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Stability and Diversity of Elite Lines of Vegetable Cowpea (*Vigna unguiculata* ssp. *unguiculata* L.)

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ABSTRACT

Background: The present study was conducted to study the stability and diversity of twenty elite breeding lines of vegetable cowpea developed at ICAR-Indian Institute of Vegetable Research, Varanasi through AMMI analysis and cluster analysis respectively.

Methods: All the 20 elite lines were laid out in randomized block design with three replications during three years of sowing *viz.*, *Kharif*-2018, *Kharif*- 2019 and *Kharif*-2021. Each year was considered as one location and the dependant variable pod yield per plant was subjected to AMMI analysis for GE interaction study. The mean of all the yield and yield attributes was subjected to cluster analysis for genetic divergence study.

Result: AMMI ANOVA showed significant variation for environments (E), genotypes (G) and G×E interactions. The graphical representation of principal component 1 (PC1) vs yield (Y) showed that the genotypes 12,15,11,13,18 were most stable and the PC1 vs PC2 graph showed that the genotypes 12,11,13,18 were most stable as they were positioned towards the origin. The cluster analysis grouped all the twenty genotypes into four clusters with two genotypes (7,20) in first cluster, five genotypes (17,14,16,8,19) in second cluster, eight genotypes (9,6,1,13,11,12,2,15) in third cluster and five genotypes (5,3,18,4,10) in fourth cluster.

Key words: AMMI analysis, Clusters, Elite lines or genotypes, GE interaction, Stability.

INTRODUCTION

Cowpea [*Vignaunguiculata* (L.) Walp.] is a legume crop cultivated worldwide as pulse, vegetable, forage, green manure and cover crop (Smartt, 1990). Cowpea is one of the most important legumes which serve as vital source of protein in the diet of the people of developing countries. Due to its high protein content in leaves, pods and grains it is widely regarded as “poor men’s meat” (Boukar *et al*., 2018). It is one of the best crops that fit well in rice-wheat cropping systems. Africa is considered as primary centre of origin of cowpea with chromosome number 2n=22. Cowpea is grown primarily in the third world for its cheap source of dietary protein, lysine and as a supplement for meat.

Vegetable cowpea refers to varieties of cowpea (*Vigna unguiculata* L.) grown for their immature succulent pods, popularly known as long bean, bodi, bora, sitao, snake pea and aspargus bean in different parts of the world. The indigenous varieties of vegetable cowpea were climbing types. In recent times, many erect bushy varieties with increased yields have been developed. The cowpea crop is used in a variety of ways. It is used at all stages of growth as a vegetable crop. Tender pods are used in the same way as snap beans while the green cowpea seeds are boiled as fresh vegetable, can be canned or frozen. Dry mature seeds used as pulse suitable for boiling and canning. Cowpea leaves are also rich source of protein, iron and β-carotene and also increases the bioavailability of calcium, iron due to absence of phytic acid.

If the yield of the genotypes responds differentially to any changes in environment, Genotype×Environment (GE) interaction occurs. Multi environment trial (MET) is needed for the analysis of GE interaction. Additive main effect and multiplicative interaction model (AMMI) is theoretically the most effective model to catch the GE interaction sum of squares with a minimum number of degrees of freedom (Yan and Hunt, 1998). This model is a combination of ANOVA and Principal Component Axis (PCA) analysis and it applies PCA to the GE interaction part of the ANOVA. So, it is also called as Interaction PCA (IPCA) (Yan and Hunt, 1998).

MATERIALS AND METHODS

The study was conducted with 20 elite lines (Table 1) of vegetable cowpea during *Kharif*-2018, *Kharif*- 2019 and *Kharif*-2021 at the research farm of ICAR- Indian Institute of Vegetable Research, Varanasi to know the stability and diversity of these elite lines. Each year considered was considered one location and hence, the three environments were E1 (*Kharif*-2018), E2 (*Kharif*- 2019), E3 (*Kharif*-2021).

