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Phenotyping for genetic divergence under transplanted and low-cost direct-seeded rice (*Oryza sativa*) production systems

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ABSTRACT

A set of 25 rice (*Oryza sativa* L.) genotypes belonging to different maturity groups and genetic background (Basmati, non-Basmati and hybrids) were phenotyped in two experiments at the experimental farm of the Rice Research Station, CCS Haryana Agricultural University, Kaul during *kharif* season (June-November) 2012. The experiments consisted of direct seeded and transplanted production systems in RBD with three replications each. The plot size was kept at 2× 0.20 × 5 m^2. The data were recorded on 5 randomly selected plants per genotype per replication for 12 traits, viz. grain yield (GY), days to flowering (DTF), days to maturity (DTM), plant height (PHT), effective tillers/ plant (T/PT), percent filled spikelets (FSPK), test weight (TWT), biological yield/plant (BYD), harvest index (HI), hulling per cent (H%), milling per cent (M%), and head rice recovery (HRR). The analysis of variance revealed significant differences among the genotypes for all the characters. The genetic dissimilarities measurement using generalized Mahalanobis distance (D^2) indicated that the genotypes with greater dissimilarity were different under high cost transplanted (TPR) than those under low cost direct seeded rice (DSR) production system. Similarly, the range of D2 values and the most divergent clusters were different in two production systems. Although genotypes were grouped into 6 clusters under both the systems, yet their members were different. Plant height showed maximum (18.67%) contribution towards divergence under low cost while DTF (29.67%) under high cost. Accordingly, genotypes were identified and recommended for evaluation in large trials and for hybridization for trait wise improvement for direct seeded production system. The results obtained thus have great relevance to the future rice improvement programme.

Key words: Cluster, DSR, Genetic divergence, Low cost, Mahalanobis's D^2, Rice, TPR

Traditionally rice (*Oryza sativa* L.) is cultivated in high cost transplanted production system. It's both water consuming and labour intensive due to non-mechanized nature of Indian farming. All these concerns are forcing farmers to diversify cultivation to other crops or switch over to direct seeded rice (DSR) cultivation, a low cost water saving technique demanding less labour. This DSR technique is in practice in several countries of Southeast Asia (Pandey and Velasco 2005). At present, 23% of rice is direct-seeded globally (Rao *et al*. 2007). To meet current challenges of non- availability of labour, its increasing costs and water scarcity as well as to overcome stagnated production and low productivity researchers have to devise alternative production system and evolve genetic materials suitable for the same.

None of the available varieties have been bred for direct seeded cultivation. Evaluation of genetic materials in alternative production system is the initial step in any breeding programme. The genetical phenomenon like genetic divergence, a pre-requisite for any crop improvement program could play a significant role in the evaluation of genetic materials. It helps in the evolution of superior recombinants. Within a certain limit, hybridization between the more diverged parents is expected to enhance the level of heterosis in hybrids and generate wide range of variability in segregating generations (Joshi and Dhawan 1966). Several measures of genetic distances have been proposed so far, of which Mahalanobis generalized distance (D^2 statistic) is a powerful tool to measure the genetic divergence. The present investigation was therefore, aimed to ascertain the genetic divergence among the available varieties belonging to different maturity groups and genetic background (Basmati, non-Basmati and hybrids) in direct seeded vis-a-vis transplanted rice production systems to identify genotypes and traits which could be used directly and indirectly via hybridization to create materials for low cost direct seeding production system .

MATERIALS AND METHODS

The experimental materials consisted of twenty five genotypes of which 19 were released varieties and 6 advanced breeding lines belonging to different maturity groups and

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genetic background (Basmati, non-Basmati and hybrid). They were evaluated in two experiments during kharif season (June-November) 2012 at the experimental farm of Rice research station, CCS Haryana Agricultural University campus, Kaul situated at latitude 29^0 51' N, longitude 76^0 39' E and altitude 230.87 m above msl. It falls in sub-tropical region of North India and is located in North Eastern part of Haryana, which is the heart of the rice-growing region, called 'Rice Bowl of Haryana'. The soil was clay loam. The two experiments one of direct seeded and 2nd of transplanting production systems were carried out in a randomized complete block design with three replications each. Plot size was kept at $2 \times 0.20 \times 5$ m^2. Under direct-seeding the seeds after priming for 24 hours were dibbled on 30 June, 2012 in the puddled soil in dry field in rows 20 cm apart at a seed rate of 25 kg/ha. The field was irrigated lightly immediately after sowing and again five days after sowing to ensure germination. Simultaneously, for transplanting sowing was done on raised nursery bed, the same day as for direct seeding. Seedlings were transplanted on 27 July, 2012 in the main field. One seedling per hill was maintained in a spacing of 15 cm. In direct seeded experiment thinning was carried out after two weeks to maintain one seedling per hill spaced at 15 cm. Hand weeding/hoeing twice at 30 and 50 days after sowing (DAS) was also done to control weeds in direct seeding. After initial light irrigation at 0 and 5 DAS for germination, subsequent irrigations were applied at 10 days interval throughout the crop period, delaying the irrigation by one day with 1 cm of rainfall (if it occurred before irrigation). The irrigation was stopped 10 days prior to harvest. Fertilizers applications were given as per conventional method. In conventional transplanting following recommended agronomic practices, irrigation was given to 5-cm depth one day after disappearance of ponded water from planting to maturity. Phenotyping was done on 5 randomly selected plants per genotypes per replication for 12 quantitative traits. D^2 Statistics of Mahalanobis (1936) was followed for genetic divergence analysis. Clustering was done according to the method suggested by Tocher (Rao 1952).

