

Genetic Association Studies for Yield and Yield Attributes in BC₂F₂ Population of rice (*Oryza sativa* L.)

Sowmiya C.A.¹, Arumugam Pillai M.^{2*}, Ramalingam J.³, Pushpam R.⁴, Shoba D.⁵ and Kumar K.K.³

¹Ph.D. Research Scholar, Department of Genetics and Plant Breeding,

V.O.C. Agricultural College and Research Institute, Killikulam, Thoothukudi dt, (Tamil Nadu), India.

^{2*}Professor and Head, Department of Genetics and Plant Breeding,

V.O.C. Agricultural College and Research Institute, Killikulam, Thoothukudi dt, (Tamil Nadu), India.

³Professor, Centre for Plant Molecular Biology and Biotechnology,

Tamil Nadu Agricultural University, Coimbatore, (Tamil Nadu), India.

⁴Professor, Centre for Plant Breeding and Genetics,

Tamil Nadu Agricultural University, Coimbatore, (Tamil Nadu), India.

⁵Assistant Professor, Department of Genetics and Plant Breeding,

V.O.C. Agricultural College and Research Institute, Killikulam, Thoothukudi dt, (Tamil Nadu), India.

(Corresponding author: Arumugam Pillai M.*)

(Received: 21 July 2023; Revised: 19 August 2023; Accepted: 18 September 2023; Published: 15 October 2023)

(Published by Research Trend)

ABSTRACT: Yield in rice is a complex trait influenced by multiple genes and environmental factors. This complexity makes it difficult to pinpoint the exact genetic variants responsible for differences in yield. It's essential to carefully control and minimize environmental noise in the phenotype data. The BC₂F₂ population of ADT43 × RP-Bio-Patho-2 was used for the present experiment. Through genotypic correlation coefficient and path analysis, sixteen quantitative variables from 58 genotypes were evaluated in this study. The genetic correlation between two traits is quantified by the genotypic correlation coefficient. The results of the experiment showed that there is potential to concurrently enhance the number of productive tillers, the number of filled grains per panicle, and the number of grains per panicle features to raise grain yield per plant, as indicated by the significant and positive correlation between the traits. The investigation of the direct and indirect relationships between variables in a complex system is conducted using path coefficient analysis. It facilitates comprehension of the contributions of several factors to the variation in a target variable by dividing the entire effect into its direct and indirect components. Based on path analysis, the number of productive tillers per plant, number of grains per panicle, and number of filled grains per panicle had a significant positive direct impact on grain yield; thus, this characteristic needs to be given top priority during selection.

Keywords: Genotypic correlation coefficient, path analysis, direct effects, indirect effects, significance.

INTRODUCTION

The grass family Poaceae includes rice. *Oryza sativa*, sometimes known as Asian rice, and *Oryza glaberrima*, often known as African rice, are the two most widely grown varieties of rice. The two subspecies of *Oryza sativa*, *indica*, and *japonica*, each have their distinctive traits. A sizeable majority of the world's population receives crucial nutrients and energy from rice in addition to being an important source of carbs. Energy-giving carbs can be found in rice. It also has a low fat content and vital nutrients including iron, thiamine, and niacin (Mohidem *et al.*, 2022). However, depending on the type and processing technique, the nutritional value can change.

Although there are many kinds of rice, they can be essentially divided into two groups: long-grain and short-grain. The size, shape, flavor, and texture of these types vary. Popular varieties include sushi, basmati,

jasmine, and arborio rice. More than half of the world's population relies on rice as a staple grain, particularly in nations like China, India, Indonesia, and many African countries. It is essential to ensure food security and reduce poverty in many regions of the world. The world economy benefits significantly from the rice sector. Pest and disease infestations, disease outbreaks, water scarcity, and the effects of climate change all pose problems for rice farming (Priyadarshini *et al.*, 2018). Sustainable rice farming techniques and more resilient rice cultivars are constantly being developed by scientists and farmers.

Studies on variation also concentrate on locating rice plants that have resistance or tolerance to pests and illnesses. Using this knowledge can help breeders create rice types that are naturally resistant to common rice diseases, cutting down on the use of chemical pesticides. To create new, improved rice varieties that can meet the changing needs of agriculture, food security, and

sustainability, variability studies in rice are an essential part of rice research and breeding operations. This research contributes to ensuring that rice remains an essential staple crop for populations around the world.

