Genetics Divergence Studies in Temperate Rice (*Oryza Sativa* L.) Grown under High Altitude Irrigated Ecosystem

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Abstract

Selection of parents for hybridization has widely been associated with degree of divergence among the selects. Mahalanobis D² analysis was carried out involving a set of 75 temperate germaplasm accessions which got grouped into 10 clusters. Thirty genotypes having their origin from geographically diverse indigenous and exotic sources were categorized into Cluster-I followed by cluster III and othes. Inter-cluster distance was maximum between cluste VII and Cluster IX. Cluster VIII had highest mean values for grain yield and important yield attributes. Some promising genotypes were idientified which could be utilized in hybridization program for development of varieties suitable for high altitude cold temperate areas.

Hill rice occupies about 4% of the total area of 45 million hectares under rice cultivation in the country. The rice cultivars are grown within a altitudinal variation of 1300 m to 2200 m amsl an particularly are temperate indica or temperate japonica ecotypes. The germaplasm base for high altitude temperate rices is relatively low in the country as compared to typical sub-tropical/tropical indica cultures. Therefore, germplasm collections from temperate exotic sources serve as valuable repositories of genes for intogression and utilization for genetic improvement. After preliminary evaluation, the measure of extent of genetic divergence among the accessions collected becomes pre-requisite step before starting any directional hybridization program. Nahalanobis D² statistic under the present study was used to quality the degree of divergence within a set of genotypes.

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Materials and Methods

Present investigations were carried out involving 75 germplasm accessions (49 exotic and 26 indigenous) having their origin from IRRI, Turkey, China, Korea, Japan, Italy, Chile, Russia, Australia, Thailand and various inland research centres. The experiment was laid in the year 2007 under irrigated conditions in Randomized Block Design with three replications at Rice Research and Regional Station, Khudwani, a constituent unit of Sher-e-Kashmir. The observations were recorded on 10 randomly selected plants for 15 agro-morphological traits viz., plant height (PH), days to 50% flowering (DF), days to maturity (DM) leaf length (LL), leaf width (LW), total tillers per plant (TT), effective tillers per plant (PP), panicle lénth (PL), number of grains per panicle (GP), grain density per panicle (GD), 1000 seed weight (SW), kernel length (KL), kernel breadth (KB), kernel length breadth ratio (LB) and grain yield per ha (GY). The estimation of genetic divergence was done using Mahalanobis D² analysis as described by Rao (1952). Grouping of genotypes as per the Tocher's method was done following Rao (1952).

Results and Discussion

Significant variances among the genotypes were recorded for all the traits under study. Based on the relative magnitude of D² values, 75 genotypes were categozed into 10 clusters (Table 1). Cluster-1 acommodated maximum of 30 accessions followed by cluster-III (16), Cluster-1 cluster-V(11) and cluster-11 (9). Cluster –VI and –VII each had 2 genotypes, while cluster VIII, -IX and cluster-X were monogentypic. Since, genotypes having their origin from different geographical origin got scattered across clusters, thereby, indicated lack of

Table 1: clustering pattern shown by 75 genotypes on the basis of D² values

Cluster No	Designation	Origin	No. of genotypes
Cluster 1	IR 68352-14-1-1-1, IR 68349-131-2-2-3, PR 26881-PJ16-4B-78-5-1, IR 71163-4-1-1-1, IR 61727-4B -1-1-1, IR 54465-B-B-3-2-2-2, IR 59614-26-2	IRRI, Philippines	30
	NONG 49, NONG 57, WON 122, WON 124, WON 125, PYONGBUK 5, SU 105, CHOJANG, SU 98, HWANGHEZO	Korea	
	Barkat, Chenab, k.312-25, K-450-3-2-2, VL 81	India	
	LANGI, NAMAGA, LLABONG	Australia	
	YUNLEN 2	China	
	PADANO	Italy	
	OSMANCIK-97	Turkey	
	Koshihikari	Japan	
Cluster 2	IR 600010-4B-1-1-1, IR 62728-2B-5-2-2-2, IR 61673-Ac 201-1-3,	IRRI, Phillipines	9
	PYONGBUK 7, PYONGBUK 21	Korea	
	K-508, K-681-9-1	India	
	84107-tr745-12-1	Turkey	
	Hexi 4	China	
Cluster 3	K-39, K-312-15, K-332, HPR 1070, SK/PBG/50, SK/PBG/68, SK/PBG/78, SK/PBG/56	India	16
	IR 59471-2B-20-2-1, IR 57301-199-2-3, IR 62443-2B-4-3-2	IRRI, Philippines	
	84032-TR76-4-1, 84037-TR765-6-2	Turkey	
	AMAROO	Australia	
	PYOONGBUK 10	Korea	
	STEJAREE	Russia	
Cluster 4	IR 62443-2B-7-2-2-1	IRRI, Philliphines	12
	ZHATONMAZAIGU	China	
Cluster 5	SK/PBG/51, SK/PBG/58, SK/PBG/81, SAW/GML/08, VL 93-3548, VL 93-3635, HPR 2047	India	11
	IR 58614-B-B-2-2, IR 57301-37-2-2	IRRI, Phillipines	
Cluster 6	CNTLR 80076-44-1-1	Thailand	
	VL 95-3336	India	2
Cluster 7	SR 12192 –T15	Korea	
	SK/PBG/79	India	2
	SR 13349-59-1	Korea	
Cluster 8	YUNLEN 19	China	1
Cluster 9	SK/PBG/62	India	1
Cluster 10	CT 6749-21-4-3-M	Chile	1

