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Genetic Analysis of Rice (*Oryza sativa* L.) Genotypes Under Wet Direct Seeding Condition

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ABSTRACT

Present investigation was carried out with 35 rice genotypes under wet direct seeding condition at Regional Agricultural Research Station, Jagtial, PJTSAU, Telangana, India during *kharif* (June to October), 2016. High GCV and PCV values for important yield contributing traits *viz.*, 1000 grain weight (24.41, 24.62) and number of grains panicle^{-1} (26.17, 29.30) were observed. High heritable and genetic advance values for 1000 grain weight (98.30, 49.86) and number of grains panicle^{-1} (79.80, 48.16) indicated the role of additive genes and these traits can be improved by simple selections. Effective bearing tillers m^{-2} recorded low values of heritability (25.40) and genetic advance (5.19) suggesting the exploitation of heterosis for improvement of this important yield character. Effective bearing tillers m^{-2} (0.7097**), plant height (0.5014**) and panicle length (0.3219**) exhibited significant correlations with yield, hence direct selection for these traits could improve the yield. Highest inter cluster distance was observed between clusters IV and VI (27.75) followed by III and VI (24.69), IV and V (22.34) and III and V (22.23) thus high heterotic hybrids can be developed by making crosses between genotypes of the clusters. 1000 grain weight (44.2%) contributed highest towards total divergence followed by days to 50% flowering (40.17%) and plant height (10.76). Genotypes from cluster V and VI can be used as parents in breeding programme for development of extra early varieties. Cluster II and IV recorded lowest means for plant height and hence genotypes from these clusters can be used as parents for development of dwarf varieties desirable for wet direct seeding condition.

KEYWORDS: Rice, wet direct seeding, correlation, genetic divergence, yield

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1. INTRODUCTION

Rice, a major food crop of the globe is being cultivated in an area of 165 million ha in the world. It is one of the world's leading staple crops, as more than half of the world's population relies on the significant source of calories and protein daily (Rohit and Parmar, 2011). Rice is crucial for Indian food security as it provides approximately 60% of the daily energy requirements or 41% of total food grain production from 35% of the national food grain area (Nirmala et al., 2022). Future rice farming faces several challenges, such as the urgent need to produce more rice to meet the world's rising demand from an increasing population, global climate change, environmental degradation linked with intensive cultivation practices, increasing competition for water-labor-land-energy, industrialization, and urbanization (Sandhu et al., 2021). At present, over 70% of global rice is grown in wetlands with puddling followed by transplanting which requires large quantities of water (Chakraborthy et al., 2017). Rice crop is generally grown by transplanting of seedlings into the puddle soil, which is a very water-labor-energy intensive system of cultivation (Kumar et al., 2011). Compared with other cereal crops such as wheat and maize, transplanted flooded rice consumes two or three times more water (Barker et al., 1998, Carriger and Vallee, 2007). It has been reported that water up to 5000 liters is used to produce 1 kg of rough rice (Bouman, 2009). Crop establishment in transplanted rice consists of major operations like nursery raising for 25–30 days in nursery bed, seedling uprooting and transplanting in the main field which in turn requires much time, labour and water. Puddled transplanted rice-based production systems are high energy and cost intensive, and result in a less profitable production system (Kumar et al., 2022 and Jat et al., 2012). This system is known to degrade the soil system and negatively impact succeeding winter crops (Rao et al., 2021).The productivity and sustainability of rice-based systems are threatened because of the increasing scarcity of resources, especially water and labor, changing climate, the emerging energy crisis and the rising cost of cultivation (Ladha et al., 2009 and Zhisheng et al., 2017). These factors triggered the scientific community in search of alternate methods of paddy cultivation in place of traditional transplanting method. Wet direct seeding is one of the alternate crop establishment methods of rice skips the nursery phase which is an important step in traditional transplanting method thereby saves the lot of time, water and labor and also reduces the crop duration by 7 to 10 days (Marasini et al., 2016 and Pathak et al., 2011). Although factors like high yielding varieties with lodging nature, shallow root system, increased weed growth, heavy rains during sowing time are some of the reasons for low yield levels in direct seeding condition when compared to transplanting method, development of suitable varieties with non-lodging nature could be one of the best approaches to reduce these yield gaps. A little research has been done regarding the genetic analysis of rice under wet direct seeding condition, hence, the present investigation was carried out to study the gene action governing the yield traits and type of association among the characters under this situation and to exploit the heritable variation present in the experimental material for desirable traits in framing the breeding methodologies to develop varieties suitable for wet direct seeding conditions.

