



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(9): 2292-2295
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www.thepharmajournal.com
Received: 10-06-2022
Accepted: 30-08-2022

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Assessment of genetic variability, heritability and genetic advance for yield and its contributing traits in Upland rice (*Oryza sativa* L.) genotypes of Manipur

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Abstract

The present experiment was conducted at experimental field of Department of Genetics and Plant Breeding, College of Agriculture, Central Agricultural University, Imphal during *kharif*, 2021 to study the extent of genetic variability, heritability and genetic advance in fifty rice genotypes along with five checks for fifteen yield traits under upland condition. The analysis of variance showed highly significant variations among all the genotypes for all the yield and its contributing traits, showing the presence of significant amount of variance. Proline content, grain yield per plant, number of unfilled grains per panicle, flag leaf length and plant height showed high estimates of phenotypic and genotypic coefficient of variation. This suggests that direct selection for these traits will result in genetic improvement. High board sense heritability estimates are observed for character days to 50% flowering, days to maturity, plant height, culm diameter, flag leaf length, panicle length, number of filled grains per panicle, number of unfilled grains per plant, grain yield, 1000 grain weight, proline content, biological yield and harvest index. High heritability coupled with high genetic advance as percent mean were observed for grain yield per plant, plant height, number of filled grains per panicle, number of unfilled grains per panicle, flag leaf length, culm thickness, biological yield and harvest index. This indicates that additive gene action influenced the inheritance of these traits, thus providing scope for further improvement through selection.

Keywords: Genetic variability, heritability, genetic advance, rice, proline, upland

Introduction

Rice ($2n=2x=24$) belongs to grass family i.e, Poaceae (Graminae), sub-family Bamboosoideae, tribe Oryzaceae. Rice (*Oryza sativa* L.) has been cultivated as a crop for a minimum of 8000 years (Maclean *et al.*, 2002)^[13] and currently 50% of the world's population depends on rice as their staple diet. Rice is mostly comprised of carbohydrate, which makes up 80% of its total dry weight. Most of the carbohydrate in rice is starch. India is the second largest producer of rice after China and it is the top country by rice exports quantity in the world. The area, production and productivity of rice in India during 2019-2020 is 43.78 million hectares, 118.43 million tonnes and 2705 kg/ha respectively (Anonymous, 2020). The rainfed upland environment is outspread in most of the states, across the country, covering about 7 million hectares with maximum (>90%) area coverage in Eastern India including NE region. Large area in the states of Jharkhand, Orissa, Chhattisgarh, Eastern Uttar Pradesh, parts of Assam, West Bengal and North-Eastern states are covered under upland rice as it is the staple diet of the populations of this region, and land holding which are mostly undulating, allow only rice to be grown during the monsoons. To overcome the effect of water stress in upland condition, upland rice plants have evolved adaptive mechanisms like metabolic responses such as accumulation of organic osmolytes such as proline and soluble sugars (Singh *et al.*, 2013)^[23]. Proline accumulation is maximum during the flowering stage. Developing a high yielding variety with stable performance, largely depends on the extent of variability of desirable characters in the population. The knowledge of genetic variability present in rice crop for the trait under improvement is of great importance for the success of any plant breeding programmes. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more useful in estimating the gain under selection than heritability estimates alone. Therefore, the present study was conducted to assess the heritability, genetic advance and genetic variability of upland genotypes of rice for yield contributing traits.

Materials and Methods

The materials for the present investigation consist of 50 upland genotypes of rice including 5 checks namely Bhalum-V, Sahbhagi, CAU R2, IR-64 and Swarna. These genotypes were sown in Randomized Block Design (RBD) with three replications at experimental field of Department of Genetics and Plant Breeding, College of Agriculture, CAU, Imphal during *kharif* 2021 and laboratory work was done at PG Lab, Department of Genetics and Plant Breeding, College of Agriculture, CAU. Each genotype was sown as row to row and plant to plant distance of 20 cm and 15 cm, respectively. The observations on 15 quantitative characters were recorded based on ten randomly taken plants from each genotype for some observations and for other observations will be recorded on whole plot basis. Data was recorded on flag leaf length, culm thickness, panicle length, plant height, number of panicles per plant, number, number of effective tillers per plant, number of filled grains per panicle, number of unfilled grains per panicles, 1000 grain weight, grain yield per plant, biological yield per plant, harvest index per plant, proline content, days to 50% flowering and days to maturity. Proline content was estimated for the leaves using the method of Bates *et al.* (1973) [5]. Heritability in a broad sense was calculated by the formula suggested by Allard (1960) [3]. Expected genetic advance (GA) was calculated by the method suggested by Johnson *et al.* (1955) [11]. The coefficient of variation for different characters was estimated by formula suggested by Burton and Devane (1953) [8].

