RESEARCH ARTICLE OPEN ACCESS

Variability, heritability and genetic advance analysis for grain yield in rice

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ABSTRACT

Ten diverse genotypes of rice (*Oryza sativa* L.) were crossed in a diallel fashion to study variability , heritability and genetic advance for 12 quantitative characters . A considerable amount of variability (gcv) varied from 5.95 for no. of leaves per tiller to 17.40 for grain yield per plant and the estimates of pcv varied from 7.08 for days to 50% flowering to 17.49 for grain yield per plant. The heritability estimates ranged from 0.721 for total biological yield per plant to 1.000 for plant height . Since the heritability in broad sense was estimated , therefore . other parameters should also be considered for selecting the genotypes. The genetic advance varied from 0.71 for no. of leaves per tiller to 46.23 for no. of spikelets per panicle. High estimates of genetic advance was reported for plant height , days to maturity , days to 50% flowering and total biological yield per plant . However, high heritability estimates was associated with high predicted genetic advance for plant height , days to maturity ,days to 50% flowering and no. of spikelets per panicle. The situation is encouraging since selection based on these characters being of additive in nature , is likely to be more effective for their improvement. As such phenotypic selection for those traits is likely to be more effective for their improvement. The estimates of phenotypic coefficient of variation were higher than those of genotypic coefficient of variation for all the traits except plant height. High estimates of heritability and genetic advance were obtained for plant height , number of spikelets per panicle , days to 50 per cent flowering and days to maturity . These traits were mostly governed by additive gene action. And these characters are important for the breeder to construct selection indices.

Key words: Diallel fashion, Variability, Heritability, Genetic advance

I. INTRODUCTION

Variation is the basis of plant breeding. Thus the success of any improvement programme will largely depend on the magnitude and range of variability in the available genetic stocks. To increase productivity and to bridge the gap between national average and the potential available. Under the present investigation a set of ten (10) genetic diverse stock of rice was assessed for twelve quantitative characters of economic importance to generate more basic information on the nature of genetic variability which will be great use to scientists in rice improvement work . A quantitative assessment of available germplasms for various yield and yield determining traits like numbers of tillers , number of grains per panicle , days to maturity , dry matter production , harvest index , etc. and their association with yield as well as among themselves is the basic necessity for a successful execution of any varietal improvement programme.

The genetic variability and combining ability provides the basis in selecting the suitable genotypes in any breeding programme(Tiwari and Jatav 2014). The effectiveness of selection depends on the magnitude of heritability for the traits being selected. The knowledge of heritability enables the breeder to predict the genetic gain under selection which will assist the breeder to formulate the suitable breeding methodology. Heritability and genetic advance are two selection parameters which were also estimated during the course of present investigation. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson, *et. al.* 1955). Heritability is a good index of the transmission of character from parents to their offspring (Falconer, 1981). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations.

Genetic advance is the measure of genetic gain under selection. The success of genetic advance under selection depends on genetic variability, heritability and selection intensity.

II. MATERIALS AND METHODS

Ten diverse parental line viz.(i)Basmati 370 (ii) Dular(iii)Govind(iv) H.U.R.52 (v) U.P.R. 79 (vi) I.R. 50(vii) Jaya (viii) Ratna (ix) Saket -4(x)Pusa 150 were crossed in all possible combinations to produce 45 F1 s (excluding reciprocals) during the rainy season of year 1996 . In the next season , that is , in rainy season of 1997, F1 plants along with their parents were grown in a randomized block design with three replications at Research Farm of the Department of Agricultural Botany Kisan (Post Graduate) College Simbhaoli, Ghaziabad, UP India. F1s and parents were planted in a single and three rows respectively of 4 meter length. Obviously , there were 45 rows of F1s and 30 rows of parental lines so, there were 75 rows in each replication. All together, there are overall 225 rows in the entire experiment. The row spacing was maintained at 20 cm and plant to plant 15 cm . During transplanting single seedling were planted per hill for recording observations on 12 quantitative characters viz., days to 50 % flowering , days to maturity, plant height , number of leaves per tiller, number of spikelets per panicle , panicle length , panicle number per plant , 1000 grain weight , grain yield per plant , straw yield per plant , total biological yield per plant and harvest index .