RESULTS AND DISCUSSION

Genetic divergence in a population, especially with respect to characters in which improvement is sought, is an indispensable pre-requisite for successful crop improvement program. Several measures of genetic distances have been proposed so far, of which Mahalanobis generalized distance is a powerful tool to measure the genetic divergence. Mahalanobis D^2 statistic considers the variation produced by any character and the consequent effect that it bears on the other character. In the present investigation the pooled divergence reflected as the aggregate effect of all the 12 characters tested by Wilk's criterion indicated highly significant differences among the genotypes. Group constellation was carried out following Tocher's method (Rao 1952), which utilizes the D^2 value. The D^2 values (table not given) of the genotypes ranged from 9.84 to 146.55 in TPR and from 7.05 to 67.06 in DSR production system, indicating that the material was quite diverse.The genetic dissimilarity measurement indicated that the genotypes with greater dissimilarity were HKR-04-487 and HKR-46 under TPR while Basmati 370 and HKR-127 under DSR production system.

With regard to contributions of each character towards the expression of genetic divergence, it was different under TPR and DSR production systems. Character-wise rank showed no single character had a major share in the total divergence. GY and TWT being contrast in contribution, T/PL, F SPK and HI were non-contributing while DTF, BYD, HRR% and PHT were major contributing traits in both the systems. In TPR production system these traits accounted for 84% of total genetic divergence and in DSR system collectively they constituted about 59% of total divergence. This revealed the differences in expression of traits in two

Table 1 Clusters and their genotypes in TPR and DSR (Italics Letters) production systems

Clusters	I	II	III	IV	V	VI
No. of genotypes	2 (2)	3 (3)	2 (*9*)	8 (*3*)	8 (*6*)	2 (*2*)
Genotypes	Basmati-370	HKR-03-408	PB-1	HKR-06-434	PR-106	CSR-30
	HKR-06-443	HKR-120	HB-1	JAYA	HKR-46	HKR-04-487
		Taraori Basmati		HKR-07-147	HKR-47	
	Basmati-370		*Pusa-1121*	IR-64	HKR-48	*HKR-06-47*
	HKR-04-487	*CSR-30*	*HKR-120*	PAU-201	HKR-126	*HKR-48*
		PB-1	*HKR-03-408*	GOVIND	HKR-127	
		Taraori Basmati	*HKR-06-443*	PUSA-1121	HKR-06-47	
			Govind	HSD-1	HKRH-1094	
			HB-1			
			HKR-47	HKR-127	HKR-126	
			HKRH-1094	PR-106	JAYA	
			HSD-1	HKR-06-434	HKR-46	
					HKR-07-147	
					IR-64	
					PAU-201	

Table 2 Cluster mean for different quantitative characters in TPR production systems

Clusters	DTF	DTM	PHT	T/PT	FSPK	T WT	B YD	GY	HI	H %	M %	HRR	Cluster mean*
I	101.8	133.0	144.1	10.9	85.0	23.7	75.3	16.9	25.5	80.3	63.3	54.6	67.9
II	107.1	137.9	144.6	12.7	84.7	22.2	98.9	31.3	34.4	85.3	68.3	63.8	74.3
III	99.7	131.0	113.9	11.6	82.1	21.0	68.8	17.9	30.7	81.4	68.4	54.3	65.1
IV	98.0	132.0	113.2	11.7	83.2	24.7	57.7	23.9	46.8	85.0	71.6	65.2	67.7
V	93.1	125.2	98.5	9.7	87.4	25.0	57.3	23.9	44.4	86.9	73.5	67.0	66.0
VI	106.8	141.8	143.1	12.8	77.4	22.0	173.5	32.3	24.0	81.8	63.5	57.6	78.1

