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Genetic analysis of yield and its attributing traits in advanced breeding lines of rice (*Oryza sativa* L.) under aerobic condition

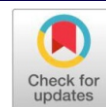
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ABSTRACT

To select improved rice lines under aerobic conditions according to a selection index, degree of association between grain yield and yield attributing characters and their direct, indirect effects on grain yield, a field experiment was conducted using forty advanced breeding lines of rice during kharif season of 2024 at field of All India Coordinated Research Project, Nagpur. The examination used a Randomized Complete Block Design with two replications. All the traits exhibited highly significant differences, indicating the existence of genetic variability among the progenies. The findings revealed that traits like grain yield plant⁻¹ exhibited highest value of genotypic and phenotypic coefficient of variability along with high heritability and genetic advance percentage of mean however, number of spikelet's panicle⁻¹, panicle length and 1000 grain weight displayed moderate genotypic and phenotypic coefficient of variability along with high heritability and genetic advance percentage of mean. Correlation studies revealed that grain yield plant⁻¹ showed a significant positive correlation with plant height, number of panicles plant⁻¹, panicle length, number of spikelet's panicle⁻¹, spikelet fertility and 1000 grain weight, while number of spikelet's panicle⁻¹ had the strongest direct positive impact on grain yield plant⁻¹ followed by panicle length, number of panicles plant⁻¹. The selection index based on the combination of plant height, panicle length, number of panicles plant⁻¹, number of spikelets panicle⁻¹ and grain yield plant⁻¹ has the highest genetic advance and relative efficiency percentage. This indicated that indirect selection via, these traits would be more efficient than direct selection using grain yield alone. The selection index based on the combination of Grain yield plant⁻¹ + Plant height, No. of panicles plant⁻¹ + Panicle length + No. of spikelet panicle⁻¹ has the highest genetic advance and relative efficiency. This indicated that indirect selection via these traits would be more efficient than direct selection using yield alone. Therefore, the progenies SKL-19-01-120-44-32-60, SKL-19-02-77-221-98-83 and SKL-19-02-77-221-98-94 could be selected based on multiple traits selection under aerobic condition for further evaluation.

Keywords: Aerobic rice, variability, heritability, genetic advance, correlation, path coefficients, selection index.

Introduction

Rice (*Oryza sativa* L.) is the most important staple food crop. Rice is commonly cultivated by transplanting seedlings into the puddled soil. This transplanting method is water-intensive and labour-intensive and hence, less profitable. [19]. Aerobic rice is one such strategy to decrease water requirements in rice production. Direct sowing of high-yielding varieties in non-puddled conditions without standing water and maintenance of aerobic soils throughout the growing season describe this novel technique for cultivating rice, whenever necessary, supplemental irrigation is required. Hence, for this condition there should be special bred aerobic genotypes which combine the features of both upland (drought tolerance) and lowland (high yielding) which is pre-requisite for successful cultivation

of rice with limited water resource. [18].

Assessment of variability for the grain yield and yield attributes is essential for the successful yield improvement through breeding. Further grain yield depends on various component characters and knowledge of correlation with yield and among yield component traits in addition to identification of the direct and indirect effects of the traits on yield would help in effective yield improvement. [26]. It is necessary to choose individuals with the best combination of desirable traits when considering several traits. The basis for this selection is a selection index, which is a combination of traits to select, according to their relative weighting. [9].

The present investigation was undertaken in this context to elucidate information on variability, heritability, genetic advance, character association, path coefficients and selection indices with their relative efficiencies among existing aerobic rice progenies to find promising lines for further multilocal yield trials.

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Materials and Methods

The experiment was conducted at the field of All India Coordinated Research Project, Nagpur during the *kharif* season of 2024. The experiment involved thirty- eight F_6 advanced rice progenies of 21 crosses along with two checks viz., Samleshwari and Vandana and was laid out in a randomized complete block design (RCBD) with two replications, utilizing a spacing of 20 cm $\times$ 10 cm under aerobic conditions. The recommended agronomic practices were followed to raise a good and healthy crop. The observations were documented for nine agromorphological traits which are days to 50% flowering, days to maturity, plant height, number of panicles plant⁻¹, panicle length, number of spikelets panicle⁻¹, spikelet fertility, 1000 grain weight and grain yield plant⁻¹. Ten plants from each progeny and five plants from checks under each replication were chosen to collect data from yield related traits. The inner middle rows of each plot were used to randomly select competitive plants in both replications. In each replication, data was collected using tagged plants from each progeny.

