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Research Article

Exploring the genetic diversity for yield and quality traits in indigenous landraces of rice (*Oryza sativa* L.)

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Abstract
An investigation on 41 genotypes of rice revealed that estimates of variability, heritability and genetic advance was high for grain yield plant^{-1}, gel consistency, number of filled grain panicle^{-1},number of total grain panicle^{-1}, alkali spreading value, number of chaffy grain panicle^{-1}, grain size and test weight indicating the predominance of additive gene action for these traits. Mahalanobis D^2 analysis grouped 41 genotypes into 8 different clusters and grain breadth contributed maximum towards divergence. Maximum inter-cluster distance was observed between cluster III and VII followed by cluster II and III indicating, maximum genetic diversity between these clusters. Character association and path-analysis revealed that, among yield attributing characters, number of filled grains panicle^{-1}, number of total grain panicle^{-1}, harvest index, test weight, number of chaffy grains panicle^{-1},number of panicles plant^{-1} and grain length had significant positive association with grain yield plant^{-1} and among grain quality traits, kernel length and kernel length after cooking exhibited significant association with amylose content.

Keywords: Rice, land races, genetic parameters, divergence

INTRODUCTION

The dwarfing gene, *Dee-Geo-Woo-Gen* played a pivotal role in tremendous increase in rice productivity worldwide by exploiting the genetic potential of semi dwarf and dwarf high yielding varieties which could adapt to varied agro climatic regimes. In this process, yield plateau has been reached and there is a loss of hidden genetic variability due to the concerted efforts for development of varieties in rice crop. Now is the time for exploitation of untapped variability existing in the land races which were available in the germplasm not only with respect to yield but also quality traits and resistance to various pests and diseases prevalent in respective locations. Even though, land races were morphologically recognizable at their place of origin and exhibit lower diversity but the variability was higher than that present in cultivated varieties in the respective locations. Thirty percent high diversity for allele richness was observed in land races with respect to biotic and abiotic stress tolerance, superior quality and nutritional aspects (Thomson *et al.,* 2007). Therefore, study of land races for various genetic parameters may help in identification of suitable and potential donors for future use in breeding programmes. In this context, a total of 39 indigenous land races and two checks (NLR 33892 and NLR 9674) were studied for generating the data on yield, yield components and quality aspects.

MATERIALS AND METHODS

Thirty-nine rice land races along with two checks *viz,* NLR 33892 and NLR 9674, were raised in a randomized block design with three replications adopting spacing of 20x15cm during *kharif,* 2021 at Agricultural Research Station, Nellore, ANGRAU. The field was located at 14^{0}21'N latitude and 79^{0}59E longitude and at an altitude of 20m above mean sea level and the soil was of sandy

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clay loam type. All the cultural practices were followed as per the standard recommendations to raise a healthy crop. Observations were recorded in randomly selected plants in each genotype in each replication for all yield attributes except days to 50% flowering. A total of 14 yield components along with yield and seven quality traits were studied.

The treatment means over three replications were subjected to analysis of variance (ANOVA) (Panse and Sukathme, 1967); genetic parameters *viz*., Variance (Burton,1952), Heritability (Lush, 1940), Genetic advance (Johnson *et al*., 1955); Genetic divergence (Mahalanobis, 1936), Association analysis (Johnson *et al.,* 1955) and Path analysis (Wright 1921, Dewey and Lu 1959).

RESULTS AND DISCUSSION

Results of ANOVA revealed the significance of mean squares for all the traits indicating presence of significant differences among the land races (**Table 1**).

The traits *viz*., grain yield plant^{-1}, gel consistency, number of filled grain panicle^{-1}, number of total grain panicle^{-1}, alkali spreading value, number of chaffy grain panicle^{-1}, grain size and test weight exhibited high estimates of GCV and PCV which indicated the effectiveness of direct selection for improvement of these traits. Moderate GCV and PCV values were exhibited by grain length, number of panicles plant^{-1}, protein content, kernel length, amylose content, kernel breadth, harvest index, grain breadth, plant height and kernel breadth after cooking indicating that these characters were highly influenced by environment and selection would be ineffective.

