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GENETIC VARIABILITY, HERITABILITY AND TRAIT ASSOCIATION ANALYSIS IN RICE (*ORYZA SATIVA* L.) GENOTYPES UNDER EASTERN UTTAR PRADESH AGRO-CLIMATIC CONDITIONS

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ABSTRACT

Rice (*Oryza sativa* L.) is a principal staple food supporting the dietary needs of over 3.5 billion people globally, particularly in Asia, where over 90% of production and consumption occur. In India, especially in the state of Uttar Pradesh, rice plays a crucial role in rural livelihoods and contributes significantly to the state's agricultural GDP. In the face of increasing food demand due to population growth, enhancing rice yield and quality through improved genotypes is vital. A field experiment was conducted during Kharif 2021-22 at the Crop Research Station, Masodha, Ayodhya, Uttar Pradesh, to evaluate genetic variability, heritability, genetic advance, and correlation among 34 rice genotypes (30 genotypes and 4 check varieties) under randomized block design with three replications. Analysis of variance (ANOVA) revealed significant differences among genotypes for all 17 studied traits, indicating sufficient genetic variability. The findings in the research highlight the importance of specific traits in rice yield improvement and suggest that selection based on harvest index, biological yield, and spikelets per panicle can effectively enhance grain yield. The identified genotypes with favourable traits can be utilized in future rice breeding and hybridization programs aimed at boosting productivity and ensuring food security.

Key words: Genetic Variability, Heritability, Trait Association Analysis, Rice (*Oryza sativa* L.)

Introduction

Rice is the most important staple and cereals that sustains more than 3.5 billion people which comprises around half of the world's population (Wing *et al.*, 2018). The chief livelihood of human beings abundantly relies on rice due to their sovereignty, nutritive property and energy value (Burlando and Cornara, 2014). Rice provides 50-80% of daily calorie intake among the poor class of society. More than 90% of the world's rice is produced and consumed in Asia (Khush, 2013). In 2020, over 756 million tons of rice were produced in 143 countries, however, it was 598 million tons in 2000 (FAO, 2022). Global rice demands are expected to climb from

439 million tonnes (milled rice) in 2010 to 496 million tonnes in 2020, and 555 million tonnes in 2035, based on population projections from the United Nations and revenue projections from the Food and Agricultural Policy Research Institute (FAPRI). This represents a normal increase of 26 percent over the next 25 years, while demand will reduce over time as population growth slows and people diversify their diets away from rice. Despite a continued reduction in per capita rice consumption, Asian rice consumption is expected to account for 67 percent of worldwide growth, rising from 388 million tonnes in 2010 to 465 million tonnes in 2035.

Uttar Pradesh is an important rice-growing state in

Table 1: List of genotypes used in present investigation.

S.	GENOTYPES	S.	GENOTYPES
1	ORJ1342	18	IRH-130
2	WGL 1355	19	MALI-348
3	RP 6317-RMS-S35	20	KR 19015
4	Bhata Mansuri	21	KR 19005
5	HKR 17-33	22	KR 19011
6	R 2454-1R1-10	23	ADT -39(RP)
7	OR 2517-8	24	KMP-245
8	RP 6467-IR	25	KMP-225-3
9	Lalat	26	RP 6529-RMS-1777-55-87-24
10	INDAM -200-053	27	RP 6531-RMS-1778-45-17-84
11	PHI-21103	28	RP 6529-RMS-1714-36-22
12	MEPH-164	29	RP 6529-RMS-15-67-91
13	RRX-271	30	MTU 1010
14	RNC-0457	31	Naveen (NC)
15	UPLRH-180839	32	US-312(C)
16	PH-21104	33	NDR 3211-1(Local Check)
17	ARRH-23316	34	IR-64(International Check)

the country. Agriculture is the most important in the state, because about 80% of its population resides in rural areas and 75% of the total workers are involved directly or indirectly in cultivation/farming which accounts for 27% of the state's GDP. Agriculture is the main source of income for families in the state. It has 11.56 million hectares of cultivated area, constituting 70% of the total geographical area. The irrigated area is over 13.43 million hectares. Rice area with salt problems in the state is estimated to be $\leq 2\%$. Inland salinity areas are mainly concentrated in Raebareli, Azamgarh, Sultanpur, Faizabad, Lucknow, Unnao and Pratapgarh districts. Although the average productivity of rice is much lower in India than the average productivity at the world level, the development of high-yielding widely adapted pure-line rice varieties coupled with advances in production technology in the past four decades has enabled us to cope with the demand for rice to a satisfactory level. However, rapidly increasing demand due to the ever-increasing Indian population has forced us to search for another quantum jump in rice productivity. The projection of India's rice production target for 2020 AD is 115-120 million tonnes, which can be achieved only by increasing rice production by over 2.0 million tonnes per year in the coming decade.

