Bangladesh J. Bot. **47**(2): 321-328, 2018 (June)

SELECTION ON STABLE GENOTYPES THROUGH GENOTYPE-ENVIRONMENT INTERACTION IN YARDLONG BEAN (*VIGNA UNGUICULATA* SSP. *SESQUIPEDALIS* (L.) VERDC.)

MOHAMMED KAMAL HOSSAIN*, ROKIB HASAN, ABUL BASHAR, SAIDUL ISLAM, AKM MAHMUDUL HUQUE[1], BHABENDRA KUMAR BISWAS[2] AND NAZMUL ALAM

Department of Botany, Jahangirnagar University, Savar, Bangladesh

Keywords: Yardlong bean, G × E interaction, Stability parameters, GGE biplot

Abstract

An experiment was conducted to study the genotype-environment interaction (GEI) and stability of performance for yield in yardlong bean (*Vigna unguiculata* ssp. *sesquipedalis* (L.) Verdc.). G × E interaction and yield stability were estimated using stability parameters and genotype plus G × E interaction (GGE) biplot. Pooled analysis of variance for yield showed significant ($p \leq 0.01$) differences among the genotypes, environments and for G × E interaction effects. This indicated that the genotypes differentially responded to the changes in the test environments. Genotypes were subjected to total rank method constructed by summing of the ranks of different stability parameters. According to this ranking method, the lowest rank referred the stable genotype, therefore, G18 was the most stable genotype followed by G1, G4, G11, G6 and G9. GGE biplot facilitated the visual comparison and identification of superior genotypes according to their yield performance.

Introduction

Yardlong bean (*Vigna unguiculata* ssp. *sesquipedalis* (L.) Verdc.) is a distinct form of cowpea grown as a vegetable crop in the Southern Asia and the Far East forits immature pods (Vavilapalli *et al*. 2014). It is cultivated mainly for crisp and tender pods that are consumed both fresh and cooked (Kongjaimun *et al*. 2012). It is strictly a self-pollinated crop due to its cleistogamous nature of flowers and its chromosome number is 2n = 2x = 22 (Ullah *et al*. 2011**)**. It is one of the important leguminous vegetables, well known as Barboti, grown widely in summer season in Bangladesh (Huque *et al*. 2012).

The genotype × environment (G × E) interaction has great importance in breeding programmes for identifying stable genotypes that are widely or specifically adapted to unique environments (Verma *et al*. 2008, Ebdon and Gauch 2002). Genotype × environment interaction has been studied in many leguminous crops, including cowpea (*Vigna unguiculata* L.) (Ddamulira *et al*. 2015), haricot bean (*Phaseolus vulgaris* L.) (Tolessa and Gela 2014) and mungbean (*Vignaradiata* L.) (Nath and Dasgupta 2013). Different methods have been observed in literature to study the stable performance of genotypes over environments (Mohammadi and Amri 2008). Mostly used multivariate methods include principal component analysis (PCA) (Gower 1967), cluster analysis (Mungomery *et al*. 1974) and additive main effects and multiplicative interaction (AMMI) models (Gauch and Zobel 1977). The differences in genotypic performance across environments had been assessed by the graphical biplots based on the significant principal component scores (Olayiwola *et al*. 2015 and Vita *et al*. 2010).

Bangladesh is a disaster prone country, it is inevitable to use suitable genotypes to avoid substantial economic losses. Most of the high yielding varieties are not cultivated frequently due to inconsistent performance in diverse environments and only a few varieties with stable

*Author for correspondence: <kamal_juniv@yahoo.com>. [1]Department of Molecular Biology, Division of Life Sciences, Block A, Hana Science Hall, Korea University, Seoul 02841, Republic of Korea. [2]Department of Genetics and Plant Breeding, Hajee Mohammad Science and Technology University, Dinajpur, Bangladesh.

performance remain cultivated repeatedly. Analysis of genotype-environment interaction with other agro-ecological conditions would help to get information on the adaptability and stability performance of genotypes. But the information of genotype × environment interaction on yardlong bean for yield and its related characters is very limited in the world scientific literature. Therefore, keeping the above facts in mind the present composition is oriented to evaluate the stability for yield of yardlong bean using stability parameters and GGE (Genotype and Genotype × Environment Interaction) biplot.