High heritability along with high genetic advance as per cent of mean was recorded for number of chaffy grain panicle^{-1}, gel consistency, number of total grain panicle^{-1}, number of filled grain panicle^{-1}, alkali spreading value, protein, grain size, grain length, amylase content, grain breadth, plant height, kernel length, grain yield plant^{-1}, kernel breadth, test weight and kernel breadth after cooking indicating the predominance of additive gene action. This was in conformity with the findings of Priyanka *et al.* (2020) for number of total grain panicle^{-1}and alkali spreading value, Koshle *et al.* (2020) for number of filled grain panicle^{-1}, Dhanwani *et al.* (2013) for number of chaffy grain panicle^{-1}, Sharma *et al.* (2020) for grain yield panicle^{-1} and Priyanka and Gauraha (2020) for test weight.

The characters *viz.,* for days to 50 % flowering, days to maturity, kernel length after cooking, panicle length, zinc content, harvest index and number of panicles plant^{-1} exhibited high heritability coupled with moderate genetic advance as per cent of mean indicating that additive gene action plays a prominent role in the inheritance of these traits and express consistently in succeeding generations. Similar trend was also observed by Lingaiah *et al.* (2019) for plant height, Kumar *et al.* (2018) for number of panicles plant^{-1}, Priyanka *et al.* (2020) for harvest index, Radha *et al.* (2019) for grain length, Gokulakrishnan *et al*. (2014) for grain breadth, Jan and Kashyap (2020) for kernel breadth after cooking, Thakur and Pandey (2020) for amylose content and Sarmah *et al.*(2017) for protein.

The data was subjected diversity analysis using D^{2}statistics (Mahalanobis, 1936) by Tocher's method (Rao 1952). It revealed that 41 genotypes were grouped in to eight clusters and clustering pattern was at random. Out of the eight clusters, cluster I was the largest with 32 genotypes followed by cluster III and V each with 2 genotypes, cluster II, IV, VI, VII and VIII were solitary in nature which indicates the wide range of genetic diversity among the genotypes under study (**Table 2**). Most of the land races were grouped into one cluster indicating the genetic relatedness among the genotypes and close resemblance for the traits *viz.*, gel consistency, amylose content and protein content. This may be due to free flow of genes between the accessions. Cluster III consisted of two genotypes developed at ARS, Nellore which might be due to unidirectional selection practiced by the respective breeders. Cluster V comprised of two aromatic genotypes which recorded high mean values for panicle length and kernel length after cooking. Five genotypes were found to constitute solitary clusters and showed separate identity from rest of the others.

D^2 values among the clusters are presented in **Table 3** which is in the range of 0.0 to 1858.09. Maximum intra cluster distance was observed in cluster I (1858.09) followed by cluster V (986.79). This suggests considerable variation among the genotypes with in the clusters and it may be due to heterogeneity, genetic architecture of the population, past history of the selection in the development of the traits and the degree of combining ability. Hence, it is advisable that selection of genotypes could be attempted from cluster I for producing good recombinants.

The inter cluster distance was found to be maximum between cluster IV and VII (12407.61) followed by cluster II and III (11693.38) and cluster III and IV(9097.02) which in turn indicate that the genotypes in these clusters possess maximum genetic diversity. Hence, genotypes from these clusters could be utilized in crossing programme. Minimum inter cluster distance was recorded between cluster I and II (2588.81) suggesting that the genotypes found in these clusters were closely related with each other.

Grain breadth contributed maximum towards total genetic diversity followed by alkali spreading value, kernel

Table1. Variability and Genetic parameters for yield and grain quality traits in 41 genotypes of rice

