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Principal Component Analysis of Quantitative Traits Governing Drought Tolerance in Germplasm Accessions of Green gram [*Vigna radiata* (L.)]

Kanavi M.S.P.^{1*}, Prakash Koler², Somu G.³, Nagesha N.⁴ and N. Marappa⁵

 ¹Dept. of Genetics and Plant Breeding, ²Dept. Crop Physiology,
 College of Agriculture, Hassan, University of Agricultural Sciences, Bangalore, Karnataka
 ³Assistant Breeder, AICRP on Sorghum, Chamarajanagara, University of Agricultural Sciences, Bangalore, Karnataka
 ⁴Dept. of Plant Biotechnology, ⁵Dept. of Genetics and Plant Breeding,
 College of Agriculture, G.K.V.K, University of Agricultural Sciences, Bangalore, Karnataka
 *Corresponding Author E-mail: kanavi.uasb@gmail.com
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ABSTRACT

An experiment was conducted to evaluate 200 green gram germplasm accessions along with five check entries for drought tolerance using augmented design during summer 2015 by imposing drought stress condition. Observations were recorded on 17 quantitative traits. ANOVA revealed high significant differences among germplasm accessions for yield, yield component traits and also for drought tolerance traits. Mean squares attributable to 'Genotypes vs check entries' were significant for all the traits except seeds per pod and relative water content. Principal component analysis was carried out for 14 variables showing positive correlation with yield. Out of 14 factors generated by PCA, there are only 4 factors with eigenvalues more than or close to one contributing for more than 79.65 % of variability. Among the variables studied, variable proline content (11.91) had highest per cent contribution to the total variability followed by spad chlorophyll meter reading (10.80), leaf water potential (10.75) seeds per pod (9.34), pod length (9.07), relative water content (8.51), harvest index (7.49), specific leaf area (6.31), pods per cluster (6.28), plant height (5.74), pods per plant (3.79) and clusters per plant (1.95). Two variables namely; test weight (0.85) and threshing percentage (0.46) had negligible percentage of contribution to total variability.

Keywords: Green gram germplasm, Drought tolerance screening, Principal component analysis, Biplot analysis

INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek] is a prehistoric crop and grown throughout Asia. Green gram is also known as mung bean is an

important short duration pulse crop of the tropical and subtropical countries of the world. Green gram is the third most important pulse crop of India after chickpea and red gram.

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Kanavi et al.

ISSN: 2582 - 2845

Green gram as a legume crop has the ability to fix atmospheric nitrogen via root rhizobial symbiosis leading to improved soil fertility and texture (Graham & Vance, 2003). Mung bean when inter-cropped in rice–rice and rice–wheat systems increases the yield of the subsequent cereal crop and reduces pest incidence (Yaqub et al., 2010 & Defaria, 1989).

India is the largest producer and consumer of green gram in the world accounting for 55% of total world acreage and 45% of total production. In India mung bean is cultivated in an area of 40.70 lakh hectare with production of 19.01 lakh tones and productivity of 467 kg ha⁻¹. Average productivity of mung bean in India is one of the lowest compared to world average because it is cultivated on marginal and poor fertile soils under rainfed condition in rabi or late rabi season utilizing available residual soil moisture after harvesting main kharif crop. Hence crop is expected to experience several kinds of droughts during its cropping period. Crop is likely to experience severe droughts in days to come because of climate change and global warming which are adding to the woes of reduced soil moisture availability to crop production. Drought is the major environmental stress severely impairing plant growth and development limiting production and performance of crop plants than any other environmental stress (Shao et al., 2009). Drought is the major constraint for green gram production due to insufficient and erratic rainfall in India (Baroowa & Gogoi., 2015). Drought, also referred to as low-moisture stress, is a multidimensional stress which not only disturbs normal metabolism and yield of crop plants but also affects all living organisms in terms of health and food. Global climate change is rapidly increasing the frequency of severe drought conditions (Dai,

2012). The plants possess a wide range of genetic and physiological adaptations innate or triggered to cope with the stress ranging from transient responses to low soil moisture to major survival mechanisms of escape by early flowering in absence of seasonal rainfall (Supratima, 2016).

