



SELECTION OF DIVERSE PARENTAL LINES FOR HETEROTIC HYBRID DEVELOPMENT IN RICE (*Oryza sativa* L.)

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SUMMARY

Hybrid rice is a proven technology to increase the yield levels to meet the demands of increasing population. An investigation was carried out with 55 genotypes to assess genetic variability and select divergent parents for high yielding hybrid development. The ANOVA revealed the significant amount of variability among the genotypes studied was noticed for all nine characters. The predominance of additive gene effect in expression of number of grains per panicle and test weight was revealed by high heritability coupled with high genetic advance values, indicating good scope for selection using their phenotypic performance for improvement of the traits. The correlation results clearly indicated that for selection of high yielding parental lines and hybrids, days to flowering, effective bearing tillers per plant, plant height and panicle length should be given more importance. Among five clusters, Cluster I had highest number of genotypes (42), followed by Cluster II (9), Cluster III (2) and two mono-genotypic clusters (cluster IV and V). Cluster III had two maintainers of different grain types and its genetic distance with other clusters, indicates possibility of development of heterotic hybrids by using restorers of cluster II and IV. Highest genetic distance was observed between mono-genotypic (JGL11470) cluster V and two genotypic cluster III (JMS2 and CMS23B). Genotypes selected from these clusters may be used for development of maintainer lines with medium slender grain type.

Key words: *Oryza sativa* L., hybrid rice, divergent parents, variability, genetic advance, correlations, gall midge donor

Key findings: This study identified two diverse early-flowering maintainers (JMS2 and CMS23B) with average grain yield and test weight, indicating the possibility of developing high yielding early hybrids by using these genotypes (corresponding A lines) as females and genotypes from cluster I and II as restorers. CMS11B, CMS14B and CMS 46B of cluster I should be crossed to restorers of cluster II and cluster IV for development of heterotic medium maturity hybrids.

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INTRODUCTION

Rice (*Oryza sativa* L.) is a staple food for more than half of the world population and grown on about one tenth of earth's arable land. With the

tremendous increase in population there is need to identify high yielding genotypes (varieties or hybrids) in case of rice. There are more than 600 varieties released in India in last five decades and presently there is a plateau in yield levels of rice

varieties. After green revolution there is only one percent annual yield increase in rice (Latha *et al.*, 2013). Hence there is an immediate requirement to enhance yield levels by utilizing available new technologies. Hybrid rice is a proven technology to increase yield levels in rice, which was practically demonstrated in China as well as south and south-east Asian countries. Hybrid rice varieties have clearly shown a 1-1.5 t/ha yield advantage over semi-dwarf inbred high-yielding varieties in farmers' fields in China and other countries (Virmani and Kumar, 2004; Shivakumar *et al.*, 2010). Genetic knowledge of a trait and availability of diverse parental lines are the key factors for development of heterotic hybrids. Careful selection of maintainer and restorer lines on the basis of their genetic diversity may lead to the development of hybrids with higher yield potential than parents and standard check varieties (Hasan *et al.*, 2012)

Knowledge on the nature and magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement and is a pre-requisite for initiating any crop improvement programme as well as adopting appropriate selection techniques. Heritability estimated along with genetic advance is normally more helpful in predicting the genetic gain under selection than heritability estimates alone. Yield is the end product of multiplicative interaction between various yield components and this necessitates a thorough understanding of character association and direct and indirect effects contributed by each character on grain yield before launching any breeding programme. In addition, quantification of the degree of divergence in a given experimental materials of immense value in the identification of divergent genotypes for further use in hybridization to create new variability and to develop hybrids. Mahalanobis D statistic has been proven to be powerful tool for quantifying genetic divergence in a given population.

Very limited work has been done on genetic analysis and genetic divergence in rice in relation to hybrid rice breeding. Keeping in view the importance of hybrid rice, This investigation was undertaken to estimate genetic parameters,

the nature and magnitude of genetic divergence and characters contributing to the genetic divergence using 40 restorer lines, five maintainer lines and 10 varieties. This study will help to select more distantly related restorer as well as maintainer lines for using in crossing programme and ultimately help to develop more heterotic rice hybrids with wider adaptability and good grain quality.

