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Genetic Variability, Heritability and Genetic Advance for Yield and its Related Traits of 27 Genotypes in *Oryza sativa* L.

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Abstract: Knowledge of the magnitude of genetic variability, heritability and genetic gains in selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programmes. This study was carried out to assess the extent of genetic variability for yield and yield related traits and to estimate heritability and genetic advance in rice genotypes. Twenty-Seven genotypes were evaluated in randomized complete block design with three replications. Number of filled grain per panicle and total number of spikelet per panicle showed higher influence of environment for the expression of these characters. Days to maturity and number of unfilled grain per panicle showed moderate influence of environment for the expression of these characters. This variability would be high potential for genetic improvement of genotypes. Days to maturity exhibits the highest value of heritability (97.91) while number of unfilled grain per panicle (58.99) exhibits the lowest value of heritability. High heritability with moderate genetic advance was observed for days to flowering, days to maturity and panicle length indicating medium possibility of selecting genotypes. Hence, the direct selection of these characters may be useful for future improvement of genotypes under respective environment for improvement and higher grain yield. Therefore, it could be recommended that due emphasis should be given for these traits for the improvement of inbred lines.

Key word: Variability · Heritability · Genetic Advance · Rice Yield

INTRODUCTION

Rice is the staple food for nearly half of the world's population [1,2]. Rice is a self-pollinated cereal crop belonging to the family Gramineae under the order Cyperales and class monocotyledon having chromosome number 2n=24. The genus *Oryza* is known to consist of two cultivated species i.e., Asian rice (*O. sativa*, 2n=24=AA) and African rice (*O. glaberrima*, 2n=24=AA) and 22 wild species (2n=24, 48) [3]. The Asian cultivated rice (*Oryza sativa* L.) is the first fully sequenced crop genome and is a model crop species. Rice is considered as a major food crop across major countries worldwide.

Bangladesh is an agro-based country. Rice is the principal food of this country from time immemorial. It occupies 77% of total cropped area. At present rice alone constitutes about 92% of the total food grains produced annually in the country. It provides 75% of the calories and 55% of the proteins in the average daily diet of the people. Rice is rich in carbohydrate. The protein content is about 8.5 percent. The thiamin and riboflavin contents are 0.27 and 0.12 micrograms, respectively [4]. The vast majority of the populations (87%) residing in rural areas that depend on rice as a major source of food.

Despite the success in rice production, the country has reached to saturation in the recent years and still faces many challenges to achieve long-term food security. Breaking the existing yield plateau is necessary by developing more promising high yielding varieties. Bangladesh is a great reservoir of rice with diverse high yielding varieties, landraces and many less known varieties. Landraces are crucial germplasm having diverse source of adaptability genes and incorporation of those genes could ensure optimum grain yield [5-8]. But, high-

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yielding rice cultivars intruded by green revolution which substituted the traditional rice landraces results in reduced genetic base and increased genetic vulnerability [6, 9-15]. So, there is an urgent need to collect, evaluate and utilize these underexplored germplasms. Genetic variability forms the basic factor to be considered while making selection. Heritability indicates transmissibility of a character in future generations [14-17].

Heritability of a trait is important in determining its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program [18]. Heritability, a measure of the phenotypic variance attributable to genetic causes, has predictive function of breeding crops. Generally, heritability indicates the effectiveness with which selection of genotypes could be based on phenotypic performance.

Genetic advance expected from selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity [19]. Since high heritability does not always indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties.

A successful breeding program depends on the genetic diversity of a crop for chieving the goals of improving the crop and producing high yielding varieties. The low heritability of grain yield characters made selection for high yielding varieties possible usually using various components traits associated with yield. However, information on relationship of grain yield and yield contributing traits for upland rice of agro-ecology is not sufficiently available. In view of the above gaps, the present study was undertaken to investigate the genetic variability, heritability and genetic advance for yield related traits as a basis for selection of high yielding rice genotypes in upland ecology. Hence, the present study aims at the assessment of the extent of genetic variability for yield and yield related traits and estimation of heritability and genetic advance in rice genotypes.

Therefore, the present investigation was undertaken to gather some useful information on genetic variability, heritability, genetic advance and character association analysis in a set of 27 rice landraces to be used as suitable breeding materials for developing high yielding rice inbreeds and hybrids.

