International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

IJBSM August 2024, 15(8): 01-13

Article AR5448

Research Article

Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2024.5448

Assessment of Genetic Variability and Character Association for Morpho-physiological and Quality Traits in Rice under Aerobic Conditions

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0009-0009-3621-0636

ABSTRACT

The experiment was conducted during *kharif* season (June–October, 2022) at Rice Research Station, Kaul, CCSHAU, Hisar using 48 rice genotypes to evaluate the genetic variability and character association under aerobic conditions. Analysis of variance revealed that the mean sum of squares was highly significant for all the traits examined. The magnitude of phenotypic coefficient of variation exceeded the genotypic coefficient of variation for all the traits analysed in the study. High genotypic coefficient of variation and phenotypic coefficient of variation were observed for root dry weight plant^{-1} followed by number of grains panicle^{-1}, grain yield plant^{-1}, biological yield plant^{-1}, number of effective tillers plant^{-1} and flag leaf length. High heritability coupled with high genetic advance as per cent of mean was observed for grain yield plant^{-1}, number of grains panicle^{-1}, biological yield plant^{-1}, root fresh weight plant^{-1} and root dry weight plant^{-1} indicating the presence of additive gene action. Grain yield plant^{-1} showed a highly significant and positive association with biological yield plant^{-1}, harvest index percentage, root fresh weight plant^{-1}, number of effective tillers plant^{-1} and 1000 seed weight. Path analysis revealed that biological yield plant^{-1} and harvest index percentage showed highest positive direct effect on grain yield plant^{-1}. Furthermore, regression analysis revealed that biological yield plant^{-1}, harvest index percentage, numbers effective of tillers plant^{-1}, number of grains panicle^{-1}, plant height and head rice recovery % as important traits contributing to grain yield plant^{-1}. Therefore, phenotypic selection could be a viable approach for genetically improving these traits to obtain promising genotypes for future rice breeding programs.

KEYWORDS: Aerobic, correlation, genetic advance, heritability, path, regression, variability

Citation* (VANCOUVER)*: Das et al., Assessment of Genetic Variability and Character Association for Morpho-physiological and Quality Traits in Rice under Aerobic Conditions. *International Journal of Bio-resource and Stress Management,* 2024; 15(8), 01-13. HTTPS://DOI.ORG/10.23910/1.2024.5448.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 11th May 2024 RECEIVED in revised form on 25th July 2024 ACCEPTED in final form on 10th August 2024 PUBLISHED on 17th August 2024

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the most consumed cereal crop in the world after wheat, meeting over 20% of world food energy (Kombali et al., 2016; Patel et al., 2017). Phylogenetically, rice is semi-aquatic plant and generally cultivated in submerged conditions. However, it thrives in a wide range of habitats on every continent except Antarctica (Kahani and Hittalmani, 2015). Conventionally, rice is transplanted into flooded fields, consuming around 50% of the water needed for irrigation (Das et al., 2016). It takes 2500–5000 litres of water to produce 1 kg of rice (Thuy et al., 2023; Rathod et al., 2021). However, the viability of the irrigated rice systems is increasingly threatened by water shortage and labour scarcity (Vanitha et al., 2016). The rapid extraction and slow groundwater recharge lowered the groundwater table from 8 to 16 meters in northern India (Kumar et al., 2021). Further, predictions suggested that 17 m ha of Asia's irrigated rice may encounter "physical water scarcity" and 22 m ha of "economic water scarcity" by 2025 (Tuong and Bouman, 2003; Vijayakumari et al., 2022). Over the last two decades, many water-saving techniques have emerged, including alternate wetting and drying, aerobic rice system, system of rice intensifications and non-flooded mulching cultivation (Kesh et al., 2022a). The International Rice Research Institute (IRRI) introduce "aerobic rice technology" to conserve water. This method involves direct seeding of rice into non-puddled and unsaturated soil with supplement irrigation (Zayed et al., 2023).. Compared to puddled transplanted rice (PTR), aerobic rice requires 50% less water (Parthasarathi et al., 2012;), leads to 32–88% higher crop output (Nie et al., 2012), a labour cost saving of 50% (Tuti et al., 2022) and an 80-85% reduction in greenhouse gas emissions (Weller et al., 2016). Despite the potential of water saving, aerobic rice faces yield loss due to unavailability of suitable cultivars (Kesh et al., 2022a; Tiruneh et al., 2019). It is crucial to develop novel rice varieties by integrating traits of lowland (high yielding) and upland cultivars (drought-tolerance) to boost the yield potential of aerobic rice (Satturu et al., 2023). When combined with improved management practices and input-responsive cultivars, this water-saving technology can yield 4–6 t ha^{-1} (Dey et al., 2021).

The presence of genetic variability is a prerequisite for an efficient breeding programme (Sreedhar, 2018; Pravalika et al., 2024), offering a wide array of genotypes that can be selected to develop a variety with desirable traits. Therefore, understanding genetic parameters in terms of genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2_{bs}) and genetic advance as per cent of mean (GAM) helps in formulating efficient breeding programmes (Gupta et al., 2020). Genotypic and phenotypic coefficients of variation partition the variability into genetic and environmental components (Girma et al., 2018). Heritability determines the degree of genetic improvement transmitted to the next generation (Akter et al., 2018; Saisupriya et al., 2022) and determines selection response. Genetic advances quantify the amount of gain achieved in a trait under a particular selection pressure. However, utilizing both heritability and genetic advance together offers the most effective strategies for the selection of desired traits (Lakshmi et al., 2020; Pasha et al., 2019). Grain yield is a complex trait and influenced by environmental and genetic factors (Edukondalu et al., 2023). Therefore, knowledge of inter-relationship between yield and its component traits is important to develop effective selection strategy. (Devi et al., 2017). However, correlation merely reflects the degree and direction of association between traits. To distinguish between direct and indirect effect path analysis is essential. The present investigation was aimed to determine the genetic variability, inter-relationship, and regression analysis among existing aerobic rice genotypes to find promising candidates for future hybridization programs.

