



Research Note

Variability studies for quantitative traits in upland rice (*Oryza sativa* L.)

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Abstract

The present experiment comprised with twenty two advanced rice cultures collected from various research institutes and was conducted during Rabi 2015-16 under upland rice ecosystem. The analysis of variance revealed that all the treatments are significant for various characters under studied *i.e.* days to 50% flowering, plant height, number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, grain yield per plot, straw yield per plot and harvest index. The higher magnitude of PCV was recorded for number of productive tillers per plant, number of filled grains per panicle, grain yield per plot and harvest index and higher magnitude of GCV was recorded for number of filled grains per panicle. Days to 50% flowering, plant height, number of panicles per square metre plot area, panicle length and number of filled grains per panicle showed high broad sense heritability and moderate for grain yield per plot, straw yield per plot and harvest index. High heritability coupled with high genetic advance was recorded for plant height and number of filled grains per panicle indicated the major role of additive gene action in the inheritance of these characters. Thus, these characters may serve as an effective selection parameter during breeding programme in the upland rice ecosystem.

Key words

Variability, heritability, genetic advance, upland rice

Rice is one of the principle food crops and one third of the world population and two thirds of the Indian population is utilizing rice as staple food. It contributes 43 per cent of caloric requirement and 20-25% of agricultural income. In India, rice is grown in an area of 43.5 million ha (23% of gross cropped area) with an annual production of 90 million tons. Most of the Asian countries have been able to keep pace between rice production growth rate and that of population during the last four decades. This has been mainly possible due to the contributions made by the green revolution technologies. However, it is of great concern to note that the rate of growth in rice production has started declining during 90's and there has been a plateauing effect. The population growth in most of the Asian countries, except China, continues to be around 2% per year. Hence it is very pertinent to critically consider whether the rice production can be further increased to keep pace with population growth. Yield is a complex character, which is highly influenced by the environment, hence direct selection for yield alone limit the selection efficiency and ultimately results in limited success in yield improvement. Genetic variability studies are important in selection of parents for hybridization (Chaudhary and Singh, 1982) because crop improvement depends upon magnitude of genetic variability in base population (Adebisi *et al.*, 2001). Once genetic variability has been ascertained, crop improvement is possible through the use of appropriate selection method and increasing total yield would be made easier by selecting for yield components because they are more often easily inherited than total yield itself. An attempt was made in the present investigation to assess the variability, heritability and genetic

advance of some quantitative characters in upland rice.

The experimental material comprised with twenty three improved rice cultures collected from various research institutes which were evaluated in a randomized block design with three replications at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi during Rabi 2015-16. The experimental site is located at 9° 21' N latitude, 78° 22' E longitudes and an altitude of 242 m above mean sealevel with average annual rainfall of 840 mm. This site has clay loam soil texture with pH of 8.0. Each genotype was raised in 5 x 2 m plot keeping 15 x 10 cm spacing. The recommended agronomic practices followed to raise good crop stand. The data were recorded on ten randomly selected plants from each replication for various quantitative traits studied were *viz.*, days to 50% flowering, plant height (cm), number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, grain yield per plot (kg), straw yield per plot (kg) and harvest index (%). Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse & Sukhatme (1967). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula given by Burton (1952), heritability in broad sense and genetic advance were calculated as per Johnson *et al.*, (1955).

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. Thus, the primary objective of germplasm conservation is to collect and preserve

the genetic variability in indigenous collection of crop species to make it available to present and future generations. The analysis of variance (Table 1.) revealed that for treatments are significant for various characters under studied *i.e.* days to 50% flowering, plant height, number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, grain yield per plot, straw yield per plot and harvest index. High phenotypic variations were composed of high genotypic variations and less of environmental variations, which indicated the presence of high genetic variability for different traits and less influence of environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. This result was in conformity with the earlier findings of Babu *et al.* (2012), Vanisree *et al.* (2013) and Allam *et al.* (2015).

The perusal of coefficient of variability indicated that wide range of variability was present at both phenotypic and genotypic levels for all the characters under studied. The magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits which may be due to higher degree of interaction of genotypes with the environment (Kavitha & Reddy 2002). The differences in the magnitude of PCV and GCV for number of productive tillers per plant, grain yield per plot and harvest index were of high order. The higher magnitude of Phenotypic coefficient of variation was recorded for number of productive tillers per plant, number of filled grains per panicle, grain yield per plot and harvest index whereas moderate magnitude of PCV was recorded in plant height, panicle length and straw yield (Table 2.).

