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ASSESSMENT OF GENETIC VARIABILITY IN F_5 GENERATION UNDER TRANSPLANTED CONDITION IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

The present study was conducted to estimate genetic variability for different characters, to estimate heritability and genetic advance and to identify promising genotypes suited for transplanted condition in rice. The study has been carried out on F_5 families consist twenty-six families from thirteen crosses along with four checks were evaluated in two replication. Analysis of variance indicated that the mean square due to between family were highly significant for all characters under study, which revealed the presence of significant genetic variability between the families. Intra class correlation lead the interference that differences between individuals within family is small and each family differentiated distinctly from the other at higher level in F_5 generation. Moderate GCV and high PCV were recorded for gain yield plant^{-1} and moderate for others. High heritability was recorded for days to 50% flowering, days to maturity, 1000 grain weight (g), number of spikelets panicle^{-1}, grain yield plant^{-1} (g), number of filled grains panicle^{-1}, plant height (cm) and moderate for others. Genetic advance as percentage of mean were high for grain yield plant^{-1}, number of filled grains panicle^{-1}, 1000 grain weight (g), number of spikelets panicle^{-1}, days to 50% flowering and moderate for other characters. Grain yield plant^{-1}(g) was character which recorded moderate GCV and high PCV, heritability and genetic advance as influenced by additive gene action selection would be effective. Hence, nine families exhibited superiority over check for grain yield plant^{-1}(g) and other yield attributing characters were identified for advancement in next generations.

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

Introduction

Rice (*Oryza sativa* L.), a crucial cereal crop within the tribe *Oryzae* of the family *Gramineae,* is a diploid species characterized by a chromosome number of 24 (2n=2x=24). It exhibits self-pollination and chasmogamous flowering traits, featuring six stamens and a stigma that is encased by the lemma and palea. The inflorescence structure, termed a panicle, comprises multiple spikelets and the rice grain is scientifically referred to as "caryopsis."

Globally, rice ranks second only to wheat and maize in terms of cultivated area, production and productivity. Approximately 90% of milled rice is allocated for human consumption, contributing to around 20% of the world's dietary energy supply and occupying nearly 15% of arable land. As a semi-aquatic plant, rice can be cultivated under both aerobic and anaerobic conditions. It is produced across 116 countries, involving approximately 144 million farming families on around 162 million hectares, resulting in a total production of 480 million tonnes of milled rice (Anonymous, 2023).

To enhance genetic resistance and implement water-efficient cultivation strategies, plant breeders must elucidate inheritance patterns to generate the desired phenotypic variability through outcrossing. This approach yields segregating populations with genetically diverse individuals, enabling the selection of favourable traits for subsequent generations. The efficacy of this selection process is influenced by heritability estimates and genetic diversity metrics (Poehlman *et al*., 1995). This study aims to genetically map the F_5 rice population, underscoring the importance of accurate genetic information including assessments of genetic variability, coefficients of genetic diversity, heritability, and the type of gene action influencing genotype expression across varied environmental conditions for the success of plant breeding programs.

Material 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. These families 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 low land condition. 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 (Sharma *et al.* (2006). Phenotypic and genotypic coefficient of variance were estimated by using formula given by (Burton *et al.*1953).

Broad sense heritability for all characters was calculated as per the method outlined by Hanson *et al*., (1956). Genetic advance was calculated as per method outlined by Robinson *et al.* (1949).

Results and Discussion

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. The intra class correlation (t) which is the ratio of two variances *i.e.* between family variances (σ^2_f) and total phenotypic variance (σ^2_f) were estimated in F_5 generation in this study. This value was observed to range from 0.19 for spikelet fertility % to 0.95 for days to 50% flowering. This indicated that differences between individuals within a family are smaller for days to 50% flowering, days to maturity, , number of spikelets panicle^{-1}, plant height (cm), panicle length (cm), number of filled grains panicle^{-1},1000 grain weight(g) and grain yield plant^{-1} (g) but each family distinctly differentiated from other at higher level. Therefore, weightage was suggested to be assigned to σ^2_f (between family) in this generation. This indicates that between family selection followed by within family selection will be more rewarding in F_5 generation were reported by Mishra *et al.* (2020), Herawati *et al.* (2021) and Saran *et al.* (2023).

Genetic parameters like mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance were calculated for eleven characters in F_5 population and presented in table 2 and table 3.

Mean and Range

The grand mean recorded for twenty-six families of F_5 population along with four checks were found to 92.62 for days to 50% flowering, 121.96 for days to maturity, 8.08 for number of tillers plant^{-1}, 7.62 for number of panicles plant^{-1}, 160.39 for number of spikelets panicle^{-1}, 114.04 cm for plant height, 23.40 cm for panicle length, 132.81 for number of filled grains panicle^{-1}, 86.02 % for spikelet fertility%, 21.66 g for 1000 grain weight and 22.80 g for grain yield plant^{-1} presented in table 2. High range of 131 was exhibited for number of filled grains panicle^{-1} followed by number of spikelets panicle^{-1}(87), days to maturity (50), plant height (cm) (45) and days to 50% flowering (42) which indicated that wide range of variation were functioning for these characters. he estimates of range provide new clue about the occurrence of of genotypes with extreme expression which varied with the trait. In accordance to these results wide range of variation for yield and contributing components were also reported by Longkho *et al.* (2020) in rice, Ferdous *et al.* (2023), Herawati *et al.* (2021), Quadri *et al.* (2023) and Saran *et al.* (2023) in rice.

