PRINCIPAL COMPONENT ANALYSIS IN ADVANCED GENOTYPES OF SOYBEAN [*GLYCINE MAX* (L.) MERRILL] OVER SEASONS

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Abstract

In present study, PCA was performed for economic traits of soybean. Out of eighteen, only five principal components (PCs) exhibited more than 1.00 Eigen value and showed about 73.44% variability among the traits studied. First principal component recorded the highest variation 37.13% followed by 13.02% (second PC), 10.17% (third PC), 6.88% (fourth PC) and 6.24% (fifth PC). Total variation of five PCs was recorded as 73.44%. Rotated component matrix revealed that the PC1, which accounted for the highest variability (37.13%) was mostly related with traits such as days to 50% flowering, days to maturity, plant height, number of branches per plant, number of nodes per plant, number of pods per plant, number of pods per node, number of seeds per plant, biological yield per plant and seed yield per plant. In second PC the traits *viz.*, number of seeds per plant and number of seeds per pod, harvest index and seed yield per plant were more related. The PC3 was dominated by single trait i.e. number of seeds per pod. The fourth component was more related to protein content, whereas PC5 was closely related to 100 seed weight. On the basis of PCA most of the important yield and yield attributing traits were present in PC1 and PC2. The characters *viz.,* days to 50% flowering, days to maturity, plant height, number of branches per plant, number of nodes per plant, number of pods per plant, number of pods per node, number of seeds per plant, biological yield per plant, harvest index and number of seeds per pod are more important yield contributing traits, and putative genotypes identified as JS 20-89, JS 20-115, JS 20-108, JS 20-122, JS 20-79 and JS 20-121 on the basis of principal component analysis.

Key words : Soybean, advanced genotypes and principal component analysis.

Introduction

Soybean (*Glycine max* L. Merill) is known as 'golden bean' and miracle crop which is an efficient producer of two most scarce items in the world food economy i.e. high quality protein (40%) and oil (20%). It is a rich source of lysine (6.4%) and other essential amino acids, vitamins and minerals. It is also used as a raw material for the nutraceuticals, functional compounds such as isoflavones, tocopherol and lecithin and industrial products like paints, varnishes, adhesives and lubricants etc. It ranks first among oilseed crops in the world and India both. It contributes 25% of the total edible oil pool and 47% of the total oilseed production of the country. In the world scenario, United States of America is the largest producer (around 50%) of soybean followed by Brazil, Argentina, China and India (Anonymous, 2014).

In the past four decades, soybean has experienced a phenomenal growth rate of 15-20% per annum. In the year 2014-15, the soybean area reached to 10.02 m ha with total production 11.64 m t and the average productivity 1062 kg ha^{-1} in India. Madhya Pradesh is the largest contributor state occupying more than 50% area of the country followed by Maharashtra, Rajasthan, Karnataka and Andhra Pradesh. Madhya Pradesh is virtually known as synonym of "Soya State" as it has played a major role ever in the development and extension of soybean in all respect. The area of Madhya Pradesh has reached to the tune of 5.55 m ha with production of 6.02 m t with productivity of 1086 kg ha^{-1}.

Yield is determined by several traits therefore, a technique is required to identify and prioritize the important traits by minimizing the number of traits for effective selection and genetic gain. PCA, basically a well known data reduction technique, identifies the minimum number

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of traits which contributes maximum variability and also ranks genotypes on the basis of PC scores.

Materials and Methods

The present study was conducted under All India Coordinated Research Project on Soybean at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidhyalaya Jabalpur (M.P.) to analyze Principal component analysis over seasons (*Rabi* 2013-14, *Kharif* 2014 and *Rabi* 2015-2016). Source and pedigree of the material are given in table 1.

The field experiment was laid out in randomized block design (RBD) with three replications. Fifty genotypes were planted with a spacing of 30 cm row to row and 10 cm plant to plant distance. All the recommended agronomical practices and plant protection measures were adopted to raise the healthy crop. The data was recorded on plant height at harvest (cm), number of nodes plant^{-1}, number of pods per plant, number of pods per node, number of seeds per plant, number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%), seed yield per plant (g), protein content

(%), oil content (%), carbohydrate (%), ash (%) and fibre (%) on a sample of 5 plants per replication in each genotypes whereas for days to flowering and days to maturity data were taken on whole plot basis.

