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**Patel HR**  
Department of Genetics and  
Plant Breeding, Navsari  
Agricultural University, Navsari,  
Gujarat, India

**Patel PB**  
Department of Genetics and  
Plant Breeding, Navsari  
Agricultural University, Navsari,  
Gujarat, India

## Heritability and genetic advance studies in segregating generation for yield, its components and quality traits in rice (*Oryza sativa* L.)

Patel HR and Patel PB

### Abstract

The present study comprised of five generation viz., P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> of following three crosses of rice (*Oryza sativa* L.) were used to study heritability and genetic advance of yield, its components and qualitative traits. The present investigation was carried out at Main Rice Research Centre, Navsari Agricultural University, Navsari during *kharif* 2018-19. High heritability coupled with high genetic advance was estimated for productive tillers per plant in all the crosses; 100 grain weight in cross-I and cross-II; grain yield per plant in cross-II; straw yield per plant in cross-II and cross-III; L:B ratio in cross-I and amylose content in cross-III 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, genetic advance, generation mean analysis, rice (*Oryza sativa* L.)

### Introduction

Rice, the world's most important cereal crop, is the primary source of food and calories for about half of the mankind (Khush, 2005) [10]. The crop is cultivated in large area but is characterized by very low productivity due to lack of high yielding varieties adapted to different seasons and agronomic conditions at different parts of country. Yield is a complex and polygenic trait which is a final product affected by the large numbers of its component traits (Renukadevi and Subbalakshmi, 2006) [14]. So, all changes in yield must be accompanied by changes in one or more of the components as have been pointed out by Grafius (1959) [8]. The eventual objective of any plant breeding programme is to develop better genotypes which are superior to their prevailing ones in one or more traits which producing the economic yield. The enrichment of mineral nutrients in rice is today's vital need to reduce malnutrition/anaemic conditions in poor people of the world. Sufficient understanding of the inheritance of quantitative traits and information about heritability of grain yield, its components and quality traits are crucial to develop an efficient breeding approach.

Assessment of heritability serves as a valuable director to the plant breeder. The heritability expresses the relative amount of heritable lot of the variation. However, the heritability assessments along with genetic advance is more useful in selecting the best population individual (Ganapati *et al.*, 2020) [5]. 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 latter 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 (Patel *et al.*, 2019) [12]. Thus, assessments of heritability are suitable in predicting the transmission of characters from the parents to their offspring.

### Material and Methods

The material comprising of five genetically diverse parents of rice (IET-25475, IET-25477, GNR-7, GNR-3 and GAR-13) selected on the basis of their geographic origin, variation in morphological characters and based on their mineral nutrient content. Three crosses (Cross-I: IET-25475 x IET-25477, Cross-II: GNR-7 x GNR-3 and Cross-III: GAR-13 x IET-25477) obtained by crossing of five diverse parents during summer 2018 at Main Rice Research

**Corresponding Author:**  
**Patel HR**  
Department of Genetics and  
Plant Breeding, Navsari  
Agricultural University, Navsari,  
Gujarat, India

Centre, Navsari Agricultural University, Navsari. A part of fresh F1s seeds of above crosses and parents kept reserve and part of F1s seeds were grown and selfed in kharif 2018 to get F2s seeds. Selfing of F2s was done during summer-2019 to get F3s seeds. The experimental material consisting of three families, each having five generations (P1, P2, F1, F2 and F3) was grown in compact family block design with three replications, whereas, different generations *viz.*, P1, P2, F1, F2 and F3 of each family represented individual experimental unit within family. The individual replication was represented by three family blocks, two rows each of P1, P2 and F1, thirty rows of F2 and fifteen rows of F3 generations of each crosses. Twenty plants were planted in each row. The experiment was surrounded by four guard rows to avoid damage and border effects. Observations were recorded for eleven different characters *viz.*, days to flowering, days to maturity, plant height, productive tillers per plant, grains per panicle, 100 grain weight, grain yield per plant, straw yield per plant, L: B ratio, amylose content and Zn content.

### 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).

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

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

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

The results obtained on these aspects for different characters studied in all the crosses are presented in table 1 and table 2.

High narrow sense heritability recorded for traits *viz.*, plant height, productive tillers per plant, 100 grain weight, L:B ratio and Zn content in cross-I (IET-25475 x IET-25477); days to flowering, days to maturity, productive tillers per plant, 100 grain weight, grain yield per plant, straw yield per plant and L:B ratio in cross-II (GNR-7 x GNR-3) and days to maturity, productive tillers per plant, grains per panicle, 100 grain weight, straw yield per plant, L: B ratio, Zn content and amylose content in cross-III (GAR-13 x IET-25477).

Moderate narrow sense heritability recorded for traits *viz.*, days to maturity, grain yield per plant, straw yield per plant and amylose content in cross-I (IET-25475 x IET-25477); amylose content and Zn content in cross-II (GNR-7 x GNR-3) and grain yield per plant in cross-III (GAR-13 x IET-25477) while rest of the traits had low heritability for all crosses.

