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Assessment of heritability and genetic advance in segregating generation for yield, its components and quality traits in rice (*Oryza sativa* L.)

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Abstract

The experiment was carried out during summer and *kharif* 2018-19 at Main Rice Research Centre, Navsari Agricultural University, Navsari. Six diversified elite lines of rice (IET-24772, IET-24783, GNR-2, GNR-3, GR-11 and GR-15) were used to study heritability and expected genetic advance under selection. High heritability coupled with high genetic advance were estimated for productive tillers per plant in all the three crosses; 100 grain weight in cross-II (GNR-2 x GNR-3) and straw yield per plant in cross-III (GR-11 x GR-15) which indicated that heritability of these traits were under the control of additive gene action. For improvement of such traits, selection will be rewarding.

Keywords: Heritability, expected genetic advance, rice

Introduction

Rice (Oryza sativa L.), the most important agronomical crop, occupies the enviable position around the world. Being a major cereal crop, nutritionally it is one of the world's most important staple foods, with greater portion of the world's population dependant on it for a significant proportion of their caloric intake in the rate of 20 per cent daily calories. India is the largest rice cultivator which accounts for almost thirty per cent rice area of the world's. India is the largest rice growing country, while China is the largest producer of rice. Thus, it is a challenging task to ensure food and nutritional security of India's ever increasing population and therefore, rice production must be increased by 50% in order to meet the growing demand (Miah *et al.*, 2013) ^[7]. Sufficient understanding of the inheritance of quantitative traits and information about heritability of grain yield, its components and quality traits are essential to develop an efficient breeding strategy. Estimate of heritability serves as a useful guide to the breeder. The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is, the heritable portion of variation in the first case, and the portion of genetic variation that is fixable in pure lines in the later case. If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. But for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Thus, estimates of heritability are useful in predicting the transmission of characters from the parents to their offspring. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program.

Materials and Methods

Six diversified elite lines of rice (IET-24772, IET-24783, GNR-2, GNR-3, GR-11 and GR-15) comprised as experimental material selected on the basis of their variation in morphological characters. The three crosses (IET-24772 x IET-24783, GNR-2 x GNR-3 and GR-11 x GR-15) obtained by crossing of six diverse parents during summer-2018 at Main Rice Research Centre, Navsari Agricultural University, Navsari. F₁s were produced during summer-2018. Selfing of F₁s was done in the *kharif*-2018 to get F₂s. F₃s were produced during summer-2019. The evaluation trial was conducted with all five generations of three crosses along with standard check GNR-7 in *kharif*-2019 at Main Rice Research Centre, Navsari Agricultural University, Navsari. F₁, F₂ and F₃) of each of the three crosses were sown during *kharif*-2019 in compact family block design with three replications.

Each three crosses consisting of five generations were randomly allotted to each plot. Each plot consisted of two rows of parents and F_{1s} , thirty rows of the F_{2} and fifteen rows of the F_{3} generations of each cross. Twenty plants were planted in each row.

Results and Discussion

Heritability is a measure of the efficiency of a selection system in separating genotypes. The quantitative traits are largely influenced by environments; therefore, those are not highly heritable. High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson *et al.*, 1949)^[12]. Heritability in broad sense, as the ratio of additive variance to the total variance was proposed by Lush (1949)^[6]. Later, Hanson *et al.* (1956)^[2] proposed heritability in broad sense as the ratio of genotypic variance to total variance in a non-segregating population.

1.	Low heritability	:	0 - 30 %
2.	Moderate heritability	:	30 - 60 %
3.	High heritability	:	> 60 %

The value of expected genetic advance for various characters is demarcated into three categories *viz.*, low, moderate and high as follows (Johnson *et al.*, 1955)^[3].

0		/	
1.	Low genetic advance	:	0 - 10%
2.	Moderate genetic advance	:	10 - 20 %
3.	High genetic advance	:	>20 %

In crop improvement, only genetic component of variation is important since that component is transmitted to the next generation. Heritability indicates the effectiveness with which the selection of genotypes could be based on phenotypic performance. This could be achieved through determining heritability and genetic gain under selection. The success of selection is governed by the degree to which the desired character is transmitted to the offspring's of the selected parents. Burton (1952)^[1] stated that an understanding of the inheritance of quantitative characters could change the art of plant breeding into a science. Therefore, a reliable estimate of heritability can be a powerful tool in determining the breeding programme.

Heritability

High to moderate narrow sense heritability was recorded for most of the characters in all the crosses. High narrow sense heritability was recorded in all the three crosses of days to flowering, days to maturity, plant height, productive tillers per plant, grains per panicle, 100 grain weight in cross-I and cross-II, grain yield per plant, straw yield per plant, L:B ratio, protein content in cross-I and cross-III. Results were in agreement with Patel *et al.* (2019)^[9], Venkatesan *et al.* (2017) ^[16] and Sadimantara *et al.* (2014)^[13]. Moderate sense heritability was estimated in cross-III for 100 grain weight and in cross-II for protein content.