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The study was conducted under the weather parameters as provided in the Fig 1a and 1b. All the 20 elite vegetable cowpea lines were developed at ICAR-Indian Institute of Vegetable Research, Varanasi through concerted breeding program of crossing and single plant selection. All the 20 elite lines were laid out in randomized block design with three replications during all the three years of sowing. The seeds were sown at a row-to-row distance of 60cm and plant-to-plant distance of 20 cm in each row in a plot size of 3 m×4 m. The data was recorded for plant height (cm), pod length (cm), number of pods per plant, 10 pod weight and yield per plant (g). The data for all the characters except yield per plant was recorded on five random plants in each replication per year (location). The data for yield was recorded on a whole plot basis and then calculated for pod yield per plant.

Each year was considered as one location and the data of the dependant variable pod yield per plant was subjected to AMMI analysis. The pod yield per plant data taken for three years considered as three different locations for Genotype×Environment (GE) interaction study. The mean data of plant height (cm), pod length (cm), number of pods per plant, 10 pod weight and yield per plant (g) recorded for all the 20 elite lines was also subjected to cluster analysis for identifying the diverse genotypes. The software used for AMMI analysis was PBSTAT while the cluster analysis was done using R software version 4.1.2 using package gclus.

RESULTS AND DISCUSSION

AMMI analysis of variance

The AMMI analysis of variance for pod yield per plant across the three environments for 20 genotypes was presented in Table 2. Significant variation was observed for environments, genotypes and G×E interactions. Of the total variations 15.99% was contributed by environments, 38.80% was contributed by genotypes and 36.69% was contributed by G×E interactions. The large portion of variation contributed by genotypes indicates that the genotypes are diverse. All the variation of the genotypes was captured in the first two principal components. The results are in accordance with the findings of Kumar *et al*. (2020) in maize, Mekonnen *et al*. (2022) in cowpea, Rajalakshmi *et al*. (2021) in black gram.

Mean yield of genotypes across three environments

The genotypes 4,5,3,6,18 were the best performing genotypes in Environment 1(E1) with 439.25, 425.58, 385.71, 363.25 and 307.25 q/ha yield respectively (Table 3). In the environment 2 (E2) the genotypes 10, 9, 1, 2, 5 recorded 366.25, 361.54, 360.50, 355.17 and 348.33 q/ha yield respectively. In the environment 3 (E3) the only genotype that recorded yield per plant of more than 300g was genotype 3 (317.50).

The genotypes 4, 10 and 3 had high yield performances in E1(2018), E2 (2019) and E3 (2021) respectively (Table 3). Highest green pod yield was recorded in the genotype 4 (439.25 g/plant) at E1 while the lowest green pod yield was recorded in genotype 7 (79.95 g/plant) at E3. The highest yield across the environments was registered for genotype 5 (343.75 g/plant) while the lowest yield across the environments was recorded for genotype 20 (140.39 g/plant). In E1 above mean average yield was recorded for 12 genotypes followed by E3 with 10 genotypes and E2 with 9 genotypes. The results are in accordance with the findings of Mekonnen *et al*. (2022).

Table 1: List of twenty genotypes of vegetable cowpea used for the study.

Genotype	Genotype code	Source	Breeding status of the genotype
VRCP 167-2	1	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 49-5	2	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 66-4	3	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 68-2	4	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 71-1	5	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 79-4	6	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 96-4	7	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 98-4	8	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 147-2	9	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 158-3	10	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 159-4	11	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 182-4	12	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 187-6	13	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 188-3	14	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 191-1	15	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 216-2	16	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 215-2	17	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 220-3	18	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 223-2	19	ICAR-IIVR, Varanasi	Elite breeding line
VRCP 230-3	20	ICAR-IIVR, Varanasi	Elite breeding line

PC1 vs Y

The genotypes that are most stable were 12,15,11,13,18. Apart from these,19,17,16,20,7 genotypes were also in accordance with stable genotypes. These genotypes were considered to be stable as they were positioned towards the origin (Fig 2). From this it can be concluded that they are adaptable to wide range of environments. While the most unstable genotypes are 4,3,6,2,1 as they were positioned away from the origin and can be concluded that they have specific adaptations. The genotype 5 is the high yielding genotype with good performance in better environment. The three environments were represented by the three arrows (Fig 2). Environment 3 had less contribution towards the interaction while the environments 2 and 3 contributed more towards the interaction. The results are in accordance with the findings of da Silveira *et al*. (2013) in sugarcane, Rajalakshmi *et al*. (2021) in black gram.

