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Understanding of Yield Stability in Jack Bean (*Canavalia ensiformis* L.) Genotypes using AMMI and GGE bi-plot Models

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ABSTRACT

Background: Jack bean is an under-exploited legume species, a source of food, medicine and cover crop. By virtue of its adaptive nature to low fertility soils, it is one of the few pulses that grow well on highly leached, nutrient depleted, lowland tropical soils. But, in India, crop improvement work is very little done. Stability of yield is a major criterion for farmer's acceptability of any variety and there are several methods to estimate the stability and G x E interaction effects of a genotype across seasons. Among these, AMMI analysis is the most recent and widely exploited in different crops for the identification of stable genotypes. In this context, yield stability of 10 accessions of jack bean is studied to identify the stable genotypes.

Methods: The experiment was conducted with 10 Jack bean genotypes in RCBD with two replications under rain fed conditions during 2017-2020 in *Kharif* for four seasons. The data was subjected to analysis of variance and then taken for AMMI and GGE analysis for identification of stable genotypes.

Result: The combined analysis of variance revealed that there was highly significant variation ($p < 0.01$) in grain yield and environments and genotype interaction among the genotypes. The average bean yield of the genotypes was 533.1 grams per plant. The highest and the lowest mean yield was recorded in PSR-12202 and CHMJB-02 respectively which was corroborated by the AMMI bi-plot as well. Similar to the AMMI bi-plot, the GGE bi-plot also confirmed that PSR-12202 was the stable genotype across the environments, whereas, G1, G2, G3, G4, G6, G7 and G8 were the other genotypes with low yields in some or all the environments. *Kharif*, 2018 and *Kharif*, 2020 are discriminating environments and are declared as the most representative than *Kharif*, 2017 and *Kharif*, 2019. Generally, PSR-12202 was the ideal genotype with higher mean yield and relatively good stability; G5 was the moderately good yielding genotype and the most unstable genotype; Whereas, G1, G2, G3, G4, G6, G7 and G8 were the poorly yielding and unstable genotypes. Both AMMI and GGE bi-plot are able to establish the genotypic stability and these models can be exploited for judging the genotypes for their GEI in other crops as well.

Key words: AMMI bi-plot, GGE bi-plot, Genotype × Environment interaction, Jack bean, Yield.

INTRODUCTION

Jack bean [*Canavalia ensiformis* (L.) DC.] belonging to family leguminosae, is one of the underexploited tropical legume species, widely distributed from West Indies (origin) to Central and South America (Anonymous, 1950). The genus *Canavalia* consisting of 48 species of which, four species are reported from India, *viz.*, *C. ensiformis, C. gladiata, C. maritima* and *C. virosa.* Out of these four species, Jack bean (*C. ensiformis*) and Sword bean (*C. gladiata*) were reported to be under cultivated especially in the North East region of India for their edible pods (Bose *et al*., 2003). According to Luckner (1990), *Canavalia ensiformis*, known as jack bean, belongs to the family Fabaceae, used as a green cover; its root system is symbiotically associated with nitrogen-fixing bacteria and does not require nitrogen fertilizers. The species *C. ensiformis* is adaptive to soils with low fertility and not much used for pasture as it is not well accepted by the animals. The Indian tribal groups belonging to Kurumba, Malayali, Irula and other Dravidian groups, consume the mature seeds of jack bean after cooking (Mittre, 1991). Its seed decoction or powdered seeds are used as an antibiotic and antiseptic (Gill and Nyawuame, 1994). In Western countries, this legume is used as a cover crop and the roasted seeds are ground to prepare a coffee-like drink (Bressani *et al*., 1987). Jack bean is considered one of the few pulses that grow well on the highly leached, nutrient depleted lowland tropical soils (Emebiri, 1996). It can be

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grown relatively easily and produce high yields in the regions of low altitude, high temperature and relative humidity (Molina *et al*., 1974).