Variance as given by Panse and Sukhatme (1967). The genetic parameters were calculated as :

$$\sigma^2 g = \frac{MSt - MSe}{r}$$

where MSt= mean squares due to treatment
MSe=mean squares due to error
r=number of replications

and $\sigma^2 p = \sigma^2 g + \sigma^2 e$

where ,
$\sigma^2 p$=estimates of phenotypic variance
$\sigma^2 g$= estimates of genotypic variance
and $\sigma^2 e$=estimates of error variance

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were calculated using the formulae suggested by Burton (1952).

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} X100$$

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} X100$$

X=is the mean of the character .

Heritability (h^2) in broad sense was calculated according to Burton(1952).

$h^2 = \sigma^2 g / \sigma^2 p$

The customary symbol h^2 stands for the heritability it self and not for its square. The symbol derives from Wright (1921) terminology, where h^2 stands for the corresponding ratio of standard deviation.

The expected genetic advance at 5% intensity of selecting defferential was calculated for each character by following the formula .

GA= K. $\sigma^2 p . h^2$

Where
K= constant value of selection intensity e.g. 2.06 at 5% selection intensity Lush (1949).

III. RESULT AND DISCUSSION

The 55 genotypes of rice exhibited highly significant differences for all the 12 characters (depicted in Table 1) indicating the presence of genetic variability among the genotypes studied during the course of present investigation.

The estimates of phenotypic coefficient of variation (pcv) ranged from (7.08) for days to 50% flowering to (17.49) for grain yield per plant.The other characters which had high phenotypic coefficient of variation (pcv) were plant hight (17.12),panicle number per plant (14.21),total biological yield (13.37),panicles number per plant (14.21) and number of spicletes per panicle (13.52).

Similarly the genotypic coefficient of variation (gcv)ranged from (5.95) for number of leaves per tiller to (17.40) for grain yield per plant . The other characters which showed high genotypic coefficients of variation were plant height (17.12),panicle number per plant (14.20),number of spikelets per panicle (12.87),straw yield per plant (11.89) and total biological yield (11.35).It was also revealed from the Table 2 that the estimates of phenotypic coefficient of variation were slightly higher than the genotypic coefficient of variation for all the characters exept plant height virtually both genotypic coefficient of variation and phenotypic coefficient of variation were found equal ,that is (17.12)during the present study.

The heritability was also estimated for all the 12 characters. The estimate of heritability was highest for plant height (1.000), while, the lowest estimate of heritability was observed for total biological yield (0.721). Obviously, it is observed that most of the characters had high estimates of heritability.

The highest estimates of genetic advance was reported for number of spikelets per panicle (46.23), whereas it was lowest for number of leaves per tiller (0.71).The other characters which showed high to moderate estimates of genetic advance were days to maturity (19.32), plant height (41.5), days to 50% flowering (14.18), total biological yield per plant (8.50) and harvest index (8.33).

Analysis of variance indicated that means sum of squares for all the characters were highly significant (table1) , indicating, thereby , that varieties differ among for all the characters during the present study similar results were also reported by Singh *et. al*. 1980. The estimates of phenotypic coefficient of variation were higher than those of genotypic coefficient of variation for all the traits except plant height, which was also reported earlier by Lal *et. al.,* (1983), Singh *et. al.* (1986) and Sundaram *et. al.,* (1988).

The data on different characters along with the estimates on variability indicating genotypic coefficient of variation(GCV) and phenotypic coefficient of variation(PCV) , heritability ,genetic advance as per cent mean are presented (table 2).

In this study, high estimates of heritability and genetic advance were obtained for plant height and number of spikelets per panicle, which supports the results of.Similar observations were reported for plant height by Singh *et. al.* (1986) and Kaul and Kumar (1982) and grains per panicle by (Paramasivam, 1980 and Shamsuddin, 1982).

