Deciphering the G x E interaction involved in milling quality of pigeon pea (Cajanus cajan) derived from interspecific hybridization

Mahadeva Swamy HK
maddygkvk@gmail.com
Sugarcane Breeding Institute
Amaresh Amaresh
Sugarcane Breeding Institute
Bajpai GC
G. B. Pant University of Agriculture and Technology
Anupama Singh
G. B. Pant University of Agriculture and Technology
Aswini Nunavath
ICAR- National Institute of Biotic Stress Management
Gopalareddy K
Sugarcane Breeding Institute
Maruthi RT
Sugarcane Breeding Institute
Sreenivasa V
Sugarcane Breeding Institute
Yathish KR
Sugarcane Breeding Institute
Chandana Behera
Odisha University of Agriculture and Technology

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Abstract

An important pulse crop, pigeon pea is primarily grown in tropical and sub-tropical climates worldwide and is a rich source of protein and dietary fibre. In India, about 80% of the pulses produced are eaten as dhal (dehusked splits), recovery of dhal plays a major role in the pulse milling industry and it increases when pulse grains are pre-treated to loosen the husk before milling. Since quality traits are highly influenced by the environment, to select stable genotypes for yield and quality traits, multi-environment trials (MET) must be carried out to study genotype × environment interaction (GEI). In the current study, seeds from inter-specific crosses derived lines involving wild species (Cajanus scarabaeoides, Cajanus acutifolius and Cajanus cajanifolius) and cultivated parental lines (ICPL 84023, Pant A134, and UPAS120) were examined for three years with pre-milling treatment and without pre milling treatment for dhal yield and hulling efficiency. The combined ANOVA revealed the existence of ample variation for all the milling quality traits among the lines derived from interspecific hybridization. The gain hardness showed a positive and significant association with the dhal yield and hulling efficiency. The AMMI and GGE analysis was employed to identify the stable genotype among the interspecific lines for dhal yield and hulling efficiency. The AMMI revealed the presence of significant G x E interaction for the milling traits. GGE grouped the pre-milling treated environment into a mega environment and distinguished it from pre-milling untreated environments. The genotypes derived from Cajanus scarabaeoides were found better under untreated environments while C. cajanifolius derived lines were found best under a pre-milling treated environment. The genotype G12 derived from the UPAS120 x C. cajanifolius was found most stable genotype with high dhal yield and hulling efficiency based on AMMI, GSI, ASV and GGE analysis.

Introduction

Redgram, or pigeon pea [*Cajanus cajan* (L.) Millspaugh], is a major legume crop rich in protein that is cultivated in semi-arid areas of Asia, Africa, Latin America, and the Caribbean which feeds over a billion individuals in developing countries[1]. For every 100 g of edible portions, pigeon pea provide 21.7 g of protein, 1.5 g of fat, 62.8 g of carbohydrates, 15.0 g of dietary fibre, 343 kcal of energy, and 130 mg of calcium[2]. It is grown for its grains and eaten as dhal. About 80% of the pulses produced in India are consumed as dhal, with the remaining 20% being consumed in various forms as whole seeds[3,4]. The process of milling began at the village level with a stone mill (chakki), which split grain under low pressure before growing into a large-scale industry[5]. Split dhal is made by milling whole pulses using a variety of techniques. Depending on the kind of pulses and the pretreatment and milling equipment used by the millers, the recovery of dhal can range from 60% to 75% [4,6]. The recovery of dhal is therefore increased when pulse grain is pretreated to loosen the husk before milling[7,8].

The main goal of plant breeding is to create high-yielding cultivars with improved quality that can be grown in a variety of environments. Since the quality traits are highly influenced by environment, resulting poor performance of genotypes. To select stable genotypes for yield and quality traits, multi-environment trials (MET) must be carried out to study genotype × environment interaction (GEI) followed by deliberate selection of stable genotypes, which may be recommended for cultivation[9]. There are two powerful methods which can effectively interpret the MET data, analyze GEI and evaluate genotypic adaptability and phenotypic stability - the additive main effects and multiplication interaction (AMMI) analysis and genotype and genotype × environment interaction[10-13].

Therefore, the present study was undertaken to identify the stable genotypes for milling quality derived from inter-specific crosses originating from cultivated parental lines, namely, ICPL 84023, Pant A134, and UPAS120, and wild species *Cajanus scarabaeoides, Cajanus acutifolius, and Cajanus cajanifolius*.

Results

Combined ANOVA and Correlation analysis for milling parameters

ANOVA revealed that there was significant variation among the genotype for milling quality traits. (Table 1). Correlation analysis showed that there was a significant positive correlation of gotta (GT) with gotta and splits (Finished Product), broken,

dhal yield and hundred seed weight and a significant negative correlation with splits. There was a significant positive correlation between the splits and finished product, hulling efficiency and dhal yield, whereas significant negative association of split with broken, powder and husk. Finished product has a perfect positive association with dhal yield and significant positive association with hulling efficiency and hardiness, negative significant correlation with broken and powder. Hulling efficiency showed a significant positive correlation with dhal yield and hardiness. Dhal yield had a significant positive correlation with gotta, splits, finished product, and significant negative correlation with broken and powder. Grain hardiness had a significant positive correlation with finished product, hulling efficiency and dhal yield and significant negative association with broken and powder (Supplementary Table 1).