The genotypic correlation coefficient is a statistical indicator that is employed in quantitative genetics and genetics to quantify the degree of relationship or correlation between the genotypic values of two distinct traits or features in individuals within a population. In other words, it evaluates the genetic link between two traits. For analyzing and measuring the complicated interactions between variables in complex systems, path coefficient analysis is a useful method that enables researchers to learn more about the variables influencing observed results. Path co-efficient analysis assists in the distribution of correlation coefficient into direct and indirect effects of traits on yield, thereby helping the breeders to hand-pick the needed components of superior genotypes. The present study was taken to determine the genotypic correlation coefficient, and the path co-efficient analysis for grain yield and its components, in BC₂F₂ generation.

MATERIALS AND METHODS:

Plant materials and crossing strategy: The V.O.C. Agricultural College and Research Institute, Killikulam, was the site of the experimental study. We selected ADT43, a common variety that is medium slender, short in duration, and particularly vulnerable to blast and bacterial blight diseases, as a recurrent parent. In the marker-assisted selection backcross breeding procedure, RP-Bio-Patho-2, a near-isogenic line of Samba Mahsuri that carries both blast and bacterial blight disease resistance genes was used as donor parent. Through foreground selection employing both gene-specific STS markers, the heterozygous F₁s with both blast and bacterial blight resistance genes were chosen. The BC₁F₁ generation was generated by further backcrossing the double-positive F₁s with the recurrent parent ADT43. Further heterozygosity for both genes was confirmed, and background selection was carried out to the double positives to maximize recurrent parent genome recovery. To create the BC₂F₁ population, the double positive line with the highest RPG was chosen and further backcrossed with the recurrent parent. The same method mentioned above was used to expose the BC₂F₁ population to choose double positive lines with the highest RPG. To create BC₂F₂ generation, the chosen lines were selfed.

Data collection: Random selection of single plants was followed and data on plant height (cm), number of productive tillers, panicle length (cm), number of grains per panicle, filled grains per panicle, thousand-grain weight (g), grain length (mm), grain width (mm), grain length/breadth ratio, kernel length before cooking (mm), kernel length after cooking (mm), kernel length/breadth before cooking, kernel length after cooking (mm), kernel length after cooking (mm), kernel elongation ratio after cooking and grain yield per plant (g) were taken.

Quantitative genetic parameters and statistical analysis:

Microsoft Excel and TNAU stat statistical software were employed for the computation of genotypic correlation coefficient, and path analysis of quantitative traits.

1. Genotypic correlation coefficient: The correlation coefficient was estimated as suggested by Miller *et al.* (1958), and Johnson *et al.* (1955).

$$\text{Genotypic correlation co-efficient } (r_g) = \frac{\text{Cov}_g 1,2}{\sqrt{\sigma_g^2 1 \times \sigma_g^2 2}}$$

Where,

Cov_g 1,2 = Genotypic covariance of traits 1 and 2

σ_g² 1 = Genotypic variance of trait 1

σ_g² 2 = Genotypic variance of trait 2

The below formula was used to 't' value to find the significance of the correlation.

$$t_{\text{cal}} = \frac{r}{SE}$$

where,

r = correlation coefficient

SE = standard error

Both the calculated 't' value and table 't' values at 5% and 1% levels of significance at n-2 df were compared to find the significance. Searle (1965) divided the correlation coefficient into the following categories to make indirect selection more effective than direct selection.

Value	Scale
< 0.30	Very weak
0.30 – 0.49	Moderately weak
0.50 – 0.64	Moderately strong
> 0.64	Very strong

2. Path co-efficient analysis: Grain yield per plant was considered as a dependent variable whereas other characters were considered as independent variables or predictors while assessing path co-efficient analysis. As suggested by Dewey and Lu (1959), the influence of independent variables either directly or indirectly was evaluated by,

$$\begin{aligned} r_{1y} &= P_{1Y}r_{11} + P_{2Y}r_{12} + P_{3Y}r_{13} + \dots + P_{nY}r_{1n} \\ r_{2y} &= P_{1Y}r_{21} + P_{2Y}r_{22} + P_{3Y}r_{23} + \dots + P_{nY}r_{2n} \\ \dots &= \dots + \dots + \dots + \dots + \dots \\ r_{ny} &= P_{1Y}r_{n1} + P_{2Y}r_{n2} + P_{3Y}r_{n3} + \dots + P_{nY}r_{nn} \end{aligned}$$

Where,

1, 2, n = Independent variables

Y = Dependent variable (grain yield per plant)

r_{1y}, r_{2y}, r_{ny} = Correlation coefficient of variation between independent and dependent variables

P_{1Y}, P_{2Y}, P_{nY} = Direct effects of characters 1 to n on 'Y'

To calculate the residual effects which are the contributions of characters not taken in the study, the following formula was used.

