MULTIVARIATE ANALYSIS IN BLACKGRAM (*VIGNA MUNGO* (L.) HEPPER) GENOTYPES FOR MUNGBEAN YELLOW MOSAIC VIRUS (MYMV) RESISTANCE

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Abstract

A present study was carried out with two hundred and twelve genotypes to discovering relationship and genetic diversity using Mahalanobis's D2 statistics and Principal Component Analysis (PCA) for eleven biometrical traits over a season. In D2 analysis, the traits *viz.,* percentage of disease infection (32.44%), number of pods per cluster (23.56%), number of pods per plant (19.38%) and number of clusters per plant (16.42%) contributed towards divergence. In PCA, the first four canonical vectors contributed only 68.96% towards genetic divergence because of which discernible overlapping was observed in group constellations of canonical vectors. The plot of PCI and PCII accounting for 48.36% total variation showed clear consistency of grouping of diverse blackgram genotypes as in D2 statistic. Genotypes belonging to the common clusters have dropped nearer to each other and vice versa. In spite of this in many instances the D2 clustering did not confirm with the PCA. The traits *viz.,* single plant seed yield, pod length, number of pods per plant and number of seeds per pod, number of clusters per plant, plant height had recorded maximum positive contribution towards genetic divergence and hundred seed weight, number of pods per cluster and percentage of disease infection (PCI), number of pods per plant, number of branches per plant, number of clusters per plant (PC II), in PC III, percentage of disease infections, days to fifty percent flowering, number of branches per plant, plant height and number of clusters per plant, in PC IV, number of branches per plant and number of seeds per pod had maximum contribution towards genetic divergence.

Key words: MYMV, Genetic Divergence, D2 Statistics, Biplot, Eigen Value, principal component analysis, PCA.

Introduction

Blackgram (*Vigna mungo* (L.) Hepper) is an crucial legume food crop because of its nutrients content and the precision to cropping practice. Blackgram is believed that was domesticated crop from a wild progenitor of *Vigna mungo* var. *silvestris* in India (Kaewwongwal *et al.,* 2015). It is an annual and diploid pulse has 22 chromosomes. Grains of blackgram highly nutritious with carbohydrates (76%), protein (25%), fiber (3-5%), fat (1.74%), oil (1.0-1.5%), minerals ((3.2%) (138mg of calcium, 7.57mg of iron, 267mg of magnesium, 379mg of phosphorus, 983mg of potassium, 38mg of sodium, 3.35mg of zinc per 100g), lesser quantity of vitamin B complex (0.273mg of thiamine (B1), 0.254mg of Riboflavin (B2), 1.447mg of Niacin (B3), 0.281mg of Vitamin (B6), 216μg of Folate (B9) per 100g) and amino acids and also it is a excellent resource of lysine for vegetarians.

A largely cultivated legume crop in many tropical and subtropical countries like India, Myanmar, Nepal, Pakistan, Sri Lanka, Thailand and etc. In ancient period it is a highly prized pulses in the world. India is the largely producing and consuming country, with 5.44mha of area, 3.56 million tonnes of production and 655kg/ha of productivity. In India area occupying about 17.13 percent of total pulse and contributing 13.40 percent of total pulse production. (Govt. of India, 2018). Because of a short duration pulses of 70-90 days, its a largely cultivated as fallow cropping and as well as intercropping. A Leguminaceae family, 150-200 kg/ha of nitrogen fix through root symbiosis by Bradyrhizobia bacteria and Rhizobium ultimately improves soil fertility (Vyas *et al.,* 2018). Pulses are the rich source of protein for human dietary, among the pulses, blackgram is a highly prised legume crop for many developing countries, comparatively a least studied and researches are less focused then other legume crops like peas and beans.

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The low productivity of blackgram due to many biotic and abiotic stresses. Among the biotic stresses, Yellow Mosaic Virus (YMV) is a major constrain limiting blackgram productivity it has given unique attention due to its severity and potential to cause up to 85% of yield losses (Nene, 1972; Verma and Malathi, 2003). MYMV shows typical yellow mosaic symptoms, which is show in the appearance of small irregular yellow spot and specks along the veins, which extend until the leaves completely turn into yellow. Infected plants are stunted with less flowers and pods that bring smaller, irregularly shrunken seeds in cruel cases and other remaining parts also completely turn into yellow. The YMV is classified into two different categorized, Mungbean Yellow Mosaic India virus (MYMIV), the disease which is caused in northern and central India and the disease which caused in southern and western India is caused known as Mungbean Yellow Mosaic Virus (MYMV).

