Research Article

Multivariate Analysis in Blackgram (*Vigna Mungo* (L.) Based on Quantitative Traits

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Abstract

An experiment was conducted to investigate the association and genetic diversity among one hundred blackgram germplasm lines using canonical (vector) analysis for thirteen yield and yield attributing traits during kharif 2015. Analysis of variance revealed significant differences among germplasm lines. The first six principal components having Eigen values more than 1 and contributed 79.80 towards variability among one hundred genotypes. The Ist principal component had contribution from the traits *viz.*, SPAD, days to 50% flowering and leaf area which was accounted 28.92% to the total variability. The remaining variability of 15.71%, 11.11%, 8.95%, 8.21% and 6.89% were accounted by second, third, fourth, fifth and sixth principal components respectively by various traits. The three PCA scores for one hundred genotypes were plotted in graph to get two dimensional and three dimensional scattered diagrams which revealed the diversity among the genotypes to exploit in crop improvement programmes for generating transgressive segregants.

Keywords: Genetic divergence, Mahalanobis D^2 statistics, Principal component analysis, Blackgram

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Introduction

Among the pulse crops, blackgram is an important pulse crop and grown over wide range of agro climatic zones of the country. The major cultivated states *viz*., Maharashtra, Andhra Pradesh, Madhya Pradesh, Uttar Pradesh, Tamilnadu, Karnataka and Rajasthan. Blackgram could be grown in inter cropping systems as a mixed crop, catch crop, sequential crop besides growing sole crop under residual moisture condition under rice fallows and also preceding and succeeding harvest of summer crops with semi irrigated or dry land situations. The urudbean grain are highly nutritious with protein (25-26%), carbohydrates (60%), fat (1.5%) and good source of minerals, amino acids and vitamins. Like other pulses, it also enhances the soil physio-chemical and biological soil health.

The major constraints in achieving higher productivity are lack of exploitable genetic variability, absence of suitable ideotypes, low harvest index and narrow genetic base due to repeated usage of parents in hybridization programmes [1]. Several biometrical approaches have been shown to be useful in selecting parents for successful hybridization programme. Multivariate statistical tools like Principal component analysis (PCA) cluster analysis and discriminate analysis are found to be most effective and widely used for classification of parental lines. Mahalanobis D^2 statistics is powerful tool for quantify the degree of divergence at phenotypic level. PCA is helpful in identification of plant character that categorizes the divergence among the genotypes. In view of above, one hundred blackgram genotypes were evaluated by PCA to identify genetically diverse parents and to identify the traits that contribute to variability in the population.

Material and Methods

The experiment was laid in augmented completely randomized block design II during kharif 2015 at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, India. The soils of the farm are deep black in nature about 6-7’ depth with good soil moisture retentive capacity with a pH of 7.4, E.C 0.6 m. mhos/cm. a total of one hundred genotypes were collected from different parts of the country was utilized for present study. Each genotype was sown in with a spacing of 30 x 10cm. All recommended agronomic practices and plant protection measures were taken to grow a healthy and good crop. The observations were recorded from five randomly selected plants of each genotype for thirteen quantitative characters *viz*., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seed per pod, 100 seed weight, leaf area, chlorophyll content, SPAD and seed yield per plant. The mean data was subjected to statistical analysis using principal component analysis (PCA).

Results and Discussion

The analysis of variance showed significant difference among the genotypes with respect to all the traits under study and indicating the presence of considerable magnitude of genetic variability among the genotypes (**Table 1**). Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating several significant principal components having eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by [2]. Results of PCA and cluster analysis are discussed hereunder.

Principal component with respect to Eigen values (latent root), per cent variability, cumulative per cent variability and component loading of different characters are presented in **Table 2**. In the present study, the first six principal components with Eigen value more than one contributed 79.80% towards the total variability. In field pea more than 89% variability contributed by Ist four components [3]. It was therefore inferred that the essential features of data set had been represented the first six principal components.