Residual effect

$$= \sqrt{(1 - r_{1Y}P_{nY} + r_{2n}P_{nY} + \dots + r_{nY}P_{nY})}$$

Scale of path analysis by Lenka and Mishra (1973):

Scale	Value of direct and indirect effects
Negligible	0.00 to 0.09
Low	0.10 to 0.19
Moderate	0.20 to 0.29
High	0.30 to 0.99
Very high	> 1.00

RESULTS AND DISCUSSION

Genotypic correlation coefficient: The genotypic correlation coefficient is used to quantify to which degree, magnitude, and direction of various components influencing the main character are associated with each other. Hence indirect selection of characters contributing to yield becomes the basis for the assortment of genotypes with high yield potential. The genotypic correlation coefficient is the genotypic connection between two characters and thereby envisages the indirect effects of the characters on the dependent character taken in the study. The genotypic correlation coefficient can range from -1 to 1. The genetic factors that raise one trait similarly increase the other trait, according to a value of 1, which denotes a perfect positive genetic association. A result of -1 denotes a perfect negative genetic correlation, in which the genetic components that boost one feature also lower the other. A value of 0 denotes the absence of any genetic link; the genetic components influencing one attribute have no bearing on the other. The genotypic correlation coefficient of yield and its contributing characters are given in Table 1 and Figs. 1 & 2.

The significant and positive association between yield and its contributing traits such as number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, and kernel length before cooking displayed the improvement of the characters along with the grain yield per plant during selection. Whereas grain yield per plant was significant and negatively intercorrelated with kernel elongation ratio after cooking.

The number of filled grains per panicle showed a positive and significant correlation with characters' thousand-grain weight, grain length, and kernel length before cooking and a negative correlation with kernel elongation ratio after cooking. Hence filled grains per panicle were insignificantly intercorrelated with all other traits taken under study. Also, the number of productive tillers per plant exhibited a significantly positive correlation with grain L/B ratio and kernel L/B ratio before cooking traits, however negatively significant with grain breadth and kernel elongation ratio after cooking. It showed an insignificant correlation at the genotypic level with the other traits. Significant positive correlation of kernel length before cooking with grain L/B ratio and grain length; grain breadth with kernel breadth after cooking.

From the table, it was found that plant height and panicle length had a significant and positive association with the number of grains per panicle and number of filled grains per panicle; thousand-grain weight was significant and positively associated with grain length, grain breadth, and kernel breadth after cooking characters. Apart from the above-mentioned characters, panicle length had a significant and positive association with plant height too.

Table 1: Correlation coefficients for grain yield and yield components in BC₂F₂ population of ADT 43 X RP-Bio-Patho-2.

Traits	PH	NPT	PL	NGP	FGP	TGW	GL	GB	G L/B	KLBC	KBBC	L/B BC	KLAC	KBAC	ERAC	GYP
PH	1.000	0.014	0.627**	0.461**	0.515**	0.211	0.101	0.104	-0.048	0.121	0.022	0.065	0.091	0.127	-0.057	0.200
NPT		1.000	0.114	0.077	0.191	-0.223	0.092	-0.409**	0.395**	0.223	-0.185	0.285*	-0.051	-0.090	-0.287*	0.780**
PL			1.000	0.607**	0.676**	0.241	0.220	-0.024	0.108	0.138	-0.118	0.164	-0.005	0.204	-0.159	0.307
NGP				1.000	0.940**	0.357**	0.210	0.124	-0.017	0.171	0.130	0.000	-0.094	0.282*	-0.253	0.356**
FGP					1.000	0.336*	0.277*	0.033	0.089	0.276*	0.022	0.139	-0.025	0.230	-0.312*	0.437**
TGW						1.000	0.477**	0.519**	-0.256	0.032	0.210	-0.188	-0.115	0.411**	-0.138	0.028
GL							1.000	-0.032	0.426**	0.322*	0.018	0.153	0.116	0.149	-0.250	0.156
GB								1.000	-0.912**	-0.157	0.246	-0.323*	-0.097	0.352**	0.096	-0.197
G L/B									1.000	0.261*	-0.215	0.347**	0.119	-0.252	-0.188	0.222
KLBC										1.000	0.057	0.546**	0.459**	-0.224	-0.665**	0.274*
KBBC											1.000	-0.782**	0.036	0.171	-0.036	0.066
L/B BC												1.000	0.201	-0.333*	-0.397**	0.109
KLAC													1.000	0.043	0.356**	-0.035
KBAC														1.000	0.271*	0.097
ERAC															1.000	-0.321*
GYP																1.000

The number of grains per panicle showed a positively significant association with the number of filled grains per panicle, thousand-grain weight per plant, and kernel breadth after cooking. The kernel L/B ratio before cooking presented a negatively significant intercorrelation with kernel breadth before cooking and kernel breadth after cooking however the grain L/B ratio showed a positively significant association with kernel length before cooking and kernel L/B ratio before cooking characters.