Multivariate statistical tools includes Principal Component Analysis (PCA), Multidimensional Scaling, Discriminate analysis, Cluster analysis and Multivariate analysis of variance (Oyelola, 2004). With use of principal component analysis can discover the similarities among variables and categorize the genotypes which is not covered in the D2 statistics, although cluster analysis conversely is concerned with categorize formerly unclassified materials (Leonard and Peter, 2009). PCA is very effective for identification of plant traits that classify the uniqueness among promising genotypes (Chakravorty *et al*., 2013). In these view of two hundred and twelve blackgram genotypes were evaluated to discover genetically diverse genotypes by multivariate analysis and to discover traits which is contribute to variability's in the population.

The present study aimed to estimate the degree of diversity for Yellow mosaic virus resistance in the blackgram and to evaluate genetic diversity it can provide additional breeding solutions and guidelines to improvement blackgram.

Material and Method

Experimental materials

The experimental materials consist of 212 blackgram genotypes collected from various sources NBPGR, New Delhi, IIPR, Kanpure and NPRC, Vamban (Tamil Nadu).

Experimental field trial

All the genotypes were grown in randomized block design (RBD) with three replications in *Karif.,* 2018 at yellow mosaic virus hotspot region in Panpozhi village, Tirunelveli district, Tamil Nadu. The 212 genotypes were sown in three row with a length of 1.5 meter and a spacing of 30×10 cm in three replications. One row of infector line was raised system was followed for providing YMV disease infection to all the genotypes. CO 5 blackgram and paiyur^{-1} green gram genotype was used as a susceptible check variety and VBN 4 blackgram genotype as a resistant check variety after every five test entries. All the recommended agronomic practices were followed. Insecticidal spray was not given to the experimental field to spread the disease through allowing whitefly population. Disease incidence was recorded periodically and the percentage disease incidence was worked out as per Bashir *et al.,* (2005).

Statistical analysis of phenotypic data

Canonical variate analysis was used to compare the clustering pattern obtained by Mahalanobis D2 statistic. The mean value of phenotypic data was figured out and the canonical roots vectors were calculated to present the genotypes in the graphical form (Rao, 1952). The data were analysed through the statistical software package *Statistical Tool for Agricultural Research (STAR), Version: 2.0.1.*

Results and Discussions

Principal Component Analysis (PCA)

In canonical variate analysis the number of variables is reduced to linear functions called canonical vectors which accounts for most of the variation produced by these traits. The eigen values, percent variance, percent cumulative variance and factor loading of different traits calculated are given in table 1.

The first three vectors, with eigen values more than one accounted for 60.14 and the fourth vector accounts for 68.96 percent of the total variability produced by all the traits under investigation. Scree plot of the eigen values also confirmed this selection criteria (Fig. 1).

The first canonical vector (PC I) observed 30.75 percent of total variability. The variables single plant seed yield (0.824) followed by pod length (0.717), number of pods per plant and number of seeds per pod (0.686), number of clusters per plant (0.649), plant height (0.579) had recorded maximum positive contribution towards genetic divergence and hundred seed weight (0.481), number of pods per cluster (0.399), percentage of disease infection (0.282) and number of branches per plant (0.155) had recorded minimum positive contributions while the trait days to fifty percent flowering (-0.029) had low negative contribution towards genetic divergence. These similar results are reported earlier worker (Sridhar *et al.,* 2020).

Table 1: The Eigen value, percent variance and percent cumulative variance for eleven principal components (PCs) and factor loading between PCs and traits studied in blackgram.

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11
Eigenvalue	3.3828	1.9375	1.2961	0.9699	0.8849	0.7571	0.7093	0.4633	0.3591	0.1882	0.0519
Variability (%)	30.7530	17.6132	11.7826	8.8171	8.0441	6.8824	6.4484	4.2119	3.2650	1.7106	0.4718
Cumulative %	30.7530	48.3662	60.1488	68.9659	77.0100	83.8924	90.3408	94.5526	97.8176	99.5282	100.0000
Trait	**Factor loadings**										
DFF	-0.029	-0.219	0.549	-0.359	0.688	-0.183	-0.088	-0.022	0.077	-0.012	0.009
PH	0.579	-0.533	0.253	0.055	-0.042	0.083	0.162	0.475	-0.224	-0.068	-0.016
NBPP	0.155	0.487	0.375	0.652	0.269	0.056	0.111	-0.165	-0.240	0.002	0.007
NCPP	0.649	0.467	0.209	0.173	0.018	0.201	0.122	0.196	0.439	0.028	-0.001
NPPC	0.399	0.074	-0.551	-0.173	0.319	-0.059	0.625	-0.073	-0.033	-0.012	0.002
NPPP	0.686	0.581	-0.094	-0.281	0.035	-0.037	-0.239	0.017	-0.141	0.039	-0.153
PL	0.717	-0.551	-0.033	0.166	-0.021	-0.162	-0.054	-0.112	0.018	0.334	0.006
NSPP	0.686	-0.264	-0.166	0.295	-0.031	-0.491	-0.154	-0.102	0.115	-0.237	-0.013
100 SW	0.481	-0.538	0.021	-0.038	0.047	0.603	-0.063	-0.306	0.029	-0.109	-0.036
PDI	0.282	0.094	0.627	-0.306	-0.480	-0.176	0.336	-0.223	-0.022	-0.023	0.000
SPSY	0.824	0.368	-0.108	-0.255	-0.013	0.084	-0.240	0.001	-0.129	-0.024	0.163

