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Inherent Variability, Correlation and Path Analysis in Lowland Rice (*Oryza sativa* L.)

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ABSTRACT: Selection of parents based on agronomic traits and grain quality requirements of consumers is the key for realizing genetic gain in any rice improvement programme. Yield attributing traits are the major target for the plant breeders along with the trait of interest. Correlation and path analysis would be the reliable tools for identifying the associations between the yield and component traits. Hence the present study aimed to assess the relationship and effects between yield and its components traits involving 12 F_1s developed through Line x Tester mating design involving four lines and three testers along with the seven parents. The trial was conducted in RBD replicated thrice. Biometrical observations were recorded on eighteen characters *viz.*, days to 50% flowering, plant height, number of tillers, number of productive tillers, panicle length, hundred grain weight, single plant yield, hulling percentage, milling percentage, head rice recovery, alkali spreading value, amylose content, gel consistency, kernel length, kernel breadth, kernel length breath ratio, kernel length after cooking and kernel breadth after cooking. Correlation and path analysis were carried out as suggested by Falconer (1964) and Dewey and Lu (1959). Much difference was not observed between PCV and the corresponding GCV for most of the traits indicating less influence of the environment on these characters. The characters *viz.*, number of productive tillers per plant, hundred seed weight, head rice recovery, amylose content, gel consistency, kernel breadth, kernel length after cooking and kernel breadth after cooking had high heritability and high genetic advance and by choosing of these characters, the selection may be effective. The genotypic correlation for single plant yield was found to be significant and positive with number of tillers, number of productive tillers, hundred seed weight and kernel length breadth ratio. In both genotypic and phenotypic correlation, number of tillers, number of productive tillers, hundred seed weight and kernel length breadth ratio with single plant yield was observed positive and significant association. Positive significant associations with high magnitude of positive direct effect were identified for hundred seed weight followed by kernel length on single plant yield. This indicated that direct selection for these traits would be rewarding for yield improvement.

Keywords: Variability, association, grain yield, head rice recovery, path effects.

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple diet for around 2.5 billion people worldwide, which is expected to increase to 4.6 billion by 2050. It is one of the most important cereal crop, providing nourishment to half of the world's population (Lopez, 2008). It is a critical nutritional and food security source for many Asian nations, as well as the only cereal crop cooked and consumed mostly as whole grains, therefore quality is much essential (Hossain *et al.*, 2009 and Wu *et al.*, 2013). Although existence of considerable genetic variability for yield and quality attributes was already recorded in the past, there are still much genetic diversity present in the germplasm, which needs to be exploited for identifying suitable parents and producing superior recombinants with regard to yield and quality components. Polygenes, which govern majority of genetic characteristics are strongly influenced by the environment. Furthermore, heritability is vital for selection-based development as it reveals the magnitude to which a character may be passed on across generations (Sabesan *et al.,* 2009). High genetic advance associated with increased heritability provide a better circumstances for character selection. The availability on magnitude and direction of genetic correlation of characters in the base population and the use of appropriate selection techniques are the basis for any crop improvement programme (Rani *et al.*, 2016; Adhikari *et al.*, 2018).

To carry out any breeding programme, it is necessary to understand the genetic variability of yield contributing characters, along with their interaction with yield. The correlation coefficient may be useful in identifying traits with little or no significance in the selection programme (Singh *et al.*, 2014). The genotypic correlation coefficient indicates the genetic proportion of a character that is heritable in nature and used to assist breeding programmes. The existence of the association may be attributed to linkage, pleiotropic effects of genes, physiological and developmental relationships and environmental impacts (Oad *et al.*, 2002). Path analysis along with correlation provide a better understanding of the cause and effect link between various pairs of characters (Jayasudha and Sharma, 2010). The association between predictor factors and responder variables has been established using path analysis (Meena *et al.*, 2020). Path coefficient analysis imparts profound knowledge to plant breeders in increasing yield via direct and indirect effects (Hasan *et al*., 2013; Moosavi *et al*., 2015). The present investigation was undertaken to estimate genetic variability, heritability, genetic advance as per cent of mean, correlation coefficients, direct and indirect effects of different yield components and quality traits among a set of seven parents and 12 hybrids.