The analysis of variance was performed to test the significance of differences between the treatments for all the characters as per the methodology suggested by [14]. The genotypic and phenotypic coefficients of variation was calculated as per the formulae given by [2]. Heritability in broad sense was estimated for various characters by the formulae suggested by [12]. The genetic advance in percent was calculated as per the method

outlined by [10]. Correlation coefficients between yield and yield components as well as among the yield components, were worked out. Path co-efficient analysis was carried out using the simple correlation coefficient to know the direct and indirect effects of the yield components on seed yield as suggested by [28] and illustrated by [5]. Selection indices were constructed using the method developed by [24] based on the discriminate function analysis of [6]. The 10 % selection intensity was used to estimate genetic advances. The estimates of genetic advance were expressed as a percentage of the genetic progress obtained from seed yield per plant alone, which was assumed to initially be 100%, and it was used to compare the relative efficiencies of the different selection indices.

Result and Discussion

Analysis of variance (mean sum of squares) for different characters

The existence of genetic variability is of utmost importance for genetic improvement of desired traits in plant breeding program. This is the fundamental factor that must be considered while making selection. Analysis of variance (ANOVA) revealed highly significant heterogeneity among rice genotypes for all the studied trait, suggesting high and inherent variation among genotypes (Table 1). The earlier scientific studies by [4], [11] and [8] also reported varied response of rice genotypes for grain yield and component traits.

Table 1: Analysis of variance (mean sum of squares) for different characters under study in rice

Characters	d.f	Days to 50% flowering	Days to Maturity	Plant height	No. of panicle	Panicle length	No. of spikelet	Spikelet fertility	1000 Grain weight	Single plant yield
Replication	1	3.84	21.50	123.11	2.02	2.04	163.96	4.88	1.52	19.6
Genotypes	39	162.09**	157.43**	138.19**	1.96**	13.24**	721.42**	12.17**	11.76**	50.86**
Error	39	23.42	18.83	39.26	0.57	1.01	60.70	5.52	0.93	5.05

**Significant at 1% level

Genetic variability parameters

The nature and degree of variation in breeding material for different traits can be analysed using the phenotypic and genotypic coefficients of variation (Table 2).

The study revealed that the magnitude of phenotypic coefficient of variations was slightly higher than the corresponding values of genotypic coefficient of variation but the difference is minimum for the traits like days to 50% flowering, days to maturity, plant height, number of spikelet panicles⁻¹, panicle length, spikelet fertility and 1000 grain weight under study suggesting that the observed variation was least influenced by environmental factors affecting genotype expression. Thus, these traits expressed the true genetic potential in varied environments. These results are true with the findings of [4], [15] and [22]. However, number of panicles plant⁻¹ and grain yield plant⁻¹ showed higher difference between genotypic and phenotypic coefficient of variability which indicates the greater role of environmental factors influencing the expression of these characters.

PCV and GCV were classified as low (0–10%), moderate (10–20%) and high (>20%) according to [2]. Based on this classification, the highest GCV and PCV were recorded for grain yield plant⁻¹ (24.87, 27.47). This showed that the environment has minimal effect on the trait's expression and that the trait is heavily influenced by genetic factors. The existence of high variability for the above-mentioned trait was previously reported by [7] and [17]. Furthermore, number of panicles plant⁻¹ (12.04%, 16.27%), the number of spikelets panicle⁻¹ (11.83%, 12.87%), 1000 grain weight (11.60%, 12.55%) and

panicle length (11.43%, 12.34%) exhibited moderate GCV and PCV, respectively. Therefore, selection of these traits would provide far more opportunities for genetic improvement of the studied genotypes. The findings of the current study in terms of GCV and PCV are broadly consistent with the earlier worker's [27] for number of panicles plant⁻¹, [22] for 1000 grain weight and panicle length. The low value for GCV and PCV were observed for days to maturity (6.98, 8.06), plant height (6.47, 8.66) and spikelet fertility (2.13, 3.48) while days to 50% flowering (9.27, 10.72) exhibited low GCV and moderate PCV values. The selection of these traits offers very little scope for genetic improvement of the progenies examined. The presence of low GCV and PCV for these traits was previously documented by [27] for plant height and spikelet fertility, [15] for days to maturity and plant height.