2. MATERIALS AND METHODS

The present investigation was carried out at Regional Agricultural Research Station, Jagtial, PJTSAU, Telangana state, India situated at 18°50'20.24" N latitude, 78°56'54.20" E longitude and 249 m above mean sea level during *kharif* (June to October), 2016. Thirty-five rice genotypes (Table 1) were evaluated for genetic analysis under wet direct seeding condition. Germinated seeds were sown on puddled and perfectly leveled field with a spacing of 20 cm between the rows and 10 cm between the plants. Each entry is sown in two replications with a plot size of 3×2 m^2 (30 hills row^{-1} and 10 rows $plot^{-1}$) ^{2}. The crop was grown with the application of N, P and K fertilizer @ 100, 50 and 40 kg ha^{-1} respectively and necessary plant protection measures were taken for raising the healthy crop. Data were recorded at maturity on 10 random plants for each entry from each replication for effective bearing tillers m^{-2}, plant height (cm), panicle length (cm) and number of grains $panicle^{-1}$. Days to 50% flowering and grain yield kg ha^{-1} were recorded on

Table 1: Details of genotypes used in the present study

Genotype	Source
JGL 26973, JGL 18047, JGL 24497, JGL 24267, JGL 24527, JGL 24548, JGL 25154, JGL 26956, JGLH 1, JGLH 37, , JGL 24423, , JGL 30090, JGL 18629, JGL 19607, JGL 21078, JGL 21820, JGL 21831, JGL 25925, JGL 27361, JGL 27371, JGL 28542, JGL 3844, JGL 24309, JGL 24513, JGL 26959, JGL 26961, JGL 23183, JGLH 6	Jagtial, Telangana
MTU 1010, MTU 1156, MTU 1121	Maruteru, Andhra Pradesh
NDR 359	Faziabad, Uttar Pradesh
NLR 34449	Nellore, Andhra Pradesh
PSBRC 1-2-1-2	IRRI. Philippines
Pusa 44	IARI, New Delhi

whole plot basis and random sample was used for recording 1000 grain weight (Days to 50% flowering was recorded in each entry by the time 50% population of that genotype comes to flowering and 10 random panicles from each entry were collected, threshed and bulked and 1000 seeds from this Bulk sample was used to record the 1000 grain weight). After computation the mean data was subjected to analysis of variance (Panse and Sukhatme, 1985). Genotypic and phenotypic coefficients of variations were estimated as per methods given by Falconer (1981). The estimates of PCV and GCV were classified as low (<10%), medium (10–20%), and high (>20%) (Sivasubramanian and Madhavamenon, 1973). Broad-sense heritability (h^2) was calculated as the ratio of the genotypic variance to the phenotypic variance using the formula according to Allard (1960) and they were categorized using the criteria of Robinson et al. (1949): 0−30%=low; 31−60%=moderate; >60%=high. Genetic advance was calculated as per Burton (1952) following standard procedures. Correlation coefficients were calculated as per the method suggested by Johnson et al. (1955) and the analysis of genetic divergence was done using Mahalanobis (1936) D2 statistics. Grouping of genotypes into clusters was carried out following Tocher's method (Rao, 1952). Intra and inter-cluster distances and cluster means for the characters were also computed. Contribution of each trait towards total genetic divergence was estimated from the number of times it appeared in first rank. WINDOSTAT software version 8.1 was used for statistical analysis.

3. RESULTS AND DISCUSSION

Table 2: Analysis of variance for yield and yield attributing traits

Source of variation	degrees of freedom	Days to 50% flowering	Effective bearing tillers m^{-2}	Plant height	Panicle length	1000 grain weight	No. of grains panicle^{-1}	Grain yield
Replications	1	2.05	2944.51*	8.64	1.20	8.77**	7140.70**	381250.8
Treatments	34	83.44**	641.39	63.36**	2.54**	47.99**	6363.18**	1311785.88**
Error	34	0.73	381.54	2.96	0.61	0.41	715.70	577386.47