Genotypic variance, phenotypic variance and their respective coefficient of variation

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 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%). The estimates of genotypic coefficient of variability and phenotypic coefficient of variability values for number of tillers plant^{-1}, number panicle plant^{-1}, panicle length(cm) and spikelet fertility% showed higher difference which indicates the greater role of environmental factors influencing the expression of these characters. However, low difference was observed for days to 50% flowering, days to maturity, number of spikelets panicle^{-1}, number of filled grains panicle^{-1},1000 grain weight and grain yield plant^{-1} which indicates less sensitivity of these characters in the fluctuating environment. This agreement with Longkho *et al.* (2020), Vijayakumari *et al.* (2022), Saran *et al.* (2023), Quadri *et al.* (2023), Sheeba *et al.* (2023) in rice.

Heritability and genetic advance

The estimates of heritability (broad sense) and genetic advance estimated in material consisting twenty-six families of thirteen crosses of F_5 population along with four checks for eleven characters are reported in Table 3. 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%). All characters show high to moderate heritability per cent except spikelet fertility % (19.26%) rewarding for selection. 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 was 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%). When all the genetic parameters for characters were considered, it was found that grain yield plant^{-1} exhibited high genotypic coefficient of variation, 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 Chuchert *et al.* (2018), Manjunath *et al.* (2018), Venketesan *et al.* (2019), Nanda *et al.* (2021), Singh *et al.* (2022), Vadodariya *et al.* (2023) and Pardhi *et al.* (2024) in rice.

Selection of superior families

In the present study only one character grain yield plant^{-1} (g) showed moderate GCV, high PCV, high heritability and genetic advance as percentage of mean and hence considered for selection in F_5 generation. This showed that this character was performed 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} and yield contributing characters.

Nine families were selected from twenty-six families to be forwarded to F_6 generation *viz.,* SKL-19-06-08-15-24, SKL-19-06-08-15-08, SKL-19-05-35-124-81, SKL-19-05-35-100-34, SKL-19-03-60-14-37, SKL-19-03-110-100-96, SKL-19-02-103-305-136, SKL-19-02-103-309-188 and SKL-19-04-64-04-26 for yield and yield contributing characters which observed to be significantly high as compared to highest check MTU 1010 for grain yield plant^{-1}. The family SKL-19-06-08-15-24 produced maximum yield of 30.60 g followed by above mentioned families respectively.

Conclusion

In the present study, genetic characters were considered, it was found that grain yield exhibited moderate genotypic coefficient of variation, high phenotypic coefficient of variation, high heritability along with high genetic advance as percentage of mean hence considered as a criteria of selection as well as result from between family variance, within family variance and intra class correlation (t) tends weightage to σ_f^2 should be given during selection. Hence, nine families from twenty-six families derived from thirteen crosses exhibiting superiority over check for grain yield plant^{-1} with yield contributing characters were identified for advancement in further generations before forwarding to yield trials.

Table 1 : Analysis of variance between family and within family variance in F_5 generation

Source of variation	Mean sum of square											
	d.f.	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} (g)
Between families	29	2324.99**	2426**	14.89**	13.74**	8359.66**	1068.82**	110.43**	8141.8**	133.9**	160.49**	358.19**
Within families	570	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)		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

Table 2 : Mean performance of 26 families along with four checks for various characters