Seed is a basic input in agriculture and it plays a vital role in boosting up to productivity and economy of the country. The need and importance of rice is increasing day by day due to the increase in the population explosion on earth. Therefore, it is the basic need of these days to boost up rice yield and quality through the development of biologically superior, stable and high yielding rice

Table 2: Analysis of variance of randomised block design for 17 characters in rice genotypes.

Characters	R D.F. (2)	T D.F. (33)	E D.F. (66)
Days to 50% flowering	5.12	120.84**	4.32
Days to maturity	0.18	221.31**	17.59
Plant height (cm)	18.30	346.08**	18.92
Number of total tillers per panicle	0.13	3.20**	0.37
No. of panicle per plant	0.76	2.85**	0.20
Panicle length(cm)	0.68	57.34**	1.51
Flag leaf length (cm)	79.73	83.55**	7.17
Flag leaf width(cm)	0.01	0.11**	0.00
Number of spikelets per panicle	255.60	1049.36**	66.19
Biological yield(g)	1.03	494.44**	17.19
Harvest index	126	304.39**	15.96
Test weight	0.82	39.35**	0.75
Seed germination	2.81	172.15**	10.68
Seed viability	0.70	251.17**	6.47
Seedling length	3.36	23.63**	3.42
Vigour index	51297.81	385576.76**	10652.65
Grain yield/plant (g)	6.12	139.63**	3.20
*, ** significant at 5% and 1% level, respectively. R: Replication; T: Treatment; E: Error			

varieties to meet the increasing food demand.

Materials and Methods

Experimental site

The experiment was conducted during *Kharif 2021-22* at the experimental field of Crop Research Station, Masodha, Ayodhya, Uttar Pradesh, India. (U.P.), India. Geographically, Narenda Nagar is positioned at 26.47°N latitude and 82.12°E longitude, with an elevation of 113 meters above sea level, situated in the Gangetic plains of eastern Uttar Pradesh, India.

Experimental details

The experimental materials for the present study consisted of 30 genotypes and 4 checks varieties namely US-312, NDR 3112-1, IR-64, NAVEEN of rice received from Department of Genetics and Plant Breeding, CRS, Masodha conducted during kharif-2021. The experiment was laid out in Randomized Block Design (RBD) with gross cultivated area of 1123.18m² which was divided into three sub-plots. The subplots were used to replicate the treatments three times with spacing of 20×15 cm. The genotype materials were sown over the nursery bed on 23th June 2021. The date of nursery sowing was 23 June, 2021 and date of transplanting was 10 July, 2021. The analysis of variance for various traits in the randomised block design followed the methodology

Table 3: Estimates of mean, range, heritability, genetic advance and coefficient for 17 characters in rice germplasm.

Characters	General mean	Range		PCV (%)	GCV (%)	Heritability (%)	GA% mean
		Min	Max				
Days to 50% Flowering	104.10	96.11	118.70	6.31	5.99	89.99	11.70
Days to Maturity	127.74	111.10	144.37	7.24	6.45	79.43	11.84
Plant Height (cm)	117.69	98.00	135.67	9.61	8.87	85.22	16.87
No. of tillers/Plant	6.93	5.31	8.59	16.52	14.02	71.99	24.50
No. of panicles/plant	8.70	7.19	10.59	11.97	10.80	81.35	20.06
Panicle Length (cm)	23.45	17.42	32.46	19.13	18.39	92.51	36.45
Flag leaf length(cm)	39.38	30.97	47.77	14.50	12.81	78.01	23.31
Flag leaf width(cm)	1.43	1.07	1.78	13.86	13.17	90.28	25.78
No. of spikelets/panicle	81.46	33.02	99.19	24.37	22.22	83.20	41.76
Biological yield(g)	65.16	24.84	75.84	20.38	19.36	90.25	37.88
Harvest index	34.64	15.42	62.21	30.57	28.31	85.76	54.00
Test weight (g)	21.11	14.33	26.87	17.48	16.99	94.48	34.02
Seed germination	79.31	61.50	86.74	10.13	9.25	83.45	17.41
Seed viability	85.34	65.61	96.72	10.99	10.58	92.65	20.98
Seedling length(cm)	21.68	15.77	25.16	14.70	11.97	66.34	20.09
Vigour index	1728.44	981.35	2140.63	21.31	20.45	92.15	40.44
Grain Yield/Plant (g)	22.13	10.13	34.97	31.53	30.48	93.42	60.68