The degree of genetic variation considered alone is of little use until augmented with information about heritability estimation, which represents the heritable portion of total variation. Heritability is a key factor in determining the selection response as it provides reliable estimates of genetic improvement of a character. [21] classified heritability as low (<30%), moderate (30–60) and high (>60). Based on the above classification, traits namely panicle length (85.86%) followed by 1000 grain weight (85.37%), number of spikelets panicle⁻¹ (84.47%), grain yield plant⁻¹ (81.94%), days to 50% flowering (74.75%) and days to maturity (74.62%) showed high heritability. The rest of the traits showed moderate magnitude of heritability. High heritability estimate indicates strong genetic effect, which make selection based on observable trait useful.

The traits that exhibit high heritability do not necessarily result in high genetic gain but may be due to environmental effects. The breeder should be careful when making a selection based solely on heritability, as this includes both additive and non-additive gene effects. High genetic advance occurs mainly because of additive gene action. Therefore, estimating heritability combined with genetic advance makes greater sense than measuring heritability alone [10]. [10] classified genetic advance as a percentage of mean into three categories: low (<10%), moderate (10-20) and high (>20%). High heritability coupled with high genetic advance as per cent of mean was recorded for grain yield plant⁻¹, number of spikelet panicle⁻¹, panicle length and 1000 grain weight. This indicates that these traits are predominantly influenced by additive gene action, and direct selection based on these traits could lead to significant improvements in grain yield. These results agreed with [22] and [25] for the 1000 grain weight, [13] and [23] for grain yield plant⁻¹, [8] for panicle length and grain yield plant⁻¹, [1] for number of spikelet panicle⁻¹.

However, the traits such as days to 50% flowering and days to maturity showed high heritability accompanied with moderate genetic advance as per cent of mean, suggesting that these traits are governed by both additive and non-additive gene action and high heritability exhibited may be due to the influence of environment rather than genotype alone. Our findings are supported by [18] for days to 50% flowering, [19] for days to maturity. Moderate heritability with moderate genetic advance was reported by the number of panicles plant⁻¹. Moderate heritability coupled with low genetic advance was reported for spikelet fertility and plant height, indicating the presence of non-additive gene action and hence simple selection for these traits would not be effective. Similar findings with these results were reported by [20] for spikelet fertility.

Table 2: Estimate of genetic variability parameters, heritability and genetic advance in rice progenies

Character	Days to 50% flowering	Days to Maturity	Plant height (cm)	No. of panicle plant ⁻¹	Panicle length (cm)	No. of spikelet panicle ⁻¹	Spikelet fertility (%)	1000 Grain weight (g)	Grain yield plant ⁻¹ (g)
Mean	89.83	119.86	108.74	6.91	21.63	154.61	85.47	20.05	19.24
Max	103.65	132.45	125.75	8.65	25.85	187.65	89.98	25.60	31.39
Min	66.86	94.86	95.23	5.38	16.40	115.75	80.28	15.23	13.08
Range	36.79	37.59	30.52	3.27	6.45	71.9	9.7	10.37	18.31
GCV%	9.26	6.98	6.47	12.04	11.43	11.83	2.13	11.60	24.87
PCV%	10.72	8.06	8.66	16.27	12.34	12.87	3.48	12.55	27.47
h ² %	74.75	74.62	55.74	54.81	85.86	84.47	37.56	85.37	81.94
GA	14.831	14.845	10.817	1.271	4.72	34.41	2.30	4.42	8.92
GA% Mean	16.509	12.39	9.95	18.37	21.82	22.41	2.69	22.08	46.38

Correlation studies

Grain yield is a multigenic traits affected by interaction of several traits called component traits. Direct selection for grain yield may mislead the final results. Therefore, association analysis of component traits with grain yield helps the plant breeders in identifying major traits influencing grain yield in plant⁻¹. Grain yield plant⁻¹ exhibited highly significant and positive association (Table 3) with plant height (0.844, 0.559), number of panicles plant⁻¹ (0.984, 0.731), panicle length (0.681, 0.579), number of spikelet's panicle⁻¹ (0.508, 0.409), Spikelet fertility (0.559, 0.338) and 1000 grain weight (0.887, 0.730) and it had significant negative association with days to 50% flowering (-0.415, -0.243) and days to maturity (-0.416, -0.248). These results are in concurrence with the findings of [27] for Spikelet fertility and 1000 grain weight, [22] for days to 50% flowering and days to maturity, [25] for plant height and panicle length.