PC1 vs PC2

The genotypes 12,11,13,18 were the most stable genotypes as these genotypes are positioned towards the origin (Fig 3). These genotypes were also in company with the genotypes 20,19,7,16,17,15,14. The genotypes that are most unstable and away from the biplot origin were 4,3,9 which represents that these genotypes had specific adaptations. Similar results were also reported by da Silveira *et al*. (2012) in sugarcane, Rajalakshmi *et al*. (2021) in black gram.

Cluster analysis

The mean data of all the twenty genotypes for the six quantitative traits *viz*., plant height (cm), pod length (cm), number of pods per plant, ten pod weight (g) and yield per plant (g) was subjected to hierarchial cluster analysis. The cluster dendrogram at a height of 100 divided all the twenty genotypes used for cluster analysis into four clusters (Table 4). The first cluster had two genotypes (7, 20), the second cluster had five genotypes (17,14,16,8,19), the third cluster had eight genotypes (9,6,1,13,11,12,2,15) and the fourth cluster had five genotypes (5,3,18,4,10). The cluster I and cluster III had the highest intercluster distance (Fig 4). By crossing the genotypes from cluster I with cluster III better transgressive segregants can be obtained. The results are in accordance with the findings of Lal *et al*. (2018), Vaggar

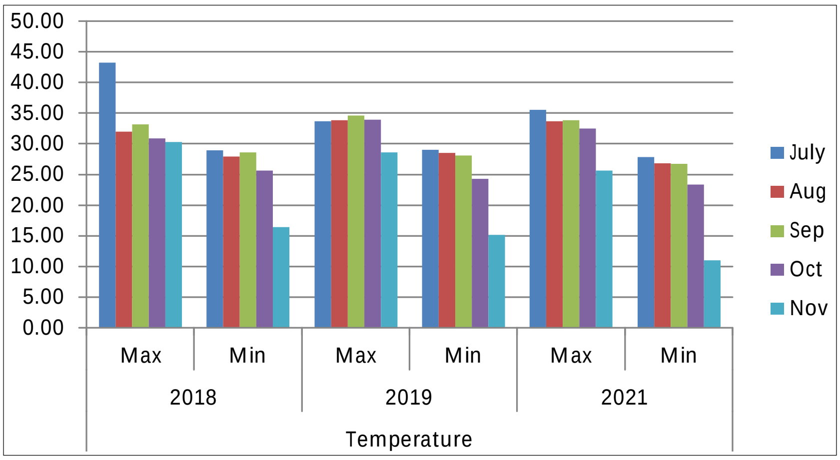

Fig 1a: Graph depicting average monthly temperature (°C) for 2018, 2019 and 2021 during crop growth.

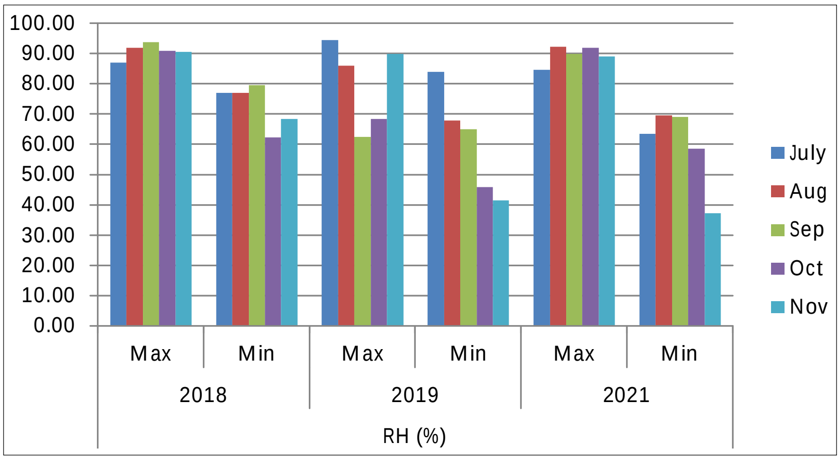

Fig 1b: Graph depicting average monthly Relative humidity (%) for 2018, 2019 and 2021 during crop growth.