The ultimate objective of most plant breeders is improving quality and/ or quantity of crops with better adaptability and stability in different growing environments. An ideal variety always combines high yield with the stability of performance (Eberhart and Russell, 1966) although it is difficult to find such a high yielding and stable variety over a wide range of variable environments. In such widely variable environments, the occurrence of significant genotype x environment interaction (GEI) is largely possible. Such occurrence of significant GEI in plant breeding is both an opportunity and a challenge for plant breeders (Baraki *et al*., 2014). Various stability models were applied for yield stability of various leguminous and other crops to isolate stable genotypes for commercial cultivation (Hemant *et al*., 2020 in chickpea, Mohanlal *et al*., 2013 in mungbean, Manorama *et al*., 2013 in potato, Suvarna *et al*., 2011 in sesame and Patel *et al*., 2009 in pigeonpea). The process of identification of a stable and high yielding genotype under different growing environments is difficult because of the occurrence of GEI. Therefore, an in-depth knowledge of the degree and pattern of GEI is important for plant breeders to minimize the cost of genotype evaluation by eliminating unnecessary spatial and temporal replication of yield trials (Basford and Cooper, 1998). In view of the above, it is indispensably important to undertake experiments over seasons and locations to identify stable and high yielding jack bean genotype.

Despite the potential of jack bean, under-exploited species as a source of less consumed food, medicine and cover crop, to our knowledge, meagre information is available on the germplasm collection from South India and its evaluation for yield potentiality. In this context, 10 accessions of jack bean were studied for their yield stability using advanced stability models *i.e.*, AMMI and GGE bi-plot.

MATERIALS AND METHODS

The present experiment was carried out at College of Horticulture, Rajendranagar, SKLTSHU Hyderabad, Telangana state from 2017-2020 in *Kharif* for four seasons under rain fed conditions with an objective to assess the adaption and stability of 10 Jack bean genotypes. Where E1, E2, E3 and E4 are *Kharif*, 2017, *Kharif*, 2018, *Kharif*, 2019 and *Kharif*, 2020 growing seasons, respectively and the 10 jack bean genotypes *viz.* CHMJB-01, CHMJB-02, IC-26174, IC-32881, IC-512946, NS/2009/053, NS/2009/059 NSA-34, NSB/2010/035 and PSR-12202 (Coded with G1…G10) were planted in randomized complete block design with two replications. Each genotype was randomly assigned and sown in a plot area of 10 m by 20 m with 2 m and 2 m buffer zone between plots and blocks, respectively, keeping inter and intra row spacing of 200 cm each. Each experimental plot received all management practices equally and properly as per the recommendations for the crop.

Statistical analysis

A combined analysis of variance was performed from the mean data of all environments to detect the presence of GEI and to partition the variation due to genotype, environment and genotype × environment interaction. Models based on principal components analysis, such as additive main effects and multiplicative interactions (AMMI) and site regression (SREG) genotypes plus genotype × environment interaction (GGE) bi-plot are linear-bilinear models with an additive component (the main effect of the environment or genotypes) and a multiplicative component (the G × E interaction). These models are defined as powerful tools for effective analysis and interpretation of multi-environment data structure in breeding programmes (Zobel *et al.,* 1988; Yan *et al.,* 2000 and Gauch, 2006). AMMI model, which combines standard analysis of variance with principal component analysis, was used to investigate the GE interaction (Gauch, 1988; Zobel *et al.,* 1998). The GGE bi-plot methodology (Yan and Tinker, 2006; Yan *et al.,* 2002) explains the variation due to genotypes main effect and genotype × environment interactions. The GGE analysis can provide the information on the cultivars that are suitable for the different environments, investigation of stability of cultivars in the various environments and identification of the mega-environments (Yan *et al*., 2002). The data was subjected to IRRI P.B. tools 1.4 version, 2014, R-packages to get AMMI and GGE analysis and Bi-plots.

RESULTS AND DISCUSSION

Combined analysis of variance

Combined analysis of variance of 10 Jack bean genotypes tested for grain yield across four seasons indicated that Jack bean grain yield was significantly ($p<0.01$) affected by environments and genotypes × environment interactions (Table 1) indicating the presence of considerable interaction of genotypes with the environments for the trait under study. The 76.0% total sum of squares was ascribed to genotype effects followed by only a small portion of (3.0%) the total sum of squares was attributed to environment effects. The 13.9% of the total sum of squares was ascribed by environmental fluctuations exhibiting that the environments were diverse causing most of the variation in yield. As genotypes, environments and genotypes × environment interactions were significant, it was proceeded to calculate AMMI and GGE stability analysis. Asfaw *et al.* (2012) and Baraki *et al.* (2020) also reported significant GEI in grain yield of mungbean and cowpea genotypes evaluated in different environments.