Multivariate analysis usually starts out with data involving a substantial number of correlated variables. Principal Component Analysis (PCA) is a very powerful dimensionreduction tool that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set. This technique reduces the dimensionality of large data sets which are often difficult to interpret. PCA is a mathematical procedure that transforms more number of correlated variables into a smaller number of uncorrelated variables called principal components. The first principal component with highest eigenvalue / PCA coefficients accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible with corresponding eigen values /PCA coefficients.

MATERIALS AND METHODS

The experiment was conducted at experimental plot of College of Agriculture, Hassan, University of Agricultural Sciences, Bangalore. The experimental site is geographically located at Southern Transitional Zone (Zone-7) of Karnataka with an altitude of 827 m above Mean Sea Level (MSL) and at 33' N latitude and 75° 33' to 76° E38' longitude. The study material consisted of 205 germplasm accessions collected from different research institutions / organizations representing different agro-climatic zones. List of germplasm accessions used in the study with their source is given in table No1.

Table 1: List of germplasm accessions used in the study and their source

Sl. No.	Germplasm	Location	Sl. No.	Germplasm	Location
1	KM13-16	ARS, Bidar	4	GG13-7	ARS, Bidar
2	KM13-19	ARS, Bidar	5	GG13-6	ARS, Bidar
3	KM13-39	ARS, Bidar	6	KM13-44	ARS, Bidar