S. No	Character	Range			Variance		Coefficient of Variation		Heritability (Broad Sense) (%)	Genetic Advance	Genetic Advance as per cent of Mean (%)
		Mean	Min	Max	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1	Days to 50% flowering	108.22	90.33	127.5	72.18	72.70	7.85	7.88	99.30	17.44	16.11
2	Days to maturity	138.79	123.33	160.00	69.64	71.24	6.01	6.08	97.80	17.00	12.25
3	Plant height (cm)	140.81	69.27	158.87	289.40	339.05	12.08	13.08	85.40	32.38	22.99
4	Panicle length (cm)	26.07	21.67	29.80	3.61	5.32	7.28	8.85	67.80	3.22	12.35
5	Number of panicles plant^{-1}	10.73	8.00	15.47	1.56	3.40	11.62	17.18	45.80	1.74	16.20
6	Number of filled grains panicle^{-1}	153.12	85.6	320.53	2043.67	2086.61	29.52	29.83	97.90	92.16	60.19
7	Number of chaffy grains panicle^{-1}	23.51	13.62	49.47	41.43	41.62	27.38	27.44	99.60	13.23	56.28
8	Number of total grains panicle^{-1}	176.94	104.00	369.99	2661.72	2707.79	29.16	29.41	98.30	105.37	59.55
9	Spikelet fertility (%)	86.50	80.92	91.22	6.59	8.44	2.97	3.36	78.10	4.68	5.41
10	Grain yield plant^{-1} (g)	31.59	15.69	63.45	134.66	161.12	36.73	40.18	83.60	21.85	69.17
11	Test weight (g)	19.38	11.67	30.67	18.07	23.14	21.94	24.82	78.10	7.74	39.93
12	Harvest index (%)	50.25	42.86	64.96	31.43	46.68	11.16	13.60	67.30	9.48	18.86
13	Grain length (mm)	7.69	5.31	11.47	1.72	1.87	17.07	17.78	92.20	2.60	33.77
14	Grain breadth (mm)	2.66	1.84	3.41	0.11	0.13	12.34	13.31	85.90	0.63	23.55
15	Grain size	2.89	1.33	4.67	0.49	0.53	24.14	25.11	92.40	1.38	47.81
16	Kernel length (mm)	5.38	4.30	7.67	0.68	0.80	14.83	16.07	85.10	1.57	28.17
17	Kernel breadth (mm)	2.63	2.22	3.45	0.08	0.11	12.37	13.87	79.50	0.53	22.73
18	Kernel length after cooking (mm)	7.14	5.24	8.87	0.44	0.64	9.02	10.90	68.50	1.13	15.39
19	Kernel breadth after cooking (mm)	3.09	2.01	3.93	0.12	0.16	11.21	12.81	76.60	0.63	20.20
20	Alkali spreading value	2.64	1.33	4.33	0.57	0.59	28.53	28.99	96.80	1.53	57.82
21	Gel consistency (mm)	41.03	16.00	91.00	201.69	203.15	37.06	37.19	99.30	29.15	76.06
22	Amylose content (%)	23.91	16.73	33.57	12.16	13.40	14.79	15.53	90.70	6.84	29.03
23	Protein (%)	7.79	6.53	14.63	1.58	1.66	16.12	16.55	94.90	2.52	32.35
24	Zinc (ppm)	16.48	14.34	20.72	1.94	2.87	8.45	10.28	67.50	2.36	14.30

Table 2. Clustering of 41 genotypes of rice based on Tocher's method

Cluster number	Number of genotypes	Landraces
I	32	Jedikahine, Eskarvanda, Red Rice, Kundadam,Motimahipal, Nagara, Ranikanda, Safari, Haldichudi, Karigejadalai, Nikko, Ramjeera, Chandraghand, Lathisali, Karameguravani, Gadakodiamahi, Kalajeera, Chyanahi, Mallepool, Narayanakamini, Dimeedi, Kakirekallu, Pohaki, Dhadega, Siddhasana, Sonamali, Kukudamande, Ambemohar, , Kistampeta Sannalu, Mudamurangi and Tikisali
II	1	Kumargoal
III	2	NLR 33892, NLR9674
IV	1	Kalabhati
V	2	Basmati, Sugandhi
VI	1	Chittimuthyalu
VII	1	Galima
VIII	1	Kistampeta Gold

Table 3. Average intra-cluster and inter-cluster distances of 41 rice genotypes for 24 traits (Tocher's method)

Cluster	I	II	III	IV	V	VI	VII	VIII
I	1858.09 (43.11)	2588.81 (50.88)	6982.37 (83.56)	2729.79 (52.25)	2864.50 (53.52)	3027.98 (55.03)	3977.89 (63.07)	4420.52 (66.49)
II		0.00 (0.00)	11693.38 (108.14)	4244.88 (65.15)	3922.03 (62.63)	2882.29 (53.69)	3163.33 (56.24)	3931.02 (62.70)
III			853.38 (29.21)	9097.02 (95.38)	6879.39 (82.94)	7652.64 (87.48)	12407.61 (111.39)	7977.17 (89.32)
IV				0.00 (0.00)	4508.35 (67.14)	4226.24 (65.01)	4767.89 (69.05)	6706.30 (81.89)
V					986.79 (31.41)	5986.66 (77.37)	4293.70 (65.53)	4235.07 (65.08)
VI						0.00 (0.00)	4644.24 (68.15)	4489.03 (67.00)
VII							0.00 (0.00)	4948.17 (70.34)
VIII								0.00 (0.00)