Further, kernel elongation ratio after cooking has a positively significant association with kernel length after cooking and kernel breadth after cooking while it had a negatively significant association with kernel length

before cooking and kernel L/B ratio before cooking. It was also found that grain breadth had a significantly negative association with grain L/B ratio and kernel L/B ratio before cooking; kernel length before cooking had a significantly positive association with kernel L/B ratio before cooking and kernel length after cooking.

Reports were given by Roy *et al.* (2015); Abhilash *et al.* (2018); Seneega *et al.* (2019); Shet *et al.* (2012); Priyanka *et al.* (2019); Shahid *et al.* (2019); Fathima *et al.* (2021); Manojkumar *et al.* (2022) for the number of productive tillers per plant and number of filled grains perpanicle showed positively significant association with grain yield per plant in their experiments.

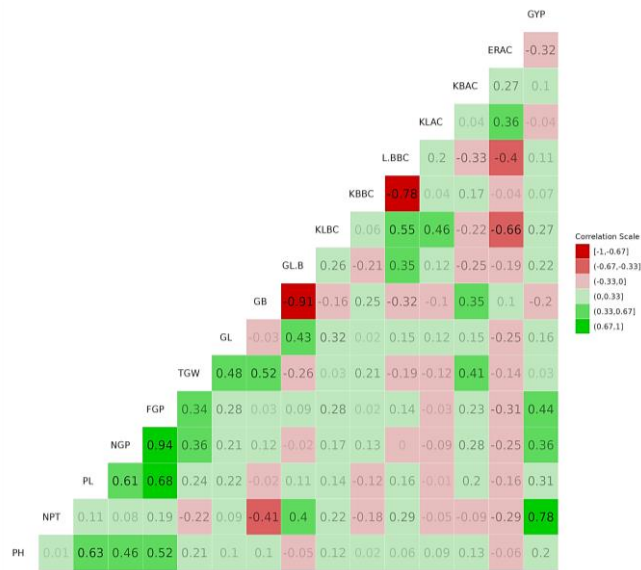


Fig. 1. Correlogram of the sixteen characters.