MATERIALS AND METHODS

This investigation was carried out at Rice Research Scheme (18°50'20.24" N latitude, 78°56'54.20" E longitude and situated 249 m above mean sea level), Regional Agricultural Research Station, Polasa, Jagtial, Karimnagar District, Telangana, India, during 2014 rainy season with 55 genotypes. The soil type of experimental plot comprised of inceptisol with a soil pH of 8.2. Among 55 genotypes, five were maintainer lines, 40 restorer lines and ten were elite genotypes (released and pre-release cultures) (Table 1). Four maintainer lines were developed at IRRI (International Rice Research Institute, Philippines) and remaining Jagtial genotypes were developed through pedigree method of breeding using different parental lines.

The experiment was laid out in randomized block design with two replications. The seed was raised on nursery beds and 25 days old seedlings were transplanted in main field under irrigated system. In each plot, entry was planted in 4 m² area by adopting row to row spacing of 15 cm and hill to hill 15 cm with 1-2 seedlings per hill. All the recommended package of practices was followed to ensure healthy crop growth. The data was recorded on five random plants per plot for effective bearing tillers per plant, plant height, panicle length and number of grains per panicle. Spikelet fertility percentage was calculated using total number of filled grains including chaffy grains. The incidence of gall midge was recorded as percent tillers affected with silver shoots (SES, IRRI, 2002) on 10 random plants and averaged. Genotypes having gall midge incidence percentage more than 5 were considered as susceptible.

Table 1. List of 55 genotypes studied along with pedigree, grain type and reaction to gall midge.

Genotype	Pedigree/Source material information	Classification	Grain type	% GM incidence	GM reaction
CMS11B	IR68902B	B line	LS	3.6	R
CMS14B	IR69628B	B line	LS	9.9	S
CMS23B	IR72081B	B line	LB	0.0	R
CMS46B	IR80559B	B line	LS	12.1	S
JMS2	JGL2933	B line	ELS	4.8	R
JGL20779-1	MTU1010 x JGL13595	R line	SS	3.4	R
JGL21770	IET20473 x JGL11118	R line	LS	0.0	R
JGL21779-1	IET20473 x JGL11118	R line	LS	5.1	S
JGL21071	MTU1010 x JGL11470	R line	LS	4.1	R
JGL20670-1	JGL11727 x JGL11470	R line	LS	3.7	R
JGL21851	JGL11118 x JGL11727	R line	LS	0.0	R
JGL21005-2	MTU1010 x JGL11727	R line	LS	0.0	R
JGL20670-2	JGL11727 x JGL11470	R line	LS	0.0	R
JGL22249	Krishna Hamsa x JGL3844	R line	LS	0.0	R
JGL21815	JGL13595 x JGL11470	R line	LS	3.8	R
JGL22311	IR64 x JGL3844	R line	LS	4.7	R
JGL22316	IR64 x JGL3844	R line	LS	1.4	R
JGL21800	MTU1010 x JGL11118	R line	MS	1.1	R
JGL20649	MTU1010 x JGL11118	R line	ELS	2.7	R
JGL5614	JGL1798 x Betagamblin	R line	MS	2.4	R
JGL21820	JGL13595 x JGL11470	R line	SS	6.1	S
JGL5868	JGL245 x Gedonzipeton	R line	SB	0.0	R
JGL22318	IR64 x JGL3844	R line	LS	0.0	R
JGL21164	MTU1010 x JGL384	R line	LS	2.3	R
JGL21101	MTU1010 x JGL3844	R line	LS	2.5	R
JGL21881	MTU1010 x JGL11470	R line	LS	1.1	R
JGL17653-2	JGL3828 x OR1032-5-2	R line	LS	0.0	R
JGL18801	MTU1010 x JGL13595	R line	SS	2.5	R
JGL21005-1	MTU1010 x JGL11727	R line	LS	2.8	R
JGL21823	JGL13595 x JGL11470	R line	SS	0.0	R
JGL21828	JGL13595 x JGL11470	R line	MS	0.0	R
JGL18213	WGL32100 x JGL3855	R line	SS	0.0	R
JGL21779-2	IET20473 x JGL11118	R line	LS	0.0	R
JGL21819	JGL13595 x JGL11470	R line	SS	0.0	R
JGL21823	JGL13595 x JGL11470	R line	SS	0.0	R
JGL21815	JGL13595 x JGL11470	R line	LS	2.3	R
JGL20769-1	MTU1001 x JGL11470	R line	LS	1.2	R
JGL21836	JGL11118 x JGL11727	R line	SS	2.6	R
JGL17653-1	JGL3828 x OR1032-5-2	R line	LS	3.4	R
JGL18624	WGL32100 x LR34452/WGL14377	R line	LS	4.3	R
JGL18230	MTU4870 x NLR34452	R line	MS	0.0	R
JGL21815	JGL13595 x JGL11470	R line	MS	6.0	S
JGL20779-2	MTU1010 x JGL13595	R line	MS	1.4	R
JGL21862	JGL11118 x JGL11727	R line	LS	0.0	R
JGL20769-2	MTU1001 x JGL11470	R line	LS	0.0	R
JGL18047	MTU1010 x JGL13595	Recently released variety	LS	5.3	S
JGL20171	MTU1010 x JGL11470	Elite line	LS	1.2	R
JGL11470	JGL418 x Gedonzibeton	Popular variety	SS	0.0	R
JGL1798	Samba Mahsuri x Kavya	Popular variety	MS	0.0	R
JGL11727	JGL420 x Vijetha	Popular variety	LS	0.0	R
JGL11118	IET8585 x JGL1798	Popular variety	SS	0.0	R
JGL17004	WGL14377 x JGL3855	Popular variety	MS	0.0	R
MTU1010	Krishnaveni x IR64	Popular variety	LS	3.5	R
JGL19621	JGL3855 x MTU1010	Elite line	SS	3.8	R
MTU1001	MTU5249 x MTU7014	Popular variety	MS	13.5	S