Materials and Methods

The field experiment was conducted at three contrasting locations including Jahangirnagar University (Dhaka), Dinajpur and Bogra using 23 yardlong bean genotypes. Complete description of the 3 test locations and 23 yardlong bean genotypes are presented in Tables 1 and 2, respectively.

The genotypes were arranged in a randomized complete block design with three replications. The unit pit was 4 × 4 feet maintaining a plant spacing of 1 × 1 feet. A distance of 2 feet in the form of drain was maintained between the block and between the plots within a block. Genotypes were randomly assigned in different blocks. The stability analysis was done according to the model of Eberhart and Russell (1966) which is defined as follows:

$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$; Where, Y_{ij} = mean of the i^{th} genotype at the j^{th} environment, (i =1,2,….,n; j = 1,2,…..,n), μ_i = mean of the i^{th} genotype over all environments, b_i = regression coefficient that measures the response of the i^{th} genotype to varying environments, δ_{ij} = deviation from regression of the i^{th} genotype at the j^{th} environment and I_j = environmental index obtained as the mean of all the genotypes at the j^{th} environment minus the grand mean. Phenotypic Index (P_i) = μ_i-X, Where, X= average mean yield. Eberhart and Russell model and Hanson model were analyzed through INDOSTAT software (Kundy *et al.* 2014 and Lodhi *et al.* 2015). AMMI stability value (ASV) and yield selection index (YSI) were calculated using "agricolae" package of R software (Mendiburu 2015). The GGE Biplot method was performed computationally in the R environment (R Development Core Team 2014) using the package "GGEBiplotGUI" (Frutos *et al.* 2014).

Table 1. Description of the test locations (BBS 2013).

Locations	Environmental parameters			
	Temperature (°C)		Average rainfall (mm)	Humidity (%)
	Min.	Max.		
Dhaka (JU)	19.40	30.50	110.75	70.25
Dinajpur	20.00	30.00	125.92	76.33
Bogra	21.10	30.80	95.00	75.17

Results and Discussion

Pooled analysis of variance of yield, using Eberhart and Russel (1966) model, studied over three locations indicated significant differences for genotypes (Table 3). Significant environments (linear) interaction showed highly significant differences among genotypes for regression means yield. G × E (linear) interaction was also highly significant for yield. The higher value of pooled deviation than the pooled error referred that there was a relationship between non-linear regression components and elite populations (Al-Aysh 2013).

The results of the different stability statistics are presented in Table 4. Eberhart and Russel (1966) suggested a stable genotype as one having high phenotypic index (P_i) with regression coefficient (b_i) near unity (1) and deviation from regression (Sd_i^2) near zero (0). None of 23 genotypes in point followed these criteria (Table 4). To some extent, genotypes G18, G9, G4 and G11 performed satisfactory result because of showing high phenotypic index (P_i) though having low regression coefficient (b_i). G1 and G13 showed perfect regression coefficient (b_i) 0.9 and 1, respectively but they had negative phenotypic index.

Table 2. Description of the 23 yardlong bean genotypes.