AMMI analysis for milling parameters

The analysis of variance (ANOVA) showed significant individual effects of Genotypes (G), Environments (E) and genotype × environment interaction (G × E) for the dhal yield and hulling efficiency (Table 2). The environmental main effects were highest for the dhal yield (53.24%) and hulling efficiency (78.06%), indicating the higher environmental influence on the performance of genotypes. The genotype main effect for dhal yield (31.74%) was higher than hulling efficiency (35.56%). The GE interaction effects were greater for dhal yield (15.02%) than hulling efficiency (8.04%). In the principal components (IPCA), the first 4

Source	Df	GT (g)	SPLT (g)	FP (g)	BKN (g)	PDR (g)	HE (%)	DY (%)	HD kg/ kernel	HSW (g)
GEN	11	382.60**	133.51**	183.03**	7.30**	40.85**	35.56**	81.33**	33.40**	2.59**
ENV	5	933.30**	1910.65**	675.26**	241.36**	218.56**	439.62**	300.09**	1.34**	1.83**
GEN X ENV	55	78.35**	55.62**	17.32**	4.15**	9.30**	4.11**	7.69**	0.14*	0.25**
Pooled error	132	3.72	3.66	0.67	0.35	0.41	0.35	0.29	0.07	0.14
Total	215									
Pooled mean		75.56	21.16	96.72	7.82	16.77	79.76	64.48	16.96	8.12

(** Significant at 1 %, * Significant at 5 % level of significance.)

Gotta (GT), Splits (SPLT), Finished Product (FP), Broken (BKN), Powder (PDR), Hulling Efficiency (HE), Dhal Yield (DY), Hardiness (HD) and Hundred Seed weight (HSW)

Table 1. Analysis of Variance (ANOVA) for the milling traits studied.

components were significant for both traits, in which the first PCA explained a maximum variance of about 54.81% for dhal yield and about 43.73% for hulling efficiency.

Biplot Analysis for Determination of Main Effect and Environment Influence

From the PC1 Vs DY (Dhal Yield), environments E2, E4 and E6 established lower average main effects, whereas environments E1, E3 and E5 expressed the highest main effects and were gainful for most of the genotypes. Genotypes G2, G9, G6, G3, and G12, expressed higher main effects; for the dhal yield, on the contrary, genotypes G5, G7 and G8 exhibited lower main effects. (Fig.1a). The AMMI biplot using PC1 and PC2 scores for the dhal yield reveals the genotypes G9 and G6 are close to the origin and so have greater environmental adaption and stable across the environments (Fig. 1b).

From the PC1 Vs HE (Hulling efficiency), environments E2, E4 and E6 showed lower average main effects, whereas environments E1 and E5, expressed the highest main effects and were gainful for most of the genotypes. The PC scores for the environment E3 were close to zero. Genotypes G2, G3, G9, and G12, expressed higher main effects; for the hulling

efficiency, in contrast, genotypes G7, G5, G1, and G6 exhibited lower main effects (Fig. 1c). Genotypes G6 and G2 are located adjacent to the origin in the PC1 Vs PC2 biplot and are stable performers (Fig. 1d).

AMMI Stability value

As per ASV, a stable variety is one with close to zero value. The ASV explained G6, G9, G11 and G12 as the top ranked genotypes for the dhal yield due to a lower ASV, hence they are considered as the most stable genotypes for the dhal yield. For, hulling efficiency the genotypes G6, G8, G11 and G12 are the most stable (Table 3).

Figure 1. AMMI biplot for Dhal yield and Hulling Efficiency (a) AMMI biplot PC1 Vs Dhal Yield, (b) AMMI biplot PC1 vs PC2 for Dhal Yield, (c) AMMI biplot PC1 Vs Hulling Efficiency, (d) AMMI biplot PC1 vs PC2 for Hulling Efficiency. Where G = Genotypes (1–12) and E1-E6 are the environments.

	DY			HE	
Source	**df**	**MS**	**VE (%)**	**MS**	**VE (%)**
ENV	5	300.09**	53.24	439.62**	78.06
GEN	11	81.33**	31.74	35.56**	13.89
ENV*GEN	55	7.70**	15.02	4.12**	8.04
IPCA 1	15	15.47**	54.81	6.60**	43.73
IPCA 2	13	10.83**	33.27	5.38**	30.91
IPCA 3	11	2.49**	6.47	2.70**	13.10
IPCA 4	9	1.73**	3.67	2.53**	10.04
Residuals	144	0.29	0	0.35	0

Table 2. AMMI Analysis of variance of main effects and interactions for Dhal yield (%) (DY) and Hulling Efficiency (%) (HE)

Genotypic stability index

According GSI, the genotypes G2, G3 and G12 were ranked higher for dhal yield whereas for hulling efficiency G12, G9 and G3 were ranked higher and are most stable (Table 3).

Mean vs. Stability

The genotypes G3, G2 and G12 were found to be stable with higher dhal yield (Fig. 2a). Whereas, the genotypes G12, G9 and G3 were shown high hulling efficiency and good stability (Fig. 2b).

