Studieson Variability, Heritability, and Genetic advance inPaddy (*Oryza sativa* L.) withspecial reference to Satna, Madhya Pradesh

Abstract:

Fourteen diverse cultivars of paddy grown in a Randomized Block Design (RBD) at AKS University, Satna, during *Kharif*season on July 2022. Data were collected foreleven quantitative traits and estimated forvariance,geneticvariability, heritability and genetic advance.The design of the experiment indicated highly significant differences for all the characters due to treatments. The analysis of variance indicated the existence of sufficient amount of variability among genotypes for all the studiedcharacters. The maximum GCV along with PCV was observed forgrain yield per plant (g) followed by panicle length (cm), number of spikelets per panicle, harvest index (%), kernel length (mm), number of panicles per plant. Higher estimates (h^2b) >80% were observed for Number of spikelets per panicle, days to development, plant level (cm), number of panicles per plant, test weight (g), grain yield per plant (g), panicle length (cm). High heritability combined with high hereditary development for the person number of panicles per plant, number of spikelets per panicle, panicle length (cm), test weight (g) and grain yield per plant (g) indicating that these characters could be prominently governed by additive gene action.

Keywords: Paddy, Variance, variability, heritability, genetic advance

Introduction:

Paddy is the world's most significant grain crop; it is the fundamental wellspring of food and calories for about portion of the humanity (Khush, 2005). For development this harvest require damp and hot climate. Rice (*Oryza sativa* L., 2n = 24) has a place with familypoaceae. It is begun in South East Asia. Other than being the central wellspring of starch and protein, it likewise gives minerals and dietary fiber (Verma*et al*., 2006). “Additionally, it contains niacin, thiamine, and riboflavin at high levels. Asia is viewed as "rice bowl" of the world, and it creates and consumes more than 90 % of world rice. China is the biggest maker of rice followed by India which produces 148.99 and 129.47 million metric lots of rice each year individually” (Annonymous, 2021-22). “Chhattisgarh is known as "rice bowl" of India. There are two developed types of rice I. e. *Oryza sativa* Linn. andStaud's*Oryzaglaberrima*. *Oryzaglaberrima*, on the other hand, is only grown in West Africa, its original region, while *Oryza sativa* is grown worldwide Linares”, (2002; Fageria and Baligar, (2003).

To do any reproducing program, it is fundamental for know the hereditary variety of yield contributing qualities, alongside their communication with yield. Hereditary improvement for quantitative characteristics relies upon the nature and measure of changeability present in the hereditary material and the degree to which the beneficial attributes are heritable Namrata*et al*.(2016). The information about hereditary changeability of yield contributing characters, bury relationship among them and their connection with yield are fundamental for a viable harvest improvement program Nayak*et al*.(2016). Breeders are able to predict the nature of the subsequent generation, make the appropriate selection, and evaluate the magnitude of genetic improvement through selection with the assistance of knowledge about heritability TuhinaKhatun*et al*.(2015) Devi B. (2016). What's more, high hereditary development combined with high heritability offers the best condition for choice for a particular quality Larik and Rajput.(2000). Estimates of heritability reveal the proportion of variation that can be passed on to offspring in subsequent generations. Genetic advancement reveals the anticipated genetic gain resulting from superior selection.

Material and method

The present investigation was conducted during *Kharif*, 2022 at Research farm, Genetics and Plant Breeding, AKS University, Sherganj, Satna, Madhya Pradesh. The material consists14 diverse genotypes of rice collected from different sources through the help from Department of Genetics & Plant Breeding, Faculty of Agriculture Science, AKS University, Satna (M. P.). The genotypes used in the study showed a wide variety of variation in yield and yield contributing characters evaluated in Randomized Block Design. The entire experimental field divided in 3 blocks of equal size and each block had 14 plots. Each plot was consisted of 4 rows 2 meters length, following row to row spacing of 25 cm. and plant to plant spacing of 15 cm.

