PHENOTYPIC STABILITY IN ELITE PIGEON PEA (*CAJANUS CAJAN* (L.) MILL.) GENOTYPES USING BIPLOT MODELS

N Sandhya Kishore*, P Jagan Mohan Rao, A Saritha, G Neelima, S Sandeep, P Madhukar Rao, Sridhar Chouhan and N Lingaiah

Professor Jayashankar Telangana State Agricultural University, Hyderabad, India

Abstract

The yield stability of promisingpigeon pea genotypes across six locations was assessed using additive main effects and multiplicative interaction and Genotype plus genotype and environment interaction biplot models. The combined analysis of variance indicated that yield was significantly affected by genotypes, environments and genotype and environment interaction. The first two interaction principal componentsfrom the AMMI analysis accounted for 68.48% and from GGE accounted for 64.4% of variation due to GxE interaction. Both AMMI and GGE biplots identified G3 and G4 as most stable andG4 with the highest yield across six locations. The "What-won-where" biplot revealed that six environments fell into four sectors *i.e.,* E1and E2fell into one mega environment (ME 1), E3and E6another (ME 2), E4in one mega environment (ME 3) andE5 into another (ME 4). Environments E5and E1were most representative while E1could be regarded as least representative environment.

Introduction

Pulses are the important component of food chain and feed system across the globe as they contribute immensely to food and nutritional security in a sustainable manner through the diversification of agricultural production system (Singh *et al*. 2020).Food legumes supplement nutritionally rich fodder and feed for ruminants. Therefore, they serve as a functional element of many viable cropping and farming systems. Pigeonpea (*Cajanus cajan* (L.) Millspaugh) is commonly known as red gram, tur and arhar. It is the second most important pulse crop after chickpea and occupies an important place under rainfed agriculture in India (Sameer Kumar *et al*. 2014). It is a crop with a large temporal variation (97-299 days) for grain maturity. Hardy, widely adapted and drought tolerant traits allow its cultivation in a wide range of environments and different cropping systems.

GxE interactions are a challenge to plant breeders because they cause difficulties in selecting genotypes evaluated in diverse environments. When G×E interaction is significant, its cause, nature, and implications must be carefully considered (Kang *et al*. 1991). AMMI analysis combines ANOVA and principal component analysis (PCA).The interpretation of results obtained from AMMI analysis is performed with a biplot that relates to genotypic means to the first or some of the principal interaction components.GGE biplot analysis enables visual (graphical) presentationof the interaction estimate. GGE analysis enables the identification of genotypes with the highest yields in different environments, comparison of their performances in different environments,identification so called "ideal" genotype, as well as "mega environments"

There are two types of biplots that have been extensively used to visualize G × E interactions, and these are the AMMI (Gauch 1988,Gauch and Zobel 1996, GGE biplots, Yan *et al.* 2000). However, the application of the two biplots in research has been debated by Gauch *et al.* (2008). The comparison studies of GGE biplot with AMMI Models validate the equal efficiency ofGGE

---

*Author for correspondence: <kishoregene@gmail.com>.

biplot and AMMI models in understanding G×E interaction(Dias *et al.*2003).However, the difference between these models is the omission of environmental component in GGE biplot (Yan *et al.* 2007,Gauch*et al.* 2008).The present study aimed to estimate the pattern of genotype × location interaction for few elite medium duration pigeon pea genotypes to take a decision on their potential and adaptability during rainy (*kharif*) season for different locations of Telangana state and also to do a comparative study of popular multivariate analysis models, *i.e.,*additive main effects and multiplicative interaction model (AMMI) and genotype, genotype ×environment interaction (GGE) model.

Materials and Methods

The experiments were conducted during the rainy season, 2019, at six research stations *viz.,*Agricultural Research Station, Tandur (E1), Regional Agricultural Research Station, Palem (E2), Agricultural Research Station, Adilabad (E3), Regional Agricultural Research Station, Warangal (E4),Regional Agricultural Research Station, Jagtial (E5) and Agricultural Research Station, Tornala (E6) working under Professor Jayashankar Telangana State Agricultural University, Telanganastate, India. The characteristics of the different sites are presented in Table 1. Fig. 1 shows the amount of rainfall received at six different locations over the trial evaluation period.

