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Studies On Variability, Heritability, Genetic Advance And Divergence For Yield And Yield Components In Various Maturity And Grain Type Groups Of Rice (*Oryza Sativa* L.) Genotypes

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ABSTRACT
Analysis of variance revealed that wide range of variability was observed among 36 genotypes of rice for all the traits except number of productive tillers per m2 under study. The magnitude of PCV was higher than the corresponding GCV for all the traits. Additive gene action was predominant for 1000-grain weight as it registered high heritability coupled with high genetic advance values. Further, high heritability coupled with moderate genetic advance estimates were recorded for days to 50 % flowering, plant height, panicle length and grain yield, whereas, low estimates of both parameters were observed for number of productive tillers per m2. Based on D2 analysis, 36 genotypes were distributed into seven clusters with cluster I containing maximum number of genotypes followed by cluster III. Maximum inter cluster distances was observed between the clusters IV and VII, II and VII, and I and VII indicating wider genetic diversity, hence, crosses involving parents belonging to these clusters likely to produce wide variability and transgressive segregants with high heterotic effects. Cluster mean analysis revealed that the genotype, KNM 1730 was identified as a potential genotype for developing high yielding long bold grain varieties. Genotypes from the clusters IV , I and II would be used in breeding programme to develop varieties of medium slender fine grain varieties as they recorded more number of grains per panicle and low 1000-grain weight and also these genotypes were characterized by early and medium duration flowering duration. The traits, 1000-grain weight and days to 50% flowering manifested highest contribution towards total divergence, thus, these traits could be given due importance for further crop improvement in the present material.
Key words: Rice, PCV, GCV, heritability, genetic advance, genetic divergence, yield

INTRODUCTION
Rice is the most important staple food crop in the world particularly in South East Asia. The need for improving productivity in long slender, long bold and medium slender fine grain rice varieties of various maturity groups by exploiting available variability in the rice germplasm has been long left. Hence, critical analysis of genetic variability is a pre-requisite for initiating rice crop improvement programme and for adopting of appropriate selection techniques. The available variability in a population can be partitioned into heritable and non heritable parts with the aid of genetic parameters such as coefficient of variation, heritability and genetic advance (13). As demand has been increasing for high yielding long slender, long bold and medium slender fine grain varieties of desired maturity groups, once genetic variability is ascertained in the population, crop improvement through appropriate selection can proceed for development of these varieties in rice.

Heritability is the heritable portion of a character from parents their offspring (8). The estimates of heritability help the plant breeders to provide information on the proportion of variation that is transmissible to the progenies in the subsequent generations and selection of elite genotypes from genetic populations. Moreover, heritability estimates in conjunction with genetic advance are normally more helpful in predicting the gain under selection. The pace and magnitude of genetic improvement are generally dependent on the amount of genetic diversity present in a population (11). Genetic divergence determines the inherent potential of a cross for hybrid vigor and frequency of desirable recombinants in

subsequent generations. Hence, selection of desirable segregants from segregating populations could be achieved through the inclusion of most divergent parents in breeding programme. Several workers (3, 17, 14) used D^2 statistics for estimation of genetic divergence in the populations. Therefore, knowledge about the genetic diversity present in the germplasm for different yield traits is the key information for any breeder for initiation of breeding programme for crop improvement.

In this context, present study was undertaken to assess the variability, heritability and genetic advance and to estimate the genetic diversity present in the experimental material to enable for selection of more divergent high yielding long slender, long bold and medium slender fine grain genotypes of various maturity groups for further improvement.