The second vector (PC II) accounted for 17.61% of total variability. The traits number of pods per plant (0.581), number of branches per plant (0.487), number of clusters per plant (0.467), single plant seed yield (0.368) had maximum positive contributions and percentage of disease infection (0.094) and number of pods per cluster (0.074) had low positive contribution towards genetic divergence while the traits pod length (-0.551), hundred seed weight (-0.538), plant height (-0.533), number of seeds per pod (-0.264) and days to fifty percent flowering (-0.219) had recorded maximum contribution in negative direction towards genetic divergence.

The vector PC III accounted for 11.78% of total variability. The traits percentage of disease infections (0.627), days to fifty percent flowering (0.549), number of branches per plant (0.375), plant height (0.253), number of clusters per plant (0.209) and hundred seed weight (0.021) had positive contribution towards genetic divergence while the traits number of pods per cluster (-0.551), number of seeds per pod (-0.166), single plant seed yield (-0.108), number of pods per plant (-0.094) and pod length had recorded negative contribution similar results are reported by previous studies (Sridhar *et al.,* 2020).
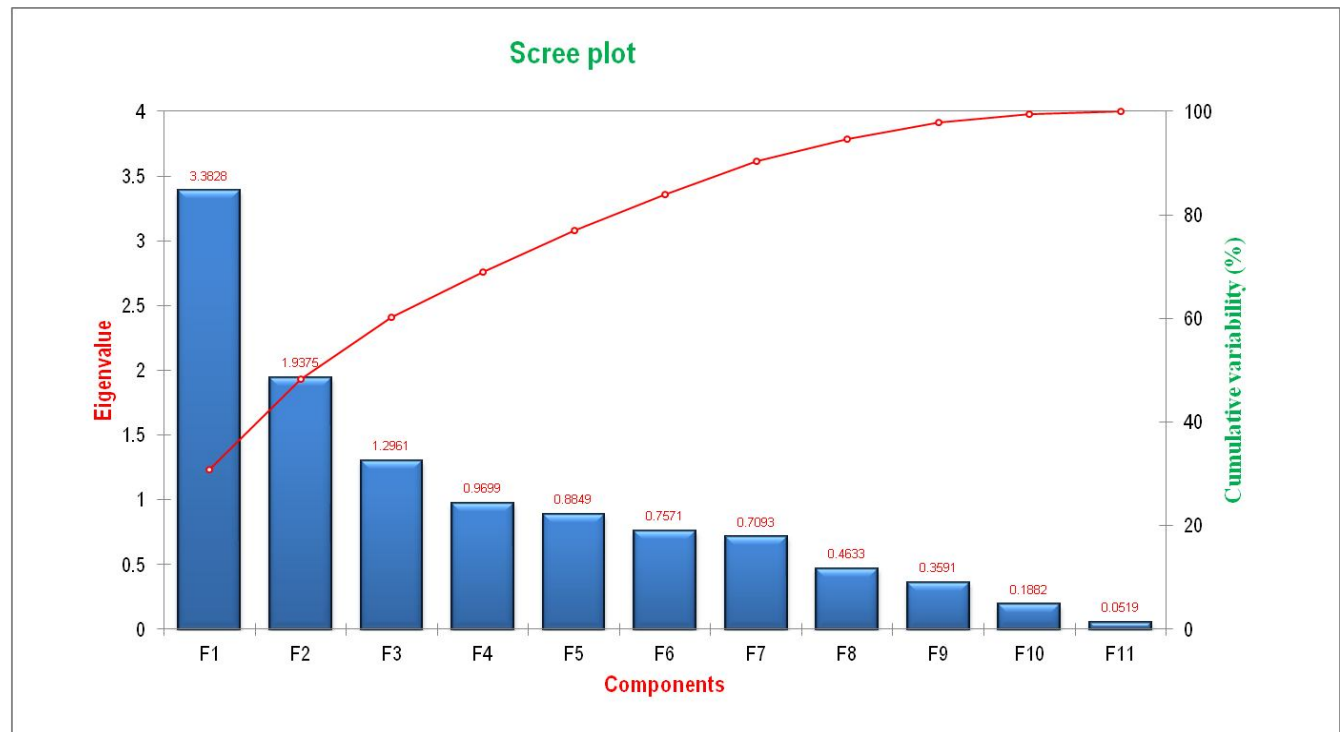

