Research article

Estimating phenotypic stability for relevant yield and quality traits in French bean (*Phaseolus vulgaris* L.) using AMMI analysis

Kartik Pramanik [a],[*],[1], Gouri Shankar Sahu [b], Gobinda Chandra Acharya [c], Pradyumna Tripathy [b], Manasi Dash [d], A.V.V. Koundinya [c], Chinmaya Jena [a],[1],[**], Duvvada Sarath Kumar [e], Priyadarshani P. Mohapatra [f], Jyostnarani Pradhan [g], S. Karubakee [h], Durga Prasad Moharana [i]

[a] *M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha, 761211, India*
[b] *Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, 751003, India*
[c] *Central Horticulture Experiment Station (CHES), ICAR- IIHR, Bhubaneswar, Odisha, 751019, India*
[d] *Department of Genetics and Plant Breeding, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, 751003, India*
[e] *Institute of Agriculture, Palli Siksha Bhavana, Visva Bharati University, Sriniketan, West Bengal, 731236, India*
[f] *MTTC and VTC, College of Community Science, Tura, Central Agricultural University, Meghalaya, 794005, India*
[g] *Department of Botany, Plant Physiology and Biochemistry, College of Basic Science and Humanities, Dr. Rajendra Prasad Central Agriculture University, Pusa, Samastipur, Bihar, 848125, India*
[h] *Department of Agronomy, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, 751003, India*
[i] *College of Horticulture, Odisha University of Agriculture and Technology, Sambalpur, Odisha, 768026, India*

ARTICLE INFO	ABSTRACT
	The presence of strong G x E (genotype by environment interaction) is a major hurdle for selecting superior genotypes when genotypes are placed into new and unfamiliar production systems. Genotype or cultivar (s) with high yield potential and having less adaptability and stability to particular environment is never a suitable choice for a breeder and farmer particularly. Purposefully, four successive seasons were chosen to enumerate the phenotypic stability of 27 French bean genotypes for yield and quality traits by involving modern statistical tools like AMMI (Additive Main Effect and Multiplicative Interaction), GGE [G + (G x E)] and cluster analysis. AMMI analysis of variance witnessed magnitude of G, E and G x E was 81.94%, 11.58% and 6.48% of the total variation respectively. The IPCA I (Interaction Principal Component Axes) was contributed with 55.44%, 73.60%, 71.81%, 81.69% and 72.16% G x E variations of days to 50% flowering, pod length, number of pods per plant, average pod weight and pod yield respectively. For qualitative traits *i.e.*, protein content (mg/100g FW), total soluble solids (%) and total phenol content (mg GAE/g FW) the involvement of IPCA I to total genotype by environment interaction variations were 89.55%, 96.07% and 66.52% respectively. The AMMI biplot revealed French bean genotypes *viz.*, IC632961, Arka Sukomal, IIHR-PV-29, IIHR-PV-30 having low AMMI stability value and higher mean value for relevant yield and quality traits in both late *kharif* and *rabi*

* Corresponding author.
** Corresponding author.
E-mail addresses: kartikouat@gmail.com, kartik.pramanik@cutm.ac.in (K. Pramanik), jenachinmaya3@gmail.com, chinmaya.jena@cutm.ac.in (C. Jena).
[1] Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha −751003, India (Past affiliation).

as two mega-environments. Multivariate analysis demonstrated significant higher contribution of pod yield associated traits towards total variations and positive correlation between them. The 27 French bean genotypes formed five groups as per Euclidean distance and the clustering revealed the nature of diversity of French bean genotypes *viz.*, IC 632961, IIHR-B-PV-24, Arka Sukomal, Arka Arjun, Ayoka and Phalguni in response to changing environments and can be utilized in future breeding programme. The study revealed pole type French bean genotypes *viz.*, IC 632961, Arka Sukomal and bush type French bean genotypes *viz.*, IIHR-B-PV-29, IIHR-B-PV-30 could be promising for utilization in future breeding programmes for the concerned traits.

1. Introduction

French bean is nutritionally valued pulse crop having worldwide importance in terms of human and animal consumption. The crop provides important vitamins including folic acid and thiamine as a food source [1] and proteins, fibers, vitamins (thiamin) and minerals (iron, zinc, and folic acid) [2,3] and Furthermore, the stems can be used as animal fodder, particularly during the dry period that follows the primary cropping season [4]. In world scenario, India is leading country in producing dry French bean seed followed by Brazil and Myanmar. However, China leads the world in green beans production preceded by Indonesia and Turkey [5].

Performance of a genotype in one environment may not same in another due to genotype × environment interactions (GEI) [6], suggest assessments and adaption breeding strategies to address this variation. Presence of GEI expressed the inconsistence performance of genotypes across diverse environments [7,8] and complicates the selection process. To identify best performing genotypes plant breeders put effort to know the genotype and environment interaction by testing genotypes across diverse environment conditions [9] and to develop superior varieties [10]. Many scientists highlighted that the genotype, environments and their interaction had significant effect on common bean grain yield [11]. The genotypes by environment interaction had significant effect in witnessing difference in grain yield in common bean [12,13]. A genotype with a low GEI will be more stable which alters its genotypic or phenotypic traits minimum in response to temporary environmental fluctuations. Genotypes should be chosen based on the least amount of interaction with environments [14] and cultivars with general and specific adaptability [15]. Hence, stability analysis of given genotypes in a given environments play essential role in crop improvement programme [16]. The necessary variety will therefore exhibit little genotype × environment interaction for agriculturally significant traits, particularly yield. So, GEI analysis suggested the best-performing crop genotypes and effective production environments. The importance of GEI has been highlighted by many crop breeders in selection of superior genotypes [17,18].

Yield component of plants is cumulative action of genotype (G), environment (E) and their interaction (G × E) [19]. French bean being a cool seasonal crop the performance usually suffers in changing season out of normal season and even changing locations due to genotype × environment interaction. Tadesse et al. [20] reported that the common bean performance was greatly affected by the environment. Significant differences in seed yield revealed among bean genotypes due to GEI have been extensively reviewed by many scientists [21,22]. Many workers also highlighted the significant grain yield variations among the genotypes or varieties in diverse environments and genotypes by environments interaction in beans [23]. G × E interaction caused variable response in grain yield relevant traits among cowpea and soybean genotypes in changing environments [24]; [25]. GEI is considered for selecting genotypes having broad adoption and rejecting specific adaptions [26]. To examine GEI, stability, and adaptation, various biometrical techniques have been developed. However, Additive Main Effects and Multiplicative Interaction (AMMI) model and the Genotype Main Effects and Genotype by Environment Interaction (GGE) models were regarded as the best models for multiple location trial for dataset analysis and discovery of genotype as per which won where pattern [27]. AMMI analysis was utilized by Ferreira et al. [28] to identify superior genotypes for specific or wider adaptation in common beans. Principal component axes (PCAs) are used in AMMI analysis to extract genotype and environment by main effects and to explain patterns in the G × E interaction or residual matrix [29]. The model determines the genotypes and environments principal component scores that compose the G × E interaction. The AMMI model considers genotypes to be broadly adaptable to all environments when they have mean values greater than the grand mean and interaction principal component axes (IPCA) scores that are close to zero. However, genotypes with high mean performance and high IPCA scores are considered to have a specific environmental adaptation. Most stable high yielding large seeded common bean genotypes were identified by employing AMMI and GGE models [30]. Furthermore, Hagos and Abay [31] suggested PCA (principal component axis) scores and AMMI stability value (ASV) of an AMMI analysis for identifying stable genotypes across locations. The IPCA1 and IPCA2 (interaction principal components axis 1 and 2, respectively) scores from the AMMI model for each genotype are utilized to determine the ASV [32]. The genotypes with a low ASV are regarded as broadly adapted. Similarly, IPCA2 scores close to zero show more stable genotypes, whereas big values show more sensitive and less stable genotypes. Purposefully, present investigation was undertaken to estimate the magnitude and pattern of G × E interaction to identify broadly or specifically adapted lines with yield and relevant traits stability for both future breeding programme and farmer adoption.

2. Material and methods

2.1. Genetic materials, experiment sites and design

Twenty seven French bean genotypes representing two growth habits *viz.*, pole and bush type including two standard check *viz.*,

Raikia (IC 632961) and Arka Arjun respectively were introduced and evaluated under two different sowing dates/Environments during the late *kharif* (E1 = September 25, 2019, E3 = September 25, 2020) and *rabi* (E2 = December 5, 2019, E4 = December 5, 2020) season over two consecutive years, 2019–20 and 2020–2021 at Central Horticulture Experiment Station (CHES), IIHR, Bhubaneswar (20.015° N latitude, 85.053° E longitude and 25.5 m AMSL) for yield and associated traits performance using randomized complete block design (Fig. 1). The precipitation code of the location was D1 E3 (B1A2B1) C1D1E2. The average temperature fluctuates from 14 °C in winter, 40 °C in summer and 30 °C in rainy season. Relative humidity varies between 49% and 90%. On a raised bed, seeds were sown with a 30 cm row to row, 15 cm plant to plant, and 60 cm row to row, 30 cm plant to plant spacing for bush type and pole type, respectively.

2.2. Traits observation

Traits of interest *viz.*, days to 50% flowering, pod length, number of pods per plant, average pod weight, pod yield were recorded for each genotype in replication and season wise over four picking in each season. For biochemical analysis randomly five fresh pods were taken from each genotype in each replication. The protein content was estimated by taking Bovine Serum Albumin (BSA) as standard and the absorbance was recorded with 660 nm in spectrophotometer and expressed as g per 100g of fresh pod proposed in Lowry method. Total soluble solids were estimated with hand refractometer as expressed as %. Using the Folin-Ciocalteu reagent, the total phenolic content of the pod was determined [33].

2.3. Statistical analysis

2.3.1. ANOVA
Data obtained on yield components and quality traits over two year and seasons were subjected combined analysis of variance employing the software package KAU GRAPES version 1.1.0 [34] after performing the test of homogeneity using Bartlet's test [35].

R1		R2	R3	R1		R2	R3
G1		G12	G5	G12		G10	G11
G5		G9	G19	G20		G15	G26
G7		G18	G23	G4		G27	G15
G2		G17	G16	G17		G11	G3
G10		G22	G18	G13		G14	G8
G9		G2	G1	G14		G6	G4
G11		G20	G22	G21		G26	G13
G24		G25	G9	G27		G4	G20
G23		G1	G12	G16		G23	G24
G18		G3	G17	G26		G5	G6
G15		G21	G2	G22		G24	G21
G25		G8	G7	G19		G13	G14
G8		G4	G10	G6		G16	G25
G3		G7	G27				

Fig. 1. RCBD experiment design followed for four seasons.

2.3.2. AMMI analysis

To estimate genotype (G), environment (E) and G × E interaction (GEI) effect on yield and relevant traits the AMMI analysis was used [36]. The G × E Interaction (GEI) sum of squares was decomposed into IPCA scores and residual values. AMM I biplot was constructed with IPCA I score and genotypes main effects to find out the stable genotypes. The degrees of freedom (df) for the IPCA were estimated as per formula mentioned by Zobel [36].

