



GENETIC DIVERGENCE ANALYSIS IN *TROPICAL JAPONICA* AND *INDICA* RICE LINES (*ORYZA SATIVA* L.)

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Abstract

Thirty-six rice lines comprising of sixteen *Tropical japonica* and same number of *indica*, were grown in Randomized Block Design to assess nature and magnitude of genetic divergence among them based on eighteen characters, *per-se* performance to grouped and arrange into seven non-overlapping clusters. Clustering pattern of genotypes showed no definite relationship between genetic divergence and geographical distribution of genotypes. The maximum inter cluster distance was observed for cluster VI and VII followed by cluster I and VII and cluster II and VII exhibiting wider genetic diversity between these groups. Therefore, it suggested that members of the respective cluster t (AAIR2, BR6926-1-1-1-1-2), VI (DR.72903-6-2-2-1, PR 33319-9-1-1-5-3-5-4-1, TJ-50836, TJ-63265, TJ-35724, TJ-25892, TJ-1739) and VII (CT 17323-1 -1 -2-2-2-2-M, CT 19558-2-17-1-2-1-1-M, PK7392-10-1-1-1-1, Sarjoo-52, CSR-36) are more distinct and any superior genotype of aforesaid clusters having high mean performance in respect of the character may be crossed with any superior genotypes of above clusters to produce desirable recombinants in hybridization programme to develop high yielding new plant type rice varieties and selection of elite segregants also.

Key words : *Tropical japonica*, *indica*, genetic divergence, clustering pattern and *per-se* performance.

Introduction

High economic yield is the prime objective of most the rice breeding programs worldwide. The knowledge of variability present in a crop species has special significance for the success of any crop improvement program. These are important selection parameters which provide clear-cut identification that selection can be practices to improve desirable characters. Tn all crops breeders try to adjust the genotype in relation to that environment, where experiment is being done to achieve hither grain yield and agronomic cum morphological traits.

Genetic diversity provides a way of selecting heavily agronomically, climate reselling and economically superior crop plants. During the beginning of agriculture process, domestication and cultivation of crop plants, wealth of generic diversity has been utilized and has been partly preserved (Mishra *et al.*, 2004). Till now date, it is estimated that not more than fifteen percent of the potential diversity has been utilized. Thousands of valuable allelic variations of traits controlling through gene action

complexes of economic significance remain unutilized in crop plants. These can be discovered and effectively used to meet the existing and emerging challenges that threaten world food security (Bhanumathi *et al.*, 2010). Developmental activities such as industrialization and exploitive manners of land-use are destroying natural habitats and modern varieties are replacing native species and landraces, resulting in a reduction of varietal diversity. Major crop species like rice and wheat and maize suffered most seriously during the green revolution. In order to successfully meet future food security challenges and changing global temperature, it is crucial to manage the continuing genetic erosion through various ways and address the issues of genetic conservation by using the advance conservation techniques and optimum utilization of genetic diversity of important crop plants.

Study of genetic divergence among the plant materials is vital tool to the crop breeder for an efficient selection of parents for improvement. Genetically diverse parents for any breeding programme would be more promising

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Table 1 : Clustering pattern of thirty-six world mini rice core collections for eighteen characters.

Cluster number	No. of genotypes	Genotypes
I	2	AAIR2, BR6926-1-1-1-1-2
II	7	B12743-MR-18-2-3, BARKE 3004, BP10620F-BB8-15-BB4, IR 80859-56-1-2-2 (IRO6N210), OM4900, PR-114, Pusa Basmati-1.
III	5	IRIONIOI (IR82493-71-1-2-2-2), PK 8573-4-1, PR 34201-B-16-1, TJ-71553, NDR-359
IV	3	TJ-39050, TJ-1819, TJ-71552
V	7	TJ-60783, TJ-67437, TJ-71511, TJ-4122, TJ-17906, TJ-67846, TJ-56698
VI	7	IR72903-6-2-2-1 (IROOA114), PR 33319-9-1-1-5-3-5-4-1, TJ-50836, TJ-63265, TJ-35724, TJ-25892, TJ-1739
VII	5	CT 17323-1-1-2-2-2-M, CT 19558-2-17-1-2-M-M, PK7392-10-1-1-1-1, Sarjoo-52, CSR-36

Table 2 : Average intra- and inter-cluster distances for eighteen characters in world mini rice core collections.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	17.845	144.177	228.057	578.451	214.541	109.594	903.034
Cluster II		66.291	178.835	351.359	95424	160.335	752.648
Cluster III			129.028	246.310	216.882	276.083	414.048
Cluster IV				191.895	335.002	587.269	322.815
Cluster V					0.000	242.534	731.310
Cluster VI						189.035	974.670
Cluster VII							0.000

Bold figures represent intra-cluster distances.

(Arunchalum, 1981 and Mehandiratta *et al.*, 1991). Grouping of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. Thus, the identification of superior donor parent for important characters is possible through assessment of generic variation in the available germplasm.