MATERIALS AND METHODS

The experimental material for present study was comprised of 36 rice cultivars (33 from Agricultural Research Station, Kunaram and three released promising varieties from APRRI, Maurteru; RARS, Jagtial and ARS, Bapatla) developed through pedigree method of breeding at Agricultural Research Station (ARS), Kunaram, Telangana (Table 1). The material was laid out in a randomized block design during *kharif*, 2015 at ARS, Kunaram. 25 days age old seedlings of each entry was transplanted in 10.53 m² area with two replications by adopting spacing of 15x15 cm between the rows and within the row. Two seedlings were planted at each hill. The crop was grown with the application of N, P and K fertilizer @ 100, 50 and 40 kg/ha respectively. All recommended package of practices and need based plant protection measures were followed to raise a good crop. Data were recorded at maturity on 5 random plants for each entry in each replication for plant height (cm), panicle length (cm), number of productive tillers per m² and number of grains per panicle. Days to 50 % flowering and grain yield (kg/plot) were recorded on whole plot basis, whereas, random sample was used to estimate 1000 grain weight (g) for each entry in each replication. Number of productive tillers per plant values were converted into the number of productive tillers per m² and grain yield values recorded from the net plot (kg/plot) were converted in to hectare (kg/ha). The mean data after computing for each trait was subjected to analysis of variance (16), genotypic and phenotypic coefficients of variation (8), heritability (h^2) in the broad sense (1) and genetic advance (4) following standard procedures. The analysis of genetic divergence was done using (12) D^2 statistics. Grouping of genotypes in to clusters was carried out following Tocher's method (18) and intra and inter cluster distances and mean performances of clusters for all the traits were also computed.

RESULTS AND DISCUSSION

The analysis of variance (Table-2) revealed highly significant differences among the genotypes for all the traits except number of productive tillers per m² studied indicating the presence of considerable amount of variability among the genotypes. The mean performances (Table-3) of 36 genotypes for seven traits revealed that days to 50 per cent flowering ranged from 78 to 107.5 days with a grand mean of 91.3 days. The released variety, JGL 3844 had the longest days to flowering and KNM 1730 was the earliest in this regard followed by KNM 1689 (81.1 days) and KNM 1704 (81.5 days). The trait, plant height varied from 88.0 to 121.9 cm with a grand mean of 105.7 cm. The tallest genotype being KNM 1643 (121.9 cm) while the shortest genotype KNM 1602 (88.0 cm) followed by the released variety, BPT 5204 (88.1 cm). The longest panicles were observed in KNM 1721 (28.4 cm) followed by KNM 1730 (27.6 cm) and KNM 1723 (27.2 cm), while, minimum length in the released variety, BPT 5204 (21.2 cm) with a grand mean of 23.8 cm. The released variety, MTU 1010 (369) possessed the maximum number of productive tillers per m² with an overall mean value of 298.8. Number of grains per panicle varied from 305.6 to 124.5. The highest grains per panicle was observed in the medium slender genotypes, KNM 1598 (305.6) followed by KNM 1632 (303.3) and KNM 1610 (299.0), while, minimum value was recorded in the long bold grain genotype, KNM 1730 (124.5) in this regard. Long bold grain genotype, KNM 1713 was found to exhibit maximum test weight (29.5 g) followed by other long bold genotypes, KNM 1716 (28.8 g) and KNM 1705 (28.7 g) and minimum was recorded for the medium slender grain genotypes, KNM 1689 (12.6 g) followed by KNM 1690 (12.7 g) and KNM 1601 (13.1 g). Highest grain yield was registered for long bold grain type genotypes, KNM 1721 (7735.5 kg/ha) followed by KNM 1723 (7518 kg/ha) and KNM 1705 (7492 kg/ha), whereas, less grain yield (4581.0 kg/ha) was observed in medium slender grain type genotype, KNM 1684.

The estimates of various genetic parameters (Table 4) for seven traits revealed that GCV values varied from 4.70 per cent in number of productive tillers per m2 to 28.39 per cent in 1000-grain weight, where as for PCV it was 6.60 per cent in days to 50% flowering to 28.54 per cent in 1000-grain weight.

The high estimates of PCV and GCV were observed for 1000-grain weight and number of grains per panicle indicated the presence of high degree of variation for these traits among the genotypes which

could be improved through selection in desirable direction. These results are in agreement with the findings were obtained by (14, 19) for both number of grains per panicle and 1000-grain weight and, (24, 6) for 1000-grain weight, whereas, low levels of PCV and GCV were observed for days to 50 % flowering, panicle length and plant height suggesting the less variability among the genotypes for these traits. Similar reports were given by (6). Moderate levels of PCV and GCV for grain yield and, moderate levels of PCV and low levels of GCV for number of productive tillers per plant indicated the considerable level of variability in this trait and suggested the possibility of improving this trait through selection. These results are in conformity with the findings of (5).