Plant height and number of spikelets per panicle recorded high heritability in broad sense coupled with high genetic advance. This indicated that, the environmental effect was low on these characters and these traits were mostly governed by additive gene action, therefore, these traits offers an ample scope for further improvement by excecising selection . Similar results were reported by (Das and Borthakur, 1974 and Chaudhary *et. al.* 1973).

High heritability coupled with high genetic advance was also recorded for days to 50% flowering and days to maturity. Hence there is ample scope of improvement for these traits as well through selection . These results are in conformity with earlier findings (Unnikrishnan, 1980). High heritability coupled with low genetic advances was recorded for harvest index. This indicate that both additive and non- additive gene actions are involved in controlling harvest index and, hence, this traits offers little scope for improvement by selection . Similar results was reported by earlier workers (Vijay Kumar, 1990 and Minidas 1990).

Among all the characters, plant height, number of spikelets per panicle, days to maturity and days to 50% flowering recorded high heritability as well as moderate to high genetic advance. These characters are important for the breeder to construct selection indices. According, the heritability estimates in combination with genetic advance were more useful than heritability alone for predicting the resultant effect of selection in a segregating population. Thus, in the present case selection based on plant height, number of spikelets per panicle, days to maturity and days to 50% flowring will be more effective. Maurya (1976) and Chaudhray *et. al. (*1980) also observed that selection based on spikelets, panicle weight and test weight is more effective.

TABLE - 1: Analysis of variance (ANOVA) for 12 quantitative characters (involving 55 genotypes) in rice.

Source of Variation	**D.F.**	**Mean Sum of Squares**											
		Days to 50% flowering	**Days to maturity**	**Plant height (cm.)**	**Number of leaves per tiller**	**Number of spikelets per panicle**	**Panicle length (cm.)**	**Panicle number per plant**	**1000 grain weight (gm.)**	**Grain yield per plant (gm.)**	**Straw yield per plant (gm.)**	**Total biological per plant (gm.)**	**Harvest index**
Replication	2	0.500	1.000	0.375	0.0456	2.7500	0.0312	0.0039	0.0039	0.1250	0.0429	0.1250	0.5625
Treatment	54	143.643**	268.214**	1197.509**	0.5512**	1726.5833**	21.4660**	7.8349**	9.7138**	25.8777**	29.7191**	79.9689	51.7558**
Error	108	0.380	1.080	0.0902	0.0597	57.9537	0.0130	0.0046	0.0523	0.0896	0.0573	9.1185	0.6855

** **Significant at 1% level of probability.**

TABLE - 2: Estimates of coefficient of variation, genotypic and phenotypic coefficients of variations, heritability and genetic advance for 12 metric characters in rice.

S.No.	**CHARACTER**	**CV**	**GCV**	**PCV**	**h^2**	**GA**	**GA (% mean)**
1	Days to 50% flowering	0.6301	7.06	7.08	0.992	14.18	14.47
2	Days to maturity	0.8405	7.53	7.58	0.988	19.32	15.43
3	Plant height (cm.)	0.2575	17.12	17.12	1.000	41.15	35.27
4	Number of leaves per tiller	4.8008	5.95	9.29	0.733	0.71	13.95
5	Number of spikelets per panicle	4.1546	12.87	13.52	0.906	46.23	25.23

6	Panicle length (cm.)	0.4268	9.97	9.98	0.998	5.50	20.52
7	Panicle number per plant	0.600	14.20	14.21	0.998	3.33	29.27
8	1000 grain weight (gm.)	0.9808	7.69	7.76	0.984	3.67	15.73
9	Grain yield per plant (gm.)	1.7769	17.40	17.49	0.990	6.01	35.66
10	Straw yield per plant (gm.)	0.9051	11.89	11.92	0.994	6.46	24.42
11	Total biological yield per plant (gm.)	7.0540	11.35	13.37	0.721	8.50	19.86
12	Harvest index	2.1290	10.61	10.82	0.961	8.33	21.42