breadth, kernel breadth after cooking, gel consistency, kernel length after cooking and number of chaffy grains per panicle.. Hence, these traits should be considered as selection parameters in the segregating generations (**Table 4**). Direct selection of these traits will give good results. Devi *et al.* (2020) reported similar results in rice. The individual cluster means of each of the character was compared with their respective overall averages and perusal of cluster means revealed considerable variation for all the traits between the clusters. Cluster VII registered lower mean values for days to 50% flowering and maturity; cluster VIII for plant height; cluster III for kernel breadth and grain breadth which was desirable. Hence, genotypes from theses clusters could be used in rice breeding programmes to improve these traits. Cluster III exhibited high mean values for number of filled grains per panicle, number of grains per panicle, grain yield per plant and harvest index and low mean values for grain breadth, grain size, kernel length and kernel length after cooking. Cluster IV exhibited high values for test weight, zinc content, intermediate alkali spreading value and amylose content and high spikelet percentage. Selection of genotypes from theses clusters would produce a broad spectrum of variability for yield and quality traits which enable further selection for genetic improvement. Based on divergence analysis the crosses between NLR 33892 (cluster III x Kalabathi (cluster IV) and NLR 9674 (Cluster III) x Kalabhathi may be identified for improvement of yield and zinc content, whereas cross between Ramjeera x NLR 33892 or NLR 9674 for grain yield and protein

Table 4. Percent contribution of yield and grain quality traits towards genetic divergence in 41 genotypes of rice

S.No.	Character	Number of Times Ranked First	Contribution towards diversity (%)
1	Days to 50% flowering	0	0.00
2	Days to maturity	0	0.00
3	Plant height (cm)	56	6.83
4	Panicle length (cm)	0	0.00
5	Number of panicles plant^{-1}	0	0.00
6	Number of filled grains panicle^{-1}	0	0.00
7	Number of chaffy grains panicle^{-1}	62	7.56
8	Number of total grains panicle^{-1}	0	0.00
9	Spikelet fertility (%)	0	0.00
10	Grain yield plant^{-1} (g)	0	0.00
11	Test weight (g)	0	0.00
12	Harvest index (%)	0	0.00
13	Grain length (mm)	103	12.56
14	Grain breadth (mm)	142	17.32
15	Grain size (mm)	0	0.00
16	Kernel length (mm)	0	0.00
17	Kernel breadth (mm)	109	13.29
18	Kernel length after cooking (mm)	97	11.83
19	Kernel breadth after cooking (mm)	104	12.68
20	Alkali spreading value	110	13.41
21	Gel consistency (mm)	28	3.41
22	Amylose content (%)	5	0.61
23	Protein (%)	4	0.49
24	Zinc (ppm)	0	0.00

content in rice for exploitation of good transgressive segregants.

Character association studies among yield attributing characters revealed that number of filled grains panicle^{-1}, total grain panicle^{-1},harvest index, test weight, number of chaffy grains panicle^{-1}, number of panicles plant-^{1}and grain length had significant positive association with grain yield plant^{-1} and selection based on these traits may be effective to develop the high yielding genotypes (**Table 5**). Kumar *et al.* (2020) and Shanmugam *et al.* (2023) also recorded similar results while working with rice crop. Among grain quality traits, kernel length and kernel length after cooking exhibited significant negative association with amylose content (**Table 6**).

Path coefficient analysis revealed number of filled grains panicle^{-1} exhibited high positive direct effect and true correlation with grain yield plant^{-1}, followed by number of panicles plant^{-1} and test weight (g) (**Table 7**). Therefore, while selecting the genotypes these characters should be considered for increasing grain yield. Among the grain quality traits, *viz.* kernel breadth after cooking and zinc had positive direct effect and positive association with amylose content (**Table 8**)

An overall perusal on different studies like variability, heritability, genetic advance as percent of mean, character association and genetic divergence elucidates the importance of characters such as number of filled grain panicle^{-1}, number of total grain panicle^{-1}, kernel breadth, kernel breadth after cooking, alkali spreading value and gel consistency to improve grain yield and quality simultaneously.