For all the traits studied, high estimates of PCV were observed than GCV indicating the role of environmental forces in the inheritance of these traits. Similar findings were earlier reported by (21, 10, 14, 19). Further, narrow differences between the estimates of PCV and GCV were observed all the traits except number of grains per panicle and number of productive tillers per m^2 indicated the presence of high genetic variability and less interference of environment on expression of these traits which may facilitate selection (22), whereas, in case of number of productive tillers per m^2 and number of grains panicle per panicle more difference was observed indicating the sensitive nature of these traits to environmental fluctuations. These findings are in agreement with the earlier reports of (21, 10, 6, 5).

High heritability was registered for the trait, 1000-grain weight followed by days to 50 % flowering, plant height, grain yield and panicle length indicated that these traits could be improved through selection based on their phenotype, whereas, number of grains per panicle and number of productive tillers per m^2 were observed to possess moderate and low levels of heritable estimates, respectively. In case of number of grains per panicle and number of productive tillers per $m^{2,}$ improvement through selection could be difficult due to masking effect of environment on the expression of these traits. The similar results were earlier reported by (2) for days to 50% flowering and 1000-grain weight, (17) for 1000-grain weight and grain yield, (14) for days to 50 % flowering and (19) for panicle length.

High heritability does not always indicate the high genetic gain. The characters those exhibit high heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process, such characters are controlled by the additive genes and less influenced by the environment (15). In the present investigation, high heritability coupled with high genetic advance values were observed for 1000-grain weight which indicated that this trait was predominantly governed by the additive genes which could be improved through simple selection procedures. Similar results were reported by (20, 19, 5) for 1000-grain weight. Similarly, high heritability coupled with moderate genetic advance estimates were recorded for days to 50 % flowering, plant height, panicle length and grain yield and moderate levels of heritability and genetic advance for number of grains per panicle suggested the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be a prospective approach (10 and 5). However, low estimates of both parameters were observed for number of productive tillers per m2 indicated the role of non additive genes in the inheritance of this trait and improvement of this trait through mere selection is not useful, therefore, breeder should go for heterosis breeding and recurrent selection methods for improvement of this character. These results are in conformity with the findings of (21, 10, 19 , 5).

Genetic divergence studies revealed that, 36 genotypes were grouped into 7 clusters (Table 5) based on their D^2 values of which cluster I was the largest comprising of 13 genotypes followed by cluster III included 12 genotypes, while, the clusters II, IV and VI comprised of three genotypes each and one genotype each in the clusters *viz.*, V and VII. Intra and inter cluster distance values among 36 genotypes were presented in Table 6. The intra cluster distances ranged from zero (cluster V and cluster VII) to 8.67 (cluster VI). Genotypes belonging to the clusters VI, IV, III, I and II which were having high degree of divergence would produce more desirable segregates to achieve greater genetic divergence. From the inter cluster distance values it was clear that highest divergence occurred between cluster IV and VII (31.64) followed by cluster II and VII (26.46), cluster I and VII (23.24), cluster III and IV (22.27), cluster V and VII (19.90), cluster VI and VII (19.53), cluster II and III (18.80) and cluster IV and VI (18.37) indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement. Genotypes belonging to clusters separated by high cluster distance could be used in breeding programme for obtaining wide spectrum of variation among the segregants (7).

Considerable amount of variation among the cluster means (Table 7) was observed for all the traits studied indicating the presence of ample diversity for these traits in experimental material. Genotypes from cluster VII and III were characterized by early in flowering, longer panicles, and more number of productive tillers per m2, higher 1000 grain weight and more grain yield, hence these genotypes could be used for obtaining high yielding early long bold grain genotypes, despite very less number of grains per