	DY			HE		
Genotype	ASV	GSI	means	ASV	GSI	means
G1	1.636	14	64.13	1.245	19	78.46
G2	3.179	13	68.58	1.153	12	80.09
G3	2.545	14	66.73	1.717	15	80.74
G4	1.081	16	62.81	1.068	12	79.38
G5	1.792	20	62.40	1.023	15	78.39
G6	0.117	5	65.13	0.503	10	78.54
G7	0.475	16	61.76	1.277	22	78.17
G8	1.465	16	62.91	0.575	10	79.22
G9	0.317	7	64.74	1.654	13	81.91
G10	1.817	18	63.14	1.101	13	79.67
G11	0.431	10	64.07	0.995	8	79.94
G12	1.053	7	67.36	1.080	7	82.59

Table 3. Mean values, AMMI stability value (ASV) and genotype selection index (GSI) for the genotypes studied for the trait Dhal Yield (DY) and Hulling Efficiency (HE).

Ranking of genotypes and environment

The genotype G12 was ranked higher and the environment E1 was ranked higher for the dhal yield (Fig. 2c and 2d). Whereas, for hulling efficiency the genotypes G12 and G9 and the environment, E6 had higher rank (Fig. 2e and 2f).

Discriminative vs. Representativeness

The environments E1, E2, E5 and E6 has high discriminating power having longest environmental vectors. The environments E3 and E4 had shorter environmental vectors having in which most of the genotypes performing equally for dhal yield (Fig. 2g). For hulling efficiency, E3 was highly representative in nature, whereas, the environments E1, E2, E4, E5 and E6 were found to have greater discriminating ability (Fig. 2h).

WWW

The biplot polygon showed that the genotypes G3, G2, G5 and G10 were vertex genotypes for the dhal yield. The six environments were classified into two mega environments, the mega environment (1) consisting of E2, E4 and E6, in which the genotype G2 and G1 had better performance. Mega environment (2) consists of E1, E3 and E5, in which well performing genotypes were G3, G12, G6 and G9 for dhal yield (Fig. 2i). The biplot polygons for hulling efficiency revealed that the vertex genotypes were G3, G4, G5, G7, G9 and G12.There were two mega environments, the mega-environment (1) include E2, E4 and E6, in which better performing genotypes were G9, G2 and G10. The second mega environment (2) comprises of E1, E3 and E5 environments, in which G3, G11 and G12 were good performing genotypes (Fig. 2j).

Discussion

Pigeon pea is used only after de-husking and splitting[14]. Both quantitative and qualitative losses occurred during dehulling, several factors influence the dhal recovery such as the method of dehulling and grain characteristics[15]. Pigeon pea grains with poor dehulling characteristics had higher uronic acid contents, according to research by Ramakrishnaiah and Kurien[16].

One of the main characteristics that breeders may take into consideration is the dehulling characteristic of pigeon pea. Processors need legumes with good dehulling qualities to meet the demands of the domestic or export markets for consumption. Processors need to use cultivars with high dhal yield recovery that are also easy to dehull[14]. Grain type and physical traits may impact the variability in dehulling characteristics of legume grains[17-19]. Hence, the present study was conducted to identify the stable and high dhal yield and high hulling efficiency genotypes derived from 9 interspecific crosses. The combined ANOVA revealed the presence of ample variability among the lines derived from interspecific hybridization for quality traits. The association studies revealed the hardness of the grain influenced the dhal yield and hulling efficiency. Grain hardness was positively associated with finished product, dhal yield and hulling efficiency, while broken and powder were negatively associated with grain hardness. This may be due to the soft gains may get crushed easily, and hard grains may not get crushed and only losses their husk. Ample variability was found for grain hardens among the interspecific derived lines, and it also found that influence by G x E as it alters the fiber content and its location in the grain legume likely play the predominant role in hardness[20].

The main goal of pigeon pea breeding is to create high-yielding with good quality cultivars that can be grown in a variety of environments. However, the development of stable, high-yielding with good milling quality cultivars is being hampered by genotype-environment interaction (GEI), which results in genotypes performing inconsistently. GEI study for choosing stable genotypes for yield and significant quality traits; farmers are then advised to use compatible and stable genotypes. Tools used by plant breeders for GEI study such as the AMMI model, put forth by Gauch[12], is a multivariate technique that describes the GEI in multiple dimensions using principal component analysis (PCA) and analysis of variance (ANOVA). Yan et al.[11] proposed the GGE biplot, which takes into account both genotype main effects and GEI effects when conducting analysis. Utilising them to assess the genotypes of groundnut[21,22], pigeon pea[23-26], chickpea[27], maize[28], barley[29,30], rapeseed[31], rice[32], wheat[33-35], and ashwagandha[36].

In the current study, AMMI analysis revealed that the analysis of variance (ANOVA) showed that significant individual effects of Genotypes (G), Environments (E) and genotype × environment interaction (G×E) for the dhal yield and hulling efficiency (Table 3). The environmental main effects were highest for the dhal yield (53.24%) and hulling efficiency (78.06%), indicating the higher environmental influence on the performance of genotypes. Genotypes G9, G6, G3, and G12, expressed higher main effects; for the dhal yield, on the contrary, genotypes G5, G7 and G8 exhibited lower main effects. (Fig. 1a). The AMMI biplot using PC1 and PC2 scores for the dhal yield reveals that genotypes G9 and G6 are close to the origin and so have greater environmental adaption and are stable across the environments (Fig. 1b). Genotypes G9, and G2, expressed higher main effects; for the hulling efficiency, in contrast, genotypes G7, G5, G1, and G6 exhibited lower main effects (Fig. 1c). Genotypes G6 and G2 are located adjacent to the origin in the PC1 Vs PC2 biplot and are stable performers (Fig. 1d).