MATERIALS AND METHODS

Twenty seven (27) genotypes (22 F_4 materials and 5 check varieties) of *Oryza sativa* L were selected for experiment. Among them, twenty two were F_4 materials and 5 check varieties (Table 1). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications.

Statistical Analysis: The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson [20]. Heritability and genetic advance were measured using the formula given by Allard [21]. Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton [22].

Estimation of Genotypic and Phenotypic Variances: Genotypic and phenotypic variances were estimated according to the formula of Johnson [20].

Genotypic variance, $\delta^2 g$ $= \frac{MSG - MSE}{r}$

where, MSG = Mean sum of square for genotypes
MSE = Mean sum of square for error and
r = Number of replication

Phenotypic Variance, $\delta^2 p = \delta^2 g + \delta^2 e$

where, $\delta^2 g$ = Genotypic variance,
$\delta^2 e$ = Environmental variance = Mean square of error

Estimation of Genotypic and Phenotypic Co-efficient of Variation: Genotypic and phenotypic co-efficient of variation were calculated by the following formula [22].

$$GCV = \frac{d_g \times 100}{\bar{x}}$$

$$PCV = \frac{d_p \times 100}{\bar{x}}$$

where, GCV = Genotypic co-efficient of variation
PCV = Phenotypic co-efficient of variation
δ_g = Genotypic standard deviation
δ_p = Phenotypic standard deviation
$\bar{x}$ = Population mean

Table 1: List of genotypes, their serial number and their sources of collection

Serial No.	Designation	Source
G_1	BR 21	BRRI
G_2	BR 24	BRRI
G_3	BRRI dhan 28	BRRI
G_4	BRRI dhan 29	BRRI
G_5	BRRI dhan 36	BRRI
G_6	BR 21 X BRRI dhan 28, S-5, P-1	SAU
G_7	BR 21 X BRRI dhan 28, S-5, P-2,	SAU
G_8	BR 21 X BRRI dhan 28,S-5, P-3	SAU
G_9	BR 21 X BRRI dhan 28,S-5, P-4	SAU
G_{10}	BR 21 X BRRI dhan 28, S-5, P-6	SAU
G_{11}	BR 21 X BRRI dhan 29, S-6, P-1	SAU
G_{12}	BR 21 X BRRI dhan 29, S-6, P-2	SAU
G_{13}	BR 21 X BRRI dhan 29, S-6, P-3	SAU
G_{14}	BR 21 X BRRI dhan 29, S-6, P-4	SAU
G_{15}	BR 21 X BRRI dhan 29, S-6, P-5	SAU
G_{16}	BR 21 X BRRI dhan 29, S-6, P-6	SAU
G_{17}	BR 21 X BRRI dhan 29, S-6, P-7	SAU
G_{18}	BR 21 X BRRI dhan 36, S-1, P-1	SAU
G_{19}	BR 21 X BRRI dhan 36, S-1, P-2	SAU
G_{20}	BR 21 X BRRI dhan 36, S-1, P-3	SAU
G_{21}	BR 21 X BRRI dhan 36, S-1, P-4	SAU
G_{22}	BR 21 X BRRI dhan 36, S-1, P-5	SAU
G_{23}	BR 24 X BRRI dhan 28, S-10, P-2	SAU
G_{24}	BR 24 X BRRI dhan 28, S-10, P-5	SAU
G_{25}	BR 24 X BRRI dhan 29, S-5, P-1	SAU
G_{26}	BR 24 X BRRI dhan 29, S-5, P-3	SAU
G_{27}	BR 24 X BRRI dhan 29, S-5, P-4	SAU

Estimation of Heritability: Broad sense heritability was estimated by the formula suggested by Allard [21].

$$h^2(\%) = \frac{d^2_g}{d^2_p} \times 100$$

where, h^2 = Heritability in broad sense.
δ^2_g = Genotypic variance
δ^2_p = Phenotypic variance

Estimation of Genetic Advance: The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard [21].

$$GA = \frac{d^2_g}{d^2_p} K.\ d_p$$

where, GA = Genetic advance
δ^2_g = Genotypic variance
δ^2_p = Phenotypic variance
δ_p = Phenotypic standard deviation
K = Selection differential which is equal to 2.06 at 5% selection intensity