Table 1. Parentage details of Pigeon pea genotypes along with environmental conditions.

Sl. No.	Code	Genotype	Parentage	Code	Environ-ments	Latitude	Longitude	MSL
1.	G1	WRG-366	ICPL-85063 × ICP-7035	E1	Tandur	$17^0 15$'N	$77^0 35$'E	553.18m
2.	G2	WRG-374	WRG-65 × ICP-7035	E2	Palem	$16^O 35^1$N	$78^0 10$'E	642.00 m
3	G3	WRG-65	WRG-13 × ICPL-87051	E3	Adilabad	$19^0 39$" N	$78^0 32$' E	268.80 m
4	G4	WRG-369	WRGE-14 × BSMR-736	E4	Warangal	$18^o 03$'N	$79^0 22$'E	270.00 m
5	G5	WRG-368	WRG-53 × BSNR-736	E5	Jagtial	$18^0 49$' N	$78^0 56$' E	243.40 m
6	G6	WRG-367	WRG-65 × BDN-2004-2	E6	Tornala	$18^0 06$' N	$78^0 44$' E	483.80 m
7	G7	IBTDRG-8	ICPL-87119 × ICPW-29	.				
8	G8	ICPL-87119	C11 × ICPL 6					

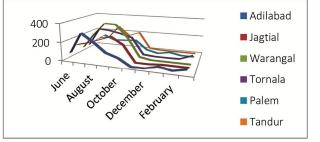

Fig. 1. Rainfall received during trial evaluation period over six environments.

The genotypes evaluatedin the present investigation were developed by pedigree method of breeding at Regional Agricultural Research Station, Warangal and Agricultural Research Station, Tandur under Professor Jayashankar Telangana State Agricultural University, Telangana State, India. The selected homozygous genotypes were evaluated in station yield trials from 2016-2018 for grain yield and also screened for traits like *Fusarium* wilt and Sterility mosaic Disease (SMD) resistance. Based on the superior performance, a total ofeight entries viz., WRG-366 (G1),WRG-374 (G2), WRG-65(G3), WRG-369 (G4),WRG-368 (G5),WRG-367 (G6), IBTDRG-8 (G7)and ICPL - 87119 (G8) were included in the multilocation testing.

Tillage at each site initiated with summer ploughings with discs (Depth adjust to 25 cm) followed by harrowing. The seeds were treated with *Rhizobium* culture. Sowing was carried out after receiving field capacity of rainfall (60mm).Field trials were carried out using RCBD with three replicates.Each genotype was planted in four rows with a length of 4 m and spaced 120 cm apart between the rows and 10 cm between plants.Each replication containing eight genotypes and 2 meters between the replications.At15 days after emergence,the plots were thinned to one plant per hill.Cultural practises such as weed,fertiliser and plant protection operations were executed. Drainage channels were laid around the trials for collecting the run-off.Comprehensive pest management methods, including the use of pheramone traps, bird perches were used. Standard crop management practices recommended by the state agricultural university were followed in raising a healthy crop across the locations. Data were recorded for grain yield on plot basis.

The combined analysis of variance was preceded to study the genotype x environment interaction of the genotypes across all environments. The AMMI model which combines standard analysis of variance with PC analysis was used to study the interactions (Zobel*et al.* 1988).

The AMMI model for G genotypes and E environments can be written as -

$$Y_{ij} = \mu + g_i + e_j + \Sigma\lambda_n\alpha_{in}\lambda_{jn} + \theta_{ij}$$

Where,

Y_{ij} is the mean yield of ith genotype in the jth environment;

μ is the general mean;

g_i is the ith genotypic effect;

e_j is the jth location effect;

$\lambda_n$is the eigen value of the principal component axis n:

α_{in} and λ_{jn} are the ith genotype,

j^{th} environment principle component analysis (PCA) scores for the PCA axis n:

$\theta_{ij}$is the residual.

n is the number of PCA axis retained in the model.

A windows based software GEA-R9genotype ×environment analysis with R for (Windows) version 4.1 developed by CIMMYT, Mexico was used for AMMI and GGE biplot analysis (Pacheco *et al.* 2015). The number of PCA axis to be retained is determined by testing the mean square of each axis with the estimate of residual through F-statistic (Gollob 1968,Gauch 1988). GGE biplot analysis was carried out by using the AMMI model R-packages 1.5 PBTools 1.4 version IRRI (PBTools 2014). The AMMI biplot is developed by placing both genotype of environment mean value on X-axis and the respective IPCA axis eigenvector on the Y-axis (Zobel*et al.* 1988).