Fig. 1: Scree plot construction for eleven components.

Table 2: Factor loading scores of first three vectors in tow hundred and twelve genotypes.

S. No.	Genotype code	PCA I X Vector	PCA II Y Vector	PCA III Z Vector	S. No.	Genotype code	PCA I X Vector	PCA II Y Vector	PCA III Z Vector
1	Variety 1	4.131	6.370	-15.604	51	Variety 51	-12.216	5.841	11.069
2	Variety 2	-9.450	-2.802	-4.985	52	Variety 52	-6.166	-7.553	15.894
3	Variety 3	2.041	5.868	-1.138	53	Variety 53	8.452	17.044	1.411
4	Variety 4	-10.740	9.289	12.813	54	Variety 54	7.372	-1.562	16.158
5	Variety 5	3.500	19.809	5.858	55	Variety 55	4.951	10.985	13.507
6	Variety 6	1.840	22.271	6.831	56	Variety 56	-17.265	10.631	2.529
7	Variety 7	1.746	19.720	5.506	57	Variety 57	8.015	0.123	3.546
8	Variety 8	-10.407	16.598	4.702	58	Variety 58	11.416	-0.865	13.622
9	Variety 9	4.714	6.976	-5.968	59	Variety 59	3.503	13.578	0.835
10	Variety 10	7.780	5.341	6.202	60	Variety 60	9.603	17.053	0.294
11	Variety 11	5.041	18.699	17.834	61	Variety 61	1.819	19.589	0.840
12	Variety 12	1.636	10.977	10.191	62	Variety 62	-1.778	21.489	0.167
13	Variety 13	0.475	7.246	11.999	63	Variety 63	6.074	4.874	-0.512
14	Variety 14	-15.167	16.071	14.366	64	Variety 64	2.869	7.668	1.021
15	Variety 15	-10.256	18.136	16.563	65	Variety 65	1.982	-2.144	2.036
16	Variety 16	-9.761	21.561	0.584	66	Variety 66	-23.717	-7.813	7.250
17	Variety 17	-10.729	13.656	9.570	67	Variety 67	-1.764	12.737	-1.558
18	Variety 18	-1.767	2.084	9.280	68	Variety 68	-14.038	13.316	6.365
19	Variety 19	-7.917	5.741	8.618	69	Variety 69	4.366	29.272	-4.945
20	Variety 20	-7.824	16.634	14.214	70	Variety 70	-0.161	-1.096	2.784
21	Variety 21	-3.657	11.066	8.982	71	Variety 71	4.404	4.376	7.533
22	Variety 22	-1.379	23.289	4.412	72	Variety 72	-9.930	2.783	12.919
23	Variety 23	-8.387	-0.473	15.478	73	Variety 73	-11.515	13.653	7.692
24	Variety 24	-4.380	25.751	1.947	74	Variety 74	1.561	-0.410	1.265
25	Variety 25	-31.282	9.592	19.005	75	Variety 75	-20.289	7.719	13.728
26	Variety 26	-26.487	19.479	3.593	76	Variety 76	-39.675	25.217	12.864
27	Variety 27	7.676	20.007	12.250	77	Variety 77	-7.926	5.900	11.444
28	Variety 28	-9.546	1.511	25.306	78	Variety 78	-4.523	4.932	14.929
29	Variety 29	3.186	10.792	6.867	79	Variety 79	-18.256	9.544	15.430
30	Variety 30	-0.999	4.354	11.754	80	Variety 80	-9.451	4.074	5.604
31	Variety 31	-1.913	17.066	17.310	81	Variety 81	-15.644	28.606	2.363
32	Variety 32	-12.644	25.172	19.032	82	Variety 82	-16.678	12.200	5.942
33	Variety 33	2.745	-5.110	19.918	83	Variety 83	-33.499	42.384	11.922
34	Variety 34	-6.680	10.614	17.306	84	Variety 84	-4.010	29.369	3.770
35	Variety 35	-10.521	19.702	13.695	85	Variety 85	-6.435	31.572	-5.801
36	Variety 36	-30.936	28.241	6.964	86	Variety 86	-13.554	-7.623	17.973
37	Variety 37	-7.673	16.173	4.195	87	Variety 87	1.208	-4.446	12.431
38	Variety 38	-15.212	16.005	10.586	88	Variety 88	5.128	8.764	5.791
39	Variety 39	-17.121	12.629	11.021	89	Variety 89	-2.070	8.144	8.479
40	Variety 40	-15.103	22.212	1.899	90	Variety 90	-17.144	20.492	-0.122
41	Variety 41	-12.858	8.372	18.782	91	Variety 91	-16.776	21.510	16.993
42	Variety 42	-7.248	15.811	6.829	92	Variety 92	3.235	17.806	-2.678
43	Variety 43	-7.322	25.061	13.253	93	Variety 93	3.983	13.502	9.065
44	Variety 44	3.956	4.184	11.581	94	Variety 94	-7.291	22.018	-4.663
45	Variety 45	10.675	17.804	7.765	95	Variety 95	-1.840	-4.966	5.584
46	Variety 46	1.364	6.883	9.962	96	Variety 96	-7.959	6.001	9.195
47	Variety 47	0.849	9.262	16.442	97	Variety 97	-16.094	33.116	-10.457
48	Variety 48	-15.659	27.841	11.857	98	Variety 98	0.869	11.169	-9.016
49	Variety 49	5.786	7.229	6.279	99	Variety 99	-19.977	26.995	-0.906
50	Variety 50	-5.992	19.383	5.444	100	Variety 100	-61.195	22.590	13.055