However, days to flowering, grain yield (t/ha) were recorded on whole plot basis, whereas random sample was taken for estimation of test weight (1000 grain weight in grams).

Statistical analysis

The data was subjected to analysis of variance (Panse and Sukhatme, 1985). The coefficient of variations (Burton, 1952), heritability in broad-sense (Lush, 1940), genetic advance (Johnson *et al.*, 1955), correlations (Robinson *et al.*, 1951), direct and indirect effects (Dewey and Lu, 1959) were calculated as per standard statistical methods. Multivariate analysis was performed as per Mahalanobis D^2 statistic and the genotypes were grouped into different clusters following Tocher's method described by Rao (1952). Contribution of each character for genetic divergence was estimated from the number of times it appeared in first rank. These parameters were estimated using Windostat software (version 8.0).

RESULTS AND DISCUSSION

Significant variation among the genotypes (hybrid rice parental lines and 10 other genotypes) studied for nine characters was revealed by the analysis of variance of the numerical data (Table 2). Gall midge incidence during the study was ranged from 0 to 13.5 % with a general mean of 2.3. Range values for other characters also observed in the material indicating huge quantum of variability (Table 2). The genotype JMS2 took only 74days to flower compared to 112 days of JGL11470. Among the genotypes JGL21071 had few tillers (6.6) compared to 11 of CMS11B. JGL11727 had longest panicle (32.5cm) with the plant height of 126.1 cm and shortest genotype was CMS23B (83cm) with shortest panicle (21.3cm). More number of grains per panicle were found in JGL21819 (348.8) and spikelet fertility was more in JGL22318 (96.3 %). JGL17653-1 had 29.5g of test weight compared to 12.3g of JGL20779. Yield of JGL20171 was highest (11.7 t/ha) and lowest yield was recorded in JGL20670-1 (6.4 t/ha). Similar type of wide variability for yield

and yield contributing characters was reported by Gokulakrishnan *et al.* (2014). The genotypes CMS11B and CMS23B having highest number of tillers and short plant stature respectively could be used for development of hybrids.