Code	Genotype	Source of collection	Code	Genotype	Source of collection
G1	BD-1516	BARI, Gazipur, BD	G12	Sobujsathi	Local market Sylhet, BD
G2	D-1533	BARI, Gazipur, BD	G13	Kgarnatki	BADC, Dhaka, BD
G3	BD-1537	BARI, Gazipur, BD	G14	Toki	Lal Teer, Dhaka, BD
G4	BD-1564	BARI, Gazipur, BD	G15	Saba	Lal Teer, Dhaka, BD
G5	BD-1591	BARI, Gazipur, BD	G16	YB-490	India
G6	BD-3064	BARI, Gazipur, BD	G17	YB-501	Chengdu, China
G7	BD-3067	BARI, Gazipur, BD	G18	YB-549	Anhui, China
G8	BD-3074	BARI, Gazipur, BD	G19	YB-550	Anhui, China
G9	BD-3078	BARI, Gazipur, BD	G20	S. Sundori	Local market, Dhaka, BD
G10	BD-10071	BARI, Gazipur, BD	G21	BARI-1	BARI, Gazipur, BD
G11	BD-10080	BARI, Gazipur, BD	G22	K. King	Local market, Dhaka, BD
			G23	T. Green	Local market, Dhaka, BD

Table 3. Pooled analysis of variance of yield of yardlong bean.

Source of variation	Degrees of freedom	Mean sum of squares
Genotypes	22	124.58**
Env. + G × Env. (linear)	46	84.65*
Env. (Linear)	1	68.64*
G × Env. (Linear)	22	84.56**
Pooled deviation	28	84.65
Pooled error	188	6.55

**= Significant at 1% level of probability. *= Significant at 5% level of probability.

The AMMI (Additive main effects and multiplicative interaction) model ranked genotypes according to their yield stability index (YSI) depending on the AMMI stability value (ASV) was proposed by Purchase *et al.* (2000). The most stable genotypes may not give the best yield performance all time, hence, there is a need for approaches that incorporate both mean yield and stability in a single index and that is why many scientists have introduced different selection criteria for simultaneous selection of yield and stability (Kang 1993, Rao and Prabhakaran 2005, Babarmanzoor *et al*. 2009, Farshadfar 2011 and Bose 2014). In this regard, as ASV takes into account both IPCA1 (interaction of principal component analysis axis 1) and IPCA2, most of the variation in the GE interaction is justified, therefore, the rank of ASV and yield mean is such that the lowest ASV takes the rank one, while the highest yield mean takes the rank one and the ranks are then summed in a single simultaneous selection index of yield and yield stability called the yield stability index (YSI). The least YSI is considered as the most stable with high grain yield. According to these conditions, genotypes G11, G4, G13, G8, G17, G9, G18 and G1 were the most stable ones. Genotypes G2, G3, G4, G5, G7, G18, G20 and G11 were the most stable ones based on composite model (D_i) of Hanson (1970) due to showing low value. Different stability parameters were used to find out the suitable stable genotypes but all parameters did not indicate the same genotypes as stable. For identifying the stable genotypes total ranking system was used that was made by combining all the rank of different parameters (Table 4). According to this ranking method the lowest rank referred the stable genotype, thus, G18 was considered the most stable genotype because of showing the lowest rank (39) followed by G1 (40), G4 (41), G11 (42), G6 (42) and G9 (45).

Fig. 1 made by using phenotypic index and regression coefficient from Eberhart and Russel (1966) model shows the adaptive nature of the genotypes over different environments. High yielding genotypes such as G18, G9, G4 and G11 showed poor sensitivity to environments indicating least fluctuation of their yield performance in any environmental changes, consequently, reinforcing their position as stable genotypes. Other high yielding genotypes showed high sensitivity to environmental changes due to having higher regression coefficient value (b_i) than 1 referring not suitable for all environments. When these genotypes get favourable environments they would show high yield performance but low performance in unfavourable environments. Therefore, keeping these genotypes in the list of desirable genotypes would not be judicious. Rests of the genotypes were not desirable due to having low performance.