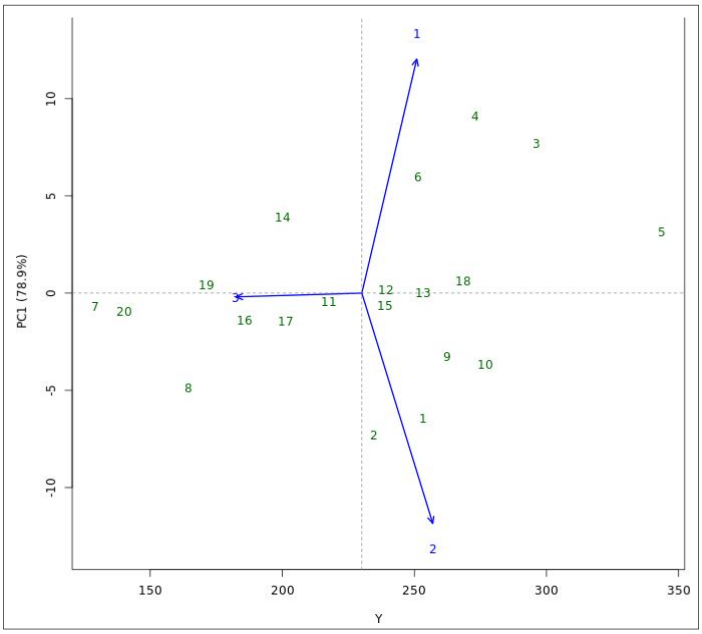

Fig 2: AMMI biplot: PC1 vs Y.

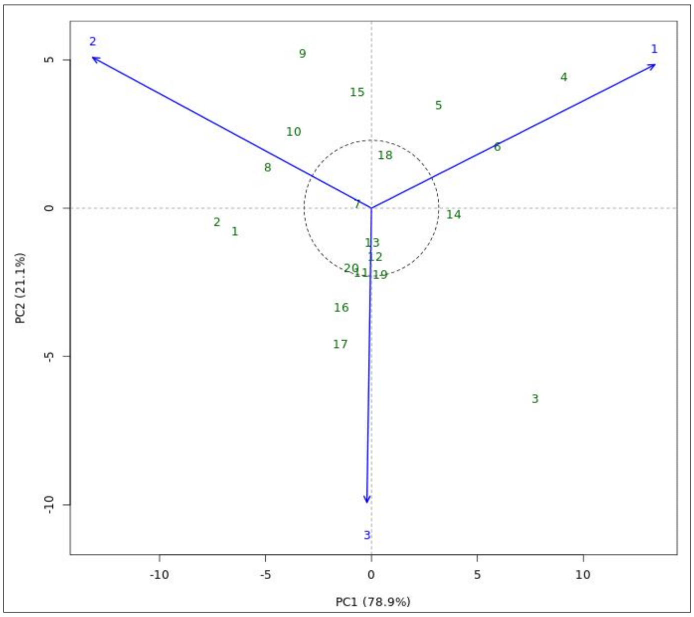

Fig 3: AMMI biplot: PC1 vs PC2.

Table 2: AMMI Analysis of variance across three environments.

	Df	Sum Sq	Mean Sq	F value	Pr (>F)	% TSS
Environment (E)	2	205329	102665	113.9558	1.688E-05***	15.99
Replication/E	6	5405	901	0.9872	0.43735	
Genotype (G)	19	498316	26227	2.1151	0.02436*	38.80
G×E	38	471208	12400	13.5882	< 2.2e-16***	36.69
PC1	20	371654	18583	20.3600	< 2.2e-16***	
PC2	18	99554	5531	6.0600	< 2.2e-16***	
Residuals	114	104034	913			
Total		1284292				

'***', '*'Significant at 0.001 and 0.05 probability levels respectively.