The phenotypic coefficient of variance values were high compared to genotypic coefficient of variance for all the nine characters studied. This indicates more influence of environment on these characters. Highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for gall midge incidence (77.3, 164.1) followed by number of grains per panicle (30.2, 35.1), test weight (20.7, 21.7), grain yield (12.1, 17.3), number of tillers (6.9, 13.4), days to flowering (8.3, 8.4), plant height (6.9, 8.4), panicle length (6.0, 7.9), and spikelet fertility (5.0, 7.5). Narrow difference between estimates of GCV and PCV was observed for three traits, *viz.*, days to flowering, test weight and panicle length (Table 2). This suggested that the absence of environmental influence on expression of these characters. These results are in conformity with the findings of Prajapati *et al.* (2011). Heritability (broad sense) values were high for days to flowering (0.96), test weight (0.90), number of grains/panicle (0.73) and plant height (0.67). Moderate heritability was observed for panicle length (0.57), grain yield (0.49) and spikelet fertility (0.43) whereas, for two traits (gall midge incidence and effective bearing tillers) estimates were low. To arrive at more reliable conclusions estimates of both genetic advance and heritability should be jointly considered. In this study, genetic advance estimate was highest for gall midge incidence (75.1) followed by number of grains/panicle, test weight, grain yield, days to flowering, plant height, panicle length, effective bearing tillers and spikelet fertility (Table 2). High heritability coupled with high genetic advance values were observed for number of grains per panicle and test weight, whereas, plant height and days to flowering had high heritability and moderate genetic advance.

Table 2. Analysis of variance and genetic parameters for grain yield and its component characters in hybrid rice parental lines.

	DF	Gall midge incidence (percent tillers)	Days to flowering	Effective bearing tillers/ Plant	Plant height (cm)	Panicle length (cm)	Number of grains/ panicle	Spikelet fertility %	Test weight (g)	Grain yield (t/ha)
MSS_	54	17.9 *	104.7 **	1.6 **	135.6 **	6.3 **	9436 **	64.8 **	34.3 **	3.7 **
Genotypes										
MSS_Error	54	11.3	1.6	0.9	26.4	1.7	1412	25.3	1.7	1.2
Mean		2.3	86.2	8.3	106.5	25.2	209.4	88.5	19.4	9.1
Range		0.0 - 13.5	74.5 - 112.5	6.6 - 11.0	83.0 - 126.1	21.3 - 32.5	93.4 - 348.8	68.7 - 96.3	12.3 - 29.5	6.4 - 11.7
GCV		77.3	8.3	6.9	6.9	6.0	30.2	5.0	20.7	12.1
PCV		164.1	8.4	13.4	8.4	7.9	35.1	7.5	21.7	17.3
h ² (broad sense)		0.22	0.96	0.26	0.67	0.57	0.73	0.43	0.90	0.49
Genetic advance as % of mean		75.1	16.8	7.4	11.7	9.3	53.5	6.8	40.6	17.4

** Significant at 1 % level; * Significant at 5 % level; MSS-Mean sum of square; GCV- Genotypic coefficient of variation; PCV- phenotypic coefficient of variation.

Grain yield had moderate heritability and moderate genetic advance. These results indicate the predominance of additive gene effects in expression of these traits and good scope for selection using their phenotypic performance for improvement of the traits. These results are in consonance with earlier reports of Tandekar *et al.* (2010) and Gokulakrishnan *et al.* (2014). Moderate heritability and low genetic advance was observed for panicle length and spikelet fertility per cent indicating the predominance of non- additive gene effects and improvement through selection for such traits may not be useful. These two traits could be improved through development of hybrids. Low heritability and genetic advance for effective bearing tillers per plant revealed that selection would be difficult for improvement of the trait. Similar results were reported in forty three rice genotypes by Mohan *et al.* (2015).