outlined Panse and Sukhatme (1967). To assess variability in different traits, the approach recommended by Burton and de Vane (1953) was employed. The heritability in the broad sense (h^2_b) was calculated using the formula proposed by Hanson *et al.*, (1956). The expected genetic advance (GA%) was estimated based on the formula suggested by Johnson *et al.*, (1955). The association among different traits at both genotypic and phenotypic levels was determined as per the methodology outlined by Searle (1961). Path coefficient analysis was carried out according to Dewey and Lu (1959).

Results and Discussion

Analysis of Variation (ANOVA)

The analysis of variance for the randomised block design accommodating 30 rice genotypes together with three checks was done for each of the 17 characters. The analysis of variance is presented in the Table 2.

The analysis of variance found that mean squares due to block were highly significant for all the grain yield contributing characters and seed quality parameters. The variation due to block was highly significant for days to 50% flowering, days to maturity, plant height (cm), number of tillers per panicle, number of tillers per plant, panicle length (cm), flag leaf length(cm), flag leaf width (cm), number of spikelets per plant, biological yield (g), harvest index, test weight, seed germination, seed viability, seedling length, vigour index, grains per plant(g). The differences among the check varieties were also found to be highly significant for all the characters.

Thus, the variance analysis shows that the genotypes

differ significantly among themselves for all the characters under study, indicating towards the presence of adequate variability. As it is clear that a high degree of variation exists among the genotypes hence these could be utilized in various selection and hybridization programmes. Similar findings were reported by Hasan-Ud-Daula and Umakanta (2020), Lakshmi *et al.*, (2021), Rahman *et al.*, (2021) and Awadh-Allah *et al.*, (2022).

Genetic variability, heritability, genetic advance and coefficient of variance

The heritability in broad sense and genetic advance as percent of mean for all the 17 yield contributing traits and seed quality parameters were estimated and are given in Table 3. The high magnitude of heritability in broad sense varied between 94.48% in case of test weight, 93.42% in case of grain yield, seed germination 92.65% and vigour index 92.15%. The high estimate (>80%) of heritability was observed for days to 50% flowering (89%), followed by harvest index (85.76%), plant height (85.22%), seed germination (83.45%), number of spikelets per plant (83.20%) and number of panicles per plant (81.35%). The moderate estimates (<80% to >50%) were observed for days to maturity (79.43%), flag leaf length (78.01%), number of tillers per plant (71.99%) and seedling length (66.34%). The genetic advance as percent of mean ranged between grain yield plant (60.68%) and days to 50% flowering (11.70%). The high estimates (>20%) for genetic advance as percent of mean was observed for grain yield (60.68%), harvest index (54%), number of spikelets per plant (41.76%), vigour index (40.44%), biological yield (37.88), panicle length

Table 4.1: Estimates of genotypic correlation coefficient among different characters in Rice genotypes.

