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Assessment of genetic variability in F5 generation across upland and lowland condition in rice (*Oryza sativa* L.)

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ABSTRACT

The present study was conducted with the objectives to estimate genetic variability for different characters, to estimate heritability, genetic advance as per cent of mean for identification of promising genotypes suited for direct seeded and transplanted condition in rice. As varietal development for direct seeded rice has been neglected which may explain why it has not become popular such comparison were made on uncertain rainfall conditions. Analysis of variance indicated that the mean square due to between family were highly significant for all characters under study under direct seeded and transplanted condition, which revealed presence of significant genetic variability between the families. Intra class correlation lead the interference that differences between family is large and each family differentiated distinctly from the other at higher level in F_5 generation. High genotypic and phenotypic coefficient of variation was recorded for grain yield plant^{-1}(g) and moderate for others under direct seeded condition and moderate GCV and PCV was recorded for grain yield plant^{-1} and moderate for others in transplanted condition. High heritability coupled with genetic advance as per cent of mean was recorded for days to 50% flowering, days to maturity, number of panicles plant^{-1}, number of spikelets panicle^{-1}, plant height (cm), number of filled grains panicle^{-1}, 1000 grain weight (g), grain yield plant^{-1}(g) and moderate for others in direct seeded and transplanted condition. This study, between-family variance was prioritized during selection to enhance genetic superiority in grain yield. Out of twenty-six families derived from thirteen crosses, seven families under direct seeding and nine families under transplanted condition exhibited superior yield traits compared to the check. Notably, six families demonstrated consistent superiority across both conditions.

Keywords: *Genotypic coefficient of variability, phenotypic coefficient of variability, heritability, within family variance, between family variance, genetic advance and intra-class correlation*

I. INTRODUCTION

Rice *(Oryza sativa* L.) is one of the most important cereal crop belonging to the tribe *oryzae* of the family *Gramineae* cultivated rice is diploid having 24 chromosomes (2n = 2x = 24). Rice is self-pollinated crop having chasmogamous nature consist six stamens and stigma enclosed by lemma and palea. The inflorescence of rice is called as panicle consists group of spikelets. Rice grain is called as 'caryopsis'. Rice is next to wheat and maize in the global area, production and productivity. Globally 90% of milled rice production is use as human food. Rice provides 20% of the world's dietary energy supply. It is cultivated on nearly 15% of world arable land. It is semi-aquatic plant and can be grown under aerobic dry and anaerobic flooded condition. It is cultivated in 116 countries globally by 144 million farm family in around 162 million hectares producing 480 million tonnes milled rice [1].

Rice is a C_3 plant. Rice is grown as dry direct seeded rice, wet seeded rice and transplanted rice or water seeded rice. Dry seeding is practice in upland, drought prone, rainfed lowland and eastern India.

Rice requires 2500 and 5000 litres of water for transplanted rice cultivation for producing one kg rice in Pakistan and India respectively. Day by day, the global temperature is increasing as well as to meet the rising population food requirement we have to maximize the production sustainably. The freshwater resources are depleting due to excess stress on fresh water bodies from where water is used for farming, so in such situation direct seeded rice is the best option for cultivation which require less water in erratic rainfall pattern impact the farmers income. Many rice varieties have been developed and released for cultivation under direct seeding condition in India. Hence, objectives of this study were to ascertain the superior rice genotypes under direct seeded and transplanted condition. While, simultaneously elucidating the genetic framework of rice through estimation of parameters related to genetic variability, we attained a comprehensive understanding genetic potential with ultimate goal of identifying superior families for advancement in further generation.

II. MATERIALS AND METHODS

The study has been carried out on F_5 families at research field of Agriculture Research Station, Sakoli (Bhandara). In *Kharif* 2023 – 24, twenty-six families from thirteen crosses along with four checks were sown in randomized block design with two replication of spacing of 20 cm was maintained to accommodate plants in plot size 4.0 x 2.0 m in direct seeded and transplanted condition.

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Data were recorded from 10 observational plants on plot basis for characters *viz.,* days to 50% flowering, days to maturity, number of tillers plant^{-1}, number of panicles plant^{-1}, number of spikelets panicle^{-1}, plant height (cm), panicle length (cm), number of filled grains panicle^{-1}, spikelet fertility%, 1000 grain weight (g) and grain yield plant^{-1} (g).

