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Principal Component Analysis and Stability of Genotypes in French Bean (*Phaseolus vulgaris* L.)

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ABSTRACT

Background: Principal component analysis and Finlay-Wilkinson stability analysis were carried out at research farm of ICAR-Indian Institute of Vegetable Research, Varanasi to identify diverse french bean genotypes for green pod yield and suitable genotypes for stable yield and yield related parameters.

Methods: All the 24 genotypes were laid out in randomized block design with two replications during winter, 2017 and 2018. Principal component analysis and stability analysis was done to identify the diverse and stable genotypes.

Result: Eight principal components were observed and the maximum variability was concentrated in the first three principal components PC1, PC2 and PC3 which contributed to 68.61% variance. Cluster analysis from principal component scores formed three clusters with a maximum of seventeen genotypes in cluster I followed by six genotypes in cluster II and one genotype in cluster III. High heritability was observed for 10 pod weight, number of pods per cluster and number of seeds per pod and moderate heritability was observed for yield per plant. Finlay-Wilkinson stability analysis identified the stable genotypes *viz*., FMGCV 1378, FMGCV 0958, Arka Suvidha, Valentino, Banoa and VRFBB-14-2 for green pod yield per plant, Cartagenta for pod length (cm) and Paulista, Slender Pack, Arka Suvidha, Valentino, FMGCV 0958, Banoa, FORC 6V 1136, VRFBB-14-1, VRFBB-14-2 for number of pods per plant.

Key words: French bean, Heritability, Principal component analysis, Stability analysis.

INTRODUCTION

French bean (*Phaseolus vulgaris* L.) is an important legume vegetable crop grown for its nutrient and protein rich pods (Carvalho *et al*., 2012). French beans used for their tender pods and green beans as vegetable are known as snap beans whereas, those used for shelled dry beans are called as “Rajmash”. Common bean or french bean originated in Central and South America (Kaplan, 1981). French bean is a highly self-pollinated diploid legume with chromosome number of 2n=2x=22. It is the legume which is devoid of root nodules and cannot fix nitrogen. The tender pods of french beans have great demand in urban areas of India. They are grown commercially as well as in kitchen gardens. Worldwide green beans are cultivated in 1.5 million hectares with a production of 24 million tonnes, out of which India contributes 0.67 million tonnes of production (FAOSTAT, 2017). The major bean producing states in India were Gujarat, Karnataka, Jharkhand, Andhra Pradesh, Uttar Pradesh, Tamil Nadu, West Bengal, Bihar and Telangana. The states with highest bean productivity were Tamil Nadu, Jammu and Kashmir, Uttar Pradesh and Jharkhand (Saxena *et al*., 2017).

About 150 species of *Phaseolus* spp. are present worldwide (Arenas *et al*., 2013) and among them four important species *viz*., *Phaseolus vulgaris* L. (common bean), *Phaseolus coccineus* L. (runner bean), *Phaseolus acutifolius* Gray (tepary bean) and *Phaseolus lunatus* L. (camber bean) were domesticated by man. The closest wild relative of the domesticated *Phaseolus vulgaris* L. is *Phaseolus aborigineus* Burk. (Berglund-Briicher and Briicher, 1976). Genetic diversity is one of the prerequisites in crop improvement. Selection of improved genotypes depends on the amount of genetic variability available within the existing genotypes. Regional diversity is one of the characteristics of the common bean. Once the diversity is established in french bean, its strong tendency to self-pollination in a cleistogamous way preserves this diversity (Kaplan, 1981).

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Genetic diversity is the total variability among different genotypes with respect to genetic makeup of the genotypes related to single species or between species. Principal component analysis (PCA) is a multivariate statistical technique that converts a lot of correlated factors to few components (Ziegel, 2002). Hanci and Cebeci (2018) evaluated the morphological variability of six pea genotypes through PCA and found that 11 of the 15 principal components had eigen value >1. Finlay-Wilkinson stability analysis, GGE biplot analysis, AMMI etc., helps to identify the stable genotypes for various characters. In common bean, yield and stability had been studied in seven genotypes by GGE biplot analysis that identified Lida and Mirsini genotypes as most desirable for yield and stability (Kargiotidou *et al*., 2019). Basavaraja *et al*. (2019) studied the diversity of 63 common bean through cluster analysis which are confined to two clusters and found significant positive correlation of seed yield with number of branches per plant, number of pods per plant, number of seeds per pod and hundred seed weight (g).