Kanavi et a	վ.	Ind. J. Pure App	. Biosci. (2	2020) 8(1),	252-261	ISSN: 2582 – 2845
Sl. No.	Germplasm	Location		Sl. No.	Germplasm	Location
7	GG13-10	ARS, Bidar		47	AKL-212	NBPGR, Akola
8	SML-668	ARS, Bidar		48	AKL-195	NBPGR, Akola
9	KM13-9	ARS, Bidar		49	AKL-211	NBPGR, Akola
10	IPM99-125	ARS, Bidar		50	KM13-11	ARS, Bidar
11	LGG-596	RARS, Guntur		51	KM13-30	ARS, Bidar
12	LGG-572	RARS, Guntur		52	KM13-45	ARS, Bidar
13	LGG-450	RARS, Guntur		53	KM13-18	ARS, Bidar
14	LGG-583	RARS, Guntur		54	KM13-5	ARS, Bidar
15	LGG-590	RARS, Guntur		55	KM13-02	ARS, Bidar
16	LGG-588	RARS, Guntur		56	KM13-37	ARS, Bidar
17	LGG-589	RARS, Guntur		57	KM13-23	ARS, Bidar
18	LGG-579	RARS, Guntur		58	KM13-55	ARS, Bidar
19	LGG-562	RARS, Guntur		59	KM13-12	ARS, Bidar
20	LGG-582	RARS, Guntur		60	GG13-9	ARS, Bidar
21	LGG-585	RARS, Guntur		61	KM13-49	ARS, Bidar
22	AKL-170	NBPGR, Akola		62	GG13-4	ARS, Bidar
23	PLM-110	UAS, Bangalore		63	GG13-54	ARS, Bidar
24	LGG-577	RARS, Guntur		64	KM13-20	ARS, Bidar
25	IC-436624	IIPR, Kanpur	-	65	GG13-5	ARS, Bidar
26	IC-436723	IIPR. Kanpur	-	66	Chinamung	ARS. Bidar
27	IC-413316	IIPR. Kanpur		67	GG13-2	ARS. Bidar
28	IC-436746	IIPR. Kanpur		68	KM13-26	ARS. Bidar
	10 100710	TNAU.		69	KM13-47	ARS, Bidar
29	VGG10-010	Coimbatore		70	KM13-41	ARS Bidar
		TNAU.		70	KM13-11	ARS, Bidar
30	VGG04-011	Coimbatore		72	KM13-42	ARS Bidar
		TNAU.		73	GG13-11	ARS Bidar
31	VGG04-007	Coimbatore		74	GG13-8	ARS, Bidar
		TNAU,		75	GG13-12	ARS, Bidar
32	COGG-93	Coimbatore		76	KM13-48	ARS Bidar
		TNAU,		77	IPM2-3	ARS, Bidar
33	VBNGG-2	Coimbatore		78	IPM2-14	ARS Bidar
24		TNAU,		79	PDM-139	ARS, Bidar
34	TARM-2013	Coimbatore		80	LGG-580	RARS Guntur
25		TNAU,		00	PM-112	TNAU
35	VGG04-005	Coimbatore		81	1101 112	Coimbatore
26		TNAU,		82	LGG-578	NBPGR, Akola
30	COGG-920	Coimbatore		83	LGG-563	NBPGR, Akola
27		TNAU,		84	LGG-594	NBPGR, Akola
57	VGG07-003	Coimbatore		85	TM-96-2	NBPGR Akola
29		TNAU,		86	LGG-593	NBPGR, Akola
50	VGG10-002	Coimbatore		87	LGG-591	NBPGR, Akola
30		TNAU,		88	PM-115	NBPGR, Akola
37	VGG-112	Coimbatore		89	LGG-587	NBPGR, Akola
40	IC-92048	NBPGR, Akola]	90	PM-113	NBPGR, Akola
41	AKL-103	NBPGR, Akola]	91	LGG-586	NBPGR Akola
42	AKL-39	NBPGR, Akola		92	IC-436775	NBPGR Akola
43	AKL-106	NBPGR, Akola		92	IC-413311	NBPGR Akola
44	AKL-225	NBPGR, Akola	1	93 Q/	IC-30808/	NBPGR Abola
45	AKL-95	NBPGR, Akola	1	05	IC-//36767	NBPGR Akola
46	AKL-194	NBPGR, Akola	1	95	IC-436573	NBPGR Abola
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Kanavi et a	al.	Ind. J. Pure App	. Biosci. (2	2020) 8(1),	252-261	ISSN: 2582 – 284
Sl. No.	Germplasm	Location		Sl. No.	Germplasm	Location
97	LGG-584	NBPGR, Akola		138	VBN-1	TNAU,
98	LGG-592	NBPGR, Akola		150		Coimbatore
99	LGG-555	NBPGR, Akola		139	VGG-119	TNAU,
100	LGG-564	NBPGR, Akola		157		Coimbatore
101	LGG-460	RARS, Guntur		140	VC3890-A	TNAU,
102	LGG-595	RARS, Guntur		140		Coimbatore
103	LGG-566	RARS, Guntur		141	DGGV-4	UAS, Raichur
104	IC-553514	IIPR, Kanpur		142	KPS-1	UAS, Raichur
105	IC-413319	IIPR, Kanpur		143	CGG-973	UAS, Raichur
106	IC-436542	IIPR, Kanpur		144	CN9-5	UAS, Raichur
107	IC-546493	IIPR, Kanpur		145	KPS-2	UAS, Raichur
108	IC-436594	IIPR, Kanpur		146	VC-6173	UAS, Raichur
109	IC-436630	IIPR, Kanpur	-	147	VC-6368	UAS, Raichur
110	IC-436668	IIPR, Kanpur		148	CO-6	UAS, Raichur
111	IC-436555	IIPR, Kanpur		149	Harsha	UAS, Raichur
112	IC-413314	IIPR, Kanpur		150	PLM-92	UAS, Bangalore
113	AKL-20	NBPGR, Akola		151	MH-709	UAS, Raichur
114	AKL-89	NBPGR, Akola	-	152	LGG-460	RARS, Guntur
115	AKL-228	NBPGR, Akola		153	KGS-5	UAS, Raichur
116	AKL-184	NBPGR, Akola	-	154	Barimung-4	UAS, Raichur
117	AKL-182	NBPGR, Akola		155	AKL-189	NBPGR, Akola
118	AKL-230	NBPGR Akola		156	AKL-168	NBPGR, Akola
110	AKL-229	NBPGR Akola	-	157	AKL-218	NBPGR. Akola
120	AKL-86	NBPGR Akola		158	AKL-179	NBPGR, Akola
120	IC-436646	IIPR Kannur	-	159	AKL-185	NBPGR, Akola
121	IC-343964	IIPR Kanpur		160	AKL-163	NBPGR, Akola
122	IC-436528	IIPR Kanpur			COGG-912	TNAU.
123	IC-436723	IIPR Kanpur	-	161		Coimbatore
124	IC-546491	IIPR Kanpur		162	IC-73451	NBPGR. Akola
125	IC-546481	IIPR Kanpur		163	IC-105690	NBPGR. Akola
120	IC-398988	IIPR Kanpur		164	IC-73534	NBPGR, Akola
127	VGG10-005			165	IC-73412	NBPGR. Akola
128	VUU10-005	Coimbatore		166	IC-39605	NBPGR, Akola
	VBN 223	TNAU		167	IC-73472	NBPGR Akola
129	V DIN-225	Coimbatore		168	IC-92053	NBPGR Akola
	COGG-912	TNAU		169	IC-73779	NBPGR Akola
130	0000-712	Coimbatore		170	IC-73462	NBPGR Akola
	VBN(G9)-3	TNAU	-	170	IC-118992	NBPGR Akola
131	(G)) 5	Coimbatore		172	IC-53783	NBPGR Akola
	ML-1165	TNAU	-	172	IC-73456	NBPGR Akola
132		Coimbatore		173	IC-73458	NBPGR Akola
	VGG04-025	TNAU	-	174	AKI -105	NBPGR Akola
133	10001 025	Coimbatore		175	AKL-213	NBPGR Akola
	VGG04-004	TNAU	-	170	AKL 160	NBPGP Akola
134		Coimbatore		170	AKI 220	NBDCD Alcolo
	VGG04-149	TNAU	-	170	AKL-220	NBDCD Alcolo
135	, 000+-147	Coimbatore		1/9	ARL-04	NDDCD Alasta
	COGG-954	TNAU	1	100	ARL-02	NDPCD Alcolo
136		Coimbatore		181	AKL-9/	NDPOR, AKOla
	VGG08-002	TNAU	-	182	ANL-220	NDPOR, AKOla
137		Coimbatore		183	ANL-24	NDPCR, AKOla
		connoutore	1	170	IC-73462	NBPGK, Akola

