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Short Communication

GENETIC DIVERGENCE ANALYSIS USING YIELD AND YIELD RELATED TRAITS IN RICE (*ORYZA SATIVA* L.)

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INTRODUCTION

Crop improvement basically depends on the extent of diversity present in the genotypes. A cross involving genetically diverse parent is expected to produce comparatively higher genetic variability in the successive segregating generations (Chaudhary *et al.*, 2002). Information on the nature and degree of divergence would help the plant breeder in choosing the right type of parents for breeding programmes (Sandhyakishore *et al.*, 2007). Hence, it is important to estimate the genetic diversity of grain yield and its component characters among the genotypes of the related crop, for planning the future crossing programme. In the present study an attempt was made to classify and understand the nature and magnitude of genetic diversity of rice germplasm consisting of rice genotypes from different rice growing regions of India and from foreign sources.

MATERIAL AND METHODS

This study consisted of 68 rice genotypes of different rice eco-geographical regions of India and some exotic genotypes. The entries were raised in a randomized complete block design with three replications during *Kharif* 2007/08. Thirty day old seedlings were transplanted at a spacing of 22.5 cm between rows and 15 cm within rows. Recommended agronomic practices were adopted to raise a good crop. Five plants of each accession per replication were randomly selected and tagged for recording observations on fourteen traits *viz,* days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, panicle length, number of grains per panicle, 1,000 grain weight, grain yield per plant, hulling (%), milling (%), head rice recovery (%), kernel length, kernel breadth and kernel length/breadth (L/B) ratio to assess the genotypes.

Fifty grams of paddy from each genotype was dehulled in a Satake Dehusker (type THU) and milled in Satake grain testing mill under standard conditions to obtain uniform 5-6% polished rice. Milled samples were sieved to separate whole kernels from the broken ones. Unbroken rice and three-fourth kernels were taken as whole milled rice for recording kernel length and kernel breadth. These were measured with the thickness gauge. L/B ratio was calculated as the ratio of mean kernel length to mean kernel breadth. The analysis of genetic divergence using Mahalanaobis D^2 statistics was carried out as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characteristics indicating existence of variability among the genotypes. Based on the relative magnitude of D^2 values, 68 genotypes were grouped into nine clusters (Table 1). The cluster I was the biggest consisting of 19 genotypes followed by cluster II with 11, cluster III with 8 , cluster IV with 7, cluster V with 6 , cluster VI with 5 and clusters VII to IX with 4 in each. The above grouping indicated existence of wide genetic divergence among genotypes. The clustering pattern of genotypes revealed that there was no relationship between clustering pattern and geographical distribution of genotypes. Similar results were observed by Sarkar *et al.* (2005), Madhavilatha *et al.* (2004; 2005), Singh *et al.* (2006).

Table 1. Grouping of rice genotypes with their origin into different clusters.

Cluster number	No. of genotypes	Genotypes	Origin/source
I	19	IR 26, IR 60, IR 36, IR 64, IR 56, IR 50, Jaya, RP 2151-40-1, CR 129-65, PR 109, Parsad, HKR 131, HKR 120, HKR 126, HKR 119, HKR 96-53, BR 827, PR 106,Pusa 21-86-6,	IRRI, Haryana, DRR/Hyderabad CRRI/Cuttack, Punjab, IARI Bangalore, UP
II	11	HKR 03-491, HKR 04-417, HKR 04-479, HKR 05-499, HKR 04-487, HKR 04-493, HKR 04-523, Basmati 370, HKR 04-524, HKR 05-475, HKR 05-476,	Haryana, Punjab
III	8	Indrasan, PR 113, PR 114, HKR 95-55, HKR 95-173, HKR 96-90,NDR 118, IRON 89-54	Pant Nagar, Punjab, Haryana, Faizabad, IRRI
IV	7	BR 51-202-8, HKR 96-54, IET 6288, PR 118, HKR 125, Pusa 44-33, CSR 13	Bangalore, Punjab Haryana, IARI, DRR/ Hyderabad
V	6	IR 20, IR 52, IR 62, HKR 95-239, HKR 112, Manhar	IRRI, Haryana, Pant Nagar
VI	5	Palman 579, Pusa 150, Pusa 169, Kogyaku, HKR 1	Punjab, IARI, Japan, Haryana
VII	4	HKR 02-430, HKR 03-428, HKR 93-49, HKR 05-416	Haryana
VIII	4	NDR 84, PR 110, HKR 86-11, HKR 128	Faizabad, Punjab, Haryana
IX	4	Taraori Basmati, CSR 30, HKR 04-489, HKR 04- 409	Haryana