Materials and Methods

The experimental material comprising of thirty-six world mini core collections were assessed for the nature and magnitude of genetic divergence among them based on eighteen characters grouped and arranged in to seven non-overlapping clusters using genetic divergence (D^2) analysis and per se performance, with four standard checks varieties of rice *viz.*, NDR-359, Sarjoo-52, Pusa Basmathi-1 and CSR-36 in Randomized Block Design with three replications during kharif 2010 at Crop Research Farm Nawabganj, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.), India. Nawabganj is situated between 27.24°N latitude, 77.50 E longitudes and at an altitude of 178 meters above the msl. in the gangetic plain of central Tjttar Pradesh.

The climate of district Kanpur is semi-arid with hot summer and cold winter. Nearly 80 percent of total rainfall occurs during the monsoon (only up to September) with a few showers in the winter. Each genotype was accommodated in three-row of 5 m length following row to row and plant to plant spacing of 20 cm and 15 cm respectively. The recommended dose of fertilizers N:P:K @ 120:60:60, cultural package and practices were followed to raise a good and healthy crop. Experimental site was sandy loam having EC = 0.34 and pH = 8.0, rich in potash and low in organic carbon, nitrogen and phosphorus. The observations were taken on ten randomly selected plants per genotype for days to 50% flowering, plant height (cm), panicle bearing tillers per plant, flag leaf length (cm), flag leaf width (cm), flag leaf area (cm²), panicle length (cm), panicle weight (g), spikelets per panicle, grains per panicle, spikelet fertility (%), 1000-grain weight (g), kernel length (mm), kernel breadth (mm), L:B ratio, biological yield per plant (g), harvest index and grain yield per plant (g). The genetic diversity between and within the members of the clusters was worked out using the techniques proposed by P. C. Mahalonobi's 1936 D^2 -statistics and Rao (1952) for the assessment of

Table 3 : Clusters means for eighteen traits in world mini rice core rice collections.

Character	DF	PH	PBT/P	FLL	FLW	FLA	PL	PW	S/P	G/P	SF	TW	KL	KB	L:B	BYP	H	GYP
Cluster I	112.33	99.47	4.19	19.29	0.94	13.68	20.08	1.63	81.45	43.17	55.37	18.91	6.08	2.18	2.79	20.35	33.44	6.70
Cluster II	104.31	85.86	12.09	26.17	1.37	27.20	28.28	2.05	131.87	110.63	83.66	22.60	6.52	2.00	3.35	47.48	35.64	16.57
Cluster III	104.72	99.92	6.89	28.10	1.56	34.00	21.15	2.60	120.91	81.03	66.26	28.01	6.45	2.37	2.77	44.38	32.45	13.02
Cluster IV	95.71	100.63	12.14	31.09	1.67	39.41	27.41	3.06	150.09	121.71	80.67	33.87	7.50	2.39	3.21	73.18	33.35	22.78
Cluster V	103.00	96.58	12.14	36.87	1.55	42.89	30.90	2.07	117.67	102.00	86.49	20.89	8.27	2.10	3.96	36.01	30.33	10.72
Cluster VI	105.56	96.02	8.95	22.35	1.28	21.60	20.08	2.38	91.98	68.67	70.18	19.64	5.64	1.87	3.18	28.23	29.01	8.99
Cluster VII	82.00	112.20	4.81	43.74	1.45	47.65	18.69	2.21	119.31	54.67	46.52	39.17	7.17	2.87	2.50	23.45	21.56	8.21

genetic divergence. The arrangement of the different genotypes in the clusters was done by Tocher method.

Results and Discussion

On the basis of genetic divergence analysis, thirty-six rice hybrids were grouped into seven non-overlapping clusters (table 1). Cluster II, V and VI have maximum 7 entries in each clusters, followed by cluster HI and VH comprising of sane number of genotypes having 5 genotypes indicated presence of adequate amount of diversity Chaudhary and Sarawgi (2002) and Nayak *et al.* (2004). Cluster IV and I have 3 and 2 entries in each respectively, reflecting narrow genetic diversity Banumathi *et al.* (2010). The maximum inter cluster distance was observed in the case of VI and VII ($D = 974.67$) Misra *et al.* (2004) and Singh *et al.* (2008) followed by cluster I and VH ($D^2 = 903.03$), Chandra *et al.* (2007) and cluster H and VQ ($D^2 = 752.65$) exhibiting wider genetic diversity between these groups. Cluster IV and I contained only three and one genotype TJ-39050, TJ-1819, TJ-71552 and AAIR2, BR6926-1-1-1-1-2 respectively. Therefore, it is suggested that members of the respective cluster I (AAIR2, BR6926-1-1-1-1-2), VI (IR72903-6-2-2-1 (IROOA114), PR 33319-9-1-1-5-3-5-4-1, TJ-50836, TJ-63265, TJ-35724, TJ-25892, TJ-I739) and VII (CT 17323-1-1-2-2-2-2-M, CT 19558-2-17-1-2-1-1-M, PK7392-10-1-1-1-1, Sarjoo-52, CSR-36) are more distinct and any superior genotype of aforesaid clusters may be crossed with any superior genotypes of above- clusters to produce desirable recombinants in hybridization programme. Intra cluster D^2 value was maximum for cluster IV ($D^2 = 191.89$) followed by cluster VI ($D^2 = 189.04$) and cluster III ($D^2 = 129.03$) while cluster V and VII ($D^2 = 0.00$) showed minimum intra cluster distance. Similar findings were also revealed by Chand *et al.* (2005) and Singh *et al.* (2008). The maximum intra cluster value indicated maximum divergence among various genotypes within the cluster whereas; minimum value reflected minimum diversity among the genotypes within the cluster. A comparison of cluster means *per-se* performance for eighteen characters under study (table 3) revealed considerable genetic differences between the clusters regarding one or more characters. Cluster I showed second highest mean value for harvest index (33.44) and Cluster II showed short plant stature, harvest index and second maximum mean value for panicle length (28.28), spikelets per panicle (131.87), grains per panicle (110.63), spikelet fertility (83.66), L:B ratio (3.35), biological yield per plant (47.48) and grain yield per plant (16.57) also reported by ChauDFary and Sarawgi 2002 and Dushyantha and Kantti