panicle were observed. Cluster IV , I and II genotypes recorded more number of grains panicle per panicle and low 1000 grain weight and these genotypes were characterized by early and medium duration flowering duration, therefore , they could be used as a parents for developing early and medium duration super fine medium slender rice varieties. The highest percent contribution (Table 7) towards total divergence was manifested by 1000-grain weight (54.29) followed by days to 50% flowering (21.75) which was on par with the contribution by the plant height (21.11) suggesting that these traits may be useful for selecting the most diverse lines in segregating populations, whereas, productive tillers per m2 and number of grains per panicle recorded least contribution (1.6) followed by the panicle length (0.48) and grain yield (2.06) which are of less importance in selection of diverse parents. Similarly, (3, 19, 5) reported higher contribution of days to flowering and 1000- grain weight towards total divergence in rice , whereas, 9 and 5 recorded least contribution of effective tillers, plant height and panicle length. Since 1000 grain weight, days to 50 % flowering and plant height exhibited more contribution to the divergence, the present experimental material could be used for developing rice varieties with desirable grain type, maturity duration and plant height.

Table -1: List of genotypes studied along with the pedigree and grain type.

S.No.	Genotype	Pedigree	Grain type
1	KNM 1590	JGL 3844 X BPT 5204	MS
2	KNM 1592	JGL 3844 X BPT 5204	MS
3	KNM 1598	JGL 3844 X BPT 5204	MS
4	KNM 1600	JGL 3844 X BPT 5204	MS
5	KNM 1601	JGL 3844 X BPT 5204	MS
6	KNM 1602	JGL 3844 X BPT 5204	MS
7	KNM 1604	JGL 3844 X BPT 5204	MS
8	KNM 1610	JGL 3844 X BPT 5204	MS
9	KNM 1616	JGL 11470 X BPT 5204	MS
10	KNM 1621	JGL 11470 X BPT 5204	MS
11	KNM 1625	JGL 11470 X BPT 5204	MS
12	KNM 1632	JGL 11727 X JGL 17004	MS
13	KNM 1638	JGL 11727 X JGL 17004	MS
14	KNM 1643	MTU 1010 X JGL 384	MS
15	KNM 1644	MTU 1010 X JGL 384	MS
16	KNM 1684	JGL 11118 X RNR 2465	MS
17	KNM 1685	JGL 11118 X RNR 2465	MS
18	KNM 1689	JGL 11118 X RNR 2465	MS
19	KNM 1690	JGL 11118 X RNR 2465	MS
20	BPT 5204	Released variety from ARS, Bapatla.	MS
21	JGL 3844	Released variety from RARS, Jagtial.	MS
22	KNM 1704	JGL 17653 X RP 2424	LS
23	KNM 1705	JGL 17653 X RP 2424	LB
24	KNM 1713	JGL 18065 X VD 82	LB
25	KNM 1716	JGL 18065 X VD 82	LB
26	KNM 1717	JGL 18065 X VD 82	LS
27	KNM 1719	JGL 18065 X VD 82	LB
28	KNM 1720	JGL 18065 X VD 82	LS
29	KNM 1721	JGL 15185 X HPR 2443	LB
30	KNM 1722	JGL 15185 X HPR 2443	LS
31	KNM 1723	JGL 15185 X HPR 2443	LB
32	KNM 1724	JGL 15185 X HPR 2443	LS
33	KNM 1728	JGL 15185 X HPR 2443	LS
34	KNM 1730	JGL 15185 X HPR 2443	LB
35	KNM 1731	JGL 15185 X HPR 2443	LS
36	MTU 1010	Released variety from APRRI, Maurteru.	LS

LS: Long slender; MS: Medium slender

Table - 2: Mean squares corresponding to various sources of variation for seven traits in rice.

Source of variation	Degrees of freedom	Days to 50% flowering	Plant height (cm)	Number of productive tillers per m²	Panicle length (cm)	Number of grains per panicle	1000-grain weight (g)	Grain yield (kg/ha)
Replications	1	4.50*	4.75	26.89	1.31	164.41	0.30	117208.70
Treatments	35	71.59**	188.69**	1481.04	7.22**	5413.31**	66.37**	1278301.44**
Error	35	0.79	3.13	1086.71	1.30	1445.10	0.34	212399.53

* =significant at P< 0.05, ** =significant at P<0.01

Table - 3: Mean performance of seven characters for 36 rice genotypes.