Yield of jack bean genotypes in different environments

Due to the existence of significant GEI, the grain yield of the genotypes varied from environment to environment in the growing locations. The highest mean yield (Table 2) was obtained from PSR-12202 (1,623.3 g/ plant) and the lowest mean yield was obtained from CHMJB-02 (277.1 g/ plant) and this variation might be due to the genetic potential of the genotypes. Regarding the mean of the genotypes across the environments, the highest grain yield (2316.7 g/plant) was obtained from PSR-12202 in E3 (*Kharif*, 2019 growing season) and the lowest grain yield (225.00 g /plant) was recorded from CHMJB-02 in E4 (grown in *Kharif,* 2020) (Table 2). Regarding growing seasons, *Kharif,* 2019 (E3) was comparatively the better with an average grain yield of 637.4 g/ plant, than *Kharif*, 2020 (E4), with average bean yield of 564.20 g/ plant, in the three growing seasons. This might be due to the reason that *Kharif*, 2019 received highest rainfall in the growing season which is favourable for jack bean production. The scarce rainfall in this growing location during the remaining seasons resulted in underdeveloped pods leading to lower yields. The performance of all the genotypes across four seasons is depicted in Fig 1.

AMMI model analysis

When genotypes are tested in multi-location yield trials, a cross over GEI most often occurs (Ceccarelli *et al*., 1996). The genotypes (G), environments (E) and the genotype × environment interaction (GEI) were significant ($P \leq 0.01$) for jack bean yield. Hence, the variation in the jack bean mean yield was affected by the above mentioned factors and the variation was due to the inherent diversity in the genotypes (76.0%), due to the environments in which the genotypes were grown (3.0%) and the interaction (GEI) (13.9%) (Table 1). This significant genotype × environment interaction effects indicate that, genotypes responded differently to the variation in environmental conditions which indicated the necessity of testing jack bean varieties during multiple seasons. Asfaw *et al.,* (2012) and Waniale *et al.,* (2014) also reported similar findings in mungbean. The AMMI model also extracted a total of four IPCAs with significant first IPCA contributing with 98.9% and 1% of the second IPCA respectively (Table 3). The performance and stability of the genotypes and the environments was depicted in AMMI1 bi-plot (Fig 2 and 3). Both the genotypes and environments become unstable as they are far away from the abscissa (with greater magnitude of IPCA1) and become stable when they are closer to the abscissa (with smaller magnitude of IPCA1). Similarly, both the Genotypes and environments become high yielding as they become far away to the right side of the ordinate and they will be low yielding as they are far away to the left side of the ordinate (Zobel *et al.,* 1988; Yan and Tinker, 2006). Accordingly, the genotype G10 (PSR-12202), which is located far away to the right side of the ordinate, was the highest yielding genotype. On the other hand, CHMJB-02 (G2), which is located far away to the left side of the ordinate, was the low yielding genotype (Fig 2). With regards to stability, the genotype G10 (PSR-12202), which has greater IPCA1 is the most unstable genotype and G5 (IC-512946), which had lower IPCA1 is the most stable genotype followed by G3 and G4 among the evaluated jack bean genotypes (Fig 3). Similar findings are reported in mungbean by Waniale *et al.* (2014).

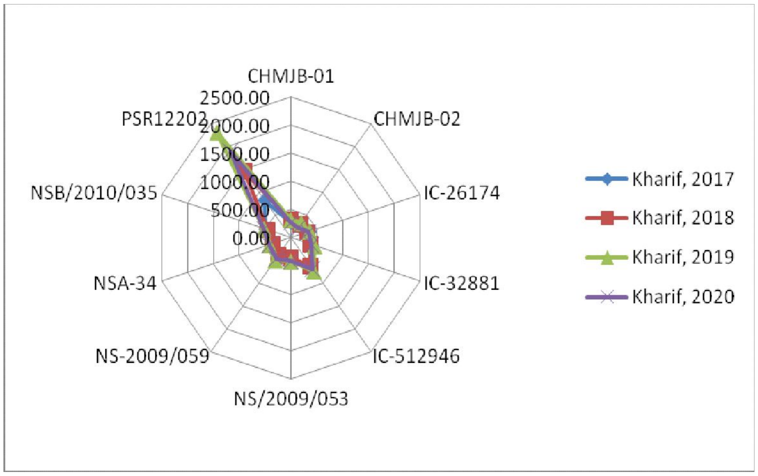

Fig 1: Yield performance of ten Jack bean genotypes across four seasons.