The maximum intra-cluster distance was observed in cluster VII (D^2=18.455) followed by cluster V (D^2=12.243) and cluster III (D^2=10.949) (results not shown). The minimum intra-cluster distance was observed in cluster IX (D^2=7.590) followed by cluster II (D^2=8.579) indicating limited genetic diversity among the genotypes. Inter cluster distance indicated greater divergence between cluster V and VII (D^2=60.902) followed by cluster VII and VIII (D^2=54.096). Mean values for different characters are presented cluster wise in Table 2. An interesting expression of the nature of diversity was provided by the cluster means. Cluster I recorded the maximum number of grains per panicle. Cluster III recorded the highest milling % and head rice recovery %. Cluster IV showed dwarf plant height. Cluster V recorded the highest kernel breadth. Cluster VI recorded the maximum 1,000 grain weight. Cluster VII had comparatively more number of effective tillers per plant, longest panicle and kernel length, highest L/B ratio with highest hulling percentage. Cluster VIII recorded early flowering, early maturing and highest grain yield per plant.

Though cluster V showed the maximum genetic distance with cluster VII, cluster V has only one desirable cluster mean value, the kernel breadth. Hence, the hybridization programme between cluster V and VII may not be successful due to lack of desirable segregants. But the hybridization programme between cluster VII and VIII may be successful because those clusters have desirable genetic divergence and higher cluster mean values for the characters contributing most to divergence. The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield and yield component traits which may enable further selection and genetic improvement.

The list of diverse and superior genotypes selected from different clusters is presented in Table 3. IR 26, IR 60 and IR 56 in cluster I exhibited early flowering and early maturity. HKR 05-499 and HKR 05-476 in cluster II registered long kernel length, narrow kernel breadth and high kernel L/B ratio. Indrasan and HKR 95-55 genotypes in cluster III recorded long panicle length, high number of grains per panicle, grain yield per plant, 1000 grain weight, milling % and high head rice recovery. HKR 93-49 and HKR 05-416 in cluster VII registered long panicle and kernel length, high milling % and kernel L/B ratio. HKR 86-11 and HKR 128 in cluster VIII recorded early flowering and early maturing, high number of grains per panicle and grain yield per plant. Taraori Basmati in cluster IX recorded high number of effective tillers per plant, 1000 grain weight, narrow kernel breadth and high kernel L/B ratio. As far as the cluster means are concerned, different clusters have higher mean values for different traits indicating that none of the cluster contained genotypes with all desirable characters. Hence, recombination breeding between genotypes of different clusters is needed. (Kandamoorthy and Govindarasu, 2005).

Table 3. Cluster means for grain yield and yield related traits of 68 rice genotypes

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Effective tillers per plant	Panicle length (cm)	No. of grains per panicle	Grain yield per plant (g)	1000 grain weight (g)	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel length / Breadth ratio
I	98.31	133.05	97.51	11.43	22.76	89.22	16.86	23.54	78.59	70.92	68.84	6.08	2.10	2.90
II	109.21	144.21	133.92	10.53	23.65	50.45	8.72	20.44	78.49	70.71	67.93	6.30	1.63	3.86
III	102.54	137.54	107.59	8.86	23.10	88.99	15.13	23.80	79.07	72.49	70.95	6.30	1.94	3.28
IV	112.33	147.33	84.08	9.46	21.09	74.25	11.82	21.63	78.55	71.62	69.11	5.82	1.98	2.88
V	103.77	138.77	96.50	10.03	22.79	81.83	14.29	23.45	76.37	68.21	66.10	6.06	2.18	2.78
VI	92.60	116.93	107.24	10.10	25.18	82.18	15.82	25.72	79.14	71.29	69.62	6.39	2.04	3.14
VII	109.08	144.08	132.35	12.63	25.19	61.63	13.05	24.01	79.28	71.64	67.72	7.00	1.64	4.26
VIII	76.50	106.50	113.10	12.57	22.61	87.73	16.95	22.61	78.76	70.49	66.73	6.03	1.85	3.34
IX	109.50	144.50	127.60	11.13	21.32	40.75	6.97	22.09	77.76	68.77	64.70	6.45	1.65	3.91
Mean	102.09	135.94	108.57	10.69	23.00	75.70	13.72	22.92	78.48	70.83	68.35	6.21	1.93	3.28
CV (5%)	0.97	1.54	8.89	2.58	2.34	11.88	2.94	2.45	1.61	3.18	3.97	0.40	0.24	0.45
SE (Mean)	0.34	0.54	3.16	0.92	0.83	4.22	1.04	0.87	0.58	1.13	1.41	0.14	0.09	0.16
Contribution to genetic divergence %	8.09	6.92	10.59	8.13	4.11	14.77	16.78	5.31	0.85	1.39	1.63	4.38	6.57	10.41

Note: CV=Coefficient of variation; SE=Standard error.