MATERIALS AND METHODS

The experiment was conducted during *kharif* 2020 at Agricultural College and Research Institute, Madurai. The experimental material was generated by involving four lines (TKM 13, ADT 49, CO 52 and ADT 52) and three testers possessing Bacterial Leaf Blight resistant genes (IRBB 21, Improved Samba Mashuri and IRBB 60) through line x tester mating design by Kempthorne (1957). The seven parents and twelve hybrids were raised in a randomized block design (RBD) with three replications. Thirty days old seedlings were transplanted in 3m row following spacing of 20cm between rows and 15cm between plants at the rate of 15 plants per row. At maturity, five plants from each genotype were selected from each replications randomly for recording the biometrical observations *viz.*, days to 50 per cent flowering, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, hundred grain weight, single plant yield, hulling percentage (%), milling percentage (%), head rice recovery (%), alkali spreading value, amylose content, gel consistency, kernel length (mm), kernel breadth (mm), kernel length breadth ratio, kernel length after cooking and kernel breadth after cooking.

Kernel length and kernel breadth of 10 whole milled rice were measured by means of dial caliper and kernel length breadth ratio was computed (Murthy and Swamy, 1967). Kernel elongation was determined by soaking 5 g of whole milled rice in 12 ml distilled water for 10 minutes and later cooked for 15 minutes in water bath. Observations on length and breadth of cooked kernels and elongation ratio were recorded with the help of graph sheet.

To estimate the Milling quality trait, the rough rice (paddy) was cleaned, dehulled by using Zaccaria's Rice Miller (Mod. PAZ-1/DTA). After cleaning and weighing the dehusked kernel (brown rice) hulling percentage was calculated. Dehusked kernels were polished to remove bran and milling percentage was calculated. From the milled paddy, percentage of head rice was measured. It is the estimate of head rice with more than 2/3 rd size and expressed as percentage.

R statistical analysis software was used for association analysis to assess their correlation and path effects. The package "Variability" was used to estimate the variability parameters and the package "Agricolae", "Metan" and "Lavaan" were used for correlation and path effects analysis.

According to Robinson *et al.* (1949), the estimates of heritability were categorized as high (> 60%), moderate (30-60%) and low (0-30%). Genetic advance as per cent of mean was calculated and classified as high (> 20%), moderate (10-20%) and low (< 10%) as given by Johnson *et al.* (1955). Correlation was worked out using the formulae suggested by Falconer (1964). Partitioning of the correlation coefficient into direct and indirect effects was carried out using the procedure suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Characterization of path coefficients was carried out as suggested by Lenka and Mishra (1973).

RESULT AND DISCUSSION

Analysis of variance. The results of the analysis of variance (ANOVA) for grain yield and yield component characteristics (Table 1) indicated highly significant mean squares for genotypes for all the traits examined, showing that there is enough variation among the genotypes, thus permitting effective selection as reported by Mazal *et al.* (2021).

Estimation of genetic variability. The mean, range, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability and genetic advance as per cent of mean, (GA %) for all the traits are presented in Table 2. For most of the characters, there was little difference between PCV and the corresponding GCV, indicating that environmental influences are minimal and that these traits have high genetic variability. Bhargava *et al.* (2021); Tiwari *et al.* (2019); Sudeepthi *et al.* (2020) previously reported similar findings in rice. High PCV and GCV were observed for head rice recovery, while moderate PCV and GCV values were noticed for number of tillers per plant, number of productive tillers per plant, hundred seed weight, amylose content, gel consistency, kernel breadth, kernel length after cooking and kernel breadth after cooking.

Table 1: Analysis of variance (mean squares) for grain yield and quality traits in rice.