2. MATERIALS AND METHODS

The experiment was conducted during *kharif* season (June–October, 2022) at Rice Research Station, Kaul, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India.

2.1. *Plant material*

The experimental material for this study consisted of 48 rice genotypes (comprising advanced aerobic lines) obtained from Rice Research Station, Kaul, CCS Haryana Agricultural University, Hisar, Haryana, India, located at 29.51°N latitude and 76.39°E longitude at an elevation of 230.7 m above from mean sea level. This area falls in subtropical and semi-arid climate zone with an average rainfall of 750 mm, most of which is received during the southwest monsoon. All the genotypes were directly sown in the field under moisture scare aerobic situation during dry season *kharif*, 2022 using randomized Block design (RBD) with three replications. Each genotype was sown in single row of 5 m length with inter and intra-row spacing of 20 cm and 15 cm respectively. The seeds were sown using dibbling, with 1–2 seeds hill^{-1}. The field underwent light irrigation immediately after sowing to ensure proper germination and further irrigation was applied when hairline cracks were noticed in the experimental plot. Recommended cultural operations and plant protection measures were followed to raise a good crop stand.

2.2. *Observations recorded*

Replication wise data based on five randomly selected competitive plants for each genotype were recorded for 23 morph-physiological and quality traits viz., days to 50%

flowering, days to maturity, flag leaf length (cm), flag leaf width (cm), plant height (cm), number of effective tillers plant^{-1}, panicle length (cm), number of grains panicle^{-1}, grain yield plant^{-1} (g), biological yield plant^{-1} (g), 1000 seed weight (g), harvest index (%), root length plant^{-1} (cm), root volume plant^{-1} (ml), root fresh weight plant^{-1} (g), root dry weight plant^{-1} (g), root fresh and dry weight ratio, kernel length (mm), kernel breadth (mm), kernel length-breadth ratio, hulling (%), milling (%) and head rice recovery (%).

2.3. Statistical analysis

Experimental data were compiled based on their mean across randomly selected plants from all three replications and analysed statistically for analysis of variance (ANOVA) as suggested by Fisher (1925). The genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) were calculated according to Burton and De Vane (1953). Heritability (in the broad sense) was calculated using the formula proposed by Lush (1949) and genetic advance was calculated using the formula proposed by Johnson et al. (1955). Correlation, path and stepwise regression analysis was carried out to prioritize the most important traits associated significantly ($p \leq 0.005$) with grain yield in rice using OPSTAT and PAST version 4.02 software.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

The existence of genetic variability is of utmost importance for genetic improvement of desired traits in plant breeding program. This is the fundamental factor that must be considered while making selection. Analysis of variance (ANOVA) revealed highly significant heterogeneity among rice genotypes for all the studied trait, suggesting high and inherent variation among genotypes (Table 1). The earlier scientific studies by Bhargava et al. (2021), Nath and Kole (2021), Tripathi et al. (2017) and Basavaraj et al. (2023) also reported varied response of rice genotypes for grain yield and component traits. The degree of genetic variation among genotypes was expressed by mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense and genetic advance as percent of mean (Table 2).

3.2. Estimation of variability parameters

The nature and degree of variation in breeding material for different traits can be analysed using the phenotypic and genotypic coefficients of variation (Table 2). The relative magnitude of the phenotypic coefficient of variation (PCV) was higher than the equivalent genotypic coefficient of variation (GCV) for all traits, denoting effect of the environment on the phenotypic expression of these traits. The difference between GCV and PCV for the studied trait was less except for number of effective tillers plant^{-1} which was relatively higher. PCV and GCV were classified as low (0–10%), moderate (10–20%) and high (>20%) according to Burton and De Vane (1953). Based on this classification, the highest GCV and PCV were recorded for root dry weight plant^{-1} (20.06% and 22.55%). This showed that the

Table 1: Analysis of variance for different morpho-physiological and quality traits under aerobic conditions

SV	Replication	Treatment	Error
Df	2	47	94
GY/P	3.79	34.31**	4.00
DTF	4.92	24.97**	1.75
DTM	6.44	33.31**	2.29
PH	69.19	351.36**	20.22
FLW	0.01	0.04**	0.01
FLL	2.28	54.00**	5.59
PL	0.01	8.94**	1.61
NG/PL	75.81	791.86**	67.19
NT/P	4.90	7.48**	2.23
TW	7.05	10.70**	2.63
BY/P	12.78	135.89**	8.35
HI	1.73	64.48**	7.50
RFW	2.05	64.00**	5.12
RDW	1.04	9.02**	0.73
RFW/RDW	0.04	1.08**	0.01
RV	3.9	50.92**	4.57
RL	4.63	5.71**	1.51
HULL	2.41	14.75**	2.91
MILL	0.60	11.28**	3.62
HRR	3.02	41.61**	4.58
KL	0.41	0.70**	0.14
KB	0.01	0.08**	0.02
KLBR	0.04	0.64**	0.05

GY/P: Grain yield plant^{-1}, DTF: Days to flowering, DTM: Days to maturity, PH: Plant height, FLW: Flag leaf width, FLL: Flag leaf length, PL: Panicle length, NG/PL: Number of grains panicle^{-1}, NT/P: Numbers effective of tillers plant^{-1}, TW: 1000 seed weight, BY/P: Biological yield plant^{-1}, HI: Harvest index percentage, RFW: Root fresh weight plant^{-1}, RDW: Root dry weight plant^{-1}, RFW/RDW: Root fresh and dry weight ratio, RV: Root volume plant^{-1}, RL: Root length plant^{-1}, HULL: Hulling %, MILL: Milling %, HRR: Head rice recovery %, KL: Kernel length, KB: Kernel breadth, KLBR: Kernel length- breadth ratio; **: Significant at (p=0.01) level of significance; *: Significant at (p=0.05) level of significance

Table 2: Mean, range, coefficient of variation%, heritability (h^2bs), genetic advance as percent of mean (GAM%)

