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Genetic divergence, variability and character association in landraces of blackgram (*Vigna Mungo* [L.] Hepper) from Odisha.

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ABSTRACT

Beside rich biodiversity, Odisha is having a potential source of indigenous gene pool of several crops. In Odisha land races of blackgram are sources of valuable genes which provide tolerance to various biotic and abiotic stresses, hence characterization and evaluation of such local germplasm may provides useful materials for breeding of good varieties. A throughout knowledge of existing genetic variation and degree of association among yield and yield contributing traits are essential for developing high yielding genotypes in blackgram. In this present investigation yield plant^{-1} contributed maximum towards divergence. The genotypes belonging to different clusters are havingshowed maximum divergence for different characters and may be successfully utilized in hybridization programmes to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters with wide inter cluster distance.

***Keywords*:** Correlation coefficient, divergence, D^2 analysis, path coefficient and lL, races

Blackgram or urdbean (*Vigna mungo* [L.] Hepper) is an important grain legume with easily digestible protein and low flatulence contents. It is highly prized pulse, rich in phosphoric acid. Grain of Black gram grain contains about 25% protein, 56% carbohydrate, 2% fat, 4% minerals and 0.4% vitamins. Urd is said to have originated in India where it is most widely grown and highly esteemed grain legume (Chatterjee and Bhattacharya, 1986). According to Vavilov (1926), blackgram has originated from Indian subcontinent. The present productivity levels of black gram in India are very low. Efforts to genetically improve the crop are still at low ebb. Further, it has been the least studied crop among the pulses and no international system under the CGIAR has this as a mandate crop (Ghafoor *et al*., 2000). The proper estimate of nature and magnitude of diversity in a crop is essential to infer about extent of variation available for yield and its component traits. The selection of highly genetically divergent parents is expected to throw superior and desirable segregants following crossing (Bhatt, 1973).

Odisha is a province situated in the eastern cost of India. Apart from rich biodiversity Odisha is a rich source of indigenous gene pool of several crops. It is believed to be the secondary centre of origin of rice. Apart from rice Odisha is also the land of the rich diversity of wild land races of pulses. Local land races of blackgram are valuable genes that provide tolerance to various biotic and abiotic stresses,stresses; hence characterization and evaluation of such local germplasm provides useful materials for breeding of good varieties. A throughout knowledge of existing genetic variation and degree of association between yield and yield contributing traits are essential for developing high yielding genotypes in blackgram. The limitations with the currently used germplasm in Odisha is the lack of knowledge on genetic base, poor yield, with low genetic diversity and vulnerability to a wide array of insect pest and diseases under monoculture. Assessment of divergence or similarity among the genotypes would help in identification of genotypes that may be used in cross breeding programme for producing transgressive segregants. Limited systematic breeding programmes for breeding superior have been taken up for developments of high yielding genotypes in blackgram. have been initiated. Vast scope lies for genetic improvement of blackgram through genetic diversity study done to understand the diversity in different landraces for assessment and creation of diverse line for further breeding. Hence a study on genetic divergence in land races of blackgram from Odisha was taken up with the view of selecting parents for hybridization programme.

MATERIALS AND METHODS

The experimental materials for the present investigation comprised of 19 genotypes of blackgram (18 land races) including one promising check. The

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experiment was conducted in Randomized Block Design, with 3 replications. Each entry was represented by 5 rows of 2.8 meter length with a spacing of 30 cm x l0 cm. A fertilizer dose of 20:40:20 kg NPK ha^{-1} was applied and need based plant protection measures were followed at Experimental Block-II of Department of Plant Breeding & Genetics, OUAT during *Rabi*, 2011-12.The mean values of three replications were used for statistical analysis. The observations were recorded on ten quantitative traits *viz,* days to 50% flowering, days to maturity, plant height, number of primary branches $plant^{-1}$, number of cluster $plant^{-1,}$ number of pods $plant^{-1}$, number of seeds $plant^{-1}$, pod length, 100 seed weight and yield $plant^{-1}$. Correlation coefficients were calculated for all character combinations at phenotypic and genotypic level by the formula given by Miller *et al*. (1958). The direct and indirect contribution of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Assessment of genetic divergence was done using Mahalanobis D^2 (Mahalanobis, 1936) statistic and the genotypes were grouped into different clusters following Tocher's method as described by Rao (1952). Average intra and inter cluster distances were determined using GENRES version 3.11, 1994 Pascal Intl. Software as suggested by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