Results and Discussion

The mean grain yield over the locations ranged from 1826 kg/ha (WRG-368) to 2033kg/ha (WRG-369), while, maximum grain yield (2344kg/ha) recorded at E6 (Tornala) and minimum at 1601 kg/ha at E1 (Tandur) among the different environments (Table 4). Combined analysis of variance of eight medium duration pigeon pea genotypes tested for grain yield over six locations indicated that pigeon pea grain yield was significantly (p<0.01) affected by environments and genotypes × environment interactions (Table 2) indicating the presence of considerable interaction of genotypes with the environments for the trait under study. Only a small portion of (2.23%) the total sum of squares was attributed to genotypic effects. 52.59% of the total sum of squares was ascribed by environmental fluctuations exhibiting that the environments were diverse, with large difference among environmental means causing the most of the variation in yield. This is in harmony with the findings of Panwar *et al.* (2008) and Mahnaz Rashidi *et al.* (2013). Genotypes × environment interactions significantly explained 26.02% of the treatment's variation for grain yield. The combined analysis of variance indicated that there was a strong interaction between genotypes and environments. The trend of mean grain yield (kg ha^{-1}) over environments is graphically represented in Fig.2.

Table 2. Combined analysis of variance of grain yield for eight medium duration Pigeon pea genotypes evaluated at six environments.

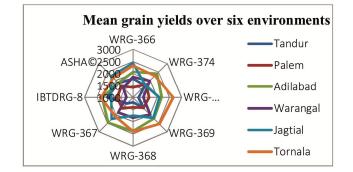| Source	d.f	S.S	M.S	Explained S.S (%)
Varieties	7	553003.34	79000.47	2.23
Environments	5	13010710.24	2602142.04	52.59
Varieties X Environments	35	6438347.89	183952.79	26.02
Error	96	4737467.24	49348.61	
Total	143	24739528.72		

Fig. 2. Yield performance of eight Pigeon pea genotypes over six environments.

To investigate the main effects and interactions across different environments, AMMI 1 and AMMI 2 biplots were constructed for yield (Table 3). AMMI 1 biplot of main effects (genotype and environments) are shown along the abscissa and the ordinate represents the first IPCA. The interpretation of biplot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive, if different, their interaction is negative. The IPCAI versus IPCAII biplot (AMMI 2 biplot) explains the magnitude of interaction of each genotype and

environment. Earlier reports confirmed that in most of the cases the maximum genotype and environment interaction could be explained through using the first two PCAs (Fikere *et al.* 2014 and Biswas *et al.*2019). Therefore, IPCA1 and IPCA2 were used for construction of AMMI1 and AMMI2 biplots. The genotype and environments that are farthest from the origin being more responsive and fit the worst genotypes and environments that fall into the same sector interact positively and negatively if they fall into opposite sectors (Anandan *et al.* 2009). The IPCA scores of genotypes in the AMMI analysis are an indication of stability over environments (Gauch and Zobel 1996 and Martin and Alberts 2004).

Table 3. AMMI analysis of variance for grain yield of eight medium duration Pigeon pea genotypes evaluated at six environments.

Source	S.S	Percent	Percent ac.	DF	M.S	F
ENV	13010059.15	65.04	65.04	5	2602011.82	52.72
GEN	552723.60	2.76	67.81	7	78960.51	1.59
ENV*GEN	6438361.68	32.18	100	35	183953.19	3.72
PC1	2788049.15	43.30	43.30	11	253459.01	5.51
PC2	1621502.26	25.18	68.48	9	180166.91	3.91
PC3	1257139.94	19.52	88.01	7	179591.42	3.90
PC4	515516.38	8.00	96.02	5	103103.27	2.24
PC5	256153.93	3.97	100	3	85384.64	1.85
PC6	0	0	100	1	0	0
Residuals	4737856	0	0	96	49352.66	