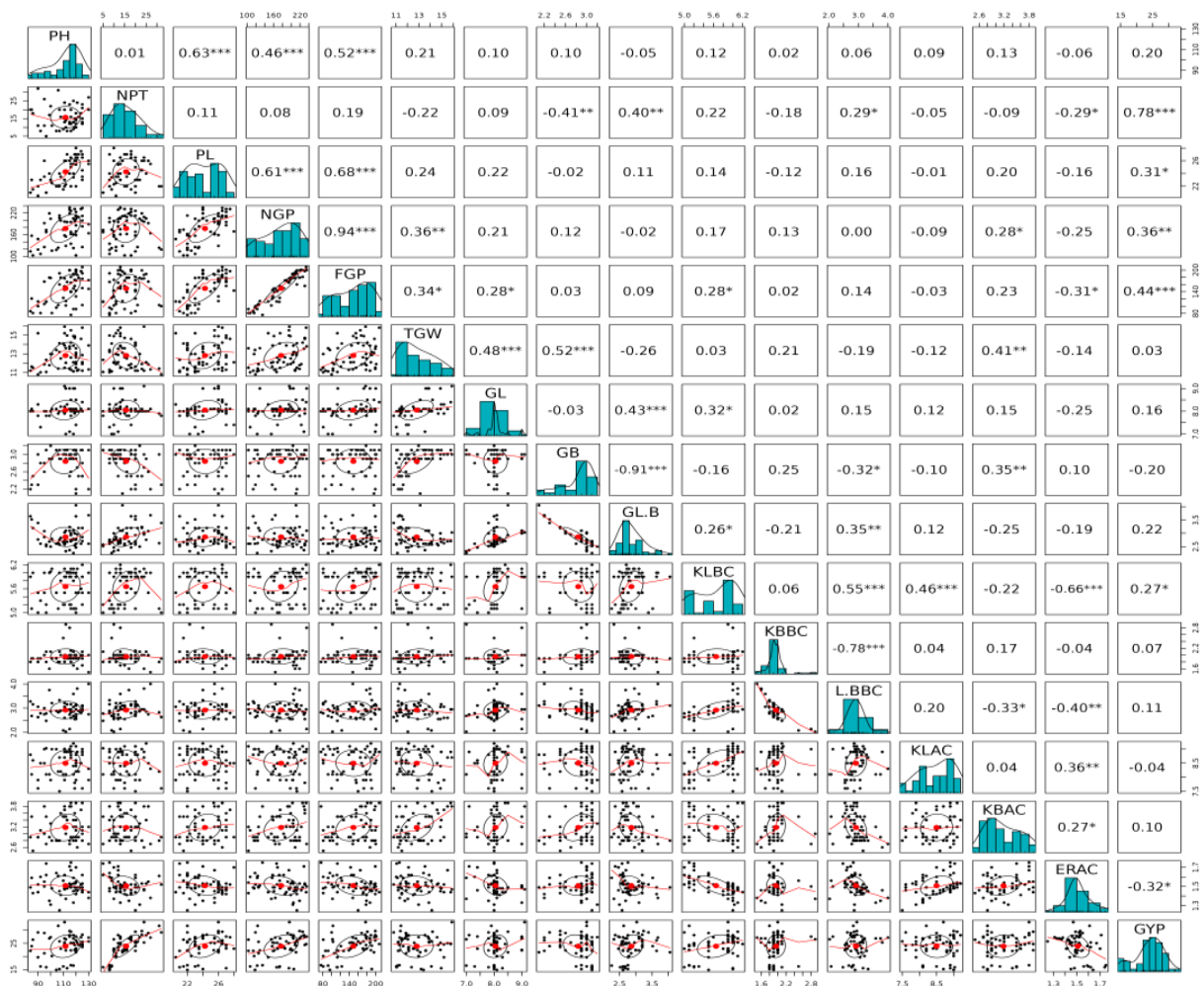


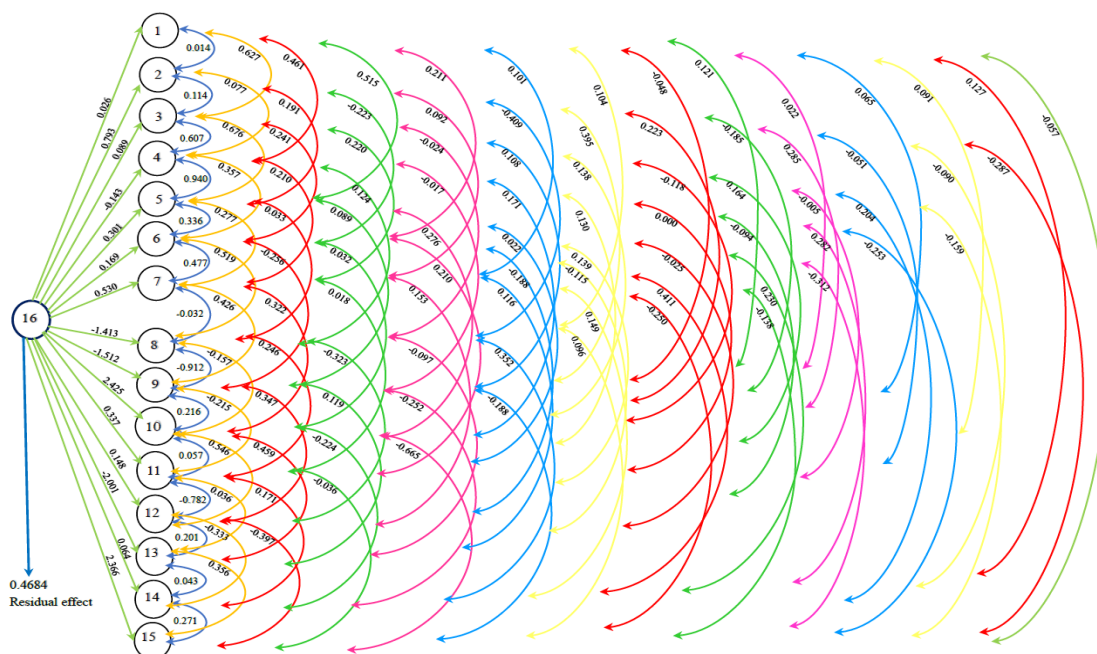
Fig. 2. Pairs plot based on genotypic correlation coefficients in sixteen characters.

Hence selection based on the number of productive tillers per plant, number of filled grains per panicle, and kernel length before cooking will indirectly focus on high-yielding genotypes. Yet, selection based on kernel elongation ratio after cooking will lead to the selection

of high-yielding and slender grain type genotypes since it showed a negatively significant association with grain yield per plant.

Table 2: Direct and indirect effects for yield component traits in BC₂F₂ population of ADT43 X RP-Bio-Patho-2.