Eleven observations of yield contributing characters were recorded. In each plot, five competitive plants were randomly selected for recording observations for all the eleven quantitative characters, which were recorded on the plot basis. The data were recorded for Days to 50% flowering, Plant height (cm), Number of panicles per plant, Panicle length (cm), Number of spikelets per panicle, Kernel length (mm), Test weight (g), Days to maturity, Harvest index (%), Biological yield per plant (g), and Grain yield per plant (g)

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme, (1967). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) was estimated by the formula suggested by Burton and de Vane, (1953). Heritability in broad sense (h^2b) was estimated using the formula suggested by Burton and de Vane, (1953). Genetic advance was calculated by the method suggested by Johnson *et al*.(1955).

Result and discussion

The analysis of variance for the design of the experiment involving 14 strains/varieties of paddy was evaluated in Randomized Block Design with three replications for the 11 quantitative characters.

Table 1 shows the analysis of variance for the experiment's design. The outcomes uncovered profoundly tremendous distinction for every one of the characters which communicated enormous measure of variety among 14 genotypes of rice.

Only one characteristic, panicle length (cm), showed a non-significant difference due to replications. These sort of similar outcomes were additionally detailed by Devi B.(2016)Lakshmi*et al*.(2021) and Manivelan*et al*.(2022).

The mean performance, grand means, range, GCV, and PCV of 14 genotypes of paddy for 11 quantitative characters are presented in

Table: 2. The magnitude of GCV ranged from grain yield per plant (g) (37.51) to days to maturity (3.23). The magnitude of PCV ranged from grain yield per plant (g) (39.00) to days to maturity (3.24). The maximum GCV along with PCV was observed forgrain yield per plant (g) followed by panicle length (cm), number of spikelets per panicle, harvest index (%), kernel length (mm), number of panicles per plant. This is an indicative of less amenability of these characters to environmental fluctuations and hence, greater emphasis should be given to these traits. United consequences of assessment of hereditary boundary uncovered that, the adequate changeability present among the genotypes, which gives adequate extension to additional rearing system. These results are in conformity with Devi*et al*.(2012), Lakshmi *et al*.(2021); Kumar *et al*.(2022) and Manivelan*et al*.(2022).

Heritability estimates are used to predict expected advance under selection so that breeders are able to anticipate improvement from different of selection intensity. Burton and De Vane (1953) suggested that “the GCV along with heritability estimate could provide better picture of the genetic advance to be expected by phenotypic selection”. Heritability h² (Broad Sense), h² (Broad Sense)%, Genetic Advancement as estimated for all the characters and has been presented in **Table: 3.**

Higher estimates (h^2b) >80% were observed for all the characters except number of pods per plant. All of the characters under study had their general heritability calculated. The heritability values went from 80.99 to 99.33 %. The most extreme worth of heritability was shown by Number of spikelets per panicle (99.33%). The characters days to development (98%), plant level (cm) (96.43%), number of panicles per plant (96.42%), test weight (g) (96.17%), grain yield per plant (g) (92.48%), panicle length (cm) (91.33%) and biological yield per plant (g) (91.08%) likewise showed higher upsides of heritability. It is suggested that the characters are least influenced by the environmental factors and also indicates the dependency of phenotypic expression which reflect the genotypic ability of strains to transmit the gene to their progenies. Similar results were reported earlier byVeni and Rani (2006); Das and Ghosh (2010), and others have also reported findings that are comparable, Patel *et al*. (2018);Acharya*et al*.(2019); Lakshmi *et al*.(2021);Sreelakshmi and Babu (2020); Kumar *et al*.(2022), as well as Manivelan*et al*.(2022) in their respective studies.

Genetic advance is a measure of genetic gain under selection which depends upon main factors viz., genetic variability, heritability, and selection index Allard RW, (1960).The expected genetic advance as percent of mean at 5% ranged from grain yield per plant (g) (74.31%) to days to maturity (6.66%). High estimate of expected genetic advance as percent of mean at 5% were found for number of pod per cluster followed by grain yield per plant (g) (74.31), test weight (g) (48.14), panicle length (cm) (45.53), number of spikelets per panicle (44.39) and harvest index (%) (37.48). High heritability combined with high hereditary development for the person number of panicles per plant, number of spikelets per panicle, panicle length (cm), test weight (g), biological yield per plant (g) and grain yield per plant (g) indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement. High degree of heritability estimate along with high genetic advance of genetic advance was also revealed earlier byVeni and Rani (2006); Das and Ghosh (2010); Patel *et al*. (2018);Acharya*et al*.(2019); Lakshmi *et al*.(2020);Sreelakshmi and Babu (2020); Kumar *et al*.(2022), as well as Manivelan*et al*. (2022)in their respective studies.in their respective studies.