Table 3: Genetic parameters for yield and yield attributes in rice

Character	Mean	Range		GCV	PCV	h^2 (Broad sense)	GA in percentage over mean
		Min	Max				
Days to 50% flowering	78.29	65.50	94.50	8.22	8.29	98.30	16.77
Effective bearing tillers m^{-2}	227.86	197.00	273.00	5.00	9.93	25.40	5.19
Plant height (cm)	90.01	69.00	98.80	6.11	6.40	91.10	12.00
Panicle length (cm)	23.85	20.70	26.10	4.11	5.27	61.00	6.61
1000 grain weight (g)	19.98	11.55	28.21	24.41	24.62	98.30	49.86
Number of grains panicle^{-1}	203.04	110.00	367.00	26.17	29.30	79.80	48.16
Grain yield (kg ha^{-1})	6573.31	5091.50	8308.00	9.22	14.79	38.90	11.84

Analysis of variance (Table 2) revealed presence of significant variation among the genotypes studied for all the characters except for number of grains panicle^{-1} and thus there was more possibility of selection for different traits in present experimental material. Mean values and range for all 7 traits under study were depicted in Table 3. The present investigation under wet direct seeding condition disclosed all three levels of magnitude of phenotypic and genotypic coefficient of variation. Low PCV and GCV values were noted for days to 50% flowering, effective bearing tillers m^{-2}, plant height and panicle length indicated less variability among the genotypes studied for these traits and thus less scope for improvement. Selection in segregating generations i.e., from F_2 to F_6 of divergent crosses for these characters under wet direct seeding condition or exploring and exploitation of natural source of variation in breeding programme could generate the variability which can be used for development of varieties suitable for direct seeding method of cultivation. High values were obtained for 1000 grain weight and number of grains panicle^{-1} whereas, grain yield recorded moderate values for PCV and GCV. Thus, it can be manifested that present experimental material has exhibited ample variability for yield contributing traits *viz.*, 1000 grain weight and number of grains panicle^{-1}and hence there was much scope for improvement of these traits through simple selection, in turn, the dependent variable yield can be maximized under wet direct seeding condition. All the characters exhibited narrow differences between PCV and GCV values indicated minimal interference of environment on expression of these traits thus selection to improve the characters could be the best practice and needs further investigation under this specific situation. Patel et al. (2014), Bassuony et al. (2021) and Prasanna et al. (2022) noted similar findings from their studies. .

The extent of transmission of a trait to its off-springs is estimated by heritability. The characters studied in the present investigations expressed low to high heritability estimates ranging from 25.40 (effective bearing tillers m^{-2}) to 98.30 (Days to 50% flowering and 1000 grain weight) (Table 3). Based on heritability studies, transmission of days to 50% flowering, plant height, panicle length, 1000 grain weight and number of grains panicle^{-1} was found high to its progeny. Hence, selection of dwarf plant types based on phenotypic appearance in segregating generations under wet direct seeding situations can be done that result in development of non-lodging varieties which are suitable for wet direct seeding condition. Similarly, as the variation present in flowering duration was highly heritable, selection of early genotypes could be an added advantage. Besides, the experimental material was the good source for development of high yielding rice varieties suitable for wet direct seeding situations as important yield contributing characters *viz.*, 1000 grain weight and number of grains panicle^{-1} exhibited high heritable variation. Based on data, it was observed moderate levels of transmission of dependent and complex trait i.e grain yield to its offspring. Characters with higher heritability values are not subject to a great amount of non-heritable or environmental variability, instead they are genetically fixed. Such values for quantitative traits are useful to plant breeders who can make selections for these traits on a phenotypic basis Kaul and Bhan (1974). The variation present in the experimental material for the trait effective bearing tillers m^{-2} might be highly influenced by the environment under present method of cultivation and was not heritable, thus improvement of this trait through simple selection is not possible and hence there is need to improve this important yield contributing character through various breeding approaches.

Generally, large heritable values show the relative ease with which selection can be made based on phenotype, but their practical utility in breeding is further enhanced if accompanied by concomitantly high genetic advance estimates (Johnson et al., 1955). As genetic advance gives the sign of amount of genetic progress for selecting the best genotype which is not possible by mere high heritable values. The estimates of genetic advance along with heritability provide a clear-cut platform for selection. In the present investigation, genetic advance values (Table 3) ranged from low (5.19) for effective bearing tillers m^{-2} to high (49.86) for 1000 grain weight. High genetic advance coupled with high heritability was observed for 1000 grain weight and number of grains panicle^{-1}. Since these two traits were important yield contributing characters and as evident by being governed by additive genes, large amount of genetic gain in yield under wet direct seeding situation could be achieved by simply selecting superior genotypes based on phenotypic performance of these two traits. Whereas, even though high heritability was observed for days to 50% flowering, plant height and panicle length, genetic advance was at low to moderate levels indicated equal role of additive and non-additive genes on these traits, thus selection along with other breeding approaches like heterosis breeding or recurrent selection could be effective for improvement of these characters. Effective bearing tillers m^{-2} ,which is most important trait contributes to higher yields in rice exhibited low levels of both heritability and genetic advance and completely governed by non-additive genes hence, improvement of this character is possible by heterosis breeding approach. Yield, a complex and dependent trait exhibited moderate levels of heritability and genetic advance governed by both additive and non-additive genes. Sameera et al. (2015), Ketan and Sarkar (2014), Kunkerkar et al. (2017), Tiwari et al. (2019), Priyanka et al. (2019) and Sravani et al. (2022) quoted similar results from their findings.