Characters	Mean	Range		Coefficient of variation %		h^2bs	GAM%
		Max.	Min.	GCV	PCV		
GY/P	24.33	33.24	17.85	13.07	15.43	71.65	22.78
DTF	88.47	95.33	82.00	3.15	3.48	81.60	5.85
DTM	120.46	129.33	113.00	2.67	2.95	81.88	4.98
PH	108.62	140.80	84.73	9.67	10.52	84.52	18.32
FLW	1.15	1.58	0.97	8.70	11.03	62.23	14.15
FLL	38.48	47.18	29.97	10.44	12.11	74.26	18.53
PL	23.76	27.97	20.60	6.58	8.48	60.19	10.51
NG/PL	110.55	145.00	80.07	14.06	15.90	78.24	25.62
NT/P	11.38	15.53	8.73	11.63	17.53	44.02	15.89
TW	23.17	27.13	18.87	7.08	9.96	50.55	10.37
BY/P	52.12	67.26	39.91	12.51	13.68	83.59	23.56
HI	46.84	56.30	35.26	9.30	10.99	71.69	16.23
RFW	24.93	40.44	19.21	17.77	19.95	79.32	32.60
RDW	8.29	12.14	3.36	20.06	22.55	79.12	36.76
RFW/RDW	3.08	6.06	2.41	18.55	21.08	77.46	33.63
RV	23.89	36.77	18.33	16.45	18.73	77.17	29.78
RL	16.07	19.73	13.57	7.37	10.62	48.19	10.54
HULL	77.24	82.15	73.81	2.57	3.39	57.62	4.02
MILL	67.31	70.47	62.65	2.38	3.69	41.40	3.15
HRR	57.09	66.47	48.12	6.16	7.21	72.96	10.83
KL	6.64	8.13	5.65	6.53	8.62	57.34	10.18
KB	2.06	2.36	1.68	7.00	9.33	56.27	10.82
KLBR	3.26	4.64	2.64	13.59	15.11	80.90	25.19

GY/P: Grain yield plant^{-1}, DTF: Days to flowering, DTM: Days to maturity, PH: Plant height, FLW: Flag leaf width, FLL: Flag leaf length, PL: Panicle length, NG/PL: Number of grains panicle^{-1}, NT/P: Numbers effective of tillers plant^{-1}, TW: 1000 seed weight, BY/P: Biological yield plant^{-1}, HI: Harvest index percentage, RFW: Root fresh weight plant^{-1}, RDW: Root dry weight plant^{-1}, RFW/RDW: Root fresh and dry weight ratio, RV: Root volume plant^{-1}, RL: Root length plant^{-1}, HULL: Hulling %, MILL: Milling %, HRR: Head rice recovery %, KL: Kernel length, KB: Kernel breadth, KLBR: Kernel length-breadth ratio

environment has minimal effect on the trait's expression and that the trait is heavily influenced by genetic factors. The existence of high variability for the above-mentioned trait was previously reported by Dey et al. (2021) and Roy et al. (2020). Furthermore, root fresh and dry weight ratio (18.55% and 21.08%), root volume plant^{-1} (16.45% and 18.73%), root fresh weight plant^{-1} (17.77% and 19.95%), number of grains panicles^{-1} (14.06% and 15.90%), grain yield plant^{-1} (13.07% and 15.43%), kernel length-breadth ratio (13.59% and 15.11%), biological yield plant^{-1} (12.51% and 13.68%), number of effective tillers plant^{-1} (11.63% and 17.53%) and flag leaf length (10.44% and 12.11%) exhibited moderate GCV and PCV, respectively. Therefore, selection of these traits would provide far more opportunities for genetic improvement of the studied genotypes. The findings of the current study in terms of GCV and PCV are broadly consistent with the earlier worker's Bhargava et al. (2021) for number of grains panicle^{-1} and biological yield plant^{-1}, Dey et al. (2021) for kernel length-breadth ratio, Sruthi et al. (2023) for number of effective tillers plant^{-1} and flag leaf length, Osman et al. (2012) for grain yield plant^{-1}. The low value for GCV and PCV were observed for 1000 seed weight (7.08% and 9.96%), kernel breadth (7.00% and 9.33%), kernel length (6.53% and 8.62%), panicle length (6.58% and 8.48%), head rice recovery % (6.16% and 7.21%), hulling % (2.57% and 3.39%), days to 50% flowering (3.15% and

3.48%), days to maturity (2.67% and 2.95%) and milling % (2.38% and 3.69%). The selection of these traits offers very little scope for genetic improvement of the genotypes examined. The presence of low GCV and PCV for these traits was previously documented by Gunasekaran et al. (2017) for days to 50% flowering, Demeke et al. (2023) for panicle length, Pavankumar et al. (2022) for 1000 seed weight, Kesh et al. (2022b) for hulling % and milling %, Dey et al. (2021) for head rice recovery%, days to maturity, kernel length and kernel breadth.