According to the AMMI model, the genotypes which are characterized by means greater than striking mean and the IPCA score nearly zero are considered as generally adaptable to all environments. According to Fig. 3, the genotypes G4,G1 and yielded above the overall genotype average, whereas the genotype G5 was the poor yielder. The Genotypes G4, G2 and G5 exhibited high grain yield than mean yield with specific adaptability for the environments E5 (Jagtial) and E3 (Adilabad). As the genotypes and environments of this adaptive group have the same sign on the IPCA axis. Genotype G1) revealed specific adaptation for the environment E5with high grain yield more than mean yield and positive interaction. Genotypes G3 and G5 exhibited specific adaptability for the environment E4with grain yield less than mean. Varieties with high mean yield and large PCA scores were considered as explicitly adapted to specific environments (Abdi and Williams 2010 and Askari *et al*. 2017). For the AMMI 2 biplot, IPCA 2 scores considered in interpreting genotype × environment interaction as suggested by Gauch and Zobel (1996). A biplot is generated using genotypic and environmental scores IPCA2, Purchase*et al.* (2000) pointed out that the closer the genotypes score to the center of the biplot, the more stable the genotypes are (Fig. 4). Allocation of genotype points in the AMMI 2 biplot revealed that the genotypes G3 and G4 dotted close to the origin, indicating least interaction of these genotypes with environments. The remaining genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. The same trend has been observed by Mahnaz Rashidi *et al.* (2013). The genotypes G5 and G2 had positive interaction with environments E6and E3. The genotypes G1 and G8 displayed positive interaction with the environment E5. The genotype G7 indicated specific adaptability and positive interaction with the environments E1and E2.

Table 4. Mean yields (kg/ha) of the pigeon pea genotypes across six environments.

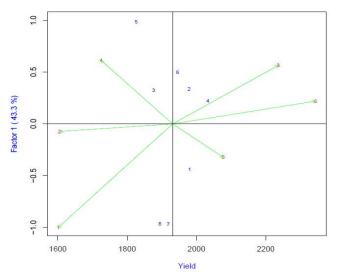| Genotype & Environment Code	Genotype & Environments names	Mean yield (kg/ha)	AMMI		GGE	
			IPCA1	IPCA2	IPCA1	IPCA2
G1	WRG-366	1980	-7.22	13.60	-242.16	379.87
G2	WRG-374	1978	5.58	-11.07	161.46	-165.63
G3	WRG-65	1876	5.35	-1.59	189.12	-190.35
G4	WRG-369	2033	3.70	5.43	89.30	217.07
G5	WRG-368	1826	16.21	-4.31	525.60	-154.84
G6	WRG-367	1946	8.22	7.65	245.74	242.19
G7	IBTDRG-8	1918	-15.96	-16.49	-481.37	-459.55
G8	ICPL-87119	1894	-15.89	6.78	-487.69	131.23
E1	Tandur	1601	-22.82	-7.32	-0.770	-0.08
E2	Palem	1605	-1.67	-6.98	-0.08	-0.152
E3	Adilabad	2236	12.88	-10.30	0.38	-0.21
E4	Warangal	1725	13.96	9.24	0.39	0.59
E5	Jagtial	2077	-7.36	20.39	-0.27	0.73
E6	Tornala	2344	5.020	-5.01	0.14	-0.18

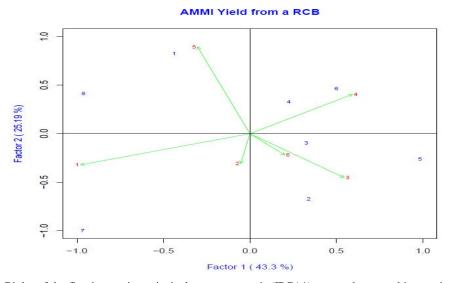Fig. 3.Biplot of the first interaction principal component axis (IPCA1) versus mean yields.

Fig. 4.Biplot of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) for pigeon pea genotypes.