The analysis of variance (Table 1) showed significant differences among the genotypes with respect to all the characters (except for number of primary branches $plant^{-1}$) and indicated high genetic variability. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters, however, large difference was observed between PCV and GCV for character *viz.,* number of primary branches $plant^{-1}$ indicating the influence of the environment in the expression of these characters (Table 2). High GCV was shown by number of primary branches $plant^{-1}$, number of clusters $plant^{-1}$, number of pods $plant^{-1}$ and yield $plant^{-1}$. Improvement could be possible through selection in these traits. Characters like 100 seed weight, pod length and plant height exhibited moderate GCV value where as low GCV value was recorded with characters like days to 50% flowering, days to maturity and seed pod^{-1}. The results are in agreement with the findings of Paramshivan and Rajashekharan (1980), Ramakrishna and Jairaj (1981), Shah and Patel (1981), Mishra (1983) and Thimmappa (1983).

The quantitative characters are governed by many genes and are more influenced by environment. The phenotype observed is not transmitted entirely to next generation. Therefore, it is necessary to know the proportion of observed variability that is heritable. Heritability estimates provides the assessment of amount of transmissible genetic variability to total variability, happens to be the most important basic component that determines the genetic improvement or response to selection. However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder. High magnitude of heritability was obtained for most of the characters except for number of primary branches/plant and number of seeds pod^{-1} (Table 2). High heritability estimate was recorded by characters *viz.,* plant height (84.00%), number of clusters $plant^{-1}$ (83.77%), number of pods $plant^{-1}$ (84.14%) and yield $plant^{-1}$ (84.88%)). However rest of the characters exhibited moderate to low heritability.

High heritability along with high genetic advance as per cent of mean (GAM) was recorded by yield $plant^{-1}$ (60.66), number of clusters $plant^{-1}$ (48.20) and number of pods $plant^{-1}$ (52.11) which revealed that selection could be effective for these characters. Genetic advance as percentage of mean is more reliable index for understanding the effectiveness of selection in improving the traits because it's estimatesed value is derived by involvement of heritability, phenotypic standard deviation and intensity of selection (Sinha and wagh, 2013). Thus genetic advance as percentage of mean along with heritability provides clear picture regarding theinfluences positively the effectiveness of selection for improving the plant characters. Estimation of heritability along with genetic gain is usually more useful in predicting the resultant effect from selecting the best individual. Mean performances of all the yield attributing characters were presented in table 3. The genotypic and phenotypic correlations among different yield attributing characters in black gram genotypes were presented in table 4. The correlation coefficient estimates, the degree and direction of association between a pair of characters and help simultaneouslywere proved useful for simustaneous improvement of the correlated traits through selection. Majority of the yield contributing traits showed significant association with yield $plant^{-1}$ except except for plant height and days to 50% flowering which implies for higher yield in case of land races for higher

Table 1: Analysis of variance (mean squares) for various biometrical traits

Source		Mean Squares									
	df	Days to 50% flowering	Days to maturity	Plant height (cm.)	Number of primary branches plant^{-1}	Number of clusters plant^{-1}	Number of pods plant^{-1}	Number of seeds pod^{-1}	Pod length (cm)	100 seed weight(g)	Yield plant^{-1} (g)
Replication	2	9.3055	0.0822	0.9802	0.2610	0.6484	1.3304	0.5394	0.0164	0.0179	0.0432
Genotype	18	29.8278**	50.1458**	22.2485**	0.3345	4.1309**	35.2845**	0.9260**	0.6784**	0.8194**	3.0347**
Error	36	3.1917	4.1838	1.3283	0.1115	0.2507	2.0855	0.1510	0.0518	0.0570	0.1701

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

Table 2: Variability and genetic parameters for different characters of blackgram genotypes