Results and Discussion

PCA provides a roadmap for how to reduce a complex data set to a lower dimension to sometimes hidden, simplified structures that often underlies it. Principal component analysis is appropriate for obtaining measures on a number of observed variables and to developing a smaller number of artificial variables (called principal component) that will account for most of the variance in the observed variables. The eigenvectors and the corresponding loadings for each individual from the PCA can be used as covariates within a logistic regression framework to account for the underlying structure.

In present investigation, PCA was performed for economic traits of soybean are presented in table. Out of eighteen, only five principal components (PCs) exhibited more than 1.00 Eigen value (table 2) and showed about 73.44% variability among the traits studied. First principal component recorded the highest variation 37.13%

Table 1 : Pedigree and source of 50 genotypes of *Glycine max* L. Merrill.

| S. no.	Variety	Pedigree	S. no.	Variety	Pedigree
01.	JS 335	JS 78-77 X JS 71-5	26.	JS 20-98	JS 97-52 X SL 710
02.	JS 93-05	2nd selection from PS 73-22	27.	JS 20-100	JS 20-30 X JS 93-05
03.	JS 95-60	2nd selection from PS 73-22	28.	JS 20-101	JS 97-52X[JS 97-51XSL 96]
04.	JS 97-52	PK 327 X L129	29.	JS 20-102	JS 97-52 X JSM 281
05.	JS 20-29	JS 97-52 X JS 95-56	30.	JS 20-103	JS 97-52 X JSM 299
06.	JS 20-34	JS 98-63 X PK 768	31.	JS 20-104	JS 92-22 X SL 517
07.	JS 20-30	JS 97-52 X SL 710	32.	JS 20-105	JS 97-52X[JS 97-51XSL 96]
08.	JS 20-35	JS 99-81 X JS 99-83	33.	JS 20-106	JS 99-76 X JSM 275
09.	JS 20-41	JS 97-52 X JS 20-02	34.	JS 20-107	JS 97-52 X JSM 281
10.	JS 20-53	JS 97-52 X JS 20-02	35.	JS 20-108	JS 97-52 X JSM 286
11.	JS 20-65	JS 97-52XJS(IS)90-5-12-1	36.	JS 20-109	JS 97-52 X JSM 299
12.	JS 20-68	JSM 240 X JSM 189	37.	JS 20-110	JS 97-52 X JS 93-05
13.	JS 20-69	JS 97-52 X SL 710	38.	JS 20-111	JS 97-52 X JS 95-60
14.	JS 20-71	JS 97-52XJS(IS)90-5-12-1	39.	JS 20-112	JS 97-52 X SL 96
15.	JS 20-72	JS 99-81 X JS 99-83	40.	JS 20-113	JS 92-22 X SL 517
16.	JS 20-76	JS 97-52 X SL 710	41.	JS 20-114	JS 99-76 X JSM 275
17.	JS 20-79	JS 97-52XJS(IS) 90-5-12-1	42.	JS 20-115	JS 97-52 X JSM 288
18.	JS 20-87	JS 97-52XJS(IS) 90-5-12-1	43.	JS 20-116	JS 97-52 X JSM 120 A
19.	JS 20-89	JS 97-52 X JSM 286	44.	JS 20-117	JS 99-76 X JSM 275
20.	JS 20-90	JS 97-52 X JS 95-56	45.	JS 20-118	JS 97-52 X JS 20-02
21.	JS 20-92	JS 97-52 X JSM 52	46.	JS 20-119	JS 97-52 X JS(IS) 90-5-12-1
22.	JS 20-94	JS 97-52 X JS 20-02	47.	JS 20-120	JS 97-52 X SL 710
23.	JS 20-95	JS 97-52 X JS 95-56	48.	JS 20-121	JS 97-52 X JSM 52
24.	JS 20-96	JS 97-52 X JSM 286	49.	JS 20-122	JS 97-52 X JSM 120
25.	JS 20-97	JSM 259 X PK 768	50.	JS 20-123	JS 97-52 X JS 95-56
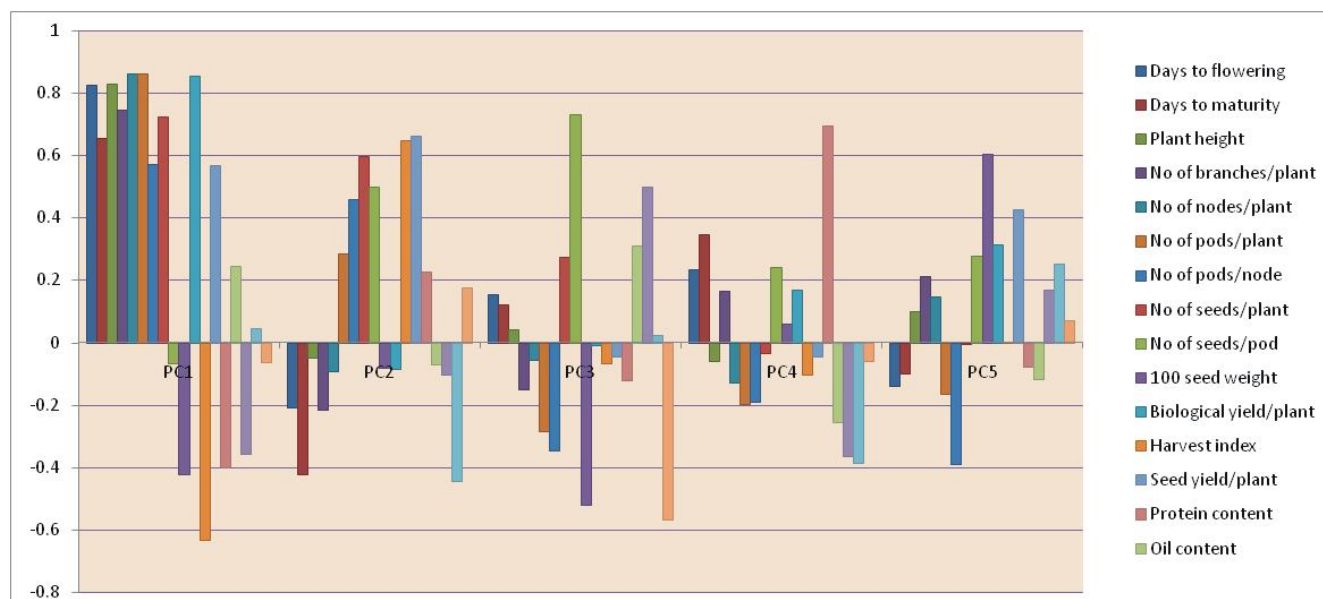
Fig. 1 : Rotated Component Matrix.