Traits	PH	NPT	PL	NGP	FGP	TGW	GL	GB	G L/B	KLBC	KBBC	L/B BC	KLAC	KBAC	ERAC	GYP
PH	0.026	0.011	0.056	-0.066	0.155	0.036	0.054	-0.147	0.073	0.292	0.008	0.010	-0.181	0.008	-0.134	0.200
NPT	0.000	0.793	0.010	-0.011	0.057	-0.038	0.049	0.578	-0.597	0.541	-0.062	0.042	0.103	-0.006	-0.680	0.780**
PL	0.017	0.090	0.089	-0.087	0.204	0.041	0.117	0.034	0.163	0.334	-0.040	0.024	0.011	0.013	-0.377	0.307
NGP	0.012	0.061	0.054	-0.143	0.283	0.060	0.112	-0.176	0.026	0.415	0.044	0.000	0.189	0.018	-0.598	0.356**
FGP	0.014	0.151	0.060	-0.135	0.301	0.057	0.147	-0.047	0.135	0.668	0.007	0.021	0.051	0.015	-0.739	0.437**
TGW	0.006	-0.177	0.022	-0.051	0.101	0.169	0.253	-0.734	0.388	0.079	0.071	-0.028	0.231	0.026	-0.326	0.029
GL	0.003	0.073	0.020	-0.030	0.083	0.081	0.530	0.045	0.643	0.780	0.006	0.023	-0.232	0.010	-0.592	0.156
GB	0.003	-0.324	-0.002	-0.018	0.010	0.088	-0.017	-1.413	1.378	-0.380	0.083	0.048	0.194	0.023	0.227	-0.197
G L/B	-0.001	0.313	0.010	0.002	0.027	-0.043	0.226	1.288	-1.512	0.632	-0.072	0.051	-0.239	-0.016	-0.444	0.222
KLBC	0.003	0.177	0.012	-0.025	0.083	0.006	0.171	0.221	0.394	2.425	0.019	0.081	-0.918	-0.014	-1.573	0.274*
KBBC	0.001	-0.147	-0.011	-0.019	0.007	0.036	0.010	-0.348	0.325	0.138	0.337	-0.116	-0.072	0.011	-0.085	0.066
L/B BC	0.002	0.226	0.015	0.000	0.042	-0.032	0.081	0.456	0.525	1.323	-0.263	0.148	-0.403	-0.021	-0.939	0.109
KLAC	0.002	-0.041	-0.001	0.014	-0.008	-0.020	0.062	0.137	0.180	1.112	0.012	0.030	-2.001	0.003	0.843	-0.035
KBAC	0.003	-0.072	0.018	-0.040	0.069	0.070	0.079	-0.497	0.380	-0.542	0.058	0.049	-0.085	0.064	0.642	0.098
ERAC	-0.002	-0.228	-0.014	0.036	-0.094	-0.023	-0.133	-0.135	0.284	-1.612	-0.012	0.059	-0.713	0.017	2.366	-0.321*



1-Plant Height; 2-Number of Productive tillers per plant; 3-Panicle Length; 4-Number of Grains per panicle; 5-Number of Filled grains per panicle; 6-Thousand grain weight; 7-Grain Length; 8-Grain Breadth; 9-Grain L/B ratio; 10-Kernel Length before cooking; 11-Kernel Breadth before cooking; 12- Kernel L/B ratio before cooking; 13- Kernel Length after cooking; 14-Kernel Breadth after cooking; 15- Kernel Elongation Ratio after cooking; 16-Grain yield per plant

Fig. 3. Diagrammatic representation of direct and indirect effects of independent traits on dependent trait via path coefficient analysis in BC₂F₂ population.

Path coefficients analysis: With the help of path coefficient analysis, correlation coefficients can be divided into direct and indirect effects, character relationships can be depicted more accurately, and the main factors influencing grain yield can be identified. Gaining those essential qualities can increase yield. Direct effects are those between two variables when there are no intermediary variables. The effects of one variable on another variable through one or more intermediary variables are known as indirect effects. Table 3 displays the direct and indirect effects of several quantitative features from the results of the current investigation. The residual effect of 0.4684 indicated that

about 53.2% of variability for grain yield per plant and other traits were studied in the present investigation. A Schematic representation of path coefficient analysis is given in Fig. 3.