2.3.3. AMMI stability value (ASV)

Stable and high yielding French bean genotypes were found out by using ASV (AMMI Stability Value). AMMI Stability Values (ASV) was estimated with the following formula [32] after testing the significance of the GEI mean square for particular traits. Genotypes having lower values of ASV were considered to be stable. The algorithm below was used to obtain the stable genotypes using the average AMMI Stability Value (AASV). ASV levels that were equal to or less than AASV were used to define stable genotypes.

2.3.4. GGE biplot

GGE biplot was constructed to reveal the interaction and adaption pattern of genotypes to environments as per proposed model [37]. The model is relied on singular value decomposition (SVD) of the first two principal components (IPCA I and IPCA II). AMMI and GGE biplot analysis were carried out by using R package. The 27 French bean genotypes comprised of pole types and bush types were subjected to clustering analysis to identify similar performing and diverse genotypes for yield components and quality traits using the software package PBSTAT-CL 2.1.2. Furthermore, principal component analysis and Pearson's correlation analyses were used to enumerate the nature and magnitude of variation prevailed over season by using KAU GRAPES version 1.1.0 [34].

3. Results and discussion

3.1. AMMI analysis

AMMI ANOVA extract GEI by mean effects and uses PCA to put straight forward explanation on patterns in the genotype × environment interaction or residual matrix in multi-seasonal or multi-location datasets [29] which is not clear in PCA, regression analysis, and conventional ANOVA. For all the examined traits ($p < 0.05$), AMMI ANOVA showed significant variation among genotypes (G), environments (E), and G × E interactions, with the exception of protein content and total soluble sugar solids, which showed non-significant variation across the environments/seasons (Table 1). The non-significant variation for protein content and total soluble sugar solids suggests that these traits are less affected by environmental factors in the study, making them potentially more predictable or consistent across different conditions. These outcomes supported the findings by Gelete et al. [38] reported significant genotype, environment, and G × L effects for many sensory attributes in cooked Andean beans. As far as contribution of different sources to the total variation is concerned, in case of pod yield, the genotypes, environment and G × E interaction accounted 81.94, 11.58 and 6.48% of the total variations. Higher contribution of G × E interaction i.e., 26.30 and 18.49% witnessed in days to 50% flowering and total phenol content respectively, indicated the traits were significantly influenced by environment over season (Table 2). Whereas maximum genotypic contribution was noticed in protein content (99.24%) and total soluble sugar (91.62%) and environment has less impact on these traits. GEI (G × E interaction) had significant lower magnitude of contribution on average pod weight (9.5%), number of pods per plant (11.02%) and length of pod (11.12%). The results corroborated with earlier findings by Thangavel et al. [39] who revealed that main effects due to environments (E), genotypes (G) and G × E interaction were found significant for plant height, number of branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight and grain yield per plant ($P < 0.01$) in mungbean. Zeleke et al. [40], indicated the presence of significant genetic variation among the common bean genotypes with differential response across environments. The GEI sum of squares had higher magnitude than genotypes indicated complicacy in superior selection and adaptable genotypes as reported by many researchers [30].

Table 1
AMMI analysis of variance for various traits of French bean.

Source	Df	Mean sum of square							
		DF	NPP	PL	APW	PY	PC	TSS	TPC
Genotype (G)	26	226.33[a]	168.38[a]	125.35[a]	82.35[a]	5287.37[a]	4.04[ns]	8.44[ns]	906.61[a]
Environment (E)	3	848.69[a]	192.74[a]	189.84[a]	87.27[a]	6477.82[a]	2.49[ns]	3.66[ns]	1691.23[a]
G x E	78	38.57[a]	3.71[a]	6.14[a]	4.50[a]	139.33[a]	7.08[ns]	0.11[ns]	83.31[a]
IPCA I	28	59.56[a]	7.61[a]	12.28[a]	10.25[a]	280.05[a]	1.80[ns]	0.31[ns]	154.38[a]
IPCA II	26	35.59[a]	1.64[ns]	4.10[a]	1.94[ns]	68.33[ns]	2.00[ns]	0.009[ns]	58.99[a]
IPCA III	24	17.30[ns]	1.41[ns]	1.19[ns]	0.58[ns]	52.06[ns]	1.00[ns]	0.004[ns]	26.75[ns]
Residual	8	23.50[ns]	2.05[ns]	2.77[ns]	1.05[ns]	56.67[ns]	6.02[a]	0.01[a]	43.34[a]
Error	208	13.89	1.29	2.66	0.97	37.23	1.91	0.17	51.43
Total	401	43.70	14.51	13.37	8.27	465.93	2.75	0.71	131.39
Grand mean		47.40	15.39	15.05	11.14	51.96	1.17	5.32	72.84
SE (m)±		1.08	0.00	0.47	0.28	1.76	0.01	0.122	2.07
CD (0.05)		3.13	0.00	1.37	0.83	5.12	0.04	0.354	6.02

[a] Significance at 5% level.

Table 2
Contribution of different sources to total variance.

Source	SS (%)							
	DF	NPP	PL	APW	PY	PC	TSS	TPC
Genotype (G)	51.44	83.46	75.66	77.74	81.94	99.24	91.62	67.07
Environment (E)	22.26	11.02	13.22	9.50	11.58	0.70	4.58	14.43
G x E	26.30	5.52	11.12	12.76	6.48	0.05	3.78	18.49
IPCA I	55.44	73.60	71.81	81.69	72.16	89.55	96.07	66.52
IPCA II	30.76	14.68	22.24	14.34	16.35	7.42	2.62	23.60
IPCA III	13.80	11.72	5.95	3.97	11.50	3.08	1.31	9.88
Residual	6.25	5.67	4.64	2.40	4.17	871.89	0.89	5.34

DF: Days to 50% flowering, **NPP**: Number of pods plant^{-1}, **PL**: Pod length (cm), **APW**: Average pod weight (g), **PY**: Pod yield (q ha^{-1}), **PC**: Protein content (g100 g^{-1} FW), **TSS**: Total Soluble Solid (%), **TPC**: Total Phenol Content (mg GAE/g FW).

To get more clarity on kind and magnitude of variation, the genotype by environments interaction was decomposed into the Interaction Principal Component Axes (IPCA) and residuals (Table 2). The first three IPCA had lager contribution towards the GEI. So IPCA I, IPCA II and IPCA III were considered for further interpretation. The IPCA I was found to be significant ($p < 0.05$) for all the traits under studies accounted for 55.44, 73.60, 71.81, 81.69, 72.16 and 66.52% of the total G x E sum of squares for DF, NPP, PL, APW, PY and TPC except protein content (89.55%) and total soluble solids (96.07%) whereas IPCA II explained significant for days to 50% flowering (30.76%), pod length (22.24%) and total phenol content (23.6%). IPCA III projected non-significant contribution towards total GEI for all traits under study. Cumulative sum of square above 70% is sufficient for interpretation of GEI [41]. According to Zobel et al. [36], first two IPCA were sufficient for the best interpretation of the interaction sum of square. Crossa et al. [42] stated that IPCA II, III and IV axes were considered for best prediction of AMMI. Hagos and Abay [31] confirmed the significance of first IPCA I score for genotype by environment interaction in bread wheat. The storage root yield of cassava showed a non-significant IPCA II with 17% variance, according to Kvitschal et al. [43]. Misra et al. [44] revealed importance of first bilinear interaction for AMMI analysis. Khan et al. [45], Tadesse et al. [20]; [46], Molosiwa et al. [47], Ejigu et al. [30] confirmed significance of first two bilinear components in stability analysis. Researchers investigated that environment effect is dominant over genotype × environment interaction and genotype with first two IPCA axes accounted maximum contribution towards total sum of square in Andean common bean genotypes [47]. These reports justified the applicability of AMMI model for our study. Non-significant interaction was witnessed for yield attributing traits revealed greater accuracy of the model. The first two bilinear terms utilized 56 of the total 78 degrees of freedom attainable in the interaction and accounted for more than 80% of the GEI sum of squares. The highest combined IPCA I and II contributions to the total G x E variance were found for TSS (98.69%), PC (96.97%), and PL (94.05%), but substantial values of the residual interaction values showed the existence of unexplained variation (noise) for PC, TSS, and TPC (Table 2). The outcomes corroborated the findings by Koundinya et al. [18] in brinjal stability experiment. For quality indicators like hulling percentage, milling percentage, and head rice percentage in paddy, Anandan et al. [48] also noted considerable residual values.

3.2. Estimation of IPCA score and AMMI stability values for stable genotypes

To obtained straight forward interpretation in identifying stable genotypes over seasons, the genotype and environment main effects assigned on *X*-axis and IPCA I on *Y*-axis having greater contribution towards to the total variance leads to construction of biplot (Fig. 2a–h). The genotypes demonstrated IPCA I score zero or near to zero regarded as stable indicated having less interaction with changing environments or less influenced by the environments. The results are concurred with earlier finding [39, 43, 48–50]. However, genotypes having IPCA score near to zero with high mean values for the traits are desirable for cultivation or utilization in crop improvement. Yan and Tinker [51] revealed the genotypes point placed at long distance from the origin indicated most responsive towards environments may not suitable general cultivation.

A Single Value Indicator (SVI) as a method to isolate stable genotypes in the context of genotype-environment interaction analysis. This approach is an alternative to the more common AMMI biplot method where relative placement of the points on biplot observed which may sometimes mislead. In this context, Purchase et al. [32] suggested AMMI Stability Value (ASV) is a numerical index used in multi-environment trials based on phenotypic stability using AMMI model [52]. It is a tool for quantifying the stability of genotypes in different environments, particularly in agricultural research and plant breeding. Farshadfar [53] and Hagos and Abay [31] utilized ASV for investigating yield stability in bread wheat. The ASV are presented in Table 3 used to distinguish stable performing genotypes having low ASV or equal to AASV (AMMI Stability Value). In the present study, the AMMI biplot and ASV consideration was found analogous for the studied traits which was corroborated with the findings of Koundinya et al. [18], who utilized the low ASV for identifying stable genotypes of brinjal.