Genotype	Days to 50 % flowering	Plant height (cm)	Panicle length (cm)	Number of productive tillers per m2	Numbers of grains per panicle	1000-grain weight (g)	Grain yield (kg/ha)
KNM 1590	92.0	113.6	23.6	286.0	266.9	16.5	6743.5
KNM 1592	88.0	116.6	23.9	281.6	242.0	15.5	6754.0
KNM 1598	92.5	108.1	24.3	259.6	305.6	16.0	5861.0
KNM 1600	92.5	109.5	23.2	325.6	255.0	15.5	7117.0
KNM 1601	93.0	101.6	24.1	299.2	237.8	13.1	6569.5
KNM 1602	93.5	88.0	23.5	290.4	248.0	13.9	5497.0
KNM 1604	93.5	92.2	22.6	294.8	210.7	16.0	5692.5
KNM 1610	92.5	105.2	24.3	308.0	299.0	14.9	7213.0
KNM 1616	93.0	107.3	24.2	277.2	236.9	16.1	7128.5
KNM 1621	94.0	94.9	22.3	330.0	230.2	15.3	6412.5
KNM 1625	87.0	101.7	24.6	303.6	226.1	19.0	7272.5
KNM 1632	101.0	112.0	22.0	321.2	303.3	16.1	7082.0
KNM 1638	91.0	103.0	22.8	299.2	260.4	16.0	6573.5
KNM 1643	92.5	121.9	27.0	255.2	214.0	18.9	5206.5
KNM 1644	93.0	119.4	25.3	277.2	186.9	18.8	5212.5
KNM 1684	87.0	102.0	22.9	286.0	225.9	19.4	4581.0
KNM 1685	86.5	100.5	23.0	272.8	228.0	13.7	5252.5
KNM 1689	81.0	94.9	21.7	321.2	202.3	12.6	7029.5
KNM 1690	87.0	111.8	21.8	303.6	243.0	12.7	7326.5
BPT 5204	107.0	88.1	21.2	290.4	270.3	17.7	6501.5
JGL 3844	107.5	96.8	21.6	286.0	273.9	17.5	6129.5
KNM 1704	81.5	101.8	23.0	325.6	172.1	25.1	5794.0
KNM 1705	88.0	112.9	22.5	347.6	180.4	28.7	7492.0
KNM 1713	87.0	101.5	22.7	250.8	148.7	29.5	5891.5
KNM 1716	94.5	95.0	23.0	299.2	138.7	28.8	5849.5
KNM 1717	94.5	96.8	21.4	308.0	158.7	26.2	7328.0
KNM 1719	89.0	96.9	22.1	316.8	152.6	28.4	7085.0
KNM 1720	97.0	91.3	22.5	264.0	144.3	26.5	6205.0
KNM 1721	87.0	114.4	28.4	272.8	146.2	26.6	7735.5
KNM 1722	87.0	113.9	25.8	286.0	177.5	24.3	7285.0
KNM 1723	93.0	113.2	27.2	321.2	149.8	28.7	7518.0
KNM 1724	91.5	119.5	26.4	272.8	162.2	26.6	6767.0
KNM 1728	92.0	117.3	26.9	321.2	153.7	23.9	6994.0
KNM 1730	78.0	111.8	27.6	347.6	124.5	28.7	7432.0
KNM 1731	93.0	120.9	24.0	286.0	184.8	16.6	7057.0
MTU 1010	87.0	109.4	24.5	369.6	154.8	25.7	7145.0
Mean	91.3	105.7	23.8	298.8	208.8	20.2	6576.0
C.V	1.0	1.7	4.8	11.0	18.2	2.9	7.0
S.E	0.6	1.3	0.8	23.3	26.9	0.4	325.9
C.D 5%	1.8	3.6	2.3	-	77.2	1.2	935.6

Table - 4: Genetic parameters for yield and yield contributing traits in rice.

