Original Research Article

Genetic variability, character association and path analysis for yield and its related traits in rice (*Oryza sativa* L.) genotypes

ABSTRACT

Assessment of variability and trait associations in a crop helps to enhance selection efficiency. With this objective, a study was conducted to estimate the genetic variability, character association and path coefficient analysis for grain yield and its component traits in 80 rice genotypes during *Kharif*-2020. Eighty genotypes including eight checks were evaluated in alpha lattice design with three replications. The results showed significant variation in all the genotypes for all the traits considered. PCV was found to be slightly more than the corresponding GCV for all the characters, indicating the role of environment in the expression of these traits. However, high GCV and high PCV were observed for number of effective tillers, grain yield per plot, number of filled grains per panicle, number of unfilled grains per panicle, biomass yield, harvest index, grain yield per plant and grain yield per hectare. Further, high heritability coupled with high genetic advance as percent of mean was recorded for all the traits studied except days to 50% flowering, days to maturity and kernel breadth. Days to first flowering, days to 50% flowering, days to maturity, spikelet fertility percentage, number of filled grains per panicle, harvest index and kernel length showed a significant and positive association with grain yield per plot. Highest direct contribution to grain yield per plot was manifested by kernel length, harvest index and spikelet fertility percent. Days to first flowering, days to maturity, number of effective tillers, number of unfilled grains per panicle, test weight, biomass yield were also found to exert a positive effect on yield, thus can be considered as desirable traits for selection in high yielding genotypes.

KEYWORDS: *Character association, Direct effects, Heritability, Rice, Variability, Yield.*

1. INTRODUCTION

Rice (*Oryza sativa* L.) is an important staple cereal crop that feeds more than half of the world's population [1]. Plant breeders' primary goal would always be to boost yields in staple food crops, given the world's expanding population. It is estimated that the world will need to produce 60% more rice by 2030 than it did in 1995 [2]. As a result, increasing rice production is crucial for providing food security. The development of high yielding varieties necessitates an understanding of existing genetic variability in the crop germplasm. The large spectrum of genetic variability in a segregating population is determined by the amount of genetic variability among genotypes and provides a better opportunity for selection [3]. The level of heritable variation in the traits studied is extremely useful in determining the genotype's potential for future breeding programs. Before planning an appropriate breeding strategy for genetic improvement, it is critical to assess variability for yield and its component characters [4]. For efficient crop development, understanding the nature and extent of genetic variation in quantitative traits such as yield and its components is critical. Selecting high yielding varieties solely on grain yield will be ineffective unless adequate information on genetic parameters is available to formulate hybridization and selection programs for further improvement. Information on character association, as well as the direct and indirect effects that each character has on yield, will be useful in the selection process. Correlation and Path analysis reveals the magnitude of the association between grain yield and its components, as well as the relative importance of their direct and indirect effects, providing a clear understanding of their association with grain yield[5]. Finally, this type of research could aid the breeder in developing selection strategies to improve grain yield. Given the above scenario, the current investigation is carried out with the objective of studying the genetic variability, character association and path coefficients in rice genotypes for yield improvement.

2. MATERIALS AND METHODS

2.1 Plant material and experimental layout:

The experimental material for the present study consisted of 80 rice genotypes including eight checks (Sarjoo-52, NDR-359, HUR-1309, NDR-97, Pantdhan-12, BPT-5204, Sahbhagi dhan and HUR-105). The investigation was carried out during *Kharif*-2020 at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, U.P. India, situated at 25^o 18’ N latitude, 83^o 03’ E longitude of 87 meters above mean sea level. The trial was laid out in Alpha lattice design with three replications. The nursery was sown on uniformly raised beds and 21day old seedlings were transplanted to the main field. Each plot consists of five rows of 2 m each with a spacing of 20 cm x 15 cm. The recommended fertilizer dose of 120 Kg N_2, 60 Kg P_2O_5, 60 Kg K_2O and 25 Kg Zn per ha was used. Standard agronomic practices were followed precisely to raise a healthy crop.

