RESEARCH ARTICLE Legume Research- An International Journal, Volume 43 Issue 5: 698-701 (October 2020)

Analysis of Multi-Environment Yield Trails of Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] Genotypes using GGE Biplot

A. Manivannan

10.18805/LR-4177

ABSTRACT

A set of 42 clusterbean genotypes were evaluated for yield attributing trait pods per plant over three environments. Pooled analysis of variance showed that Environments (E) explained highest proportion of variation for pods per plant, accounting for 42.16% of it, followed by G × E interactions (GEI) effects (31.1%) and genotype (26.7%). Higher effect of GEI compared to G alone indicated the possible existence of mega environments among the testing locations. The biplot explained 89% of the total variation relative to G plus GEI. Based on environment discrimination test, Environment 1(Madurai) is the ideal environment. Which Won Where (WWW) Polygon identified the most diverse genotypes namely M local, T local, RGC1055, RGC1033, HGS75, MRSG6 and CAZG10-2 were found to be highly diverse. These genotypes also occupied the convex of the hull. The genotype CAZG10-2 won in the Environment1 (E1) and the genotype HGS75 won in both environments E2 (Coimbatore) and E3 (Kovilpatti). Genotype stability test identified genotypes namely RGC1031, R local, HGS75, MRG1786, HGS2-1, HGS365, RGC1003, HGS2-4, HGS2-20 and PNB were stable over the other genotypes as they placed near to the Average Environment Coordination (AEC) abscissa.

Key words: Clusterbean, G × E interactions, GGE biplot, Stability.

INTRODUCTION

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] known as guar, is a drought tolerant annual legume crop, known for its versatile usage like vegetable, fodder, green manure, gum extraction, and medicinal purpose. Young tender pods of clusterbean are used as vegetable in India and African countries. Clusterbean for gum extraction largely cultivated in *kharif* (rainy season) season across the Northern India. The crop is now being cultivated in dry tracts of Chhattisgarh, Andhra Pradesh, Karnataka, Tamil Nadu and other parts in *kharif* as well as in summer season. The crop has also been able to compete with other *kharif* crops like groundnuts, pearl millet, sorghum, cotton, *etc* (Manivannan *et al.* 2016).

Crop breeding efforts focus on genetic gain of yield traits within their target environment or across the environments. Performance of a genotype across the environment is better understood by the genotype × environment interaction. Biplot methodology has greatly addressed the complex GEI in much simplistic graphical manner (Gabriel 1971). Recently GGE biplot analysis is getting popular due to powerful visual tool for making superior genotype selections and classifying test locations and also could be a quick way to visualize G×E or stability across mega-environments (Yan and Tinker 2006). GGE biplot analysis has been carried out in understanding GEI in many crop species. In spite of reports on utility of GE analysis in deciding superior genotypes and/or test environments in many crops, application of such techniques in clusterbean is not yet performed, hence the study was envisaged.

Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.

Corresponding Author: A. Manivannan, Central Institute for Cotton Research, Regional Station, Coimbatore-641 003, Tamil Nadu, India. Email: manivannan461@gmail.com

How to cite this article: Manivannan, A. (2020). Analysis of Multi-Environment Yield Trails of Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] Genotypes using GGE Biplot. Legume Research. 43(5): 698-701.

Submitted: 04-06-2019 **Accepted:** 05-09-2019 **Published:** 03-12-2019

MATERIALS AND METHODS

A set of 42 clusterbean germplasm accessions (Table 1) were obtained from various leading centers of clusterbean research which represents different agro-geographical diverse areas of India. They were evaluated in three environments namely E1 (Environment 1) Madurai; E2 (Environment 2), Coimbatore and E3 (Environment 3) Kovilpatti. Experiment was conducted as per RCBD (Randomized Complete Block Design) in plot sizes of 39×3 m during 2012-13 with two replications per entry. Each entry occupied a three meter row with crop geometry of 45×15 cm. All agronomical practices were followed as prescribed by the agronomists. Here yield is taken as pods per plant for stability analysis. The statistical method of GGE Biplot explained by Yan and Kang (2003) was employed. The software GGE biplot ver. 6.3 (Yan, 2001) was used in the analysis.

RESULTS AND DISCUSSION

Pooled analysis of variance among 42 cluster bean genotypes tested in three environments over two years showed that genotype and environments effects were significant. Environment (E) explained highest proportion of variation for pods per plant, accounting for 42.16%, followed by G×E interactions (GEI) effects (31.1%) and genotype (26.7%). Effect G×E interactions (GEI) is higher than the Genotype (G) alone. Higher effect of environment was also observed in other pulse crops (Sabaghnia *et al.* 2008). Higher effect of GEI compared to G alone indicated the possible existence of mega environments among the testing locations.

Table 1: List of germplasm used in G x E interaction studies in Clusterbean.