Correlation and path coefficient analysis

Correlation coefficients were calculated to assess the relationship among grain yield and its component traits and presented in Table 3. Grain yield had significant positive correlation with days to flowering, effective bearing tillers per plant, plant height and panicle length both at genotypic and phenotypic level and test weight and gall midge incidence had positive correlation at genotypic level. These results clearly indicated that days to flowering, effective bearing tillers per plant, plant height and panicle length should be given more importance for selection of high yielding parental lines and hybrids.

Table 3. Genotypic (G) and phenotypic (P) correlation coefficients among yield and yield contributing traits in rice and direct effects of path analysis.

		Days to flowering	Effective bearing tillers/ plant	Plant height (cm)	Panicle length (cm)	Number of grains/ panicle	Spikelet fertility %	Test weight (g)	Grain yield (t/ha)	Direct effects on yield
Gall midge incidence	G	-0.0073	0.4599 **	0.1793	0.0970	-0.5197 **	-0.1241	0.2481 **	0.1926 *	2.0404
	P	-0.0435 **	0.1380	0.0623	-0.0039	-0.1998 *	-0.1891 *	0.1239	0.0127	0.0068
Days to Flowering	G		0.1808	0.5926 **	0.4826 *	0.4731 **	-0.4618 **	-0.3793 **	0.3950 **	-0.2027
	P		0.0549	0.3917 **	0.3716 *	0.3870 **	-0.3022 **	-0.3595 **	0.3029 **	0.2536
Effective Bearing Tillers/plant	G			0.0693	-0.4372 *	-0.6215 **	-0.1737	0.1891 **	0.1992 *	0.4020
	P			-0.0632	-0.2225 *	-0.1713	-0.1128	0.0413	0.3029 **	0.0921
Plant Height (cm)	G				0.7949 *	0.5489 **	-0.0282	-0.2787 **	0.5664 **	1.3466
	P				0.4286 *	0.2348 *	-0.0458	-0.1053	0.2741 **	0.0726
Panicle Length (cm)	G					0.3838 **	-0.2292 *	-0.0018	0.3328 **	-3.5488
	P					0.2098 *	-0.0971	-0.0034	0.3839 **	0.2472
Number of grains/panicle	G						0.0852	-0.8166 **	0.0913	5.6775
	P						0.1284	-0.7294 **	0.0689	0.1792
Spikelet Fertility %	G							0.0441	-0.2110 *	-1.5922
	P							-0.0037	-0.0478	0.0462
Test Weight (g)	G								0.2338 *	4.8020
	P								0.1389	0.3648

These findings are consistent with Mohan *et al.* (2015) for days to flowering, plant height, Ramanjaneyulu *et al.* (2014) for plant height and test weight and Cyprien and Kumar (2011) for days to flowering and contrary for test weight.

Gall midge incidence had significant positive correlation with test weight and number of effective bearing tillers per plant and negative correlation with number of grains per panicle and days to flowering. These findings indicate that the gall midge induces more tillers and may delays flowering and reduces number of grains per panicle thus increases test weight. The results agree with the findings of Ogunbayo *et al.* (2010) and Mohan *et al.* (2015) and contrary to Bashir *et al.* (2013). Hence it is important to identify gall midge resistant genotypes for development of widely adoptable resistant hybrids. In this

investigation one maintainer line (CMS23B), 16 restorer lines (JGL21770, JGL21851, JGL21005-2, JGL20670-2, JGL22249, JGL5868, JGL22318, JGL17653-2, JGL21823, JGL21828, JGL21779-2, JGL21819, JGL21823, JGL18230, JGL21862 and JGL20769-2) and five released varieties (JGL1798, JGL11118, JGL11470, JGL11727 and JGL17004) were immune to gall midge incidence, hence these forms a genetic stock that needs to be exploited in resistant hybrid development.

Effective bearing tillers per plant had significant negative correlation with number of grains per panicle (Table 3) and intern number of grains per panicle had negative correlation with test weight. Simultaneous improvement of these three important yield contributing traits is found to be difficult in the present investigation as they

were negatively correlated. Genotypes with high effective bearing tillers, more number of grains and high test weight can be developed by large segregating population and selecting good plant type. Mahendra Bhati *et al.* (2015) reported negative correlation between tillers per hill, spikelets per panicle and test weight. Whereas, Ravindra Babu *et al.* (2012) reported highly significant negative correlation of test weight with number of grains per panicle.

