent with the findings of Misra et al.[22] and Nawaz et al.[23] who also reported the larger contribution of GEI than genotype effect for the observed yield variation of groundnut genotypes. Furthermore, in the present study, AMMI residual variance for groundnut kernel yield was found to be significant, thus, it is not appropriate to use AMMI biplot (AMMI-1 & AMMI-II) for stability analysis insead the GGE biplot is recommended in such a case.

The values and signs of IPCAs indicated a proportionate genotype response. The breeders preferred to select cultivars with lower IPCA1 scores than those with higher IPCA1 scores due to lower GEI effect and having less variable yields (more stable) across environments[24]. However, the low ASV and IPCAs are not the only important parameters to select genotypes for cultivation but also the high yield of the genotypes need to be considered along with the stability parameters. Dynamic stability implies that a stable genotype has a yield response parallel to the mean response of the tested environments[25]. Therefore, the genotypes could be considered for cultivation at the environments where they performed better.

The AMMI model stability parameters (ASV) for groundnut kernel yield (Table 4) exhibited that genotypes like Behagudo, Tole-1and Werer-962 had the 1st, 2nd and 3rd highest mean kernel yield but withASV ranked 10th, 16th and 15th, respectively (Table 4). Manipeter, Tole-2, Roba and Shulamithgenotypes had mean kernel yield above the average with high ASV at the rank of 12th, 13th, 9th and 11th, respectively. The AMMI stability value (ASV) has shown that Werer-961, Sedi, Bulki and Werer-963 were among the most stable genotypes for kernel yield. However, Roba, Bulki and Sedi were among

the least in mean kernel yield. When both ASV and mean kernel yield (Table 4) are considered, Behagudo and Fetene are selected as best genotypes.

GGE biplot for kernel yield: The 'which won where analysis of GGE Biplot for the 16 groundnut genotypes evaluated across six locations with respect to kernel yield identified two possible mega-environments (Fig. 1). The first mega-environments included Mechara, Fedis and Hirna; while the second mega-environment included Guba, Pawe, Babile and Hirna. This result did not correspond with the usual geographical locations in Ethiopia. This finding, however was in accordance with Lin and Binns[25] who suggested mega-environments based on the location grouping did not usually correspond with the traditional area divisions.

The which-won-where analysis of the GGE biplot (Fig. 1) has shown that the six environments fell into two sectors with different winning genotypes. Specifically, Bahagudo was the highest yielding genotype in Guba, Pawe and Babile; while Werer-962 was the highest yielding genotype (but only slightly higher than other genotypes like Manipeter and Roba with markers in close proximity to Werer-962) in Fedis, Mechara and Hirna. Dividing target environment or location into mega-environment is recommended if such crossover patterns are repeatable across years[27]. Those vertex genotypes (Fig 1) including Bahajidu, Oldhale, Sedi and Tole-1 without any site in their sectors were not highest yielding genotypes at any site; moreover, there were the poorest genotypes within the polygon, particularly those located near the plot origin like Lote, thatwere less responsive than the vertex genotypes. These findings were in agreement with previous works by Kebede and Tana[5] who conducted GEI for pod yield in groundnut; likewise for Ifrim et al.[28] who report on oil yield stability in
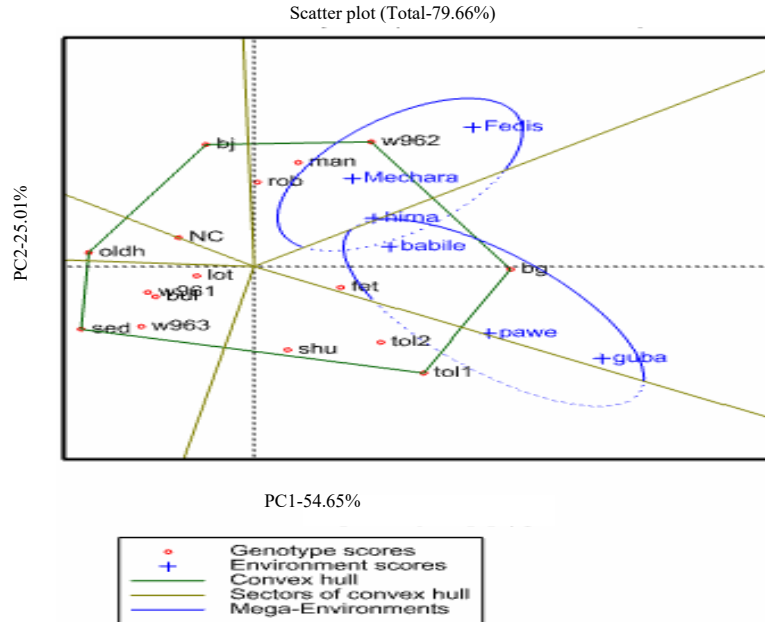
Scatter plot (Total-79.66%)

