Genetic Diversity Studies on Important Panicle Traits in Rice (*Oryza sativa* L.)

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An investigation was carried out at Tamilnadu Rice Research Institute, Aduthurai during *Thaladi* 2009 with 125 advanced breeding lines of 23 rice cross combinations to study the nature and magnitude of genetic divergence through mahalanobis D^2 statistics. Observations were recorded on important panicle traits *viz.,* panicle length, number of filled grains per panicle, panicle exertion and 100 grain weight. The breeding lines were grouped into 42 clusters. The cluster I contained highest number of genotypes (40) followed by cluster II, XXXXI, and XXXXII which had three genotypes each, the remaining 39 clusters had two genotypes each. The intra cluster distance was highest in cluster XXXXII (14.59), followed by cluster XXXXI (14.28) and cluster II (14.12). It was the lowest (0.66) in cluster III. Highest inter cluster distance was noticed between clusters XXXX and XXXV (30.35), followed by clusters XXXX and XXX (30.30), cluster XXXX and XXVIII (30.05) and lowest between clusters XIII and IV (2.04). Hundred grain weight contributes 57.67 per cent and panicle exertion contributes 19.60 per cent to the total genetic divergence. From this study it was concluded that sufficient amount of variability was observed among the breeding lines developed in the crosses *viz.,* ADT 43/ Tapaswini, ADT 46 (R)/ IET 17917, ADT 39/ AD 02202, ADT 39/ Kalinga, ASD 19/ T 317 which may be used as parents to produce highly heterotic and superior transgressive segregants upon hybridization for important panicle traits.

Key words: Genetic diversity, D^2 statistics, panicle traits, rice.

Rice (*Oryza sativa* L.) is the principal staple cereal food crop for more than half of the world's population. It accounts for 35 to 75% of calories consumed by more than three billion Asians. Genetic improvement mainly depends upon the amount of genetic variability present in the population. In any crop, germplasm serves as a valuable source of base population and providing scope for wide variability. The more diverse the parents, the greater are the chances of obtaining higher amount of heterotic expression in F_1s and broad spectrum of variability in segregating generations (Joshi and Dhawan, 1966). The estimate of genetic divergence in the available germplasm is important for the selection of desirable donors for breeding programme. Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murthy and Arunachalam, 1996 and Rahman, 1997). The use of Mahalanobis D^2 statistics for estimating genetic divergence have been emphasized by many workers (Roy and Panwar, 1993; Ramya and Senthilkumar, 2008). Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme (Vivekananda and

Subramanian, 1993). Therefore the present investigation was taken up with the objective of studying genetic divergence among 125 advanced breeding lines (F_7 generation) of 23 rice cross combinations for important panicle traits.

Materials and Methods

The experimental materials consisted of 125 advanced breeding lines of twenty three rice cross combinations *viz.*, C0 43 / BPT 5204, C0 43 / TKM 11, C0 43 / Bansakthi, C0 43 / Swarna, IWP / BPT 5204, ADT 43 / Padmini, ADT 43 / Tapaswini, ADT 43 / Vanapraba, ADT 43 / AD 00203, ASD 19 / T 317, ASD 19 / AD 01168, ADT 46 / IET 17910, ADT 46 / IET 17941, ADT46 / Kalajoha, ADT 46 / IET 17917, ADT (R) 45 / Kalajoha, ADT (R) 45 / Tapaswini, IWP / Bansakthi, Triguna / IET 17920, ADT 39 / Kalinga, ADT 39 / AD 02202, ADT 39 / Triguna and ADT 39 / TKM 12. The advanced breeding lines (F_6 generation) were raised during season *Thaladi* 2009 at the south farm, plant breeding and genetics unit, Tamilnadu Rice Research Institute, Tamil Nadu Agricultural University, Aduthurai. The materials were replicated twice and all the recommended agronomical practices were followed. The genetic diversity among the 125 advanced breeding lines was analyzed with respect to four important panicle traits viz., panicle length, number of filled grains per

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Table 1. Clustering pattern of 125 advanced breeding lines of 23 rice cross combinations