Table 1: Combined analysis of variance for grain yield of 10 Jack bean genotypes over four seasons.

Source of variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	Explained Sum of Squares (%)
Varieties	9	17145024.30	1905002.70**	76.00
Seasons	3	680331.53	226777.177**	3.02
Varieties x Seasons	27	3135166.30	116117.27**	13.90
Error	80	1592575.33	19907.19	
Total	119	22553097.46		

** indicates significance at p<0.01.

Table 2: Mean grain yield (g/ plant) of 10 jack bean genotypes across four seasons.

Genotype Code	Jack bean genotype ID	*Kharif*, 2017 (E1)	*Kharif*, 2018 (E2)	*Kharif*, 2019 (E3)	*Kharif*, 2020 (E4)	Mean yield (g/ plant) over four seasons	Genotype by Rank
G1	CHMJB-01	278.00	306.67	321.67	271.67	294.50	9
G2	CHMJB-02	255.00	298.33	330.00	225.00	277.08	10
G3	IC-26174	352.33	325.67	370.00	347.00	348.75	8
G4	IC-32881	400.33	382.67	466.00	413.33	415.58	5
G5	IC-512946	614.33	625.00	729.67	684.67	663.42	2
G6	NS/2009/053	387.67	350.67	415.33	415.00	392.17	6
G7	NS/2009/059	426.00	391.00	489.33	450.67	439.25	4
G8	NSA-34	351.00	351.67	415.33	411.67	382.42	7
G9	NSB/2010/035	485.00	448.67	520.00	523.00	494.17	3
G10	PSR-12202	816.67	1460.00	2316.67	1900.00	1623.33	1
Average of seasons		436.63	494.03	637.40	564.20		

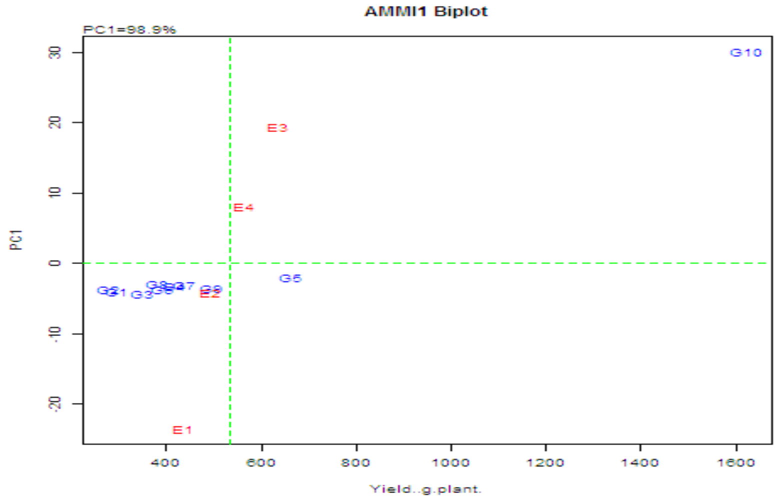

Fig 2: The AMMI bi-plot of the first interaction principal component axis (IPCA 1) versus mean yields of ten Jack bean genotypes across four environments.