A stable variety is defined by ASV as having a value near zero. G6, G9, and G11 are thought to be the most stable genotypes for the dhal yield because the ASV explained they were the top-ranked genotypes for the dhal yield owing to a lower ASV. The most stable genotypes for hulling efficiency are G6, G8, and G11. The genotypes G2, G3, and G12 were ranked higher for dhal yield, while the genotypes G9, G3, and G12 were ranked higher and are the most stable for hulling efficiency, according to GSI. It was discovered that the genotypes G3, G2, and G12 were stable and had higher dhal yields (Fig. 2a)

On the other hand, high hulling efficiency and good stability were demonstrated by the genotypes G12, G9, and G3 (Fig. 2b). For the dhal yield, the genotype G12 and the environment E1 were ranked higher (Fig. 2c and 2d). On the other hand, hulling efficiency was higher for the genotypes G12 and G9 and the environment E6 ranked higher (Fig. 2e and 2f). With the longest environmental vectors, the environments E1, E2, E5, and E6 have a high discriminating power. Most genotypes performed equally for dhal yield in the environments E3 and E4, which had shorter environmental vectors (Fig. 2g). While environments E1, E2, E4, E5, and E6 were found to have greater discriminating ability, E3 was highly representative of nature in terms of hulling efficiency (Fig. 2h). The six environments were divided into two mega environments: the first mega environment (1), which included the genotypes G2 and G1, performed better, and included the E2, E4, and E6 environments. In the mega environment (2), which is made up of the E1, E3, and E5, the genotypes G3, G12, G6, and G9 performed well in terms of dhal yield (Fig. 2i). There were two mega-environments, the first mega-environment has formed E2, E4, and E6, these are all

untreated treatment environment, in the three years they behaved almost similar for milling quality trait. The husk of the pegionpea grain contains a lot of glucuronic acids and glycol protein[5] which are responsible for poor hulling efficiency and dhal recovery[2] and it can only be overcome by premilling treatment[37]. However, the genotypes G9, G2, and G10 performed better in this environment and most of them are derived from *C. scarabaeoides*. The E1, E3, and E5 environments make up the second mega environment and were formed for the pre-milling treated group. The genotypes G3, G11, and G12 performed well in this environment (Fig. 2j), and were mostly derived from the *C. acutifolius*.

Conclusion

The pigeon pea is an important pulse crop globally and interspecific hybridization played a key role in the improvement of yield and pest and disease resistance in pigeon pea. In the present study, the nine interspecific hybrid lines were studied for their milling quality. The study revealed the presence of ample variation in milling quality traits among the interspecific hybrids studied. It found the influence of G x E interactions for dhal yield and hulling efficiency. The seed harness was found to be positively associated with dhal yield and hulling efficiency. Based on AMMI and GGE studies the genotype G12 was found to be more stable for dhal yield and hulling efficiency. It also found that genotypes derived from *Cajanus scarabaeoides* were found better under untreated environments while *C. cajanifolius* derived lines were found best under a pre-milling treated environment.

Materials And Methods

Experimental Site

The experimental investigation was carried out at the Norman E Borlaug Crop Research Centre, situated within Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand (29°N latitude; 79.30°E longitude; 243.84 meters above mean sea level).

Experimental material

The seeds collected from lines derived from nine inter-specific crosses originating from cultivated parental lines, namely, ICPL 84023, Pant A134, and UPAS 120, and wild species, *Cajanus scarabaeoides, Cajanus acutifolius, and Cajanus cajanifolius* (Table 4) were used in the study. The lines were grown in the years 2009, 2010 and 2011 and the seeds were harvested at maturity, dried, threshed, cleaned and used for milling studies.

Table 4. List of interspecific crosses and their cultivated parents

Sl.No	Designation	Genotype	Features/Remarks
1	G1	ICPL84023	Determinate, early maturing line
2	G2	ICPI84023 x *C. scarabaeoides*	Interspecific cross
3	G3	ICPL84023 x *C. acutifolius*	Interspecific cross
4	G4	ICPL84023 x *C. cajanifolius*	Interspecific cross
5	G5	PA134	Indeterminate, early maturing line
6	G6	PA134 x *C. scarabaeoides*	Interspecific cross
7	G7	PA134 x *C. acutifolius*	Interspecific cross
8	G8	pa134 x *C. cajanifolius*	Interspecific cross
9	G9	UPAS120	Indeterminate, early variety
10	G10	UPAS102 x *C. scarabaeoides*	Interspecific cross
11	G11	UPAS120 x *C. acutifolius*	Interspecific cross
12	G12	UPAS120 x *C. cajanifolius*	Interspecific cross

Determination of milling parameters

In each cross six seed (grain) samples of 150 g were formed, out of them three were given treatment with 10% sodium bicarbonate before milling and another three were milled without any treatment. A total of 27 seed samples from inter specific progeny lines and 9 seed samples from cultivated parents were given seed treatment with sodium bicarbonate before milling in each season. A total of 72 seed samples were milled by using Satake grain Testing Mill at 10% moisture content in each season. The Moisture content of the samples was measured by using the standard oven dry method. Moisture content in the milling samples was maintained at 10%.