Continue Table 2 ...

Table 2 Continue ...

101	Variety 101	-15.465	18.598	4.448	157	Variety 157	-22.057	3.746	6.486
102	Variety 102	0.904	21.452	0.043	158	Variety 158	-0.370	5.072	1.112
103	Variety 103	1.752	12.353	9.015	159	Variety 159	-7.917	2.709	-5.119
104	Variety 104	-14.727	-10.069	15.144	160	Variety 160	-5.689	7.820	-6.007
105	Variety 105	-16.589	-11.272	7.501	161	Variety 161	-5.752	2.692	3.419
106	Variety 106	10.974	11.712	12.169	162	Variety 162	-9.658	1.428	2.169
107	Variety 107	1.591	7.377	8.177	163	Variety 163	-10.585	11.149	-5.479
108	Variety 108	-14.574	13.469	7.507	164	Variety 164	-13.445	0.292	5.368
109	Variety 109	-4.180	16.371	12.044	165	Variety 165	1.693	11.922	6.811
110	Variety 110	3.089	14.694	7.237	166	Variety 166	-0.871	0.576	2.867
111	Variety 111	1.431	3.311	25.474	167	Variety 167	-49.011	13.505	12.392
112	Variety 112	-1.389	5.222	4.736	168	Variety 168	-25.327	3.582	2.848
113	Variety 113	-1.330	3.947	12.741	169	Variety 169	2.801	5.951	-4.102
114	Variety 114	7.117	24.886	0.337	170	Variety 170	-2.416	-18.793	11.473
115	Variety 115	-21.775	-1.599	5.671	171	Variety 171	7.454	-0.656	0.766
116	Variety 116	-15.971	8.765	4.246	172	Variety 172	14.408	4.991	2.253
117	Variety 117	9.538	16.897	2.750	173	Variety 173	6.889	2.455	2.454
118	Variety 118	-16.289	-1.413	21.237	174	Variety 174	9.570	8.503	19.998
119	Variety 119	-0.306	21.522	-3.035	175	Variety 175	-8.672	10.924	-1.080
120	Variety 120	-9.205	12.418	1.610	176	Variety 176	-13.814	11.440	1.551
121	Variety 121	1.633	28.673	9.093	177	Variety 177	5.549	4.462	1.416
122	Variety 122	-1.007	6.692	2.395	178	Variety 178	-12.915	5.146	1.887
123	Variety 123	4.418	9.952	11.656	179	Variety 179	-0.842	13.209	5.494
124	Variety 124	-14.897	14.227	5.303	180	Variety 180	4.955	4.701	-0.658
125	Variety 125	-0.451	-3.931	6.130	181	Variety 181	0.857	10.964	-0.036
126	Variety 126	-1.087	23.933	0.861	182	Variety 182	10.603	13.624	-4.888
127	Variety 127	-5.951	7.657	-1.723	183	Variety 183	-1.199	10.382	9.568
128	Variety 128	2.458	16.106	-9.148	184	Variety 184	4.669	4.228	10.826
129	Variety 129	-7.372	12.771	2.983	185	Variety 185	-3.635	14.473	23.451
130	Variety 130	5.576	5.242	-7.752	186	Variety 186	6.748	4.943	-4.031
131	Variety 131	9.754	7.464	-12.457	187	Variety 187	7.553	16.938	1.149
132	Variety 132	6.675	16.518	-0.287	188	Variety 188	-4.208	15.946	2.978
133	Variety 133	-4.580	11.373	10.202	189	Variety 189	-1.650	10.334	4.325
134	Variety 134	8.212	13.344	1.555	190	Variety 190	-0.222	18.131	-4.177
135	Variety 135	-2.029	20.614	-8.705	191	Variety 191	2.322	2.248	7.715
136	Variety 136	4.368	18.190	-3.478	192	Variety 192	-6.614	17.029	-1.237