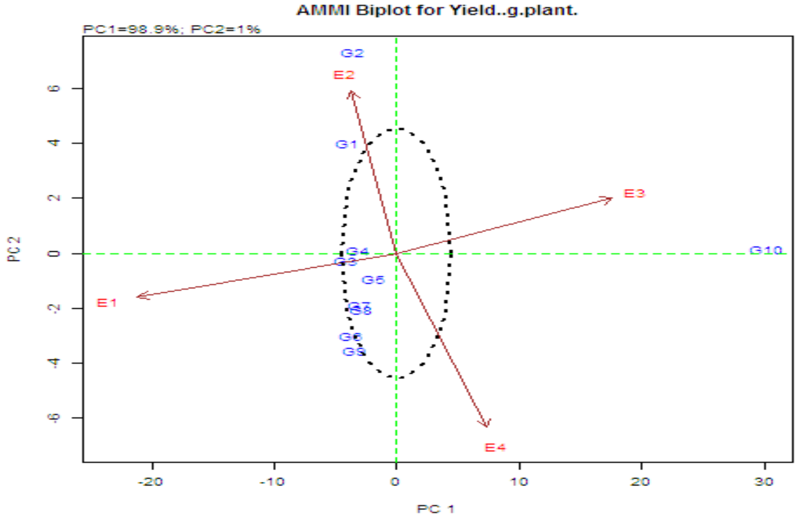

Fig 3: The AMMI 2 bi-plot of the first interaction principal component axis (IPCA 1) versus the second interaction principal component axis (IPCA 2) for Jack bean genotypes.

GGE bi-plot analysis

GGE bi-plots not only provide effective evaluation of genotypes but also allow for a comprehensive understanding of the target and test environments through various IPCAs (Table 4). GGE bi plots are helpful in understanding the target environment as a whole whether it consists of single or multiple mega environments. (Yan and Tinker, 2006). The genotype main effect (G) plus genotype × environment (GE) interaction *i.e.,* (G+E) bi-plot analysis has wider adaptability in breeding programmes and is superior to AMMI in mega-environment analysis and genotype evaluation (Yan *et al.,* 2007). It has extra property in evaluation of test environment by discriminating power versus representativeness view which is not possible in AMMI bi-plot (Bhushan Kumar *et al.,* 2018).

What-won-where view of the GGE bi-plot

The what-won-where view of the GGE bi-plot (Yan *et al.*, 2000) is best for multi-environment trial data for studying the possible existence of different mega-environments in growing locations (Gauch and Zobel, 1997). The polygon view of a GGE bi-plot explicitly displays the which-wins-where pattern and hence is a brief summary of the GEI pattern of a multi-environment trial data set (Fig 4). Hence, this GGE bi-plot is depicted to effectively identify the GEI pattern of the data to clearly show which genotype won in which environments. In the GGE bi-plot, there are two sectors on which at least one genotype is fall down on. Out of the three sectors, there is only one sector on which six of the different environments fall down. The genotypes in the vertex of the GGE bi-plot are the best genotypes in the

Table 3: Partitioning of genotype x environment interaction with AMMI model.

Source	df	SS	MS	F-value	Percent	Accumulation
Varieties X Seasons	27	3135166.30	116117.27**	5.83		
IPCA 1	11	3101809.80	281982.70**	14.16	98.9	98.9
IPCA 2	9	30051.85	3339.09	0.17	1.0	99.9
IPCA 3	7	3304.63	472.09	0.02	0.1	100.0
Total	119	22553097.46				

** indicates significance at p<0.01.

Table 4: Partitioning of genotype x environment interaction with GGE model.

Source of variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	F-value	Percent	Accumulation
IPCA 1	11	20107674.10	1827970.37**	91.82	99.1	99.1
IPCA 2	9	152546.90	16949.65	0.85	0.8	99.9
IPCA 3	7	16948.53	2421.21	0.12	0.1	100.0
IPCA 4	5	3021.05	604.21	0.03	0.0	100.0