2.2 Observations recorded:

Different quantitative traits *viz.,* Days to first flowering (DF1st), Days to 50% flowering (DF50per), Days to maturity(DM), Plant height (PH), Panicle length (PL), Effective tillers per plant (ET), Filled grains per panicle (FG), Unfilled grains per panicle (UFG), Spikelet fertility percent (SF), Kernel length (KL), Kernel breadth (KB), Kernel L/B ratio (LpB), Test weight (TW), Grain yield per plant (YLDpr plant), Grain yield per plot (YLDkgpp), Biomass yield per plot (BW), Harvest index (HI), Grain yield per hectare (YLDkgpha) were recorded. For most of the quantitative traits, the average of readings from five randomly selected plants was taken replication wise and the mean values concerning these traits were subjected to further statistical analysis. However, for the traits like Days to first flowering, Days to 50% flowering, Days to maturity, Grain yield and Biomass data were collected on plot basis.

2.3 Statistical analysis:

The mean data after computing for each character was subjected to standard method of analysis of variance following the alpha lattice design. The ANOVA was conducted using SAS *v* 9.3. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance as percent of mean were estimated by the formula as suggested by Burton and Devane [6] and Allard [7]. Categorization of the range of variation was followed as proposed by Sivasubramanian and Madhavamenon [8] *i.e.,* Less than 10% – Low; 10–20% – Moderate; More than 20% – High.

Heritability was calculated by the formula given by Allard [7] and as suggested by Johnson *et al* [9]. h^2 (b) estimates were categorized as: Less than 30% – Low; 30–60% – Moderate; More than 60% – High. Further, Genetic advance as percent of mean was estimated by the following formula suggested by Allard [7]. The range of genetic advance as percent of mean was classified as suggested by Johnson *et al* [9] *i.e.,* Less than 10% – Low; 10–20% – Moderate; More than 20% – High

The simple correlation coefficients among pairs of characters were calculated according to the formula suggested by Searle [10]. Searle [11] has suggested minimum values of correlation coefficient necessary for indirect selection to be more efficient than direct selection for yield as below:

Values of correlation coefficients	**Rate or scale**
> 0.65	Very strong
0.50 to 0.64	Moderately strong
0.30 to 0.49	Moderately weak
< 0.30	Very weak

Path coefficients were computed using correlation coefficients to know the direct and indirect effects of the component characters on yield as suggested by wright [12] and illustrated by Dewey and Lu [13]. Scale for path coefficient was reported by Lenka and Mishra [14] as below:

Values of correlation coefficients	**Rate or scale**
0.00 – 0.09	Negligible
0.1 – 0.19	Low
0.2 – 0.29	Moderate
0.30 – 0.99	High
>1	Veru high

3. RESULTS AND DISCUSSION

3.1 ANOVA:

The analysis of variance (ANOVA) revealed that the genotypes differed significantly for all the traits studied (Table 1) indicating the existence of a sufficient amount of variability among the genotypes taken for the study.

3.2 Genetic parameters:

Various genetic parameters *viz*., Variability, Heritability and Genetic Advance as percent of mean were calculated for the 18 traits included in the study. It was observed that the estimates of PCV were higher than their corresponding GCV values suggesting the effect of environment on all the traits. [1], [15], [16], [17], [18] and [19] have reported higher PCV values than GCV values in their studies. However, the difference between PCV and GCV was found to be very small, indicating that environment has little influence on the expression of traits or that genotypes are less sensitive to the environment. The trait, number of unfilled grains per panicle exhibited high GCV (34.89%) as well as PCV (36.76%). It was followed by number of effective tillers (GCV 30.11% and PCV 31.92%) and number of filled grains per panicle (GCV 29.21% and PCV 29.85%). Similar findings were reported by Singh *et al.,* [20], Gautam et al [21], Abebe *et al* [22], Gour *et al* [23], Prasad *et al* [24] and Pragnya *et al* [25]. In the case of harvest index and grain yield per plant, the differences between PCV and GCV reflect relatively greater environmental impact. Other variability parameters, such as heritability, can thus be considered.

In the present study, high heritability was recorded for all the traits studied. The values of heritability ranged from 70.79% for harvest index to 99.05% for days to first flowering. Kernel length (98.43%), days to maturity (98.27%), days to 50% flowering (97.65%), kernel L/B ratio (97.10%) and number of filled grains per panicle (95.73%) reported high heritability indicating the genetic inheritance of these traits. Similar reports were made by Ovung *et al* [26] and Tripathi *et al* [27]. This indicated the scope of selection for these traits. Heritability estimates include both additive and non-additive gene effects. So, high heritability does not serve as true indicator of high genetic gain. Together with genetic advance, heritability can be used as a tool in the selection program for better efficiency in selection.