The What-won-where GGE biplot (Fig. 5) revealed the information about which genotype is top performer in the respective environment and ideal for which particular environment. The polygon is drawn on genotypes that lie farthest from the biplot origin in such way that all other genotypes are contained within the polygon. The "what-won-where" biplot revealed that six environments fell into four sectors *i.e.,*E1and E2 fell into one mega environment (ME 1), E3 and E6 another mega environment(ME 2), E4 in one mega environment (ME 3), andE5 into another mega environment(ME 4). As E1and E2 fell under single ME 1 and E3and E6under ME 2, from each MES, any one of these environments is sufficient to study the performance of genotypes. Genotype 7was the winner in the mega environment 1, Genotype G5 was the winner in mega environment 2, genotype G6 was winner in mega environment 3 and genotype G1 was winning genotype in mega environment 4. These genotypes performed better than other genotypes in the respective mega environments.

The average environment axis (AEA) is the line passing through the average environment and the biplot origin. A test environment showing a smaller angle with the AEA is more representative than other test environments (Yan and Rajcan2002). Test environments that are consistently non discriminating provide little information on the genotypes, which is inappropriate as test environments (Kang-Bo-Shim *et al.* 2015). Discriminativeness vs Representativeness GGE biplot for grain yield revealed thatE5had the least cosine angle with average environmental axis (AEA) (Fig. 6) and could be declared as the least discriminative environment, whereas E4 was observed to be the most discriminative environment as it made the largest cosine angle with AEA followed by E1.Environment E6and E2were the test environments that had both discriminating and representative, hence could serve as good test environment for selecting generally adapted genotypes. Discriminative but non-representative test environment E4was useful for rejecting unstable genotypes if the target environment is a single mega environment. E5was most representative among all environments, while E1 was least representative of all environments.
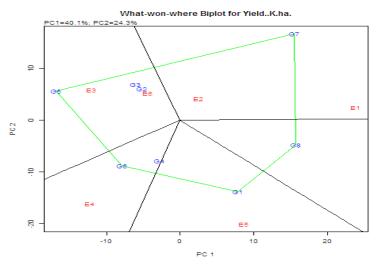
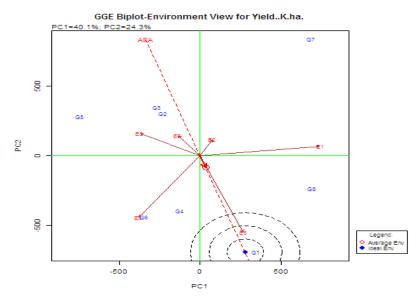Fig. 5.Polygon view of the GGE biplot of grain yield of eight genotypes over six locations.

Fig.6. GGE biplot based on environment focused for comparing environments with ideal environment.

The line that passes through the biplot origin and the average environment with single arrow is the average environment axis (AEA). Projections of genotype markers to the AEA showed the mean yield of genotypes. Greater projection onto AEA ordinate, regardless of the direction means greater instability (Kang-Bo-Shim *et al.* 2015). The genotypes G3, G2and G4 showed shorter projections and were relatively stable over environments (Fig. 7). Whereas, G7showed greater projection onto AEA ordinate indicating the greater instability. The genotype that showed good performance with stability includingG4 since it ranked first in yielding and short projection of the genotype marker lines.
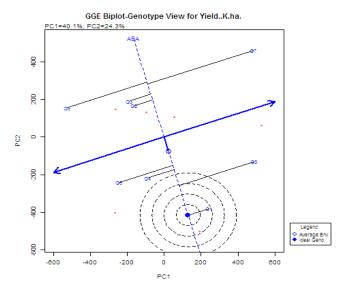
Fig. 7. Biplot of stability and mean performance of eight genotypes across average environments.

The genotypes G4, G1 and G2 yielded above the overall genotypes average, whereas the genotype G5 was the poor yielder. The Genotypes G4, G2 and G5 exhibited high grain yield than mean yield with specific adaptability for the environments E5and E3. Environments E2and E6could be regarded as more stable sites and the environment E4as the most discriminating environment while E1 was the most representative environment. Hence, the genotype G4showing most stable across six locationswith highest yield can be given to farmers field for further evaluation before its release for general cultivation.

Acknowledgements

References
Abdi H and Williams LJ 2010. Principal Component Analysis', Wiley Interdisciplinary Reviews: Comput.Stats. **2**(4): 433-459.

Askari H, Kazemitabar KS, Zarrini NH and Saberi HM 2017.Analysis of the genotype by salt interaction of Barley (*Hordeum voulgar* L) genotypes at early growth stage by graphical models. Intl. J. Agri. Envi. Res. **3**: 190-196.