Days to 50% flowering showed positive significant correlation with days to maturity (0.999, 0.984) and number of spikelet's panicle⁻¹ (0.356, 0.259) while it exhibited negative but significant correlation with plant height (-0.355, -0.230), number of panicles plant⁻¹ (-0.279, -0.228) and 1000 grain weight (-0.697, -0.525) at both genotypic and phenotypic levels.

Days to maturity exhibited a positive and significant correlation with number of spikelet's panicle⁻¹ (0.358, 0.258) while it demonstrated a negative but significant correlation with plant height (-0.358, -0.232), panicle length (-0.278, -0.226) and 1000 grain weight (-0.694, -0.527) at both genotypic and phenotypic levels. Plant height exhibited a positive and highly significant correlation with number of panicles plant⁻¹ (0.938, 0.492), panicle length (0.746, 0.429) and 1000 grain weight (0.777, 0.492). The number of panicles plant⁻¹ exhibited a positive and significant correlation with panicle length (0.571, 0.355), number of spikelet's panicle⁻¹ (0.376, 0.297), spikelet fertility (0.458, 0.277) and 1000 grain weight (0.834, 0.586) at both genotypic and phenotypic levels. Panicle length had a positive and strongly significant correlation with the number of spikelet's panicle⁻¹ (0.368, 0.324), spikelet fertility (0.609, 0.405) and 1000 grain weight (0.588, 0.469). Number of spikelet's panicle⁻¹ exhibited a positive and significant correlation with spikelet fertility (0.275, 0.255) while it demonstrated positive but non-significant correlation with 1000 grain weight (0.065, 0.076) at both genotypic and phenotypic levels. Spikelet fertility showed positive but non-significant correlation with 1000 grain weight (0.158, 0.160) at both genotypic and phenotypic levels.

Table 3: Estimates of Genotypic and phenotypic correlation coefficient (r) for different characters in rice

Characters		Days to maturity	Plant height (cm)	Panicle length (cm)	No. of panicles plant ⁻¹	No. of spikelet's panicle ⁻¹	Spikelet fertility (%)	1000 grain weight (g)	Grain Yield plant ⁻¹ (g)
Days to 50% flowering	G	0.999**	-0.355*	-0.399**	-0.279*	0.356**	-0.240*	-0.697**	-0.415**
	P	0.984**	-0.230*	-0.192	-0.228*	0.259*	-0.106	-0.525**	-0.243*
Days to maturity	G		-0.358**	-0.401**	-0.278*	0.358**	-0.238*	-0.697**	-0.416**
	P		-232**	-0.193	-0.228*	0.258*	-0.108	-0.525**	-0.248
Plant height (cm)	G			0.938**	0.746**	0.160	0.610**	0.777**	0.844**
	P			0.492**	0.429**	0.102	0.162	0.495**	0.559**
Panicle length (cm)	G				0.571**	0.376**	0.458**	0.834**	0.984**
	P				0.355**	0.297**	0.277*	0.586**	0.731**
No. of panicles plant ⁻¹	G					0.368**	0.609**	0.588**	0.681**
	P					0.324**	0.405**	0.469**	0.579**
No. of spikelet's panicle ⁻¹	G						0.275*	0.065	0.508**
	P						0.255*	0.076	0.409**
Spikelet fertility (%)	G							0.158	0.559**
	P							0.160	0.338**
1000 grain weight (g)	G								0.887**
	P								0.730**

*Significant at 5% level, **Significant at 1% level

Path coefficient Analysis

The estimates of the correlation coefficient revealed only the relationship between yield and yield associated traits, with no indication of direct and indirect effect of different characters on grain yield plant⁻¹. Path analysis on the other hand divides the association between two traits into its direct and indirect effect and provides meaningful results on the cause of the association between the grain yield as the dependent variable and the other traits as independent variable. In present study, genotypic correlation was partitioned in direct and indirect effect using path analysis, as shown in Table 4, to assess the relative importance of nine morpho-physiological traits.

Path coefficient analysis revealed that the highest positive direct effect on grain yield was exhibited by number of spikelet's panicle⁻¹ (0.986) followed by the panicle length (0.569), number of panicles plant⁻¹ (0.485), plant height (0.301) and days to 50% flowering (0.293). Therefore, these two traits should be regarded as essential for enhancing grain yield under aerobic condition. The results are in conformity with the findings of [3] for the number of spikelet's panicle⁻¹ and the number of panicles plant⁻¹, [11] for panicle length and days to 50% flowering. This indicates that direct selection of these traits is likely to result in improved grain yield. Therefore, it is advisable to prioritize these traits in the breeding programme to identify superior progenies with higher yield potential.