Table 1 Augmented RBD analysis of variance for seed yield and yield component characters in blackgram (*Vigna mungo* L.)

	d.f	Days to 50% flowering	Plant height (cm)	No. of branches/ plant	No. of clusters / plant	No. of pods / plant	Pod length (cm)	No. of seeds / pod	100 seed weight (g)	Days to maturity	Leaf area (cm²)	SPAD	Chlorophyll content (mg/g)	Seed yield/ plant (g)
Entries	103	2.31**	250.13**	0.25	8.24**	82.69**	0.15*	0.44*	0.26**	35.91**	59488.71**	45.80**	0.16**	8.43**
Varieties	99	1.08	255.60**	0.23	7.88**	59.06**	0.08	0.23	0.21**	20.67**	58804.16**	43.96**	0.16**	6.40**
Block	4	6.64**	2226.25**	0.32	30.58**	293.94**	0.24*	0.22	1.57**	163.70**	364207.91**	62.90**	0.30**	44.42**
Checks	3	1.93	19.92*	0.29	3.18**	8.55*	0.11	1.21**	0.10	3.87	19031.27**	7.84*	0.00	1.27**
Error	12	0.64	5.21	0.14	0.26	1.98	0.06	0.14	0.05	1.37	1637.74	1.65	0.00	0.07

** Significant at 1% level; * Significant at 5% level; d.f : degrees of freedom

Table 2 Eigen values, proportion of the total variance represented by first six principal components, cumulative per cent variance and component loading of different characters in blackgram (*Vigna mungo* L.)

	PC_1	PC_2	PC_3	PC_4	PC_5	PC_6
Eigen Value (Root)	3.76	2.04	1.44	1.16	1.07	0.90
% Var. Exp.	28.92	15.71	11.11	8.95	8.21	6.89
Cum. Var. Exp.	28.92	44.63	55.74	64.69	72.91	79.80
Days to 50% flowering	0.06	0.48	0.28	0.32	0.06	0.28
Plant height (cm)	-0.38	-0.10	0.13	-0.32	-0.08	-0.30
No. of branches / plant	-0.11	-0.50	0.28	-0.12	-0.08	0.15
No. of clusters / plant	-0.41	0.08	-0.36	0.12	-0.03	0.10
No. of pods / plant	-0.45	0.06	-0.28	0.14	0.02	0.10
Pod length(cm)	-0.17	-0.04	0.10	-0.24	0.76	0.24
No. of seeds/ pod	-0.20	-0.19	0.28	0.52	0.15	0.27
100 Seed weight(g)	-0.31	0.30	0.18	-0.26	0.06	-0.38
Days to maturity	-0.24	0.05	0.43	0.08	-0.54	0.08
Leaf area (cm²)	0.05	0.58	0.09	0.00	0.05	-0.13
SPAD	0.09	-0.14	-0.40	0.40	-0.01	-0.36
Chlorophyl1 content (mg/g)	-0.02	-0.14	0.36	0.40	0.29	-0.60
Seed yield /plant (g)	-0.49	0.04	-0.12	0.15	-0.02	0.01

The first principal component (PC_1) contributed maximum towards the variability (28.92%). The characters *viz.*, SPAD (0.09), days to 50% flowering (0.06) and leaf area (0.05) were loaded positively, while seed yield per plant (-0.49), number of pods per plant (-0.45), number of clusters per plant (-0.41), plant height (-0.38), 100 seed weight (-0.31), days to maturity (-0.24), number of seeds per pod (-0.20), pod length (-0.17), number of branches per plant (-0.11) and chlorophyll content (-0.02) were negatively loaded.

The second principal component (PC_2) described 15.71 % variability of total variance and it reflected through the positive loading of the characters *viz.*, leaf area (0.58), days to 50% flowering (0.48), 100 seed weight (0.30), number

of clusters per plant (0.08), number of pods per plant (0.06), days to maturity (0.05) and seed yield per plant (0.04) and negative loading of number of branches per plant (-0.50), number of seeds per pod (-0.19), SPAD (-0.14), chlorophyll content (-0.14), plant height (-0.10) and pod length (-0.04). Similar finding were also reported by [1]

The third principal component (PC_3) was characterised by 11.11% contribution towards the total variability through the characters viz., days to maturity (0.43), chlorophyll content (0.36), days to 50% flowering (0.28), number of branches per plant (0.28), number of seeds per pod (0.28), 100 seed weight (0.18), plant height (0.13), pod length (0.10) and leaf area (0.09) were positively loaded while, SPAD (-0.40), number of clusters per plant (-0.36), number of pods per plant (-0.28) and seed yield per plant (-0.12) were negatively loaded.