Anandan A, Eswaran R, Sabesan T and Prakash M 2009.Additive main effects and multiplicative interactions analysis of yield performances in rice genotypes under coastal saline environments. Adv. in Bio Res.**3**: 43-4.

Biswas T, Debasis M, Arpita D, Dinesh PK, Anirban M, Parihar AK and Gupta S 2019. Additive main effects and multiplicative interaction in field pea (*Pisum sativum* L.) genotypes across the   major agro-climatic zones in india. Leg Res.DOI:**10**.18805/LR-4166

Dias CT, Dos S and Krzanowskib WJ 2003. Model selection and cross validation in additive main effect and multiplicative interaction models. Crop Sci.**43**: 865-873.

Fikere M, Bing DJ, Tadesse T and Ayana A 2014. Comparison of biometrical methods to describe yield stability in field pea (*pisum sativum* L.) under south eastern Ethiopian conditions. Afri. J. Agric Res.**9**: 2574-2583.

Gauch HG 1988. Model selection and validation for yield trials with interaction. Biometrics.**44**: 705-715.

Gauch HG and Zobel RW 1996.AMMI analysis of yield trials.Genotype-by EnvironmentInteraction. CRCPress, Boca Raton, Florida,USA.

Gauch HG, Piepho HP and Annicchiarico P 2008.Statistical analysis of yield trials by AMMI and GGE: further considerations. Crop Sci.**48**: 866-889.

Gollob HF 1968. A statistical model which combines features of factor analytic and analysis of variance techniques. Psychometrika.**33**: 73-115.

Kang MS, Gorman DP and Pham HN 1991.Application of a stability statistic to international maize yield trials. Theor Appli.Gen. **81**: 162-165.

Kang-Bo-Shim, Seong-Hyu-Shin, Ji-Young Shon, Shin-Gu-Kang, Woon-Ho Yang and Sung-Gi-Hey2015. Interpretation of genotype x environment interaction of sesame yield using GGE biplot analysis. Koren J. Crop Sci. **60**: 349-354.

Mahnaz Rashidi, Ezatollah Farshdfar and Mohammad Mahdi Jowkar. 2013. AMMI Analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments. Int.J.Agri. Crop Sci.**5**: 253-260.

Martin Jand Alberts 2004.A comparison of statistical methods to describe genotype x environment interaction and yield stability in multi-location maize trials.Faculty of Agriculture, Department of plant Science (Plant Breeding) at the University of the Free State.

PachecoA, Vargas M, Alvarado G, Rodriguez F, Crossa Jand Burgueno 2015. GEA-R (Genotypex Environment Analysis with R for Windows) Version 4.1.Hdl.11529/10203, CIMMYT Research Data and Software Repository Network.

Panwar LL, Joshi VN and Mashiat Ali 2008.Genotype x environment interaction in scented rice.Oryza.**45**: 103-109.

PBTools, version 1.4. 2014. Biometrics and breeding informatics, PBGB division, International Rice Research Institute, Los Banos, Laguna.

Purchase JL, Hatting H and van Deventer CS 2000. Genotype x environment interaction of winter wheat (*T. aestivum*) in South Africa: stability analysis of yield performance. SouthAfrica J. Plant.Soil. **17**: 101-107.

Sameer Kumar CV, Myer G Mula, Singh IP, Mula RP, Rachit K Saxena, Ganga Rao NVPR and Rajeev K Varshney. 2014. Pigeonpea Perspective in India. Paper presented during the '1st Philippine Pigeonpea Congress. Mariano Marcos State University, Batac, Ilocos Norte, Philippines. December 16-18.

Singh NP and Praharaj CS 2020. Scenario of pulses production and consumption in India.Paper presented during the international conference on pulses as climate smart crops: challenges and Opportunities. 3-9.

Yan W, Kang MS, Ma B, Woods S and Cornelius PL 2007.GGE biplot vs AMMI analysis of genotype-by-environment data. Crop Sci**. 47**: 643-53.

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

Yan W and Rajcan I 2002. Biplot analysis of test sites and trait relations of Soybean in Ontario.Crop Sci. **42**: 11-20.

Zobel RW, Wright MJ and Gauch HG 1988.Statistical Analysis of a Yield Trial.Agronomy Journal.**80**: 388-393.