Character	Range	Mean	LSD (0.05)	Variance			GCV	PCV	h_{bs}^2 (in %)	GA(%) of mean
				GV	PV	EV				
Days to 50% flowering	32.960 – 47.600	38.387	2.959	8.879	12.070	3.192	7.7624	9.0507	73.56	13.7143
Days to maturity	72.587 – 93.727	87.313	3.387	15.321	19.504	4.184	4.4829	5.0581	78.55	8.1846
Plant height (cm)	15.903 – 25.737	20.934	1.909	6.973	8.302	1.328	12.6147	13.7638	84.00	23.8168
Number of primary branches plant^{-1}	0.803 - 2.123	1.191	0.553	0.074	0.186	0.112	22.8993	36.2086	40.00	29.8332
Number of clusters plant^{-1}	2.657 – 7.187	4.448	0.829	1.293	1.544	0.251	25.5672	27.9349	83.77	48.2044
Number of pods plant^{-1}	8.390 – 20.347	12.061	2.392	11.066	13.152	2.085	27.5818	30.0687	84.14	52.1194
Number of seeds pod^{-1}	4.703 – 6.880	5.499	0.644	0.258	0.409	0.151	9.2426	11.6342	63.11	15.1257
Pod length (cm)	3.483 – 5.093	4.205	0.377	0.209	0.261	0.052	10.8694	12.1436	80.12	20.0415
100 seed weight (gm)	3.083 – 5.317	3.797	0.395	0.254	0.311	0.057	13.2755	14.6898	81.67	24.7146
Yield plant^{-1} (gm)	2.147 – 5.840	3.057	0.683	0.955	1.125	0.170	31.9636	34.6932	84.88	60.6644

Coefficient of variation (CV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance (GA), genotypic variance(GV), phenotypic variance (PV), environmental variance (EV.)

Table 3: Mean performances of yield attributing characters of genotypes of blackgram

Serial number	Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of cluster plant^{-1}	No. of pod plant^{-1}	No. of Seeds pod^{-1}	Pod length (cm)	100 seed weight (gm)	Yield plant^{-1} (in gm)
1	*Badamba local*	37.000	85.167	17.610	**2.123**	6.227	12.010	5.070	4.453	4.097	3.373
2	*Bilipara local*	35.500	87.087	***15.903***	1.620	4.607	12.017	5.210	3.760	3.670	2.850
3	*Sheragarh local*	36.667	88.200	18.083	1.260	4.560	12.140	5.740	4.623	3.673	2.770
4	*Cheripali local*	36.333	87.333	22.027	1.087	5.443	15.393	5.447	3.670	4.090	3.523
5	*Khedapada local*	39.500	87.520	**25.737**	1.373	4.215	13.390	6.493	4.200	3.594	2.933
6	*Mahimunda local*	39.500	90.250	23.657	0.833	3.770	10.270	4.807	3.763	3.494	2.467
7	*Nayagarh local-b*	39.167	90.367	18.870	1.033	5.113	12.047	5.360	4.043	3.241	2.813
8	*Dayapali local*	39.000	88.233	22.490	1.069	4.770	13.120	5.370	3.927	4.157	2.847
9	*Sudhasarangi local*	**47.600**	**93.727**	23.147	0.863	**2.657**	9.033	5.067	3.963	**3.083**	**2.147**
10	*Deogaon local*	40.167	87.320	21.800	0.810	4.800	12.240	5.613	4.413	3.619	2.918
11	*Banapur local*	37.250	85.583	21.869	1.150	4.613	9.310	5.707	4.330	3.604	2.487
12	*Kantapada local*	39.500	88.313	18.053	**0.803**	3.507	**8.390**	**4.703**	**3.483**	3.133	2.180
13	*Kendrapara local*	40.333	90.000	23.443	1.100	3.300	9.557	5.690	4.237	3.519	2.673
14	*Pendibadi local*	34.833	87.713	19.553	1.207	*3.184*	8.143	5.910	4.170	3.892	2.345
15	*Kalahandi local*	38.333	89.000	18.487	1.077	3.940	10.997	5.150	5.057	3.434	2.452
16	*Bhawanipatna local*	36.333	85.950	24.737	1.217	3.497	10.963	6.047	3.927	4.041	2.973
17	*Bolangir local*	**32.960**	86.187	19.290	0.923	3.207	9.623	5.193	3.773	3.991	2.878
18	*B-3-8-8 (check)*	37.037	*72.587*	22.887	1.54	**5.92**	**20.347**	5.03	**5.093**	4.5	5.617
19	*Keonjhar local*	42.333	88.417	20.107	1.533	**7.187**	20.167	**6.880**	5.000	**5.317**	**5.840**
	Mean	**38.387**	**87.313**	**20.934**	**1.191**	**4.448**	**12.061**	**5.499**	**4.205**	**3.797**	**3.057**
	SEm(±)	**1.459**	**1.670**	**0.941**	**0.273**	**0.409**	**1.179**	**0.317**	**0.186**	**0.195**	**0.337**
	LSD (0.05)	**2.959**	**3.387**	**1.909**	**0.553**	**0.829**	**2.392**	**0.644**	**0.377**	**0.395**	**0.683**