1	2	3	4	5	6	7	8	9	10	11	12	13
Sr. no	**Progeny**	**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} (g)**
1	SKL-19-01-189-295-24	70.25	100.10	7.85	7.80	183.05	119.70	24.38	160.45	87.48	25.19	21.27
2	SKL-19-02-103-305-136	98.45	127.55	9.15	8.60	174.05	125.40	26.10	155.35	89.27	23.06	27.86
3	SKL-19-03-60-14-37	79.45	108.45	8.95	8.45	139.45	121.30	22.33	119.55	85.77	22.3	28.20
4	SKL-19-04-64-04-26	77.5	107.70	9.00	8.70	156.95	119.5	26.07	127.45	81.37	25.22	26.95
5	SKL-19-05-35-100-34	92.25	122.90	8.65	8.45	168.5	114.1	25.48	143.8	85.41	22.31	28.38
6	SKL-19-06-08-15-08	77.5	106.80	7.55	7.15	143.5	116.05	23.54	127.55	88.9	22.65	30.51
7	SKL-19-10-108-104-11	103.15	133.05	8.15	7.85	152.7	118.65	23.57	126.4	82.87	19.04	19.26
8	SKL-19-11-65-01-05	105.4	137.85	7.20	6.90	189.2	113.00	23.52	164.45	86.92	15.52	19.40
9	SKL-19-12-11-01-08	103.55	136.15	6.60	6.30	179.6	98.45	22.26	155	86.33	18.52	19.98
10	SKL-19-17-62-15-24	92.35	123.00	6.10	5.75	120.25	111.65	22.32	102.05	85.02	18.01	17.24
11	SKL-19-13-29-04-08	91.35	121.50	8.70	7.80	150.75	119.25	16.60	131.9	87.64	22.28	18.95
12	SKL-19-21-21-08-35	107.05	136.85	9.05	8.00	184.45	107.10	21.61	159.3	86.44	18.99	19.50
13	SKL-19-26-44-105-20	98.9	128.85	8.35	7.95	147.15	104.35	21.59	125.1	85.09	20.25	17.67
14	SKL-19-01-126-44-32	74.5	104.85	8.30	7.9	187.65	113.9	24.33	165.3	88.13	25.45	23.04
15	SKL-19-02-103-309-188	99.3	129.55	8.75	8.45	175.6	128.2	25.75	154.15	87.94	23.48	27.81
16	SKL-19-03-110-100-96	79	107.15	9.05	8.5	174	118.4	22.13	156.1	89.8	22.95	28.05
17	SKL-19-04-64-17-28	79.65	108.70	8.55	8.35	159.35	114.35	25.77	134.95	84.71	26.09	24.81
18	SKL-19-05-35-124-81	94.25	123.05	9.05	8.65	173.4	115.9	24.51	151.75	87.73	22.84	28.91
19	SKL-19-06-08-15-24	82.2	109.75	8.10	7.5	150.9	113.5	24.22	127.25	84.53	22.80	30.60
20	SKL-19-10-108-104-35	103.05	114.60	7.75	7.4	156.55	122.6	24.22	126.95	81.23	20.32	21.63
21	SKL-19-11-65-01-18	104.85	133.40	8.00	7.05	188.7	107.45	24.11	165.5	87.73	15.85	21.39
22	SKL-19-12-11-01-20	104.7	133.45	6.55	6.05	179.6	97.40	21.875	157.75	87.86	21.49	22.40
23	SKL-19-17-62-28-81	94	124.85	6.1	5.80	122.35	109.85	22.19	101.35	82.89	18.73	19.07
24	SKL-19-13-29-04-34	91.3	121.40	8	7.4	141.3	112.75	18.115	126.5	89.67	22.02	18.11
25	SKL-19-21-32-42-45	107.35	136.95	8.65	7.85	187.2	107.15	22.065	159.95	85.48	18.38	19.23
26	SKL-19-26-44-108-40	100.15	129.45	8.1	7.75	150.95	103.5	21.99	126.7	84.09	20.13	17.7
27	Samleshwari	87.05	117.5	8.2	7.55	144.45	112.65	24.675	124	86.15	21.94	21.34
28	Rajeshwari	95.3	126.15	8.1	7.7	149.15	120.75	22.3	130.85	87.80	24.68	21.36
29	Parbhani Aviskar	90.75	122.85	7.45	6.95	156.2	118	27.615	131.7	84.32	24.92	21.64
30	MTU-1010	93.95	124.2	8.5	8.05	124.6	116.15	26.745	104.8	84.36	24.44	21.85
	mean	92.61	121.95	8.08	7.62	160.39	114.03	23.4	138.13	86.09	21.66	22.80
	S.E.(m)±	1.65	2.13	0.85	0.76	4.86	3.18	1.58	5.6	3.83	0.58	1.29
	CD 5%	4.57	2.35	2.35	2.1	13.46	8.81	4.39	15.54	10.6	1.62	3.56
	CV%	1.38	1.2	11.39	11.43	1.37	1.56	5.37	1.71	2.27	3.52	4.97

Table 3 : 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	92.62	121.96	8.08	7.62	160.39	114.04	23.40	132.81	86.02	21.66	22.80
Min	68	96	4	4	111	90	10	65	61.7	14.3	14.1
Max	110	146	12	12	198	135	39	196	97.71	29.1	36
Range	42	50	8	8	87	45	29	131	36.45	14.8	21.9
Genotypic variance	115.98	120.88	0.67	0.63	415.63	52.43	5.27	402.29	5.53	8.0	17.74
Phenotypic variance	121.41	129.93	2.11	1.78	462.85	72.63	10.29	498.24	28.75	8.67	21.06
GCV (%)	11.62	9.01	10.14	10.40	12.71	6.34	9.81	15.10	2.73	13.04	18.47
PCV (%)	11.90	9.34	17.98	17.51	13.42	7.47	13.70	16.80	6.23	13.59	20.12
Heritability (%)	95.54	93.02	31.8	35.61	89.80	72.19	51.22	80.74	19.26	92.12	84.25
GA	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)	23.41	17.91	11.78	12.74	24.81	11.11	14.47	27.96	2.47	25.79	34.92

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