137	Variety 137	15.951	11.518	-1.905	193	Variety 193	-1.699	6.943	5.902
138	Variety 138	-0.613	19.189	-5.993	194	Variety 194	4.746	31.535	-9.516
139	Variety 139	9.148	19.259	1.784	195	Variety 195	8.955	12.546	-0.911
140	Variety 140	-11.821	-3.896	9.173	196	Variety 196	10.162	22.795	0.663
141	Variety 141	8.470	8.553	-11.464	197	Variety 197	-4.902	-13.706	5.168
142	Variety 142	-3.022	23.645	-14.033	198	Variety 198	1.474	4.509	5.766
143	Variety 143	5.477	1.317	1.391	199	Variety 199	1.360	15.971	-2.117
144	Variety 144	-1.196	-7.010	13.887	200	Variety 200	-7.834	14.062	-15.004
145	Variety 145	-3.939	-2.226	9.301	201	Variety 201	-2.068	13.047	0.264
146	Variety 146	-15.857	5.622	9.693	202	Variety 202	-6.281	1.104	-7.472
147	Variety 147	-10.860	5.104	6.217	203	Variety 203	-6.852	7.053	5.541
148	Variety 148	-1.740	0.036	2.911	204	Variety 204	7.947	15.481	-5.209
149	Variety 149	-13.534	8.972	16.516	205	Variety 205	4.079	3.413	7.070
150	Variety 150	-8.102	0.709	1.692	206	Variety 206	7.889	-3.203	2.073
151	Variety 151	3.353	2.020	0.099	207	Variety 207	4.716	19.981	-12.557
152	Variety 152	3.069	-1.897	1.870	208	Variety 208	-39.054	-2.492	19.457
153	Variety 153	-6.293	9.665	1.879	209	Variety 209	3.375	3.644	-4.608
154	Variety 154	-3.116	-5.028	8.067	210	Variety 210	-12.272	-2.358	-4.574
155	Variety 155	0.514	6.598	1.188	211	Variety 211	6.646	0.948	3.273
156	Variety 156	-14.045	-6.023	11.743	212	Variety 212	3.407	7.200	-0.452

The vector PC IV accounted for 8.81% of total variability. The variables number of branches per plant (0.652), number of seeds per pod (0.295), number of clusters per plant (0.173), pod length (0.166) and plant height (0.055) had recorded positive contribution while the variables days to fifty percent flowering (-0.359), percentage of disease infection (-0.306), number of pods per plant (-0.281), single plant seed yield (-0.255), number of pods per cluster (-0.173) and hundred seed weight (-0.038) had recorded minimum negative contributions towards genetics divergence.

Canonical graph and genetic distance

The principal factor scores of the canonical vectors for the first three roots PC I (X), PC II (Y) and PC III (Z) are presented in the table 2. The mean scores of first two canonical vectors were used to obtain graphical depiction of genetic distance for 212 genotypes. Using this scores, all the genotypes plotted in PC I and PC II which cumulatively explained 48.36% variability. On the contrary the first four canonical vectors contributed only 68.96% towards genetic divergence because of which discernible overlapping was observed in group constellations of canonical vectors.