Table 2: Mahalanobis intra-(diagonal) and inter-cluster D² values among 75 genotypes of rice

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	43.04	103.68	134.52	159.14	205.44	155.44	187.53	183.22	536.37	656.74
Cluster II		54.33	104.33	138.45	184.89	153.89	159.40	172.23	489.83	604.20
Cluster III			96.55	206.88	287.61	170.99	225.04	256.51	590.01	722.41
Cluster IV				17.17	284.96	177.55	198.15	102.89	812.20	635.92
Cluster V					100.49	240.98	338.55	249.33	282.66	311.90
Cluster VI						39.90	339.46	161.78	514.68	570.60
Cluster VII							45.40	312.71	904.88	938.85
Cluster VIII								0.00	673.42	586.40
Cluster IX									0.00	309.33
Cluster X										0.00

Table 3. Cluster means for 15 agro- morphological traits

	PH	DF	DM	LL	LW	TT	PP	PL	GP	GD	SW	KL	KB	LB	GY
Cluster I	82.71	91.70	125.78	29.50	1.26	14.03	5.61	17.48	111.24	6.34	27.19	4.92	2.48	1.99	40.65
Cluster II	94.72	92.36	127.68	34.00	1.22	14.18	5.67	19.22	113.44	5.82	29.52	5.24	2.52	2.08	47.51
Cluster III	94.78	93.62	126.70	35.06	1.39	16.69	6.68	19.06	115.00	6.25	28.11	5.41	2.49	2.17	50.50
Cluster IV	125.60	104.15	130.56	24.50	0.90	13.95	5.58	18.00	94.00	5.24	25.15	4.45	2.35	1.89	31.32
Cluster V	108.81	90.24	127.03	39.27	1.35	14.77	5.91	20.06	101.73	5.05	27.58	5.89	2.22	2.69	38.43
Cluster VI	82.15	97.67	129.07	32.41	1.15	13.95	5.58	13.50	74.00	5.43	21.60	4.10	2.00	2.05	17.38
Cluster VII	84.45	80.23	124.08	25.28	1.45	10.46	4.19	19.00	120.50	6.47	26.72	4.70	2.40	1.96	31.72
Cluster VIII	111.30	107.64	134.55	20.64	0.80	24.92	9.97	22.00	224.32	10.18	11.20	4.80	2.40	2.00	58.38
Cluster IX	121.60	86.71	118.60	58.00	2.10	14.95	5.98	18.00	70.00	3.89	22.00	4.60	2.20	2.09	21.50
Cluster X	97.00	97.67	124.58	38.00	1.20	6.98	2.79	21.00	126.00	6.00	28.25	8.00	1.09	4.21	23.19

parallelism between geographical diversity an dclustering pattern. This is in conformity with the previous works of Sharma et al. (2008), Ravindra Babu et al. (2006) and Manonmai and Khan (2003). The kind of genetic diversity found among the genotypes belonging to same geographical region might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions (Nayak et al. 2004).

Maximum inta-cluster distance was observed in cluster V(100.49) followed by cluster-III (96.5) (Table 2). This indicative of high expected genetic gain under selection within the cluster. The maximum inter-cluster distance were recorded between clusters VII and X (938.85) followed by Clusters VII and IX (904.88) and clusters IV and IX (812.20) Barring D^2 values involving monogenotypic clusters maximum inter-cluster distance was found between clusters VI and VII (339.46) followed by clusters V and VII (338.55). Genotypes from divergent clusters may be identified as parents with high heterotic potential in F1 and such parents may generate broad spectrum of variability in segregating generations which may enable further selection and would produce transgressive segregrants. The direct relationships between degree of genetic divergence anong parents an dtheir ability to throw out useful segregrants on hybridization has been documented by Rather et al. (2001) and Rahman et al. (1997).

On the basis of average cluster means for important yield traits, it was eastablesheds that not all the traits of interest were chatacteristic feature of a single cluster (Table 3). However, cluster VIII had highest mean values for PL (22.00 CM), GP (224.32), GD (10.18 grains per cm), TT (24.92) PP (9.97) and GY (58.38 q/ha). Cluster –IX had a genotype with a high mean values for LL, LW and showed early maturity (118.60 DAS) which is a trait useful in cold temperate high altitude regions with relatively short growing seasons. Maximum average values for PH (125.60 CM) and SW (29.52 g) were recorded for cluster –IV and cluster-II respectively.

On the basis of D^2 values and cluster mean analysis, some of the genotypes which were identified in the present study as putative parents in hybridization program include YUNLEN-19, SK/PBG/62, IR 62443-2B-7-2-2-1, IR 60010-4B-1-1-1, 84107-TR745-12-1 and Hex4. The genotype CT 6749-21-4-3 of cluster-X identified as fine grained type had LB ratio of 4.21.

Acknowledgement

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