Table 1. ANOVA table showing mean sum of squares for different characters in rice

Source	**df**	**Days to first flowering**	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Panicle length**	**Effective tillers per plant**	**Filled grains per panicle**	**Unfilled grains per panicle**	**Spikelet fertility percent**
Genotype	79	201.07**	200.87**	185.59**	339.35**	18.96**	15.11**	2634.39**	398.33**	164.47**
Rep.	2	1.31	30.92**	7.35**	9.07	12.90**	2.36	490.08**	69.12*	41.45**
Block(rep)	6	1.40	4.41	2.12	6.73	2.61	1.1	86.42	23.39	5.01

Source	**df**	**Kernel length**	**Kernel breadth**	**Kernel L/B ratio**	**Test weight**	**Grain yield per plant**	**Grain yield per plot**	**Biomass yield per plot**	**Harvest index**	**Grain yield per hectare**
Genotype	79	1.37**	0.08**	0.69**	20.17**	47.48**	0.17**	0.76**	149.06**	2712877.1**
Rep.	2	0.06**	0.01*	0.02	0.77	21.52**	0.09**	0.19*	173.21**	9259117.3**

Block(rep)	6	0.02	0.00	0.01	0.23	1.56	0.01	0.05	29.24	838100.7

*, ** - significant at 5 and 1 percent respectively

High heritability coupled with high genetic advance as percent of mean was recorded for all the traits studied except days to 50% flowering, days to maturity and kernel breadth, indicating the effectiveness of selection for the improvement of these traits. Similar reports were also made by Ovung *et al* [26] and Tripathi *et al* [27]. Whereas, high heritability along with moderate genetic advance as percent of mean were found for days to 50% flowering, days to maturity and kernel length. The results are consistent with the findings of Paikhomba *et al* [15], Prasad *et al* [24], Pandey *et al* [28], and Lingaiah *et al* [29]. The values of all these genetic parameters were presented in Table 2.

Table 2. Genetic parameters of yield and component traits **in rice genotypes**

Character	**Mean**	**Range**	**GCV %**	**PCV %**	**h^2(bs) %**	**GA% Over mean**
DF1st	98	80-121	9.89	9.94	99.05	20.27
DF50per	103	85-126	9.33	9.44	97.65	18.99
DM	125	109-150	7.50	7.56	98.27	15.31
PH	109.62	88.01-132.82	11.52	11.85	94.48	23.06
PL	26.78	19.79-32.73	11.00	11.95	84.64	20.84
ET	9	5-17	30.11	31.92	88.98	58.51
YLDkgpp	.099	0.47-1.66	28.51	30.21	89.10	55.45
FG	120	73-218	29.21	29.85	95.73	58.87
UFG	39	14-64	34.89	36.76	90.09	68.23
KL	6.34	4.99-7.63	12.72	12.82	98.43	26.00
KB	1.98	1.70-2.35	9.68	10.04	93.02	19.24
TW	21.42	14.45-26.10	14.47	14.89	94.53	28.99
BW	2.03	1.08-3.30	28.82	30.90	86.97	55.36
HI	33.55	17.92-51.63	22.85	27.16	70.79	39.60

SF	75.07	62.91-89.95	11.88	12.18	95.12	23.86
LpB	3.23	2.21-4.28	17.65	17.92	97.10	35.83
YLDpr plant	15.59	7.44-28.27	28.54	32.58	76.77	51.52
YLDkgpha	4398	2097.36-7357.99	28.51	30.21	89.10	55.45