The analysis of variance for eleven characters of twenty-six families as well as four check was computed by [18]. Phenotypic and genotypic coefficient of variance were estimated by using formula given by [3].

Broad sense heritability for all characters was calculated as per the method outlined by [6]. Genetic advance was calculated as per method outlined by [15].

III. RESULTS AND DISCUSSION

Analysis of variance

The data recorded on eleven characters in twenty-six families along with four checks were subjected to analysis of variance to know the genetic difference between families and within families. The results of analysis of variance are presented in table 1. showed highly significant mean square due to between family for all the eleven characters in direct seeded and transplanted condition presented in table1.

Intra class correlation (t)

The intra class correlation (t) which is the ratio of two variances *i.e.* between family variances **(σ^2f)** and total phenotypic variance (σ^2p) were estimated in F_5 generation in this study. This value was observed to range from 0.20 for spikelet fertility % to 0.96 for days to 50% flowering in direct seeded condition while, this value was observed to range from 0.19 for spikelet fertility % to 0.95 for days to 50% flowering under transplanted condition. This indicated that differences between individuals within a family are at lower level for all the characters but each family distinctly differentiated from other also at higher level. Therefore, weightage was suggested to be assigned to between family variances in this generation. This indicates that family selection will be more rewarding in F_5 generation.This conclusion is similar with prior findings *i.e.* [10], [7] and [16] which revealed F_5 families were highly significant for all characters indicating considerable genetic variation among F_5 families.

Components of genetic variability

Knowledge on relative contribution of genetic and non-genetic sources on the quantitative trait variability is useful in formulating appropriate selection strategies to bred improved cultivars. The estimates of genotypic coefficient of variation and phenotypic coefficient of variation, which reflects average inter-genotype differences are more useful tools to understand variability among genotypes.

In direct seeded condition, genotypic coefficient of variation (GCV)exhibited the values in high category (> 20%) for only grain yield plant^{-1}(g) was 23.38% while moderate for number of filled grains panicle^{-1} (15.58%), number of spikelets panicle^{-1} (14.80%), 1000 grain weight (g) (13.92%), days to 50% flowering (12.42%), number of panicles plant^{-1} (12.41%), number of tillers plant^{-1} (12.19%), panicle length (cm) (10.84%) while, Genotypic coefficient of variation exhibited the values in moderate category (20 – 10 %) for grain yield plant^{-1}(g) 18.47 % , number of filled grains panicle^{-1} (15.10 %), 1000 grain weight (13.04 %), number of spikelets panicle^{-1} (12.71 %), days to 50% flowering (11.62 %), number of panicles plant^{-1} (10.40 %) and number of tillers plant^{-1} (10.14 %) indicates presence of significant variability suggest the possibility of successful selection for character enrichment. Similarly, phenotypic coefficient of variation (PCV) was also observed high for grain yield plant^{-1} (g) (24.14%) and moderate phenotypic coefficient of variation observed in number of filled grains panicle^{-1} (17.24%) followed by number of tillers plant^{-1} (16.08%), number of spikelets panicle^{-1} (15.54%), number of panicles plant^{-1} (15%), panicle length (cm) (14.42%),1000 grain weight (g) (14.26%), days to 50% flowering (12.65%) under direct seeded condition,While in transplanted condition phenotypic coefficient of variation (PCV) was observed high for grain yield plant^{-1} (20.12%) and moderate phenotypic coefficient of variation observed in number of tillers plant^{-1} (17.98%) followed by number of panicles plant^{-1} (17.51%), number of filled grains panicle^{-1}(16.80%), panicle length (cm) (13.70), 1000 grain weight (g) (13.59%), number of spikelets panicle^{-1} (13.42%) and days to 50% flowering (11.90%).This agreement with [8]. found moderate GCV and PCV for plant height and high for yield plant^{-1} [11], [16], [14], and [12] in rice.