Sources	df	DF	PH	NOT	NPT	PL	HSW	SPY	HP	MP	HHR	ASV	AC	GC	KL	KB	KLBR	KLAC	KBAC
Replication	2	0.60	1.023	0.676	0.673	0.349	0.023	0.956	6.544	6.801	20.562	0.123	0.441	3.943	0.046	0.001	0.008	0.001	0.032
Treatment	18	186.13	45.294**	18.591**	29.290**	8.881 **	0.250 **	57.169**	54.897**	54.705**	59.613**	2.873**	3.88 **	235.467**	1.962 **	0.103 **	0.341**	1.343**	0.312**
Error	36	5.634	2.383	0.734	1.057	0.825	0.013	0.868	17.879	12.920	14.584	0.493	0.691	3.552	0.027	0.003	0.009	0.002	0.029

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

DFF-Days to 50% flowering, **PH**-Plant height, **NOT**- Number of tillers per plant, **NPT** - Number of productive tillers per plant, **PL** – Panicle length, **HSW** – Hundred seed weight, **SPY** – Single plant yield, **HP** – Hulling percentage **MP** – Milling percentage, **HHR** – Head Rice Recovery, **ASV** – Alkali spreading value, **AC** – Amylose content, **GC** - Gel consistency, KL – Kernel length, **KB** – Kernel breadth, **KLBR** – Kernel length breadth ratio, **KLAC** – Kernel length after cooking, **KBAC** – Kernel breadth after cooking.

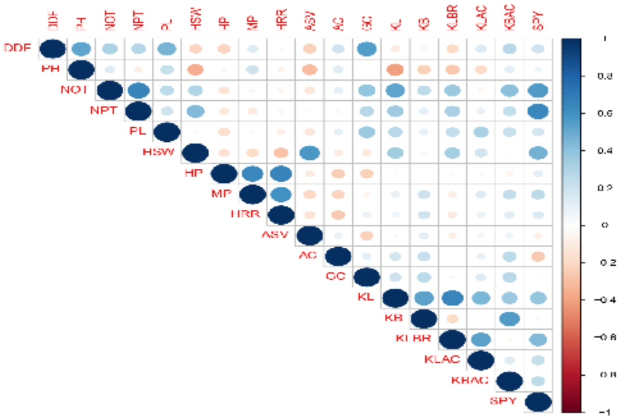
Table 2: Components of genetic parameters for grain yield and quality traits in rice.

character	Range		Mean	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability (%)	Genetic advance as per cent of mean
	MIN	MAX					
Days to 50% flowering	84	116	101.87	7.96	7.61	91.44	15.00
Plant height	86.73	101.24	93.76	4.36	4.03	85.72	7.69
Number of tillers per plant	19.67	28.77	24.49	10.56	9.96	89.02	19.36
Number of productive tillers per plant	15	25.27	20.84	15.52	14.72	89.91	28.75
Panicle length	22.03	28.43	25.07	7.47	6.54	76.49	11.78
Hundred seed weight	1.47	2.31	1.88	16.12	14.93	85.80	28.50
Single plant yield	25	41.67	33.55	7.24	4.63	40.83	6.09
Hulling percentage	68.66	82.62	75.90	7.95	5.73	51.88	8.50
Milling percentage	60.07	75.17	64.50	9.88	7.04	50.72	10.32
Head rice recovery	48.08	61.28	55.06	36.94	29.01	61.67	46.93
Alkali spreading value	1.67	5.00	3.07	5.71	4.45	60.66	7.13
Amylose content	21	25.54	23.22	11.41	11.16	95.61	22.47
Gel consistency	63.63	106.17	78.82	13.17	12.90	95.98	26.04
Kernel length	5.20	7.80	6.23	9.59	9.21	92.09	18.20
Kernel breadth	1.60	2.20	1.99	11.04	10.61	92.40	21.01
Kernel length breadth ratio	2.50	3.63	3.14	8.95	8.93	99.56	18.36
Kernel length after cooking	6.09	8.53	7.49	13.92	12.20	76.83	22.03
Kernel breadth after cooking	2.10	3.00	2.52	13.21	12.91	95.58	26.00

DFF-Days to 50% flowering, **PH**-Plant height, **NOT**- Number of tillers per plant, **NPT** - Number of productive tillers per plant, **PL** – Panicle length, **HSW** – Hundred seed weight, **SPY** – Single plant yield, **HP** – Hulling percentage **MP** – Milling percentage, **HHR** – Head Rice Recovery, **ASV** – Alkali spreading value, **AC** – Amylose content, **GC** - Gel consistency, KL – Kernel length, **KB** – Kernel breadth, **KLBR** – Kernel length breadth ratio, **KLAC** – Kernel length after cooking, **KBAC** – Kernel breadth after cooking.