Table 5. Phenotypic (r_p) and genotypic (r_g) correlation coefficients among grain yield and yield attributing traits in rice

Character		DFF	DM	PH	PL	NPP	FG	CG	TG	SF	TW	HI	GL	GB	GS	GY
DFF	r_p	1.000	0.989**	0.024	0.335**	-0.114	0.273**	0.409**	0.275**	-0.109	-0.088	-0.066	-0.085	-0.099	0.042	0.101
	r_g	**1.000**	0.997**	-0.004	0.359**	-0.170	0.278**	0.411**	0.280**	-0.128	-0.094	-0.083	-0.109	-0.136	0.027	0.115
DM	r_p		**1.000**	-0.021	0.304**	-0.110	0.325**	0.453**	-0.328**	-0.117	-0.077	-0.037	-0.089	-0.117	0.050	0.149
	r_g		**1.000**	-0.050	0.327**	-0.183*	0.335**	0.459**	0.337**	-0.145	-0.087	-0.044	-0.113	-0.154	0.039	0.158
PH	r_p			**1.000**	0.614**	0.050	-0.404**	-0.359**	-0.407**	0.198*	0.089	-0.234**	-0.033	0.338**	-0.196*	-0.235**
	r_g			**1.000**	0.528**	0.092	-0.441**	-0.394**	-0.441**	0.201*	0.141	-0.310**	-0.155	0.229*	-0.317**	-0.265**
PL	r_p				**1.000**	-0.112	-0.155	-0.069	-0.166	0.159	-0.059	-0.269**	-0.020	0.229*	-0.090	-0.188*
	r_g				**1.000**	-0.187*	-0.187*	-0.091	-0.197*	0.151	-0.029	-0.394	-0.218*	0.028	-0.271**	-0.228*
NPP	r_p					**1.000**	0.004	-0.099	0.002	0.075	-0.083	0.333**	0.091	0.030	0.055	0.396**
	r_g					**1.000**	0.007	-0.159	0.005	0.140	-0.052	0.444**	0.153	0.057	0.076	0.340**
FG	r_p						**1.000**	0.851**	0.995**	0.030	-0.080	0.335**	0.048	-0.308**	0.142	0.695**
	r_g						**1.000**	0.863**	0.996**	0.013	-0.090	0.380**	-0.049	-0.334**	0.152	0.755**
CG	r_p							**1.000**	0.872**	-0.230*	-0.152	0.272**	0.069	-0.397**	0.301**	0.480**
	r_g							**1.000**	0.882**	-0.265**	-0.166	0.334**	0.069	-0.434**	0.311**	0.527**
TG	r_p								**1.000**	-0.063	-0.103	0.319**	-0.045	-0.336**	0.162	0.674**
	r_g								**1.000**	-0.074	-0.116	0.360**	-0.044	-0.361**	0.174	0.731**
SF	r_p									**1.000**	0.121	0.132	-0.058	0.205*	-0.172	0.166
	r_g									**1.000**	0.197	0.174	-0.099	0.212*	-0.221*	0.210*
TW	r_p										**1.000**	0.230*	0.288**	0.490**	-0.060	0.484**
	r_g										**1.000**	0.326**	0.364**	0.624**	-0.043	0.465**
HI	r_p											**1.000**	0.090	0.015	0.075	0.541**
	r_g											**1.000**	0.125	0.020	0.083	0.659**
GL	r_p												**1.000**	0.152	0.774**	0.185*
	r_g												**1.000**	0.056	0.774**	0.224*
GB	r_p													**1.000**	-0.367**	0.051
	r_g													**1.000**	-0.503**	0.070
GS	r_p														**1.000**	0.115
	r_g														**1.000**	0.142

DFF- Days to 50% flowering	DM- Days to maturity	PH- Plant height (cm)	PL- Panicle length (cm)
NPP- Number of panicle plant^{-1}	FGP- Number of filled grains panicle^{-1}	CGP- Number of chaffy grain panicle^{-1}	TGP- Number of total grain panicle^{-1}
SF- Spikelet fertility (%)	GY- Grain yield plant^{-1}(g)	TW- Test weight (g)	HI- Harvest index (%)
GL- Grain length (mm)	GB- Grain breadth (mm)	GS- Grain size	

Table 6. Phenotypic (r_p) and genotypic (r_g) correlation coefficients among amylose content and grain quality attributes traits in rice