Genotype code	Genotype	Source
1	RGC1002	RAU, Durgapur
2	HFG119	HAU, Hisar
3	HGS884	HAU, Hisar
4	HGS16	HAU, Hisar
5	GAU512	SDAU, Krushinagar
6	HGS365	HAU, Hisar
7	RGC1066	RAU, Durgapur
8	HGS75	HAU, Hisar
9	HVG2-30	HAU, Hisar
10	HGS2-4	HAU, Hisar
11	RGC471	RAU, Durgapur
12	T local	Local landraces from Thiruvanamalai, Tamil Nadu
13	RGC1017	RAU, Durgapur
14	HGS3-52	HAU, Hisar
15	HGS563	HAU, Hisar
16	RGM2	RAU, Durgapur
17	SRG1058	CAZRI, Jodhpur
18	HGS2-20	HAU, Hisar
19	RGC936	RAU, Durgapur
20	HGS258	HAU, Hisar
21	RGC1055	RAU, Durgapur
22	HGS2-1	HAU, Hisar
23	FS277	HAU, Hisar
24	RGC197	RAU, Durgapur
25	Amrit 11	Local variety from Gujarat
26	HGS870	HAU, Hisar
27	CAZG10-2	CAZRI, Jodhpur
28	MRG1786	CAZRI, Jodhpur
29	HGS182	HAU, Hisar
30	RGC1038	RAU, Durgapur
31	M local	Local landraces from Mettur, Tamil Nadu
32	MRSG6	CAZRI, Jodhpur
33	RGC1003	RAU, Durgapur
34	RGM1	RAU, Durgapur
35	R local	Local landraces from Rajasthan
36	RGC986	RAU, Durgapur
37	PNB	IARI, New Delhi
38	GAU 513	SDAU, Krushinagar
39	RGC1031	RAU, Durgapur
40	HGS3-2	HAU, Hisar
41	HGS832	HAU, Hisar
42	RGC1033	RAU, Durgapur

GGE Biplot

The genotype plus genotype × environment (GGE) biplot Yan (1999) was used to visualize winning genotypes and their environmental niches. This procedure grouped homogenous environments based on a similar genotype response and identifies the best performing genotypes at their most influential environments for the traits studied. In GGE biplot analysis, G×E interaction (GEI) partitioned into different Principal components (PCs) and data set is presented graphically against various PC (Yan and Tinker 2006). If the first two PC explain more than 60% of the (G + GE) variability and the combined (G + GE) effect account for more than 10% of the total variability, then the biplot adequately approximates the variability in G×E data (Yan *et al*. 2010). In our present study, the percentage of GGE for pods per plant explained by PC1 and PC2 was 89% of the total variation. Further, relative to G plus GEI and the combined effect (G+GEI) was accounting for 57 percentages. This result revealed that there was a differential yield performance among clusterbean genotypes across testing environments due to the presence of GEI. The presence of GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance through minimizing the association between phenotype and genotype. Yan and Hunt 1998 also obtained 78% of total variation of G+GEI (PC1 = 59% and

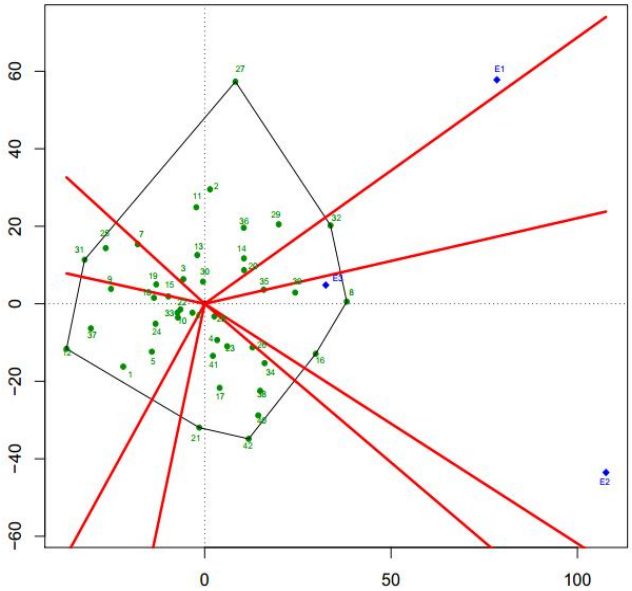


Fig 1: Which-Won-Where (WWW) pattern. (genotype codes given in Table 1).

PC2 = 19%) in winter wheat trails. Therefore, studying yield performances, patterns and GEI of clusterbean is crucial in genotype evaluation and test environment investigation.