The extent of transmission of traits to its off-springs is estimated by heritability. Such estimate facilitates the evaluation of genetic and environmental effect aiding in selection. Heritability per cent ranged from 20.36% (spikelet fertility %) to 96.39% (days to 50% flowering). High heritability was recorded for days to 50% flowering (96.39%) followed by 1000 grain weight (g) (95.23%), grain yield plant^{-1} (g) (93.86%), number of spikelets panicle^{-1} (90.79%), days to maturity (90.73%), number of filled grains panicle^{-1}(81.67%), plant height (cm) (77.14%), number of panicles plant^{-1} (68.40%), number of tillers plant^{-1} (51.43%), panicle length (cm) (56.49%) under direct seeded condition. However, Heritability percent ranged from 19.26% (spikelet fertility %) to 95.54% (days to 50% flowering). High heritability was recorded for days to 50% flowering (95.54%) followed by days to maturity (93.02%), 1000 grain weight (g) (92.12%), number of spikelets panicle^{-1} (89.80%), grain yield plant^{-1} (84.25%), number of filled grains panicle^{-1}(80.74%), plant height (72.19%) and moderate heritability were recorded for panicle length (51.22%) followed by number of panicles plant^{-1} (35.61%) and number of tillers plant^{-1} (31.8%) in transplanted condition. High to moderate estimate of heritability for above traits suggested less influence of environmental factors in the expression of these traits.

Genetic advance as percentage of mean under direct seeded condition was high for grain yield plant^{-1} (g) (46.68%) followed by number of filled grains panicle^{-1} (29.01%), number of spikelets panicle^{-1} (29.06%), 1000 grain weight (g) (27.98%), days to 50% flowering (25.12%), number of panicles plant^{-1} (21.14%) and moderate for number of tillers plant^{-1} (19.02%), days to maturity (18.25%), panicle length (cm) (16.79%), plant height (cm) (11.50%). While, high for grain yield plant^{-1} (g) (34.92%) followed by number of filled grains panicle^{-1}(27.96%), 1000 grain weight (25.79%), number of spikelets panicle^{-1} (24.81%) and days to 50% flowering (23.41%) and moderate for days to maturity (17.91%), panicle length (14.47%), number of panicles plant^{-1} (12.74%), number of tillers plant^{-1} (11.78%), plant height (11.11%) under transplanted condition. When all the genetic parameters for characters were considered, it was found that grain yield plant^{-1} (g) exhibited high genotypic coefficient of variation in direct seeded condition while moderate in transplanted condition, high heritability along with high genetic advance per cent of mean.

This indicated that these were influenced by additive gene action operating in the expression of these traits in F_5 generation and help as criteria for making selection. Similar findings were also reported by [4], [5], [9], [20], [11] found high heritability coupled with genetic advance for number of filled grains panicle^{-1} and grain yield plant^{-1} (g) [17] and [19] also reported similar findings in rice.

Selection of superior families

Any appraisal of the breeding material permitting elimination of material of low potential is clearly advantageous because all important programme has limitation and elimination of poor material enhances the probability of finding superior segregants in remaining material [2]. Individual families were selected from F_4 generation raised in F_5 generation to test the performance and homozygosity. These families which were subjected to evaluation for further generation till homozygosity is attained.

Selection of superior families on the basis of grain yield plant^{-1} (g) may not be effective and hence plant breeder has to involve large number of component characters simultaneously in the selection.But handling of large number of component characters simultaneously become cumbersome and hence selections of plants on the basis characters having moderate to high GCV, PCV, high heritability and genetic advance as percentage of mean was considered. In the present study only one character grain yield plant^{-1} (g) showed high GCV, high PCV, high heritability and genetic advance as percentage of mean in direct seeded condition and moderate GCV, high PCV high heritability and genetic advance as percentage of mean under transplanted condition. The efficacy of this selection process is influenced by heritability estimates and genetic diversity metrics [13]. Hence, considered for selection in F_5 generation. This showed that this character was performed under additive gene action and selection would be rewarding in improving this trait, hence was considered as criteria for selection.

Superior families from F_5 generation which was selected from twenty-six families derived from thirteen crosses on the basis of grain yield plant^{-1} (g) along with other yield contributing traits under direct seeded, transplanted, and superior in both conditions presented on table 3, table 4 and table 5 respectively.

IV. CONCLUSIONS

In the present study, the result from between family variance, within family variance and intra-class correlation (t) weightage should be given to between family variance (σ^2_f) during selection. Seven families from direct seeded condition and nine families under transplanted condition obtained from twenty-six families from thirteen crosses exhibiting superiority over check for grain yield plant^{-1} (g) with yield and yield contributing characters were identified. From which six families were found similarly superior under direct seeded and transplanted condition. Superior families were identified for advancement in further generations before forwarding to yield trials.

Future scope of study

To mitigate the challenge of food security as rice is major staple food crop globally, mostly cultivated by the water intensive methods.The productivity and sustainability of rice-based system hampered due to changing climatic condition and reduction in the global water table regime and to find elite genotypes with best performance under adverse climatic condition.