Kanavi et a	d.	Ind. J. Pure App	. Biosci. (2	2020) 8(1),	252-261	ISSN: 2582 – 2845
Sl. No.	Germplasm	Location		Sl. No.	Germplasm	Location
171	IC-118992	NBPGR, Akola		186	AKL-180	NBPGR, Akola
172	IC-53783	NBPGR, Akola		187	AKL-222	NBPGR, Akola
173	IC-73456	NBPGR, Akola		188	AKL-187	NBPGR, Akola
174	IC-73458	NBPGR, Akola		189	AKL-216	NBPGR, Akola
175	AKL-105	NBPGR, Akola		190	AKL-29	NBPGR, Akola
176	AKL-213	NBPGR, Akola		191	AKL-90	NBPGR, Akola
177	AKL-169	NBPGR, Akola		192	AKL-227	NBPGR, Akola
178	AKL-220	NBPGR, Akola		193	AKL-200	NBPGR, Akola
179	AKL-84	NBPGR, Akola		194	AKL-92	NBPGR, Akola
180	AKL-82	NBPGR, Akola		195	AKL-183	NBPGR, Akola
181	AKL-97	NBPGR, Akola		196	AKL-176	NBPGR, Akola
182	AKL-226	NBPGR, Akola		197	AKL-191	NBPGR, Akola
183	AKL-24	NBPGR, Akola		198	AKL-165	NBPGR, Akola
184	AKL-174	NBPGR, Akola		199	AKL-164	NBPGR, Akola
185	AKL-161	NBPGR, Akola		200	AKL-192	NBPGR, Akola

2.1 Layout of the experiment

The experiment was conducted in an Augmented Randomized Complete Block Design with 205 germplasm accessions. As per the augmented RCBD, the check entries were replicated twice randomly in each block. There were 5 blocks, each block had 5 plots of size $3x3 \text{ m}^2$ thus each block size was 15 m². The gross area of experimental plot was 75 m². The row spacing was 30 cm and inter plant distance was 10 cm. The experiment was conducted during *summer* 2015.

Recommended crop production practices were followed to raise healthy crop.

2.2 Imposing drought condition

Drought condition was imposed by withholding irrigation 25 days after sowing (Baroowa & Gogoi, 2015; & Pooja et al., 2019). Since the experiment was conducted during *summer* season, there were no unpredicted rains during the entire cropping period hence the drought condition was effectively imposed. The rainfall data of experimental site during the cropping period is given in table No.2.