Pre-milling treatment

Samples were treated with 10% sodium bicarbonate at the rate of 20:1 grain solution ratio for five hours and then the samples were dried to bring the moisture level to 10% before milling (Table 5).

Table 5. Details of environment used for the study

Sl.No	Designation	Environment
1	E1	First year, Treated
2	E2	First year, Un-treated
3	E3	Second year, Treated
4	E4	Second year, Un-treated
5	E5	Third year, Treated
6	E6	Third year, Un-treated

Milling of the samples

Milling of grins was done by using Stake grain testing mill (Stake Engg. Co. Ltd. Tokyo, Japan).

The milling parameters were worked as follows

Dhal yield: It can be obtained by using formulae,

Dhal yield = (S+G)/ (W x 100)

Where,

S= Splits (dehusked & separated),

G= Gotta (dehusked whole),

W= Total amount of sample feed.

Hulling efficiency: It was obtained by the formulae,

Hulling efficiency = (1-Un/T) x (Fp/ Fp+Br+Po) x 100

Where,

Un= Hulled grain,

Fp= Finished product consists of split and whole dehusked grain,

Br= Broken,

Po= Powder.

Statistical Analysis

Combined ANOVA and Correlation analysis were performed in Statistical Tool for Agricultural Research (STAR) Version: 2.0.1. All other statistical analyses were conducted in the statistical software R version 4.1.1. The “metan” package[38] was employed to conduct the AMMI analysis of variance. Prediction assessment was carried out utilising the AMMI approach for all the above-mentioned traits across environment trials[39]. This was the AMMI model:

$$Y_{ij} = \mu + a_i + \beta_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} \delta_{jk} + \varepsilon_{ij}$$

where, Y_{ij} is the yield of ith genotype in jth environment over all replications, μ is the grand mean, a_i is the ith genotype mean deviation (genotype mean minus grand mean), β_j is the jth environment mean deviation, λ_k is the singular value for IPC axis k, γ_{ik} is the ith genotype eigenvector value for IPC axis k, δ_{jk} is the jth environment eigenvector value for IPC axis k, and ε_{ij} is the error term.

AMMI Stability Value (ASV)

As described by Purchase et al. [40], the AMMI stability value (ASV), which was used to compare the stability of genotypes, was calculated as follows:

$$ASV=\sqrt{[SSIPC1/SSIPC2\ (IPC1)^2] + (IPC2)^2}$$

By dividing the IPC1 sum of squares by the IPC2 sum of squares, SSIPC1/SSIPC2 represents the weight applied to the IPC1 value. A genotype is more particularly adapted to a given environment the higher the IPC score, whether negative or positive. Greater genetic stability across contexts is indicated by lower ASV scores.

Genotype Selection Index (GSI)

Each genotype's genotype selection index (GSI), which combines the mean of the characteristic and the ASV index into a single criterion, was determined.

$GSI_i = RM_i + RASV_i$

where GSI_i is the i^{th} genotype's genotype selection index, RM_i is the rank of that genotype's based on trait mean, and $RASV_i$ is the rank of that genotype's based on AMMI stability value. This parameter's low value indicates genotypes with high mean and stability that are desirable.

Genotype plus genotype by environment (GGE) biplot analysis

The “metan” package[38] was employed to conduct the GGE (genotype plus genotype by environment) biplot analysis in the statistical software R version 4.1.1.

Declarations

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Author contributions

MSHK, BGC, AS: Conceptualization, Methodology, and Writing—Original-draft preparation, Data curation; A, AN, MSHK: Data curation, Visualization, Writing-Review and Editing; MSHK, GK, MRT, SV, YKR, CB: Data curation, Visualization, Validation.

Declarations

The study adhered to applicable institutional, national, and international guidelines and legislation, ensuring that all experiments on plants were conducted in accordance with relevant regulations. Additionally, the plant collection and use was in accordance with all the relevant guidelines.

The wild genotypes have been obtained through the nodal agency for germplasm exchange i.e. National Bureau of Plant Genetic Resources, New Delhi following the prescribed guidelines. Also, the authors have all the required permissions and rights to collect and use the genotypes for research purpose. The experimental research and field experiments in the present study are duly approved by the student research advisory board and Department of Genetics and plant breeding, College of Agriculture, GBPUA&T, Pantnagar, Uttarakhand, India-263145.

Data Availability Statement

All data generated and analyzed supporting the findings of this study are available within the manuscript and within its supporting information files given.

Competing interests

The authors declare no competing interests.

Correspondence and requests for materials should be addressed to MSHK

References

1. Valenzuela, H. Pigeon pea: a multipurpose crop for Hawaii, *March–April–May edn. Hanai'Ai/The Food Provider, Hawaii*, p. 1–8 (2011).