Character		KL	KB	KLAC	KBAC	ASV	GC	PR	Zn	AC
KL	r_p	**1.000**	0.225 *	0.685 **	0.311 **	0.264 **	-0.254 **	0.073	-0.078	-0.318**
	r_g	**1.000**	0.065	0.616**	0.157	0.222*	-0.271**	0.092	-0.146	-0.359**
KB	r_p		**1.000**	0.209 *	0.492 **	0.169	-0.204 *	-0.036	-0.101	0.059
	r_g		**1.000**	-0.056	0.353**	0.108	-0.224*	-0.028	-0.183	0.077
KLAC	r_p			**1.000**	0.313 **	0.332 **	-0.069	0.129	-0.136	-0.304**
	r_g			**1.000**	0.061	0.294**	-0.074	0.176	-0.268**	-0.377**
KBAC	r_p				**1.000**	0.362 **	-0.170	0.018	-0.136	0.061
	r_g				**1.000**	0.328**	-0.188*	0.037	-0.244	0.083
ASV	r_p					**1.000**	-0.259 **	-0.133	0.130	0.004
	r_g					**1.000**	-0.263**	-0.134	0.145	0.004
GC	r_p						**1.000**	0.050	0.176	0.092
	r_g						**1.000**	0.048	0.208*	0.101
PR	r_p							**1.000**	-0.112	-0.109
	r_g							**1.000**	-0.113	-0.114
Zn	r_p								**1.000**	0.129
	r_g								**1.000**	0.188

KL : Kernel length (mm)
KB : Kernel breadth (mm)
KLAC : Kernel length after cooking (mm)
KBAC : Kernel breadth after cooking (mm)
ASV : Alkali spreading value
GC : Gel consistency (mm)
AC : Amylose content (%)
PR : Protein (%)
Zn : Zinc (ppm)

Table 7. Phenotypic and genotypic path analysis of yield attributing traits in rice

Character		PH	PL	NPP	FG	CG	TG	SF	TWG	HI	GL	GY
PH	P	**-0.0444**	0.0232	0.0211	-0.1787	0.0259	-0.1384	0.0117	0.0504	-0.0052	-0.0009	-0.2353**
	G	**-0.0123**	0.0228	0.0282	-0.5599	0.0561	0.1646	-0.0048	0.0698	-0.0224	-0.0075	-0.2654**
PL	P	-0.0272	**0.0378**	-0.0477	-0.0684	0.0050	-0.0565	0.0094	-0.0334	-0.0060	-0.0005	-0.1877*
	G	-0.0065	**0.0432**	-0.0577	-0.2367	0.0130	0.0734	-0.0036	-0.0143	-0.0285	-0.0105	-0.2281*
NPP	P	-0.0022	-0.0042	**0.4257**	0.0016	0.0071	0.0007	0.0044	-0.0468	0.0074	0.0023	0.3960**
	G	-0.0011	-0.0080	**0.3082**	0.0094	0.0226	-0.0017	-0.0033	-0.0256	0.0320	0.0074	0.3399**
FG	P	0.0179	-0.0059	0.0015	**0.4421**	-0.0613	0.3381	0.0018	-0.0454	0.0075	-0.0012	0.6952**
	G	0.0054	-0.0080	0.0023	**1.2689**	-0.1229	-0.3713	-0.0003	-0.0446	0.0274	-0.0024	0.7545**
CG	P	0.0159	-0.0026	-0.0422	0.3763	**-0.0720**	0.2965	-0.0135	-0.0861	0.0061	0.0018	0.4801**
	G	0.0048	-0.0039	-0.0489	1.0953	**-0.1424**	-0.3290	0.0063	-0.0823	0.0242	0.0033	0.5273**
TG	P	0.0181	-0.0063	0.0008	0.4397	-0.0628	**0.3400**	-0.0037	-0.0582	0.0071	-0.0012	0.6735**
	G	0.0054	-0.0085	0.0014	1.2633	-0.1256	**-0.373**	0.0017	-0.0574	0.0260	-0.0021	0.7311**
SF	P	-0.0088	0.0060	0.0318	0.0133	0.0166	-0.0213	**0.0588**	0.0683	0.0029	-0.0015	0.1661
	G	-0.0025	0.0065	0.0432	0.0161	0.0377	0.0276	**-0.0237**	0.0974	0.0125	-0.0048	0.2101*
TW	P	-0.0040	-0.0022	-0.0353	-0.0355	0.0110	-0.0350	0.0071	**0.5650**	0.0051	0.0074	0.4836**
	G	-0.0017	-0.0012	-0.0160	-0.1144	0.0237	0.0433	-0.0047	**0.4945**	0.0236	0.0176	0.4647**
HI	P	0.0104	-0.0102	0.1418	0.1479	-0.0196	0.1086	0.0078	0.1299	**0.0223**	0.0023	0.5412**
	G	0.0038	-0.0170	0.1367	0.4818	-0.0476	-0.1341	-0.0041	0.1613	**0.0722**	0.0060	0.6590**
GL	P	0.0015	-0.0008	0.0388	-0.0213	-0.0050	-0.0153	-0.0034	0.1627	0.0020	**0.0260**	0.1848*
	G	0.0019	-0.0094	0.0472	-0.0623	-0.0098	0.0164	0.0023	0.1799	0.0090	**0.0483**	0.2237*