MATERIALS AND METHODS

The experimental material consists of 24 bush type french bean genotypes (Table 1) that include cultivars developed both at National and International level. All the genotypes were laid out in a randomized block design with two replications during winter, 2017 and 2018. The study was conducted at the research farm of ICAR-Indian Institute of Vegetable Research, Varanasi which is located at 25° 10' N latitude and 82° 52' E longitude and 128.93 m of mean sea level. Each genotype was grown in a plot size of 4m × 3m. The seeds were sown at a spacing of 60 cm between the rows and 20 cm within the row in the mechanically prepared layout. All the standard package of practices was done agronomically in raising the crop.

Table 1: List of french bean genotypes used for present study.

S.No	Genotype	S.No	Genotype
1.	Kashi Rajhans	13.	FORC6V 1137
2.	FMGCV 1378	14.	VRFBB-6
3.	Paulista	15.	VRFBB-7
4.	Contender	16.	Ribera
5.	FMGCV 0958	17.	Cartagenta
6.	FMGCV 1187	18.	Rivergaro
7.	FMGCV 1006	19.	VRFBB-14-1
8.	Arka Suvidha	20.	Valentino
9.	Giolli	21.	FMGC6V 1379
10.	FORC 6V 1136	22.	Banoa
11.	Swarn Priya	23.	Slender Pack
12.	FMGCV1007	24.	VRFBB-14-2

The data on eight characters *viz*., plant height (cm), number of branches per plant, pod length (cm), number of pods per plant, 10 pod weight (g), number of pods per cluster and number of seeds per pod was recorded from 10 random plants in each genotype per replication while the pod yield (kg/plant) was calculated on whole plot basis. The statistical analysis for principal component analysis and cluster analysis was done using *SAS version 9.2* and the stability analysis for two environments (seasons) was done using PBSTAT (Suwarno *et al*., 2008).

RESULTS AND DISCUSSION

The principal component analysis for eight traits revealed eight principal components out of which maximum variability was concentrated in the first three principal components PC1, PC2 and PC3 which contributed to 68.61% variance (Table 2). The remaining five principal components were considered irrelevant as their eigen values were less than unity. The eigen values for the significant principal components were 2.3955 (PC1), 1.7101 (PC2) and 1.3830 (PC3).

The first principal component (PC1) contributed a maximum of 29.94% towards variance which was contributed mainly by pod length (cm) and number of pods per cluster. The second principal component explained 21.38% of variance which was contributed mainly by number of pods per plant, number of seeds per pod and 10 pod weight (g). The third principal component contributed 17.29% of total variance which was contributed mainly by yield per plant (g) and number of branches per plant. The results are in accordance with the findings of Shama *et al*. (2019), Alice *et al*. (2018), Sofi *et al*. (2014) and Verma *et al*. (2014) for number of pods per plant, 10 pod weight (g), pod length (cm), number of seeds per pod and yield per plant.

The clustering of genotypes into different clusters based on principal component scores and their intercluster distances. At an RMS distance of 79.76 all the 24 genotypes of french bean were grouped into three clusters (Table 3) based on the principal component scores from the standardized data. Cluster I comprised of 17 genotypes, Cluster II had 6 genotypes and Cluster III had only one genotype. Greater intercluster distance was observed

Table 2: Eigen values, percent variance and cumulative variance of the principal components.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigen Value	2.3955	1.7102	1.3830	0.8131	0.5670	0.5511	0.3977	0.1825
% Variance	29.9400	21.3800	17.2900	10.1600	7.09	6.8900	4.9700	2.2800
% Cumulative Variance	29.9400	51.3200	68.6100	78.7700	85.8600	92.7500	97.7200	100.0000

Table 3: Clustering of genotypes at RMS (Root mean square distance) of 79.76.