2. Hiregoudar, S., Sandeep, T. N., Nidoni, U., Shrestha, B., & Meda, V. Studies on dhal recovery from pre-treated pigeon pea (*Cajanus cajan* L.) cultivars. *J. Food Sci. Technol.* **51**, 922-928 (2014).
3. Chacko, J., Saxena, R.P., Kumbhar, B.K. & Agrawal, U.S. Pigeon pea milling: A status report. *National seminar on emerging trends in processing, handling, storage and by-product utilization of pulses and soybean*. GBPUAT, Pantngar (2001).
4. Mangaraj, S., Agrawal, S., Kulkarni, S. D., & Kapur, T. Studies on physical properties and effect of pre-milling treatment on cooking quality of pulses. *J. Food Sci. Technol.* **42**(3), 258–262 (2005).
5. Kurien, P.P., & Parpia HAB. Pulse milling in India I—processing and milling of tur, *arhar* (*Cajanus cajan* L.) *J Food Sci. Technol.* **5**, 203–207 (1968).
6. Sahay, K. M., & Bisht, B. S. Development of a small abrasive cylindrical mill for milling pulses. *Int. J. Food Sci. Technol.* **23**(1), 17–22 (1988).
7. Sahay, K.M., Agrawal, S.P., & Bisht, B.S. Optimization of emery/ carborundum grade for pulse dehusking for 100 kg/h capacity. RPF-III, project No.111, CIAE, Bhopal, India (1985).
8. Mangaraj, S., Agrawal, S., Kapur, T., & Kulkarni, S. D. Effect of pre-milling treatment and abrasive rollers on milling of pulses. Journal of Agricultural Engineering, **41**(4), 10–5 (2004).
9. Zali, H., Farshadfar, E & Sabaghpour, S. H. Non-parametric analysis of phenotypic stability in chickpea (*Cicer arietinum* L.) genotypes in Iran. *Crop Br. J.* **1**(1), 89-100 (2011).
10. Yan W. & Rajcan I. Biplots analysis of the test sites and trait relations of soybean in Ontario. *Crop Sci.* **42**, 11-20 (2002.).
11. Yan, W., Hunt, L. A., Sheng Q. & Szlavnics Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.* **40**(3), 597-605 (2000).
12. Gauch H. G. Statistical analysis of regional yield trials: AMMI analysis offactorial designs. *Elsevier*, Amsterdam (1992).
13. Samonte, S. O. P., Wilson, L. T., Mc Clung, A.M. & Medley, J. C. Targeting cultivars on to rice growing environments along AMMI and SREG GGE biplot analysis. *Crop Sci.* **45**, 2414-2424 (2005).
14. Opoku, A., Tabil, L., Sundaram, J., Crerar, W. J., & Park, S. J. Conditioning and dehulling of pigeon peas and mung beans. *CSAE/SCGR Paper*, 03-347 (2003).
15. Goyal, R. K., Vishwakarma, R. K., & Wanjari, O. D. Optimisation of the pigeon pea dehulling process. *Biosyst. Eng.* **99**(1), 56-61 (2008).
16. Ramakrishnaiah, N. & P. P. Kurien. Non-starchy polysaccharides of pigeon pea and their influence on dehulling characteristics. *J. Food Sci and Technol* **22**, 429 – 430 (1985).
17. Ramakrishnaiah, N. & P. P. Kurien. Variabilities in the dehulling characteristics of pigeon pea (*Cajanus cajan* L.) cultivars. *J Food Sci Technol.* 20, 287 – 291 (1983).
18. Ehiwe, A.O.F. & R.D. Reichert. Variability in dehulling quality of cowpea, pigeon pea, and mung bean cultivars determined with the tangential abrasive dehulling device. *Cereal Chem.* **64**(2), 86 – 90 (1987).
19. Singh, U., B.A.S. Santosa & P.V. Rao. Effect of dehulling methods and physical characteristics of grains on dhal yield of pigeon pea (*Cajanus cajan* L.) genotypes. *J Food Sci Technol.* **29**(6): 350 – 353 (1992).
20. Tyler, R. T. Impact milling quality of grain legumes. *J Food Sci Technol.* 49, 925 (1984).
21. Kumar, N. *et al.* Multi-environment evaluation of Spanish bunch groundnut genotypes for fresh seed dormancy. *Indian J. Genet.* **79**(3), 572-582 (2019). doi:10.31742/IJGPB.79.3.7.
22. Ajay, B. C., Bera, S. K., Singh, A., Kumar, N., Gangadhar & Praveen K. Evaluation of genotype × environment interaction and yield stability analysis in peanut under phosphorus stress condition using stability parameters of AMMI model. *Agric. Res.* **9**, 477-486 (2020). doi: 10.1007/s40003-020-00458-3.
23. Pagi, N. *et al.* Phenotypic stability and GGE biplot analysis in Pigeon pea [*Cajanus cajan* (L.) Mill sp.] genotypes across the environments. *J. Exp. Biol. Agric. Sci.* **5**(3), 359-367 (2017).
24. Singh J., Kumar A., Fiyaz R. A. & Singh M. K. Stability analysis of pigeon pea genotypes by deployment of AMMI model under rainfed environment. *Legume Res.* **41**(2), 182-188 (2018).