Phenotypic stability for all component traits in a genotype(s) is not obvious always. In our experiment, traits which are correlated with yield were considered along with some quality parameters for consumer point of view. Genotypes having yield stability with associated traits are selected for breeding purpose [54].
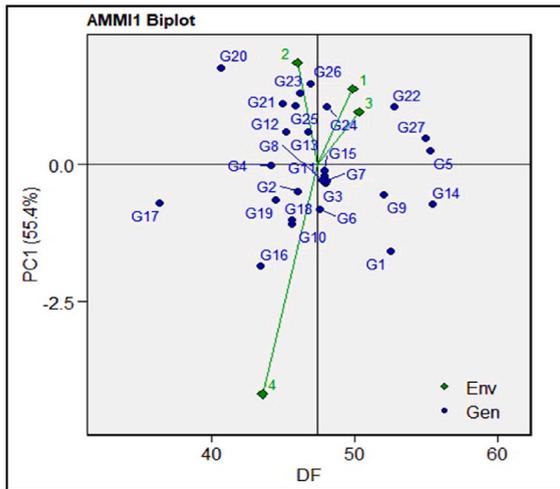
a. AMMI biplot for days to 50% flowering
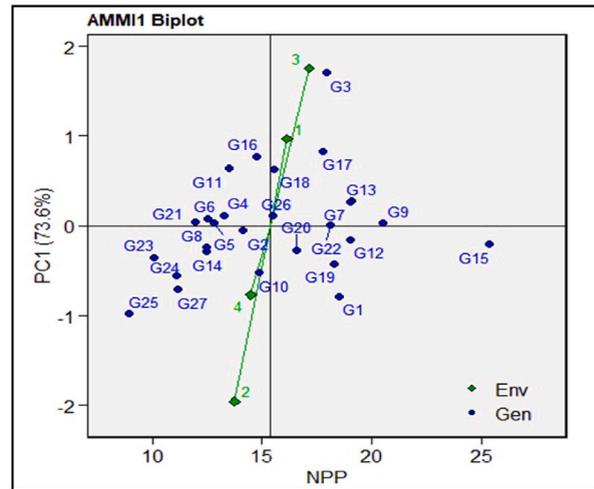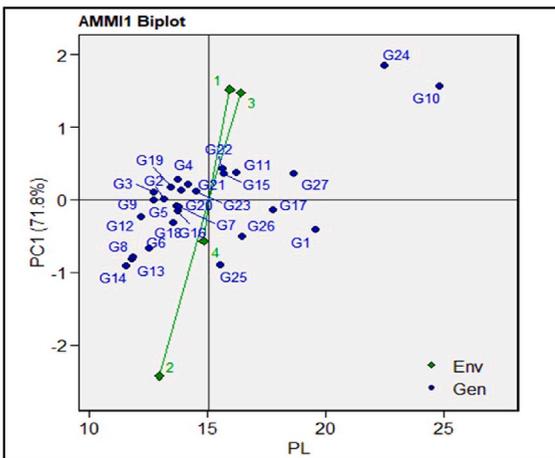
b. AMMI biplot number of pod plant⁻¹

c. AMMI biplot for pod length (cm)
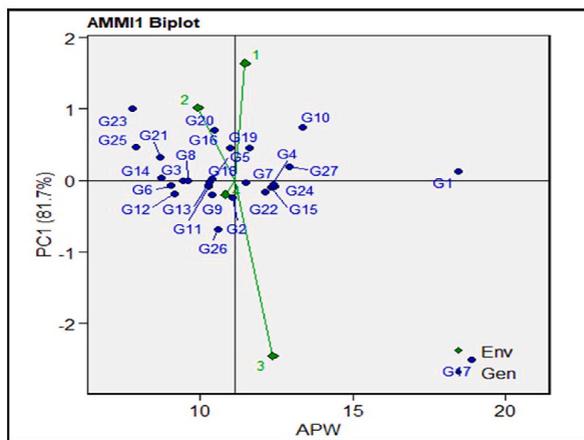
d. AMMI biplot for average pod weight (g)
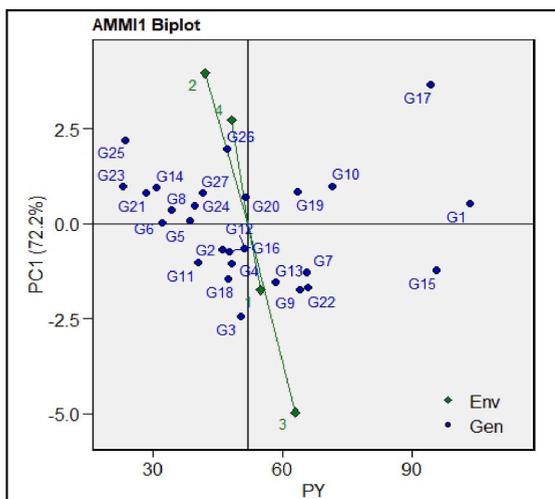
e. AMMI biplot for pod yield (qha⁻¹)
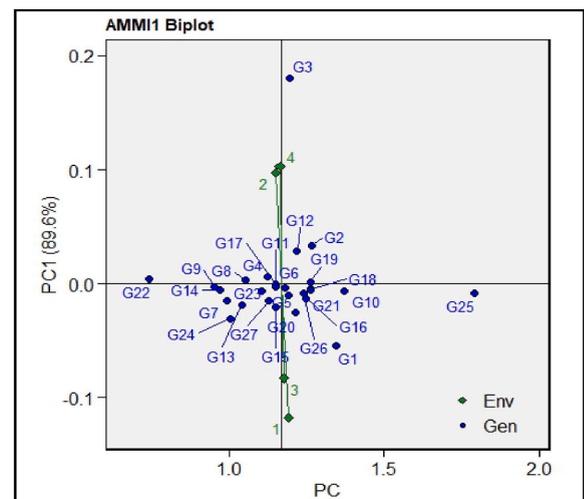
f. AMMI biplot for protein content (g100⁻¹ FW)

Fig. 2. (a) AMMI biplot for days to 50% flowering. **(b)** AMMI biplot number of pod plant^{-1}. **(c)** AMMI biplot for pod length (cm). **(d)** AMMI biplot for average pod weight (g). **(e)** AMMI biplot for pod yield (qha^{-1}). **(f)** AMMI biplot for protein content (g100^{-1} FW). **(g)** AMMI biplot for TSS (%). **(h)** AMMI biplot for total phenol content (mg GAE/g FW). **Genotypes: G1** = IC 632961, **G2** = IIHR-B-PV-26, **G3** = IIHR-B-PV-16, **G4** = IIHR-B-PV-

4, **G5** = IIHR-B-PV-5, **G6** = IIHR-B-PV-9, **G7** = IIHR-B-PV-11, **G8** = IIHR-B-PV-12, **G9** = IIHR-B-PV-15, **G10** = Arka Sukomal, **G11** = IIHR-B-PV-17, **G12** = IIHR-B-PV-20, **G13** = IIHR-B-PV-21, **G14** = IIHR-B-PV-22, **G15** = IIHR-B-PV-24, **G16** = IIHR-B-PV-25, **G17** = Arka Arjun, **G18** = IIHR-B-PV-27, **G19** = IIHR-B-PV-29, **G20** = IIHR-B-PV-30, **G21** = Anupam, **G22** = Ranar, **G23** = Phulbani local, **G24** = Ayoka, **G25** = Phalguni, **G26** = Baisnavi, **G27** = Angul local.
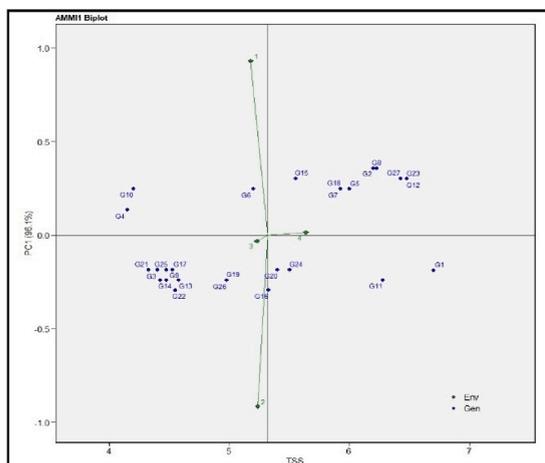
g. AMMI biplot for TSS (%)
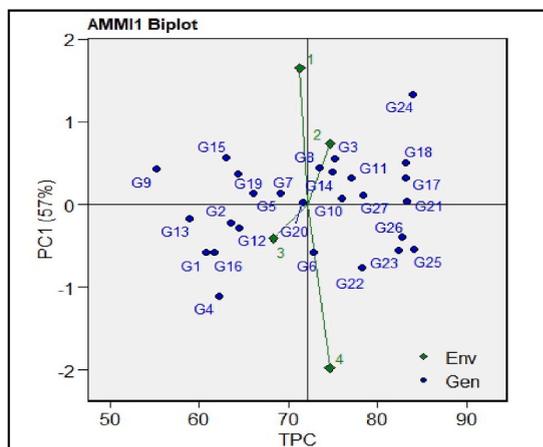
h. AMMI biplot for total phenol content (mg GAE/g FW)

Fig. 2. (*continued*).

3.3. Stable genotypes

Genotypes with low AMMI Stability Value or IPCA I score near zero along with higher mean values for the concerned trait was considered as stable [18]. Earliness is an important trait in French bean preferred by grower. Therefore, to find out the stable genotypes for days to 50 percent flowering, low mean value was considered. Genotypes; G4 (0.87, 44.15), G8 (0.76, 55.27), G11 (0.48, 47.85), G7 (0.86, 47.99) having low ASV (ASV ≤ AASV) and observed with early flowering were considered as most stable for the trait (Table 3; Fig. 2a). For number pods per plant, genotypes G3, G9, G7, G12, 17, G19, G22, G20 found to be most stable having maximum number of pods per plant (>16) with less environment interaction (below average ASV i.e., ≤1.54) as per ASV and AMMI biplot (Table 3; Fig. 3b).

As per AMMI biplot (Fig. 2c) and ASV (Table 3) genotypes; G21, G22, G23, G15 and G26 were observed with high average pod length (>14 cm) and below AASV (<2.11). The data on average pod weight (Fig. 2d) depicted that 19 genotypes were below average AMMI stability value (<1.97) or IPCA I score nearing to zero. Out of which, 6 genotypes viz., G1, G4, G15, G22, G24 and G27 having high average fruit weight (>12) could be considered for general cultivation and crop improvement prospects for the traits. Similarly, 16 genotypes of French bean observed with below AASV (<5.19) or low IPCA I score indicated these genotypes performed stable for pod yield (Fig. 2e). Out of these, G1 reported with maximum pod yield (103.4 q ha^{-1}) proceeded by G10 (71.49 q ha^{-1}), G19 (63.32 q ha^{-1}), G20 (51.31 q ha^{-1}) and G12 (51.22 q ha^{-1}) could be recommended for commercial cultivation and included in the crop breeding program for the relevant trait (Table 3).

Similarly, the stable performing genotypes for important qualitative parameters were identified based on lower AMMI stability value and IPCA I score presented as AMMI biplots. There were 19 and 15 genotypes out of 27 having less than average ASV and IPCA score near to zero although 10 and 4 genotypes were observed with high average value for protein content (>1.22 g100 g^{-1} FW) and TSS (>5%) respectively indicated less interaction with environment and suitable for inclusion in crop improvement (Table 3, Fig. 2f and g). In our experiment, 16 genotypes witnessed lower ASV and IPCA I score nearing to zero (Fig. 2h) out of which 8 genotypes viz., G8, G18, G21, G22, G24, G25, G26 and G27 having higher mean value for TPC (>75 mg GAE/g FW).

Similar context of research findings was reported by many workers [[20,30,38,40,47,55]] who considered lower IPCA and AMMI stability value for identifying stable genotypes with wider adaptations for yield and component traits in common bean breeding programme.