Cluster	Number of genotypes	Genotypes
I Cluster	17	FORC 6V 1136, Swarn Priya, FMGCV1007, FORC6V 1137, VRFBB-6, VRFBB-7, Ribera, VRFBB-14-1, FMGCV 1378, Valentino, FMGC6V 1379, Banoa, VRFBB-14-2, Paulista, Contender, FMGCV 0958, Arka Suvidha
II Cluster	6	Cartagenta, Rivergaro, Slender Pack, FMGCV 1187, FMGCV 1006, Giolli
III Cluster	1	Kashi Rajhans

between clusters III and II followed by clusters III and I while the least inter cluster distance was observed between clusters I and II. The genotypes from clusters with greater intercluster distance can be utilized as donor parents to obtain better transgressive segregants. The results are in accordance with the findings of Shama *et al*. (2019) and Alice *et al*. (2018).

Broad sense heritability for various traits is presented in Table 4. High heritability (> 60%) was observed for 10 pod weight (97.09), number of pods per cluster (94.25), number of seeds per pod (60.87). Moderate heritability (31-60%) was observed for pod length (50.61), number of pods per plant (46.10) and yield per plant (42.45) and low heritability (0-30%) was observed for plant height (22.27) and number of branches per plant (0.05). The traits with high heritability *viz*., 10 pod weight (g), number of pods per cluster, number of seeds per pod can be improved by simple selection. Jhanavi *et al*. (2018), Singh and Singh (2013), Ahmed and Kamaluddin (2013) reported high heritability for 10 pod weight (g), number of pods per cluster, pod length (cm), yield per plant, plant height (cm), number of primary branches per plant and number of pods per plant.

The correlation between various traits under study was presented in Table 4. Pod yield per plant had a significant positive correlation with number of pods per plant (0.7154), 10 pod weight (0.6482) and number of branches per plant (0.4785) while pod yield per plant had significant negative correlation with number of seeds per pod (-0.4182). Number of branches per plant and number of pods per plant (0.4167) had significant positive correlation whereas, significant negative correlation exists between plant height and number of seeds per pod (-0.4817). Similar findings of positive correlation of yield with number of pods per plant, average pod weight and number of branches per plant were reported by Shama *et al*. (2019), Verma *et al.* (2014) and Karasu and Oz (2010).

All the twenty four bush type french bean genotypes were significantly different for the characters studied *viz*., number of branches per plant, pod length (cm), number of pods per plant, 10 pod weight (g), number of seeds per pod, number of pods per cluster and yield per plant (g) whereas, no significant difference was observed for plant height in these bush type genotypes of french bean. Significant genotype × environment interactions were observed for the traits number of branches per plant, pod length, number of pods per plant and yield per plant (Table 5) while there was no significant G × E interactions observed for 10 pod weight (g), number of seeds per pod, plant height (cm) and number of pods per cluster.

Finlay-Wilkinson stability analysis was done to identify stable genotypes for various characters. A genotype is considered stable if its response to environment is parallel

Table 4: Correlation coefficients between the eight traits of french bean.

	NBR	POL	PON	TPW	NSP	PH	PPC	YLD	h^2bs (%)
NBR	1.0000	0.1302	0.4167*	0.1611	-0.4848*	0.1775	0.2285	0.4785*	0.05
POL		1.0000	-0.2654	0.6868**	-0.2081	0.1048	-0.0075	0.2728	50.61
PON			1.0000	-0.0075	-0.3024	0.0508	0.1069	0.7154**	46.10
TPW				1.0000	-0.1887	0.1568	0.0517	0.6482**	97.09
NSP					1.0000	-0.4817*	-0.0911	-0.4182*	60.87
PH						1.0000	-0.0740	0.2352	22.27
PPC							1.0000	0.0800	94.25
YLD								1.0000	42.45

NBR- Number of branches per planr; POL- Pod length; PON- Number of pods per plant; TPW- 10 pod weight (g); NSP- Number of seeds per pod; PH- Plant height (cm); PPC- Number of pods per cluster; YLD- Yield per plant (g); h^2 bs (%)- Broad sense heritability*=P value <0.05; **=P value <0.01.

Table 5: ANOVA for stability over two years.