The fourth principal component (PC_4) was conspicuously characterised by 8.95% contributed to the total variance and observed high positive loading values from number of seeds per pod (0.52), SPAD (0.40), chlorophyll content (0.40), days to 50% flowering (0.32), seed yield per plant (0.15), number of pods per plant (0.14), number of clusters per plant (0.12) and days to maturity (0.08) and negative loading values from plant height (-0.32), 100 seed weight (-0.26), pod length (-0.24) and number of branches per plant (-0.12).

The fifth principal component (PC_5) describes 8.21 % of total variance and the characters viz., pod length (0.76), chlorophyll content (0.29), number of seeds per pod (0.15), days to 50% flowering (0.06), 100 seed weight (0.06), leaf area (0.05) and number of pods per plant (0.02) were positively loaded. While, days to maturity (-0.54), plant height (-0.08), number of branches per plant (-0.08), number of clusters per plant (-0.03), seed yield per plant (-0.02) and SPAD (-0.01) were negatively loaded [4].

The sixth principal component (PC_6) was characterised by 6.89% contribution towards the total variability through the characters, days to 50% flowering (0.28), number of seeds per plant (0.27), pod length (0.24), number of branches per plant (0.15), number of clusters per plant (0.10), number of pods per plant (0.10), days to maturity (0.08) and seed yield per plant (0.01) were positively loaded and the characters chlorophyll content (-0.60), 100 seed weight (-0.38), SPAD (-0.36), plant height (-0.30) and leaf area (-0.13) were negatively loaded. These results are in agreement with [5].

Conclusion

The PCA scores of one hundred genotypes for the first three principal components computed and considered as three axes, x, y, z and squared distances of each genotype from these three axes were calculated and presented in **Table 3**. It is important to study variance as the relative contribution than the signs (indicative of directions) in PCA. The three PCA scores for one hundred genotypes were plotted in graph to get two dimensional and three-dimensional scattered diagrams (**Figures 1** and **2**) which revealed the diversity among the genotypes to exploit in crop improvement programmes for generating transgressive segregants.

Table 3 PCA scores of divergences in 100 blackgram (*Vigna mungo* L.) genotypes

Genotype	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5	Vector 6
TU 68	-7.72	315.30	5.68	40.94	21.90	-70.63
RU-44	-7.58	289.19	14.34	33.93	19.69	-65.61
VBG04-005	-4.00	295.13	11.41	36.33	21.42	-64.24
UH 2289	-12.98	234.50	16.92	34.05	7.56	-53.62
KU 1006	-4.97	291.90	15.14	34.68	17.55	-63.82
AKU10-4	-8.68	302.56	21.26	27.96	22.56	-63.23
LBG 726	12.83	478.93	11.11	31.79	53.35	-102.66
PU 212	-17.84	146.31	20.23	33.82	-5.90	-33.71
OBG 35	-7.51	225.58	19.29	35.29	6.17	-49.85
UH07-06	-5.77	282.28	12.06	38.10	15.60	-64.49
P 205	-6.46	273.30	10.59	39.02	15.91	-62.33
PU 30	-11.98	278.68	7.86	39.45	15.92	-62.22
PGRU3-38	-7.68	217.10	21.63	34.59	5.54	-47.21
U 150	-15.01	162.55	21.53	35.06	-4.62	-37.22
KPU 26	-1.94	296.76	19.09	31.91	21.70	-64.13
LBG 771	-4.13	318.17	19.37	30.73	24.60	-68.84
RVSU11-8	-13.11	177.95	21.17	36.36	-3.29	-40.52
COBG 1045	-21.60	408.72	6.15	28.08	39.13	-96.07
KPU 67-08	-9.01	427.87	9.66	25.75	44.45	-95.75
IPU 2-43	-35.60	252.15	14.84	27.66	9.63	-67.17
PLU 710	-9.87	391.39	10.31	29.21	37.54	-89.17