** indicates significance at p<0.01.

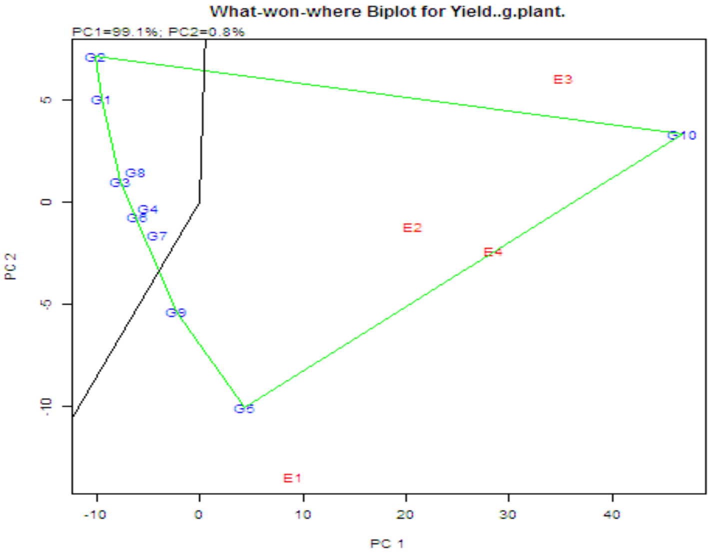

Fig 4: What-won-where GGE bi-plot of grain yields of ten Jack bean genotypes across four environments.

respective environments or the worst genotypes in some or all of the environments (Yan and Tinker, 2006). Accordingly, G10 (PSR12202), on which all, the environments fall down, is the winning genotype in most of the environments followed by G5 (IC-512946); whereas, G1 (CHMJB-01), G2 (CHMJB-02), G3 (IC-26174), G4 (IC-32881), G6 (NS/2009/053), G7 (NS/2009/059) and G8 (NSA-34), which fall down in the sectors without any environments, were the low yielding genotypes in some or all the environments.

Discriminating and representativeness of the test environments

A test environment which has a smaller angle with the AEA is highly representative of other test environments (Frutos *et al*., 2014) and a test environment which has a long vector length is considered as discriminating environment (Yan, 2002 and (Yan *et al*., 2007). Accordingly, environments E2 (*Kharif*, 2018) and E4 (*Kharif*, 2020) having smaller angle with the AEA are declared as the most representative than E1 (*Kharif*, 2017) and E3 (*Kharif*, 2019) which are with a relatively higher degree with the AEA (Fig 5). Furthermore, environments E2 and E4 are also with longer vector length and are considered as good test environments for selecting widely adapted genotypes. Asfaw *et al.* (2012) and Baraki *et al.* (2020) also used the discriminating representativeness view of the GGE bi-plot to evaluate the testing environments for mungbean and cowpea genotypes, respectively.

Mean performance and Stability of genotypes

The genotype, G10 (PSR-12202) is the ideal genotype with a higher mean yield and relatively good stability (Table 5 and Fig 6). The genotype G5 (IC-512946) was also the genotype with relatively higher yield and stability, while the remaining eight genotypes are the poor yielding genotypes

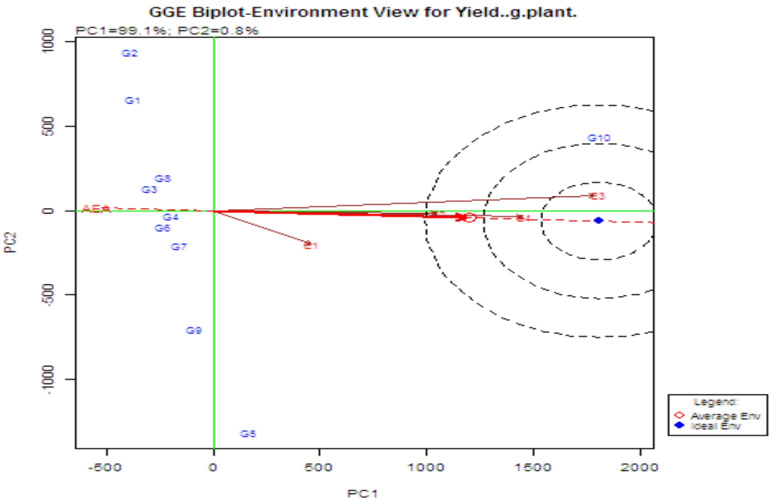

Fig 5: GGE bi-plot based on environment focused for comparing environments with ideal environment.

Table 5: Genotypes mean yield and principal component scores of mean yield of AMMI and GGE for Jack bean genotypes.