Table 4. List of diverse and superior genotypes selected from different clusters and their promising characteristics

Cluster no.	Genotype	Promising Characteristics
I	IR 26	Days to 50% flowering, Days to maturity, No. of effective tillers / plant, No. of grains per panicle, Grain yield per plant
	IR 60	Days to 50% flowering, Days to maturity, 1000 grain weight, Hulling (%), Head rice recovery (%)
	IR 56	Days to 50% flowering, Days to maturity, No. of effective tillers / plant, Hulling (%), Milling (%)
II	HKR 05-499	No. of effective tillers / plant, Hulling (%), Milling (%), Kernel length, Kernel breadth, Kernel length/ breadth ratio
	HKR 05-476	1000 grain weight, Kernel length, Kernel breadth, Kernel length/ breadth ratio
III	Indrasan	Panicle length, No. of grains per panicle, Grain yield per plant, 1000 grain weight, Milling (%), Head rice recovery (%)
	HKR 95-55	Panicle length, No. of grains per panicle, Grain yield per plant, 1000 grain weight, Milling (%), Head rice recovery (%), Kernel breadth
IV	IET 6288	Plant height, 1000 grain weight, Milling (%), Head rice recovery (%)
VI	Pusa 150	Days to 50% flowering, Days to maturity, No. of effective tillers / plant, Panicle length, Grain yield per plant, Kernel length
	HKR 1	Days to 50% flowering, Days to maturity, Milling (%), Head rice recovery(%), Kernel length
VII	HKR-93-49	Panicle length, Milling (%), Kernel length, Kernel length/ breadth ratio
	HKR 05-416	No. of effective tillers / plant, Panicle length, No. of grains per panicle, Hulling (%), Milling (%), Kernel length, Kernel breadth, Kernel length/ breadth ratio
VIII	HKR 86-11	Days to 50% flowering, Days to maturity, No. of grains per panicle, Grain yield per plant, 1000 grain weight, Kernel breadth
	HKR 128	Days to 50% flowering, Days to maturity, No. of effective tillers / plant, No. of grains per panicle, Grain yield per plant
IX	Taraori Basmati	No. of effective tillers / plant, 1000 grain weight, Kernel breadth, Kernel length/ breadth ratio

CONCLUSIONS

The present study revealed that due emphasis in breeding programme should be given to varieties such as IR 26 of cluster I, HKR 05-476 of cluster II, HKR 95-55 of cluster III, Pusa 150 of cluster VI , HKR 05-416 of cluster VII and HKR 86-11 of cluster VIII. Intercrossing of genotypes from different clusters showing good mean performances may help in obtaining high yield with better grain quality. Out of the fourteen characteristics studied grain yield per plant, number of grains per panicle, plant height and kernel L/B ratio were the most potential traits contributing to the genetic diversity as these characters accounted for more than 50% of the total genetic divergence. Therefore, during the selection of parents for hybridization programmes and during selection of superior segregants in segregating populations/generations above mentioned characteristics should be considered.

REFERENCES

Chaudhary, M. and A.K. Sarawgi. (2002). Genetic divergence in traditional aromatic rice accessions of Madhya Pradesh and Chhattisgarh, India. Crop Improvement, 29 (2): 146-50.

Kandamoorthy.S. and R. Govindarasu. (2005). Genetic divergence in extra early rice (*Oryza sativa* L.) under two culture systems. Indian Journal of Genetics, 65(1): 43-44.

Madhavilatha, L., M.R. Sekhar, Y. Suneetha and T. Srinivas. (2005). Studies on genetic divergence and isozyme variability in rice (*O. Sativa* L.). Research on Crops, 6(3): 520-526.

Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Willy and sons, New York.

Sandhyakishore, N., V. Ravindra Babu, N.A. Ansasi and Ravi Chandran. (2007). Genetic divergence analysis using yield and quality traits in rice (*Oryza sativa* L.) Crop improvement, 34(1): 12-15.

Sarkar, K.K., K.S. Bhutia, B.K. Senapati, S.K. Roy, S. Panda and A.B. Mondal (2005). Genetic variability and relationships between grain yield and its component traits in rice (*Oryza sativa* L.). Environment and Ecology, 23S(4): 702-706.

Singh, P.K., M.N. Mishra, D.K. Hore and M.R. Verma. (2006). Genetic divergence in lowland rice of north eastern region of India. Communications in Biometry and Crop Science, 1(1): 35-40.