Cluster number	Name of Genotypes	Number of genotypes
I	C0 43 / BPT 5204 2-3-3-1-3, :C0 43 / BPT 5204 2-3-3-1-6, C0 43 / BPT 5204 2-3-3-2-5, C0 43 / BPT 5204 2-3-3-3-4, C0 43 / BPT 5204 2-3-3-5-6, C0 43 / BPT 5204 19-2-1-3-1-1, C0 43 / BPT 5204 19-2-1-3-3-1, C0 43 / BPT 5204 19-2-1-3-5-11, C0 43 / BPT 5204 21-1-2-1-2, C0 43 / BPT 5204 21-2-2-1-2, C0 43 / TKM 11 1-1-2-1-3, C0 43 / TKM 11 1-1-2-1-5, C0 43 / TKM 11 1-1-2-1-9, C0 43 / TKM 11 1-1-2-1-10, C0 43 / TKM 11 1-1-2-1-11, C0 43 / Bansakthi 1-3-1-1, C0 43 / Swarna 7-3, IWP / BPT 5204 1-2-2-1-1, IWP / BPT 5204 2-2-2-2 IWP / BPT 5204 8-3-1-2-3-1, IWP / BPT 5204 8-3-1-2-4-1, IWP / BPT 5204 10-3-3-1-3, IWP / BPT 5204 10-3-3-2-3, IWP / BPT 5204 10-3-3-2-4, IWP / BPT 5204 14-2-1-2-1-1, IWP / BPT 5204 14-2-1-2 3-1, IWP / BPT 5204 14-2-1-2-3-5, IWP / BPT 5204 16-1-1-2-1-2, ADT 43 / Padmini 1-3-1-3-1-1, ADT 43 / Padmini 1-3-3-2-1, ADT 43 / Padmini 4-1-1-1-2-1-1, ADT 43 / Padmini 4-1-1-2-1-2, :ADT 43 / Padmini 4-1-1-1-2-1-3 ADT 43 / Padmini 1-5-2-4, ADT 43 / Padmini 12-1-1-2-4-1, ADT 43 / Padmini 9-3-1-3 2-2, ADT 43 / Tapasmini 2-2-1-2-1	40
II	ADT 43 / Tapasmini 2-2-1-2-1-3 , ADT (R) 45 / Tapasmini 2-2-2-2-1, ADT 39 / Triguna 10-1-1-2-3	3
III	ADT 39 / ADO 2202 6-1-1-1, ADT (R) 45 / Kalajoha 2-14-3-1-1	2
IV	ADT 46 / IET 17917 4-2-3-4, ADT 46 / IET 17917 4-2-3-5	2
V	ADT 46 / IET 17917 4-2-4-2, ADT (R) 45 / Kalajoha 9-2-4-4-2-2	2
VI	ADT 39 / ADO 2202 3-1-2-1, ADT 43 / Tapaswini 6-4-2-2-2-1	2
VII	ADT 43 / AD 00203 1-2-1-1, IWP / Bansakthi 1-2-1-2-1-1	2
VIII	ADT (R) 45 / Kalajoha 6-1-3-3-4, ADT 39 / Triguna 6-1-1-2	2
IX	ADT 39 / Triguna 10-2-1-1, ADT 39 / Triguna 10-2-1-2	2
X	Triguna / IET 17920 15-2-1-2-2-5, ASD 19 / AD 01168 10-1-3-1	2
XI	ADT (R) 45 / Tapaswini 2-2-2-2-3, ADT (R) 45 / Tapaswini 2-2-2-2-4	2
XII	ADT (R) 45 / Kalajoha 9-2-4-4-3-1, :ADT 46 / IET 17910 7-1-2-3-2	2
XIII	ADT 46 / IET 17917 4-2-3-1, ADT 46 / IET 17917 4-2-3-8	2
XIV	ADT (R) 45 / Kalajoha 4-2-4-4-1-3, ADT (R) 45 / Tapaswini 2-2-2-1-4	2