Estimation of Genetic Advance as Percentage of Mean: Genetic advance as percentage of mean was calculated by the following formula given by Comstock and Robinson [23].

$$\text{Genetic Advance as percentage of mean} = \frac{\text{Genetic advance}}{\bar{x}} \times 100$$

RESULTS AND DISCUSSION

Variation and Performance of the 27 Genotypes: The analysis of variance of 27 genotypes (22 F_4 populations and 5 check varieties) of rice for yield related different characters are shown in Table 2. The combined analysis of variance was revealed significant differences among rice genotypes for all traits studied ($P<0.05$) (Table 2). The results showed that there is a presence of acceptable amount of variability among the genotypes. This gives an opportunity for rice breeders to improve those traits through selection and hybridization to improve the desired traits.

The phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study. Number of filled grain per panicle and total number of spikelet per panicle showed higher influence of environment for the expression of these characters. Days to maturity and number of unfilled grain per panicle showed moderate influence of environment for the expression of these characters.

On the other hand, days to maturity, days to flowering, plant height, total number of tiller per plant, total number of effective tiller per plant, panicle length, number of primary branches per panicle, number of secondary branches per panicle, yield per plant, thousand seed weight and yield per hectare showed least difference phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

Genetic Parameters: The genotypic variance (σ^2g), phenotypic variance (σ^2p) and environmental variance (σ^2e), genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), environmental co-efficient of variation (ECV) for all the quantitative characters under study are presented in Table 3 and Figure 1. The difference between genotypic and phenotypic coefficient of variation was less for all characters studied except panicle length and number of unfilled grains per panicle, which in the indication of the

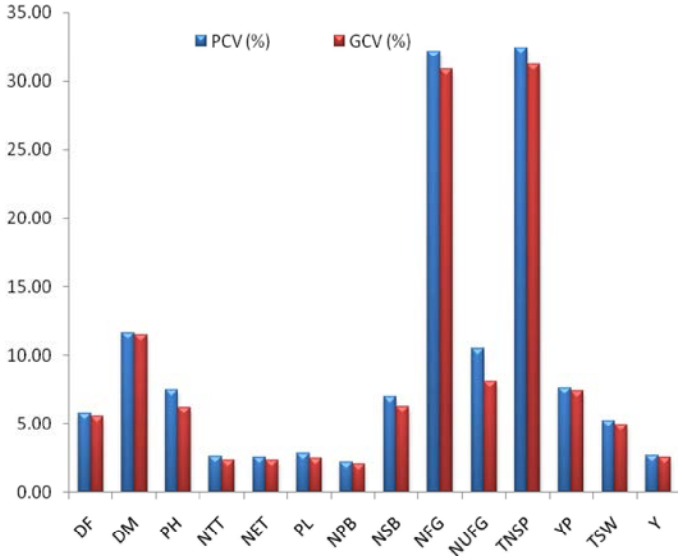

Fig. 1: Genotypic and phenotypic coefficient of variation in *Oryza sativa* L

Table 2: Analysis of variance (ANOVA) for yield and its related characters of 27 genotypes in *Oryza sativa* L

		Mean sum of squares (MSS)		
	Characters	Replication	Genotypes	Error
Sl. No.	df	2	26	52
1	Days to flowering	581.123	37.844**	2.803
2	Days to maturity	561.123	66.594**	1.675
3	Plant Height (cm)	891.590	355.106**	7.039
4	Total no. of tiller/ plant	84.303	7.431**	0.480
5	No. of effective tiller/ plant	75.250	7.415**	0.411
6	Panicle length (cm)	114.779	8.516**	0.844
7	No. of primary branches/panicle	40.920	1.628*	0.223
8	No. of secondary branches/ panicle	424.515	48.760**	3.755
9	No. of filled grain /panicle	11171.155	1256.086**	34.253
10	No. of unfilled grain of main/panicle	10263.601	1130.072**	35.308
11	Total no. of spikelet/ panicle	32.772	100.390**	18.890
12	Yield/ plant (g)	556.075	48.936**	1.346
13	1000 seed weight (g)	124.790	11.853**	1.111
14	Yield (ton/ hectare)	45.644	1.442*	0.284