Fig. 1: The "which-won-where" analysis of the GGE biplot based on the G×E data for grain yield. NC:NC-343; bg: Bahagudo; Bj: Bahajidu; bul: Bulki; fet: Fetene; lot: Lote; man: manipeter; oldh: Oldhale; ro: = Roba; sed: Sedi; shul: Shulamith; tol1:Tole-1; tol2: Tole-2; W961:Werer-961; W962:Werer-962; W963:Werer-963
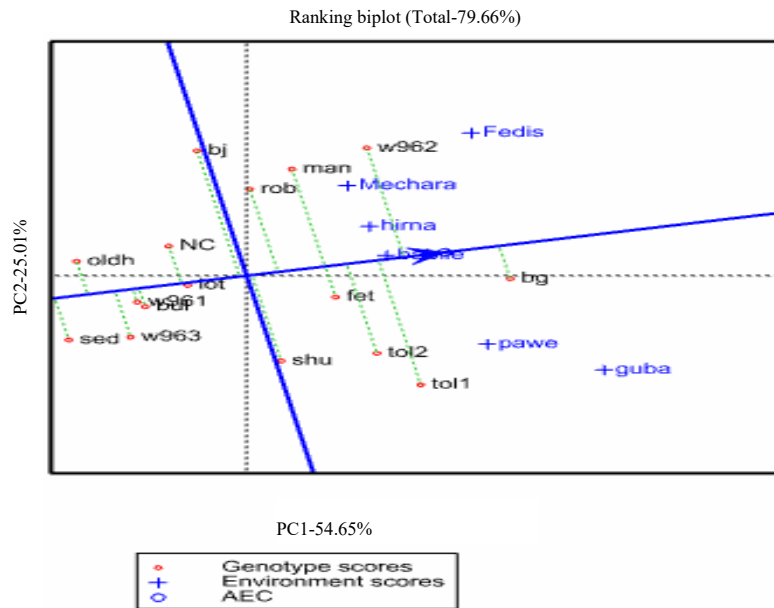
Ranking biplot (Total-79.66%)

Fig. 2: The ranking and stability based on mean data of GGE biplot for kernel yield in groundnut.NC:NC-343; bg: Bahagudo; Bj: Bahajidu; bul: Bulki; fet: Fetene; lot: Lote; man: manipeter; oldh: Oldhale; rob: Roba; sed: Sedi; shul: Shulamith; tol1:Tole-1; tol2:Tole-2; W961:Werer-961; W962:Werer-962; W963:Werer-963

soybean and Khan *et al*.[29] who worked on GEI for various agronomic traits in sunflower. The mean and stability based on GGE biplot (Fig. 2) facilitates genotype comparisons based on mean performance and stability across environments within a mega-environment. The genotypes are ranked according to G means as follows: Behagudo>Werer-962>Tole-1>Tole-2>Fetene = Manipeter> Roba> Shulamith> mean> Behajidu> Lote>
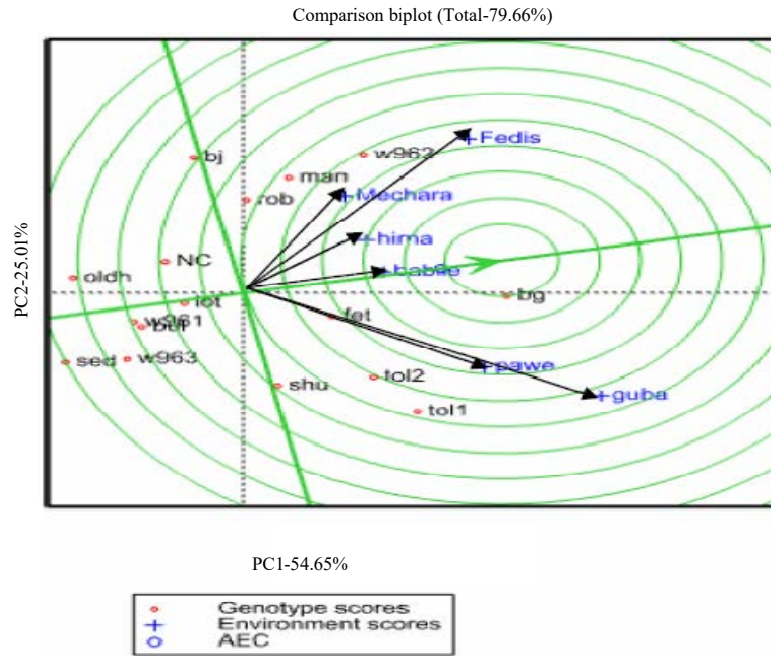
Comparison biplot (Total-79.66%)