Days to maturity (-0.716) had highest negative direct effect on grain yield plant⁻¹ (-0.157) but it demonstrated positive indirect effect on grain yield through panicle length, number of spikeletes panicle⁻¹, spikelet fertility and 1000 grain weight. The direct expression of 1000 grain weight (-0.323) and spikelet fertility (-0.157) was negative on grain yield however it had positive indirect effect on grain yield through plant height, number of panicles plant⁻¹, panicle length and number of spikelet panicle⁻¹. These results are in agreement with the findings of [16] who estimated that days to maturity had highest negative effect on grain yield followed by spikelet fertility. Our studies are in agreement with the result of [1] for 1000 grain weight.

In the present investigation, path coefficient analysis revealed that the number of spikelet's panicle⁻¹ had maximum positive direct effect on grain yield as well as indirect effect on other traits which suggest that selection based on this trait for yield improvement in direct seeded condition would be most effective strategy. The residual effect signifies the unexplained variability of the dependent factor, grain yield plant⁻¹. The moderate value of 0.12 suggests that the traits analysed in the path coefficient analysis accounted for 87.04% of the variation in grain yield plant⁻¹. The residual effect on grain yield plant⁻¹ in this study could be attributed to various factors such as other unaccounted traits, environmental influences and sampling errors that were not included in present investigation.

Table 3: Path coefficient analysis showing direct and indirect effects of various characters on grain yield plant⁻¹ of rice genotypes

Characters	Days to 50% flowering	Days to Maturity	Plant height	No. of panicles plant ⁻¹	Panicle length	No. of spikelet plant ⁻¹	Spikelet fertility	1000 grain weight	Genotypic correlation with grain yield per plant
Days to 50% flowering	0.293	-0.716	-0.6832	0.57983	0.2907	0.42542	-0.0306	-0.5744	-0.415**
Days to maturity	0.29283	-0.716	-0.6878	0.58343	0.2891	0.42709	-0.03041	-0.57413	-0.416**
Plant height	-0.104	0.25592	0.301	-0.285	-0.5382	0.49673	0.07788	0.64049	0.844**
No. of panicles plant ⁻¹	-0.31677	-0.2872	0.214	0.485	0.39504	0.14918	0.05846	0.28684	0.984**
Panicle length	-0.08171	0.3986	-0.662	-0.6306	0.569	0.4392	0.16481	0.48465	0.681**
No. of spikelet panicle ⁻¹	0.10434	0.06599	-0.3073	-0.547	0.38321	0.986	-0.23012	0.05372	0.508**
Spikelet fertility%	-0.07019	0.17045	0.934	-0.6499	-0.335	0.32846	-0.1577	0.33948	0.559**
1000 grain weight	-0.20417	0.49875	0.684	-0.353	-0.6129	0.67785	0.52122	-0.3238	0.887**

Values in the bold are direct effect Residual effect = 0.12966

Table 4: Estimates of direct and indirect effect of different traits on grain yield plant⁻¹ in rice in terms of percentage

Characters	Genotypic correlation with grain yield plant ⁻¹	Direct effect	% Direct effect	Total indirect effect	% indirect effect	Character contributing through indirect effect
Days to 50% flowering	-0.415**	0.293	-70.602	-0.708	170.60	NPP, NSP, PL
Days to maturity	-0.416**	-0.716	172.11	0.98791	-237.47	NPP, NSP, PL, DFF
Plant height	0.844**	0.301	35.66	0.54378	64.33	TW, NSP, DM, SF
No. of panicles plant ⁻¹	0.984**	0.485	49.28	0.4996	50.71	PL, TW, PH, NSP, SF
Panicle length	0.681**	0.569	83.55	0.11299	16.44	TW, NSP, DM, SF
No. of spikelet panicle ⁻¹	0.508**	0.986	194.09	-0.47716	-93.91	PL, DFF, DM, TW
Spikelet fertility%	0.559**	-0.1577	-28.08	0.71737	128.26	PH, TW, NSP, DM
1000 grain weight	0.887**	-0.3238	-36.50	1.21179	136.60	PH, NSP, DM