Genotypic coefficient of variation was high for number of filled grains per panicle and was moderate for plant height, grain yield per plot, straw yield per plot and harvest index (Table 2.). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. Coefficients of variability for various characters observed in the present study were in agreement with the findings of Babu *et al.* (2012), Vanisree *et al.* (2013), Shinde *et al.* (2015) and Allam *et al.* (2015).

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush, 1949). Robinson *et al.* (1949) viewed that the knowledge of heritability of a

character is important to the breeder, as it indicates the possibility and extent to which improvement is possible through selection. It is a measure of genetic relationship between parents and their progeny and has been widely used in determining the degree to which a character may be transmitted from parents to offspring. High heritability is not enough to make efficient selection in the advanced generations unless it is accompanied by substantial amount of genetic advance. Burton (1952) pointed out that the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Thus, genetic advance is yet another important selection parameter which although independent, represents the expected genetic advance under selection. It measures the differences between the mean genotypic values of the selected lines and the mean genotypic values of original population from which these were selected. According to Panse (1957) if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provided good scope for further improvement. In the present study, high broad sense heritability estimates were obtained for days to 50% flowering, plant height, number of panicles per square metre plot area, panicle length and number of filled grains per panicle (Table 2.), indicating the major role of additive gene action in inheritance of these traits. The broad sense heritability of these characters is in accordance with those of Babu *et al.* (2012), Shinde *et al.* (2015) and Allam *et al.* (2015).

High heritability alone does not guarantee large gain from selection unless sufficient genetic advance (GA) attributed to additive gene action is present. High heritability coupled with high genetic advance was recorded for plant height and number of filled grains per panicle (Table 2.). It indicates that most likely the heritability if due to additive gene effects then the selection may be effective. This finding is in close agreement with the findings of Vaithiyalingan and Nadarajan (2006), Babu *et al.* (2012), Shinde *et al.* (2015) and Allam *et al.* (2015). Low heritability coupled with low genetic advance was recorded for number of productive tillers per plant which indicates that this character is highly influenced by environmental effect and selection would be ineffective.

An overall consideration of results revealed that high heritability coupled with high genetic advance was recorded for plant height and number of filled grains per panicle and the major role of additive gene action involved in the inheritance of these characters. Thus, these characters may serve as effective selection parameters during breeding programme in the upland rice ecosystem.

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Table 1. Analysis of variance for different traits in rice

Source of variation	Degrees of freedom	Days to 50% flowering	Plant Height	Productive tillers per plant	Panicles per square metre	Panicle length	Filled grains per panicle	Grain yield per plot	Straw yield per plot	Harvest index
Replication	2	7.06	12.88	3.99	180.91	4.05	897.26	0.69	0.40	0.002
Treatment	22	167.29*	832.84*	5.23*	698.16*	11.48*	3983.62*	1.46*	1.90*	0.013*
Error	44	2.51	23.43	2.19	20.94	1.47	201.47	0.27	0.35	0.004

*significant at P=0.05 level

Table 2. Estimates of mean, variability, heritability and genetic advance in rice

Traits	Mean \pm SE	PV	GV	GCV	PCV	h^2	GA	GAM
Days to 50% flowering	75.99 \pm 0.92	57.44	54.93	9.75	9.97	95.63	14.93	19.65
Plant height	113.51 \pm 2.79	293.23	269.80	14.47	15.09	92.01	32.46	28.59
Productive tillers per plant	8.46 \pm 0.96	3.19	0.40	7.47	21.11	12.53	0.46	5.45
Panicles per square metre	220.57 \pm 2.64	246.68	225.74	6.82	7.12	91.51	29.61	13.42
Panicle length	21.70 \pm 0.70	4.81	3.34	8.42	10.10	69.46	3.14	14.46
Filled grains per panicle	131.04 \pm 8.19	1462.19	1260.71	27.10	29.18	86.22	67.92	51.83
Grain yield per plot	3.34 \pm 0.30	0.67	0.40	18.86	24.44	59.59	1.00	29.99
Straw yield per plot	5.45 \pm 0.34	0.87	0.52	13.18	17.13	59.24	1.14	20.90
Harvest index	0.37 \pm 0.03	0.01	0.01	14.80	21.75	46.33	0.08	20.76

SE= Standard Error; **GV**= Genotypic Variation; **PV**= Phenotypic Variation; **GCV**= Genotypic Co-efficient of Variation; **PCV**= Phenotypic Co-efficient of Variation; **h^2** = Heritability (Broad sense); **GA**= Genetic Advance; **GAM**= Genetic Advance as % of Mean.