Maximum and minimum values of each character are printed in bold and italics, respectively

Table 4: Genotypic (G) and phenotypic (P) correlation among different yield attributing characters in blackgram genotypes

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of clusters plant^{-1}	No. of pod plant^{-1}	No. of Seeds pod^{-1}	Pod length (cm)	100 seed weight (g)	Yield plant^{-1} (g)
Days to 50% flowering	G	1.000	0.523	0.373	-0.303	-0.061	0.068	0.048	0.120	-0.244	0.019
	P	1.000	0.374	0.285	-0.212	-0.011	0.027	0.079	0.071	-0.137	-0.025
Days to maturity	G		1.000	-0.059	-0.545**	-0.451*	-0.584**	0.096	-0.465*	-0.527*	-0.658**
	P		1.000	-0.053	-0.351	-0.379	-0.518*	0.043	-0.330	-0.405*	-0.560**
Plant height (cm)	G			1.000	-0.380	-0.206	0.135	0.304	-0.039	0.037	0.086
	P			1.000	-0.169	-0.187	0.083	0.283	-0.058	0.042	0.037
No. of primary branches plant^{-1}	G				1.000	0.821**	0.579**	0.347	0.582**	0.650**	0.661**
	P				1.000	0.418*	0.329	0.133	0.254	0.405	0.356
No. of clusters plant^{-1}	G					1.000	0.888**	0.305	0.537**	0.766**	0.850**
	P					1.000	0.720**	0.240	0.449*	0.586**	0.692**
No of pods plant^{-1}	G						1.000	0.391*	0.598**	0.845**	0.958**
	P						1.000	0.272	0.471*	0.644**	0.911**
No. of seeds pod^{-1}	G							1.000	0.383	0.561**	0.393*
	P							1.000	0.268	0.424*	0.317
Pod length (cm)	G								1.000	0.481*	0.615**
	P								1.000	0.390*	0.524*
100 seed weight (g)	G									1.000	0.934**
	P									1.000	0.741**
Yield plant^{-1} (g)	G										1.000
	P										1.000

*,**= *Significant at 5% and 1% levels respectively*

Table 5: Path coefficient analysis for blackgram genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of clusters plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Pod length (cm)	100 seed weight (g)	Genotypic yield correlation
Days to 50% flowering	**0.31898**	-0.04139	-0.03135	-0.14876	0.04404	0.05809	-0.00934	-0.01284	-0.15858	0.019
Days to maturity	0.16675	**-0.07917**	0.00493	-0.26797	0.32581	-0.49606	-0.01874	0.04967	-0.34321	-0.658**
Plant height (cm)	0.11891	0.00465	**-0.08410**	-0.18668	0.14882	0.11498	-0.05956	0.00419	0.02439	0.086
No. of primary branches plant^{-1}	-0.09650	0.04315	0.03193	**0.49172**	-0.59368	0.49137	-0.06786	-0.06220	0.42296	0.661**
No. of clusters plant^{-1}	-0.01944	0.03569	0.01732	0.40390	**-0.72276**	0.75395	-0.05959	-0.05736	0.49849	0.850**
No. of pods plant^{-1}	0.02183	0.04627	-0.01139	0.28464	-0.64196	**0.84884**	-0.07646	-0.06386	0.55044	0.958**
No. of seeds pod^{-1}	0.01522	-0.00758	-0.02560	0.17055	-0.22013	0.33172	**-0.19566**	-0.04098	0.36547	0.393
Pod length (cm)	0.03832	0.03679	0.00330	0.28616	-0.38790	0.50719	-0.07503	**-0.10688**	0.31313	0.615**
100 seed weight (g)	-0.07769	0.04173	-0.00315	0.31942	-0.55335	0.71760	-0.10983	-0.05140	**0.65110**	0.934**