Characters with moderate PCV and GCV values are likely to provide a decent scope of improvement through selection in their particular environment due to their moderate genetic variability (Garg *et al.*, 2011; Paswan *et al.*, 2014). Low estimates of these two parameters were observed for the characters days to 50 per cent flowering, plant height, panicle length, single plant yield, hulling percentage, milling percentage, alkali spreading value, kernel length and kernel length breadth ratio indicating little scope of improvement in these traits due to lack of requisite variability. The characters *viz.*, number of productive tillers per plant, hundred seed weight, head rice recovery, amylose content, gel consistency, kernel breadth, kernel length after cooking and kernel breadth after cooking had high heritability and high genetic advance and selection may be rewarding for these characters. Similar findings were reported by Lakshmi *et al.*, 2021; Yadav *et al.*, 2021 in rice. Days to 50 per cent flowering, number of tillers per plant, panicle length and kernel length, and kernel length breadth ratio all showed high heritability along with moderate genetic progress as obtained in rice by Singh *et al.* (2021). Plant height and alkali spreading value had high heritability, but low genetic advance as per cent of mean. Either high heritability coupled with high genetic advance or moderate heritability accompanied with high genetic advance indicated the presence of additive gene effect and selection may be effective in such cases. Low heritability combined with low genetic progress showed the presence of non-additive gene action, and selection for such characteristics may be ineffective. (Nadarajan *et al.*, 2018).

Phenotypic correlation. Phenotypic correlation between yield and yield attributing characters are presented in Table 3 and Fig. 1. Highly positive and significant phenotypic association was observed between yield with number of tillers (0.568**), number of productive tillers (0.644**), hundred seed weight (0.475**), kernel length (0.391**) and kernel length breadth ratio (0.434**), whereas positive non significant association with days to 50% flowering (0.203), plant height(0.063), panicle length(0.184), hulling percentage(0.115), milling percentage(0.260), gel consistency(0.015), kernel length after cooking (0.235) and kernel breadth after cooking(0.258). This significant relationship between single plant yield and yield attributing features indicated that increasing the dimension of these qualities lead to an increase in grain production.



Circles represents relative correlation (r) values; circle dark color represents the high phenotypic correlation values; circle light color represents low phenotypic correlations; red color represents negative correlation; blue color represents positive.

Fig 1. Diagrammatic representation of phenotypic correlation in yield and yield contributing traits.

Table 3: Phenotypic correlation for grain yield and quality traits in rice.