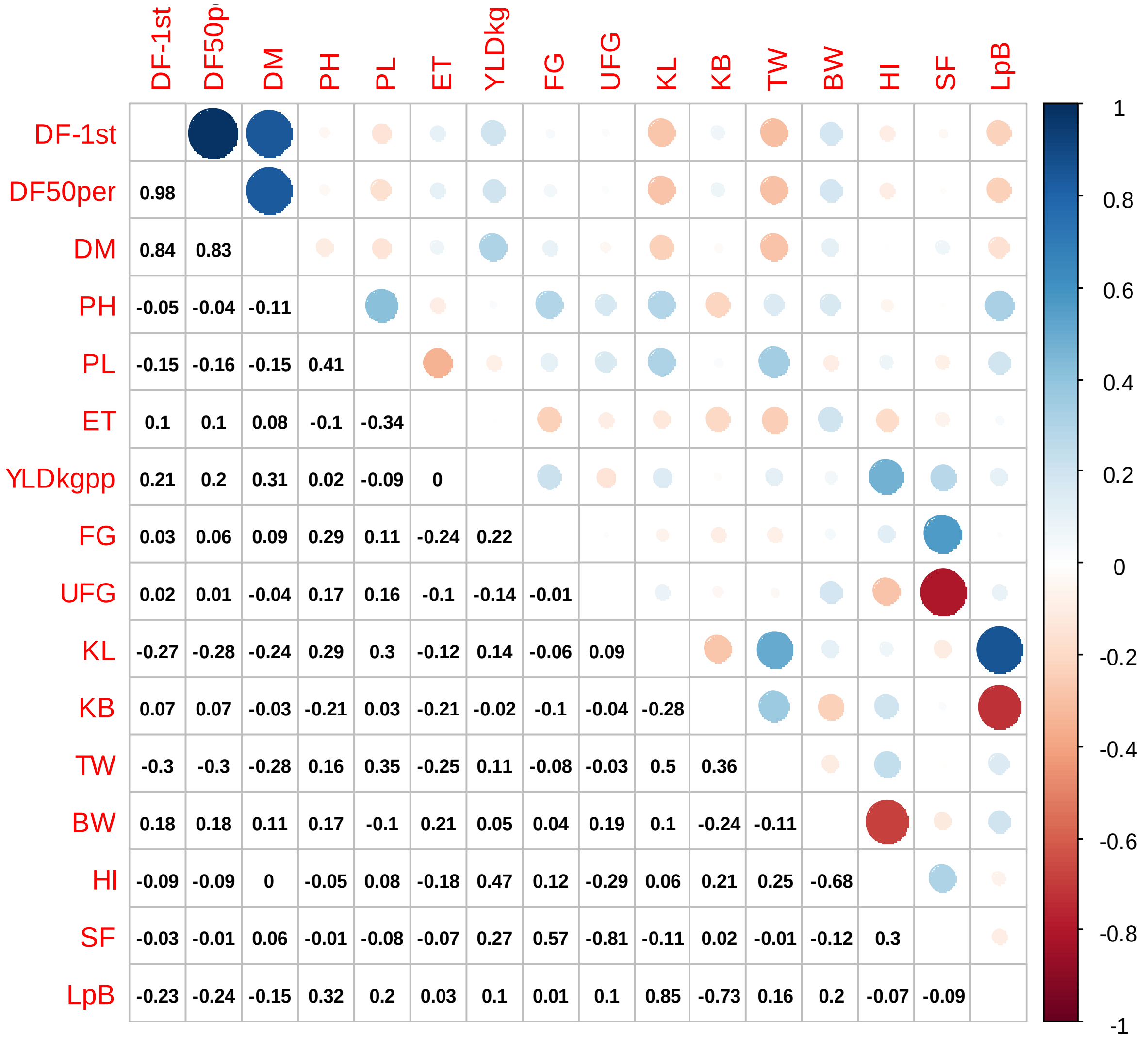
3.3 Character association and path coefficient analysis:

3.3.1 Character association:

The direction and level of correlation/association between yield and its contributing traits, as well as among themselves, determines the efficiency of selection for yield. Correlation coefficients give us information about the nature and extent of association and thus help in the selection for the improvement of traits. The results pertaining to correlation are presented in Figure 1.

In the present study, grain yield had a significant and positive correlation with harvest index (0.47), days to maturity (0.31), spikelet fertility percent (0.27), number of filled grains per panicle (0.22), days to first flowering (0.21) and days to 50% flowering (0.2) and kernel length (0.14). These results were in agreement with the research findings of Seyoum *et al* [30], Aditya *et al* [31], Sarker *et al* [32], Naseer *et al* [33] and Ratna *et al* [34]. This indicates the importance of these traits as a selection criterion in yield improvement programs. Number of unfilled grains per panicle (-0.14) showed a significant negative association with grain yield. These results agree with the research findings of Sarker *et al* [32] and Fentie *et al* [35].