Year	Months	Temperature (°C)	Relative humidity (%)	Rainfall (mm)
2015	January	21.32	61.03	0.59
	February	23.10	50.72	Nil
	March	25.34	58.70	2 mm (25.03.2015)
	April	25.87	66.55	Nil

 Table 2: Meteorological data of experimental site for the year 2015

2.3 Plant sampling and data collection

Observations were recorded on five randomly chosen competitive plants from each germplasm accession for all the characters except days to 50 *per cent* flowering and days to maturity, which were recorded on plot basis. The values of five competitive plants were averaged and expressed as mean of the respective characters. The observations were taken on the traits like; Days to 50% flowering, Days to maturity, Plant height (cm), Clusters per plant, Pods per cluster, Pods per plant, Pod length (cm), Seeds per pod, test weight, Threshing %, Harvest index (%), SCMR (SPAD Chlorophyll meter reading), Leaf water potential (Mpa), Proline content ($\mu g g^{-1}$), Relative water content, Specific leaf area and Seed yield per plant.

2.4 Statistical Analysis

2.4.1 Analysis of variance (ANOVA)

The quantitative trait mean value of five randomly selected plants in each of the genotype and check entries were used for statistical analysis. ANOVA was performed to

Kanavi et al.

partition the total variation among genotypes and check entries into sources attributable to 'Genotypes + Check entries', Genotypes', Check entries' and Genotypes vs check entries', following the augmented design as suggested by Federer (1956) using statistical package for augmented design SAS version 9.3 and IndoStat. The adjusted trait mean of each of the genotype was estimated (Federer, 1956) and the same was used for all subsequent statistical analysis.

2.4.2 Multivariate analysis

Factor analysis, using the Principal Component Analysis (PCA) as extraction method and Varimax rotation, was performed to verify if the assay data variation and obtained factors could explain genotype performance and identify drought tolerance controlling factors. Biplot analysis was presented by first two principal component analysis (PCA) which were computed based on rank correlation matrix using data from 17 quantitative traits by Microsoft Excel (2007) and XLSTAT 2014, Copyright Addinsoft 1995-2014 (http://www.xlstat.com) as described by Iqbal et al. (2014).

RESULTS AND DISCUSSION

3.1 Analysis of variance (ANOVA)

Analysis variance of revealed highly significant mean squares attributable to germplasm accessions for all the traits. Significant mean squares were recorded for all the traits. (Table 3). Mean squares attributable 'Genotypes vs check entries' to were significant for all the traits except seeds per pod and relative water content. These results suggest significant differences among the germplasm accessions. The germplasm accessions as group differed significantly for all of the traits under investigation, similarly, check entries as group differed significantly for most of the traits under study.

3.2 Multivariate analysis

The first principal component with highest eigenvalue / PCA coefficients accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible with corresponding eigen values /PCA coefficients. Principal component analysis has to be performed only for those traits (independent variables) having positive correlation with dependent variable yield. Hence correlation studies were first carried out to identify traits to be considered for principal component analysis

3.3 Correlation coefficient analysis

Correlation coefficients are used to measure the strength of the relationship between two (dependent and independent). variables Pearson correlation is one of the most commonly used statistics hence, Pearson correlation was performed. The correlation coefficient analysis revealed that out of 17 independent variables, 15 variables showed positive correlation with dependent variable yield. Two variables which did not show positive correlation with yield are; days to flowering and days to maturity. Among the independent variables, pods per cluster had highest positive correlation with seed yield per plant (0.84) followed by pods per cluster (0.77), cluster per plant(0.71), plant height (0.68), proline content (0.63), spad chlorophyll meter reading (0.62), leaf water potential (0.61), harvest index and seeds per pod (0.60). Other independent variables showed lower positive magnitude of relation with dependent variable yield such as; pod length (0.56), primary branches per plant (0.52), relative water content (0.51), specific leaf area (0.41), test weight (0.40) and threshing percentage (0.17). Sandhiya and Saravanan (2018) have also reported significant positive correlation with the traits, number of pods per plant, number of clusters per plant and number of pods per cluster.

3.4 Principle component analysis

Principal component analysis was carried for 14 variables showing positive correlation with yield. The fourteen variables considered for principal component analysis are; plant height, cluster plant⁻¹, pods cluster⁻¹, pods plant⁻¹, pod length, seeds pod⁻¹, test weight, threshing percentage, harvest index, spad chlorophyll meter reading, leaf water potential, proline content, relative water content and specific leaf area.