Path coefficient analysis allows separating the direct and indirect effects through other attributes by apportioning the correlations (Wright, 1921) for better interpretation of cause and effect relationship. The results clearly showed significant difference in genotypic and phenotypic direct effects indicating the predominance of environmental influence in expression of the traits (Table 3). Perusal of results obtained in path analysis revealed that maximum direct effect on grain yield was exhibited by number of grains per panicle and test weight. However, highest negative direct effect was exerted by panicle length at genotypic level on grain yield. These results are in line with the earlier reports of Mohan *et al.* (2015) and contrary to the reports of Babu *et al.* (2012). Though number of grains per panicle and test weight had direct positive effect on grain yield, simultaneous improvement of both the traits is not possible as they are negatively correlated with each other. Hence appropriate balance has to be attained between them to get high yield.

Genetic divergence

Genetic divergence has been considered as an important factor in discriminating the genetically diverse parents for efficient and successful hybridization programme. Genetic divergence determines the inherent potential of a cross for hybrid vigour and frequency of desirable recombinants in subsequent generations for parental line development. Genetic divergence analysis was conducted to identify suitable parents out of 55 rice genotypes to initiate a breeding programme for development of heterotic hybrids for nine yield and yield

contributing characters using Mahalanobis's D^2 analysis. Genotypes were grouped in to five clusters based on D^2 values (Table 4). Cluster I had highest number of genotypes (42), followed by Cluster II (9), Cluster III (2), whereas, cluster IV and V were monogenic clusters. Most of the restorers and poplar varieties were grouped in to cluster I. Two maintainers (JMS2 and CMS23B) were grouped in to cluster III. Among them JMS2 was developed at RARS, Jagtial and CMS23B was developed at International Rice Research Institute (IRRI), Manila, Philippines. The clustering pattern revealed that the genotypes from different sources clustered together, was an indication of no association between eco-geographical distribution of genotypes and genetic divergence. The possible reason for grouping of genotypes of different states/countries in one cluster could be the free exchange of germplasm among the breeders of different regions, or unidirectional selection practiced by breeder in tailoring the promising cultivars for different regions. Similar findings were reported by Bhati *et al.* (2015). This indicated that, in general, selection has been towards the same goal in the different centers of origin of these genotypes and yet, there is sufficient genetic variability, which distinctly differentiated them into five clusters. High yielding hybrids with different grain type and maturity groups is possible by using females from cluster III and restorers from cluster I and cluster II.

Intra and inter cluster distance analysis among five clusters revealed that intra cluster distance values ranged from zero to 5.41 and inter cluster distance ranged from 7.84 to 25.11 (Table 5). The inter cluster distances in all the clusters were higher than the intra cluster distances suggesting wider genetic diversity among the genotypes of different cluster groups. These results are in line with the earlier reports of Mohan *et al.* (2015). The relative divergence of each from other cluster *i.e.* inter-cluster distance, indicated greater divergence between cluster III and cluster V (25.11) followed by cluster I and cluster V (19.42); cluster II and cluster III (15.15);

Table 4. Distribution of 55 hybrid rice parental lines into different clusters based on 9 traits.

Cluster	No. of genotypes	Genotypes
Cluster I	42	JGL22249, JGL22318, JGL21005-2, MTU1010, JGL20171, JGL21005-1, JGL21164, JGL18047, JGL20649, JGL21779-1, JGL21779-2, JGL21862, JGL11118, JGL21881, JGL21815, JGL21770, JGL21815, JGL20769-2, JGL22316, JGL20670-1, JGL20670-2, JGL22311, JGL21851, JGL21815, JGL21820, JGL21800, JGL21836, JGL21101, JGL17004, JGL20769-1, JGL21828, JGL18624, CMS14B, JGL21823, CMS46B, JGL19621, JGL21819, JGL18801, JGL21823, JGL20779-1, JGL20779-2, CMS11B.
Cluster II	9	JGL18213, JGL18230, JGL17653-2, JGL21071, JGL5614, JGL5868, MTU1001, JGL1798, JGL11727.
Cluster III	2	JMS2, CMS23B
Cluster IV	1	JGL17653-1
Cluster V	1	JGL11470

Table 5. Average intra (diagonal) and inter cluster (above diagonal) distance values in rice.