The higher estimates of narrow sense heritability indicates that these traits were comparatively less affected by environment and their phenotypes are good reflection of genotypes and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matric traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement. The moderate estimates of heritability indicated the preponderance of non-additive variance for yield and yield attributes in the material under study.

Genetic advance

Since heritability estimates vary with change in environment, experimental material etc, their scope is restricted. Hence, heritability values used in conjuction with the genetic advance would be more reliable than heritability alone (Johnson *et al.*, 1955) ^[3] which will be helpful in forming selection procedures.

In the present investigation, low genetic advance was recorded for most of the traits in all the three crosses. However, most of the crosses revealed low to high genetic advance for some more traits. High genetic advance was reported for productive tillers per plant in all the three crosses; 100 grain weight in cross-II (GNR-2 x GNR-3) and straw yield per plant in cross-III (GR-11 x GR-15). Moderate expected genetic advance was recorded for days to flowering in cross-II; grains per panicle in cross-II; 100 grain weight in cross-II; grain yield per plant in cross-II and cross-II; protein content in cross-II and cross-III. Kiani *et al.* (2013) ^[4], Montazeri *et al.* (2014) ^[8], Shahid *et al.* (2014) ^[14], Patel *et al.* (2015) ^[10], Rani *et al.* (2015) ^[11], Sultana *et al.* (2016) ^[15] and Kumar *et al.* (2017) ^[5] which supported the present results.

Heritability coupled with genetic advance

High heritability coupled with high genetic advance were estimated for productive tillers per plant in all the three crosses; 100 grain weight in cross-II (GNR-2 x GNR-3) and straw yield per plant in cross-III (GR-11 x GR-15) which indicated that heritability of these traits were under the control of additive gene action. For improvement of such traits, selection will be rewarding.

Moderate to high heritability coupled with moderate genetic advance was observed for days to flowering in cross-II; grains per panicle in cross-II; 100 grain weight in cross-I and cross-III; grain yield per plant in cross-II and cross-III; straw yield per plant in cross-I and cross-II; protein content in cross-II and cross-III which indicate that heritability of these traits were due to additive gene action, suggesting that these characters can be further improved by adopting selections in succeeding generations Patel *et al.* (2019) ^[9].

Most the traits studied under present study showed high to moderate heritability coupled with low genetic advance in all the three crosses indicate the presence of non-additive gene action. The moderately high heritability was exhibited due to favorable influence of environment rather than genotype and selection for such traits may not be rewarding.

Shift in the gene frequency towards selection pressure is termed as genetic advance. Johnson *et al.* (1955) ^[3] found it more useful to estimate heritability values together with genetic advance in predicting the ultimate choice of best individuals by selection.

Table 1: Estimates of heritability and genetic advance for days to flowering, days to maturity, plant height (cm), productive tillers per plant,
grain per panicle, 100 grain weight in cross-I, II, III

Estimates (%)	Days to flowering	Days to maturity	Plant height (cm)	Productive tillers per plant	Grains per panicle	100 grain weight (g)
Cross-I (IET-24772 x IET-24783)						
Heritability (NS) %	118.00	140.00	83.22	91.25	104.00	91.36
Genetic Advance %	9.35	7.04	1.89	24.07	6.83	14.95
Cross-II (GNR-2 x GNR-3)						
Heritability (NS) %	156.20	123.29	117.53	92.26	100.94	95.59
Genetic Advance %	10.51	6.06	5.85	29.81	14.15	32.64
Cross-III (GR-11 x GR-15)						
Heritability (NS) %	80.40	131.22	75.18	109.95	78.84	39.80
Genetic Advance %	9.51	2.79	6.20	24.78	3.12	13.85
	*	** significant at	5% and 1% level of	f significance respectively		

 Table 2: Estimates of heritability and genetic advance for grain yield per plant (g), straw yield per plant (g), L:B ratio, protein content (%) and amylose content (%) in cross-I, II, III

Estimates (%)	Grain yield per plant (g)	Straw yield per plant (g)	L:B ratio	Protein content (%)	Amylose content (%)		
Cross-I (IET-24772 x IET-24783)							
Heritability (NS) %	66.85	96.88	133.26	122.71	91.47		
Genetic Advance %	-0.59	13.22	-2.46	4.60	3.83		
Cross-II (GNR-2 x GNR-3)							
Heritability (NS) %	89.96	97.21	162.22	49.02	70.58		
Genetic Advance %	12.04	14.12	9.04	12.86	-1.83		
Cross-III (GR-11 x GR-15)							
Heritability (NS) %	87.92	91.06	70.32	97.80	106.58		
Genetic Advance %	13.35	21.71	2.68	13.06	1.16		

*,** significant at 5% and 1% level of significance respectively

Conclusion

The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotypes are good reflection of genotypes and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these matric traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement. The moderate to low estimates of heritability for most of the traits including yield components indicated the preponderance of non-additive variance for yield and yield attributes in the material under study. High heritability coupled with high genetic advance indicated that heritability of these traits were under the control of additive gene action and moderate to high heritability coupled with high to moderate genetic advance indicate that heritability of these traits were due to additive gene action, suggesting that these characters can be further improved by adopting selections in succeeding generations.

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