** = Significant at 1% level of probabilities,*=Significant at 5% level of probabilities, df=Degrees of freedom

Table 3: Estimation of genetic parameters of 27 genotypes in *Oryza sativa* L

Parameters	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	ECV(%)
Days to flowering	47.82	45.01	2.80	5.71	5.54	1.38
Days to maturity	56.31	55.14	1.18	11.59	11.47	1.67
Plant Height (cm)	23.06	16.02	7.04	7.42	6.18	4.10
Total no. of tillers/ plant	2.80	2.32	0.48	2.58	2.35	1.07
No. of effective tillers/ plant	2.75	2.33	0.41	2.56	2.36	0.99
Panicle length (cm)	3.40	2.56	0.84	2.85	2.47	1.42
No. of primary branches/panicle	2.02	1.80	0.22	2.20	2.07	0.73
No. of secondary branches/ panicle	20.09	16.34	3.76	6.92	6.24	2.99
No. of filled grain /panicle	433.56	398.25	35.31	32.16	30.82	9.18
No. of unfilled grain of /panicle	46.06	27.17	18.89	10.48	8.05	6.71
Total no. of spikelet/ panicle	441.53	407.28	34.25	32.45	31.17	9.04
Yield/ plant (g)	23.88	22.53	1.35	7.55	7.33	1.79
1000 seed weight (g)	11.36	10.25	1.11	5.20	4.94	1.63
Yield (ton/ hectare)	3.00	2.72	0.28	2.68	2.55	0.82

σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and ECV = Environmental Coefficient of Variation

Table 4: Estimation of heritability and genetic advance of 27 genotypes in *Oryza sativa* L

Parameters	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to flowering	94.14	13.41	11.08
Days to maturity	97.91	15.14	10.52
Plant Height (cm)	69.48	6.87	6.17
Total no. of tillers/ plant	82.84	2.85	21.45
No. of effective tillers/ plant	85.03	2.90	22.75
Panicle length (cm)	75.19	2.86	11.99
No. of primary branches/panicle	88.99	2.61	24.37
No. of secondary branches/ panicle	81.31	7.51	22.44
No. of filled grains /panicle	91.86	39.40	25.42
No. of unfilled grains/panicle	58.99	8.25	41.77
Total no. of spikelet/ panicle	92.24	39.93	22.85
Yield/ Plant (g)	94.36	9.50	26.98
1000 seed weight (g)	90.22	6.26	29.63
Yield (ton/ hectare)	90.54	3.23	38.58

more influence of the environment over this two characters. The slight difference between GCV and PCV was also reported by [24-26].

Phenotypic and genotypic variance for days to flowering was observed as (47.82) and (45.01), respectively with little differences between them, suggested considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (PCV) (5.71) was higher than the genotypic coefficient of variation (GCV) (5.54) (Table 3). There was a little difference between GCV and PCV on this character. Such values of GCV with least difference were also observed by Padmaja [27] for days to flowering. Phenotypic and genotypic variance for days to maturity was observed (56.31) and (55.14), respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling this trait. The moderate phenotypic coefficient of variation (PCV) (11.59%) was close to genotypic coefficient of variation (GCV) (11.47%) (Table 4), which suggested that environment has a role on the expression of this trait. Phenotypic variance and genotypic variance were observed as 23.06 and 16.02 respectively. The phenotypic variance appeared to be higher than the genotypic variance which suggested considerable influence of environment on the expression of the genes controlling this trait. The estimates of PCV (7.42) and GCV (6.18) also indicated presence of variability among the genotypes for this trait (Table 4). Ketan and Sarker [28] also showed that the PCV was higher than the GCV in this character. Phenotypic variance and genotypic variance were observed as 2.80 and 2.32, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The PCV (2.58) and GCV (2.35) were relatively low indicating the apparent variation not only due to genotypes but also due to the influence of environment (Table 3). Tuwar [29] found high GCV and PCV value in this character. Phenotypic variance and genotypic variance were observed as 2.7 and 2.33, respectively. The phenotypic variance appeared to be higher than the genotypic variance which suggested considerable influence of environment on the expression of the genes controlling this trait. Relatively low difference between PCV (2.56%) and GCV (2.36%) value indicating the apparent variation not only due to genotypes but also due to the influence of environment. Length of panicle showed phenotypic variance (3.40) and genotypic variance (2.56) with low difference between them indicating that they were minimum responsive to environmental factors for their phenotypic expression and relatively lower PCV (2.85%) and GCV (2.47%) indicating that the genotype has minimum variation for this trait (Table 3). In this respect, Padmaja [27] found low GCV and PCV along with little difference between them. Phenotypic variance and genotypic variance were observed as 3.40 and 2.56, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggesting considerable influence of environment on the expression of the genes controlling this trait and relatively low difference between PCV (2.20%) and GCV (2.07%) value indicating the apparent variation not only due to genotypes but also due to the influence of environment (Table 3). Karim [30] found higher differences between GCV and PCV for this trait Phenotypic variance and genotypic variance were observed as 20.09and 16.34, respectively. Low PCV (6.92%) and GCV (6.24%) values are closely to each other which indicated the presence of considerable variability among the genotypes for this trait