Residual value phenotypic = 0.02648 and genotypic = 0.00895

PH : Plant height (cm)
PL : Panicle length (cm)
NPP : Number of panicles plant $^{-1}$
FG : Number of filled grains panicle $^{-1}$
CG : Number of chaffy grains panicle $^{-1}$
TG : Number of total grains panicle $^{-1}$
SF : Spikelet fertility (%)
TWG : Test weight (g)
HI : Harvest index (%)
GL : Grain length (mm)
GY : Grain yield plant $^{-1}$

Table 8. Phenotypic and genotypic path analysis of quality attributing and amylose in rice

Character		KL	KB	KLAC	KBAC	ASV	GC	PR	Zn	AC
KL	P	**-0.2313**	0.0199	-0.1453	0.0490	0.0170	-0.0172	-0.0037	-0.0068	-0.3184**
	G	**-0.2274**	0.0038	-0.1344	0.0204	0.0139	-0.0150	-0.0036	-0.0165	-0.3588**
KB	P	-0.0521	**0.0884**	-0.0444	0.0775	0.0108	-0.0138	0.0018	-0.0088	0.0594
	G	-0.0147	**0.0586**	0.0123	0.0459	0.0068	-0.0124	0.0011	-0.0207	0.0769
KLAC	P	-0.1587	0.0185	**-0.2118**	0.0493	0.0214	-0.0046	-0.0065	-0.0119	-0.3044**
	G	-0.1401	-0.0033	**-0.2181**	0.0079	0.0184	-0.0041	-0.0070	-0.0303	-0.3466**
KBAC	P	-0.0721	0.0435	-0.0664	**0.1573**	0.0233	-0.0115	-0.0009	-0.0119	0.0613
	G	-0.0358	0.0207	-0.0132	**0.1299**	0.0206	-0.0104	-0.0015	-0.0276	0.0827
ASV	P	-0.0612	0.0149	-0.0705	0.0570	**0.0642**	-0.0176	0.0067	0.0114	0.0049
	G	-0.0504	0.0063	-0.0642	0.0468	**0.0627**	-0.0146	0.0053	0.0164	0.0042
GC	P	0.0588	-0.0180	0.0145	-0.0268	-0.0167	**0.0677**	-0.0025	0.0153	0.0924
	G	0.0616	-0.0131	0.0162	-0.0244	-0.0165	**0.0554**	-0.0019	0.0236	0.1009
PR	P	-0.0169	-0.0032	-0.0274	0.0028	0.0086	0.0034	**-0.0502**	-0.0098	-0.1098
	G	-0.0209	-0.0017	-0.0383	0.0049	-0.0084	0.0027	**-0.0397**	-0.0128	-0.1142
Zn	P	0.0181	-0.0089	0.0288	-0.0214	0.0084	0.0119	0.0056	**0.0872**	0.1297
	G	0.0331	-0.0107	0.0583	-0.0316	0.0091	0.0115	0.0045	**0.1133**	0.1875

Residual effect phenotypic= 0.9075$^{@}$ and genotypic = 0.8885$^{@}$

KL : Kernel length (mm)
KB : Kernel breadth (mm)
KLAC : Kernel length after cooking (mm)
KBAC : Kernel breadth after cooking (mm)
Zn : Zinc (ppm)

ASV : Alkali spreading value
GC : Gel consistency (mm)
AC : Amylose content (%)
PR : Protein (%)

$^{@}$The data on quality traits include cooking as well as chemical quality and don't follow a specific pattern for correlation. The material needs to test one more season for better accuracy or to reduce the residual effect.

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