The degree of genetic variation considered alone is of little use until augmented with information about heritability estimation, which represents the heritable portion of total variation. Heritability is a key factor in determining the selection response as it provides reliable estimates of genetic improvement of character. Robinson et al. (1949) classified heritability as low (<30%), moderate (30–60%), and high (>60%). Based on above classification, traits namely plant height (84.52%), biological yield plant^{-1} (83.59%), days to 50 % flowering (81.60%), days to maturity (81.88), kernel length- breadth ratio (80.90%), root fresh weight plant^{-1} (79.32%), root dry weight plant^{-1} (79.12%), number of grains panicle^{-1} (78.24%), root fresh and dry weight ratio (77.46%), flag leaf length (74.26%), head rice recovery (72.96%), Harvest index percentage (71.69%), grain yield plant^{-1} (71.65%), flag leaf width (62.23%) and panicle length (60.19%) showed high heritability. The rest of the traits showed moderate to low magnitude of heritability. High heritability estimate indicates strong genetic effect, which make selection based on observable trait useful. Moderate to high heritability for different rice traits were earlier studied by Nusrat et al. (2017) for grain yield plant^{-1}, plant height and panicle length, Basavaraj et al. (2023) for plant height and days to 50% flowering, Devi et al. (2022) for biological yield plant^{-1}, Dey et al. (2021) for head rice recovery%, kernel length-breadth ratio, root fresh weight plant^{-1} and root dry weight plant^{-1}, Bhargava et al. (2021) for days to maturity, number of grains panicle^{-1}, Kumari et al. (2023) for flag leaf width and flag leaf length, Demeke et al. (2023) for Harvest index percentage. The traits that exhibit high heritability do not necessarily result in high genetic gain but may be due to environmental effects. The breeder should be careful when making a selection based solely on heritability, as this includes both additive and non-additive gene effects. High genetic advance occurs mainly because of additive gene action. Therefore, estimating heritability combined with genetic advance make greater sense than measuring heritability alone (Johnson et al., 1955). Johnson et al. (1955) classified genetic advance as percent of mean into three categories: low (<10%), moderate (10–20%), and high (>20%). High heritability coupled with high genetic advance as per cent of mean was recorded for biological yield plant^{-1} (83.59% and 23.56%), kernel length breadth ratio (80.90% and 25.19%), root fresh weight plant^{-1} (79.32% and 32.60%), root dry weight plant^{-1} (79.12% and 36.76%), number of grains panicle^{-1} (78.24% and 25.62%), root fresh and dry weight ratio (77.46% and 33.63%), root volume plant^{-1} (77.17% and 29.78%) and grain yield plant^{-1} (71.65% and 22.78%). This indicates that these traits are predominantly influenced by additive gene action and direct selection based on these traits could lead to significant improvements in grain yield. These results agreed with Dey et al. (2021) for biological yield plant^{-1}, root fresh weight plant^{-1}, root dry weight plant^{-1} and root volume plant^{-1}, Salunkhe et al. (2024) for grain yield plant^{-1}and number of grains panicle^{-1}, Gupta et al. (2022) for kernel length - breadth ratio. However, the traits such as plant height (84.52% and 18.32%), flag leaf length (74.26% and 18.53%), head rice recovery % (72.96% and 10.83%), harvest index percentage (71.69% and 16.23%), flag leaf width (62.23% and 14.15%) and panicle length (60.19% and 10.51%) showed high heritability accompanied with moderate genetic advance as per cent of mean, suggesting that these traits are governed by both additive and non-additive gene action and high heritability exhibited may be due to influence of environment rather than genotype alone. Our findings are supported by Bhargava et al. (2021) for harvest index percentage, Chuchert et al. (2018) for flag leaf length and plant height, Pavankumar et al. (2021) for flag leaf width, Kesh et al. (2022b) for panicle length, Dey et al. (2021) for panicle length and head rice recovery %.

3.3. Association analysis

Grain yield is a multigenic traits affected by interaction of several traits called component traits. Direct selection for grain yield may mislead the final results. Therefore, association analysis of component traits with grain yield (Figure 1) helps the plant breeders in identifying major traits influencing grain yield. Grain yield per plant exhibited highly significant and positive association (Table 3) with biological yield plant^{-1}, number of effective tillers plant^{-1}, root fresh weight plant^{-1}, numbers of grains panicle^{-1}, root dry weight plant^{-1}, root volume, 1000 seed weight, kernel breadth, harvest index percentage, root length followed by plant height, panicle length and flag leaf length and it had significant negative association with milling %, kernel length breadth ratio and days to maturity. Days to 50% flowering and flag leaf width exhibited significant and positive association with days to maturity, while showed a negative association with number of grains panicle^{-1}, panicle length, harvest index percentage and plant height. Flag leaf length showed significant and positive association with root length, plant height, panicle length, flag leaf width, biological yield plant^{-1}, number of grains panicle^{-1} and number of effective tillers plant^{-1}. Root fresh weight

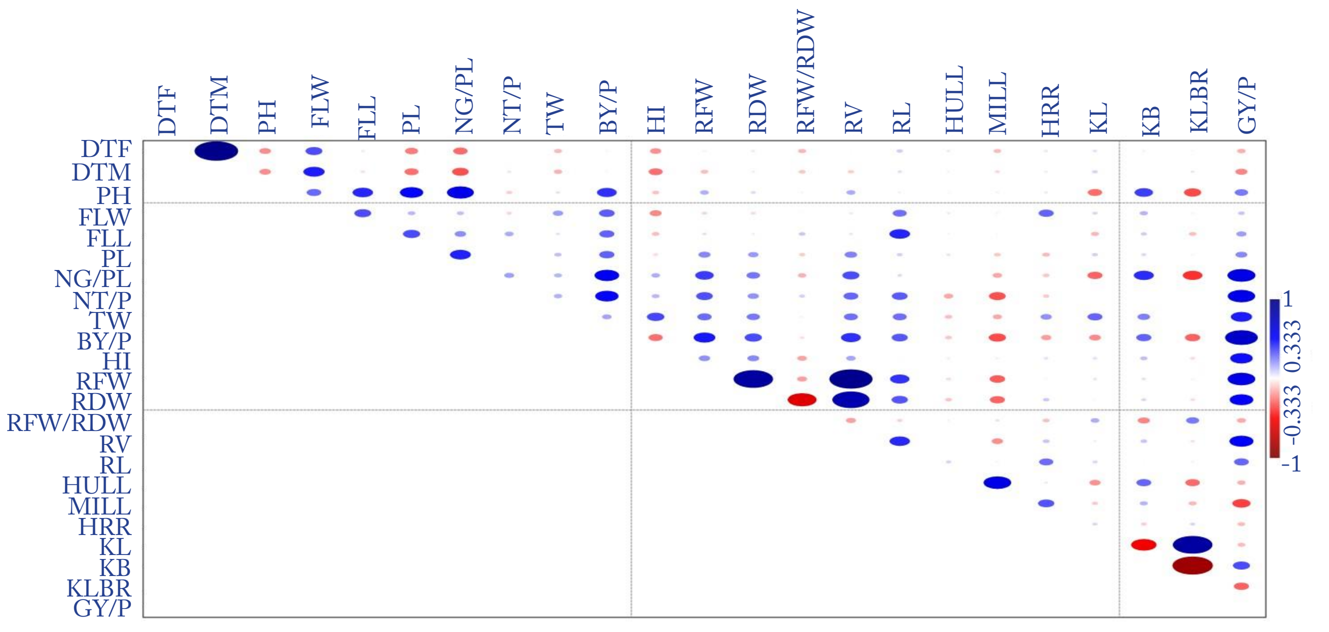

Figure 1: Association analysis among grain yield and its component traits in 48 genotypes of rice