Fig. 3: GGE biplot for discriminativeness and representativeness of the environments for kernel yield in groundnut. NC:NC-343; bg: Bahagudo; Bj: Bahajidu; bul: Bulki; fet: Fetene; lot: Lote; man: manipeter; oldh: Oldhale; rob:Roba; sed:Sedi; shul: Shulamith; tol1:Tole-1; tol2:Tole-2; W961:Werer-961; W962:Werer-962; W963:Werer-963

NC-343>Bulki>Werer-961>Werer-963>Oldhale>Sedi. The stability ranking of genotypes based on increasing absolute difference between the genotype markers and the mean environment axis was: Lote> Werer-961>Bulki>Fetene=Oldhale> Behagudo=NC-343>Sedi>Werer-963>Roba> Shulamith>Tole-2=Manipeter>Werer-962 >Tole-1= Bahajidu. Even though Bahagudo was the highest yielding cultivar, it was the fifth in stability and although Lote was the first in stability, it was among the least in yielding ability. When both yield and stability rankings were considered, it was Behagudo that qualified as best among the sixteen genotypes.

The discriminative vs representative analysis of GGE biplot is indicated in Fig. 3. According to GGE interpretation, an ideal test environment should be both discriminating and representative. An 'ideal' environment probably does not exist in reality but can be used as a reference point[7]. In this study "ideal" test environment which is a virtual environment that has the longest vector of all test environments (most discriminating) was Guba and it is the most desirable among the six environments. In this study Bahagudo, followed by Fetene and Werer-962 genotypes were among the closest to the concentric center of circles (Fig. 3) and thus, considered to be most representative of "ideal genotypes". The interactions between genotypes and environment for groundnut yield also were found in many other studies[5, 23, 3-32].

CONCLUSION

In this study, the results obtained for the Eberhart and Russell regression model were almost consistent with that of the AMMI Model. However, the regression models account for only a small proportion of the variance and they do not distinguish the best genotypes with respect to both yield and stability. When both ASV and mean kernel yield are considered, Behagudo and Fetene were considered as best genotypes. The best genotypes are those that have large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability). A similar result as that of the AMMI model was obtained by using the GGE biplot model; that is, Bahagudo was best, followed by Fetene and Werer-962 genotypes, because they were among the closest to the concentric center of circles; thus, they were considered to be the ideal genotypes.

Authors' contributions: Zekeria Yusuf: field experiment, data collection and analysis; Habtamu Zeleke: initiation and design of the study: Arno Hugo; acquisition of data and doing the laboratory phase; Wassu Mohammed and Shimelis Hussein: Analysis and interpretation of data. All authors contributed to drafting the article and revising it critically for important intellectual content

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REFERENCES

01. DeLacy, I.H., R.L. Eisemann and M. Cooper, 1990. The Importance of Genotype-by-Environment Interaction in Regional Variety Trials. In: Genotype-by-Environment Interaction and Plant Breeding, Kang, M.S. (Ed.). Louisiana State University, Baton Rouge, Louisiana, USA., pp: 287-300.

02. Roy, D., 2000. Plant Breeding, Analysis and Exploitation of Variation. Alpha Science International Ltd., Pangbourne, India.

03. Ramagosa, I. and P.N. Fox, 1993. Genotype-Environment Interaction and Adaptation. In: Plant Breeding: Principles and Prospects, Hayward, M.D., N.O. Bosemark, I. Ramagosa and M. Carezo (Eds.). Chapman and Hall, London, UK., ISBN-13: 9789401115247, pp: 373-390.

04. Gauch Jr., H.G., P.C. Rodrigues, J.D. Munkvold, E.L. Heffner and M. Sorrells, 2011. Two new strategies for detecting and understanding QTL× environment interactions. Crop Sci., 51: 96-113.

05. Kebede, A. and T. Tana, 2014. Genotype by environment interaction and stability of pod yield of elite breeding lines of groundnut (*Arachis hypogaea* L.) in Eastern Ethiopia. Sci. Technol. Arts Res. J., 3: 43-46.

06. Eberhart, S.A. and W.A. Russell, 1966. Stability parameters for comparing varieties. Crop Sci., 6: 36-40.

07. Yan, W., 2001. GGEbiplot-A windows application for graphical analysis of multi environment trial data and other types of two-way data. Agron. J., 93: 1111-1118.

08. Zobel, R.W., M.J. Wright and H.G. Gauch, 1988. Statistical analysis of a yield trial. Agron. J., 80: 388-393.

09. Gabriel, K.R., 1971. The biplot graphic display of matrices with application to principal component analysis. Biometrika, 58: 453-467.