Cluster No	I	II	III	IV	V
I	5.41				
II	9.96	5.13			
III	7.84	15.15	3.01		
IV	10.97	8.03	14.16	0.00	
V	19.42	11.49	25.11	15.14	0.00

cluster IV and cluster V (15.14); cluster III and cluster IV (14.16); cluster II and cluster V (11.49) and cluster I and IV (10.97) suggesting highest genetic divergence existing between the genotypes of these clusters. Highest genetic distance was noticed between mono-genotypic (JGL11470) cluster V and two genotypic cluster III (JMS2 and CMS23B). Genotypes selected from these clusters may be used for development of maintainer lines with medium slender grain type. Cluster III had two maintainers of different grain types and genetic distance between this and other two clusters (II and IV), indicates possibility of development of heterotic hybrids by using restorers of cluster II and IV.

Selecting genotypes from divergent cluster I, V, II and IV and use in a hybridization programme will be useful for good restorer development. Since hybridization between divergent parents is likely to produce wide variability and transgressive segregants with high heterotic effects (Bhati *et al.*, 2015). Lowest inter cluster distance was observed between the cluster

I and cluster III (7.84) followed by cluster II and cluster IV (8.03) and cluster I and cluster II (9.96) indicating the genetic resemblance between these cluster genotypes.

Considerable emphasis should be given to the characters contributing most to the divergence, while selecting genotypes. Among the traits studied, test weight and days to flowering contributed considerably, accounting for 80.07% of total divergence indicating the importance of these traits for effective selections (Table 6). Similar findings were reported by Ramanjaneyulu *et al.* (2014) and Mohan *et al.* (2015). However, results were contrary to the findings of Pandey *et al.* (2009) for days to flowering. Number of grains per panicle had better contribution (9.43%) towards divergence compared to least contribution of gall midge incidence, effective bearing tillers, panicle length, spikelet fertility, grain yield and plant height.

The genotype, JGL11470 in cluster V had highest number of grains per panicle (339)

and lowest test weight (12.50) with short slender grain type and gall midge resistance is revealed by the data on cluster means for nine characters (Table 6). This genotype could be exploited as donor to develop gall midge resistant parental lines. Another mono-genotypic (JGL17653-1) cluster IV recorded highest grain yield and test weight and least number of grains per panicle. This reconfirms the negative correlation between number of grains per panicle and test weight. The cluster III, having two maintainers had least

number of days to flowering with average grain yield and test weight. This indicates the possibility of development of high yielding early maturing hybrids by making use of corresponding A lines of JMS2 and CMS23B with the restorers of cluster I and II. Similarly, corresponding CMS lines of CMS11B, CMS14B and CMS 46B should be crossed to restorers of Cluster II and IV for development of heterotic medium maturity hybrids.

Table 6. Cluster mean values and character contribution towards genetic divergence in 55 hybrid rice parental lines.

Cluster	Days to flowering	Effective bearing tillers/plant	Plant height (cm)	Panicle length (cm)	Number of grains/panicle	Spikelet fertility %	Test weight (g)	Gall midge incidence (percent tillers)	Grain yield (t/ha)
I	83.90	8.27	106.04	25.10	210.44	89.52	19.48	2.33	9.03
II	97.38	8.64	113.33	26.63	220.31	87.50	18.38	2.49	10.24
III	75.75	8.18	85.20	22.20	127.50	87.25	22.75	2.38	8.93
IV	95.50	9.45	107.60	24.70	111.50	68.50	29.50	3.35	11.20
V	112.50	7.90	113.30	26.40	339.50	80.00	12.50	0.00	6.60
Times Ranked 1st	821	11	47	24	140	26	368	8	40
% Contribution	55.29	0.74	3.16	1.62	9.43	1.75	24.78	0.54	2.69

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