Table 3: Phenotypic (below diagonal) and Genotypic (above diagonal) correlation coefficients under aerobic conditions

	DTF	DTM	PH	FLW	FLL	PL	NG/PL	NT/P	TW	BY/P	HI	RFW
DTF	1	0.959**	-0.226**	0.388**	-0.041	-0.298**	-0.312**	-0.015	-0.146	0.01	-0.246**	-0.041
DTM	0.946**	1	-0.224**	0.500**	-0.06	-0.334**	-0.369**	-0.07	-0.161	-0.029	-0.323**	-0.147
PH	-0.225**	-0.222**	1	0.344**	0.467**	0.562**	0.620**	-0.122	0.058	0.430**	-0.125	0.164*
FLW	0.277**	0.354**	0.225**	1	0.416**	0.188*	0.135	-0.133	0.255**	0.372**	-0.289**	-0.084
FLL	-0.049	-0.072	0.359**	0.263**	1	0.429**	0.225**	0.164*	0.061	0.324**	-0.151	0.072
PL	-0.209*	-0.210*	0.392**	0.066	0.256**	1	0.525**	0.025	0.170*	0.373**	-0.113	0.273**
NG/PL	-0.254**	-0.297**	0.493**	0.111	0.219**	0.311**	1	0.207*	0.168	0.529**	0.153	0.420**
NT/P	0.006	-0.03	-0.075	-0.038	0.147	-0.026	0.162	1	0.254**	0.573**	0.166*	0.417**
TW	-0.137	-0.141	0.051	0.124	0.054	0.07	0.112	0.039	1	0.212*	0.434**	0.332**
BY/P	0.024	-0.009	0.368**	0.244**	0.278**	0.219**	0.503**	0.406**	0.137	1	-0.320**	0.489**
HI	-0.172*	-0.218**	-0.113	-0.161	-0.101	-0.024	0.166*	0.095	0.276**	-0.232**	1	0.245**
RFW	-0.014	-0.104	0.142	-0.094	0.046	0.186*	0.321**	0.237**	0.240**	0.398**	0.178*	1
RDW	0.055	-0.025	0.063	-0.067	-0.024	0.162	0.235**	0.152	0.202*	0.307**	0.169*	0.824**
RWF/RDW	-0.128	-0.103	-0.012	-0.026	0.093	-0.07	-0.122	0.067	-0.021	-0.046	-0.154	-0.141
RV	-0.023	-0.096	0.142	-0.051	0.01	0.212*	0.295**	0.202*	0.234**	0.374**	0.139	0.816**
RL	0.084	0.059	0.038	0.230**	0.294**	0.089	0.008	0.159	0.180*	0.183*	0.008	0.382**
HULL	-0.039	-0.02	-0.024	-0.046	-0.018	0.026	0.002	-0.115	-0.084	-0.102	-0.026	-0.059
MILL	-0.078	-0.024	0.015	0.007	-0.036	-0.054	-0.127	-0.236**	-0.156	-0.280**	-0.001	-0.255**
HRR	0.025	0.024	0.041	0.264**	-0.024	-0.084	-0.092	-0.091	0.14	-0.16	0.106	-0.022
KL	0.027	0.045	-0.251**	0.062	-0.098	0.077	-0.249**	0.024	0.192*	-0.213*	0.041	-0.001
KB	-0.012	-0.015	0.348**	0.118	0.087	0.023	0.299**	-0.024	0.225**	0.248**	0.028	0.067
KLBR	0.01	0.036	-0.336**	-0.026	-0.121	0.045	-0.354**	0.033	-0.04	-0.307**	-0.047	-0.064
GY/P	-0.117	-0.181*	0.218**	0.084	0.177*	0.178*	0.561**	0.444**	0.343**	0.700**	0.527**	0.496**

Table 3: Continue...

	RDW	RFW/ RDW	RV	RL	HULL	MILL	HRR	KL	KB	KLBR	GY/P
DTF	0.042	-0.154	0.003	0.113	-0.056	-0.187*	0.059	0.085	0.063	0.02	-0.182*
DTM	-0.052	-0.122	-0.102	0.066	-0.037	-0.125	0.041	0.119	0.024	0.058	-0.278**
PH	0.077	-0.034	0.175*	0.014	-0.003	0.038	0.043	-0.316**	0.401**	-0.365**	0.298**
FLW	-0.084	0	-0.05	0.329**	-0.06	-0.081	0.326**	0.08	0.177*	-0.043	0.129
FLL	-0.051	0.12	0.074	0.544**	-0.03	-0.004	0.01	-0.177*	0.111	-0.132	0.199*
PL	0.225**	-0.12	0.272**	0.094	0.078	-0.167*	-0.176*	0.109	0.111	0.006	0.278**
NG/PL	0.292**	-0.173*	0.384**	0.121	0.001	-0.224**	-0.126	-0.347**	0.498**	-0.437**	0.615**
NT/P	0.260**	0.113	0.366**	0.481**	-0.233**	-0.474**	-0.135	-0.017	0.035	-0.035	0.700**
TW	0.319**	-0.041	0.320**	0.390**	-0.173*	-0.188*	0.282**	0.406**	0.268**	0.011	0.535**
BY/P	0.387**	-0.072	0.432**	0.451**	-0.122	-0.429**	-0.217**	-0.245**	0.347**	-0.315**	0.708**
HI	0.272**	-0.202*	0.200*	-0.027	-0.052	-0.065	0.028	0.076	0.202*	-0.088	0.439**
RFW	0.883**	-0.220**	1.025**	0.424**	-0.079	-0.381**	0.038	0.086	0.039	-0.005	0.659**
RDW	1	-0.634**	0.889**	0.355**	-0.134	-0.397**	0.129	0.051	0.08	-0.062	0.570**
RWF/ RDW	-0.591**	1	-0.209*	-0.102	-0.016	0.108	-0.123	0.172*	-0.312**	0.284**	-0.188*
RV	0.677**	-0.154	1	0.503**	-0.015	-0.293**	0.112	0.039	0.128	-0.064	0.565**
RL	0.310**	-0.07	0.333**	1	0.15	-0.086	0.365**	0.136	-0.009	0.048	0.412**
HULL	-0.084	-0.047	0.01	0.012	1	0.565**	-0.012	-0.291**	0.372**	-0.351**	-0.161
MILL	-0.211*	-0.008	-0.142	0.03	0.613**	1	0.291**	-0.145	0.205*	-0.198*	-0.479**
HRR	0.067	-0.122	0.119	0.197*	0.106	0.387**	1	0.064	-0.079	0.068	-0.182*
KL	-0.035	0.137	0.022	0.018	-0.125	-0.06	0.098	1	-0.660**	0.918**	-0.138
KB	0.061	-0.143	0.082	0	0.212*	0.089	-0.11	-0.396**	1	-0.948**	0.458**
KLBR	-0.081	0.214*	-0.061	0	-0.213*	-0.081	0.097	0.793**	-0.797**	1	-0.333**
GY/P	0.396**	-0.132	0.441**	0.177*	-0.119	-0.267**	-0.07	-0.136	0.231**	-0.283**	1