Which-Won-Where (WWW)

Which-Won-Where is a polygon-view of a GGE biplot, provides an effective and elegant means of visualizing the MET dataset (Fig 1). For the trait pods per plant, the polygon was drawn by joining the genotypes namely CAZG10-2, M Local, T local, RGC1055, RGC1033, HGS75 and MRSG6 as they were located farthest from the origin, and all other genotypes contained inside of the polygon (These genotypes considered to be diverse). The genotype CAZG10-2 won in the Environment 1 (E1) and it is clearly

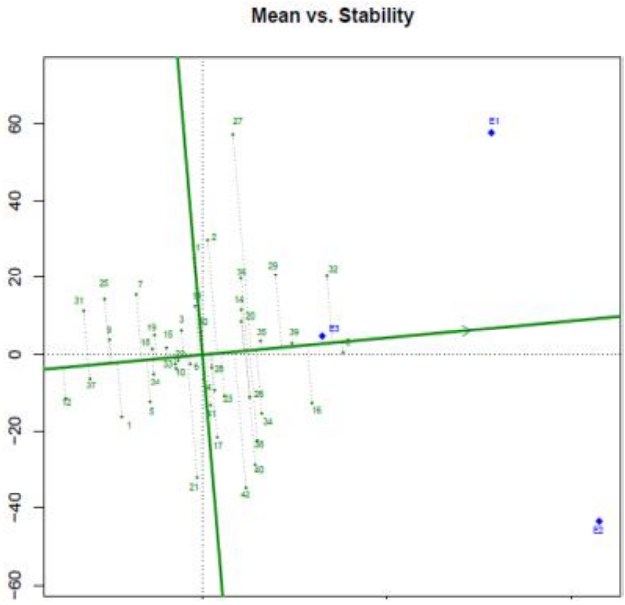


Fig 2: Forty two clusterbean genotypes evaluated based on mean and stability. (genotype codes given in Table 1).

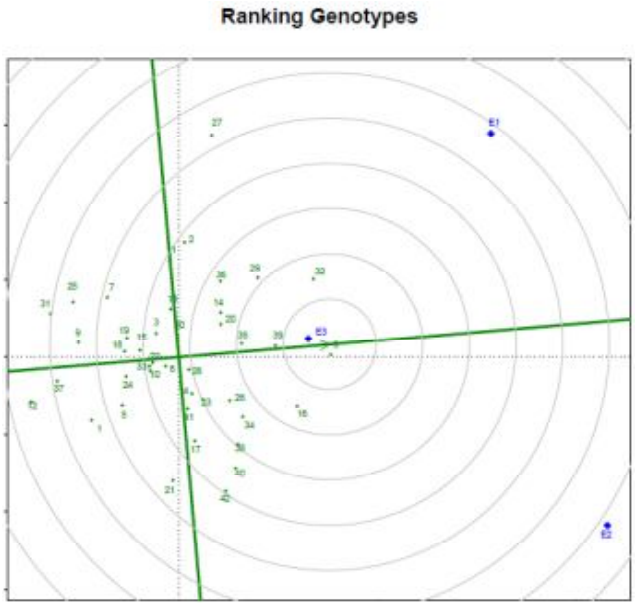


Fig 3: Comparison of genotypes in relation to the 'ideal' genotype. (genotype codes given in Table 1).

Table 2: Pooled mean performance of 42 clusterbean genotypes across the environments.

Code	Genotypes	E1	E2	E3	PE	Code	Genotypes	E1	E2	E3	PE
1	RGC1002	21.30	44.00	25.40	30.23	23	FS277	43.90	69.00	31.20	48.03
2	HFG119	59.60	47.50	41.00	49.37	24	RGC197	31.70	47.00	34.90	37.87
3	HGS884	43.60	50.30	33.60	42.50	25	Amrit11	34.00	27.90	24.00	28.63
4	HGS16	37.80	61.90	55.70	51.80	26	HGS870	49.50	76.40	28.00	51.30
5	GAU512	28.30	49.60	29.40	35.77	27	CAZG10-2	81.60	45.60	29.20	52.13
6	HGS365	43.20	57.80	22.20	41.07	28	MRG1786	45.80	63.00	28.80	45.87
7	RGC1066	41.50	36.50	21.50	33.17	29	HGS182	71.00	71.10	29.90	57.33
8	HGS75	72.10	95.20	41.10	69.47	30	RGC1038	48.90	57.10	25.20	43.73
9	HVG2-30	29.30	33.10	25.40	29.27	31	MLOCAL	26.90	22.40	30.30	26.53
10	HGS2-4	37.20	52.50	34.20	41.30	32	MRSG6	78.20	82.70	45.50	68.80
11	RGC471	53.80	45.10	44.00	47.63	33	RGC1003	36.60	51.00	40.00	42.53
12	TLOCAL	13.10	27.70	21.10	20.63	34	RGM1	48.80	80.40	33.20	54.13
13	RGC1017	50.60	52.40	28.90	43.97	35	RLOCAL	56.10	71.10	45.10	57.43
14	HGS3-52	53.20	60.30	60.70	58.07	36	RGC986	58.50	58.20	54.70	57.13
15	HGS563	38.80	48.40	30.80	39.33	37	PNB	19.30	31.10	28.40	26.27
16	RGM2	57.80	91.20	46.10	65.03	38	GAU513	43.50	81.40	36.60	53.83
17	SRG1058	36.70	71.00	31.60	46.43	39	RGC1031	63.20	80.70	39.60	61.17
18	HGS2-20	35.60	44.60	31.30	37.17	40	HGS3-2	39.70	83.20	37.10	53.33
19	RGC936	37.50	43.60	33.10	38.07	41	HGS832	36.60	63.70	46.80	49.03
20	HGS258	57.20	65.80	33.00	52.00	42	RGC1033	34.80	83.10	36.10	51.33
21	RGC1055	27.70	69.80	29.30	42.27		**Mean**	44.43	58.31	34.41	45.71
22	HGS2-1	41.40	54.40	21.20	39.00		**SEd**	4.17	3.08	2.04	9.19