3.4. Genotypes adapted to favourable environment

A favourable environment is characterized with suitable system of weather and available resources in which plants attained proper growth and development. In this environment the genotypes interact positively and usually perform better for quantitative and qualitative traits. These are spotted in 2nd quarter of AMMI biplot above the horizontal interaction line having high ASV and IPCA I score along with high mean value for the traits. Perusal of Table 3 and AMMI biplot (Fig. 2b) depicted genotypes G13, G17 and G18 observed with high positive environment interaction with higher value of number of pods per plant (>15) performed better under

Table 3

AMMI Stability values for pod yield associated and quality traits of French bean.

Genotypes	DF		NPP		PL		APW		PY		PC		TSS		TPC	
	ASV	Mean	ASV	Mean	ASV	Mean	ASV	Mean	ASV	Mean	ASV	Mean	ASV	Mean	ASV	Mean
G1	3.07	52.52[abc]	1.41	18.53[c]	3.95	19.59[c]	0.75	18.44[a]	2.52	103.40[a]	0.67	1.34[b]	6.87	6.70[a]	1.56	61.61[hi]
G2	0.89	46.00[d]	0.48	14.13[fgh]	0.59	13.16[hijk]	1.40	11.06[def]	3.06	45.90[efg]	0.40	1.27[c]	13.11	6.20[bc]	1.14	64.35[ghi]
G3	1.24	47.98[bcd]	0.53	17.95[cd]	8.60	12.72[hijk]	0.21	9.44[ghi]	10.72	50.19[def]	2.19	1.19[fg]	8.74	4.43[fg]	0.72	75.26[bcde]
G4	0.87	44.15[de]	1.07	13.28[ghi]	0.65	13.77[ghijk]	0.62	12.38[bcd]	4.59	48.29[defg]	0.08	1.12[ij]	5.03	4.15[g]	2.80	63.10[hi]
G5	0.76	55.27[a]	0.48	12.83[hij]	0.38	13.70[ghijk]	0.40	10.40[efgh]	1.09	38.48[ghi]	0.12	1.19[fg]	9.13	6.00[c]	1.63	66.88[fgh]
G6	1.49	47.56[cd]	2.20	12.52[hij]	0.42	12.56[hijk]	0.42	9.06[hij]	0.55	32.15[hij]	0.05	1.18[gh]	9.13	5.20[de]	3.95	76.17[abcde]
G7	0.86	47.99[bcd]	0.53	19.01[bc]	1.37	13.80[ghijk]	0.47	11.50[cde]	5.84	65.67[bc]	0.18	0.99[l]	9.17	5.93[c]	4.53	71.67[defg]
G8	0.76	47.70[bcd]	2.56	12.50[hij]	1.45	11.84[jk]	0.02	9.59[fghi]	1.65	34.16[hi]	0.04	1.05[k]	13.14	6.23[bc]	1.84	75.18[bcde]
G9	1.13	51.99[abc]	0.07	20.52[b]	0.26	12.73[hijk]	1.23	10.37[efgh]	7.67	63.84[bc]	0.03	0.95[m]	6.80	4.48[fg]	1.99	56.82[i]
G10	1.99	45.62[d]	5.22	14.87[fg]	2.65	24.85[a]	4.24	13.33[b]	4.39	71.49[b]	0.08	1.37[b]	9.13	4.20[fg]	3.85	78.57[abcd]
G11	0.48	47.85[bcd]	1.37	13.48[ghi]	3.20	16.25[def]	0.50	10.28[efgh]	4.49	40.52[efg]	0.01	1.15[hi]	8.77	6.28[bc]	6.57	78.79[abcd]
G12	1.48	45.21[de]	0.89	19.01[bc]	0.84	12.22[ijk]	1.06	9.14[hij]	2.85	51.22[de]	0.34	1.22[def]	11.10	6.48[ab]	6.17	62.81[hi]
G13	1.46	46.73[d]	2.66	19.08[bc]	1.40	11.84[jk]	0.54	10.25[efgh]	6.76	58.41[cd]	0.23	1.04[k]	8.77	4.58[f]	4.83	63.05[hi]
G14	1.32	55.43[a]	2.96	12.48[hij]	1.48	11.59[k]	0.24	8.71[ij]	4.21	30.88[hij]	0.06	0.97[lm]	8.77	4.48[fg]	3.37	73.34[cdef]
G15	1.58	47.84[bcd]	1.20	25.37[a]	1.05	15.70[efg]	0.61	12.32[bcd]	5.51	95.47[a]	0.25	1.15[hi]	11.17	5.55[d]	6.48	63.88[ghi]
G16	3.36	43.37[de]	0.55	14.78[fg]	3.94	13.78[ghijk]	2.65	10.99[defg]	4.89	47.75[efg]	0.16	1.25[cd]	10.71	5.33[de]	2.80	62.56[hi]
G17	1.27	36.27[f]	0.56	17.77[cd]	4.18	17.77[cd]	14.29	18.87[a]	16.21	94.27[a]	0.03	1.15[hi]	6.74	4.53[fg]	5.18	83.96[a]
G18	2.83	45.61[d]	1.07	15.54[ef]	3.17	13.58[ghijk]	0.13	10.29[efgh]	6.39	47.33[efg]	0.05	1.26[c]	9.17	5.93[c]	0.96	82.26[ab]
G19	1.15	44.48[de]	0.68	18.31[cd]	2.16	13.48[ghijk]	2.61	11.61[cde]	3.88	63.32[bc]	0.02	1.26[c]	8.77	4.98[e]	3.31	63.48[hi]
G20	3.31	40.59[ef]	0.60	16.59[cd]	1.38	13.90[ghij]	4.09	10.47[efgh]	3.15	51.31[de]	0.31	1.21[efg]	6.77	5.40[d]	1.65	69.93[efgh]
G21	2.02	44.93[de]	0.81	11.96[ij]	0.22	14.19[fghi]	1.84	8.70[ij]	3.72	28.39[ij]	0.07	1.26[c]	6.74	4.33[fg]	1.48	84.19[a]
G22	2.08	52.73[ab]	1.45	18.11[cd]	0.24	15.63[efg]	1.05	12.12[bcd]	7.44	65.89[bc]	0.05	0.74[n]	10.78	4.55[fg]	2.08	79.95[abc]
G23	2.46	46.19[d]	0.49	10.08[kl]	1.78	14.53[efgh]	5.70	7.79[j]	4.40	22.92[j]	0.08	1.10[j]	11.10	6.48[ab]	4.86	80.64[abc]
G24	2.04	48.04[bcd]	6.04	11.08[jk]	2.77	22.48[b]	0.51	12.44[bcd]	2.13	39.64[fgh]	0.37	1.00[l]	6.77	5.50[d]	2.44	83.18[ab]
G25	1.94	45.80[d]	2.92	8.95[l]	4.91	15.58[efg]	2.68	7.88[j]	9.71	23.56[j]	0.10	1.79[a]	6.77	4.40[fg]	1.29	84.06[a]
G26	2.68	46.86[d]	1.62	15.52[ef]	0.58	16.47[de]	3.96	10.58[efgh]	8.81	47.15[efg]	0.10	1.24[cde]	8.77	4.98[e]	2.08	81.95[ab]
G27	0.85	54.96[a]	1.33	11.18[jk]	3.57	18.68[c]	1.10	12.90[bc]	3.64	41.40[efgh]	0.18	1.13[ij]	11.14	6.43[ab]	1.35	79.18[abcd]
AASV	1.681		1.545		2.117		1.975		5.194		0.231		9.003		2.997	

Genotypes: G1 = IC 632961, **G2** = IIHR-B-PV-26, **G3** = IIHR-B-PV-16, **G4** = IIHR-B-PV-4, **G5** = IIHR-B-PV-5, **G6** = IIHR-B-PV-9, **G7** = IIHR-B-PV-11, **G8** = IIHR-B-PV-12, **G9** = IIHR-B-PV-15, **G10** = Arka Sukomal, **G11** = IIHR-B-PV-17, **G12** = IIHR-B-PV-20, **G13** = IIHR-B-PV-21, **G14** = IIHR-B-PV-22, **G15** = IIHR-B-PV-24, **G16** = IIHR-B-PV-25, **G17** = Arka Arjun, **G18** = IIHR-B-PV-27, **G19** = IIHR-B-PV-29, **G20** = IIHR-B-PV-30, **G21** = Anupam, **G22** = Ranar, **G23** = Phulbani local, **G24** = Ayoka, **G25** = Phalguni, **G26** = Baisnavi, **G27** = Angul local. Traits: **DF**: Days to 50% flowering, **NPP**: Number of pod plant^{-1}, **PL**: Pod length (cm), **APW**: Average pod weight (g), **PY**: Pod yield (qha^{-1}), **PC**: Protein content (g100^{-1} FW), **TSS**: Total soluble solids (%), **TPC**: Total phenol content (mg GAE/g FW).

a. GGE biplot for days to 50% flowering

b. GGE biplot number of pod plant^{-1}

c. GGE biplot for pod length (cm)

d. GGE biplot for average pod weight (g)

e. GGE biplot for pod yield (qha^{-1})

f. GGE biplot for protein content (g100^{-1} FW)

Fig. 3. (a) GGE biplot for days to 50% flowering. **(b)** GGE biplot number of pod plant^{-1}. **(c)** GGE biplot for pod length (cm). **(d)** GGE biplot for average pod weight (g). **(e)** GGE biplot for pod yield (qha^{-1}). **(f)** GGE biplot for protein content (g100^{-1} FW). **(g)** GGE biplot for TSS (%). **(h)** GGE biplot for total phenol content (mg GAE/g FW). **Genotypes: G1** = IC 632961, **G2** = IIHR-B-PV-26, **G3** = IIHR-B-PV-16, **G4** = IIHR-B-PV-4, **G5** = IIHR-B-PV-5, **G6** = IIHR-B-PV-9, **G7** = IIHR-B-PV-11, **G8** = IIHR-B-PV-12, **G9** = IIHR-B-PV-15, **G10** = Arka Sukomal, **G11** = IIHR-B-PV-17, **G12** =

IIHR-B-PV-20, **G13** = IIHR-B-PV-21, **G14** = IIHR-B-PV-22, **G15** = IIHR-B-PV-24, **G16** = IIHR-B-PV-25, **G17** = Arka Arjun, **G18** = IIHR-B-PV-27, **G19** = IIHR-B-PV-29, **G20** = IIHR-B-PV-30, **G21** = Anupam, **G22** = Ranar, **G23** = Phulbani local, **G24** = Ayoka, **G25** = Phalguni, **G26** = Baisnavi, **G27** = Angul local.
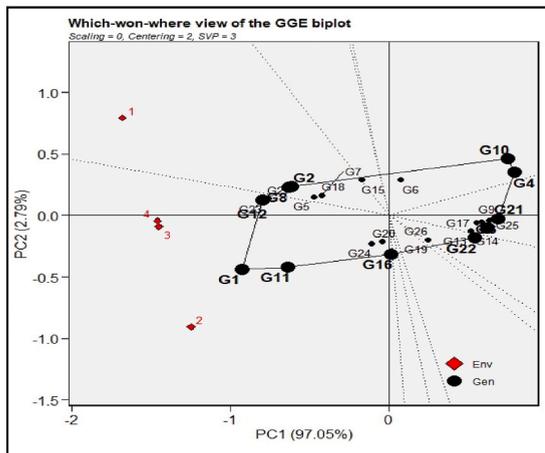
g. GGE biplot for TSS (%)
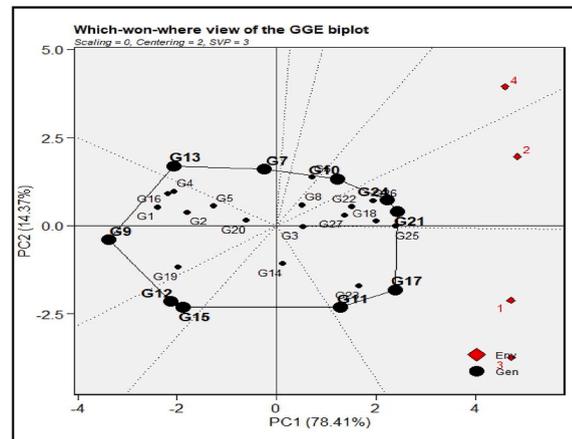
h. GGE biplot for total phenol content (mg GAE/g FW)