Genotype	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5	Vector 6
UH 85-5	-18.67	332.94	7.17	35.41	24.66	-77.01
IPU 10-4	-28.71	254.22	16.59	27.22	11.63	-61.27
LBG 710	-32.96	203.28	18.23	29.53	0.80	-49.55
UPU 88-86	-33.83	250.35	16.43	26.44	9.58	-57.83
TBG 104	-50.93	169.94	20.29	23.46	-6.26	-49.30
LBG 765	-28.27	218.47	19.59	28.31	5.34	-51.69
KU 323	-43.56	159.58	27.87	19.42	-6.82	-46.43
LBG 785	-43.18	174.08	28.86	15.56	-2.81	-54.33
LBG 758	-26.75	276.26	27.28	16.70	16.28	-72.43
GKU 02-1	-24.67	318.98	24.69	17.93	21.68	-82.34
LBG 20	-47.19	222.70	23.21	24.27	-0.69	-58.87
LBG 766	-21.11	279.34	20.82	30.72	12.22	-66.23
P 1053	-28.17	420.75	18.80	20.28	38.14	-101.62
P 710	-39.59	244.07	26.65	21.40	5.08	-67.58
P 705	-27.38	366.72	18.49	23.03	28.99	-89.76
P 728	-32.57	335.73	18.52	22.58	21.85	-82.97
LBG 746	-36.32	223.58	24.30	25.38	-0.41	-58.67
LBG 726	-33.21	302.67	24.33	21.57	14.31	-75.71
P 1060	-26.31	308.86	21.92	23.41	16.52	-82.82
P 112	-41.91	224.36	31.01	16.50	1.81	-63.42
UH 07-13	-48.15	221.71	32.67	11.02	1.49	-70.21
PLU 2146	-44.15	211.68	29.90	18.27	-1.56	-57.17
P 1070	-43.62	260.28	21.17	25.19	5.81	-66.90
PU 31	-50.52	175.11	27.16	22.27	-8.05	-47.37
LBG 752	-69.41	137.94	25.29	20.11	-17.27	-41.36
CN 8072	-27.40	290.12	20.71	25.96	13.82	-66.36
LBG 780	-23.03	250.75	18.01	33.09	6.47	-58.20
LBG 786	-34.85	152.94	23.01	34.55	-14.10	-33.79
PBG 32	-24.46	144.72	37.67	23.48	-12.05	-36.55
ACM 05-007	-19.80	273.08	21.06	31.95	11.23	-62.28
UTTARA	-26.94	235.72	22.80	30.88	3.30	-55.22
NDU12-300	-7.09	392.13	10.52	36.28	31.20	-91.02
KKBU-5011	-6.24	418.53	24.06	24.01	37.51	-96.47
LBG 747	-2.80	419.43	10.48	35.96	37.58	-93.43
LBG 787	-40.72	187.78	21.29	30.68	-7.94	-47.10
UG 708	-23.43	239.61	23.82	23.89	7.86	-58.17
PGRU 99058	-31.57	138.93	27.77	26.11	-10.77	-25.97
TU10-3	-32.56	169.98	26.32	24.76	-4.41	-40.97
NUL 388	-19.69	262.74	25.24	25.11	10.56	-60.24
VBG 10-014	-9.82	288.42	21.65	31.31	13.64	-69.81
P 1032	-21.27	230.98	21.92	32.30	3.10	-53.38
KU 708	-14.24	325.79	18.58	31.61	19.96	-72.83
CPS 35	-17.20	296.05	20.30	32.65	13.37	-68.89
P 726	-30.49	164.79	20.27	33.90	-9.53	-42.42
NDUK 20	-6.82	362.71	8.62	34.33	30.53	-84.35
TU 136	-29.29	198.57	23.33	24.45	1.11	-53.04
T9	-42.43	157.50	23.43	28.77	-11.38	-38.65
SMS 131	-13.80	349.43	10.87	37.71	24.40	-76.51
SPS 26	-17.32	429.19	8.27	33.39	35.86	-102.22
LBG 770	-12.12	470.92	3.27	36.24	44.73	-109.27
LBG 784	5.47	494.93	11.33	33.67	50.38	-115.23
LBG 788	-27.04	239.06	28.38	22.82	6.48	-56.31
LBG 797	-21.53	274.43	24.58	31.66	7.30	-65.54
LBG 623	-4.25	416.03	13.17	31.64	36.38	-96.88
LBG 782	-11.92	354.29	14.21	33.79	26.17	-83.03