Table 2 : Eigen values, % variance and cumulative eigen values of promising lines of soybean over seasons.

Traits	Principal Component	Eigen values	% variation	Cumulative %
Days to 50% flowering	PC1	6.684	37.131	37.131
Days to maturity	PC2	2.344	13.024	50.155
Plant height	PC3	1.831	10.173	60.328
No. of branches plant^{-1}	PC4	1.238	6.876	67.203
No. of nodes plant^{-1}	PC5	1.123	6.240	73.443
No. of pods plant^{-1}	PC6	0.809	5.606	79.049
No. of pods node^{-1}	PC7	0.818	4.544	83.593
No. of seeds plant^{-1}	PC8	0.764	4.246	87.839
No. of seeds pod^{-1}	PC9	0.645	3.582	91.421
100 seed weight	PC10	0.445	2.473	93.894
Biological yield plant^{-1}	PC11	0.411	2.284	96.178
Harvest index	PC12	0.318	1.767	97.945
Seed yield plant^{-1}	PC13	0.157	0.871	98.817
Protein content	PC14	0.124	0.688	99.505
Oil	PC15	0.050	0.280	99.785
Carbohydrate	PC16	0.021	0.115	99.900
Ash	PC17	0.016	0.087	99.988
Fibre	PC18	0.002	0.012	100.000

followed by 13.02% (second PC), 10.17% (third PC), 6.88% (fourth PC) and 6.24% (fifth PC). Total variation of five PCs was recorded as 73.44%. Semi curve line obtained after fifth PC with little variation observed in each PC indicated that maximum variation was found in first PC, therefore selection for characters under first PC may be desirable.

Rotated component matrix (tables 3 and 4) revealed that the PC1, which accounted for the highest variability (37.13%) was mostly related with traits such as days to

50% flowering, days to maturity, plant height, number of branches per plant, number of nodes per plant, number of pods per plant, number of pods per node, number of seeds per plant, biological yield per plant and seed yield per plant. In second PC the traits *viz.*, number of seeds per plant and number of seeds per pod, harvest index and seed yield per plant were more related. The PC 3 was dominated by single trait *i.e.* number of seeds per pod. The fourth component was more related to protein content, whereas PC 5 was closely related to 100 seed

Table 3 : PC values of rotation component matrix for eighteen variables of fifty genotypes of soybean over seasons.