*Residual effect = 0.201, *, **= Significant at 5% and 1% levels respectively*,

Table 7: Clustering of blackgram genotypes using Tocher's method

Cluster	Genotypes	Number of genotypes
I	*Badamba local, bilipara local, sheragarh local, cheripali local, khedapada local, mahimunda local, nayagarh local-b, dayapali local*	8
II	*Deogaon local, banapur local*	2
III	*Pendibadi local, bolangir local*	2
IV	*Sudhasarangi local, kantapada local, kendrapara local, kalahandi local, bhawanipatna local*	5
V	*B-3-8-8 (check)*	1
VI	*Keonjhar local*	1

Table 8: Average intra (diagonal) and inter-cluster distance

Cluster	I	II	III	IV	V	VI
I	**7.624**	6.180	8.284	9.521	15.428	16.899
II		**3.546**	6.565	7.281	14.974	17.697
III			**3.949**	8.471	18.200	20.834
IV				**8.630**	19.191	21.574
V					**0.000**	12.027
VI						**0.000**

** figures given the diagonal are intra cluster distance*

Table 9: Cluster wise mean values of ten characters in blackgram

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of clusters plant^{-1}	No. of pods plant^{-1}	No. of Seeds pod^{-1}	Pod length (cm)	100 seed weight (g)	Yield plant^{-1} (g)
I	37.833	88.020	20.547	1.300	4.838	12.548	5.437	4.055	3.752	2.947
II	38.708	86.452	21.830	0.980	4.707	10.775	5.660	4.372	3.611	2.702
III	33.897	86.950	*19.422*	1.065	*3.195*	8.883	5.552	*3.972*	3.941	2.611
IV	40.420	**89.398**	21.573	1.012	3.380	9.788	5.331	4.133	*3.442*	*2.485*
V	37.037	*72.587*	**22.887**	**1.540**	5.920	**20.347**	*5.030*	**5.093**	4.500	5.617
VI	**42.333**	88.417	20.107	1.533	**7.187**	20.167	**6.880**	5.000	**5.317**	**5.840**

Maximum and minimum values of each character are printed in bold and italics, respectively

Table 6: Value of D^2 for combinations of 19 genotypes of blackgram

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.000	51.100	48.554	57.033	110.053	132.830	64.979	58.325	278.758	66.016	66.142	171.428	131.881	104.304	90.730	97.632	101.908	156.713	185.648
2		0.000	24.868	75.352	107.084	88.050	27.588	63.459	195.796	61.202	46.158	62.614	89.301	35.020	60.187	76.897	35.402	311.530	353.869
3			0.000	71.294	56.433	75.133	20.938	45.004	164.081	25.300	22.639	87.804	56.507	30.064	16.361	54.411	52.544	254.196	298.936
4				0.000	60.088	77.955	60.878	11.949	240.648	46.046	66.671	164.711	106.250	111.753	123.377	49.226	85.342	160.752	184.403
5					0.000	44.399	50.411	31.019	118.375	19.122	34.800	133.190	31.746	81.274	66.730	23.942	101.778	226.586	286.805
6						0.000	36.428	39.904	59.904	28.514	33.408	48.658	15.134	62.236	68.246	30.259	57.363	313.988	418.056
7							0.000	36.603	104.724	18.881	24.417	49.690	36.788	44.858	34.244	52.954	55.891	297.651	332.487
8								0.000	160.586	16.940	34.889	117.487	55.828	74.037	73.652	25.008	64.191	182.703	224.409
9									0.000	107.766	122.577	79.037	46.126	143.343	114.438	136.199	175.952	527.988	615.377
10										0.000	12.574	84.356	24.255	52.257	30.966	24.764	62.178	206.321	278.149
11											0.000	62.657	23.949	23.014	29.593	19.282	34.950	242.093	348.199
12												0.000	53.988	46.860	78.462	94.029	49.367	471.729	590.151
13													0.000	43.745	41.706	28.654	63.875	321.817	413.178
14														0.000	40.932	40.733	15.592	349.851	440.290
14															0.000	72.154	74.579	295.337	385.060
16																0.000	38.257	224.507	323.320
17																	0.000	312.663	427.809
18																		0.000	144.638
19																			0.000