GY/P: Grain yield plant^{-1}, DTF: Days to flowering, DTM: Days to maturity, PH: Plant height, FLW: Flag leaf width, FLL: Flag leaf length, PL: Panicle length, NG/PL: Number of grains panicle^{-1}, NT/P: Numbers effective of tillers plant^{-1}, TW: 1000 seed weight, BY/P: Biological yield plant^{-1}, HI: Harvest index percentage, RFW: Root fresh weight plant^{-1}, RDW: Root dry weight plant^{-1}, RFW/RDW: Root fresh and dry weight ratio, RV: Root volume plant^{-1}, RL: Root length plant^{-1}, HULL: Hulling %, MILL: Milling %, HRR: Head rice recovery %, KL: Kernel length, KB: Kernel breadth, KLBR: Kernel length- breadth ratio; **: Significant at (p=0.01) level of significance; *: Significant at (p=0.05) level of significance

plant^{-1} depicted highly significant and positive correlation with root volume, root dry weight plant^{-1}, biological yield plant^{-1}, root length, number of grains panicle^{-1}, number of effective tillers plant^{-1}, 1000 seed weight, panicle length and harvest index. Milling % had significant and positive correlation with hulling %, head rice recovery % and kernel breadth while exhibited a negative association with number of effective tillers plant^{-1}, biological yield plant^{-1}, root dry weight plant^{-1}, root fresh weight plant^{-1}, root volume, number of grains panicle^{-1}, kernel length breadth ratio, 1000 seed weight and panicle length. Similar to current study Kumari et al. (2023) described that grain yield plant^{-1} was positively correlated with 1000 seed weight and biological yield plant^{-1}. Patel et al. (2017) detected that grain yield plant^{-1} exhibited significant positive association with panicle length, number of effective tillers plant^{-1}, number of grains panicle^{-1} and harvest index percentage. Kesh et al. (2022b) also reported strong positive association of grain yield with number of effective tiller plants^{-1}, 1000 seed weight and panicle length. Mohankumar et al. (2012) studied that root volume and root weight showed significant positive correlation with grain yield, indicated importance of root in achieving higher grain yield under upland conditions. Chuchert et al. (2018) reported that flag leaf length had significant and positive association with grain yield plant^{-1}. Gupta et al. (2020) observed significant positive association of number of grains panicle^{-1} with panicle length. Himaja et al. (2022) found 1000 seed weight and kernel length had significant negative correlation with number of grains per panicle.

3.4. *Regression analysis*

A statistical technique known as step-by-step regression is used to determine which variable contributes the most to the amount of variability towards dependent variables, such economic yield. In present study, the results indicated that biological yield plant^{-1}, harvest index percentage, numbers effective of tillers plant^{-1}, number of grains panicle^{-1}, plant height and head rice recovery accounted for the maximum variation of grain yield in rice with cumulative R^2=99.45. A significantly positive regression coefficient of biological yield plant^{-1}, harvest index percentage, numbers effective of tillers plant^{-1}, number of grains panicle^{-1}, plant height and head rice recovery suggested that an increase in the mean of these variables might improve the grain yield of rice. Because of regression coefficients of significant variables, the predicted model equation for rice grain yield (Table 4) was calculated as: Predicted grain yield =-24.33+(0.44×BYP)+(-0.01×PH)+(0.10×NTP)+(0.01×NGL)+(-0.01×PH)+(0.01×HRR)

Table 4: Stepwise regression approach for traits prioritization under aerobic conditions in rice.

Dependent Variable	Steps and Variables	C(p)	R-square	Adj. R-square
GY/P (Grain yield plant^{-1})	BY/P	3582.3	49.77	48.68
	BY/P+HI	13.17	99.24	99.2
	NT/P+BY/P+ HI	6.00	99.40	99.35
	NG/PL+NT/P + BY/P+HI	4.17	99.42	99.37
	PH+NG/PL+ NT/P+BY/P+ HI	3.74	99.44	99.38
	PH+NG/PL+ NT/P+BY/P+ HI+HRR	3.61	99.45	99.36

GY/P: Grain yield plant^{-1}, PH: Plant height, NG/PL: No. of grains panicle^{-1}, NT/P: No. effective of tillers plant^{-1}, BY/P: Biological yield plant^{-1}, HI: Harvest index percentage, HRR: Head rice recovery %

The highly positive and negative coefficients of characteristics show that the final grain yield plant^{-1} will either increase or decrease with an increase or decrease in their respective values. In the previous research, Krishna et al. (2022) also reported that number of effective tillers, thousand seed weight, kernel length, and gel consistency are the major traits for prosperous breeding programs in rice. Similarly to this, Saed-Moucheshi et al. (2013) determined that spike weight and chlorophyll content were important characteristics for wheat breeding programmes operating in various water regimes.