Fig. 3. (*continued*).

suitable environment condition and the number of pods may reduce under adverse conditions (temperature above 27 °C). Similarly, the study also identified genotypes suitable for favourable environment with high ASV and mean value of concerned traits i.e., G10, G24 and G27 for pod length (Fig. 2c); G10 for average pod weight (Fig. 2d); G17 for pod yield (Fig. 2e); G2, G3 and G20 for protein content (Fig. 2f); G12, G23, G27, G8, G2, G5, G18, G7 and G15 for TSS (Fig. 2g) and G10, G11 and G14 for total phenol content (Fig. 2h). For days to 50% flowering positive IPCA I value and lower mean trait value is desirable which indicate the early flowering characteristics of the genotype. Genotypes were located 1st quadrant of AMMI biplot above the horizontal interaction line. The data on ASV and mean value for days to 50% flowering revealed G20, G21, G23, G25 and G26 produced early flowering with positive interaction with environment indicated suitability of these genotypes to rich environment conditions (Fig. 2a).

3.5. Genotypes adapted to adverse environments

An adverse or poor environment characterized by unfavorable weather conditions and limited input resources which exert pressure on critical growth phases of plants. The French bean is being a cool seasonal crop prefers optimum temperature of 20–25 °C [56] and extreme temperature affects the growth and development and ultimately the pod yield [57]. The genotypes perform better for quantitative traits with high negative IPCA I score and low ASV indicated negative interaction with environments. In AMMI biplot, the genotypes located 4th quadrant below the horizontal interaction line. Genotypes; G15, G22, G9, G7 and G13 having high mean value for pod yield and negatively interacting with environments demonstrating these performing better under adverse environment condition (Fig. 2e). Though their pod yield was not increasing under suitable environment conditions. Similarly, the experiment screened out genotypes suitable in adverse environments for yield relevant traits i.e., G1 and G15 for NPP; G1, G17 and G25 for PL; G17 for APW; G1 for DF (Fig. 2a–d). Similarly, genotypes suitable for poor environment for qualitative traits also identified which having higher trait value and ASV viz., G1 for PC; G1, G11 for TSS and G6, G23 for TPC (Fig. 2f–h) indicating these genotypes perform better under adverse climatic conditions of high temperature (>27 °C).

3.6. Genotypes observed with low mean trait value

In the present investigation genotypes were screened out for less trait value which may have negative or positive environmental interaction scattered in 1st and 3rd quadrant of AMMI biplot having negative or positive IPCA I score (Fig. 2a–h). Less number of pods per plant obtained in genotypes; G25, G27, G24, G23, G14 had negative environmental interaction and G11, G16 had positive environmental interaction (Fig. 2b). Likewise, Fig. 2c revealed minimum trait value was observed for pod length in genotypes; G14, G13, G8, G6 had negative interaction with environment whereas G19, G4 had positive environmental interaction. Genotypes; G26 and G23, G25, G21 observed with lesser value of average pod weight had negative and positive environmental interaction respectively (Fig. 2d). Minimum pod yield was obtained in G3, G11, G18 and G25, G23, G21, G14 under rich and poor environment respectively indicating their adoption to the particular environment (Fig. 2e). Similarly, the studied genotypes interacted differently with environments for qualitative traits viz., protein content, total soluble solids and total phenol content demonstrated in AMMI biplot (Fig. 2f–h). Lower protein content (G24), TSS (G22, G14, G13), TPC (G4, G1, G16) obtained under adverse weather conditions with

negative IPCA I score and high ASV. Whereas genotypes; G10 and G9, G15 produced less TSS and TPC under favourable climatic conditions indicated their performance may not be better even under favourable conditions.

3.7. Interaction of genotypes and environments for different traits

The AMMI biplot enumerate the differential interaction of late *kharif* and *rabi* season of 2019–2020 and 2020–2021 with genotypes for yield and quality traits in French bean. The interaction between the four environments indicated by angle formed by the vector *i.e.*, if the angle is less than 90° indicating positive interaction and placed near on IPCA I axis. If the angle is obtuse than negative correlation is noticed between the environments placed far on IPCA I axis [39, 48, 51, 58]. The represented length of vector in AMMI biplot indicated the contribution of the environment towards total variation. Environments with long vector indicated high interactive and create discrimination among genotypes whereas, short vector mean less interaction and provide less information on differences in performance of genotypes [59]. The environments: E1 = September 25, 2019, E2 = December 5, 2019 and E3 = September 25, 2020 interacted positively for days to 50% flowering as these formed vectors placed near on the AMMI biplot whereas weather conditions of E4 = December 5, 2020 interacted differently as this scattered to different place (Fig. 2a). The long vector of E4 demonstrated maximum contribution to the variation created for days to 50% flowering among the 27 French bean genotypes. The well adopted genotypes were congregated to respective environments as per their correlation. For number of pods per plant and pod length, E1; E3 and E2; E4 interacted similar way whereas between the late kharif and rabi sowing window there was opposite correlation. E3 and E4 contributed maximum towards total variations for NPP (Fig. 2b) as joined with long vectors from the center whereas for PL (Fig. 2c), E2 had more contribution towards total variations.

Differential interaction was demonstrated among the studied environments for average pod weight and pod yield. The AMMI biplot (Fig. 2d) showed positive correlation between environments; E1, E2 and E4 for average pod weight of 27 genotypes. But E4 exert opposite correlation adjoined with long vector indicated its bigger contribution to total variation exist for the traits. Similarly, for pod yield traits, the weather conditions of environment E2; E4 and E1; E3 interacted positively and negatively within and between the groups. In E3, the genotypes demonstrated much variation in pod yield (Fig. 2f).

The AMMI biplot also revealed the association of environments with genotypes for various quality traits. There was close positive association between environment group; E2 & E4 and E1 & E3 placed same IPCA I axis for protein content of fresh pod of 27 genotypes (Fig. 2f). Between these group opposite correlation was demonstrated as the weather parameters differs and that was reflected in the expression of protein content in pods of genotypes. The weather conditions of the E1 demonstrated much more contribution towards total variation for the trait. For TSS and total phenol content of the genotypes, all studied environments reacted differentially adjoined with different length and direction of vectors from the center. Though the contribution towards total variation was attributed in E1; E2 for TSS (Fig. 2g) and E1; E4 for total phenol content (Fig. 2h). The genotypes were well scattered on AMMI biplot revealed the differential interaction of weather conditions of four environments for the studied traits.

3.8. GGE (Which Won Where) biplot analysis

GGE stands for Genotype Main Effects and Genotype by Environment Interaction Effects [G + (G x E)] explained the phenotypic expression of individual is the combined effect of genotype and how it interacts with the prevailing environmental circumstances. In a multiple environments (locations or seasons) experiment, GGE biplot analysis endorses the selection of genotypes that suitable for different environments by demonstrating mean performance and stability and genotype effect and G × E interaction [[49,52,60,61]]. Hence, the analysis is also termed as "Which Won Where". Souza et al. [62] highlighted greater efficacy of first two main components of GGE biplot in evaluating twenty seven genotypes.

In our experiment, we observed the similar results demonstrated in both AMMI biplot and GGE biplot indicating accuracy of the model. The GGE biplot is constructed with decomposition of a set of linear data into two principal components [49]. The biplot constituted a polygon made up joining the extreme performing genotypes in such way all other genotypes fall inside the polygon area considering each and every genotypes interaction with prevailing weather conditions. Interaction vectors were drawn from center and are perpendicular to the sides of the polygon or its extensions. By this, the polygon area divides into number of sectors (n+1) by the interaction vectors (n) and the sectors contains the genotypes and environments at the vertex and withing the polygon [[49,52]] indicated the adaptability of the genotypes to the environments explains "Which Won Where" (Fig. 3a–h). Environment E1 (September 25, 2019) and E4 (December 5, 2020) fall in same sector for pod yield and the genotypes; G1 and G15 were placed at vertex demonstrated the weather conditions were suitable for G1 and G15 in producing high pod yield. Similarly, E2 (December 5, 2019) favoured genotype G17 in yielding more pod weight. E1; E3 and E2; E4 forming two mega-environments placed at proximity distance indicating positive correlation (Fig. 3e). For average pod weight, the genotype G17 placed at vertex of the sector containing environment E3 and E4 explained these environments had favourable weather conditions influence G17 in gaining maximum pod weight but E3 was the most suitable season for full expression of the traits. Likewise, genotypes G1 and G10 performed superior in term of maximum average pod weight in both E1 and E2 (Fig. 3d).

The GGE biplot for pod length demonstrated all four environments viz., E1, E2, E3 and E4 in same sector containing genotypes; G1, G10, G24 at the vertex and G17, G27, G11 within the sectoral polygon depicted these environments had congenial weather conditions for gaining long pod of these genotypes. More precisely, it is revealed E1 and E3 were most suitable for Genotype G24 and E2 for G1 for pod length (Fig. 3c). Similarly, all environments fall in a sector scattered with genotypes G15, G1 at the vertex and G9, G12, G22, G13, G17, G18, G26, G19, G20 within the sectoral polygon indicated these genotypes yielded maximum number of pods per plant under prevailed weather conditions. December 5, 2020 sowing was most appropriate for G15 in producing maximum number of pods per

plant (Fig. 3b). The data on days to 50% flowering (Fig. 3a) revealed environments E1 and E2 fall in the sector where genotype G22 observed at the vertex explained G22 took less days to 50% flowering. Genotypes; G27 and G5 received congenial weather conditions in environment E3 for attaining minimum days to 50% flowering.