25. Lal, C., Ajay, B. C., Chikani, B. M. & Gor H. K. AMMI and GGE biplot analysis to evaluate the phenotypic stability of recombinant inbred lines (RILs) of peanut under mid-season water stress conditions. *Indian J. Genet.* **79**(2), 420-426 (2019). doi:10.31742/IJGPB.79.2.5.
26. Gaur, A. K., Verma, S. K., Panwar, R. K. & Sharma R. K. Estimation of G x E interaction by AMMI model in some elite pigeon pea [*Cajanus cajan* (L.) Millspaugh] genotypes. *Indian J. Genet.* **80**(2), 173- 178 (2020). doi: 10.31742/IJGPB.80.2.7.
27. Kanouni, H. Stability of Chickpea (*Cicer arietinum* L.) landraces in National Plant Gene Bank of Iran for Drylands. *J. Agril. Sci. Technol.* **20**, 387-400 (2018).
28. Choudhary, M. *et al.* GGE biplot analysis of genotype × environment interaction and identification of megaenvironment for baby corn hybrids evaluation in India. *Indian J. Genet.* **79**(4): 658-669 (2019). doi: 10.31742/ IJGPB.79.4.3.
29. Kumar V., Verma R. P. S., Kumar D., Kharub A. S. & Singh G. P. Assessment of barley genotypes for malting quality: Genotype x environment interactions. *Indian J. Genet.* **78**(4): 523-526 (2018). doi: 10.31742/IJGPB.78.4.16.
30. Yadav, O. P., Razdan, A. K., Kumar, B., Singh P. & Singh A. K. Using AMMI approach to delineate genotype by environment interaction and stability of barley (*Hordeum vulgare* L.) genotypes under northern Indian Shivalik hill conditions. *Indian J. Genet.* **80**(3): 339-342 (2020). doi: 10.31742/IJGPB.80.3.15.
31. Sara, M., Abbas, R., Reza, A & Alireza, E. Yield stability of rapeseed genotypes under drought stress conditions. *Indian J. Genet.* **79**(1): 40-47 (2019). doi: https://doi.org/10.31742/IJGPB.79.1.6.
32. Dwivedi, A., Basandrai, D & Sarial, A. K. AMMI biplot analysis for grain yield of basmati lines (*Oryza sativa* L.) in North Western Himalayan Hill regions. *Indian J. Genet.* **80**(2): 140-146 (2020). doi: 10.31742/ IJGPB.80.2.3.
33. Bavandpori F., Ahmad J. & Hossaini S. Stability analysis of bread wheat landraces and lines using biometrical genetic models. *Genetika*, **50**, 449-464 (2018). doi: 10.2298/GENSR1802449B.
34. Lozada, D.N. & Carter, A.H. Insights into the genetic architecture of phenotypic stability traits in winter wheat. *Agron*omy **10**(3), 368 (2018). doi:10.3390/agronomy 10030368.
35. Manu, B. *et al.* Genetic gain and morphophysiological characterization of BILs (Backcross Inbred Lines) under different moisture regimes in wheat (*Triticum aestivum* L). *Indian J. Genet*. **80**(1), 84-93 (2020). doi: 10.31742/IJGPB.80.1.11.
36. Kumar, M. et al. Delineating G × E interactions by AMMI method for root attributes in ashwagandha [*Withania somnifera* (L.) Dunal] *Indian J. Genet.* **80**(4), 441- 449 (2020). doi: 10.31742/IJGPB.80.4.10.
37. Saxena, R.P. A technical report on comparison of different premilling treatments of pigeon pea grain on a laboratory dhal mill. Res. Bull no. 5/PHT of pulses/1999, Govind Ballabh. Pant University of Agriculture and Technology, Pantnagar (1999).
38. Olivoto, T., & Lúcio, A. D. C. metan: An R package for multi-environment trial analysis. *Methods Ecol. Evol.* **11**(6), 783-789 (2020).
39. Gabriel, K. R. Analysis of meteorological data by means of canonical decomposition and biplots. *J. Appl. Meterol. Climatol.* **11**(7), 1071-1077 (1972).
40. Purchase, J. L., Hatting, H., & Van Deventer, C. S. Genotype× environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *S. Afr. J. Plant Soil.* **17**(3), 101-107 (2000).