10. Gollob, H.F., 1968. A statistical model which combines features of factor analytic and analysis of variance techniques. Psycometrika, 33: 73-115.

11. Gauch, H.G. and R.W. Zobel, 1996. AMMI Analysis of Yield Trials. In: Genotype-by-Environment Interaction, Kang, M.S. and H.G. Gauch Jr. (Eds.). Taylor and Francis, Boca Raton, FL., ISBN: 9780849340031, pp: 85-122.

12. Purchase, J.L., H. Hatting and C.S. van Denventer, 2000. Genotype x environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. South Afr. J. Plant Soil, 17: 101-107.

13. Burgueno, J., J. Crossa and M. Vargas, 2001. SAS Programs for Graphing GE and GGE Biplots. CIMMYT Int., Mexico.

14. Crossa, J., P.L. Cornelius and W. Yan, 2002. Biplots of linear-bilinear models for studying crossover genotype x environment interaction. Crop Sci., 42: 619-633.

15. VSN International, 2012. GenStat for Windows. Hemel Hempstead, UK.

16. Cruz, C.D., 2013. A software package for analysis in experimental statistics and quantitative genetics. Acta Scientiarum Agron., 35: 271-276.

17. Pacheco, A., M. Vargas, G. Alvarado, F. Rodriguez, M. Lopez, J. Crossa and J. Burgueno, 2015. GEA-R (genotypeXenvironment analysis with R for windows. version 2.0. CIMMYT research data and software repository network.

18. Nachit, M.N., G. Nachit, H. Kenata, H.G. Gauch and R.W. Zobel, 1992. Use of AMMI and linear regression models to analyze genotype-environment interactions in durum wheat. Theoret. Applied Genet., 83: 597-601.

19. Patil, A.S., H.R. Nandanwar, A.A. Punewar and K.P. Shah, 2014. Stability for yield and its component traits in groundnut (*Arachis hypogaea* L.). Int. J. Bio-resource Stress Manage., 5: 240-245.

20. Reddy, A.L., T. Srinivas, A.P. Rajesh and P. Umamaheshwari, 2016. Genotype x environment interaction studies in rainfed groundnut (*Arachis hypogaea* L.). Electron. J. Plant Breed., 7: 953-959.

21. De Vita, P., A.M. Mastrangelo, L. Matteu, E. Mazzucotelli and N. Virzi *et al.*, 2010. Genetic improvement effects on yield stability in durum wheat genotypes grown in Italy. Field Crop Res., 119: 68-77.

22. Misra, R.C., S. Das and M.C. Patnaik, 2009. AMMI model analysis of stability and adaptability of late duration finger millet (*Eleusine coracana*) genotypes. World Applied Sci. J., 6: 1650-1654.

23. Nawaz, M.S., N. Nawaz, M. Yousuf, M.A. Khan, M.Y. Mirza *et al*., 2009. Stability performance for pod yield in groundnut. Pak. J. Agric. Res., 22: 116-119.

24. Oliveira, E.J.D., J.P.X.D. Freitas and O.N.D. Jesus, 2014. AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. Sci. Agric., 71: 139-145.

25. Annicchiarico, P., 2002. Genotype X Environment Interactions: Challenges and Opportunities for Plant Breeding and Cultivar Recommendations. Vol. 1, FAO, Rome, ISBN: 9789251048702, Pages: 115.

26. Lin, C.S. and M.R. Binns, 1988. A superiority measure of cultivar performance for cultivar x location data. Can. J. Plant Sci., 68: 193-198.

27. Yan, W., M.S. Kang, B. Ma, S. Woods and P.L. Cornelius, 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci., 47: 643-653.

28. Ifrim, S.E., I. Has and E. Muresanu, 2012. The stability of yield and quality characters in some soybean *Glycine max* (L. Merr.) genotypes. Res. J. Agric. Sci., 44: 67-71.

29. Khan, H., H.U. Rehman, J. Bakht, S.A. Khan, I. Hussain, A. Khan and S. Ali, 2013. Genotype× environment interaction and heritability estimates for some agronomic characters in sunflower. J. Anim. Plant Sci., 23: 1177-1184.

30. Kasno A., 2010. Talam 1, peanut varieties adaptive dry acid soil and tolerant to aspergillus flavus. Bull. Crops, 19: 19-26.

31. Mothilal, A., V.P. Vindhiya and N. Manivannan, 2010. Stability analysis of foliar disease resistant groundnut genotypes (*Arachis hypogaea* L.). Electron. J. Plant Breed., 1: 1021-1023.

32. Kasno, A. and T. Trustinah, 2015. Genotype-environment interaction analysis of peanut in Indonesia. SABRAO J. Breed. Genet., 47: 482-492.