XV	ADT46 / Kalajoha 6-1-1-3-2-1, ADT 46 / IET 17941 18-2-1-2-1-2	2
XVI	ADT (R) 45 / Tapaswini 2-2-2-2-2, ADT 39 / ADO 2202 10-1-4-1	2
XVII	ADT (R) 45 / Tapaswini 2-2-2-1-2, ASD 19 / T 317 2-1-2-2-1	2
XVIII	ADT (R) 45 / Kalajoha 2-1-1-3-2-2, IWP / Bansakthi 1-5-2-2-2-1	2
XIX	ADT (R) 45 / Tapaswini 2-2-2-3-2, ADT 46 / IET 17917 4-2-3-2	2
XX	ADT (R) 45 / Kalajoha 9-2-4-4-3-3, ADT (R) 45 / Kalajoha 9-2-4-4-3-4	2
XXI	ADT 46 / IET 17910 7-1-3-3-4, ADT 46 / IET 17910 7-1-3-3-5	2
XXII	ADT 46 / IET 17941 2-1-1-2, ADT 39 / TKM 12 8-2-1	2
XXIII	ADT 39 / Triguna 10-1-1-2, ADT 43 / AD 00203 6-4-2-2-1-1	2
XXIV	IWP / Bansakthi 1-2-1-2-1-2, IWP / Bansakthi 1-2-1-2-3-2	2
XXV	ADT 46 / IET 17910 7-1-2-3-4, ADT 39 / TKM 12 8-1-1	2
XXVI	Triguna / IET 17920 9-3-4-3-2, ADT 46 / IET 17941 15-3-1-2-2-1	2
XXVII	Triguna / IET 17920 15-2-1-2-2-2, Triguna / IET 17920 15-2-1-2-2-4	2
XXVIII	ADT 39 / Kalinga 7-2-2-2-2-2, ASD 19 / T 317 2-1-2-3-2	2
XXIX	ASD 19 / T 317 2-1-2-1-1, ADT 46 / IET 17941 15-3-1-2-3-5	2
XXX	ADT 43 / Tapaswini 2-2-1-2-2-2, ADT 46 / IET 17917 4-2-4-1	2
XXXI	ADT 46 / IET 17941 18-2-1-2-1-3, ADT 46 / IET 17941 17-2-2-3-2-1	2
XXXII	ASD 19 / T 317 2-1-2-1-2, ASD 19 / T 317 2-1-2-2-1	2
XXXIII	ADT46 / Kalajoha 6-1-1-3-2-2, ADT 39 / TKM 12 8-1-2	22
XXXIV	ADT 46 / IET 17910 7-1-3-3-6, ADT 46 / IET 17941 18-3-2-3-6	2
XXXV	ADT 46 / IET 17917 8-2-2-1-2, ADT 39 / ADO 2202 3-3-2	2
XXXVI	ADT 39 / Triguna 10-1-1-1, ADT 43 / Tapaswini 6-4-2-2-1-2	2
XXXVII	ADT 46 / IET 17941 18-3-2-3-8, Triguna / IET 17920 9-3-4-2-2	2
XXXVIII	IWP / Bansakthi 1-5-2-2-4-1, ADT 46 / IET 17941 18-2-2-2-3	2
XXXIX	ADT 46 / IET 17941 18-3-2-3-2, ADT (R) 45 / Kalajoha 6-1-3-3-1-1	2
XXXX	ADT 43 / Tapaswini 2-2-1-2-2-1, ADT 43 /Tapaswini 6-4-2-2-1-1	2
XXXXI	ASD 19 / T 317 2-1-2-3-1, ADT (R) 45 / Kalajoha 2-1-1-3-2-1, ADT (R) 45 / Tapasmini 2-2-2-1-3	3
XXXXII	Triguna / IET 17920 8-1-2-2-1, ADT 39 / Kalinga 7-2-2-2-2-1, ADT 39 / ADO 2202 3-3-1	3