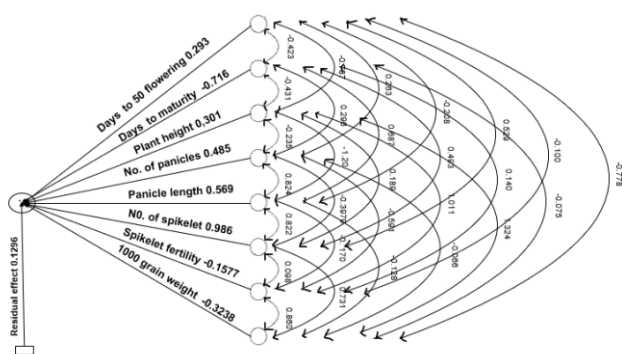


Fig. 1. Path diagram for grain yield in rice

Selection Indices

Selection for grain yield plant⁻¹ in rice based on single character may not be effective. On the other hand, it is a very cumbersome process for a breeder to involve a large number of component characters simultaneously in a selection program. Hence, knowledge of major yield components is necessary for evolving effective selection criteria. Selection indices provide the means for making use of correlated traits for higher efficiency in selection for yield. Hence different selection indices have been constructed and the results on the formulation of selection indices of different characters, the genetic advance and relative efficiency over straight selection for grain yield plant⁻¹ of rice are presented below. Forty-five different selection indices were constructed in advanced breeding progenies of rice under aerobic condition.

Table 5. Selection indices for seed yield and their relative efficiency in advanced breeding lines of rice under aerobic condition

Sr. No.	Index	Genetic gain/plant	Relative efficiency	Relative efficiency %
1	X8	12.70	100	0
2	X1	13.30	104.68	4.47
3	X5	34.40	270.80	63.07
4	X8+X2	26.02	204.78	51.16
5	X8+X3	19.60	154.31	35.19
6	X8+X4	32.96	259.47	61.46
7	X8+X5	50.04	393.83	74.60
8	X8+X1+X2	16.08	126.55	20.98
9	X8+X1+X4	23.02	181.23	44.82
10	X8+X1+X5	40.10	315.59	68.31
11	X8+X2+X3	32.92	259.1	61.40
12	X8+X2+X4	46.28	364.26	72.54
13	X8+X2+X5	63.35	498.62	79.94
14	X8+X2+X7	19.62	154.42	35.24
15	X8+X3+X4	39.87	313.79	68.13
16	X8+X3+X5	56.94	448.15	77.68
17	X8+X3+X7	13.20	103.95	3.8
18	X8+X4+X5	70.30	553.3	81.92
19	X8+X4+X7	26.56	209.1	52.17

The efficiencies of different indices were determined by calculating genetic advance and comparing it with that for straight selection for grain yield plant⁻¹ taken as 100%. It was observed that among all selection indices, the index based on grain yield plant⁻¹ + plant height, number of panicles plant⁻¹ + panicle length + number of spikelets panicle⁻¹ had the maximum genetic advance (90.52) with 85.96% increase in relative efficiency. Among the others, the indices based on grain yield plant⁻¹ + plant height + number of panicles plant⁻¹ + panicle length + number of spikelets panicle + 1000 grain weight showed 84.89% increase in relative efficiency with high genetic gain (84.12) over straight selection for grain yield alone followed by grain yield plant⁻¹ + days to 50 % flowering + plant height + number of panicles plant⁻¹ + panicle length + number of spikelets panicle⁻¹ showed 84.23% increase in relative efficiency with 84.58 % genetic gain.

Selection based on yield alone may be often misleading due to high environmental influence and multiple traits selection can improve selection efficiency and can attain largest economic gain. Therefore, the relative genetic score of each genotype was determined by utilizing the best selection index grain yield plant⁻¹ + plant height, number of panicles plant⁻¹ + panicle length + number of spikelets panicle⁻¹ (Table 6). It was found that the 18 genotypes performed better over the best check Samleshwari (275.45). SKL-19-01-120-44-32-60, SKL-19-02-77-221-98-83, SKL-19-02-77-221-98-94 and SKL-19-05-64-188-102-105 were found as a superior among all genotypes tested, having the optimal combination of attributes. These genotypes should be used for further evaluation.