Days to first flowering showed a very strong correlation with days to 50% flowering (0.98%) and days to maturity (0.84). Kernel length showed very strong correlation with kernel L/B ratio (0.85). Number of filled grains per panicle displayed significant positive correlation with spikelet fertility percent (0.57), plant height (0.29) and grain yield (0.22). Test weight showed a significant positive correlation with kernel breadth (0.36), panicle length (0.35) and harvest index (0.21). Harvest index showed significant positive correlation with grain yield (0.47), spikelet fertility (0.3) and test weight (0.25). Kernel L/B ratio showed significant positive correlation with kernel length (0.85), plant height (0.32), panicle length (0.2), biomass yield (0.2) and test weight (0.16). Similar findings were reported by Venkatesan *et al* [36]It reveals that selecting high performing genotypes for the above-mentioned traits can increase grain yield. Characteristics like days to first flowering and maturity showed negative correlation with panicle length; and exhibited a positive correlation with number of filled grains per panicle and grain yield, reflecting that decrease in panicle length leads to an increase in number of filled grains per panicle and grain yield in late flowering and maturing genotypes. Grain yield was positively correlated with kernel L/B ratio and plant height reflecting that increase in grain dimension leads to an increase in grain yield in tall plants.



	DF-1st	DF50p	DM	PH	PL	ET	YLDkg	FG	UFG	KL	KB	TW	BW	HI	SF	LpB
DF-1st																
DF50per	0.98															
DM	0.84	0.83														
PH	-0.05	-0.04	-0.11													
PL	-0.15	-0.16	-0.15	0.41												
ET	0.1	0.1	0.08	-0.1	-0.34											
YLDkgpp	0.21	0.2	0.31	0.02	-0.09	0										
FG	0.03	0.06	0.09	0.29	0.11	-0.24	0.22									
UFG	0.02	0.01	-0.04	0.17	0.16	-0.1	-0.14	-0.01								
KL	-0.27	-0.28	-0.24	0.29	0.3	-0.12	0.14	-0.06	0.09							
KB	0.07	0.07	-0.03	-0.21	0.03	-0.21	-0.02	-0.1	-0.04	-0.28						
TW	-0.3	-0.3	-0.28	0.16	0.35	-0.25	0.11	-0.08	-0.03	0.5	0.36					
BW	0.18	0.18	0.11	0.17	-0.1	0.21	0.05	0.04	0.19	0.1	-0.24	-0.11				
HI	-0.09	-0.09	0	-0.05	0.08	-0.18	0.47	0.12	-0.29	0.06	0.21	0.25	-0.68			
SF	-0.03	-0.01	0.06	-0.01	-0.08	-0.07	0.27	0.57	-0.81	-0.11	0.02	-0.01	-0.12	0.3		
LpB	-0.23	-0.24	-0.15	0.32	0.2	0.03	0.1	0.01	0.1	0.85	-0.73	0.16	0.2	-0.07	-0.09	

Figure 1. Correlation coefficients between yield per plot (kg) and its component traits in 80 rice genotypes

3.3.2 Path analysis:

Correlation just shows the relationship between two variables whereas, path coefficient analysis allows separation of direct and indirect effects by partitioning the correlation. Path analysis was carried out taking the grain yield as dependent characters and the remaining 15 traits as independent characters. The direct and indirect effects of various traits on grain yield were depicted in table 3.

Path coefficient analysis revealed nine out of fifteen characters showed a positive and direct effect on grain yield *viz.,* days to first flowering (0.197), days to maturity (0.261), number of effective tillers (0.052), number of unfilled grains per panicle (0.740), kernel length (0.981), test weight (0.058), biomass yield (0.535), harvest index (0.843) and spikelet fertility percent (0.877). Similar reports were made by Reddy *et al [37],* Allam *et al* [38], Mahendera *et al* [39] and Dhurai *et al* [40]. While the characters *viz.,* days to 50% flowering (-0.179), plant height (-0.012), panicle length (-0.096), number of filled grains per panicle (-0.378), kernel breadth (-0.731) and kernel L/B ratio (-1.251) showed negative direct effect on grain yield. Days to first flowering and days to maturity had a direct and positive effect on grain yield per plot indicating more days to flowering and maturity is effective in grain yield. Spikelet fertility percent demonstrated a very high positive and direct effect on grain yield per plot (0.877) but through number of unfilled grains per panicle (-0.708) and biomass yield (-0.104) it exhibited negative indirect effect with positive indirect effect through number of filled grains per panicle (0.497) and harvest index (0.267). The current study found that the trait spikelet fertility percent had a greater positive and direct effect on grain yield per plot, indicating that this trait could be effective in selection for increasing grain yield.