Chrs	DF-50	DM	PH (cm)	NTPP	NPH	PL (cm)	FLL (cm)	FLW (cm)	NSPP	BY (g)	HI	TW	SG	S V	SL	VI	GY (g)
DF-50	1.000	-0.036	-0.282**	0.243*	-0.612**	-0.703**	0.685**	0.260**	-0.712**	-0.514**	-0.488**	-0.816**	-0.098	-0.097	-0.663**	-0.494**	-0.805**
DM			-0.133	-0.035	0.073	0.036	0.035	0.352**	0.066	-0.243*	0.334**	-0.016	-0.194	-0.574**	0.074	0.239*	0.081
PH (cm)				0.109	0.158	0.245*	0.002	-0.116	0.307**	0.154	0.308**	0.385**	0.093	0.177	0.212*	0.101	0.353**
NTPP					-0.370**	-0.104	0.283**	-0.154	-0.145	-0.361**	0.130	-0.221*	0.224*	0.199*	-0.123	-0.248*	-0.138
NPH						0.585**	-0.197*	-0.230*	0.295**	0.333**	0.166	0.541**	-0.104	-0.107	0.557**	0.308**	0.398**
PL (cm)							-0.707**	-0.295**	0.632**	0.351**	0.639**	0.869**	0.151	0.144	0.705**	0.370**	0.863**
FLL (cm)								0.149	-0.746**	-0.503**	-0.385**	-0.781**	-0.284**	-0.261**	-0.651**	-0.615**	-0.730**
FLW (cm)									-0.085	-0.135	-0.103	-0.268**	-0.269**	-0.573**	-0.526**	-0.310**	-0.243*
NSPP										0.723**	0.270**	0.884**	0.209*	0.274**	0.746**	0.646**	0.786**
BY (g)											-0.273**	0.658**	0.112	0.287**	0.506**	0.522**	0.542**
HI												0.445**	0.249*	0.049	0.441**	0.227*	0.642**
TW													0.247*	0.249*	0.891**	0.631**	0.886**
SG														0.724**	0.527**	0.375**	0.263**
SV															0.491**	0.388**	0.281**
SL																0.798**	0.775**
VI																	0.603**
GY (g)																	1.000

Table 4.2: Estimates of phenotypic correlation coefficient among different characters in Rice genotypes.

Chrs	DF-50	DM	PH (cm)	NTPP	NPH	PL (cm)	FLL (cm)	FLW (cm)	NSPP	BY (g)	HI	TW	SG	S V	SL	VI	GY (g)
DF-50	1.000	-0.018	-0.272**	0.210*	-0.493**	-0.650**	0.535**	0.255**	-0.605**	-0.463**	-0.427**	-0.750**	-0.103	-0.098	-0.527**	-0.452**	-0.734**
DM			-0.126	-0.011	0.038	0.008	0.037	0.265**	0.055	-0.190	0.258**	0.002	-0.135	-0.483**	-0.015	0.202*	0.075
PH (cm)				0.058	0.080	0.245*	0.061	-0.109	0.223*	0.137	0.266**	0.342**	0.088	0.158	0.186	0.101	0.313**
NTPP					-0.271**	-0.074	0.193	-0.115	-0.095	-0.309**	0.119	-0.176	0.189	0.177	-0.140	-0.198*	-0.088
NPH						0.502**	-0.150	-0.200*	0.274**	0.297**	0.117	0.500**	-0.070	-0.079	0.390**	0.252*	0.339**
PL (cm)							-0.601**	-0.247*	0.563**	0.313**	0.566**	0.814**	0.124	0.132	0.578**	0.342**	0.794**
FLL (cm)								0.122	-0.633**	-0.426**	-0.313**	-0.668**	-0.222*	-0.204*	-0.459**	-0.507**	-0.628**
FLW (cm)									-0.070	-0.113	-0.103	-0.248*	-0.236*	-0.531**	-0.370**	-0.297**	-0.233*
NSPP										0.607**	0.248*	0.782**	0.197*	0.263**	0.517**	0.561**	0.706**
BY (g)											-0.324**	0.613**	0.098	0.245*	0.380**	0.467**	0.480**
HI												0.391**	0.204*	0.041	0.349**	0.217*	0.649**
TW													0.230*	0.244*	0.677**	0.586**	0.828**
SG														0.678**	0.405**	0.353**	0.234*
SV															0.337**	0.369**	0.249*
SL																0.679**	0.616**
VI																	0.567**
GY (g)																	1.000

*, ** significant at 5% and 1% level, respectively

(36.45%), number of tillers per plant (24.50%), flag leaf length (23.31%). The moderate estimates (<20% to >10%) for genetic advance as percent of mean were observed for 20.98% (seed viability), seedling length (20.09%), seed germination (17.41%), plant height (16.87%), days to maturity (11.84%) and days to 50% maturity (11.75%).