Different environments and yardlong bean genotypes were subjected to GGE biplot analysis to facilitate the visual interpretation of existing G × E interaction. The GGE biplot can effectively determine the magnitude and pattern of G × E interaction effect among the genotypes. Yan *et al*. (2000) proposed the GGE (Genotype and Genotype-by-Environment Interaction) biplot analysis based on the SREG (Sites Regression) model, suggested by Cornelius *et al*. (1996) and Crossa and Cornelius (1997). Fig. 2 showed the ranking of 23 genotypes based on their mean yield and stability performance across 3 diversified environments. The line passing through the biplot origin horizontally is called the average environment coordinate (AEC), which is defined by the average PC1 and PC2 scores of all environments (Yan and Kang 2003). The line passes through the origin and is perpendicular to the AEC represents the average yield performance of the genotypes. Genotypes located on the right hand side of the perpendicular line showed higher mean than average yield such as G18, G4, G9 and G11 (Fig. 2). Those genotypes located on the left hand side of the perpendicular line showed lower mean than average yield such as G2, G3, G7, G10 and G23. On the other hand, G13 showed nearly an average yield and G8, G16 and G17 showed above average yield performance.

An ideal genotype is one that has both high mean yield and high stability. The center of the concentric circles represents the position of an ideal genotype (Fig. 2). A genotype is more desirable if it is closer to the ideal genotype. Although such an ideal genotype may not exist in reality, it can be used as a reference for genotype evaluation (Yan and Kang 2003). Therefore, genotype G18, fell into the centre of concentric circle, was ideal genotype in terms of higher yield ability and stability, compared with the rest of the genotypes. Genotypes G9, G4 and G11 were near to the ideal genotype and were more desirable than others. Genotypes G2, G23 and G3 were unfavorable because they were far away from the ideal genotype.

Table 4.Estimates of stability parameters for yield of yardlong bean.

Code	Mean	Rank	Eberhart and Russell model					AMMI model			Hanson's model		Total rank
			P_i	b_i	Rank	S^2d_i	Rank	ASV	Rank	YSI	D_i	Rank	
G1	427.9	15	–111.78	0.9	2	–390.29	6	1.83	4	19	47.579	13	40
G2	152.48	23	–387.19	–0.34	15	–736.45	18	3.01	9	32	17.396	2	67
G3	252.07	21	–287.61	–1.13	21	–672.96	14	4.83	19	40	8.982	1	76
G4	744.6	3	204.93	–0.24	14	–596.79	10	3.04	10	13	22.767	4	41
G5	389.65	16	–150.03	0.33	7	–709.67	16	1.63	3	19	31.988	5	47
G6	383.53	17	–156.14	0.59	5	–187.83	4	2.41	6	23	43.834	10	42
G7	311.49	19	–228.19	–0.37	17	–671.96	13	3.19	11	30	18.567	3	63
G8	629.13	9	89.46	2.03	10	–544.9	9	2.63	7	16	69.287	16	51
G9	816.62	2	276.94	0.38	6	503.71	8	3.59	15	17	48.061	14	45
G10	294.95	20	–244.72	0.32	8	209.37	5	3.35	13	33	43.959	11	57
G11	707.03	7	167.35	0.66	4	–743.34	21	0.8	2	9	38.553	8	42
G12	743.61	4	203.93	2.35	16	1411.06	22	5.25	21	25	87.937	20	83
G13	509.48	14	–30.2	1	1	–737.37	19	0.38	1	15	45.718	12	47
G14	627.73	10	88.06	1.2	3	1555.75	23	4.6	17	27	69.323	17	70
G15	716.3	6	176.62	3.57	23	–717.84	17	5.7	22	28	100.835	23	91
G16	606.8	12	67.12	2.43	18	–692.43	15	3.22	12	24	76.607	19	76
G17	609.7	11	70.02	1.73	9	–597.15	11	1.97	5	16	62.5	15	51
G18	970.72	1	431.04	–0.21	13	31.52	3	3.71	16	17	34.29	6	39
G19	727.35	5	187.67	3.01	20	–462.38	7	4.8	18	23	90.345	21	71
G20	373.49	18	–166.18	–0.09	11	17	2	3.52	14	32	35.558	7	52
G21	631.21	8	91.53	3.3	22	16.32	1	5.82	23	31	98.851	22	76
G22	577.9	13	38.23	2.14	12	–647.12	12	2.74	8	21	70.811	18	63
G23	208.81	22	–330.86	–0.56	19	743.23	20	5.13	20	42	40.596	9	90