The direct and indirect effects of predictor traits on yield are presented in Table 3. The predictor traits number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, and kernel length before cooking showed a significant positive effect on grain yield per plant at the genotypic level whereas kernel elongation ratio after cooking showed significant negative effect at the genotypic level on grain yield per plant. The yield attributing traits such as plant height,

panicle length, thousand-grain weight, grain length, grain L/B ratio, kernel breadth before cooking, kernel L/B ratio before cooking, and kernel breadth after cooking showed a positive insignificant effect on grain yield per plant in the present study but grain breadth and kernel length after cooking showed a negative insignificant effect on grain yield per plant.

The breakdown of direct and indirect effects of path analysis exposed that the highest positive direct effect was discovered in kernel length before cooking (2.425), followed by kernel elongation ratio after cooking (2.366), number of productive tillers per plant (0.793), grain length (0.530) and kernel breadth before cooking (0.337) at the genotypic level. The highest negative direct effect of kernel length after cooking (-2.001), tailed by grain L/B ratio (-1.512) and grain breadth (-1.413) on grain yield per plant was detected.

A very high indirect positive effect of grain L/B ratio through grain breadth, kernel length before cooking through kernel L/B ratio before cooking, and kernel length after cooking on grain yield per plant was estimated at the genotypic level. Positive high indirect effects of kernel elongation ratio after cooking via kernel length after cooking and kernel breadth after cooking, kernel length before cooking utilizing grain length, number of filled grains per panicle, grain L/B ratio, number of productive tillers per plant, number of grains per panicle, and panicle length on grain yield per plant was found. Further, a high indirect positive effect of grain breadth through the number of productive tillers per plant and kernel L/B ratio before cooking and grain L/B ratio through kernel breadth after cooking and thousand-grain weight on yield was detected.

An indirect negative very high effect of kernel length before cooking through kernel elongation ratio after cooking on yield per plant was observed. High negative indirect effects of kernel elongation ratio after cooking through kernel L/B ratio before cooking, number of filled grains per panicle, number of productive tillers per plant, grain length, number of grains per panicle, and grain L/B ratio on yield per plant was found. Added, high negative indirect effects of kernel length after cooking on yield through kernel length before cooking and kernel elongation ratio after cooking; grain breadth via thousand-grain weight and kernel breadth after cooking; and grain L/B through grain length, number of productive tillers per plant and kernel L/B ratio before cooking on grain yield per plant was unveiled. All the other predictor traits showed moderate to negligible negative indirect effects through the other independent traits on the dependent trait, grain yield per plant.

Reports of Aditya and Bhartiya (2013); Saha *et al.* (2019) were similar to our present investigation. Additionally, Sameera *et al.* (2014); Kishore *et al.* (2015); Manojkumar *et al.* (2022) reported a low direct effect of the number of filled grains per panicle on yield per plant. Shet *et al.* (2012); Kishore *et al.* (2015); Abhilash *et al.* (2018); Priyanka *et al.* (2019); Saha *et al.* (2019); Seneega *et al.* (2019); noticed a highly positive effect of for the number of productive tillers per plant on grain yield.

Bhadru *et al.* (2012), Nagaraju *et al.* (2013); Sameera *et al.* (2014); Padmaja *et al.* (2011) exposed that thousand-

grain weight had indirect positive effects on yield per plant. Shet *et al.* (2012); Seneega *et al.* (2019); Shahid *et al.* (2019); sighted low to negligible direct effect of panicle length on yield per plant contrary to the present study. These characteristics, FG and TGW significantly benefited the YP. As a result, the number of productive tillers per plant, number of grains per panicle, and number of filled grains per panicle may be utilized as the main selection criteria for improving the grain yield per plant, with kernel length before cooking serving as a secondary selection criterion.

CONCLUSIONS

The genetic parameters of yield and qualities that contribute to yield were examined in BC₂F₂ populations of 58 backcross-derived rice genotypes (ADT43 X RP-Bio-Patho-2), recipient parent ADT43, and donor parent RP-Bio-Patho-2. A high degree of positive correlation and a direct positive effect of a number of productive tillers per plant, number of grains per panicle, and number of filled grains per panicle with the grain yield per plant, suggested that this yield-contributing trait could be a selection criterion for improving the yield of the rice genotypes under study. Additionally, kernel length before cooking may be useful selection criteria.

Acknowledgment. Innovation in Science Pursuit for Inspired Research (INSPIRE), Department of Science & Technology, India, provided funding for the research project.

Conflict of Interest. None.