20	X8+X5+X7	43.64	343.46	70.88
21	X8+X1+X2+X3	22.98	180.87	44.71
22	X8+X1+X2+X4	36.34	286.02	65.03
23	X8+X1+X2+X5	53.41	420.38	76.21
24	X8+X2+X3+X4	53.1	418.58	76.1
25	X8+X2+X3+X5	70.25	552.93	81.91
26	X8+X2+X3+X7	26.52	208.74	52.09
27	X8+X3+X4+X5	77.2	607.62	83.54
28	X8+X4+X5+X6	67.62	532.18	81.2
29	X8+X4+X5+X7	63.90	502.93	80.11
30	X8+X1+X2+X3+X4	43.24	340.34	70.61
31	X8+X1+X2+X3+X5	60.31	474.70	78.93
32	X8+X1+X2+X3+X7	16.58	130.5	23.37
33	X8+X1+X2+X4+X5	73.67	579.85	82.75
34	X8+X1+X2+X4+X7	29.94	235.65	57.56
35	X8+X1+X2+X5+X7	47.01	370.01	72.97
36	X8+X2+X3+X4+X5	90.52	712.41	85.96
37	X8+X2+X3+X4+X7	46.78	368.21	72.84
38	X8+X2+X3+X5+X7	63.85	502.57	80.1
39	X8+X3+X4+X5+X7	70.80	557.25	82.05
40	X8+X1+X2+X3+X4+X5	80.58	634.17	84.23
41	X8+X1+X2+X3+X4+X7	36.84	289.97	65.51
42	X8+X1+X2+X3+X5+X7	53.91	424.33	76.43
43	X8+X1+X2+X4+X5+X7	67.27	529.49	81.11
44	X8+X2+X3+X4+X5+X7	84.12	662.04	84.89
45	X8+X1+X2+X3+X4+X5+X7	74.18	583.81	82.87

Note: X1-Days to 50% flowering, X2-Plant height, X3-Number of panicles plant⁻¹, X4- Panicle length, X5-Number of spikelets panicle⁻¹, X7-1000 grain weight, X8-Grain yield plant⁻¹.

Table 6: Comparison between relative genetic score of 38 rice genotypes along with two checks based on the best selection index (Grain yield plant⁻¹ + Plant height + No. of panicles plant⁻¹ + Panicle length + No. of spikelets panicle⁻¹)

Rank	Genotypes	Selection index (selection score)	Rank	Genotypes	Selection index (selection score)
1	SKL-19-01-120-44-32-60	334.00	21	SKL-19-03-110-100-96-84	274.55
2	SKL-19-02-77-221-98-83	332.93	22	SKL-19-19-124-154-80-86	273.29
3	SKL-19-02-77-221-98-94	330.53	23	SKL-19-06-55-225-95-135	270.74
4	SKL-19-05-64-188-102-105	318.52	24	SKL-19-15-134-138-95-60	268.14
5	SKL-19-05-64-188-102-88	311.27	25	Vandana	266.66
6	SKL-19-21-203-250-134-112	307.65	26	SKL-19-26-51-151-80-48	265.77
7	SKL-19-04-108-225-108-105	307.32	27	SKL-19-26-81-151-80-77	265.30
8	SKL-19-11-194-116-89-98	306.71	28	SKL-19-15-134-138-95-70	264.66
9	SKL-19-21-203-260-134-124	304.99	29	SKL-19-15-134-138-95-78	264.44
10	SKL-19-11-194-116-89-112	303.79	30	SKL-19-19-124-154-80-98	264.23
11	SKL-19-14-45-105-50-88	291.48	31	SKL -19-13-29-09-53-33	261.92
12	SKL-19-23-137-127-85-112	289.42	32	SKL-19-18-45-60-44-84	252.31
13	SKL-19-23-137-127-85-134	288.04	33	SKL-19-18-45-60-44-116	250.96
14	SKL- 19-14-45-105-50-99	286.93	34	SKL-19-08-35-42-63-68	246.32
15	SKL-19-16-120-100-102-97	286.83	35	SKL-19-09-123-91-100-128	240.6
16	SKL-19-11-194-116-29-105	285.71	36	SKL-19-09-123-91-100-138	239.09
17	SKL-19-10-108-120-65-149	283.33	37	SKL-19-09-123-91-100 -147	237.99
18	SKL-19-16-120-100-102-112	281.70	38	SKL-19-17-204-215-127-124	233.78
19	Samleshwari	275.45	39	SKL-19-17-204-215-127-318	232.79
20	SKL-19-03-110-100-96-77	275.28	40	SKL-19-17-204-229-127-102	231.20

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