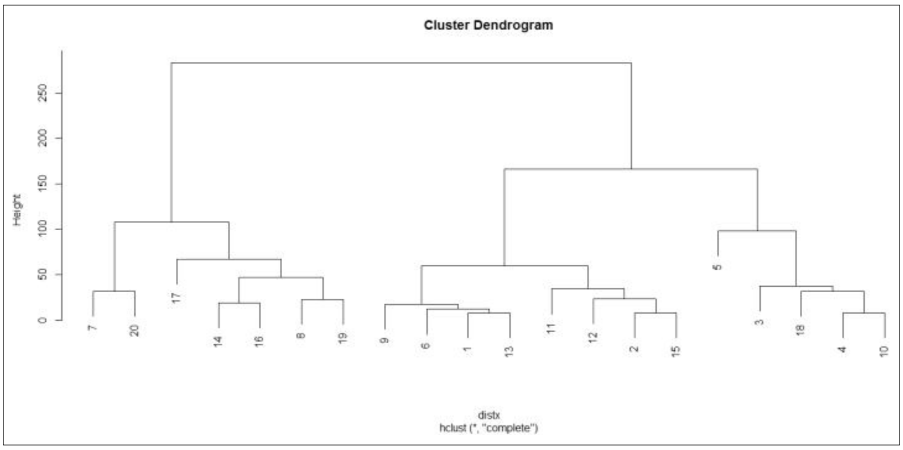

Fig 4: Cluster dendrogram representing diversity of 20 vegetable cowpea elite lines.

Table 3: Mean of dependant variable Yield per plant (g) across three environments in descending order.

Genotype	Environment 1 (2018)	Genotype	Environment 2 (2019)	Genotype	Environment 3 (2021)
4	439.25	10	366.25	3	317.50
5	425.58	9	361.54	5	257.33
3	385.71	1	360.50	13	218.47
6	363.25	2	355.17	1	215.65
18	307.25	5	348.33	12	209.58
14	272.00	18	297.00	17	204.70
15	272.00	15	296.58	10	201.41
13	268.21	13	272.92	18	200.92
9	267.88	8	263.33	11	193.92
10	262.58	12	254.63	2	193.73
12	253.33	11	238.00	6	179.60
11	220.50	17	221.63	16	175.30
19	185.79	16	212.50	4	174.63
1	183.88	6	211.75	9	158.13
17	178.08	4	205.50	14	154.04
16	170.00	3	185.25	15	148.53
2	155.83	19	180.33	19	148.40
7	141.58	14	174.38	20	115.13
20	138.04	20	168.00	8	102.67
8	127.33	7	165.67	7	79.95
Mean	250.90		256.96		182.48
LSD 0.05	41.21		49.62		32.06
CV (%)	11.93		14.03		12.76

LSD: Least significant difference; CV: Coefficient of variation.

Table 4: Grouping of genotypes based on cluster analysis.

Cluster name	Genotypes
Cluster I	7, 20
Cluster II	17, 14, 16, 8, 19
Cluster III	9, 6, 1, 13, 11, 12, 2, 15
Cluster IV	5, 3, 18, 4, 10

et al. (2022) and Suganthi *et al*. (2023) in cowpea, Reddy *et al*. (2021) in french bean and Bishnoi *et al*. (2022) in pea.

CONCLUSION

The stability study of pod yield per plant by AMMI analysis showed significant variation due to environments, genotypes and G×E interactions for twenty elite lines of vegetable cowpea. The large portion of variation was contributed by genotypes followed by G×E interactions indicates that the genotypes are diverse and had significant G×E interactions. The total variation was captured in the first two principal components. Based on AMMI biplot study of PC1 vs Yield and PC1 vs PC2 the most stable genotypes were 12, 11, 13 and 18 as they were positioned towards the origin in biplot. The most unstable genotypes were 4 and 3 as they were positioned away from the origin representing they were suitable for specific environments. The mean data of six quantitative traits subjected to cluster analysis grouped all the twenty elite lines into four clusters. The highest intercluster distance was observed between cluster I and cluster III. By crossing the genotypes between cluster I and cluster III better transgressive segregants can be obtained.

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Conflict of interest: None.

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