Results and Discussions

Analysis of variance

Analysis of variance was used to estimate the degree of variation of studied characters among 50 upland genotypes of rice and the results are presented in table 1. For all the characters studied, the study of variance indicated highly significant variations among the 50 upland rice genotypes, suggesting significant genetic variation in the material. For all yield contributing characters tested, an F-test revealed that the values of mean sum of squares were significant (at 1% level of significance). High genetic variability for different yield contributing traits in rice was also reported by Singh *et al.*, (2021) [22] and Patel *et al.*, (2014) [17].

Phenotypic and genotypic coefficient of variation (PCV & GCV)

Phenotypic variability refers to total variation which is observable in a character. It includes both genotypic and environmental variation. Genotypic variability refers to variability which remains unaffected by environmental conditions, this type of variability is more useful to a plant breeder for exploitation in selection or hybridization. For all yield contributing characters, the value for GCV and PCV ranged from low to high. For all characters, the GCV was smaller than PCV, this suggests a masked influence of the environment on the expression of the characters. (Table 2). The high estimates of the GCV were recorded for proline content (36.03) followed by grain yield per plant (24.37), number of unfilled grains per panicle (23.83), flag leaf length (21.49) and plant height (20.8). The moderate estimates of the GCV were recorded for number of filled grains per panicle (18.21) followed by culm thickness (17.92), harvest index (13.49), biological yield (13.42), number of panicles per plant (11.45), number of effective tillers per plant (11.45) and

panicle length (10.09) whereas low estimates of the GCV were recorded for days to 50% flowering (8.52) followed by 1000 grain weight (8.33) and days to maturity (8.01) (Table 2). Similar results recorded by Padmaja *et al.*, (2008) [16] for genotypic coefficient of variation (GCV) in days to 50% flowering and panicle length and also recorded by Srujana *et al.*, (2017) [24] for number of effective tillers per plant, flag leaf length, and number of panicles per plant and Patel *et al.*, (2014) [17] for days to maturity. The results were in unison with the findings of Biju *et al.*, (2020) [6] for culm thickness and Mohan *et al.* (2011) [14] for plant height and Singh *et al.*, (2020) [20] for number of filled grains per panicle and Saha *et al.*, (2019) [18] for number of unfilled grains per panicle and Akhand *et al.*, (2018) [2] for grain yield per plant and Aditiya *et al.*, (2013) [1] for 1000 grain weight and Singh *et al.*, (2018) [21] for proline content and Neha *et al.*, (2018) [15] for biological yield and Dey *et al.*, (2021) [9] for harvest index.

Heritability

Heritability in broad sense refers to the ratio of genotypic variance to the phenotypic variance or total variance. Heritability is a good index of the transmission of characters to the offsprings from their parents. Heritability was classified as low (<30%), medium (30-60%) and high (>60%) as suggested by Johnson *et al.*, (1955) [11]. In the present study, highest broad sense heritability value was estimated for proline content (99.98%) followed by days to maturity (99.11%), days to 50% flowering (99.09%), culm thickness (99.06%), plant height (98.98%), biological yield (94.02%), 1000 grain weight (93.1%), flag leaf length (92.35%), panicle length (88.74%), number of filled grains per panicle (83.92%), number of unfilled grains per panicle (82.49%), grain yield per plant (80.45%) and harvest index (61.71%). Moderate heritability estimates are observed for number of effective tillers (42.51%) and number of panicles per plant (42.51%). The similar results were found by Vivek *et al.*, (2005) [25] for moderate heritability estimates for number of effective tillers and number of panicles per plant. Lingaiah *et al.*, (2019) [12] recorded similar results for 1000 grain weight and panicle length. Similar results recorded by Gupta *et al.*, (2021) [10] for days to 50% flowering and also recorded by Srujana *et al.*, (2017) [24] for number of effective tillers per plant, flag leaf, biological yield, harvest index, grain yield per plant, effective tillers per plant and 1000 seed weight and also recorded by Biju *et al.*, (2020) [6] for culm thickness and Singh *et al.*, (2018) [21] for proline content. It indicates the heritability is due to additive gene effect and selection may be effective.