Characters contribution

The principal component analysis sorted out the total characters into four main principal components. The contribution of the main characters for variance easily identified by the characters loaded on the PC I as it explained maximum variance. In D2 analysis, the traits *viz.,* percentage of disease infection (32.44%), number of pods per cluster (23.56%), number of pods per plant (19.38%) and number of clusters per plant (16.42%)
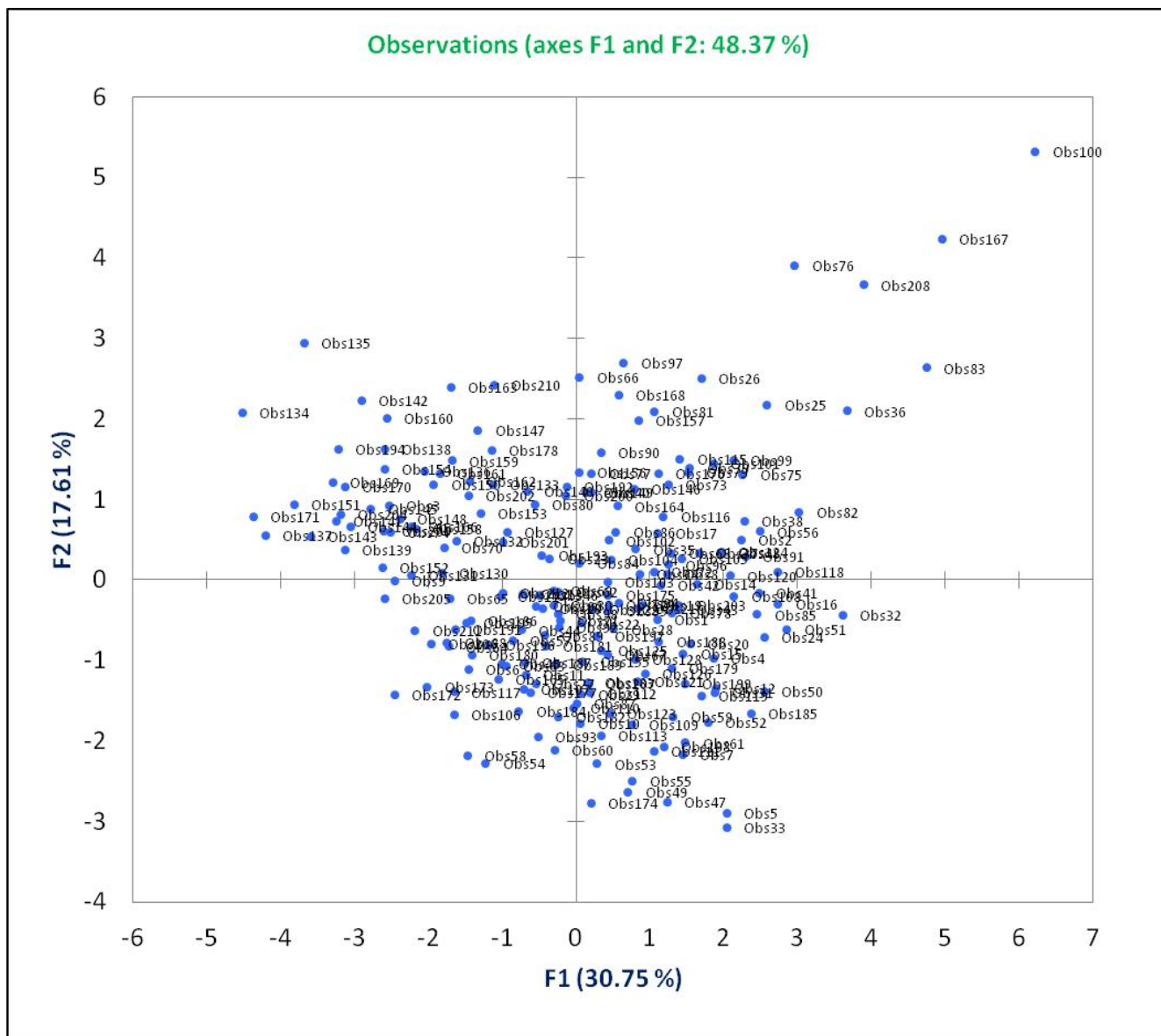