Correlation coefficients

The coefficient of variation was observed for 17 characters for 34 genotypes together with Grain yield per plant presented in Table 4.1 and 4.2. The highest estimates (>10%) of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed in case of number of tillers per plant (PCV=16.52%, GCV=14.02), number of panicles per plant (PCV=11.97, GCV=10.80), panicle length (PCV=19.13, GCV=18.39), flag leaf length (PCV=14.50, GCV=12.18), flag leaf width (PCV=13.86, GCV=13.17), number of spikelets per panicle (PCV=24.37, GCV=22.22), biological yield (PCV=30.57, GCV=28.31), harvest index (PCV=30.57, GCV=28.31), test weight (PCV=17.48, GCV=16.99), seed germination (PCV=10.13, GCV=9.25), seed viability (PCV=10.99, GCV=10.58), seedling length (GCV=14.70, PCV=11.97), vigour index (PCV=21.31, GCV=20.45) and grain yield per plant (PCV=31.53%, GCV=30.48%, GCV=10.20%). The moderate estimates (>5% to <10%) were exerted by days to 50% flowering (PCV=6.31%, GCV=5.99%), days to maturity (PCV=7.24%, GCV=6.45%), plant height (PCV=9.61%, GCV=8.87%). Similar results were observed by Behera *et al.*, (2020), Palaniyappan *et al.*, (2020), Alhassan and Musa (2021), Giri *et al.*, (2021) and Devi *et al.*, (2022).

Path Coefficient Analysis

The path coefficient analysis was worked out by using simple correlation among 17 characters to estimate the direct and indirect effect of different characters on grain yield per plant. The direct and indirect effects of different characters are depicted in Table 5. The highest positive direct effect on grain yield per plant was exhibited by harvest index (1.1433) followed by biological yield (1.0067), days to 50% flowering (0.3125), number of panicles per plant (0.2207) and number of spikelets per plant (0.2007), while highest negative direct effect were exerted by test weight (-0.3072) followed by flag leaf length (-0.1946) and seedling length (-0.1215). The direct and indirect effects of rest of the characters were found very low. The highest positive indirect effect on grain yield per plant was exhibited by harvest index *via* harvest index (1.1433) followed by biological yield *via* biological yield (1.0067) and panicle length *via* harvest index

Table 5: Direct and indirect effect of different characters on grain yield per plant in Rice genotypes.