1. Badamba local; 2. Bilipara local;3. Sheragarh local; 4. Cheripali local; 5. Khedapada local; 6. Mahimunda local 7. .nayagarh local-b; 8. Dayapali local ; 9. Sudhasarangi local; 10. Deogaon local; 11. Banapur local; 12.kantapada local; 13. Kendrapada local; 14. Pendibadi local; 15.kalahandi local; 16. Bhawanipatna local; 17. Bolangir local; 18. B-3-8-8(check); 19. Keonjhar local

yield early flowering and plant height of the plant are not playing any sorts of pivotal rolefailed to play any pivotal role. Similar findings were reported by Choi *et al.* (1986), Damodaran *et al.* (1989), Varma (1992) *et al.* Naidu and Rosaiah (1993) and Rao (1995).

A path coefficient is simply a standardized partial-regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effects (Dewey and Lu, 1959). The path coefficient analysis was used to partition the correlation coefficients of all the component characters studied with yield plant^{-1}, into direct and indirect effects. The results of various causes influencing yield plant^{-1} (direct and indirect effect) are shown in Table 5. The path coefficient analysis of different traits contributing towards yield plant^{-1} revealed that positive direct effect was exhibited by days to 50% flowering, number of primary branches plant^{-1}, number of pods plant^{-1} and 100 seed weight, while days maturity, plant height, number of clusters plant^{-1}, number of seeds pod^{-1} and pod length expressed negative direct effect on yield plant^{-1}. The result of negative direct effect indicated that these characters had low association and selection based on these characters would not be effective.

Table 10: Percent contribution of different characters towards diversity in blackgram genotype

Names of characters	No. of time ranked 1st	Percent contribution
Days to 50% flowering	6	3.5088
Days to maturity	2	1.1696
Plant height (cm)	13	7.6023
Primary branches plant^{-1}	4	2.3392
No. of cluster plant^{-1}	20	11.6959
Pod plant^{-1}	15	8.7719
Seed pod^{-1}	4	2.3392
Pod length (cm)	10	5.8480
100 seed weight (gm)	34	19.8830
Yield plant $^{-1}$ (gm)	63	36.8421
Total		**100**

The D^2 values for all comparisons between pairs of genotypes are calculated (Table 6). On the basis of divergence 19 genotypes under investigation have been grouped into six distinct clusters (Table 7), indicating wide diversity in the experimental materials for majority of the characters. Distance between all pairs of genotypes was calculated using squared Euclidean distance method and the genotypes were clustered based on Tocher's method. Cluster I had maximum 8 genotypes (8) followed by cluster IV with 5 where as cluster II and III were digenotypic. Cluster V and VI had solitary genotype. The pattern of clustering proved the existences of significant amount of variability. It is obvious that the genotypes have grouped into different cluster irrespective of their geographical origins. It means that the genetic constitution of the varieties was more important than their origin and distribution (Rai *et al*., 2009). The divergence within the cluster indicates the divergence among the genotypes in the same cluster. On the other hand inter cluster divergence suggests the distance (divergence) between the genotypes of different clusters. Inter and intra cluster D^2 values were worked out from divergence analysis. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relation.

The lower D^2 value between their characters suggested that the genetic constituents of these genotypes in one cluster were in close proximity with those genotypes in other cluster. Similar result was reported earlier by *Gadakh et.al.* (2013).