Table 4 : Top ten superior genotypes identified on the basis of their genetic distances and other important traits.

Clusters	Superior genotype	Important traits
V	CT 17323-1-1-2-2-2-M	Medium plant height, Flag leaf length, Flag leaf area, kernel length, L:B ratio
V	CT 19558-2-17-1-2-1-1-M	Medium plant height, shortest plant stature, flag leaf width, biological yield per plant
II	OM-4900	Panicle length, spikelet per panicle, grains per panicle, spikelet fertility
VII	PK7392-10-1-1-1-1	Panicle length, spikelet fertility, L:B ratio, biological yield per plant, grain yield per plant
III	PR34201-B-16-1	Spikelet per panicle, grains per panicle, test weight, grain yield per plant
III	TJ-71553	Panicle bearing tillers per plant, flag leaf length, flag leaf width, flag leaf area, panicle length, panicle weight, grains per panicle, test weight, kernel length, biological yield per plant, grain yield per plant
VI	TJ-63265	Flag leaf width, flag leaf area, spikelets per panicle, biological yield per plant
VI	TJ-35724	Flag leaf length, flag leaf width, flag leaf area, panicle length
VI	TJ-1739	Flag leaf length, flag leaf area, test weight, kernel length, kernel breadth
V	TJ-4122	Medium days to flowering, medium plant stature, flag leaf length, flag leaf area, harvest index

2010. Cluster HI emerged with second highest mean for flag leaf width (1.56), panicle weight (2.60) and third highest mean value for spikelets per panicle (120.91), test weight (28.01), kernel breadth (2.37), biological yield per plant (44.38), grain yield per plant (13.05) Chaudhary and Sarawgi (2002). The cluster IV stand with early days to flowering (95.71), first highest mean for flag leaf width (1.67), panicle weight (3.06), spikelets per panicle (150.09), grains per panicle (121.71), biological yield per plant (73.18) and grain yield per plant (22.78) and second highest mean for test weight (33.87), kernel length (7.50), and kernel breadth (2.39). These findings are in agreement with the results of Misra *et al.* (2004), Nayak *et al.* (2004) and Dushyantha and Kantri (2010). Cluster V showed first highest mean value for panicle bearing tillers per plant (12,14), panicle length (30,90), spikelet fertility (86.49), kernel length (8.27) and L:B ratio. Cluster VIII exhibited early days to flowering, first highest mean for flag leaf length (43.74), flag leaf area (47.65), test weight (39.17) and kernel breadth (2.87). The results indicated that selection on genotypes having high values for a particular trait could be made and used in the further hybridization programme for exploitation of hybrid vigour with respective character. The lowest intra cluster distance between pairs of clusters indicated members of genotypes belonging to these clusters cannot be taken in consideration in formulating the further breeding programme.

The result pertaining to the contribution of each character was ranked on the basis of per cent contribution of that character. The perusal of divergence showed that 1000-grain weight contributed (52.06%) maximum to total

divergence followed by kernel length (13.49%), panicle weight (8.89%), kernel breadth (4.92%), days to flowering (4.44%), grain yield per plant (4.44%), panicle length (4.13%), plant height (2.86%), flag leaf width (1.27%) and rest of the character contributed low to very low towards genetic divergence. These findings were also noted by Singh *et al.* (2008) and Banumathi *et al.* (2010). The data on inter cluster distance and *per se* performance of the genotypes was used to select genetically diverse and agronomically superior lines among nine genotypes. On the basis of seven genetically diverse groups, superior genotypes were selected (table 4), they belong to different clusters. Interacting of different genotypes would be lead to greater opportunity for crossing over which release latent variability by breaking linkage and progenies derived from cross are expected to show broad spectrum of genetic variability providing a greater scope for finding transgressive segregants for increasing sustainable yields and broadening the genetic base of existing varieties/formers variety can be obtained through international exchange evaluation and use of diverse germplasm. Unrestricted sharing and exchange of germplasm across geographical, political boundaries requires sound neat work and for the commitments of research.

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