	DFF	**PH**	**NOT**	**NPT**	**PL**	**HSW**	**HP**	**MP**	**HRR**	**ASV**	**AC**	**GC**	**KL**	**KB**	**KLBR**	**KLAC**	**KBAC**	**SPY**
DFF	1	0.523**	0.318*	0.283*	0.466**	-0.212	-0.214	0.149	0.021	-0.234	0.207	0.558**	-0.108	0.045	-0.196	0.158	0.275 *	0.203
PH		1	0.128	-0.086	0.233	-0.352**	-0.047	0.206	-0.057	-0.305*	0.142	0.001	-0.404**	-0.240	-0.263*	-0.189	0.122	0.063
NOT			1	0.672**	0.264*	0.299*	-0.148	0.039	-0.044	-0.133	0.120	0.401**	0.519**	0.252	0.367**	-0.047	0.426**	0.568**
NPT				1	0.1998	0.436**	-0.120	-0.121	-0.039	0.017	-0.037	0.277*	0.361**	0.112	0.329*	0.093	0.24	0.644**
PL					1	-0.0212	-0.171	0.024	-0.097	-0.135	0.104	0.37 **	0.275*	0.102	0.250	0.323*	0.242	0.184
HSW						1	-0.161	-0.200	-0.278*	0.572**	-0.102	-0.122	0.351**	0.034	0.332*	0.200	0.005	0.475**
HP							1	0.647**	0.690**	-0.105	-0.235	-0.231	0.014	0.007	-0.022	0.028	-0.058	0.115
MP								1	0.622**	-0.217	-0.216	-0.063	0.099	0.199	-0.095	0.140	0.235	0.260
HRR									1	-0.144	-**0.**269*****	0.085	0.073	0.207	-0.100	0.087	0.136	0.153
ASV										1	0.080	-0.224	0.033	0.116	-0.087	0.057	0.068	-0.075
AC											1	0.112	0.189	0.228	0.008	0.094	0.268*	-0.261*
GC												1	0.206	0.264*	0.029	0.140	0.273*	0.015
KL													1	0.539**	0.66 **	0.455**	0.37**	0.391**
KB														1	-0.184	0.016	0.564**	-0.036
KLBR															1	0.534**	-0.047	0.435**
KLAC																1	0.141	0.235
KBAC																	1	0.258
SPY																		1

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

DFF-Days to 50% flowering, **PH**-Plant height, **NOT**- Number of tillers per plant, **NPT** - Number of productive tillers per plant, **PL** – Panicle length, **HSW** – Hundred seed weight, **SPY** – Single plant yield, **HP** – Hulling percentage **MP** – Milling percentage, **HHR** – Head Rice Recovery, **ASV** – Alkali spreading value, **AC** – Amylose content, **GC** - Gel consistency, KL – Kernel length, **KB** – Kernel breadth, **KLBR** – Kernel length breadth ratio, **KLAC** – Kernel length after cooking, **KBAC** – Kernel breadth after cooking.

Days to fifty per cent flowering possessed positive significant association with plant height (0.523**), number of tillers (0.318*), number of productive tillers (0.283*), panicle length (0.466**), gel consistency (0.558**) and kernel breadth after cooking (0.275*). Similar findings were obtained by Hema *et al*. (2019) in rice. Number of tillers per plant and productive tillers per plant were found to be positive and significant among themselves along with hundred seed weight, gel consistency, kernel length, kernel length breadth ratio and single plant yield. Apart from this number of tillers per plant also exhibited positive and significant association with panicle length and kernel breadth after cooking. It was revealed that number of total tillers per plant and productive tillers per plant were important factors in enhancing rice production potential. The plant height unveiled negative association with hundred seed weight (-0.352**), alkali spreading value (-0.304*), kernel length (-0.404**) and length breadth ratio (-0.262*). Positive and significant correlation was found among panicle length with gel consistency (0.37**), kernel length (0.274*) and kernel length after cooking (0.323*). The alkali spreading value, kernel length and kernel length breadth ratio all had a positive relationship with hundred seed weight, however the head rice recovery (-0.278*) had a negative relationship. As a result, careful selection is required when seeking to increase these quality features without reduction in yield.

Hulling and milling percentages were shown to have a positive and significant relationship with one another as well as with head rice recovery, while head rice recovery had a significant negative relationship with amylose content (-0.269*). Kernel breadth and kernel breadth after cooking exhibited positively significant association with kernel length and gel consistency. Kernel length and kernel length breadth ratio were shown to have a positive relationship with kernel length after cooking. These findings showed that through careful selection, these quality characteristics might be improved simultaneously with yield.

Genotypic correlation: The genotypic correlation for single plant yield was found to be significant and positive with number of tillers (0.645**), number of productive tillers (0.709**), hundred seed weight (0.506**) and kernel length breadth ratio (0.478). Similar results were obtained for tiller number per plant by Saha *et al.*, (2019); Singh *et al.* (2020). Kernel length (0.405), milling percentage (0.389), kernel breadth after cooking (0.278), and kernel length after cooking (0.405) all had non-significant positive association (0.236) with yield per plant (Table 4).