Character	Mean	Range		GCV	PCV	h² (Broad Sense)	GA in % over mean
		Min	Max				
Days to 50% flowering	91.3	78.0	107.5	6.52	6.60	97.8	13.29
Plant height (cm)	105.7	88.0	121.9	9.11	9.27	96.7	18.47
Panicle length (cm)	23.8	21.2	28.4	7.23	8.67	69.4	12.40
Number of productive tillers per m2	298.8	250.8	369.6	4.70	12.00	15.4	3.79
Number of grains per panicle	208.8	124.5	305.6	21.34	28.05	57.9	33.44
1000- grain weight (g)	20.2	12.6	29.5	28.39	28.54	99.0	58.18
Grain yield (kg/ ha)	6576.0	4581.0	7735.5	11.10	13.13	71.5	19.34

GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation

Table - 5: Distribution of 36 rice genotypes in different clusters.

Cluster Number	Number of genotypes	Genotype
I	13	KNM 1643, KNM 1644, KNM 1731, KNM 1590, KNM 1592, KNM 1600, KNM 1598, KNM 1616, KNM 1610, KNM 1638, KNM 1601, KNM 1690 and KNM 1685
II	3	KNM 1604, KNM 1621 and KNM 1602
III	12	KNM 1722, MTU 1010, KNM 1721, KNM 1705,KNM 1724, KNM 1723, KNM 1728, KNM 1713, KNM 1719, KNM 1704, KNM 1717 and KNM 1716
IV	3	BPT 5204, JGL 3844 and KNM 1632
V	1	KNM 1720
VI	3	KNM 1625, KNM 1684 and KNM 1689
VII	1	KNM 1730

Table - 6: Average intra (diagonal) and inter cluster distances (Tocher method) for 36 rice genotypes.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	6.68	9.58	16.71	14.31	16.70	10.09	23.24
Cluster II		3.21	18.80	11.03	14.40	10.45	26.46
Cluster III			8.14	22.27	11.44	14.95	12.17
Cluster IV				8.62	16.40	18.37	31.64
Cluster V					0	15.40	19.90
Cluster VI						8.67	19.53
Cluster VII							0

Table - 7: Cluster means and percent contribution of each character towards total divergence of 36 rice genotypes for 7 characters.

Cluster	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Number of Productive tillers per m2	Number of grains per Panicle	1000- grain weight (g)	Grain yield (kg/ha)
Cluster I	91.27	110.71	23.94	287.02	243.10	15.69	6462.69
Cluster II	93.67	91.67	22.78	305.07	229.63	15.05	5867.33
Cluster III	89.33	107.69	24.47	307.63	157.95	26.85	6907.04
Cluster IV	105.17	98.93	21.58	299.20	282.50	17.08	6571.00
Cluster V	97.00	91.25	22.50	264.00	144.30	26.50	6205.00
Cluster VI	85.00	99.52	23.02	303.60	218.10	16.98	6294.33
Cluster VII	78.00	111.75	27.55	347.60	124.50	28.65	7432.00
% Contribution of character	21.75	21.11	0.48	0.16	0.16	54.29	2.06
Number of times ranked first	137	133	3	1	1	342	13

CONCLUSION

In the present investigation, it is concluded that most important yield contributing trait, 1000-grain weight could be improved through simple selection procedures using present experimental material. Based on the cluster means and inter cluster distances in the divergent studies, it would be rewarding to attempt crosses between the genotypes belonging to the clusters IV and VII, II and VII, and I and VII could be used in breeding programme to produce desirable transgressive segregants. The genotype, KNM 1730 was identified as a potential genotype for developing high yielding long bold grain varieties. In view of increasing demand for medium slender fine grain varieties, genotypes from the clusters IV, I and II would be used in breeding programme to develop varieties of medium slender fine grain varieties as they recorded more number of grains per panicle and low 1000-grain weight and also these genotypes were characterized by early and medium duration flowering duration. Hence, more emphasis would be given to 1000-grain weight and days to 50% flowering for deriving the lines of different maturity groups and grain types in the present material.

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Salient points of this article are:
1. The present investigation could be useful in identifying parents based on divergence for further improvement in yield.
2. Present experimental material could be a good source for developing genotypes with varying degrees of grain types *viz.,* medium slender, long slender and long bold grain types with various maturity groups.