Conflict of interest

It is very difficult to identify the promising genotypes due to environmental variation occurred as per the different weather conditions. The genetic variability reached to plateau by the excessive gene fixation causes the non-responsiveness of genotypes to further selection.

Table 1. Analysis of variance between family and within family variance in F5 generation under direct seeded and transplanted condition

Source of variation		d.f.	Mean sum of square									
			Days to 50% flowering	Days to maturity	No. of tillers plant^{-1}	No. of panicles plant^{-1}	No. of spikelets panicle^{-1}	Plant height (cm)	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility %	1000 grain weight (g)	Grain yield plant^{-1}
Between families	DSR	29	2428.48**	2419.60**	18.17**	16.30**	10545.62**	1052.45**	125.69**	8618.90**	137.19**	175.61**	455.20**
	Transplant		2324.99**	2426**	14.89**	13.74**	8359.66**	1068.82**	110.43**	8141.80**	133.9**	160.49**	358.19**
Within families	DSR	570	4.53	12.29	0.65	0.37	53.22	15.56	4.66	95.65	22.44	0.44	1.48
	Transplant		5.43	9.06	1.44	1.15	47.22	20.20	5.02	95.95	23.37	0.68	3.32
Intra class correlation (t)	DSR		0.96	0.91	0.57	0.68	0.91	0.78	0.56	0.81	0.20	0.95	0.94
	Transplant		0.95	0.93	0.32	0.35	0.9	0.72	0.51	0.80	0.19	0.92	0.84

*** - Significant at 1% level of significance*

Table 2. Genetic parameters estimate for different characters in F_5 generation

Parameters		Days to 50% flower	Days to maturity	No. of tillers plant^{-1}	No. of panicles Plant^{-1}	No. of spikelets panicle^{-1}	Plant height (cm)	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility %	1000 grain weight (g)	Grain yield plant^{-1} (g)
Mean	DSR	88.51	117.91	7.67	7.19	154.71	113.26	22.68	132.46	86.03	21.25	20.36
	Trans	92.62	121.96	8.08	7.62	160.39	114.04	23.40	132.81	86.02	21.66	22.80
Min	DSR	61	91	4	4	101	89	10	58	61.26	14	11.5
	Trans	68	96	4	4	111	90	10	65	61.7	14.3	14.1
Max	DSR	107	137	13	9	203	135	32	199	98.43	32.9	29.7
	Trans	110	146	12	12	198	135	39	196	97.71	29.1	36
Range	DSR	46	46	9	5	102	46	22	141	37.17	18.9	18.2
	Trans	42	50	8	8	87	45	29	131	36.45	14.8	21.9
Genotypic variance	DSR	120.94	120.36	0.88	0.8	524.62	51.85	6.05	426.16	5.737	8.75	22.69
	Trans	115.98	120.88	0.67	0.63	415.63	52.43	5.27	402.29	5.53	8.0	17.74
Phenotypic variance	DSR	125.47	132.65	1.52	1.16	577.83	67.21	10.71	521.81	28.17	9.20	24.17
	Trans	121.41	129.93	2.11	1.78	462.85	72.63	10.29	498.24	28.75	8.67	21.06
GCV (%)	DSR	12.42	9.30	12.19	12.41	14.80	6.35	10.84	15.58	2.78	13.92	23.38
	Trans	11.62	9.01	10.14	10.40	12.71	6.34	9.81	15.10	2.73	13.04	18.47
PCV (%)	DSR	12.65	9.76	16.08	15	15.54	7.23	14.42	17.24	6.16	14.26	24.14
	Trans	11.90	9.34	17.98	17.51	13.42	7.47	13.70	16.80	6.23	13.59	20.12
Heritability (%)	DSR	96.39	90.73	57.43	68.40	90.79	77.14	56.49	81.67	20.36	95.23	93.86
	Trans	95.54	93.02	31.8	35.61	89.80	72.19	51.22	80.74	19.26	92.12	84.25
GA	DSR	22.24	21.52	1.46	1.52	44.95	13.02	3.80	38.43	2.22	5.94	9.5
	Trans	21.69	21.85	0.95	0.97	39.79	12.67	3.89	37.13	2.12	5.58	8.0
GA (% of mean)	DSR	25.12	18.25	19.02	21.14	29.06	11.50	16.79	29.01	2.58	27.98	46.68
	Trans	23.41	17.91	11.78	12.74	24.81	11.11	14.47	27.96	2.47	25.79	34.92