Days to fifty per cent flowering had a positive significant association with the traits such as plant height (0.594**), panicle length (0.538**) and gel consistency (0.602**), whereas the traits, number of productive tillers (0.727**), kernel length (0.562*) and kernel breadth after cooking (0.526*) exhibited significantly positive association with number of tillers per plant. Association of kernel length with kernel breadth (0.558*), kernel length breadth ratio (0.725**), kernel length after cooking (0.467*) and kernel breadth after cooking (0.471*) were positive and significant. Further, kernel breadth had highly significant and positive association with kernel breadth after cooking (0.674**). The relationship between kernel length and kernel length breadth ratio was positive and significant comparable to that of Archana *et al.* (2018); Singh *et al.* (2020) in rice. Kernel length breadth ratio was significantly associated with kernel length after cooking (0.560*). Hulling and milling percentage had highly positive and significant correlation with each other along with head rice recovery as reported by Srinivas *et al.* (2021).

Table 4: Genotypic correlation for grain yield and quality traits in rice.

	DFF	PH	NOT	NPT	PL	HSW	HP	MP	HRR	ASV	AC	GC	KL	KB	KLBR	KLAC	KBAC	SPY
DFF	1	0.594**	0.351	0.309	0.538*	-0.238	-0.234	0.280	0.088	-0.280	0.268	0.602**	-0.118	0.063	-0.204	0.167	0.353	0.214
PH		1	0.153	-0.102	0.264	-0.401	-0.084	0.401	-0.138	-0.469	0.170	-0.012	-0.415	-0.257	-0.330	-0.208	0.128	0.053
NOT			1	0.727**	0.354	0.327	-0.125	0.038	-0.032	-0.155	0.313	0.441	0.562*	0.255	0.389	-0.047	0.526*	0.645**
NPT				1	0.246	0.499*	-0.104	-0.185	-0.046	0.036	0.035	0.306	0.379	0.100	0.332	0.101	0.310	0.710**
PL					1	-0.019	-0.263	0.223	-0.166	-0.125	0.311	0.427	0.309	0.124	0.279	0.366	0.228	0.194
HSW						1	-0.359	-0.393	-0.411	0.726**	-0.143	-0.119	0.368	0.018	0.422	0.216	-0.006	0.506*
HP							1	0.790**	1.036**	-0.272	-0.567	-0.275	0.008	0.091	-0.026	0.047	-0.091	0.205
MP								1	0.796**	-0.317	-0.408	-0.043	0.071	0.224	-0.102	0.194	0.446	0.389
HRR									1	-0.442	-0.493	0.160	0.095	0.321	-0.146	0.111	0.079	0.229
ASV										1	0.074	-0.289	0.074	0.221	-0.063	0.055	-0.047	-0.134
AC											1	0.152	0.257	0.292	0.049	0.127	0.441	-0.402
GC												1	0.228	0.289	0.023	0.145	0.303	0.017
KL													1	0.558*	0.725**	0.467*	0.4716*	0.405
KB														1	-0.212	0.019	0.674**	-0.040
KLBR															1	0.560*	-0.069	0.478*
KLAC																1	0.154	0.237
KBAC																	1	0.278
SPY																		1

*Significant at 0.05 level **Significant at 0.01 level

DFF-Days to 50% flowering, **PH**-Plant height, **NOT**- Number of tillers per plant, **NPT** - Number of productive tillers per plant, **PL** – Panicle length, **HSW** – Hundred seed weight, **SPY** – Single plant yield, **HP** – Hulling percentage **MP** – Milling percentage, **HHR** – Head Rice Recovery, **ASV** – Alkali spreading value, **AC** – Amylose content, **GC** - Gel consistency, KL – Kernel length, **KB** – Kernel breadth, **KLBR** – Kernel length breadth ratio, **KLAC** – Kernel length after cooking, **KBAC** – Kernel breadth after cooking.