Traits	Principal components				
	PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	**0.824**	-0.207	0.156	0.234	-0.141
Days to maturity	**0.655**	-0.424	0.121	0.346	-0.100
Plant height	**0.831**	-0.047	0.042	-0.060	0.101
No. of branches plant^{-1}	**0.745**	-0.216	-0.151	0.167	0.212
No. of nodes plant^{-1}	**0.862**	-0.094	-0.057	-0.129	0.146
No. of pods plant^{-1}	**0.862**	0.284	-0.284	-0.198	-0.166
No. of pods node^{-1}	**0.571**	0.461	-0.345	-0.189	-0.390
No. of seeds plant^{-1}	**0.724**	**0.597**	0.273	-0.033	-0.003
No. of seeds pod^{-1}	-0.068	**0.500**	**0.730**	0.240	0.278
100 seed weight	-0.424	-0.080	-0.521	0.061	**0.603**
Biological yield plant^{-1}	**0.854**	-0.086	-0.009	0.169	0.313
Harvest index	-0.634	**0.647**	-0.067	-0.105	0.002
Seed yield plant^{-1}	**0.567**	**0.662**	-0.045	-0.044	0.426
Protein content	-0.402	0.228	-0.122	**0.695**	-0.078
Oil	0.246	-0.069	0.310	-0.255	-0.119
Carbohydrate	-0.358	-0.103	0.498	-0.366	0.168
Ash	0.045	-0.444	0.025	-0.388	0.251
Fibre	-0.063	0.175	-0.566	-0.060	0.072

Table 4 : Interpretation of rotated matrix for the traits having values >0.5 in each PCs over seasons.

PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	No. of seeds plant^{-1}	No. of seeds pod^{-1}	Protein content	100 seed weight
Days to maturity	No.of seeds pod^{-1}	-	-	-
Plant height	Harvest index	-	-	-
No.of branches plant^{-1}	Seed yield plant^{-1}	-	-	-
No. of nodes plant^{-1}	-	-	-	-
No. of pods plant^{-1}	-	-	-	-
No. of pods node^{-1}	-	-	-	-
No. of seeds plant^{-1}	-	-	-	-
Biological yield plant^{-1}	-	-	-	-
Seed yield plant^{-1}	-	-	-	-

weight. On the basis of PCA most of the important yield and yield attributing traits were present in PC1 and PC2 (fig. 1).

Among 50 genotypes, the top principal component scores (PC score) for all the traits were estimated in these five components and presented in table 5. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of principal component. High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype.

JS 20-89 had the highest score 4.467 value followed by JS 20-112 (4.175), JS 20-103 (3.845), JS 20-108 (3.730), JS 95-60 (3.502), JS 20-122 (2.996), JS 20-116 (2.430), JS 20-120 (2.351), JS 20-69 (2.207), JS 20-118 (1.999), JS 20-109 (1.929), JS 20-90 (1.628), JS 20-79 (1.583), JS 20-53 (1.452), JS 20-121 (1.150), JS 20-104 (1.142), JS 20-110 (1.399), JS 20-107 (1.270) and JS 20-101 (1.094) in PC1 indicating that they had high value for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of nodes per plant, number of pods per plant, number of pods per node, number of seeds per plant, biological yield per plant and seed yield per plant. JS 20-115 (3.509), JS 20-102 (2.688), JS 20-111 (2.328), JS 20-109 (2.092), JS 20-65 (2.061), JS 20-121 (1.779), JS 20-107 (1.705), JS 93-05 (1.621), JS 20-30 (1.559), JS 20-96 (1.460), JS 20-108 (1.133)