Low genetic advance was reported for days to flowering, days

to maturity, grains per panicle, grain yield per plant, straw yield per plant, amylose content and Zn content in cross-I (IET-25475 x IET-25477); plant height, grains per panicle, amylose content and Zn content in cross-II (GNR-7 x GNR-3) and days to flowering, days to maturity and Zn content in cross-III (GAR-13 x IET-25477).

Moderate expected genetic advance was recorded for plant height in cross-I (IET-25475 x IET-25477); days to flowering, days to maturity and L:B ratio in cross-II (GNR-7 x GNR-3) and plant height, grains per panicle, 100 grain weight and L:B ratio in cross-III (GAR-13 x IET-25477).

High expected genetic advance was recorded for productive tillers per plant, 100 grain weight and L: B ratio in cross-I (IET-25475 x IET-25477); productive tillers per plant, 100 grain weight, grain yield per plant and straw yield per plant in cross-II (GNR-7 x GNR-3) and productive tillers per plant, grain yield per plant, straw yield per plant and amylose content in cross-III (GAR-13 x IET-25477).

High heritability coupled with high genetic advance was estimated for productive tillers per plant in all the crosses; 100 grain weight in cross-I and cross-II; grain yield per plant in cross-II; straw yield per plant in cross-II and cross-III; L:B ratio in cross-I and amylose content in cross-III which indicated that heritability of these traits were under the control of additive gene action. For improvement of such traits, selection will be rewarding. The results are matching with the results of Ghosh and Sharma (2012) [7], Shet *et al.* (2012) [20], Gangashetty *et al.* (2013) [6], Kumar and Senapati (2013) [17], Sala *et al.* (2013) [17], Sadimantara *et al.* (2014) [16], Savitha and Usha (2015) [19] and Venkatesan *et al.* (2017) [21].

Moderate to high heritability coupled with high to moderate genetic advance was observed for days to flowering and days to maturity in cross-II; plant height in cross-I; grains per panicle, 100 grain weight and grain yield per plant in cross-III and L: B ratio 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. These findings are similar to those of Samak *et al.* (2011) [18], Babu *et al.* (2012) [3] and Rahman *et al.* (2015) [13].

High to moderate heritability coupled with moderate to low genetic advance was observed for days to maturity in cross-I and cross-III; grain yield per plant and straw yield per plant in cross-I; amylose content in cross-I and cross-II and Zn content in all crosses shows that little progress can be made in the improvement of these traits by phenotypic selection. The results are in accordance with the results of Samak *et al.* (2011) [18], Babu *et al.* (2012) [3] and Rahman *et al.* (2015) [13].

Low to moderate heritability coupled with low to moderate genetic advance was estimated for days to flowering and grains per panicle in cross-I and cross-II and plant height in cross-II and cross-III, which indicated that heritability was under the control of non-additive gene action and selection would be ineffective for this trait. These findings are similar to those of Fiyaz *et al.* (2011) [4], Ahmadikhah (2012) [1] and Anyanwu Chinyere and Obi (2014) [2].

**Table 1:** Estimates of narrow sense heritability (NS) and genetic advance for days to flowering, days to maturity, plant height, productive tillers per plant, grains per panicle and 100 grain weight in three crosses of rice

Estimates (%)	Days to flowering	Days to maturity	Plant height (cm)	Productive tillers per plant	Grains per panicle	100 grain weight (g)
<b>Cross-I (IET-25475 x IET-25477)</b>						
Heritability (NS) %	25.72	50.13	136.24	96.50	-	121.68
Genetic Advance %	8.61	9.54	16.12	28.68	8.54	21.05

Cross-II (GNR-7 x GNR-3)						
Heritability (NS) %	179.98	176.42	11.87	85.19	-	102.27
Genetic Advance %	12.32	11.02	6.12	25.12	8.47	30.82
Cross-III (GAR-13 x IET-25477)						
Heritability (NS) %	-	66.96	-	77.82	82.09	155.54
Genetic Advance %	4.68	5.15	10.15	30.01	13.15	13.51

'-' indicate negative value

**Table 2:** Estimates of narrow sense heritability (NS) and genetic advance for grain yield per plant, straw yield per plant, L: B ratio, amylose content and Zn content in three crosses of rice

Estimates (%)	Grain yield per plant (g)	Straw yield per plant (g)	L: B ratio (mm)	Amylose content (%)	Zn content (ppm)
Cross-I (IET-25475 x IET-25477)					
Heritability (NS) %	30.60	48.97	118.31	51.57	73.22
Genetic Advance %	6.53	8.93	24.52	9.37	5.66
Cross-II (GNR-7 x GNR-3)					
Heritability (NS) %	132.69	131.96	117.60	44.13	56.72
Genetic Advance %	30.09	30.26	14.58	3.47	5.01
Cross-III (GAR-13 x IET-25477)					
Heritability (NS) %	34.69	87.20	122.16	98.10	124.44
Genetic Advance %	22.24	33.48	14.45	26.84	9.96

## 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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