Genotypic correlation coefficient for the traits *viz.*, number of tillers and number of productive tillers, hundred seed weight and kernel length breadth ratio with single plant yield were found to be higher than the phenotypic correlation coefficient, indicating that there is a strong genetic correlation than environmental association between these traits and single plant yield. Similar results were obtained by Devi *et al.* (2022).

Path analysis. Selections based on the results of correlation coefficient analysis may not produce the expected outcome, it is necessary to include path coefficient analysis for estimation of degree of association (Prasanna Kumari *et al.*, 2020). Path analysis was undertaken to study the direct and indirect effects of the different traits on yield, the dependent variable. The results of response variable, single plant yield and other polygenic and qualitative traits results are presented in Table 5. Majority of the values were less than unity in path analysis revealing that inflation due to multi-collinearity is less (Gravois and Helms, 1992). Hundred seed weight had high magnitude of positive direct effect on single plant yield (0.507) followed by days to fifty per cent flowering (0.357) and kernel length (0.347**)**, whereas number of productive tillers (0.250), head rice recovery (0.236) and kernel breadth after cooking (0.276) recorded moderate direct effect on single plant yield. Singh *et al.*, 2020 found that the number of productive tillers and hundred seed weight had a highly positive direct influence on single plant yield. These variables with high and moderate direct effects are considered to be crucial aspects of single plant yield and direct selection of these traits might significantly increase single plant yield.

Kernel breadth (-0.316) exhibited high and negative direct effect on single plant yield whereas, gel consistency (-0.273), alkali spreading value (-0.250) and amylose content (-0.214) were found to have moderate and negative direct effect on single plant yield. The negative direct effects showed that selection through these traits would be ineffective for enhancing rice productivity. In the present study, the residual effect was 0.185 which revealed that the characters chosen in this study contributed 81.5 per cent to the yield.

Alkali spreading value (0.289) exhibited the highest positive indirect effect followed by number of productive tillers (0.223) on grain yield through hundred seed weight. Kernel length breadth ratio (0.229) exhibited positive and moderate indirect effect on single plant yield via kernel length. As a result, indirect selection based on these traits should be examined simultaneously for yield enhancement.

The association between number of tillers, number of productive tillers, hundred seed weight, and kernel length breadth ratio with single plant yield were positive and significant at both genotypic and phenotypic levels. Positive and significant correlation with high positive direct effects were found on single plant yield by hundred seed weight followed by kernel length. This suggested that direct selection for these attributes might be advantageous for yield enhancement.