(DSR- Direct seeded condition and Trans- Transplanted condition)

Table. 3 Superior families selected for yield and yield contributing characters under direct seeded condition

Sr. No.	Families selected	Characters of progeny for which selected under direct seeded condition
1.	SKL-19-05-35-124-81	Grain yield plant^{-1} (27.73 g), number of tillers plant^{-1} (8.8), number of panicles plant^{-1} (8.55), number of spikelets panicle^{-1} (163.9) and panicle length (25.51 cm).
2.	SKL-19-04-64-17-28	Grain yield plant^{-1} (27.52 g), days to 50% flowering (75 days), number of tillers plant^{-1} (8.55), panicle length (25.32 cm) and 1000 grain weight (25.68 g).
3.	SKL-19-04-64-04-26	Grain yield plant^{-1} (27.50 g), days to 50% flowering (73.35 days), number of tillers plant^{-1} (8.4)and 1000 grain weight (25.42 g).
4.	SKL-19-03-60-14-37	Grain yield plant^{-1} (27.4 g), days to 50% flowering (75.45 g) and number of tillers plant^{-1} (8.55).
5.	SKL-19-05-35-100-34	Grain yield plant^{-1}(27.25 g), number of tillers plant^{-1} (8.5), number of panicles plant^{-1} (8.4) and number of spikelets panicle^{-1} (165.7).
6.	SKL-19-03-110-100-96	Grain yield plant^{-1} (27.23 g) days to 50% flowering (74.55) and number of tillers plant^{-1} (8.5).
7.	SKL-19-02-103-309-188	Grain yield plant^{-1} (26.91 g), number of tillers plant^{-1} (8.55), number of panicles plant^{-1} (8.35) and number of spikelets panicle^{-1} (170.3), number of filled grains panicle^{-1} (147.85) and 000 grain weight (23.30 g).

Table. 4 Superior families selected for yield and yield contributing characters transplanted condition

Sr. No.	Families selected	Characters of progeny for which selected under transplanted condition
1.	SKL-19-06-08-15-24	Grain yield plant^{-1} (30.60 g), number of tillers plant^{-1} (8.1) and number of panicles plant^{-1} (7.5) .
2.	SKL-19-06-08-15-08	Grain yield plant^{-1} (30.51 g), days to 50% flowering (77.5 days), number of tillers plant^{-1} (7.55) and 1000 grain weight (22.65 g).
3.	SKL-19-05-35-124-81	Grain yield plant^{-1} (28.91 g), number of tillers plant^{-1} (9)and 1000 grain weight (22.84 g).
4.	SKL-19-05-35-100-34	Grain yield plant^{-1} (28.38 g), and number of tillers plant^{-1} (8.65) and number of spikelets panicle^{-1} (168.5).
5.	SKL-19-03-60-14-37	Grain yield plant^{-1}(28.20 g), days to 50% flowering (79.45 days), number of tillers plant^{-1} (8.95) and number of panicles plant^{-1} (8.45).
6.	SKL-19-03-110-100-96	Grain yield plant^{-1} (28.05 g) days to 50% flowering (79), number of tillers plant^{-1} (9.05) and number of spikelets panicle^{-1} (174).
7.	SKL-19-02-103-305-136	Grain yield plant^{-1} (27.86 g), number of tillers plant^{-1} (9.15), number of panicles plant^{-1} (8.60), number of spikelets panicle^{-1} (174.05) and number of filled grains panicle^{-1} (155.35).
8.	SKL-19-02-103-309-188	Grain yield plant^{-1} (27.81 g), number of spikelets panicle^{-1} (175.6) and panicle length (25.75 cm) and number of filled grains panicle^{-1} (154.15).
9.	SKL-19-04-64-04-26	Grain yield plant^{-1} (26.95 g), days to 50% flowering (77.5 days), panicle length (26.07 cm) and 1000 grain weight (25.22 g).

Table. 5 Superior families selected in both direct seeded and transplanted condition

Sr. No.	Selected families
1.	SKL-19-05-35-124-81
2.	SKL-19-04-64-04-26
3.	SKL-19-03-60-14-37
4.	SKL-19-03-110-100-96
5.	SKL-19-05-35-100-34
6.	SKL-19-02-103-309-188

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