Genotype	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5	Vector 6
LBG 798	-9.90	336.94	25.95	24.72	23.08	-80.65
LBG 783	-25.39	182.89	27.65	27.83	-5.56	-43.62
LBG 767	5.58	500.39	8.00	31.38	57.88	-113.42
LBG 772	13.59	603.33	1.95	34.15	75.51	-135.96
LBG 794	-23.70	257.44	20.25	30.96	8.04	-60.46
LBG 801	-18.64	365.29	19.38	24.46	28.57	-89.28
LBG 791	-7.22	385.64	16.73	27.55	36.12	-86.28
LBG 795	8.14	528.60	7.50	34.21	59.41	-119.24
LBG 802	16.17	612.05	-3.20	35.19	78.49	-139.84
LBG 799	-19.52	370.02	8.09	34.04	28.94	-85.22
LBG 812	-9.34	401.63	10.15	32.16	37.47	-93.27
LBG 805	-9.84	362.06	11.61	34.35	28.94	-83.29
MBG 207	69.09	1039.62	-21.93	35.88	157.55	-233.75
LBG 806	-10.71	356.92	14.17	27.03	30.86	-84.13
LBG 823	-12.54	396.50	7.50	31.63	37.25	-89.52
LBG 808	1.81	498.78	-0.57	32.57	58.10	-113.22
LBG 815	-23.58	370.85	2.15	35.52	29.15	-81.64
WBG 26	-7.34	391.31	12.20	33.36	33.51	-83.72
LBG 818	-9.40	371.43	7.10	30.88	33.87	-85.30
LBG 822	5.63	479.73	4.80	36.07	52.45	-104.40
LBG 798	-11.54	363.33	9.05	33.21	29.90	-79.73
LBG 753	20.25	660.92	-10.16	38.85	86.85	-147.36
LBG 777	-3.98	461.15	4.77	35.25	45.43	-101.71
TU94-2	40.53	775.01	-7.81	35.14	109.94	-177.51