The GGE biplot also revealed genotypes G15, G1, G3 fall on the vertex of polygon in the sector consist of all four environments depicted genotypes won in these environments in gaining more protein content in pod (Fig. 3f). Likewise, for TSS, the environments E2, E3, E4 fall on same sector where G11, G1, G12, G8, G16 placed at vertex and G24, G20, G23 fall within sectoral polygon performed well for gaining high TSS. Whereas environment E1 observed in different sector suitable for higher TSS of genotypes G2 pointed at the vertex and G18, G15, G7, G23, G5 scattered within the sectorial polygon (Fig. 3g). Regarding, total phenol content of the genotypes, the environments E4; E2 and E1, E3 interacted differently formed three groups which included best performing genotypes *viz*; G10, G8, G6 in E4; G24, G21 (at vertex), G22, G18, G26, G27 (within sector) in E2; G11, G17 (at vertex), G3, G25 (within sector) in E1 and E3 environments (Fig. 3h). Asfaw et al. [63] and Correa et al. [64] used the GGE biplot in evaluating common bean genotypes having high grain yield and stability across diverse environments. Zeleke and Berhanu [17], identified broadly adopted lines in small red common bean by employing GGE biplots. Gelete et al. [38] emphasized significance of GGE biplots in estimating the GEI variation for canning and cooking quality in common bean genotypes.

3.9. Multivariate analysis and clustering of traits and genotypes

Multivariate analysis, a statistical technique, is used to determine and separate complex and substantial datasets. The Fisher's least significant difference (LSD) analysis was employed to estimate the relationship between five quantitative traits and three qualitative traits in the 27 genotypes of French bean under study. To determine a specific number of linear combinations for variable traits, the PCA analysis was employed. There was a total of 8 principal components (PCs) found, although only three of them were deemed significant (P value is ≤ 0.05) because of eigenvalues greater than 1 and remaining were nonsignificant (Table 4). Based on Eigenvalue (≥ 1) first two components were demonstrated 56.7% of the total variation (Table 4). The PCA biplot (Fig. 4a) depicted the Component 1 (PC1) explained 33.4% and Component 2 (PC2), 23.3% of the total variance. Depending on correlation, the traits were dispersed in various ordinates in biplot with different vector length and colour indicted how well the qualities are represented and how much they contribute to the principal components and ultimately formed groups (Fig. 4a).

Trait groups I (average pod weight and pod yield) and V (number of pods per plant) appear to be contributed maximum to PC1 (Fig. 4a and b). Trait group II (pod length), III (protein content and total phenol content) and IV (days to 50% flowering and TSS) contributed more towards PC2 and subsequent principal components. Correlation studies demonstrated positive correlation between pod lengths, number of pods and average pod weight with pod yield. Whereas, days to 50% flowering had negative correlation with all traits under consideration except TSS. The protein content and total phenol content of pods witnessed only positive correlation with pod length (Fig. 4c).

The 27 genotypes were congregated on axis as per mean value for the traits subjected to clustering based on their response and performance in the four seasons/environments *viz*., E1, E2, E3, and E4 presented into five cluster (Table 5; Fig. 5). The Cluster C2 included the most genotypes (21) while Clusters C1, C3, C4 and C5 contained genotypes i.e., 2, 1, 1, and 1, respectively (Fig. 5). When compared to the other genotypes, the presence of one or two genotypes in a cluster suggested their heterogeneous nature in response to seasonal fluctuations. Genotypes were categorized in a single cluster revealed their similar response to changing environment conditions. Genotype G1 (IC 632961), G15 (IIHR-B-PV-24), G17 (Arka Arjun) and G10 (Arka Sukomal) were found most diverse with high pod yield and relevant yield traits. The clustering is utmost important to select best performing varieties or genotypes for general cultivation as well as utilization in future breeding programme.

4. Conclusion and recommendation

Understanding the genotype by environment interaction is crucial in plant breeding and agricultural practices. It allows researchers

Table 4
Extracted Eigenvalues and correlation values for yield and associated traits with the first three principal components.

Variables	Principles components		
	PC1	PC2	PC3
Extracted Eigenvalues	2.671	1.864	1.305
Explained variance (%)	33.393	23.302	16.309
Cumulative variance (%)	33.393	56.695	73.004
Yield traits			
Days to 50% flowering	−0.091	−0.427	0.728
Pod length (cm)	0.831	−0.341	−0.249
Number of pods plant^{-1}	0.273	0.789	0.416
Average Pod weight (g)	0.792	0.458	0.201
Pod yield (qha-1)	0.977	0.131	−0.033
Protein content (g100^{-1} FW)	−0.28	0.507	−0.37
TSS (%)	0.018	−0.194	0.576
Total phenol content (mg GAE/g FW)	−0.486	0.649	0.169
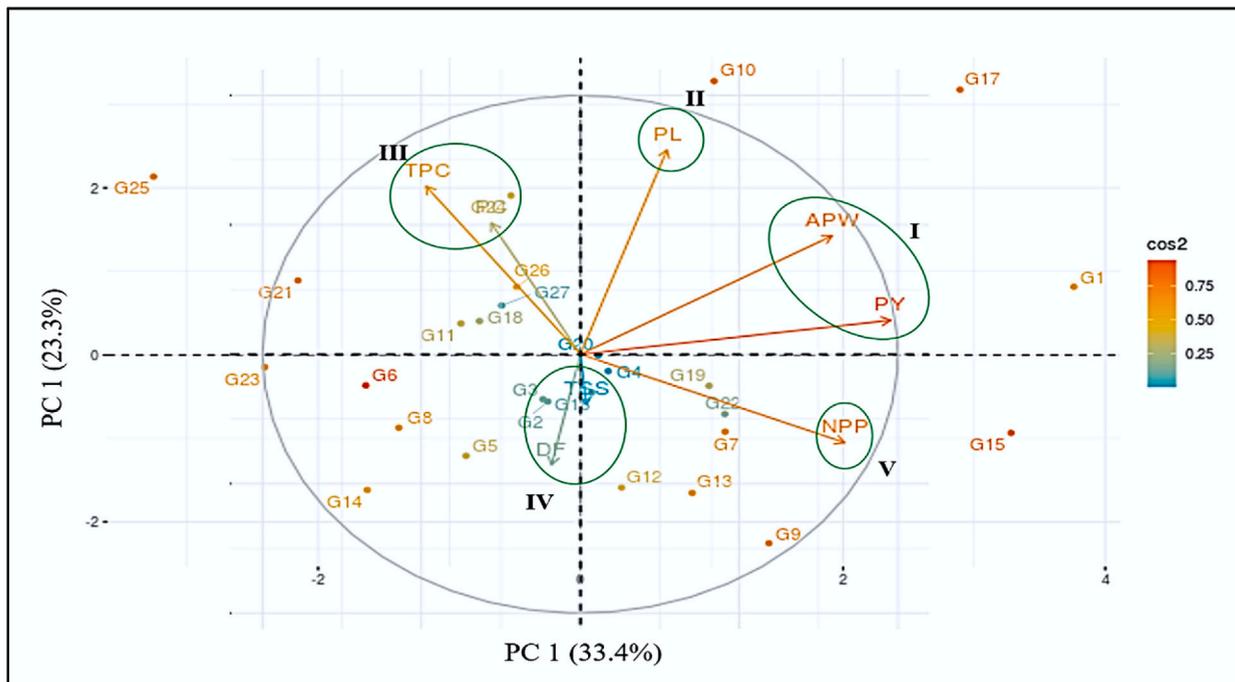
(a)
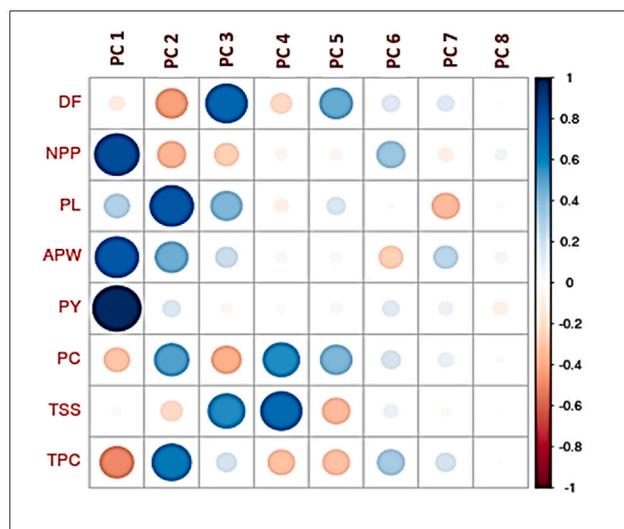
(b)
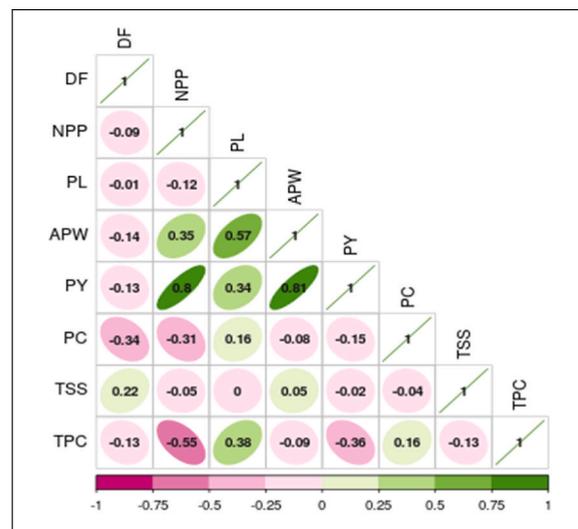
(c)

Fig. 4. a PCA biplot for showing interaction and grouping of seven French bean traits, Fig. 4b: Correlation between traits and PCs, Fig. 4c: Pearson's correlation analysis for yield associated and qualitative traits

DF: Days to 50% flowering, **NPP:** Number of pod plant^{-1}, **PL:** Pod length (cm), **APW:** Average pod weight (g), **PY:** Pod yield (qha^{-1}), **PC:** Protein content (g100^{-1} FW), **TSS**: Total soluble solids (%), **TPC**: Total phenol content (mg GAE/g FW). **Genotypes: G1** = IC 632961, **G2** = IIHR-B-PV-26, **G3** = IIHR-B-PV-16, **G4** = IIHR-B-PV-4, **G5** = IIHR-B-PV-5, **G6** = IIHR-B-PV-9, **G7** = IIHR-B-PV-11, **G8** = IIHR-B-PV-12, **G9** = IIHR-B-PV-15, **G10** = Arka Sukomal, **G11** = IIHR-B-PV-17, **G12** = IIHR-B-PV-20, **G13** = IIHR-B-PV-21, **G14** = IIHR-B-PV-22, **G15** = IIHR-B-PV-24, **G16** = IIHR-B-PV-25, **G17** = Arka Arjun, **G18** = IIHR-B-PV-27, **G19** = IIHR-B-PV-29, **G20** = IIHR-B-PV-30, **G21** = Anupam, **G22** = Ranar, **G23** = Phulbani local, **G24** = Ayoka, **G25** = Phalguni, **G26** = Baisnavi, **G27** = Angul local.

and farmers to select or develop varieties of crops that are better suited to the local environment, ultimately improving overall productivity and quality. The present study revealed the existence of significant genotype by environment interaction due to seasonal changes influenced the yield and quality in French bean. Higher contribution of genotype by environment interaction witnessed in days to 50 percent flowering and total phenol content respectively, indicated the traits were significantly influenced by environment

Table 5
Euclidian distance between 27 French bean genotypes for four quantitative yield traits and three qualitative traits.