panicle, panicle exsertion and 100 grain weight. Observations were recorded on three randomly selected plants for each trait and the genetic distance between the individual breeding lines were worked out using Mahalanobis D^2 statistics and the grouping of genotypes was done following the Tocher's method as described by Rao (1952).

Results and Discussion

The analysis of variance revealed that the presence of significant amount of variability among

Table 2. Contribution of different characters to total genetic divergence

Character	Times ranked 1st	Per cent contribution
Panicle length	327	4.22
Number of filled grains per panicle	1436	18.53
Panicle exertion	1519	19.60
100 grain weight	4468	57.65

the breeding lines for all the characters studied. D^2 statistics was performed after ascertaining the presence of significant amount of variability among

Table 3. Mean intra and inter cluster distances among 42 clusters in rice

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX	XXI	XXII	XXIII
I	11.10	15.08	10.78	9.40	8.17	8.80	10.04	9.44	9.62	11.19	9.79	9.27	8.67	9.45	9.29	9.35	9.78	10.46	8.28	13.65	9.48	9.10	10.42
II		14.12	11.55	15.26	12.50	12.78	10.77	12.17	10.69	9.67	12.27	15.26	14.39	14.32	9.95	10.26	15.31	14.55	11.91	17.77	15.47	13.97	10.77
III			0.66	7.04	6.26	4.25	1.98	4.40	4.66	9.38	8.31	8.14	7.08	11.83	4.95	5.85	11.26	11.64	5.07	17.16	9.11	8.49	2.28
IV				0.80	4.41	3.57	6.70	5.31	6.52	11.27	9.07	3.80	2.03	9.56	7.81	8.09	8.10	10.46	2.14	15.43	5.00	4.88	7.12
V					1.15	3.41	5.01	3.34	3.89	7.92	7.44	5.05	3.01	6.27	4.90	4.26	7.60	9.08	2.67	13.49	4.41	4.58	5.64
VI						1.17	3.77	3.90	4.41	8.91	6.54	7.44	3.36	9.19	4.69	5.74	7.72	8.93	3.97	14.34	6.40	5.05	4.28
VII							1.20	3.59	2.98	7.72	7.56	4.85	6.33	10.44	3.60	4.44	10.26	10.75	3.76	16.05	8.34	7.32	1.57
VIII								1.31	3.51	9.11	9.20	6.56	4.77	8.58	5.42	3.99	10.48	11.62	3.34	16.33	5.28	7.01	4.31
IX									1.33	6.20	7.93	11.26	5.64	8.92	3.77	3.81	9.45	10.52	3.76	15.33	7.39	5.90	3.36
X										1.46	7.31	10.28	9.93	9.57	5.32	6.66	9.27	9.08	7.71	12.50	11.79	8.08	7.76
XI											1.77		8.25	9.98	5.11	8.03	5.69	4.00	6.46	9.58	11.17	7.17	7.73
XII												1.80	2.64	7.79	8.31	7.39	9.04	11.39	3.86	15.58	2.59	5.64	7.99
XIII													1.80	7.96	6.83	6.91	7.20	9.49	7.27	14.20	4.32	3.93	6.81
XIV														2.07	8.82	7.20	8.99	9.77	3.85	11.16	6.78	8.38	11.04
XV															2.15	3.91	8.35	8.15	3.95	13.06	8.98	6.69	3.94
XVI																2.16	10.23	10.43	7.74	14.44	7.29	7.84	5.07
XVII																	2.18	4.16	8.64	8.39	10.10	5.10	10.49
XVIII																		2.29	2.31	6.35	12.12	7.90	10.98
XIX																			2.31	13.44	5.73	5.26	4.63
XX																				2.31	15.73	12.53	16.34
XXI																					2.22	7.15	8.97
XXII																						2.46	7.56
XXIII																							2.66

the genotypes. Genotypes' clustering was performed with the critical D^2 value of 399.42. Based on the relative magnitude of D^2 values all the 125 advanced breeding lines were grouped into 42 clusters (Table 1). Maximum 40 breeding lines were grouped into Cluster I, followed by three genotypes each in clusters II, XXXXI and XXXXII. The remaining clusters from III to XXXX are having two genotypes each. Cluster I exhibited a genetic similarity within them. Since, among the 40 breeding lines in cluster I, 21 lines having BPT 5204 as common parent.