P_i= Phenotypic index, b_i = Regression coefficient, S^2d_i=Deviation from linearity, ASV= AMMI stability value, YSI = Yield stability index, D_i= Hanson's composite paramet

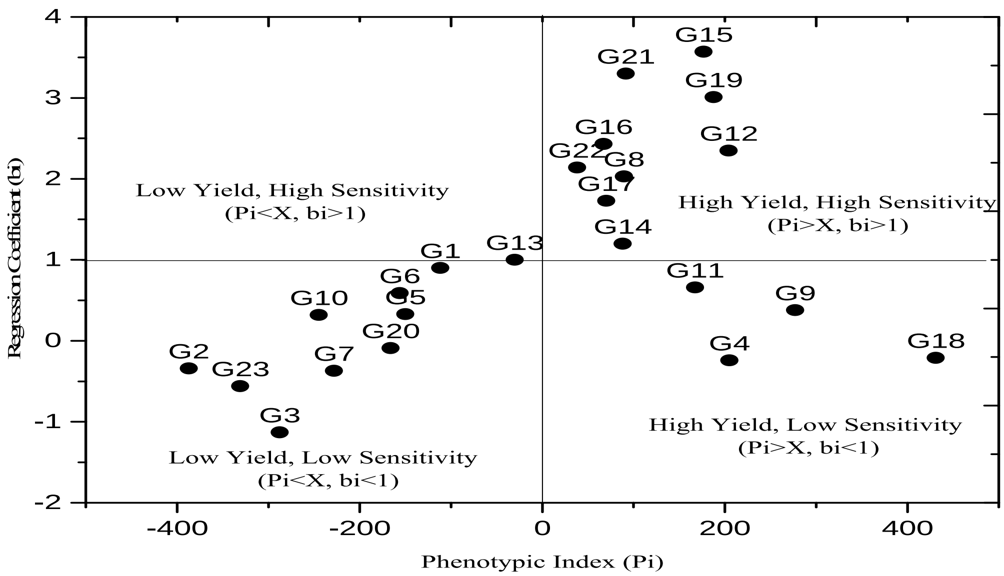

Fig. 1. Adaptive specificities of 23 yardlong genotypes. (X= Average value of Pi).