	Environment	Replication × Environment	Genotype	Genotype × Environment	CV (%)
Degrees of freedom	1	2	23	23	
Number of branches per plant	24.99**	5.59**	0.52**	5.22**	12.39
Pod length (cm)	0.16ns	5.91**	2.02**	2.75**	6.53
Number of pods per plant	2,581.30**	0.06ns	1.86**	4.83**	17.37
10 pod weight (g)	4.23**	3.24*	34.32**	1.18ns	8.66
Number of seeds per pod	0.22ns	0.85ns	4.21*	0.49ns	8.7
Plant height (cm)	0.58ns	2.19ns	1.44ns	0.66ns	21.37
Number of pods per cluster	0.13ns	6.43**	17.40**	1.08ns	7.22
Yield per plant (g)	529.99**	0.46ns	1.74**	6.48**	20.36

*=P value <0.05; **=P value <0.01.

Table 6: Pooled mean values for different yield and yield related traits along with their regression coefficients (bi).

	Number of branches per plant		Pod length (cm)		Number of pods per plant		10 pod weight (g)		Number of seeds per pod		Plant height (cm)		Number of pods per cluster		Yield per plant (g)	
	Mean	bi	Mean	bi	Mean	bi	Mean	bi	Mean	bi	Mean	bi	Mean	bi	Mean	bi
Kashi Rajhans	3.30	0.43	11.92	-3.74	44.68	0.02	60.00	1.29	5.98	-3.32	36.38	-0.21	2.95	-6.86	267.11	0.23
FMGCV 1378	3.00	2.16	11.60	0.01	34.91	1.57	47.50	2.58	5.73	-5.53	37.88	-0.71	2.95	2.29	170.30	1.28
Paulista	3.03	0.38	13.80	0.01	36.97	0.99	62.50	2.58	6.08	1.11	39.59	-0.60	3.50	4.57	211.50	1.56
Contender	3.50	1.08	14.18	-6.34	24.70	0.42	75.75	1.68	5.94	1.66	42.08	-0.53	2.55	11.43	188.43	0.53
FMGCV 0958	2.95	0.32	12.05	6.64	32.35	1.12	55.00	1.29	5.68	-16.59	41.31	-0.40	3.25	-2.29	156.45	1.37
FMGCV 1187	3.38	0.16	12.38	-1.51	17.13	-0.11	34.78	0.66	5.88	5.53	38.88	-1.26	2.90	9.14	64.49	-0.11
FMGCV 1006	2.80	-0.43	12.25	4.23	19.50	0.40	33.50	0.77	6.10	4.42	34.80	0.97	2.90	4.57	71.88	0.12
Arka Suvidha	3.10	0.43	13.90	2.42	21.15	0.89	72.50	2.58	6.15	-2.21	38.99	0.30	3.00	0.01	132.38	1.47
Giolli	2.95	-0.32	11.65	-4.23	20.20	0.29	32.50	-1.29	6.13	3.32	35.11	-0.62	3.03	-10.29	66.10	-0.01
FORC 6V 1136	3.45	0.97	12.30	6.04	28.21	1.14	71.25	-1.93	5.43	-5.53	46.94	6.60	3.50	-4.57	200.09	0.74
Swarn Priya	2.70	0.43	13.63	-16.00	20.39	-0.09	80.00	3.87	6.35	-2.21	40.42	0.97	3.25	-2.29	160.55	0.23
FMGCV 1007	3.60	1.30	13.54	11.29	36.60	1.86	66.25	1.93	5.20	-8.85	39.60	1.67	3.20	0.01	218.70	2.34
FORC6V 1137	3.28	1.35	11.91	12.53	27.65	2.03	55.00	1.29	6.51	9.40	34.84	0.55	3.95	2.29	148.45	1.60
VRFBB-6	3.48	2.65	13.28	-2.20	31.16	2.82	68.75	-0.64	5.35	8.85	67.47	15.93	3.30	-4.57	217.40	2.21
VRFBB-7	3.28	2.22	14.62	5.83	25.10	2.02	83.75	1.93	5.45	-6.64	33.60	1.59	3.70	4.57	218.33	2.19
Ribera	2.65	1.51	14.08	-4.53	14.95	0.65	90.00	-1.29	6.33	1.88	31.92	0.79	3.60	9.14	139.36	0.55
Cartagenta	2.78	-0.59	11.85	1.81	30.92	0.33	28.75	0.64	6.25	2.21	33.45	-0.16	3.50	4.57	89.95	0.19
Rivergaro	3.08	0.92	13.79	-1.06	20.92	-0.31	50.00	1.29	6.00	8.85	36.38	-0.69	3.60	0.01	101.45	-0.05
VRFBB-14-1	2.65	0.76	13.00	0.01	24.36	1.32	69.50	1.55	6.10	8.85	35.61	0.04	1.60	0.01	156.21	1.58
Valentino	3.10	1.51	12.20	10.87	30.05	0.88	60.00	1.29	6.50	-8.85	38.18	0.16	4.00	9.14	170.15	1.02
FMGC6V 1379	3.65	2.49	11.78	6.34	30.35	2.47	64.50	1.55	6.00	0.01	28.50	0.01	3.55	2.29	191.65	2.30
Banoa	3.23	2.76	12.90	12.08	28.53	0.86	55.75	0.90	5.95	-2.21	27.71	1.11	3.40	-4.57	137.80	1.14
Slender Pack	2.70	0.86	11.30	-22.34	23.28	0.98	50.50	-1.55	5.33	21.01	40.14	-1.00	3.40	0.01	117.65	0.45
VRFBB-14-2	2.70	0.65	12.06	5.89	26.68	1.45	54.50	1.03	6.05	8.85	32.10	-0.49	2.70	-4.57	148.74	1.08