A perusal of results on cluster means (Table 4) for important panicle traits revealed that cluster XXXII characterized by genotypes with long panicle length (27.24 cm) and genotypes in cluster XXXI were characterized by higher number of filled grains per panicle (265.95). Panicle exertion (1.09) was poor in cluster VIII. Cluster XXXX were characterized by breeding lines with higher 100 grain weight (2.62 gm) but it was low in cluster XXX. Cluster XXX is characterized by advanced breeding lines with reduced panicle length (21.70 cm) and 100 grain weight (1.31 gm). A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. Interestingly, all the maximum and minimum cluster mean values were distributed in relatively different clusters. The similar results were reported by Bose and Pradhan (2005) and Monika et al (2008). There by understanding the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Hence, depending on the per se performance of the best genotypes within the clusters may be directly used as parents in future hybridization programme.

The inter cluster distance (Table 3) ranged from 1.57 to 30.24 between clusters VII and XXII and between clusters XXX and XXXX respectively. Inter cluster distance was observed to be maximum between XXX and XXXX (30.24) which is followed by clusters XXXV and XXXX (30.18) and between clusters XXVIII and XXXX (30.05). Pradhan and Roy (1990) and De and Rao (1987) suggested that selection of parents should be done from the two clusters having maximum inter cluster distance to get more variability in succeeding segregating generations and also to generate high heterotic effect. The minimum inter cluster distance (1.57) was between clusters VII (ADT 43 / AD 00203 1-2-1-1, Improved White Ponni / Bansakthi 1-2-1-2-1-1) and XXIII (ADT 39 / Triguna 10-1-1-2, ADT 43 / AD 00203 6-4-2-2-1-1) revealed the close relationship between them. Unidirectional selection practiced in the past and the use of certain genotypes (Co43, ADT39, ADT43, ADT45, ADT46, Triguna, Tapaswini and Kalajoha) as only source for enhancing the yield, grain quality, insect or disease resistance in repeated hybridization programmes might have

Table 3. Mean intra and inter cluster distances among 42 clusters in rice (Continued)