REFERENCES

- Abhilash, R., Thiruvengadam, T., Dhatchinamoorthy, S. and Chitra, S. (2018). Genetic studies in F₂ for biometrical traits in Rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 9(3), 1067-1076.
- Aditya, J. and Bhartiya, A. (2013). Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand Hills.
- Bhadru, D., Mohan, Y. C., Rao, V. T., Bharathi, D., Krishna, L., Poalasa, J. and Pradesh, K. D. A. (2012). Correlation and path analysis studies in gall midge resistant cultures of rice (*Oryza sativa* L.). *International journal of applied biology and pharmaceutical technology*, 3(2), 137-140.
- Dewey, D. R. and Lu, K. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production 1. *Agronomy journal*, 51(9), 515-518.
- Fathima, M. A., Geetha, S., Amudha, K. and Uma, D. (2021). Genetic variability, frequency distribution and association analysis in ADT (R) 48 x Kavuni derived F₂ population of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 12(3), 659-666.
- Johnson, H. W., Robinson, H. and Comstock, R. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*, 47(7), 314-318.
- Kishore, N. S., Srinivas, T., Nagabhushanam, U., Pallavi, M. and Sameera, S. (2015). Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. *SAARC Journal of Agriculture*, 13(1), 99-108.
- Lenka, D. & Mishra, B. (1973). Path coefficient analysis of yield in rice varieties. *Indian J. Agric. Sci.*, 43(4), 376.
- Manojkumar, D., Srinivas, T., Rao, L. S., Suneetha, Y., Sundaram, R. and Kumari, V. P. (2022). Study of genetic variability and trait associations in F₂

- Population of YH3 x AKDRMS 21-54 intra-specific cross of rice.
- Miller, P., Williams Jr, J., Robinson, H. and Comstock, R. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection 1. *Agronomy journal*, 50(3), 126-131.
- Mohidem, N. A., Hashim, N., Shamsudin, R. and Che Man, H. (2022). Rice for food security: Revisiting its production, diversity, rice milling process and nutrient content. *Agriculture*, 12(6), 741.
- Nagaraju, C., Sekhar, M. R., Reddy, K. H. and Sudhakar, P. (2013). Correlation Between Traits and Path Analysis Coefficient for Grain Yield and other Components in Rice (*Oryza Sativa* L.) Genotypes.
- Padmaja, D., Radhika, K., Rao, L. and Padma, V. (2011). Correlation and path analysis in rice germplasm. *ORYZA-An International Journal on Rice*, 48(1), 69-72.
- Priyadarshini, S., Raveendran, M., Manonmani, S. and Robin, S. (2018). Studies on early backcross generation inbred lines of Rice (*Oryza sativa* L.) for yield under stress evaluated under different moisture regimes. *Journal of Pharmacognosy and Phytochemistry*, 7(1S), 1236-1243.
- Priyanka, A., Gnanamalar, R., Banumathy, S., Senthil, N. and Hemalatha, G. (2019). Genetic variability and frequency distribution studies in F₂ segregating generation of rice. *Electronic Journal of Plant Breeding*, 10(3), 988-994.
- Roy, R. K., Majumder, R. R., Sultana, S., Hoque, M. and Ali, M. (2015). Genetic variability, correlation and path coefficient analysis for yield and yield components in transplant aman rice (*Oryza sativa* L.). *Bangladesh Journal of Botany*, 44(4), 529-535.
- Saha, S. R., Lutful, H., Haque, M. A., Islam, M. M. and Rasel, M. (2019). Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *Journal of the Bangladesh Agricultural University*, 17(1), 26-32.
- Sameera, S., Rajesh, A. P., Jayalakshmi, V., Nirmala, P. and Srinivas, T. (2014). Assessment of Variability for Grain Yield and Quality Characters in Rice (*Oryza sativa* L.). *The Journal of Research, PJTSAU*, 42(3).
- Searle, S. (1965). The value of indirect selection: I. Mass selection. *Biometrics*, 682-707.
- Seneega, T. A., Gnanamalar, R., Parameswari, C., Vellaikumar, S. and Priyanka, A. (2019). Genetic variability and association studies in F₂ generation of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 10(2), 512-517.
- Shahid, S., Islam, M., Hossain, M., Begum, S. and Hassan, L. (2019). Green Global Foundation©. *Int. J. Sustain. Crop Prod*, 14(1), 27-36.
- Shet, R. M., Rajanna, M., Ramesh, S., Sheshshayee, M. and Mahadevu, P. (2012). Genetic variability, correlation and path coefficient studies in F₂ generation of aerobic rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 3(3), 925-931.

How to cite this article: Sowmiya C.A., Arumugam Pillai M., Ramalingam J., Pushpam R., Shoba D. and Kumar K.K. (2023). Genetic Association Studies for Yield and Yield Attributes in BC₂F₂ Population of rice (*Oryza sativa* L.). *Biological Forum – An International Journal*, 15(10): 221-227.