(Table 3). Ketan and Sarker [28] also observed PCV value was higher than the GCV value in number of secondary branches per panicle.

Phenotypic variance and genotypic variance were observed as 441.53 and 407.28, respectively. Higher estimate of PCV (32.45%) and GCV (31.17%) values indicated presence of considerable variability among the genotypes for this trait. The phenotypic and genotypic variances for this trait were 433.56 and 398.25, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggesting considerable influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were (32.16%) and (30.82%) respectively for number of filled grain per panicle which indicating that medium variation exists among different genotypes (Table 3). Similar variability was also recorded by Bisne [31]. The phenotypic and genotypic variances for this trait were 46.06 and 27.17, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggesting considerable influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 10.48% and 8.05%, respectively for number of unfilled grain per panicle which indicated that medium variation exists among different genotypes. The yield/plant showed high genotypic (22.53) and phenotypic (23.88) variance with little differences indicating that they were low responsive to environmental factors. The phenotypic coefficient of variation (7.55%) was greater than genotypic coefficient of variation (7.33%) (Table, 3). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. Dhanwani [32] and Singh [33] found higher phenotypic co-efficient of variation (PCV) than the genotypic co-efficient of variation (GCV) for spikelet yield/plant. Thousand seed weight showed genotypic (10.25) and phenotypic (11.36) variance with little differences indicating that they were low responsive to environmental factors. The phenotypic coefficient of variation (5.20%) and genotypic coefficient of variation (4.94%) were close to each other. There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. The phenotypic variances and genotypic variances for this trait were 3.00 and 2.72, respectively. The values were very close to each other indicated less environmental influences on this trait. The values of GCV and PCV were 2.55% and 5.71% indicating lower environmental influence in the expression of this character (Table 3).

Heritability and Genetic Advance: The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. The estimates of heritability are more advantageous when expressed in terms of genetic advance, knowledge of heritability of a character is important as it indicate the possibility and extend to which improvement is possible through selection.

Days to flowering exhibited high heritability (94.14%) with moderate genetic advance as percentage of mean (11.08%) indicated that this trait was controlled by additive gene and moderate possibility of selecting genotypes that would mature earlier (Table 4). This results support the reports of Hasan [34] and Singh [35]. Days to maturity showed high heritability (97.91%) with moderate genetic advance as percentage of mean (10.52%) indicated that this trait was controlled by additive gene and moderate possibility of selecting genotypes that would mature earlier. Plant height showed high heritability (69.48%) with low genetic advance as percentage of mean of (6.17%) which indicated that this trait was controlled by non-additive gene. Total number of tiller per plant showed high heritability (82.84%) with high genetic advance as percentage of mean (21.45%) indicating that this trait was controlled by additive gene and higher possibility of selecting genotypes. High heritability coupled with high genetic advance for this trait was also observed. Total number of effective tiller per plant showed high heritability (85.03%) with high genetic advance as percentage of mean (22.75%) indicating that this trait was controlled by additive gene and higher possibility of selecting genotypes. Satheeshkumar [16] also found high heritability with high genetic advance as percentage of mean for the character of effective tillers per plant. Panicle length showed high heritability (75.19%) with medium high genetic advance as percentage of mean (11.99%) indicating that this trait was controlled by additive gene. High heritability coupled with moderate genetic advance for this trait was observed by Padmaja [27]. Number of primary branches per panicle exhibited moderately high heritability (88.99%) with high genetic advance as percentage of mean of (24.37%) which revealed that this trait was controlled by additive gene (Table 4). As a whole, the high heritability and the consequent high genetic advance indicated the higher possibility of selecting genotypes for this trait.