Table 5: PATH analysis for grain yield and quality traits in rice

	DDF	PH	NOT	NPT	PL	HSW	HP	MP	HRR	ASV	AC	GC	KL	KB	KLBR	KLAC	KBAC	SPY
DDF	**0.357**	0.035	-0.004	0.070	-0.018	-0.106	0.008	0.012	0.005	0.057	-0.043	-0.153	-0.038	-0.016	-0.019	-0.021	0.074	0.203
PH	0.186	**0.067**	-0.002	-0.023	-0.009	-0.177	0.002	0.016	-0.014	0.075	-0.030	0.015	-0.139	0.076	-0.025	0.024	0.033	0.063
NOT	0.114	0.009	**-0.014**	0.168	-0.010	0.147	0.006	0.003	-0.012	0.032	-0.024	-0.109	0.180	-0.079	0.036	0.006	0.116	0.568 **
NPT	0.100	-0.006	-0.009	**0.250**	-0.008	0.223	0.005	-0.010	-0.007	-0.005	0.006	-0.077	0.125	-0.035	0.032	-0.012	0.066	0.644**
PL	0.168	0.015	-0.004	0.050	**-0.038**	-0.010	0.007	0.002	-0.021	0.035	-0.024	-0.101	0.094	-0.032	0.024	-0.041	0.066	0.184
HSW	-0.075	-0.023	-0.004	0.110	0.001	**0.507**	0.006	-0.015	-0.066	-0.142	0.021	0.033	0.121	-0.013	0.032	-0.026	0.003	0.475 **
HP	-0.075	-0.003	0.002	-0.030	0.006	-0.081	**-0.040**	0.051	0.158	0.025	0.051	0.063	0.007	-0.003	-0.002	-0.004	-0.017	0.115
MP	0.054	0.013	-0.001	-0.030	-0.001	-0.096	-0.025	**0.080**	0.142	0.052	0.045	0.016	0.035	-0.063	-0.009	-0.018	0.066	0.260
HRR	0.007	-0.004	0.001	-0.008	0.003	-0.142	-0.027	0.048	**0.236**	0.037	0.054	-0.022	0.024	-0.063	-0.010	-0.012	0.036	0.153
ASV	-0.082	-0.020	0.002	0.005	0.005	0.289	0.004	-0.017	-0.035	**-0.250**	-0.017	0.060	0.010	-0.038	-0.008	-0.008	0.019	-0.075
AC	0.071	0.009	-0.002	-0.008	-0.004	-0.051	0.009	-0.017	-0.059	-0.020	**-0.214**	-0.030	0.062	-0.073	0.001	-0.012	0.074	-0.261
GC	0.200	0.012	-0.005	0.070	-0.014	-0.061	0.009	-0.005	0.019	0.055	-0.024	**-0.273**	0.069	-0.082	0.003	-0.018	0.077	0.015
KL	-0.039	-0.027	-0.007	0.090	-0.010	0.177	-0.001	0.008	0.017	-0.007	-0.039	-0.055	**0.347**	-0.171	0.064	-0.059	0.102	0.391 **
KB	0.018	-0.016	-0.003	0.028	-0.004	0.020	0.000	0.016	0.047	-0.030	-0.049	-0.071	0.187	**-0.316**	-0.018	-0.003	0.154	-0.036
KLBR	-0.071	-0.017	-0.005	0.083	-0.010	0.167	0.001	-0.007	-0.024	0.020	-0.002	-0.008	0.229	0.057	**0.097**	-0.068	-0.011	0.434 **
KLAC	0.057	-0.013	0.001	0.023	-0.012	0.101	-0.001	0.011	0.021	-0.015	-0.019	-0.038	0.160	-0.006	0.052	**-0.129**	0.039	0.235
KBAC	0.096	0.008	-0.006	0.060	-0.009	0.005	0.002	0.019	0.031	-0.017	-0.058	-0.077	0.128	-0.177	-0.004	-0.018	**0.276**	0.258

Residual = 0.185

* Significant at 1% level

** Significant at 5% level

Diagonal values indicate direct effects

DFF-Days to 50% flowering, **PH**-Plant height, **NOT**- Number of tillers per plant, **NPT** - Number of productive tillers per plant, **PL** – Panicle length, **HSW** – Hundred seed weight, **SPY** – Single plant yield, **HP** – Hulling percentage **MP** – Milling percentage, **HHR** – Head Rice Recovery, **ASV** – Alkali spreading value, **AC** – Amylose content, **GC** - Gel consistency, KL – Kernel length, **KB** – Kernel breadth, **KLBR** – Kernel length breadth ratio, **KLAC** – Kernel length after cooking, **KBAC** – Kernel breadth after cooking.

CONCLUSION

In the present investigation wide range of variation was observed among the traits. High heritability combined with high genetic advance was exhibited by number of productive tillers per plant, hundred seed weight, head rice recovery, amylose content, gel consistency, kernel breadth, kernel length after cooking and kernel breadth after cooking. The association between number of tillers, number of productive tillers, hundred seed weight and kernel length breadth ratio with single plant yield were positive and significant both at phenotypic and genotypic levels. Path analysis revealed that number of tillers, number of productive tillers, hundred seed weight, and kernel length breadth ratio exhibited a positive direct effect on single plant yield. Thus selection for these characters with high heritability, high genetic advance as per cent of mean and positive direct effects help in selection of superior genotypes for further breeding programmes.

FUTURE SCOPE

The characters with high heritability, high genetic advance as per cent of mean and positive direct effects on single plant yield could be used either for selection of parents for effecting new crosses or hybrids for recombination breeding.

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Conflict of Interest. None.

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