Genotypes	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27
G1	1																										
G2	0.84	1																									
G3	0.83	1	1																								
G4	0.87	1	0.99	1																							
G5	0.75	0.98	0.98	0.97	1																						
G6	0.68	0.97	0.97	0.95	0.98	1																					
G7	0.92	0.98	0.98	0.99	0.93	0.9	1																				
G8	0.7	0.97	0.98	0.96	0.98	1	0.92	1																			
G9	0.95	0.96	0.94	0.96	0.91	0.85	0.98	0.87	1																		
G10	0.92	0.97	0.96	0.98	0.91	0.89	0.99	0.9	0.95	1																	
G11	0.74	0.98	0.99	0.97	0.98	0.99	0.94	1	0.89	0.93	1																
G12	0.88	0.99	0.99	0.99	0.96	0.94	0.99	0.95	0.98	0.97	0.96	1															
G13	0.92	0.98	0.98	0.99	0.94	0.91	1	0.92	0.99	0.98	0.94	1	1														
G14	0.67	0.96	0.96	0.94	0.99	0.99	0.89	0.99	0.86	0.87	0.98	0.93	0.9	1													
G15	0.99	0.87	0.86	0.89	0.78	0.72	0.95	0.74	0.96	0.93	0.78	0.91	0.94	0.7	1												
G16	0.87	1	1	1	0.97	0.95	0.99	0.96	0.96	0.98	0.97	1	0.99	0.94	0.89	1											
G17	0.95	0.9	0.9	0.92	0.8	0.78	0.96	0.8	0.92	0.97	0.84	0.92	0.94	0.75	0.96	0.92	1										
G18	0.78	0.99	0.99	0.98	0.97	0.98	0.96	0.99	0.91	0.95	0.99	0.97	0.95	0.95	0.82	0.96	0.88	1									
G19	0.94	0.97	0.97	0.98	0.92	0.88	1	0.89	0.99	0.98	0.92	0.99	1	0.87	0.96	0.98	0.96	0.94	1								
G20	0.86	0.99	1	0.99	0.95	0.95	0.99	0.96	0.95	0.98	0.97	0.99	0.98	0.93	0.89	0.99	0.93	0.99	0.98	1							
G21	0.62	0.94	0.95	0.92	0.95	0.99	0.87	0.99	0.8	0.86	0.99	0.9	0.87	0.98	0.66	0.92	0.75	0.97	0.84	0.93	1						
G22	0.9	0.99	0.99	1	0.95	0.93	1	0.94	0.97	0.99	0.96	1	0.99	0.92	0.92	1	0.94	0.98	0.99	1	0.9	1					
G23	0.57	0.92	0.93	0.9	0.95	0.99	0.84	0.98	0.77	0.83	0.97	0.88	0.84	0.98	0.61	0.9	0.7	0.95	0.81	0.9	0.87	1	1				
G24	0.71	0.97	0.97	0.96	0.97	0.99	0.91	0.99	0.85	0.92	0.99	0.94	0.91	0.97	0.74	0.96	0.82	0.98	0.89	0.96	0.99	0.94	0.98	1			
G25	0.57	0.92	0.93	0.9	0.94	0.99	0.84	0.98	0.76	0.83	0.97	0.87	0.83	0.97	0.62	0.9	0.71	0.95	0.81	0.9	1	0.87	1	0.98	1		
G26	0.78	0.99	0.99	0.98	0.97	0.98	0.96	0.99	0.91	0.95	1	0.97	0.95	0.97	0.82	0.99	0.88	1	0.94	0.99	0.97	0.98	0.95	0.99	0.96	1	
G27	0.74	0.98	0.98	0.97	0.99	0.99	0.93	0.99	0.89	0.92	1	0.95	0.93	0.99	0.76	0.97	0.82	0.98	0.91	0.96	0.98	0.95	0.97	0.99	0.97	0.99	1

DF: Days to 50% flowering, **NPP**: Number of pod plant^{-1}, **PL**: Pod length (cm), **APW**: Average pod weight (g), **PY**: Pod yield (qha^{-1}), **PC**: Protein content (g100^{-1} FW), **TSS**: Total soluble solids (%), **TPC**: Total phenol content (mg GAE/g FW). **Genotypes: G1** = IC 632961, **G2** = IIHR-B-PV-26, **G3** = IIHR-B-PV-16, **G4** = IIHR-B-PV-4, **G5** = IIHR-B-PV-5, **G6** = IIHR-B-PV-9, **G7** = IIHR-B-PV-11, **G8** = IIHR-B-PV-12, **G9** = IIHR-B-PV-15, **G10** = Arka Sukomal, **G11** = IIHR-B-PV-17, **G12** = IIHR-B-PV-20, **G13** = IIHR-B-PV-21, **G14** = IIHR-B-PV-22, **G15** = IIHR-B-PV-24, **G16** = IIHR-B-PV-25, **G17** = Arka Arjun, **G18** = IIHR-B-PV-27, **G19** = IIHR-B-PV-29, **G20** = IIHR-B-PV-30, **G21** = Anupam, **G22** = Ranar, **G23** = Phulbani local, **G24** = Ayoka, **G25** = Phalguni, **G26** = Baisnavi, **G27** = Angul local.

Fig. 5. Clustering of 27 French bean genotypes as pereucldian distance.

over season. Whereas maximum genotypic contribution was noticed in protein content and total soluble sugar hinted environment has less impact on these traits. G1(IC 632961), G10 (Arka Sukomal), G19 (IIHR-B-PV-29), G20 (IIHR-B-PV-30) and G12 (IIHR-B-PV-20) were found most stable and suitable for economic cultivation and included in future crop breeding programme. September–December sowing window showed negative interaction for pod yield and relevant traits forming two mega-environment explaining major influence on phenotypes of French bean. Genotype G1 (IC 632961), G15 (IIHR-B-PV-24), G17 (Arka Arjun) and G10 (Arka Sukomal) were found most diverse with high pod yield and relevant yield traits as compared to other genotypes. So, it is noted, the AMMI model and GGE biplot are useful statistical tool for the purpose of the study as per its accuracy and we suggest the pole type French bean genotypes *viz.*, IC 632961, Arka Sukomal and bush type French bean genotypes *viz.*, IIHR-B-PV-29, IIHR-B-PV-30 could be promising for utilization in future breeding programmes for the concerned traits.

Funding

Research content

The search content of manuscript is original and has not been published elsewhere.

Ethical approval

The research design, data collection, and analysis procedures were guided by established ethical principles. No ethical concerns arose during the course of this study.

Data availability

The data used to support the findings of the study are included within the article.

Consent to publish

All authors agree to publish the paper in Heliyon.

CRediT authorship contribution statement

Kartik Pramanik: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Resources, Methodology, Investigation, Data curation, Conceptualization. **Gouri Shankar Sahu:** Supervision. **Gobinda Chandra Acharya:** Supervision, Resources, Project administration, Methodology. **Pradyumna Tripathy:** Validation, Supervision, Conceptualization. **Manasi Dash:** Writing – review & editing, Validation, Supervision, Methodology, Conceptualization. **A.V.V. Koundinya:** Writing – review & editing, Validation, Software, Methodology, Formal analysis, Data curation, Conceptualization. **Chinmaya Jena:** Writing – review & editing,

Validation, Data curation. **Duvvada Sarath Kumar:** Software, Formal analysis, Data curation. **Priyadarshani P. Mohapatra:** Writing – review & editing. **Jyostnarani Pradhan:** Writing – review & editing. **S. Karubakee:** Writing – review & editing, Methodology. **Durga Prasad Moharana:** Data curation, Software.

Declaration of competing interest

The authors declare that there is no conflict of interest.