*Over traits. DTF = Days to flowering; DTM = Days to maturity; PHT = Plant height; T/PT = Effective tillers/plant; FSPK = Per cent filled spikelets; T WT = Test weight; B YD = Biological yield/plant; GY = Grain yield; HI = Harvest index; H % = Hulling per cent; M % = Milling per cent; HRR = Head rice recovery per cent.

production environments and suggested that these characters are the basic attributes of plant architecture, which needs greater attention, as they accounted for major share of the total divergence in the material. According to Pandya and Sarial (2013), plant height, contributed maximum among all the traits toward divergence Kandamoorthy and Govindarasu (2005) reported that plant height and days to flowering were among the maximum contributory traits towards divergence in transplanted condition while days to flowering also contributed in direct sowing condition. Contribution of days to 50% flowering towards genetic divergence was also confirmed by Pandya and Sarial (2013) While, Ishfaq *et al*. (2006) reported the contribution of head rice recovery in genetic divergence and Singh *et al*. (2008) reported per cent filled spikelets and harvest index as the main contributing characters to the total divergence contrary to our findings of low contribution of these traits in both the production systems.

Based on the genetic divergence as measured by D^2 values, genotypes were grouped into 6 clusters under both the production systems (Table 1). Cluster IV and V were the largest clusters, contained eight genotypes in TPR while cluster III contained nine genotypes in DSR. The clustering pattern revealed that the late maturing Basmati genotypes were grouped into four different clusters under TPR and into three clusters under DSR production systems while the non-Basmati, hybrids and genotypes of different maturity clustered together irrespective of their maturity group and genetic background.

Cluster means revealed a wide range of variation for all the quantitative characters studied under TPR (Table 2) and DSR (Table 3) production systems. In general, cluster mean over traits were higher under TPR than DSR production system. In TPR production environment, Cluster VI represented traits of both extremes. Traits like; GY, BYD and T/PT showed greatest value in cluster VI among all the clusters, thus, recognized as the best cluster for these traits. Howerver, cluster VI had the lowest value for F/SPK, H1 and HRR% traits. Under direct seeded production system Cluster IV was the best with respect to GY, BYD, HI and TWT. So, the genotypes of this cluster could be evaluated in larger trials in direct seeded production system and be utilized in breeding programme aimed to improve the grain yield and other desirable traits. But, as this cluster contained genotypes which performed poorly for other traits like DTF and DTM, F SPK and PHT etc. So genotypes from different and divergent clusters should be involved in crossing programme to get high heterotic hybrids as well as high yielding segregants with desirable traits. The results obtained thus, have great relevance to the future rice breeding programme.

With regards to clusters response for average intra and inter-cluster distance. In TPR, the maximum intra cluster D^2 value for cluster II and in DSR for cluster VI indicated the existence of maximum variability within cluster. Maximum inter cluster distance signifying most divergent clusters was

Table 3 Cluster mean for different quantitative characters in DSR production systems

Clusters	DTF	DTM	PHT	T/PT	FSPK	T WT	B YD	GY	HI	H %	M %	HRR	Cluster mean*
I	105.5	143.5	107.2	10.2	85.1	19.2	58.8	14.8	25.2	82.7	67.2	60.4	65.0
II	107.7	139.7	94.8	10.1	73.5	20.7	42.8	11.1	26.5	79.5	61.8	47.8	59.7
III	103.5	137.7	89.3	10.6	80.5	22.2	53.0	18.8	36.0	84.7	70.2	52.0	63.2
IV	119.6	149.4	59.3	6.9	65.2	22.6	48.0	19.1	40.7	79.8	67.3	57.5	61.3
V	107.7	144.7	78.4	9.2	79.7	21.9	35.4	16.6	47.2	79.7	66.3	56.5	61.9
VI	94.2	127.8	77.8	9.3	81.1	23.0	30.5	14.6	48.5	87.0	74.5	61.7	60.8

*Over traits. DTF = Days to flowering; DTM = Days to maturity; PHT = Plant height; T/PT = Effective tillers/plant; FSPK = Per cent filled spikelets; T WT = Test weight; B YD = Biological yield/plant; GY = Grain yield; HI = Harvest index; H % = Hulling per cent; M % = Milling per cent; HRR = Head rice recovery per cent.

observed for cluster V and VI under TPR condition while clusters I and IV were the widely divergent clusters under DSR production environment. This revealed that considerable amount of genetic diversity among the genotypes was present and the genotypes in these clusters could be used as parents in hybridization programme. Highly divergent genotypes will produce a broad spectrum of variability enabling further selection and improvement. The hybrids developed from these genotypes within the limit of compatibility may produce high magnitude of heterosis or desirable transgressive segregants which would be rewarding for successful breeding programme for rice.