Study of association between yield and yield traits at genotypic level under wet direct seeding condition could be much helpful to the breeders in understanding association among the desirable traits which play a key role in development of varieties suitable for direct seeding. Genotypic correlations, which are based on the heritable part of the observed variation, enable the assessment of the pattern of inherent relationship that existed between various traits. In present investigation, the important yield contributing traits *viz.*, effective bearing tillers m^{-2} , plant height and panicle length exhibited significant correlations with yield in positive direction (Table 4), hence practicing of strong selection for these traits for generations would ultimately end up with high yielding elite genotypes which can be either used as varieties for wet direct seeding situations or could be used as source for development of varieties. The remaining traits exhibited very week association with yield. Effective bearing tillers m^{-2} and plant height exhibited higher and significant correlations at genotypic level compared to corresponding phenotypic correlations which might be due to masking effect of the environment (Singh, 1980). Significant and positive correlations among the traits indicated strong association of effective bearing tillers m^{-2} with panicle length, plant height with panicle length and 1000 grain weight and panicle length with 1000 grain weight clearly indicated that selection for any one of these traits leads to simultaneous improvement of other trait. The similar findings were reported by Patel et al. (2014), Ronghua et al. (2019), Tiwari et al. (2019), Vennela et al.

Table 4: Phenotypic and genotypic correlation coefficients among yield and yield contributing traits in rice

Character		Days to 50% flowering	Effective bearing tiller m^{-2}	Plant height	Panicle length	1000 grain weight	No. of grain panicle^{-1}	Grain yield
Days to 50% flowering	P	1	0.0344	-0.071	-0.0221	-0.1477	0.0672	-0.1044
	G	1	0.0554	-0.06	0.0005	-0.1493	0.0605	-0.1027
Effective bearing tillers m^{-2}	P		1	-0.081	0.146	-0.0142	-0.246*	0.2344
	G		1	-0.172	0.3998**	-0.0249	-0.5307**	0.7097**
Plant height	P			1	0.4389**	0.347**	-0.1635	0.3484**
	G			1	0.5071**	0.3588**	-0.1974	0.5014**
Panicle length	P				1	0.3342**	-0.1422	0.3219**
	G				1	0.4261**	-0.1946	0.1183
1000 grain weight	P					1	-0.5763**	0.1429
	G					1	-0.6522**	0.2018
No. of grainspanicle^{-1}	P						1	-0.0697
	G						1	-0.132

P: Phenotypic correlation coefficients, G: Genotypic correlation coefficients

(2021) and Sucharitha et al. (2022)

The distribution of 35 genotypes into 6 clusters (Table 5) was random and highest number of genotypes (16) were grouped into cluster I followed by cluster II (10) and cluster III (6). Single genotype is allotted to each of IV, V and VI clusters. Grouping of genotypes into different clusters suggested the presence of ample amount of divergence in present experimental material studied and allotment of genotypes from various sources to same cluster and genotypes developed from same geographical area into different clusters indicates that grouping pattern does not relate to geographical origin. Murty and Arunachalam (1966) stated that genetic drift and selection in different environments could cause greater diversity than geographical distance. These findings are similar to the reports of Toshimenla et al. (2016), Chandramohan et al. (2016), Ashok et al. (2017) and Shaili et al. (2022). Highest intra cluster distance of 8.34 (Table 6) was observed for cluster III suggested the exploitation of genotypes from these cluster as parents based on their highest mean performance. Least intra cluster distance (6.77) of cluster I indicated the presence of less divergence among the genotypes of this cluster for the characters studied as these genotypes might be developed by practicing unidirectional selection pressure for one or more traits. Degree of divergence between the parents is the key for a successful breeding programme. Highest inter cluster distance of 27.75 (Table 6) was observed between clusters IV and VI, followed by cluster III and VI (24.69), cluster IV and V (22.34) and cluster III and V (22.23),thus crosses between these clusters would result high heterosis in F_1 progeny. Contribution of each trait to the total divergence (Table 7) indicated that the present experimental material is more divergent for the character 1000 grain weight (44.2%) followed by days to 50% flowering (40.17%) and plant height (10.76%), whereas, panicle length (1.18%), number of grains panicle^{-1} (1.85%) and grain yield (1.85%) contributed least to the total divergence. Singh et al. (2021) reported highest contribution of divergence by test weight and plant height from their studies. Cluster means (Table 7) for the traits under study pointed out that, greater range was observed for 1000 grain weight i.e. from 13.61 g (cluster II)