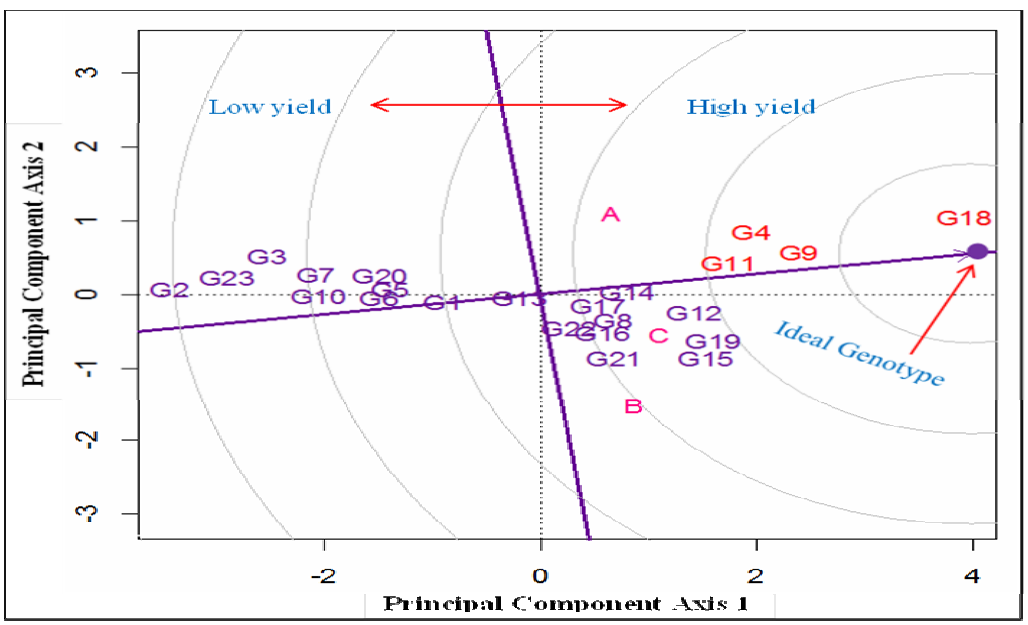

Fig. 2. Identification of superior genotypes through GGE biplot method. A = Dhaka (JU), B = Dinajpur, C= Bogra.

According to different stability parameters and GGE biplot method G18, G9, G4 and G11 showed promising high mean yield and adaptable nature over three locations. These genotypes can be recommended for national release for wider cultivation and also can be used in breeding programmes as stable gene sources in future yardlong bean research work.

Acknowledgements

The authors are grateful to Dept. of Genetics and Breeding, Hajee Mohammad Danesh Science & Technology University, Dinajpur and Dr. Mustafizur Rahman, Bogra for their kind support during the research.

References

AL-Aysh FM 2013. Analysis of performance, genotype-environment interaction and phenotypic stability for seed yield and some yield components in faba bean (*Vicia faba* L.) populations. Jord. J. Agri. Sci. **9**(1): 43-51.

Babarmanzoor A, Tariq MS, Ghulam A and Muhammad A 2009. Genotype × environment interaction for seed yield in Kabuli chickpea (*Cicer arietinum* L.) genotypes developed through mutation breeding. Pak. J. Bot. **41**(4): 1883-1890.

BBS 2013.Yearbook of Agricultural Statistics.p. 209.

Bose LK, Jambhulkar NN, Pande K and Singh ON 2014. Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. Chil. J. Agri. Res. **74**(1):3-9.

Cornelius PL, Crossa J and Seyedsader MS 1996. Statistical tests and estimators of multiplicative models for genotypeby-environment interaction. *In:* Kang MS and Gauch HG (Eds.) Genotype-by-environment interaction. CRC Press, Boca Raton, pp. 199-234.

Crossa J and Cornelius PL 1997. Sites regression and shifted multiplicative model clustering of cultivar trial sites under heterogeneity of error variances. Crop Sci. **37**: 405-415.

Ddamulira 1 G, Santos CAF, Obuo P, Alanyo1 M and Lwanga CK 2015. Grain yield and protein content of brazilian cowpea genotypes under diverse Ugandan environments. Amer. J. Plant Sci. **6**: 2074-2084.

Ebdon JS and Gauch HG 2002. Additive main effect and multiplicative interaction analysis of national turfgrass performance trials II: Cultivar recommendations. Crop Sci. **42**: 497-506.

Eberhart SA and Russell WW 1966. Stability parameters for comparing varieties. Crop Sci. **6**: 36-40.

Farshadfar E, Mahmodi N and Yaghotipoor A 2011. AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). Aus. J. Crop Sci. **5**(13): 1837-1844.

Frutos E, Galindo MP and Leiva V 2014.An interactive biplot implementation in R for modeling genotype-by-environment interaction. Stoch. Envir. Res. Ris. Ass. **28**: 1629-1641.

Gauch HG and Zobel RW 1997. Identifying mega environment and targeting genotypes. Crop Sci. **37**:311-326.

Gower JC 1967. Multivariate analysis and multivariate geometry. Statistician **1**7:13-28.

Hanson WD 1970. Genotypic stability. Theoret. Appl. Genet. **40**: 226-231.

Huque AKM, Hossain MK, Alam N, Hasanuzzaman M and Biswas BK 2012. Genetic divergence in yardlong bean (*Vigna unguiculata* subsp. *sesquipedalis* L. Verdc.). Bang. J. Bot. **41**(1): 61-69.