Kanavi et al.	Ind. J. Pure App. Biosci. (2020) 8(1), 252-261	ISSN: 2582 – 2845
Table 3: Summary of augment	ed ANOVA for grain yield and component traits of	f germplasm accessions

under drought condition

Sources of Variations	DF	DFF	DM	РН	СРР	PPC	PPP	PL	SPP	TW
Blocks (b)	4	14.74 **	8.18***	65.31**	2.23**	0.11*	25.23**	1.49**	5.05**	1.77 **
Entries (e) (Genotypes + Checks)	204	17.10 **	18.01**	84.47**	3.60**	0.51**	72.94**	0.75**	2.70**	0.35 **
Checks	4	34.57 **	37.01**	22.56**	1.40**	0.42**	12.50**	0.87**	3.98**	0.81 **
Genotypes	199	14.215 **	15.14**	85.71**	3.67**	0.51**	73.91**	0.73**	2.69**	0.31 **
Checks vs Genotypes	1	521.64 **	513.06**	85.01**	0.16**	1.45**	121.60**	4.52**	0.03	5.42 **
Error	16	1.32	0.74	0.98	0.04	0.02	0.98	0.009	0.05	0.05

Sources of Variations	DF	ТР	HI	SCMR	LWP	РС	RWC	SLA	SYPP
Blocks (b)	4	37.12*	247.54 **	396.55 **	1.17 **	470.90 **	423.68 *	4067.34 *	2.11 **
Entries (e) (Genotypes + Checks)	204	37.20 **	54.41 *	98.71 **	2.45 **	1707.90 **	425.40 **	4283.10 **	7.01 **
Checks	4	17.09	64.39 *	24.49	0.82 **	942.07 **	63.06	1924.20	3.76 **
Genotypes	199	27.67 *	53.01 *	79.58 *	2.33 **	1712.67 **	433.68 **	4294.15**	7.10 **
Checks vs Genotypes	1	2014.79 **	293.20 **	4203.25 **	32.57 **	3822.09 **	227.32	11518.68**	0.42*
Error	16	9.83	19.57	31.14	0.03	1.48	130.64	1339.95	0.09

*Significant at P =0.05, ** Significant at P=0.01

DFF : Days to 50% flowering	
DM : Days to maturity	
PH: Plant height (cm)	
CPP : Cluster plant ⁻¹	
PPC : Pods cluster ⁻¹	

Pods plant⁻¹ PL : Pod length (cm) SPP : Seeds per pod TW: test weight (g) TP : Threshing %

HI : Harvest index (%) SCMR : SPAD Chlorophyll meter reading LWP : Leaf water potential(Mpa) PC : Proline content ($\mu g g^{-1}$) RWC : Relative water content (%) SLA : Specific leaf area SYPP : Seed yield plant⁻¹

3.5 Kaiser-Meyer-Olkin (KMO) Test

KMO test measures whether the data is suitable for **factor analysis like PCA**. The test measures sampling adequacy for each variable in the model **and** for complete model. Lower the proportion, more the data is suited for factor analysis. KMO values between 0.8 and 1 indicate the sampling is adequate. KMO values less than 0.6 indicate the sampling is not adequate and that remedial action should be taken. KMO test results are given in table 4.

	Tunte to Transfer Total interstate of Sampling autoquity								
Traits	PH	PBPP	СРР	PPC	PPP	PL	SPP	TW	
KMO Values	0.91	0.93	0.50	0.67	0.60	0.93	0.95	0.56	
Traits	TP	HI	SCMR	LWP	PC	RWC	SLA		
KMO Values	0.45	0.94	0.90	0.82	0.81	0.93	0.94		

Table 4: Kaiser-Meyer-Olkin measure of sampling adequacy

Out of 14 traits considered for study, 11 traits satisfied the conditions of KMO test and only three traits namely; clusters per plant (0.50), test weight (0.56) and threshing percentage (0.45) did not satisfy the conditions.

3.6 Identifying principal component numbers controlling maximum variability

Identifying principal component number contributing for maximum variability is decided based on eigenvalues and also scree plot. Out of 14 factors generated by PCA, there are only 4 factors with eigenvalues more than or close to one (table 5). Hence these are the only four factors contributing for more

Ind. J. Pure App. Biosci. (2020) 8(1), 252-261

Kanavi et al. Ind. J. Pure App. I than 79.65 % of variability. This could also be cross verified with scree plot. A scree plot shows the eigenvalues on the y-axis and the number of factors on the x-axis. It always displays a downward curve. The point where the slope of the curve is clearly leveling off

(the 'elbow') indicates the number of factors that should be generated by the analysis. From the scree plot (figure 1) it is evident that principal component analysis would identify four factors explaining maximum variability.