3.5. *Path coefficient*

The estimates of correlation coefficient revealed only the relationship between yield and yield associated traits, with no indication of direct and indirect effect of different characters on grain yield. Path analysis on the other hand divide the association between two traits into its direct and indirect effect and provides meaningful results on the cause of the association between the grain yield as dependent variable and the other traits as independent variable. In present study, genotypic correlation was partitioned in direct and indirect effect using path analysis, as shown in Table 5, to assess the relative importance of 23 morpho-physiological and quality traits. Path coefficient analysis revealed that the highest positive direct effect on grain yield was exhibited by biological yield plant^{-1} and Harvest index percentage. Therefore, these two traits should be regarded as essential for enhancing grain yield under aerobic condition. The results are in conformity with the findings of Sravan et al. (2012) and Farheen et al. (2023). In addition to these two traits, days to 50% flowering, 1000 seed weight, flag leaf length, number of grains panicle^{-1}, panicle length, root fresh weight plant^{-1}, root dry weight plant^{-1}, number of effective tillers plant^{-1}, hulling %, head rice recovery % and milling % all showed a positive direct impact on grain yield plant^{-1}. This indicates that direct selection of these traits is likely to result in improved grain yield. Therefore, it is advisable to prioritize these traits in the breeding programme to identify superior genotypes with higher yield potential. The results were consistent with the findings of Chuchert et al. (2018) for flag leaf length and 1000 seed weight, Vennela et al. (2021) for number of grains panicle^{-1}, Chandra and Nilanjaya (2017) for number of effective tillers plant^{-1}, Lakshmi et al. (2020) for panicle length, and Gupta et al. (2020) for panicle length and plant height. Flag leaf width had negative direct effect on grain yield plant^{-1} but it demonstrated positive indirect effect on grain yield through biological yield plant^{-1}, 1000 seed weight and number of grains panicle^{-1}. Plant height expressed positive indirect effect on grain yield through biological yield plant^{-1}, flag leaf length, number of grains panicle^{-1} and root fresh weight plant^{-1}. The direct expression of kernel breadth was negative on grain yield however it had positive indirect effect on grain yield through biological yield plant^{-1}, harvest index percentage, 1000 seed weight, kernel length, hulling % and milling %. Kernel length head negative direct effect on grain yield while it showed positive indirect effect on grain yield through kernel breadth, 1000 seed weight and harvest index. The major positive indirect effect via biological yield plant^{-1} and harvest index percentage primary contribute to the correlation of plant height, number of grains panicle^{-1}, number of effective tillers plant^{-1}, root fresh weight plant^{-1},

Table 5: Genotypic path analysis of twenty-three traits on grain yield in rice genotypes under aerobic conditions

	DTF	DTM	PH	FLW	FLL	PL	NG/PL	NT/P	TW	BY/P	HI	RFW
DTF	0.0289	0.1693	0.0054	-0.0397	-0.0039	-0.0043	-0.0463	-0.0009	-0.0382	0.0102	-0.1780	-0.0078
DTM	0.0277	0.1766	0.0054	-0.0512	-0.0058	-0.0049	-0.0548	-0.0039	-0.0422	-0.0282	-0.2341	-0.0282
PH	-0.0065	-0.0396	-0.0240	-0.0352	0.0447	0.0082	0.0919	-0.0068	0.0154	0.4215	-0.0902	0.0314
FLW	0.0112	0.0882	-0.0083	-0.1024	0.0398	0.0027	0.0200	-0.0074	0.0671	0.3648	-0.2097	-0.0160
FLL	-0.0012	-0.0106	-0.0112	-0.0426	0.0957	0.0063	0.0334	0.0092	0.0160	0.3170	-0.1092	0.0137
PL	-0.0086	-0.0589	-0.0135	-0.0193	0.0411	0.0146	0.0778	0.0014	0.0445	0.3656	-0.0815	0.0523
NG/PL	-0.0090	-0.0652	-0.0149	-0.0138	0.0216	0.0076	0.1483	0.0115	0.0441	0.5186	0.1107	0.0805
NT/P	-0.0005	-0.0123	0.0029	0.0136	0.0157	0.0004	0.0307	0.0557	0.0667	0.5610	0.1205	0.0798
TW	-0.0042	-0.0284	-0.0014	-0.0262	0.0058	0.0025	0.0249	0.0142	0.2624	0.2081	0.3143	0.0636
BY/P	0.0003	-0.0051	-0.0103	-0.0381	0.0310	0.0054	0.0785	0.0319	0.0558	0.9797	-0.2319	0.0936
HI	-0.0071	-0.0571	0.0030	0.0296	-0.0144	-0.0016	0.0227	0.0093	0.1139	-0.3137	0.7243	0.0470
RFW	-0.0012	-0.0260	-0.0039	0.0086	0.0069	0.0040	0.0623	0.0232	0.0872	0.4789	0.1778	0.1914
RDW	0.0012	-0.0091	-0.0018	0.0086	-0.0049	0.0033	0.0434	0.0145	0.0837	0.3796	0.1972	0.1691
RFW/RDW	-0.0045	-0.0216	0.0008	0.0000	0.0115	-0.0018	-0.0256	0.0063	-0.0109	-0.0709	-0.1464	-0.0421
RV	0.0001	-0.0179	-0.0042	0.0051	0.0071	0.0040	0.0570	0.0204	0.0840	0.4231	0.1446	0.1963
RL	0.0033	0.0116	-0.0003	-0.0337	0.0521	0.0014	0.0180	0.0268	0.1023	0.4418	-0.0192	0.0811
HULL	-0.0016	-0.0065	0.0001	0.0061	-0.0029	0.0011	0.0001	-0.0130	-0.0454	-0.1199	-0.0375	-0.0152
MILL	-0.0054	-0.0220	-0.0009	0.0083	-0.0004	-0.0024	-0.0332	-0.0264	-0.0493	-0.4200	-0.0470	-0.0730
HRR	0.0017	0.0072	-0.0010	-0.0334	0.0010	-0.0026	-0.0186	-0.0075	0.0740	-0.2126	0.0204	0.0073
KL	0.0025	0.0210	0.0076	-0.0082	-0.0169	0.0016	-0.0515	-0.0009	0.1065	-0.2402	0.0553	0.0165
KB	0.0018	0.0042	-0.0097	-0.0182	0.0107	0.0016	0.0739	0.0019	0.0704	0.3398	0.1466	0.0075
KLBR	0.0006	0.0102	0.0088	0.0044	-0.0126	0.0001	-0.0649	-0.0019	0.0029	-0.3083	-0.0636	-0.0009

Table 5: Continue...