Number of secondary branches per panicle exhibited moderately high heritability (81.31%) with high genetic advance as percentage of mean (22.44%) such results revealed that this trait was controlled by additive gene (Table 4). As a whole, the high heritability and the

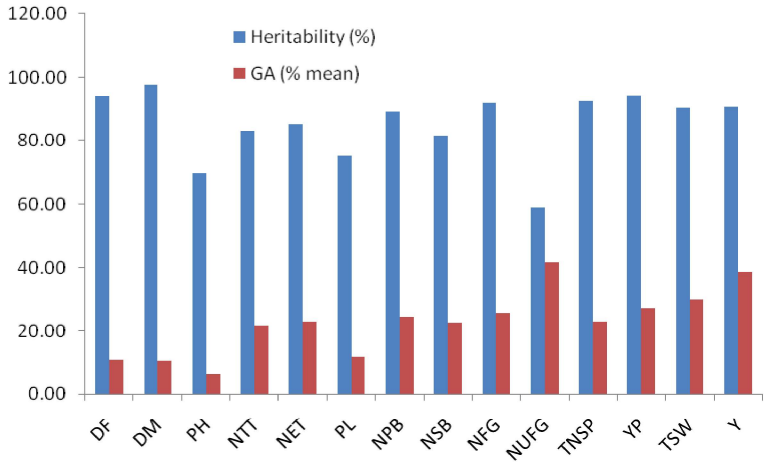

Fig. 2: Heritability and Genetic Advance as percentage of mean in *Oryza sativa L.*

consequent high genetic advance indicated the higher possibility of selecting genotypes. High heritability coupled with high genetic advance was also found by Ketan and Sarkar [28].

Total number of spikelet per panicle exhibited high heritability (92.24%) with high genetic advance as percentage of mean (22.85%), such results revealed that this trait was controlled by additive gene. As a whole, the high heritability and the consequent high genetic advance indicated the higher possibility of selecting genotypes. Dhanwani [32] also found such results. Number of filled grain per panicle exhibited moderately high heritability (91.86%) with high genetic advance as percentage of mean (25.42%), such results revealed that this trait was controlled by additive gene. As a whole, the moderately high heritability and the consequent high genetic advance indicated the effective possibility of selecting genotypes. Singh [19] and Tuwar [29] also found high heritability coupled with high genetic advance as percentage of mean for the trait of filled grains per panicle. Number of unfilled grain per panicle exhibited moderate heritability (58.99%) with and high genetic advance as percentage of mean (41.77%), such results revealed that this trait was controlled by non-additive gene. Similar results for number of grains per panicle and number of filled grains per panicle were previously supported by Edukondalu [36]. Seed yield per plant in dried condition showed high heritability (94.36%) with high genetic advance as percentage of mean (26.98%) indicating this trait was controlled by additive gene and selection for this character would be more effective. High heritability coupled with high genetic advance for this trait was also observed by Mishra and Verma [37]. Thousand seed weight exhibiting high heritability (90.22%) with high genetic advance as percentage of mean (29.63%) revealed that this trait was controlled by additive gene and selection of this character would be more effective. Similar results for 100 seed weight, number of unfilled grains per panicle and number of effective tillers per plant were earlier recorded [38-43] respectively. Yield (ton per hectare) showed high heritability (90.54%) with high genetic advance as percentage of mean (38.58%) indicated this trait was controlled by additive gene and selection for this character would be highly effective (Table 4 and Figure 2). Significant positive correlations at both genotypic and phenotypic levels were recorded for flag leaf area with yield per plant which was supported by Devi [44].

CONCLUSION

In conclusion, the present study identified the presence of adequate genetic variability among 27 tested genotypes. Therefore, it is advisable to repeat the study at least more than one season considering major rice growing areas to make sound recommendations. Moreover, it is recommended that future rice research explore molecular means to further confirm the outcome of these study findings. These estimates suggested that selection on the basis of these traits is helpful for hybridization program otherwise no genetic gain can be achieved.

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