E1-Environment 1, E2-Environment 2, E3-Environment 3, PE-Pooled Environments.

evidenced from the mean value (Table 2) of the genotype was the highest (86.1) in E1. The genotype HGS75 won in both environments E2 and E3, this is evidenced from the mean value of the genotype HGS75 in E2 (95.20) and E3 (41.10).

Genotype evaluation based on mean performance and stability

Genotype evaluation based on mean and stability was depicted in Fig 2 of GGE Biplot. The AEC ordinate is the double-arrowed line that passes through the biplot origin and is perpendicular to the AEC abscissa. The genotypes namely RGC1031, R local, HGS75, MRG1786, HGS2-1, HGS365, RGC1003, HGS2-4, HGS2-20 and PNB were stable over the other genotypes as they placed near to the abscissa. In contrast, the genotypes namely CAZG10-2 and RGC1033 located far away from the AEC abscissa, it indicates these two genotypes were much more variable towards their environments (less stable).

Ranking of genotypes based on ideal genotype

The small circle in Fig 3 which is located on the AEC abscissa and an arrow pointing to it represents the ideal genotype (as they will be having highest yield and most stable one). The genotype HGS75 plotted proximate to the ideal genotype and the genotypes were ranked based on ideal genotype in the order of HGS75, MRSG6, RGM2, RGC1031, HGS182, R local, RGM1, CAZG10-2, GAU513, RGC986, HGS870, HGS3-52, HGS258, RGC1033, FS277, HFG119, HGS3-2, MRG1786, SRG1058, HGS832, HGS16, RGC1038, RGC471, RGC1017, HGS365, RGC1055, HGS884, HGS2-1, RGC1003, HGS2-4, HGS563, RGC936, HGS2-20, RGC197, GAU512, RGC1066, RGC1002, HVG2-30, Amrit11, M local, PNB and T local.

CONCLUSION

The genotype plus genotype × environment (GGE) biplot useful in identifying the homogenous test environments, which would be helpful to reduce the test locations especially in conducting mega environment analysis and in AICRP trails, which involves large number of test locations across the country. However, the WWW pattern needs to be reconfirmed over years before attempting to the exercise. GGE biplot is more reliable because it displays the relative magnitude of the G (environment main effect) and IPCA1. In contrast, AMMI biplot 1 is misleading regarding the "Which-Won-Where" issues, if associate the genotypes closer to the particular environment based on location in AMMI 1 Biplot. "Which Won Where" pattern in AMMI biplot 1 is not a true representative when compare to GEB Biplot's "Which Won Where" pattern.

REFERENCES

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

Manivannan, A., Anandakumar, C.R., Ushakumari, R and Dahiya, G.S. (2016). Characterization of Indian clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] genotypes using qualitative morphological traits. Genet. Resour. Crop Evol. 63: 483-493.

Sabaghnia, N., Dehghani, H and Sabaghpour S.H. (2008). Graphic analysis of genotype by environment interaction for lentil yield in Iran. Agron. J. 100: 760-764.

Yan, W. (1999). Methodology of cultivar evaluation based on yield trial data-with special reference to winter wheat in Ontario. Ph.D. Thesis, University of Guleph, Guleph, Ontario, Canada.

Yan, W. (2001). GGE biplot-a windows application for graphical analysis of multi-environment trial data and other types of two-way data. Agron J. 93: 1111-1118.

Yan, W. and Hunt, L.A. (1998). Genotype-by-environment interaction wheat breeding and crop yield. Plant Breed. Rev. 16: 135-178.

Yan, W. and Kang, M.S. (2003). GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists. CRC Press, Boca Raton.

Yan, W. and Tinker, N.A. (2006). Biplot analysis of multi-environment trial data: principles and applications. Can. J. Plant Sci. 86: 623-645.