References

[1.] Burton,G.W. 1952 Quantitative inheritance in grasses. Proc. 6th Int. Grassland Cong ., 1:227-83.
[2.] Chaudhury, D, Rao, M.J.B.K, Parsad, A.B., Rao Suriya, A.V. (1980). Heritability and correlation in rice. Oryza.**17**(3) : 194-199.
[3.] Chaudhury, D, Srivastava, D.P, Ghose, K, Arun, R, Seetha Raman (1973). Genetic variability and correlation for yield components in rice.Oryza **10**(4) : 205-206.
[4.] Das, G.R. and Borthakur, D.N. (1974). Variability parameters for quantitative characters in potoperiod insensitive tall and semidwarf rice varieties. Indian J. Agric. Sci. **44** : 613-616.
[5.] Falconer, D.S. (1981). Introduction to Quantitative Genetics, 2nd ed. Longman, New York.
[6.] Johnson, H.W, Robinson, H.F, Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. Agron.**47** : 314-318.
[7.] Kaul, M.L.H. and V. Kumar (1982). Genetic veriability in rice. Geneti-ca Agraria, **36**(3-4): 257-268.
[8.] Lal, J.P, Richaria, J.A.K, Agarwal, R.K. (1983). Coheritability, correlation and genetic parameters in semi-dwarf cultivars of rice. Oryza **200**(4): 195-203.
[9.] Lush, J.L. (1949). Heritability of quantitative characters in farm animals. Hereditas, suppl 356-375.
[10.] Maurya, D.M. (1976). Heritability and genetic advance in rice. Oryza **13** (2) : 97-100.
[11.] Minidas (1990). Studies on genetic variability, character association and path analysis in aromatic Rice (Oryza-sativa L.) M.Sc. (Agri.) Thesis University of Agricultural Sciences, Bangalore.
[12.] Paramasivan, K.S. (1980). Study of genotypic and phenotypic variability in quantitative characters in hybrids of tall and dwarf indica rice varieties, Crop Improvement **7**: 141-142.
[13.] Panes, V.G and Sukhatme, P.V. 1967. Statistical methods for agricultural workers. ICAR New Delhi:, 2nd Edn. PP.381.
[14.] Shamsuddin, A.K.M. (1982). Analysis of genetic variation for panicle and grain characteristics in relation to grain yield in rice. Pakistan J. Sci. Res. **34** : 75-78.
[15.] Singh, R.P, Pandey, D.D, Rai, J.N. (1980). Genetic variability and correlation studies in rice. Madras Agric. J. **67**(10) : 682-686.
[16.] Singh, R.S., Chauhan, S.P., Maurya, D.M. (1986). Genetic variability in 98 upland rice cultivars of Inida. Intern. Rice Res. Newsl., **11**: 9-10.
[17.] Sundram, T, Wilfred Manuwl, W, Palanisamy, S. (1988). Genetic varia-bility and correlation coefficients in early rice (Oryza-sativa L.) Ind. Agric. Sci. **58**(8): 629-630.
[18.] Tiwari,G.C., Jatav ,N.K.(2014). Combining ability analysis for grain yield and its related characters in rice (*Oryza-sativa* L.). Trends in Biosciences. J.**7** (13): 1444-1448.
[19.] Unnikrishnan, A. (1982). Studies on genetic variability and selection indices for grain yield in three F_2 populations of rice (Oryza sativa). Thesis abstract B. 71-72.
[20.] Vijay Kumar, S.B. (1990). Estimates of combining ability and gene action of Jaya and Mahsuri Derivatives of rice through F_1, F_1 Ratoon and F_2 generation analysis. M.Sc (Agri.) Thesis. University of Agricultural Sciences, Banglore.
[21.] Wright, S. (1921). Correlation and causation. J. Agric. Res. **20**: 557-585