and JS 20-95 (1.291) in PC2. They had high value for number of seeds per plant and number of seeds per pod, harvest index and seed yield per plant. JS 20-108 (3.134) followed by JS 20-90 (2.417), JS 20-29 (2.339), JS 20-79 (2.033), JS 20-100 (1.823), JS 93-05 (1.786), JS 20-113 (1.562), JS 20-92 (1.547), JS 20-87 (1.356), JS 20-101 (1.285) and JS 335 (1.188) in PC3, which exhibited high value for number of seeds per pod. In PC4 JS 20-79 recorded the highest PC score (1.877) followed by JS 20-121 (1.849), JS 20-109 (1.717), JS 20-90 (1.667), JS 20-92 (1.541), JS 20-116 (1.523), JS 20-89 (1.441), JS 20-119 (1.386), JS 20-97 (1.251), JS 20-104 (1.213), JS 97-52 (1.190), JS 20-53 (1.150) and JS 20-117 (1.073) indicating that they had high value for protein content. JS 20-122 (2.057) exhibited the highest PC score followed by JS 20-101 (1.964), JS 97-52 (1.825), JS 93-05 (1.722), JS 20-68 (1.470), JS 20-94 (1.351), JS 20-111 (1.281), JS 20-121 (1.225), JS 20-120 (1.172), JS 20-116 (1.007) and JS 20-65 (1.003) in PC5 indicating that they had high value for 100 seed weight.

JS 20-121 was found in PC1, PC2, PC4 and PC5, whereas JS 20-108 was present in PC1, PC 2 and PC3, JS 20-116 in PC1, PC4 and PC5, JS 20-109 in PC1, PC2 and PC4, JS 20-101 in PC1, PC3 and PC5, JS 20-90, JS 20-89 and JS 20-79 were present in PC1, PC3 and PC4, JS 93-05 in PC2, PC3 and PC5, JS 97-52 in PC4 and PC5, JS 20-53, JS 20-89, JS 20-104, JS 20-116 in PC1 and PC4, JS 20-65 in PC2 and PC5, JS 20-92 in PC3 and

Table 5 : PCA scores of soybean genotypes over seasons.

Genotype	PC1	PC2	PC3	PC4	PC5
JS 335	-2.089	-0.323	**1.188**	0.180	-1.815
JS 93-05	-5.797	**1.621**	**1.786**	0.475	**1.722**
JS 95-60	**3.502**	0.518	0.542	-0.776	-0.645
JS 97-52	0.016	-1.499	0.021	**1.190**	**1.825**
JS 20-29	-5.643	-0.248	**2.339**	-2.549	0.645
JS 20-34	-3.151	-0.042	-0.573	0.375	-0.546
JS 20-30	-0.844	**1.559**	-2.039	-1.333	0.145
JS 20-35	-0.928	-0.032	-2.590	-0.929	0.797
JS 20-41	-1.632	-0.609	-0.822	0.852	-0.752
JS 20-53	**1.452**	-0.149	0.229	**1.150**	0.379
JS 20-65	-5.572	**2.061**	-1.134	0.213	**1.003**
JS 20-68	-0.538	-1.576	0.901	-1.564	**1.470**
JS 20-69	**2.207**	-2.240	-1.888	-0.235	-0.512
JS 20-71	-0.699	0.556	-2.229	-0.171	0.743
JS 20-72	-1.430	-0.199	-0.103	-0.056	-0.976
JS 20-76	0.786	-1.642	0.350	-0.879	-0.464
JS 20-79	**1.583**	-0.118	**2.033**	**1.877**	0.179
JS 20-87	-2.325	-2.294	**1.356**	-0.863	0.594
JS 20-89	**4.467**	0.748	0.637	**1.441**	0.565
JS 20-90	**1.628**	0.631	**2.417**	**1.667**	-0.550
JS 20-92	-1.308	-1.130	**1.547**	**1.541**	0.364
JS 20-94	0.106	-2.198	-1.764	0.128	**1.351**
JS 20-95	-1.470	**1.291**	0.506	-0.646	0.037
JS 20-96	-7.857	**1.460**	-1.802	0.906	-0.982
JS 20-97	-1.776	-1.492	-0.137	**1.251**	-0.798
JS 20-98	-1.255	-0.768	0.809	0.476	0.235
JS 20-100	0.998	-0.840	**1.823**	-1.306	-0.375
JS 20-101	**1.094**	0.308	**1.285**	-1.903	**1.964**
JS 20-102	0.961	**2.688**	-0.343	-1.125	-1.104
JS 20-103	**3.845**	0.835	-0.112	-0.778	0.785
JS 20-104	**1.142**	-0.667	-1.994	**1.213**	-1.819
JS 20-105	0.374	-0.691	-0.302	-0.708	-1.599
JS 20-106	-0.414	-1.562	-1.675	0.195	-0.668
JS 20-107	**1.270**	**1.705**	-1.798	-0.321	-0.207
JS 20-108	**3.730**	**1.133**	**3.134**	-1.365	-1.081
JS 20-109	**1.929**	**2.092**	0.207	**1.717**	-0.873
JS 20-110	**1.399**	-2.013	-0.898	-0.835	-0.227
JS 20-111	0.454	**2.328**	-1.335	-0.932	**1.281**
JS 20-112	**4.175**	0.317	-1.280	-0.885	0.014
JS 20-113	-1.022	0.862	**1.562**	-1.622	-1.947
JS 20-114	-0.500	0.819	0.200	0.097	-0.426
JS 20-115	0.526	**3.509**	0.086	0.209	-1.973
JS 20-116	**2.430**	0.848	-0.344	**1.523**	**1.007**
JS 20-117	-1.695	-3.171	0.778	**1.073**	-0.119
JS 20-118	**1.999**	-3.412	-0.917	-1.042	-1.168
JS 20-119	-0.629	-1.717	0.547	**1.386**	0.065
JS 20-120	**2.351**	0.338	-0.442	-0.276	**1.172**
JS 20-121	**1.150**	**1.779**	0.789	**1.849**	**1.225**
JS 20-122	**2.996**	0.627	-0.553	0.113	**2.057**
JS 20-123	-1.089	-0.326	0.188	0.280	-1.515