Thus, on the basis of inter cluster distances the following genotypes could be hybridized for further improvement of different traits like; GY and T/PT, PUSA 1121 × HKR-03-487, PUSA 1121 × CSR-30, HKR-46 × CSR-30, HKR-03-487 × HKR-127 and Basmati 370 × HKR-127 under both production system; for DTM, HKR-120 × CSR-30 and Basmati 370 × HKR-127; for HI and F SPK, PUSA 1121 × HKR-03-487 under TPR and Basmati 370 × HKR-04-434 under DSR; for TWT, PUSA 1121 × CSR-30 in TPR and HKR-04-487 × HKR-127 in DSR and for HRR trait improvement PR-106 × HKR-03-484 under transplanted and HKR-04-434 × HKR-04-487 under direct seeded rice production system. Padmaja *et al*. (2010) divulged that genotypes contained in clusters which have maximum inter-cluster distance may be used as potential donor in hybridization programme to obtain desirable recombinants. Sharma *et al*. (2011) studied 63 genotypes and grouped them into 8 clusters based on mean performance and inter-cluster distances they suggested few genotypes from most divergent groups for use in hybridization programme. Bos *et al*. (2012) estimated forty nine genotypes for genetic divergence suitable for boro ecosystem and grouped them into five clusters: found most genotypes from divergent cluster II and IV suggested for used in hybridization programme. Pandya and Sarial (2013) based on inter cluster distances suggested genotypes from divergent clusters for hybridization programme to get the transgressive segregants of various traits.

REFERENCES

Anonymous. 2015. Directorate General of Commercial Intelligence and statistics (DGCIS) Annual Export 2014-15, www.dgciskol.nic.in

Anonymous. 2013.www.fao.org, Food and Agriculture Organization, Rome, Italy. APEDA, Report, Vol 4, AgriNet Solutions, 24 October 2013.

Anonymous. 2014. National Conference on Agriculture for *kharif* Campaign, NAAS, New Delhi, 26-27 Feb 2014.

Bose L K, Kar M K, Singh O and Pande K. 2012. Genetic divergence studies in puddle wetland boro rice. *Indian Journal of Plant Genetic Resources* **25**(2): 183–85.

Ishfaq A, Zargar M A, Gullzaffar Ali G, Rather, A G and Ahmad Z. 2006. Genetic divergence in rice germplasm under temperate conditions. *Agricultural and Biological Research* **22**(2): 135–43.

Joshi A B and Dhawan N L. 1966. Genetic improvement of yield with special reference to self-fertilizing crops. *Indian journal of Genetics and Plant Breeding* **26A**: 101–13.

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

Mahalanobis P C. 1936. On the generalized distance in statistics. *Proc. Nat. Inst. Sci*. (Indian) **2**: 49–55.

Padmaja D, Radhika K, Rao L V and Padma V. 2010. Studies on genetic divergence in rice (*Oryza sativa* L.) germplasm. *Crop-Research Hisar* **40**(1-3)**:** 117–21.

Pandey S and Velasco L. 2005. Trends in crop establishment methods in Asia and research issues. (*In*) *Rice Is Life: Scientific Perspective for the 21st Centuary*, pp 178–81. International Rice Research Institute, Los Banos, Philippines and Tsukuba, Japan.

Pandya T and Sarial A K. 2013. Genetic divergence and cluster analysis of Basmati and non-Basmati rice genotypes (*Oryza sativa L.). African Journal of Agriculture Science*. (In press).

Rao A.N, Johnson D E, Siyaprasad B, Ladha J K and Mortimer A K. 2007. Weed management in direct-seeded rice. *Adv. Agron.* **93:** 153–255.

Rao C R. 1952. *Advanced Statistical Methods in Biometrical Research*, edn 1.John Willy and Sons, New York.

Sarial A K. 1995.Exploitation of hybrid vigor in rice 1995. 33rd IARI Convocation, Post-Graduate Students Significant Research Findings Journal 1995: 24–25.

Singh S, Pradhan S K and Virk P. 2008. Genetic divergence in new plant type rice under shallow lowland ecosystem.*Sabrao Journal of Breeding and Genetics* **40**(1): 1–8.

Sharma S K, Nandan R, Singh S K, Sharma A K, Kumar S, Sharma P K, Singh M K and Kumar V. 2011. Genetic divergence in rice (*Oryza sativa* L.) genotypes under irrigated condition. *Progressive Agriculture* **11**(2): 321–5.

USDA. 2016. United States Department of agriculture; http://www.fas.usda.gov/ data/ india-grain-and-feed-annual.