Figures

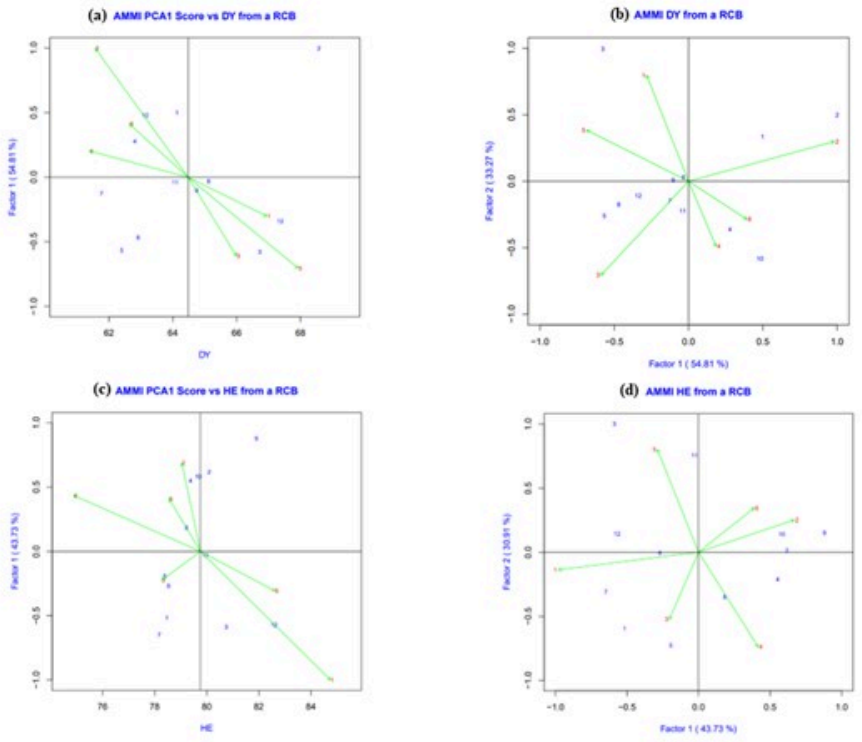

Figure 1

AMMI biplot for Dhal yield and Hulling Efficiency (a) AMMI biplot PC1 Vs Dhal Yield, (b) AMMI biplot PC1 vs PC2 for Dhal Yield, (c) AMMI biplot PC1 Vs Hulling Efficiency, (d) AMMI biplot PC1 vs PC2 for Hulling Efficiency. Where G = Genotypes (1–12) and E1-E6 are the environments.

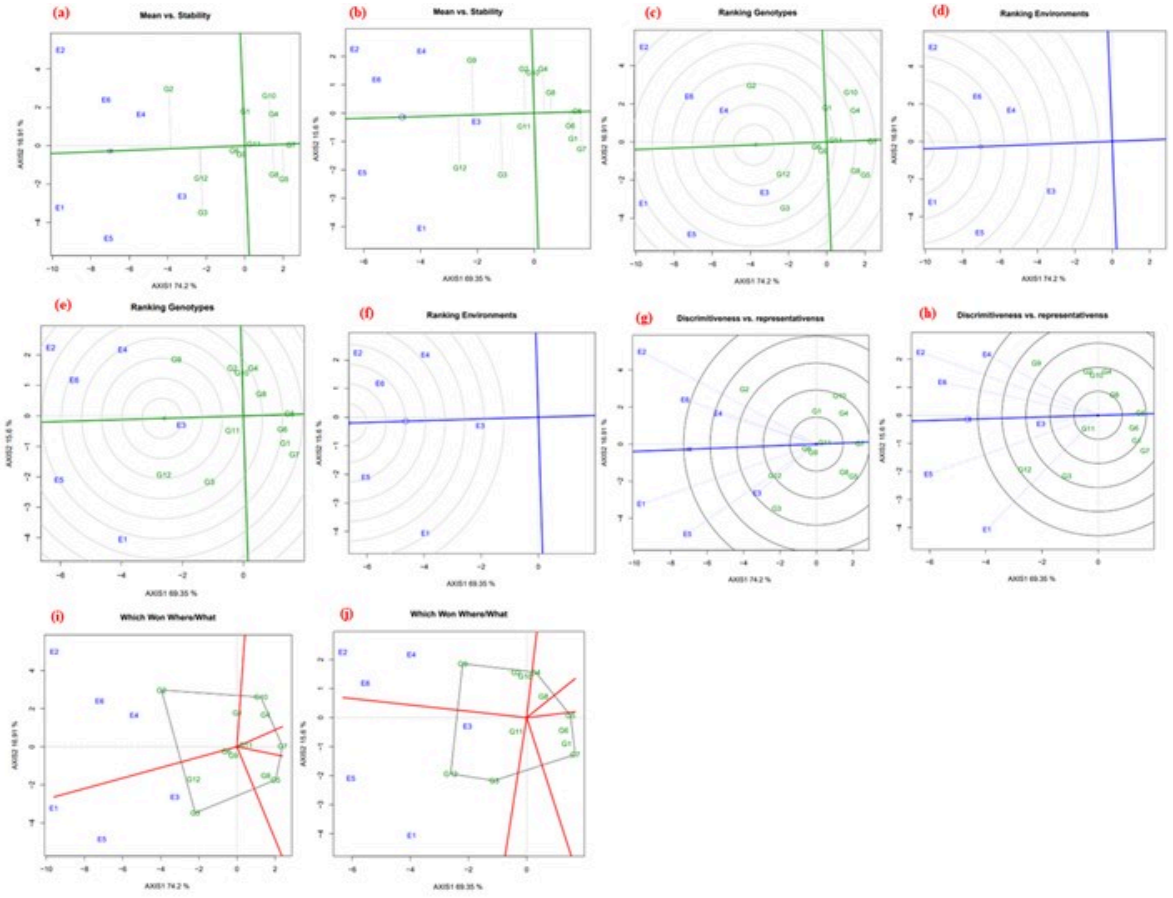

Figure 2

(a) Mean Vs Stability biplot for dhal yield, (b) Mean Vs Stability biplot for hulling efficiency, (c) Ranking Genotypes biplot for dhal yield, (d) Ranking Environment biplot for dhal yield, (e) Ranking Genotypes biplot for hulling efficiency, (f) Ranking Environment biplot for hulling efficiency, (g) Discriminative vs. Representativeness for dhal yield (h) Discriminative vs. Representativeness for hulling Efficiency, (i) Which Won Where/What Biplot for dhal yield (j) Which Won Where/What Biplot for dhal yield hulling Efficiency; Where G = Genotypes (1–12) and E1-E6 are the environments.

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