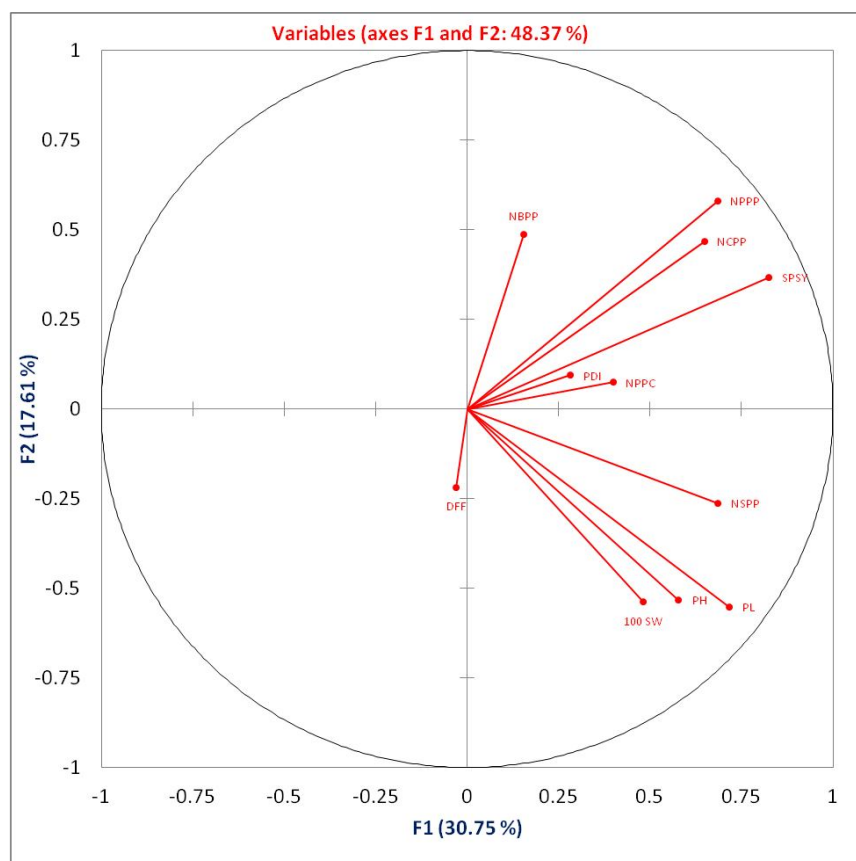**Fig. 2:** Biplot of Distribution of genotypes across first two (PC-1 and PC-2) components.

Fig. 3: Distribution of various traits across two components.

The PCA biplot (Gower and Hand, 1996), represents the variables with observations and calibrated axes as points allowing to predict the annotations onto the axis to construct an estimation of the original values of the variables. In the vector view of the biplot (Fig. 2), the vector has drawn from a biplot origin to every sign of the character to facilitate illustrating of the associations among and between the characters. If the biplot explain a proper amount of the total variation, the correlation coefficient between any two traits are positively correlated if the angle is<90°, negatively correlated if the angle is >90° and independent of each other if the angle is =90°. Major correlation predictions can be confirmed from the original data but some are not reliable with the data. Such discrepancies occurs as the biplot usually explains less than 100% rather than 100% of the variation. Characters with longer vectors are high responsive to the genotypes; Characters with shorter vectors are low responsive to the lines and those represent at the biplot origin is not responsive at all (Divayabharathi, 2019).

contributed towards divergence. In PCA, the traits *viz.,* single plant seed yield, pod length, number of pods per plant and number of seeds per pod, number of clusters per plant, plant height had recorded maximum positive contribution towards genetic divergence and hundred seed weight, number of pods per cluster and percentage of disease infection (PC I), number of pods per plant, number of branches per plant, number of clusters per plant (PC II), in PC III, percentage of disease infections, days to fifty percent flowering, number of branches per plant, plant height and number of clusters per plant, in PC IV, number of branches per plant and number of seeds per pod had maximum contribution towards genetic divergence early studies also reported the similar results (Ajay Kumar Singh *at al.,* 2010).

Clustering of genotypes

The plot of PC I and PC II accounting for 48.36% total variation showed clear consistency of grouping of diverse blackgram genotypes as in D2 statistic. Genotypes belonging to the common clusters have dropped nearer to each other and vice versa. In spite of this in many instances the D2 clustering did not confirm with the PCA.

Biplot analysis of PC and its contribution with character association.

Among the two hundred and twelve genotypes, single plant seed yield was highly positively correlated with number of cluster per plant and number of pods per plant indicating that higher the values of these two characters, more will be the seed yield. It was also positively correlated with number of pods per cluster and percentage of disease infection and number of seeds per plant. However, single plant seed yield was negatively correlated (obtuse angle) with number of branches per plant and days to fifty percent flowering. The traits plant height, pod length and hundred seed weight had low negative correlations. The single plant seed yield was highly positively correlated with number of clusters per plant and number of pods per plant. The sharing out of genotypes based on PC I and PC II exhibit the phenotypic variation among the genotypes and its illustrates how they extensively distributed along the both axes (Fig. 3).

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