	RDW	RFW/RDW	RV	RL	HULL	MILL	HRR	KL	KB	KLBR	rg
DTF	0.0057	-0.0076	-0.0009	-0.0176	-0.0066	-0.0187	0.0013	-0.0143	-0.0185	0.0002	-0.182*
DTM	-0.0069	-0.0060	0.0316	-0.0103	-0.0044	-0.0125	0.0009	-0.0200	-0.0071	0.0005	-0.278**
PH	0.0103	-0.0017	-0.0545	-0.0021	-0.0003	0.0038	0.0010	0.0531	-0.1187	-0.0030	0.298**
FLW	-0.0113	0.0000	0.0156	-0.0516	-0.0071	-0.0081	0.0074	-0.0135	-0.0524	-0.0004	0.129
FLL	-0.0069	0.0059	-0.0230	-0.0852	-0.0036	-0.0004	0.0002	0.0298	-0.0330	-0.0011	0.199*
PL	0.0301	-0.0059	-0.0845	-0.0148	0.0092	-0.0167	-0.0040	-0.0184	-0.0328	0.0001	0.278**
NG/PL	0.0391	-0.0085	-0.1193	-0.0190	0.0001	-0.0224	-0.0028	0.0585	-0.1473	-0.0036	0.615**
NT/P	0.0347	0.0055	-0.1138	-0.0753	-0.0277	-0.0474	-0.0030	0.0028	-0.0103	-0.0003	0.700**
TW	0.0427	-0.0020	-0.0994	-0.0610	-0.0205	-0.0188	0.0064	-0.0683	-0.0793	0.0001	0.535**
BY/P	0.0518	-0.0035	-0.1342	-0.0706	-0.0145	-0.0429	-0.0049	0.0413	-0.1025	-0.0026	0.708**
HI	0.0364	-0.0099	-0.0620	0.0042	-0.0062	-0.0065	0.0006	-0.0128	-0.0599	-0.0007	0.439**
RFW	0.1182	-0.0108	-0.3186	-0.0663	-0.0094	-0.0381	0.0009	-0.0145	-0.0116	0.0000	0.659**

Table 5: Continue...

	RDW	RFW/ RDW	RV	RL	HULL	MILL	HRR	KL	KB	KLBR	rg
RDW	0.1338	-0.0310	-0.2763	-0.0556	-0.0160	-0.0397	0.0029	-0.0086	-0.0236	-0.0005	0.570^{**}
RFW/ RDW	-0.0848	0.0490	0.0650	0.0161	-0.0019	0.0109	-0.0028	-0.0290	0.0921	0.0024	-0.188^{*}
RV	0.1190	-0.0102	-0.3107	-0.0788	-0.0018	-0.0293	0.0025	-0.0066	-0.0378	-0.0005	0.565^{**}
RL	0.0475	-0.0050	-0.1564	-0.1566	0.0178	-0.0086	0.0082	-0.0228	0.0026	0.0004	0.412^{**}
HULL	-0.0180	-0.0008	0.0046	-0.0235	0.1188	0.0565	-0.0003	0.0490	-0.1100	-0.0029	-0.161
MILL	-0.0531	0.0053	0.0910	0.0135	0.0671	0.1000	0.0066	0.0244	-0.0607	-0.0016	-0.479^{**}
HRR	0.0173	-0.0060	-0.0349	-0.0572	-0.0015	0.0291	0.0226	-0.0108	0.0232	0.0006	-0.182^{*}
KL	0.0069	0.0084	-0.0123	-0.0212	-0.0346	-0.0145	0.0015	-0.1683	0.1950	0.0076	-0.138
KB	0.0107	-0.0153	-0.0397	0.0014	0.0442	0.0205	-0.0018	0.1110	-0.2956	-0.0078	0.458^{**}
KLBR	-0.0083	0.0139	0.0199	-0.0075	-0.0417	-0.0198	0.0015	-0.1546	0.2802	0.0083	-0.333^{**}

GY/P: Grain yield plant^{-1}, DTF: Days to flowering, DTM: Days to maturity, PH: Plant height, FLW: Flag leaf width, FLL: Flag leaf length, PL: Panicle length, NG/PL: No. of grains panicle^{-1}, NT/P: Numbers effective of tillers plant^{-1}, TW: 1000 seed weight, BY/P: Biological yield plant^{-1}, HI: Harvest index percentage, RFW: Root fresh weight plant^{-1}, RDW: Root dry weight plant^{-1}, RFW/RDW: Root fresh and dry weight ratio, RV: Root volume plant^{-1}, RL: Root length plant^{-1}, HULL: Hulling %, MILL: Milling %, HRR: Head rice recovery %, KL: Kernel length, KB: Kernel breadth, KLBR: Kernel length-breadth ratio; Residual effect: 0.00238; **: Significant at (p=0.01) level of significance; *: Significant at (p=0.05) level of significance

root dry weight plant^{-1}, root volume and kernel breadth to the grain yield plant^{-1}. Therefore, these traits may be included in breeding programme for simultaneous yield improvement.

4. CONCLUSION

Considerable genetic variability was found among 48 rice genotypes. High heritability with high genetic advance as per cent of mean indicating the influence of additive gene action. The study revealed that biological yield plant^{-1}, number of grains panicle^{-1}, harvest index percentage, root fresh weight plant^{-1}, number of effective tillers plant^{-1} and 1000 seed weight were the major contributing traits to grain yield. Thus, these traits significantly contribute to grain yield, underscoring their importance in genetic improvement.

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