Table 5: Grouping of genotypes into different clusters in rice

Cluster	No. of genotypes	Genotype
I	16	JGL 26973, JGL 18047, JGL 24497, MTU 1010, JGL 24267, JGL 24527, JGL 24548, JGL 25154, JGL 26956, JGLH 1, JGLH 37, WDR 359, JGL 24423, MTU 1156, JGL 30090
II	10	JGL 18629, JGL 19607, JGL 21078, JGL 21820, JGL 21831, JGL 25925, JGL 27361, JGL 27371, JGL 28542, JGL 3844 NLR 34449
III	6	JGL 24309, JGL 24513, JGL 26959, JGL 26961, PSBRC 1-2-1-2, MTU 1121
IV	1	JGL 23183
V	1	Pusa 44
VI	1	JGLH 6

Table 6: Average intra (diagonal) and inter cluster distances (Tocher method) for 35 rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	6.77	13.63	14.01	17.91	12.75	13.14
Cluster II		7.33	15.15	11.58	13.97	19.76
Cluster III			8.34	11.16	22.23	24.69
Cluster IV				0	22.34	27.75
Cluster V					0	10.35
Cluster VI						0

Table 7: Cluster means and percent contribution of each character towards total divergence of 35 rice genotypes for 7 characters

Cluster	Days to 50% flowering	Effective bearing tillers m^{-2}	Plant height (cm)	Panicle length (cm)	1000 grain weight (g)	No. of grains $panicle^{-1}$	Grain yield (kg ha^{-1})
Cluster I	75	226	91.5	24.3	23.43	184	6808
Cluster II	80	228	86.2	23.0	13.61	259	6383
Cluster III	87	231	92.6	23.9	22.52	169	6664
Cluster IV	89	227	92.2	25.1	14.12	229	6242
Cluster V	66	219	93.4	23.1	16.29	150	5717
Cluster VI	66	246	82.9	24.0	22.73	173	5367
Percentage contribution of character	40.17	0	10.76	1.18	44.2	1.85	1.85
Number of times ranked first	239	0	64	7	263	11	11

to 23.43 g (cluster I) followed by for days to 50% flowering i.e. from 65.5 days to (cluster VI) to 88.5 days (cluster IV). Early maturity character in rice is more advantageous as it accommodates 2–3 crops per year. Thus, genotypes from cluster V and VI can be use as parents for development of extra early varieties. Non lodging nature is most important feature for a rice variety to make it suitable for wet direct seeding method of cultivation. Plant height is one of the stem morphology traits associated with the lodging anomaly (Assefa et al., 2000) and dwarfness is a desirable trait contributes for non-lodging nature. Hence, genotypes fell in clusters II and IV are the best choice for developing high yielding dwarf varieties. As observed greater divergence for the trait 1000 grain weight, present experimental material could be the great source for development of fine, super fine and coarse grain varieties. Genotypes from clusters II, IV and V can be used for development of fine varieties whereas, coarse grain varieties could be developed by using genotypes from clusters I, III and VI as parents in breeding programme.

4. CONCLUSION

High PCV, GCV, heritability and genetic advance values for 1000 grain weight and number of grains $panicle^{-1}$ indicated the role of additive gene action, thus direct selection was effective for improvement of these traits. Effective bearing tillers m^{-2}, plant height and panicle length had significant positive association with yield under wet direct seeding situation. As wet direct seeded rice was more prone to lodging due to shallow or peripheral sowing, intermediate or low plant height was desirable trait for lodging resistance. Hence, genotypes from clusters II and IV with low mean values for plant height might be used for development of non-lodging cultivars suitable for wet direct seeding method.

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