Kang MS 1993. Simultaneous selection for yield and stability in crop performance trials: Consequences for growers. Agron. J. **85**: 754-757.

Kongjaimun A, Kaga A, Tomooka N, Somta P, Vaughan DA and Srinives P 2012. The genetics of domestication of yardlong bean, (*Vigna unguiculata* L. Walp. subsp. *unguiculata* cv.-gr. *sesquipedalis*). Ann. Bot. pp. 1-16.

Kundy AC, Mkamilo GS and Misangu RN 2014. Genotype × environment interaction and stability analysis for yield and its components in selected cassava (*Manihot esculent* Crantz) genotypes in Southern Tanzania. J. Bio. Agri. Health. **19**(4): 29-39.

Lodhi RD, Prasad LC, BornareSS, Madakemohekar AH and Prasad R 2015. Stability analysis of yield and its component traits of barley (*Hordeum vulgare* L.) genotypes in multi-environment trials in the North Eastern Plains of India. SAB. J. Breed. Genet. **47**(2): 143-159.

Mendiburu FD 2015. Agricolae: Statistical procedures for agricultural research. R Package Version 1.2-3.

Mohammadi R and Amri A 2008. Comparison of parametric and non-parametric methods for selecting stable and adapted durum wheat genotypes in variable environments. Euphytica **159**: 419-432.

Mungomery VE. Shorter R and Byth DE 1974. Genotype × environment interaction and environment adaptation. 1. Pattern analysis- application to soya bean population. Aust. J. Agric. Res. **25**:59-72.

Nath D and Dasgupta T 2013. Genotype × environment interaction and stability analysis in mungbean. J. Agri. Veter. Sci. **5**(1):62-70.

Olayiwola MO, Soremi PAS and Okeleye KA 2015.Evaluation of some cowpea (*Vigna unguiculata* L. [Walp]) genotypes for stability of performance over 4 years.Cur. Res. Agri. Sci. **2**(1):22-30.

Purchase JL, Hatting H and Vandeventer CS. 2000. Genotype × environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: Π. Stability analysis of yield performance. S. Africa. J. Plant Soil. **17**: 101-107.

R Development Core Team 2014. R: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing.

Rao AR and Prabhakaran VT 2005. Use of AMMI in simultaneous selection of genotypes for yield and stability. Ind. Soc. Agril. Statist. **59**(1): 76-82.

Tolessa TT and Gela TS 2014.Sites regression GGE biplot analysis of haricot bean (*Phaseolus vulgaris* L.) genotypes in three contrasting environments. World J. Agri. Res. **2**(5): 228-236.

Ullah MZ, Hasan MJ, Rahman AHMA and Saki AI 2011.Genetic variability, character association and path analysis in yardlong bean. SAARC J. Agri. **9**(2): 9-16.

Vavilapalli SK, Celine VA and Vahab AM 2014. Assessment of genetic divergence among yardlong bean (*Vigna unguiculata* ssp. *sesquipedalis* L.) genotypes. Leg. Genom.Genet.**5**(1): 1-3.

Verma SK, Tuteja OP and Monga D 2008. Evaluation for genotypes × environment interaction in relation to stable genetic male's sterility based Asiatic cotton (*Gossypium arboreum*) hybrid of north zone. Ind. J. Agri. Sci. **78**(4): 375-378.

Vita PD, Mastrangetoa AM, Mattena L, Mazzncotellib E, Virzi N, Paluenboc M, Stortod ML, Rizzab F and Cattivelli L 2010. Genetic improvement effects on yield stability in durum wheat genotypes grown in Italy. Field crop Res. **119**:68-77.

Yan W and Kang MS 2003. GGE biplot analysis: A graphical tool for breeders, geneticists and agronomists. Boca Raton, FL: CRC Press.

Yan W, Hunt LA, Sheng Q and Szlavnics Z 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. **40**: 597-605.

(Manuscript received on 4 October, 2017; revised on 15 January, 2018)