	XXIV	XXV	XXVI	XXVII	XXVIII	XXIX	XXX	XXXI	XXXII	XXXIII	XXXIV	XXXV	XXXVI	XXXVII	XXXVIII	XXXIX	XXXX	XXXXI	XXXXII
I	10.74	9.30	9.15	11.09	10.94	11.37	10.66	12.93	11.51	9.18	9.20	10.42	10.28	10.07	11.90	9.12	26.52	14.00	13.48
II	15.18	12.31	11.43	13.03	16.54	8.88	18.05	16.42	11.13	10.46	13.57	16.55	13.33	11.76	9.62	14.01	19.21	15.92	15.08
III	11.37	6.87	9.48	12.92	12.13	8.90	10.58	15.06	11.93	6.37	6.35	8.42	7.47	8.92	7.14	10.94	22.74	15.52	9.79
IV	8.68	6.54	9.79	12.44	9.79	11.98	4.66	13.43	12.82	7.49	3.98	3.47	7.77	9.88	11.90	8.94	28.30	15.38	11.12
V	6.30	3.33	5.83	8.42	9.75	8.31	6.94	10.24	9.25	4.15	3.09	6.82	5.49	7.67	8.73	5.93	24.78	13.12	11.09
VI	9.33	5.69	7.87	11.26	8.99	9.16	7.39	13.34	10.71	5.29	4.15	5.15	6.98	7.40	8.86	8.30	25.48	13.80	9.55
VII	10.11	5.67	8.07	11.33	11.60	7.46	10.31	13.76	10.33	4.72	5.52	8.36	6.87	7.93	6.56	9.69	22.40	14.51	9.84
VIII	7.17	3.03	7.60	10.17	12.20	8.96	7.86	11.26	11.12	5.22	3.22	7.92	4.27	9.43	7.87	8.20	23.31	15.10	11.32
IX	8.26	4.44	7.11	9.62	11.69	6.72	9.97	12.15	8.92	3.19	4.72	8.56	6.70	7.87	7.44	8.55	22.83	14.00	10.71
X	11.27	8.75	6.63	8.30	11.64	3.42	14.49	13.18	4.22	4.86	9.77	12.49	11.07	6.39	8.25	9.38	21.78	11.56	12.24
XI	12.98	9.84	7.15	10.91	5.63	7.42	12.18	15.15	7.67	6.65	9.46	9.06	11.25	3.22	9.08	8.85	25.17	10.22	9.75
XII	6.06	4.99	8.94	10.81	11.17	11.88	4.03	10.95	12.52	7.38	3.24	5.91	6.30	10.71	11.81	7.66	27.54	15.49	12.56
XIII	7.49	5.44	8.24	10.75	9.28	10.69	5.14	12.03	11.29	6.24	3.39	4.55	7.09	8.86	11.03	7.47	27.36	14.24	11.12
XIV	5.72	6.57	4.74	4.39	11.11	9.67	9.66	5.98	8.58	7.65	8.05	11.50	7.94	9.61	11.00	3.62	24.99	12.10	14.86
XV	10.15	6.20	5.69	9.23	9.72	4.99	11.19	12.84	7.34	3.36	6.66	9.14	7.82	5.25	5.86	8.05	22.05	12.01	9.84
XVI	7.57	3.69	4.87	7.50	11.93	5.86	10.45	9.98	8.22	3.89	5.71	10.29	5.19	7.80	5.50	6.97	20.79	13.13	11.69
XVII	11.86	10.48	8.58	11.03	4.39	10.61	10.33	14.51	9.04	8.19	9.39	7.75	12.38	6.44	13.11	8.29	29.36	10.93	11.70
XVIII	13.70	11.67	8.07	11.03	3.75	9.64	12.74	15.30	8.11	8.84	11.22	10.11	13.19	4.96	12.01	8.84	27.68	9.40	11.71
XIX	7.82	4.17	5.85	9.09	9.34	7.75	7.82	11.32	9.18	4.04	3.93	6.89	5.78	6.89	7.71	6.61	24.09	12.87	10.30
XX	16.23	15.55	10.56	11.71	8.03	12.93	16.58	15.97	9.80	13.20	15.74	15.29	16.96	9.59	15.86	10.83	29.57	9.65	16.48
XXI	4.72	4.59	8.52	9.90	12.11	12.10	4.50	9.23	12.67	7.96	4.08	7.74	5.45	11.43	11.75	7.00	26.87	15.64	13.65
XXII	8.91	7.25	8.23	10.46	8.24	9.69	8.07	13.06	9.44	5.74	5.77	5.80	9.59	7.55	11.71	7.95	27.90	13.01	11.04
XXIII	10.70	6.33	8.60	11.83	11.83	7.59	10.84	14.37	10.51	5.07	6.09	8.62	7.56	8.09	6.86	10.27	22.47	14.74	9.82
XXIV	2.58	5.02	8.25	7.67	14.53	11.68	8.34	6.10	11.84	8.42	6.48	11.38	6.42	12.66	12.16	7.02	25.42	15.91	15.80
XXV		2.59	6.37	8.05	12.60	8.66	8.12	8.81	10.19	5.21	3.89	9.28	3.89	9.74	8.29	6.73	23.02	14.56	12.64
XXVI			2.95	4.74	10.13	5.97	11.40	8.78	5.95	5.47	8.11	11.47	7.79	6.67	7.50	4.80	22.07	10.59	12.83
XXVII				2.98	13.23	8.11	13.25	6.28	6.87	8.06	10.30	14.40	9.54	10.05	10.32	5.89	22.30	11.95	15.97
XXVIII					3.03	12.23	11.70	16.66	11.08	10.46	11.47	8.80	13.84	7.06	13.77	10.03	30.05	11.17	11.84
XXIX						3.22	14.97	12.87	4.96	5.45	10.19	13.35	10.38	6.57	6.17	9.37	19.52	11.59	12.37
XXX							3.46	12.59	15.32	10.59	6.26	6.29	8.48	12.89	14.44	9.43	30.24	17.06	14.05
XXXI								3.80	12.38	11.44	11.12	15.86	9.28	14.54	13.34	7.91	24.01	16.02	18.84
XXXII									3.81	6.94	11.46	13.91	12.25	6.62	9.62	8.61	22.44	10.00	13.75
XXXIII										3.88	5.92	9.22	7.50	6.40	7.30	7.31	22.76	12.31	10.91
XXXIV											3.96	6.71	5.49	9.77	9.96	7.80	25.54	15.08	11.74
XXXV												4.05	10.39	10.20	13.50	10.65	30.18	15.70	11.02
XXXVI													4.86	11.32	8.59	7.97	22.60	15.82	13.53
XXXVII														5.26	8.88	8.70	24.38	10.05	10.53
XXXVIII															5.48	10.44	17.68	13.96	12.44
XXXIX																5.95	25.04	11.75	13.88
XXXX																	8.18	26.51	26.85
XXXXI																		14.28	15.94
XXXXII																			14.59

resulted in uniform features with limited genetic divergence among the breeding lines.