Conclusion

The design of the experiment indicated highly significant differences for all the characters among treatments. Wide range of variation was found for all the studied characters of pea.The maximum GCV along with PCV was observed for grain yield per plant (g) followed by panicle length (cm), number of spikelets per panicle, harvest index (%), kernel length (mm), number of panicles per plant. Higher estimates (h^2b) >80% were observed for Number of spikelets per panicle, days to development, plant level (cm), number of panicles per plant, test weight (g), grain yield per plant (g), piece length (mm) and natural yield per plant (g)indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement.

Table 1 Analysis of variance for 11 characters in 14 genotypes of paddy.

Sr. No.	Characters	Mean sum of squares		
		Replications d.f. = 2	Treatment d.f. = 13	Error d.f. = 26
1	Days to 50% flowering	20.738**	67.269***	2.610
2	Plant height (cm)	18.002**	175.076***	2.136
3	Number of panicles per plant	2.1800***	10.5946***	0.1297
4	Panicle length (cm)	2.473	48.857***	2.026
5	Number of spikelets per panicle	40.17***	1264.61***	2.85
6	Kernel length (mm)	0.30310*	2.25634***	0.06925
7	Test weight (g)	18.199***	38.320***	0.502
8	Days to maturity	32.667***	42.791***	0.010
9	Harvest index (%)	82.163***	122.030***	8.853
10	Biological yield per plant (g)	13.976*	89.880***	2.842
11	Grain yield per plant (g)	9.799**	45.982***	1.213

Significant.codes:'***' 0.001 '**' 0.01 '*' 0.05 .

Table 2 Estimation of genetic parameters for 11 characters in 14 genotypes of paddy.

Sr. No.	Characters	Range		Grand Mean	Critical Difference (CD) 5%	Genotypic variance	Phenotypic variance	GCV	PCV	CV%
		Min.	Max.							
1	Days to 50% flowering	70.00	88.00	76.83	2.71	21.55	24.16	6.04	6.39	2.10
2	Plant height (cm)	95.36	124.61	110.51	2.45	57.64	59.78	6.87	6.99	1.32
3	Number of panicles per plant	8.60	16.00	10.74	0.60	3.48	3.61	17.38	17.70	3.35
4	Panicle length (cm)	6.80	23.40	16.81	2.38	15.61	17.63	23.49	24.97	8.46
5	Number of spikelets per panicle	63.59	128.61	94.84	2.83	420.58	423.43	21.62	21.69	1.78
6	Kernel length (mm)	3.50	6.80	4.79	0.44	0.72	0.79	17.80	18.63	5.48
7	Test weight (g)	9.35	23.45	14.89	1.18	12.60	13.10	23.83	24.29	4.75
8	Days to maturity	107.00	123.00	116.76	0.01	14.26	14.27	3.23	3.24	0.01
9	Harvest index (%)	18.80	49.19	30.38	4.99	37.72	46.57	20.21	22.46	9.79
10	Biological yield per plant (g)	24.36	46.35	33.52	2.82	29.01	31.85	16.06	16.83	5.02
11	Grain yield per plant (g)	6.12	20.19	10.29	1.84	14.92	16.13	37.51	39.00	10.69

Table 3 Estimation of heritability and genetic advance 11 characters in 14 genotypes of paddy.

Sr. No.	Characters	Heritability (%) (h2)	Genetic advance (GA)	Genetic Advance as % means
1	Days to 50% flowering	89.20	9.03	11.75
2	Plant height (cm)	96.43	15.35	13.89
3	Number of panicles per plant	96.42	3.77	35.16
4	Panicle length (cm)	88.51	7.65	45.53
5	Number of spikelets per panicle	99.33	42.10	44.39
6	Kernel length (mm)	91.33	1.68	35.05
7	Test weight (g)	96.17	7.17	48.14
8	Days to maturity	98.00	7.78	6.66
9	Harvest index (%)	80.99	11.38	37.48
10	Biological yield per plant (g)	91.08	10.58	31.58
11	Grain yield per plant (g)	92.48	7.65	74.31

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