to the mean response of all genotypes in the trial (Lin *et al*., 1986). Genotype with b_i = 1.0 is considered dynamically stable, if b_i value greater than 1.0 it is suitable for more favorable environments and if b_i value less than 1.0 the genotype is expected to be suitable for less favorable environments.

The mean values and linear regression coefficient (b_i) of the different genotypes and various characters presented in Table 6. For the trait number of branches per plant the genotypes that could be considered stable were Contender (1.08), FORC6V 1136 (0.97), FMGCV 1007 (1.30), FORC6V 1137 (1.35) and Rivergaro (0.92). The genotype Cartagenta (1.81) could be considered stable for pod length (cm) when compared to all other genotypes. The genotypes Paulista (0.99), Slender Pack (0.98), Arka Suvidha (0.89), Valentino (0.88), FMGCV 0958 (1.12), Banoa (0.86), FORC 6V 1136 (1.14), VRFBB-14-1 (1.32) and VRFBB-14-2 (1.45) were considered stable for number of pods per plant. The genotypes FMGCV 1378 (1.28), FMGCV 0958 (1.37), Arka Suvidha (1.47), Valentino (1.02), Banoa (1.14) and VRFBB-14-2 (1.08) were found stable for yield per plant.

For yield per plant the genotypes FMGCV 1007 (2.34), VRFBB 6 (2.21), VRFBB 7 (2.19), FMGC6V 1379 (2.30) were suitable for cultivation under more favourable environments. FMGCV 1006 (0.12), Cartagenta (0.19), Swarn Priya (0.23), Kashi Rajhans (0.23) and Slender Pack (0.45) were suitable for less favourable environments. The results are in accordance with the findings of Singh *et al*. (2020), Jain *et al*. (2018) in rice, Chavan *et al*. (2009) in groundnut, Singh *et al*. (2018) and Haydar *et al*. (2018) in Wheat.

CONCLUSION

Based on the principal component analysis, it was observed that the first three principal components contributed for 68.61% variance. Selection of genotypes from cluster III and cluster II for crossing will help to create new genetic diversity and better transgressive segregants for future use. Due to high heritability, the traits 10 pod weight, number of pods per cluster and number of seeds per pod can be improved by simple selection in early generations. The genotypes FMGCV 1378, FMGCV 0958, Arka Suvidha, Valentino, Banoa and VRFBB-14-2 could be considered stable for yield per plant and were grouped in the same cluster indicating their similar genotypic response.

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Conflict of interest

All the authors of this research manuscript declare no conflict of interest with any one regarding this manuscript submission.

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