Acknowledgment

References

[1] N. Petry, E. Boy, J.P. Wirth, R.F. Hurrell, Review: the potential of the common bean (*Phaseolus vulgaris*) as a vehicle for iron biofortification, Nutrients 7 (2015) 1144–1173.
[2] W.J. Broughton, G. Hernández, M. Blair, S. Beebe, P. Gepts, J. Vanderleyden, Beans (*Phaseolus* spp.)–model food legumes, Plant Soil 252 (2003) 55–128.
[3] A. Mora-Avilés, B. Lemus-Flores, R. Miranda-López, D. Hernández-López, J.L. Pons-Hernández, J.A. Acosta-Gallegos, S.H. Guzmán-Maldonado, Effects of common bean enrichment on nutritional quality of tortillas produced from nixtamalized regular and quality protein maize flours, J. Sci. Food Agric. 87 (5) (2007) 880–886.
[4] Z. Wondatir, Y. Mekasha, Feed resources availability and livestock production in the central rift valley of Ethiopia, Int. J. Livest. Prod. 5 (2014) 30–35.
[5] Faostat, Food and agriculture organisation of the united nations. FAOSTAT database, Available online: http://www.fao.org/faostat/en/#data/QC, 2019.
[6] A. Asfaw, F. Alemayehu, F. Grum, M. Atnaf, AMMI and SREG GGE biplot analysis for matching varieties in to soybean production environments in Ethiopia, Sci. Res. and Essay 4 (11) (2009) 1322–1330.
[7] J.L. Araus, G. Slafer, C. Royo, M.D. Serret, Breeding for yield potential and stress adaptation in cereals, Crit. Rev. Plant Sci. 27 (2008) 377–412.
[8] W. Asnake, H. Mwambi, Z. Temesgen, T. Girma, Additive main effects and multiplicative interaction model (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot analysis of multi-environmental wheat variety trials, Afr. J. Agric. Res. 8 (2013) 1033–1040.
[9] M.W. Akash, S.M. Kang, G.O. Myers, GGE biplot analysis of wheat cultivars evaluated in a Multi-Environment trial, J. N. Seeds 10 (2009) 88–97.
[10] B.S. Blanche, G.O. Myers, M.S. Kang, GGE Biplot and traditional stability measures for interpreting genotype by environment interactions, J. Crop Improv. 20 (2007) 123–135.
[11] L.D. Barili, N.M. Vale, L.M. Moura, R.G. Paula, F.F. Silva, J.E.S. Carneiro, Genetic progress resulting from forty three years of breeding of the carioca common bean in Brazil, Genet. Mol. Res. 15 (3) (2016) 1–8.
[12] S.A. Raffis, M.A. Newaz, N. Khan, Stability analysis for pod and seed production in dry bean (*Phaseolus vulgaris* L.), Asian J. Plant Sci. 3 (2) (2004) 239–242.
[13] S.A. Dar, F.A. Pir, A. Manzar, A.A. Lone, Studies on genotype x environment interaction and stability for seed yield in common bean (*Phaseolus vulgaris* L.), Trends Biosci 2 (2) (2009) 21–22.
[14] R.W. Allard, A.D. Bradshaw, Implication of genotype environmental interactions in applied plant breeding, Crop Sci. 4 (1964) 503–598.
[15] R. Rodríguez-González, J. Ponce-Medina, E. Rueda-Puente, L. Avendaño-Reyes, P. Hernández, J. Santillano-Cazares, M. Cruz-Villegas, Interacción genotipo-ambiente para la estabilidad de rendimiento en trigo en la regiónd Mexicali, B.C., México, Tropical and Subtropical Agroecosytems 14 (2) (2011) 543–558.
[16] M.S. Kang, Genotype-by-environment Interaction and Plant Breeding, Louisana State University Agricultural Center, Baton Rouge, LA, USA, 1990, p. 392.
[17] A.A. Zeleke, F.A. Berhanu, AMMI and GGE models analysis of stability and GEI of common bean (*Phaseolus vulgaris* L.) lines in Ethiopia, Journal of Biology, Agriculture and Healthcare 6 (9) (2016) 127–135.
[18] A.V.V. Koundinya, A. Das, P. Pradeep Kumar, M.K. Pandit, Profiling of growth and yield parameters of eggplant as influenced by the cropping season, Int. J. Curr. Microbiol. Appl. Sci. 6 (5) (2017) 440–448.
[19] A.A. Elias, K.R. Robbins, R.W. Doerge, M.R. Tuinstra, Half a century of studying genotype x environment interactions in plant breeding experiments, Crop Sci. 56 (5) (2016) 2090–2105.
[20] T. Tadesse, G. Sefera, B. Asmare, A. Teklaign, Agronomic performance and yield stability of large red bean genotypes using AMMI model in midlands of bale zone, South-Eastern Ethiopia, Chemical and Biomolecular Engineering 3 (3) (2018), 35-35.
[21] S.P. Singh, H. Terán, M. Lema, D.M. Webster, Seventy-five years of breeding dry bean of the western USA, Crop Sci. 47 (2007) 981–989.
[22] G. Keneni, E. Bekele, M. Imtiaz, E. Getu, K. Dagne, F. Assefa, Breeding chickpea (*Cicer arietnum* [Fabaceae]) for better seed quality inadvertently increased susceptibility to adzuki bean beetle (*Callosobruchus chinensis* [Coleoptera: Bruchidae]), Int. J. Trop. Insect Sci. 31 (4) (2011) 249–261.
[23] L.D. Barili, N.M. Vale, L.M. Moura, R.G. Paula, F.F. Silva, J.E.S. Carneiro, Genetic progress resulting from fortythree years of breeding of the carioca common bean in Brazil, Genet. Mol. Res. 15 (3) (2016) 1–8.
[24] A. Gerrano, W. van Rensburg, I. Mathew, A. Shayanowako, M. Bairu, S. Venter, W. Swart, A. Mofokeng, J. Mellem, M. Labuschagne, Genotype and genotype environment interaction effects on the grain yield performance of cowpea genotypes in dryland farming system in South Africa, Euphytica (2020) 216–280.
[25] H. Mushoriwa, I. Mathew, E.T. Gwata, P. Tongoona, J. Derera, Grain yield potential and stability of soybean genotypes of different ages across diverse environments in Southern Africa, Agronomy 12 (2022) 1147.
[26] A.I. Adjei, S.O. Dapaah, I.K. Dontwi, Predicting the best genotype from analysis of genotype by environment interaction, European J. Sci. Res. 45 (1) (2010) 128–135.
[27] S. Aarthi, J. Suresh, N.K. Leela, D.D. Prasath, Multi environment testing reveals genotype-environment interaction for curcuminoids in turmeric (*Curcuma longa* L.), Ind. Crop. Prod. (2020) 145.
[28] D.F. Ferreira, C.G.B. Demetrio, B.F.J. Manly, A.A. Machado, R. Vencovsky, Statistical model in agriculture: biometrical methods for evaluating phenotypic stability in plant breeding, Cerne Lavras 12 (4) (2006) 373–388.
[29] I. Romagosa, P.N. Fox, Genotype-environment interaction and adaptation, in: M.D. Hayward, N.O. Bosemark, I. Romagosa (Eds.), Plant Breeding: Principles and Prospects, Chapman and Hall, Cambridge, UK, 1993, pp. 373–390.
[30] G.K. Ejigu, H. Mohammed, B.A. Fenta, Yield stability analysis of large-seeded common bean varieties in major bean growing areas of Ethiopia, Ethiop. J. Crop Sci. 9 (2) (2022) 75–94.
[31] H.G. Hagos, F. Abay, AMMI and GGE biplot analysis of bread wheat genotypes in the northern part of Ethiopia, J. Plant Breed. Genet. 1 (2013) 12–18.
[32] J.L. Purchase, H. Hatting, C.S. van Deventer, Genotype x environment interaction of wheat in South Africa: stability analysis of yield performance, S. Afr. J. Plant Soil 17 (3) (2000) 101–107.
[33] V.L. Singleton, R. Orthofer, R.M. Lamuela-Raventós, Analysis of total phenols and other oxidation substrates and antioxidants by means of folin-ciocalteu reagent, Methods Enzymol. 299 (1999) 152–178.

[34] P.P. Gopinath, R. Parsad, B. Joseph, V.S. Adarsh, GRAPES: General Rshiny Based Analysis Platform Empowered by Statistics, 2020, https://doi.org/10.5281/zenodo.4923220.

[35] M.S. Bartlett, Properties of sufficiency and statistical tests, Proc. R. Soc. Lond. 160 (1937) 268–282.

[36] R.W. Zobel, M.S. Wright, H.G. Gauch, Statistical analysis of a yield trial, Agron. J. 80 (1988) 388–393.

[37] H.G. Gauch, Statistical analysis of yield trials by AMMI and GGE, Crop Sci. 46 (2006) 1488–1500.

[38] S.H. Gelete, F. Mekbib, B.A. Fenta, M. Teamir, Genotype-by-environment interaction on canning and cooking quality of advanced large-seeded common bean genotypes, Heliyon 7 (2021) e06936.

[39] P. Thangavel, A. Anandan, R. Eswaran, AMMI analysis to comprehend genotype-by-environment (G× E) interactions in rainfed grown mungbean ('*Vigna radiata*'*L.*), Aust. J. Crop. Sci. 5 (13) (2011) 1767–1775.

[40] Zeleke Ashango, Berhanu Amsalu, Kidane Tumisa, Kassaye Negash, Asnake Fikre, Seed yield stability and genotype x environment interaction of common bean (*Phaseolus vulgaris* L.) lines in Ethiopia, International Journal of Plant Breeding and Crop Science 3 (2) (2016) 135–144.

[41] H.S. Pereira, L.C. Melo, L.C. de Faria, J.L. Cabrera Díaz, M.J. Del Peloso, C.G. da Costa, A. Wendland, Stability and adaptability of carioca common bean genotypes in stated of the central South Region of Brazil, Crop Breeding and Applied Biotechnology 9 (2009), 181-18.

[42] J. Crossa, H.G. Gauch, R.W. Zobel, Additive main effects and multiplicative interaction analysis of two international maize cultivar trials, Crop Sci. 30 (1990) 493–500.

[43] M.V. Kvitschal, P.S. Vidigal Filho, C.A. Scapim, M.C. Gonçalves-Vidigal, M.G. Pequeno, E. Sagrilo, F. Rimoldi, Evaluation of phenotypic stability of cassava clones by AMMI analysis in northwestern Paraná state, Crop Breeding and Applied Biotechnology 6 (3) (2006).

[44] R.C. Misra, S. Das, M.C. Patnaik, AMMI model analysis of stability and adaptability of late duration finger millet (*Eleusine coracana*) genotypes, World Applied Sci. J. 6 (12) (2009) 1650–1654.

[45] A.A. Khan, M.A. Alam, M.R. Kabir, AMMI analysis for stability and environmental effects on grain yield of eight spring wheat varieties (*Triticum aestivum L.*) in Bangladesh, Bull. Inst. Trop. Agr., Kyushu Univ. 37 (2014) 93–103.

[46] H. Tadesse, F. Abay, Additive main effects and multiplicative interactions analysis of yield performance of sesame genotypes across environments in northern Ethiopia, Journal of the Drylands 4 (1) (2011) 259–266.

[47] O.O. Molosiwa, J. Pharudi, S. Seketeme, P. Mashiqa, R. Chirwa, Assessing yield stability and adaptability of Andean common bean genotypes in the semi-arid environment of Botswana, Afr. J. Agric. Res. 14 (32) (2019) 1593–1600.

[48] A. Anandan, R. Eswaran, T. Sabesan, M. Prakash, Additive main effects and multiplicative interactions analysis of yield performances in rice genotypes under coastal saline environments, Adv. Biol. Res. 3 (1–2) (2009) 43–47.

[49] Shadi Heidari, Reza Azizinezhad, Reza Haghparast, Yield stability analysis in advanced durum wheat genotypes by using AMMI and GGE biplot models under diverse environment, Indian J. Genet. Plant Breed. 76 (2016) 274–283.

[50] K. Nowosad, A. Liersch, W. Popławska, J. Bocianowski, Genotype by environment interaction for seed yield in rapeseed (*Brassica napus L.*) using additive main effects and multiplicative interaction model, Euphytica 208 (2016) 187–194.

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

[52] M.N. Rad, M.A. Kadir, M.Y. Rafii, H.Z. Jaafar, M.R. Naghavi, F. Ahmadi, Genotype environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions, Aust. J. Crop. Sci. 7 (7) (2013) 956.

[53] E. Farshadfar, Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat, Pak. J. biol. Sci. 11 (14) (2008) 1791–1796.

[54] S.A. Eberhart, W.A. Russel, Stability parameters for comparing varieties, Crop Sci. 6 (1966) 36–40.

[55] Buno Haleke Besaye, Gebre Garmame Galgaye, Impact of common bean (*Phaseolus vulgaris L.*) genotypes on seed yield, and seed quality at different locations of Eastern Ethiopia, Cogent Food Agric. 8 (1) (2022) 2115674.

[56] S.S. Singh, Crop Management, Kalyani Publishers, New Delhi, India, 2005, p. 538.

[57] T.Y. Reddy, G.H. Reddi, Principles of Agronomy, second ed., Kalayani Publisher, New Delhi, India, 2005, p. 552.

[58] M. Kandus, M.D. Almorza, R. Ronceros, J.C. Salerno, Statistical methods for evaluating the genotype by environment interaction in Maize (*Zea mays L.*), FYTON 79 (2010) 39–46.

[59] W. Yan, Singular-value partitioning in biplot analysis of multi-environment trial data, Agron. J. 94 (2002) 990–996.

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

[61] W. Yan, L.A. Hunt, Q. Sheng, Z. Sclavnica, Cultivar Evaluation and Mega environmental investigation based on GGE biplot, Crop Sci. 40 (2000) 597–605.

[62] M.A. Souza, O.P. Morais, R.E.C. Herán, A. Cargnin, A.J.B. Pimentel, Progresso genético do melhoramento de arroz de terras altas no período de 1950 a 2001, Pesqui. Agropecuária Bras. 42 (2007) 371–376.

[63] A. Asfaw, T. Assefa, B. Amsalu, K. Negash, F. Alemayehu, F. Grum, Y. Rezene, C. Finensa, M. Atnaf, C. Daba, Adaptation and yield stability of small red bean elite lines in Ethiopia, Int. J. Plant Breed. Genet. 2 (2) (2008) 51–63.

[64] A.M. Correa, P.E. Teodoro, M.C. Gonçalves, L.M.A. Barroso, Selection of common bean (*Phaseolus vulgaris L.*) genotypes using a genotype plus genotype x environment interaction biplot, Genet. Mol. Res. 15 (2016) 15038427.