Further, the maximum inter cluster distance (14.59) was observed in cluster XXXXII and followed by the clusters XXXXI (14.28) and II (14.12). Hence, selection within these clusters may be exercised

Table 4. Cluster means for four different panicle traits in rice

Clusters	Panicle length	Filled grains/ Panicle	Panicle exsertion	100 grain weight
I	23.30	183.62	3.11	1.53
II	25.19	152.57	2.55	1.94
III	21.71	135.50	1.26	1.70
IV	22.59	163.20	1.57	1.41
V	23.75	180.35	2.12	1.56
VI	22.39	153.05	2.06	1.55
VII	22.85	145.30	1.50	1.70
VIII	22.87	172.05	1.09	1.63
IX	24.68	159.85	1.50	1.67
X	27.17	161.40	3.29	1.77
XI	23.05	144.30	4.51	1.61
XII	23.27	187.55	1.35	1.43
XIII	23.31	172.30	1.92	1.45
XIV	24.94	229.40	3.48	1.56
XV	23.68	154.30	2.77	1.71
XVI	23.74	180.95	2.08	1.73
XVII	24.75	164.25	4.58	1.40
XVIII	23.75	159.55	5.60	1.51
XIX	23.03	169.75	2.30	1.59
XX	25.08	195.80	7.59	1.49
XXI	23.11	205.00	1.38	1.46
XXII	25.30	163.55	2.61	1.45
XXIII	22.99	139.75	1.45	1.70
XXIV	25.45	230.25	1.25	1.54
XXV	23.89	193.95	1.37	1.63
XXVI	24.35	200.30	3.76	1.69
XXVII	26.45	232.60	3.72	1.70
XXVIII	22.39	152.80	5.49	1.40
XXIX	25.71	165.05	3.41	1.85
XXX	21.70	193.70	1.46	1.31
XXXI	25.59	268.95	2.43	1.63
XXXII	27.24	182.30	4.56	1.75
XXXIII	25.06	167.90	2.44	1.67
XXXIV	23.41	177.90	1.24	1.53
XXXV	22.08	146.60	2.08	1.35
XXXVI	22.19	199.40	1.13	1.65
XXXVII	23.96	151.35	4.49	1.65
XXXVIII	22.41	163.30	2.56	1.90
XXXIX	24.15	215.60	3.62	1.56
XXXX	23.39	187.50	1.55	2.62
XXXXI	24.93	182.47	6.13	1.64
XXXXII	22.03	119.13	2.85	1.60

based on the highest mean for the desirable traits *viz.,* panicle length and panicle exertion, which could be made use of in improvement through inter varietal hybridization programme.

The utility of D^2 statistics is a potent tool to quantify the extent of divergence in biological populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence. Present investigation revealed that 100 grain weight (Table 2) alone contributes about 57.65 per cent to the total genetic divergence which is followed by panicle exsertion (19.60 per cent) and number of filled grains per panicle (18.53 per cent). The present finding were in accordance with the results of Subudhi *et al* (2008).

The advanced breeding lines *viz.,* Triguna / IET 17920, ADT 39 / Kalinga, ADT 39 / AD 02202, ASD 19 / T 317, ADT (R) 45 / Kalajoha, ADT (R) 45 / Tapaswini, ADT 43 / Tapaswini and ADT 39 / Triguna are found to be highly diverse for number of filled grains per panicle. Hence, these advanced breeding lines may be used as diverse parents in intervarietal hybridization programme to generate transgressive segregants higher heterotic effect for important panicle related traits in rice.

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