Table 5: Eigen values of principal component analysis										
Descriptives	F1	F2	F3	F4						
Eigen value	7.47	2.39	1.11	0.95						
Variability (%)	49.82	15.98	7.45	6.39						
Cumulative %	Cumulative % 49.82 65.81 73.26 79.65									



Fig. 1: Scree plot of principal component analysis for 15 variables



Fig. 2: Loading plot of principal component analysis for 14 variables

Ind. J. Pure App. Biosci. (2020) 8(1), 252-261

Kanavi et al.

The analysis will simply identify factors / principal component numbers. It is the researcher who has to decide which variable to be considered. In making decision to identify variables depending upon our research interest one should refer to factor loadings or component coefficient values which are correlation coefficients between variables and the factors. These values will help in making decision to identify variables having maximum contribution for total variability (table 6).

Traits	F1	F2	F3	F4
Plant height	0.66	0.46	0.05	0.17
Cluster plant ⁻¹	0.38	0.83	0.03	-0.16
Pods cluster ⁻¹	0.69	0.49	-0.06	-0.07
Pods plant ⁻¹	0.53	0.81	-0.01	-0.12
Pod length	0.82	-0.25	0.13	0.22
Seeds pod ⁻¹	0.84	-0.29	0.09	-0.02
Test weight	0.25	0.19	-0.48	0.80
Threshing percentage	0.19	0.13	0.86	0.35
Harvest index	0.75	0.03	-0.15	-0.08
Spad chlorophyll meter reading	0.90	-0.19	-0.02	0.02
Leaf water potential	0.90	-0.12	-0.16	-0.20
Proline content	0.94	-0.22	-0.07	-0.10
Relative water content	0.80	-0.41	-0.11	-0.03
Specific leaf area	0.69	-0.36	0.15	0.03

nent coefficient values of PCA
)

The PCA revealed *per cent* contribution made by each of the traits to the total variability (table 7). Among the fifteen variables studied, variable proline content (11.91) had highest *per cent* contribution to the total variability followed by spad chlorophyll meter reading (10.80), leaf water potential (10.75), seeds per pod (9.34). pod length (9.07), relative water content (8.51), harvest index (7.49), specific leaf area (6.31), pods per cluster (6.28), plant height (5.74), pods per plant (3.79) and clusters per plant (1.95). Two variables namely; test weight (0.85) and threshing percentage (0.46) had negligible percentage of contribution to total variability. Our results are on par with the results of Mohammad and Sharif (2015) who reported that factor analysis indicated four independent factors explaining 75% of total variability in control condition and 78% variability in drought stress condition in mung bean. Srikanth et al. (2017) has also reported similar findings on principal component analysis.

			v	
Traits	F1	F2	F3	F4
Plant height	5.74	8.74	0.21	3.16
Cluster plant ⁻¹	1.95	28.85	0.08	2.72
Pods cluster ⁻¹	6.28	10.14	0.27	0.46
Pods plant ⁻¹	3.79	27.56	0.00	1.61
Pod length	9.07	2.58	1.44	5.22
Seeds pod ⁻¹	9.34	3.63	0.78	0.06
Test weight	0.85	1.47	20.81	67.10
Threshing percentage	0.46	0.69	66.70	13.00
Harvest index	7.49	0.05	2.12	0.59
Spad chlorophyll meter reading	10.80	1.44	0.02	0.04
Leaf water potential	10.75	0.57	2.26	4.36
Proline content	11.91	2.02	0.38	0.94
Relative water content	8.51	6.86	1.16	0.11
Specific leaf area	6.31	5.39	2.14	0.07

Table 7: Per cent contribution of the traits to the total variability in PCA

Kanavi et al.

CONCLUSIONS Principal component analysis identified 4 factors with eigenvalues more than or close to one contributing for more than 79.65 % of variability. Among the variables studied, variable proline content (11.91) had highest *per cent* contribution to the total variability followed by spad chlorophyll meter reading (10.80), leaf water potential (10.75) and seeds per pod (9.34).

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