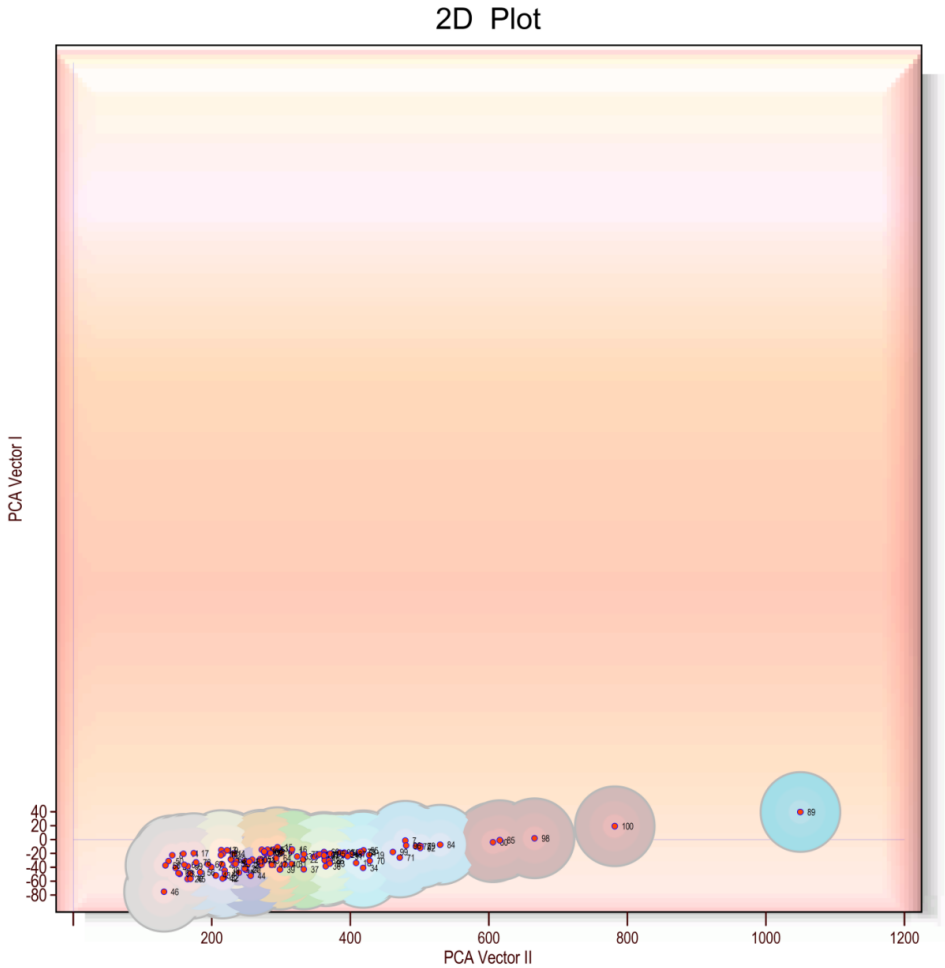

Figure 1 Two dimensional graph showing relative position of 100 blackgram genotypes based on PCA scores

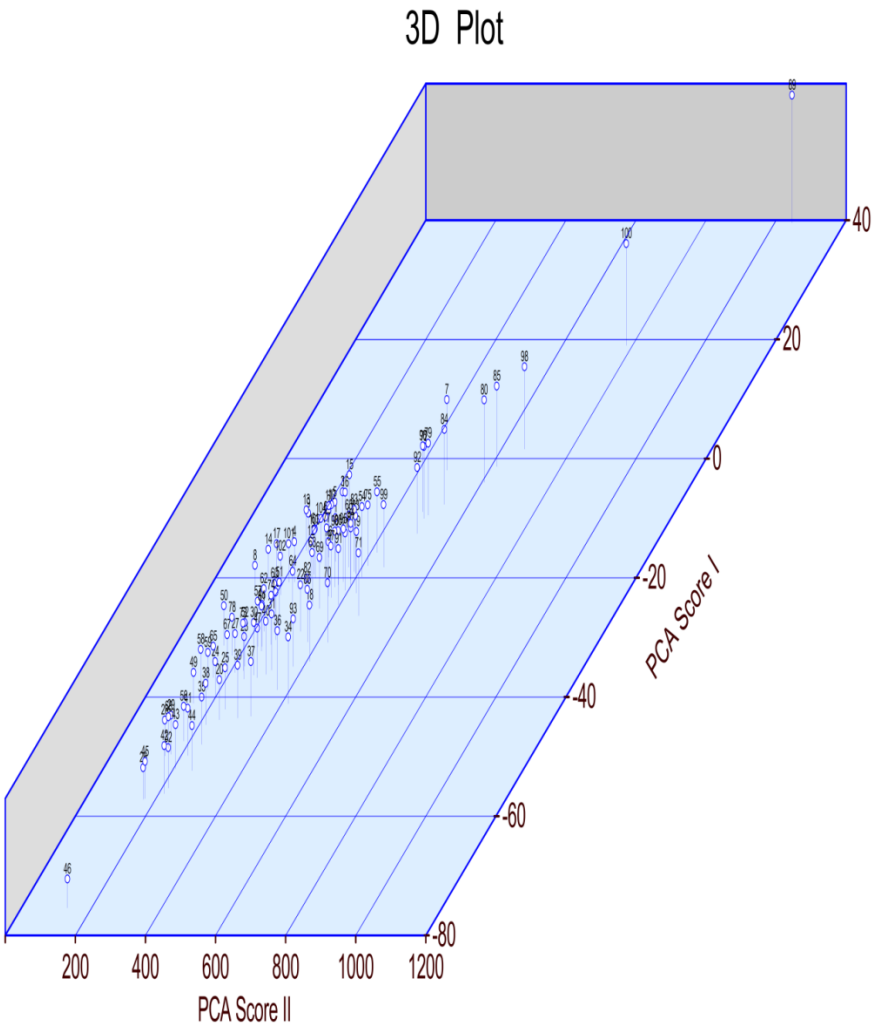

Figure 2 Three dimensional graph showing relative position of 100 blackgram genotypes based on PCA scores

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