Genetic Advance

Genetic advance refers to the improvement in the mean genotypic value of selected plants over the parental population. Genetic advance or genetic gain is a more useful estimate which reflects the possible improvement in the new population through selection in contrast to the original population. High genetic advance was recorded for proline content (512.87) followed by plant height (48.36) and number of filled grains per panicle (44.96). Moderate genetic advance was recorded for days to maturity (19.59), culm thickness (17.63), Days to 50% flowering (16.32), harvest index (15.66), flag leaf length (12.66) and grain yield (10.03). Biological yield (8.19), number of unfilled grains per panicle (7.92), panicle length (4.64), 1000 grain weight (4.09),

number of effective tillers per plant (1.06) and number of panicles per plant (1.06) showed the low genetic advance. Moderate estimates of genetic advance as per cent of mean was recorded for characters days to 50% flowering (17.47%), days to maturity (16.42%), number of effective tillers per plant (15.38%), panicle length (19.58%), number of panicles per plant (15.38%) and 1000 grain weight (16.55%) High estimates of genetic advance as per cent of mean was recorded for characters plant height (42.63%), culm diameter (36.74%), flag leaf length (42.53%), number of filled grains per panicle (34.37%), number of unfilled grains per panicle (44.58%), grain yield (45.03%), proline content (74.23%) biological yield (26.8%) and harvest index (21.83%) (Table 2). Similar results were found by Vivek *et al.*, (2005) [25], Singh *et al.*, (2020) [20], Biju *et al.*, (2020) [6] and Singh *et al.*, (2018) [21]. High heritability coupled with high genetic advance as per cent mean were observed for grain yield per plant, plant height, number of filled grain per panicle, number of unfilled grains per panicle, culm thickness, flag leaf length, proline content, biological yield and harvest index. This indicated that these characters were controlled by additive type gene action and selection may be effective for these characters. Similar results were found by Bisne *et al.*, (2009) [7] for harvest index and grain yield per plant and also found

by Sameera *et al.*, (2015) [19] for number of filled grains per panicle and Biju *et al.*, (2020) [6] for culm thickness and Singh *et al.*, (2018) [21] for proline content.

Table 1: Analysis of variance for yield contributing characters in rice

S. No	Characters	Mean sum of Squares		
		Replication	Treatments	Error
	Degree of freedom	2	49	98
1	Days to 50% flowering	4.05	191.69**	1.73
2	Days to maturity	6.02	276.29**	2.46
3	Plant height (cm)	47.53	1687.18**	17.08
4	No. of effective tillers per plant	6.66	4.35**	2.5
5	Culm thickness (mm)	6.14	223.86**	2.09
6	Flag leaf length (cm)	23.95	132.92**	10.17
7	Panicle length (cm)	2.34	19.36**	2.18
8	No. of panicles per plant	6.66	4.35**	2.5
9	No. of filled grain per panicle	829.29	2029.54**	326.35
10	No. of unfilled grain per panicle	22.01	65.09**	11.39
11	Grain yield/ plant (g)	59.11	109.83**	21.47
12	1000 grain weight (g)	2.59	13.71**	0.95
13	Proline content ($\mu\text{g/g}$)	52.34	185991.17**	21.05
14	Biological yield (g)	8.47	53.71**	3.21
15	HI (%)	324.29	455.44**	174.37

*,**Significant at 5% and 1% level of probability respectively

Table 2: Genotypic and phenotypic coefficient of variability, heritability and genetic advance for different characters in rice

Sl. No.	Character	PCV (%)	GCV (%)	h^2_b (%)	GA	GA as % of mean
1	Days to 50% flowering	8.56	8.52	99.09	16.32	17.47
2	Days to maturity	8.04	8.01	99.11	19.59	16.42
3	Plant height (cm)	20.91	20.8	98.98	48.36	42.63
4	No. of effective tillers per plant	17.56	11.45	42.51	1.06	15.38
5	Culm thickness (mm)	18.01	17.92	99.06	17.63	36.74
6	Flag leaf length (cm)	22.36	21.49	92.35	12.66	42.53
7	Panicle length (cm)	10.71	10.09	88.74	4.64	19.58
8	No. of panicles per plant	17.56	11.45	42.51	1.06	15.38
9	No. of filled grain per panicle	19.88	18.21	83.92	44.96	34.37
10	No. of unfilled grain per panicle	26.24	23.83	82.49	7.92	44.58
11	Grain yield per plant (g)	27.17	24.37	80.45	10.03	45.03
12	1000 grain weight (g)	8.63	8.33	93.1	4.09	16.55
13	Proline content ($\mu\text{g/g}$)	36.04	36.03	99.98	512.87	74.23
14	Biological yield (g)	13.84	13.42	94.02	8.19	26.8
15	HI (%)	17.17	13.49	61.71	15.66	21.83

Conclusion

Among the characters, proline content, grain yield per plant, number of unfilled grains per panicle, flag leaf length and plant height exhibited high estimate of GCV and PCV. High heritability along with high genetic advance as percent of mean was observed for grain yield per plant, plant height, number of filled grain per panicle, number of unfilled grains per panicle, culm thickness, flag leaf length, proline content, biological yield and harvest index. It indicates that the heritability is due to additive gene effect and variation exists in the genotypes, which provides opportunities for genetic improvement through selection.

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