Chrs	DF-50	DM	PH (cm)	NTPP	NPH	PL (cm)	FLL (cm)	FLW (cm)	NSPP	BY (g)	HI	TW	SG	SV	SL	VI	GY (g)
DF-50	0.3125	0.0019	0.0061	0.0186	-0.1351	0.0401	-0.1333	-0.0428	-0.1430	-0.5175	-0.5582	0.2506	0.0045	0.0069	0.0805	0.0030	-0.805**
DM	-0.0113	-0.0522	0.0029	-0.0027	0.0161	-0.0021	-0.0069	-0.0578	0.0132	-0.2442	0.3815	0.0050	0.0088	0.0411	-0.0090	-0.0015	0.081
PH (cm)	-0.0881	0.0069	-0.0216	0.0084	0.0348	-0.0140	-0.0004	0.0191	0.0616	0.1549	0.3525	-0.1184	-0.0042	-0.0127	-0.0258	-0.0006	0.353**
NTPP	0.0761	0.0018	-0.0024	0.0766	-0.0816	0.0059	-0.0552	0.0253	-0.0291	-0.3639	0.1482	0.0680	-0.0102	-0.0142	0.0149	0.0015	-0.138
NPH	-0.1913	-0.0038	-0.0034	-0.0283	0.2207	-0.0334	0.0384	0.0379	0.0591	0.3352	0.1901	-0.1661	0.0047	0.0077	-0.0677	-0.0019	0.398**
PL (cm)	-0.2197	-0.0019	-0.0053	-0.0079	0.1292	-0.0571	0.1376	0.0485	0.1268	0.3537	0.7310	-0.2669	-0.0069	-0.0103	-0.0857	-0.0023	0.863**
FLL (cm)	0.2141	-0.0018	0.0000	0.0217	-0.0435	0.0403	-0.1946	-0.0246	-0.1497	-0.5064	-0.4401	0.2399	0.0129	0.0187	0.0790	0.0038	-0.730**
FLW (cm)	0.0812	-0.0183	0.0025	-0.0118	-0.0508	0.0168	-0.0291	-0.1645	-0.0170	-0.1355	-0.1180	0.0823	0.0122	0.0409	0.0639	0.0019	-0.243*
NSPP	-0.2226	-0.0034	-0.0066	-0.0111	0.0650	-0.0361	0.1451	0.0139	0.2007	0.7279	0.3089	-0.2717	-0.0095	-0.0196	-0.0906	-0.0040	0.786**
BY (g)	-0.1607	0.0127	-0.0033	-0.0277	0.0735	-0.0201	0.0979	0.0222	0.1451	1.0067	-0.3120	-0.2021	-0.0051	-0.0205	-0.0614	-0.0032	0.542**
HI	-0.1526	-0.0174	-0.0067	0.0099	0.0367	-0.0365	0.0749	0.0170	0.0542	-0.2747	1.1433	-0.1366	-0.0113	-0.0035	-0.0536	-0.0014	0.642**
TW	-0.2550	0.0009	-0.0083	-0.0169	0.1193	-0.0496	0.1520	0.0441	0.1775	0.6623	0.5083	-0.3072	-0.0112	-0.0178	-0.1082	-0.0039	0.886**
SG	-0.0306	0.0101	-0.0020	0.0172	-0.0229	-0.0086	0.0552	0.0443	0.0419	0.1131	0.2849	-0.0759	-0.0454	-0.0517	-0.0640	-0.0023	0.263**
SV	-0.0303	0.0300	-0.0038	0.0152	-0.0237	-0.0082	0.0508	0.0942	0.0551	0.2888	0.0558	-0.0765	-0.0328	-0.0715	-0.0597	-0.0024	0.281**
SL	-0.2071	-0.0039	-0.0046	-0.0094	0.1229	-0.0403	0.1266	0.0866	0.1497	0.5090	0.5046	-0.2736	-0.0239	-0.0351	-0.1215	-0.0049	0.775**
VI	-0.1543	-0.0124	-0.0022	-0.0190	0.0679	-0.0211	0.1197	0.0511	0.1296	0.5258	0.2594	-0.1939	-0.0170	-0.0277	-0.0969	-0.0062	0.603**

Resi- 0.0161; *, ** significant at 5% and 1% level, respectively

(0.7310). The highest negative indirect effect on grain yield per plant was exerted by days to 50% flowering *via* harvest index (-0.5582) followed by days to 50% flowering *via* biological yield (-0.5172). The remaining estimates of the indirect effect on grain yield per plant were too low to be considered. The residual effect observed was 0.0161 which indicates that some of the characters which might contribute to yield have not been included in the study. Similar results were observed by Behera *et al.*, (2020), Palaniyappan *et al.*, (2020), Sabri *et al.*, (2020), Alhassan and Musa (2021), Giri *et al.*, (2021) and Devi *et al.*, (2022).

Summary

Rice is a critical staple crop, sustaining over half the global population, with more than 90% of production and consumption occurring in Asia. India, particularly Uttar Pradesh, plays a significant role in rice cultivation. To meet the escalating food demands of a growing population, the development of high-yielding, stable, and biologically superior rice varieties is essential. This study was conducted during *Kharif 2021* at the Crop Research Station, Masodha (Ayodhya, U.P., India) to evaluate genetic variability, heritability, genetic advance, and trait associations in 30 rice genotypes, including four check varieties with three replications was used to assess 17 agro-morphological and seed quality traits. Analysis of variance revealed significant differences among genotypes for all traits, indicating substantial genetic variability. High heritability (>80%) was recorded for most traits, notably test weight (94.48%), grain yield (93.42%), and vigour index (92.15%), coupled with high genetic advance as percent of mean (GA%), suggesting the predominance of additive gene action. Grain yield exhibited strong positive correlations with panicle length, test weight, biological yield, harvest index, and number of spikelets per panicle. Path coefficient analysis revealed that harvest index, biological yield, and number of spikelets per panicle exerted the most substantial positive direct effects on grain yield, while test weight and flag leaf length showed negative direct effects. These findings highlight the presence of considerable genetic diversity and identify key yield-contributing traits, which can be utilized in future breeding programs aimed at enhancing rice productivity and seed quality in salt-affected and normal environments.

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