Genotype code	Jack bean genotype name	Mean yield (g/plant over four seasons	AMMI		GGE	
			Interaction principal component scores		Interaction principal component scores	
			IPCA 1	IPCA 2	IPCA 1	IPCA 2
G1	CHMJB-01	294.50	-3.97	4.02	-489.28	75.73
G2	CHMJB-02	277.08	-3.61	7.33	-517.26	107.86
G3	IC-26174	348.75	-4.23	-0.245	-392.18	15.18
G4	IC-32881	415.58	-3.20	0.122	-256.18	-4.02
G5	IC-512946	663.42	-1.90	-0.94	217.21	-151.53
G6	NS/2009/053	392.17	-3.73	-2.98	-305.83	-10.95
G7	NS/2009/059	439.25	-3.08	-1.88	-210.93	-24.18
G8	NSA-34	382.42	-2.92	-2.04	-313.84	22.35
G9	NSB/2010/035	494.17	-3.51	-3.53	-114.80	-80.79
G10	PSR-12202	1623.33	30.19	0.15	2383.12	50.34
E1	*Kharif*, 2017	436.63	-23.50	-1.75	0.17	-0.89
E2	*Kharif*, 2018	494.03	-4.15	6.54	0.40	-0.08
E3	*Kharif*, 2019	637.40	19.50	2.21	0.69	0.40
E4	*Kharif*, 2020	564.20	8.16	-7.01	0.56	-0.16

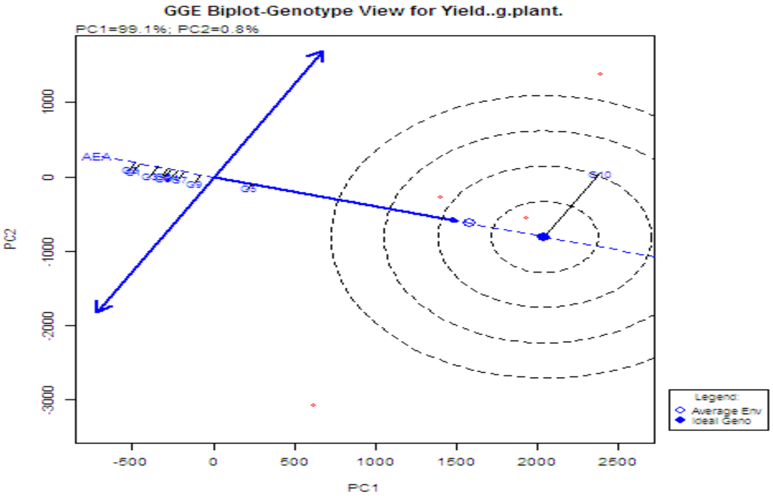

Fig 6: GGE bi-plot of stability and mean performance of ten Jack bean genotypes across average environments.

which are too far from the ideal genotype and are relatively stable since, they are with short vector length from the AEA. Asfaw *et al.* (2012) and Baraki *et al.* (2020) also used the GGE bi-plot of the mean and stability to evaluate the performance and stability of mungbean and cowpea genotypes respectively against the ideal genotypes.

CONCLUSION

The genotypes (G), environments (E) and the genotype × environment interaction (GEI) were significant ($P \leq 0.01$) for jack bean confirming there was a cross over interaction in this study. The highest mean yield was obtained from PSR-12202. According to AMMI 1 bi-plot, PSR-12202, was the high yielding genotype while, CHMJB-02 was the low yielding genotype. Furthermore, according to the what-won-where view of the GGE bi-plot, PSR-12202 was the winning genotype in most of the environments, whereas, CHMJB-01, CHMJB-02, IC-26174, IC-32881, NS/2009/053, NS/2009/059 and NSA-34 were the low yielding genotypes in some or all the environments. Finally, G10 (PSR-12202) was the ideal genotype with higher mean yield and relatively good stability and G5 (IC-512946) was the moderately good yielding and highly stable genotype. Whereas, the genotypes CHMJB-01, CHMJB-02, IC-26174, IC-32881, NS/2009/053, NS/2009/059 and NSA-34 were the poor yielders and unstable. Both the models indicated that the genotype G10 (PSR-12202) is the preferred genotype as it was high yielding with moderate stability. The two stability models, AMMI and GGE bi-plot are established as powerful tools for effective genotypic stability analysis and interpretation of multi-environment data structure and hence, these models can be exploited for judging the genotypes for their GEI in other crops as well.

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