Table 3. Direct and indirect effects of component traits attributing to grain yield per plot (kg)

	DF-1st	**DF50per**	**DM**	**PH**	**PL**	**ET**	**FG**	**UFG**	**KL**	**KB**	**TW**	**BW**	**HI**	**SF**	**LpB**	**linear**
DF-1st	**0.197**	0.193	0.166	-0.009	-0.029	0.020	0.007	0.004	-0.054	0.013	-0.059	0.036	-0.019	-0.006	-0.045	0.210
DF50per	-0.175	**-0.179**	-0.148	0.007	0.029	-0.018	-0.010	-0.003	0.050	-0.013	0.053	-0.032	0.016	0.002	0.042	0.201
DM	0.220	0.217	**0.261**	-0.028	-0.039	0.020	0.025	-0.012	-0.062	-0.007	-0.074	0.030	-0.001	0.017	-0.040	0.309
PH	0.001	0.000	0.001	**-0.012**	-0.005	0.001	-0.003	-0.002	-0.003	0.002	-0.002	-0.002	0.001	0.000	-0.004	0.023
PL	0.014	0.015	0.014	-0.040	**-0.096**	0.033	-0.011	-0.015	-0.029	-0.003	-0.033	0.009	-0.007	0.008	-0.019	-0.089
ET	0.005	0.005	0.004	-0.005	-0.018	**0.052**	-0.012	-0.005	-0.006	-0.011	-0.013	0.011	-0.010	-0.004	0.002	0.003
FG	-0.013	-0.022	-0.036	-0.110	-0.042	0.090	**-0.378**	0.004	0.024	0.037	0.032	-0.016	-0.046	-0.214	-0.005	0.217
UFG	0.016	0.011	-0.033	0.129	0.119	-0.073	-0.008	**0.740**	0.064	-0.033	-0.025	0.139	-0.212	-0.597	0.073	-0.145
KL	-0.268	-0.275	-0.231	0.286	0.296	-0.120	-0.062	0.085	**0.981**	-0.270	0.494	0.103	0.063	-0.107	0.837	0.143
KB	-0.049	-0.052	0.020	0.157	-0.019	0.153	0.071	0.032	0.201	**-0.731**	-0.263	0.175	-0.152	-0.015	0.533	-0.017
TW	-0.017	-0.017	-0.016	0.009	0.020	-0.015	-0.005	-0.002	0.029	0.021	**0.058**	-0.006	0.014	0.000	0.009	0.113
BW	0.098	0.097	0.061	0.091	-0.052	0.112	0.022	0.101	0.056	-0.128	-0.059	**0.535**	-0.366	-0.063	0.107	0.051
HI	-	-	-	-	0.0	-	0.1	-	0.0	0.1	0.2	-	**0.8**	0.2	-	0.4

	0.080	0.078	0.002	0.045	65	0.154	01	0.241	54	75	08	0.576	**43**	56	0.055	74
SF	-0.026	-0.010	0.056	-0.007	-0.071	-0.061	0.497	-0.708	-0.095	0.018	-0.007	-0.104	0.267	**0.877**	-0.082	0.271
LpB	0.287	0.295	0.191	-0.401	-0.247	-0.038	-0.016	-0.123	-1.067	0.913	-0.196	-0.251	0.082	0.117	**-1.251**	0.103

4. CONCLUSION

From the study on genetic parameters, it is clear that number of effective tillers, grain yield per plot, number of filled grains per panicle, number of unfilled grains per panicle, biomass yield, harvest index, grain yield per plant and grain yield per hectare display higher PCV and GCV, very high heritability with high genetic advance. Selection based on these traits would be effective in increasing yield. Correlation and path coefficients envisaged characteristics such as harvest index, days to first flowering, days to maturity, spikelet fertility percent, kernel length, test weight and kernel L/B ratio showed positive direct effect and positive correlation with grain yield per plot, indicating the effectiveness of these traits in selection.

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