The composition of cluster and values of inter and intra cluster distances are given in Table 8 and Fig.1. The inter cluster distance were greater than the intra cluster distance revealing that significant amount of diversity existed among the accession. The intra cluster distance ranged from 0.000 to 8.630 and the inter cluster distance ranged from 6.180 to 21.574 indicating that the land races were divergent (Table 8). The cluster V and VI had only one entry each so the intra cluster distance in these cases were nullified. The minimum intra cluster distance was recorded in cluster II (3.546) followed by cluster III (3.949). Cluster IV had highest (8.630) intra cluster distance. The genotypes within the cluster were less divergent. The maximum inter cluster distance was observed between cluster IV and VI (21.574) followed by cluster III and VI (20.834). The inter cluster distance between cluster VI with rest of the cluster were more, suggesting that the land race Keonjhar Local belonging to this cluster may be used as a parent for further hybridization programme to develop desirable type because divergent parents results in transgressive segregants. Least inter cluster distance was recorded between cluster I and II (6.180) followed by clusters II and III (6.565).

The cluster mean values were estimated over genotypes for ten yield attributing characters in black gram related to yield, which revealed that a wide range of variation (Table 9). Minimum days to 50% flowering was observed in genotype of cluster III followed by cluster V. A maximum day to 50% flowering was recorded in cluster VI. Earliest maturing entries were belonged to cluster V followed by cluster II. Genotypes requiring maximum time to mature belonged to cluster IV. Highest mean value for plant height was recorded with cluster V. Cluster III had lowest mean value for plant height. Number of primary branches plant^{-1} was more with the genotypes of cluster V. The maximum number of cluster plant^{-1} was observed in cluster VI. Similarly genotype belonged to cluster V had maximum pod plant^{-1} and pod length. Highest mean values for number of seeds pod^{-1}, 100 seed weight and yield plant^{-1} were more in genotype ofrecorded in cluster VI. The characters contributing maximum divergence needs greater emphasis for deciding on the clusters for the purpose of selection of parents in the respective cluster for hybridization. The number of times each of the yield component characters appeared first in rank and its respective percent contribution towards genetic divergence was presented in Table 10. Among the yield attributing traits the maximum contribution towards divergence was made by yield plant^{-1} (36.84%) followed by 100 seed weight (19.88%) (Table 10) and number of clusters plant^{-1} (11.69%). Genotypes belonging to different clusters having high means for desired characters and with maximum divergence may be successfully used in hybridization programmes.

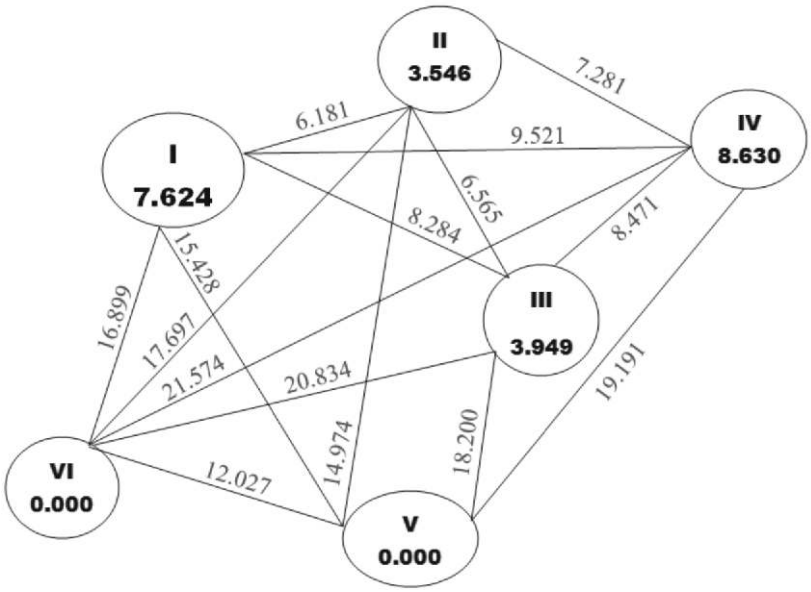

Fig. 1: Mahalanobis Distance Cluster Diagram (Not to scale)

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