Table 6 : Five genotypes are selected on the basis of PC score in decreasing order in each component.

PC1	PC2	PC3	PC4	PC5
JS 20-89	JS 20-115	JS 20-108	JS 20-79	JS 20-122
JS 20-112	JS 20-102	JS 20-90	JS 20-121	JS 20-101
JS 20-30	JS 20-111	JS 20-29	JS 20-109	JS 97-52
JS 20-108	JS 20-109	JS 20-79	JS 20-90	JS 93-05
JS 95-60	JS 20-65	JS 20-100	JS 20-92	JS 20-68

PC4, JS 20-107 in PC1 and PC2, JS 20-111 in PC2 and PC5 and JS 20-120 in PC1 and PC5. On the basis of top PC scores in each principal component, genotypes are selected and summarized in table 6.

Similar results were obtained by Miladinovic *et al.* (2006) reported three principal components in his investigation and found first one, which explained 58.92% of the total variance included harvest index, reproductive period, seed weight and vegetative period respectively. The second component explained 23.63% of the total variance. The third component, explaining 16.16% of the total variance, included yield and plant height. Iqbal *et al.* (2008) studied three principal components; first three components accounted 69.77% of the total variance. PC1 included number of filled pods per plant, grain yield and biological yield per plant, while 100-seed weight and harvest index were included in PC2 and days to maturity and number of branches per plant in PC3. Uguru *et al.* (2012) screened seven genotypes of soybean under varying soil pH conditions. The PCA indicated that the first three principal components contributed 71.12 and 69.28 % of the total variability among the genotypes. Wang *et al.* (2013) performed PCA and showed cumulative contribution rates of the former four principal components to the variation of semi-determinate and determinate summer sowing soybean were 79.92% and 79.50%, respectively. Aondover *et al.* (2013) for pods/plant, seed yield and plant height. Badkul *et al.* (2014) for vegetative phase, plant height, number of branches per plant and yield per plant. Hashash (2016) observed principle components analysis showed that PC1 and PC2 having eigen values highest than unity explained 82.55% of total variability among soybean genotypes attributable to seed yield and accounted with values 67.77% and 14.78%, respectively. PC1 and PC2 noticed positive association with all and most genotypes, respectively and Jha *et al.* (2016) performed PCA for Identification and ranking of advanced genotypes of soybean based on combination of various phenotypic traits. Out of total principal components, five principal components were considered to be more important because they have more than one Eigen value that showed total variation among

50 soybean genotypes under study.

Conclusion

The characters *viz.,* days to 50% flowering, days to maturity, plant height, number of branches per plant, number of nodes per plant, number of pods per plant, number of pods per node, number of seeds per plant, biological yield per plant, harvest index and number of seeds per pod are more important yield contributing traits, and putative genotypes identified as JS 20-89, JS 20-115, JS 20-108, JS 20-122, JS 20-79 and JS 20-121 on the basis of principal component analysis.

Conflict of interest

The author declares no conflicts of interests.

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