***Original Research Article***

**Estimation of heritability and genetic advance in segregating generations for grain yield and yield contributing traits in upland condition of rice**

**(*Oryza sativa* L.)**

**ABSTRACT**

The experiment was carried out during *kharif* 2024 in upland condition at Regional Rice Research Station, N.A.U., Vyara to study the narrow sense heritability and genetic advance from segregating generations of four different crosses of rice *viz*., NVSR 2565 × NVSR 2272, NVSR 2565 × Dhanhar black, Devli kolam × NVSR 2272 and Devli kolam × Dhanhar black. For the majority of the attributes being studied, moderate to high genetic advance and moderate to high heritability (narrow-sense) estimations were found in all four crosses. Additive gene effects were undoubtedly the cause of the high heritability and high genetic advance, and it would be advantageous to use selection to improve these attributes.

**KEYWORDS:** Rice, heritability (narrow sense), genetic advance, segregating generation, upland conditions

**INTRODUCTION**

Rice (*Oryza sativa* L.), referred to as the "princess of the cereals," is the world's second-most important cereal food crop in terms of annual production for human consumption, after maize. More than 90% of the world's rice is produced and consumed in Asia, hence it is known as the "rice bowl" of the globe (Tyagi *et al*., 2004) [15]. Over two billion people in Asia alone rely on rice and items made from it for their calorie requirements. Rice kernels are nevertheless low in sodium and cholesterol. Since, rice is the primary source of calories in food, it is becoming more and more important in the production of baby food, snack foods, morning cereals, beer, fermented products and rice bran oil. India is ranked second in terms of rice production and first in terms of area. The demands of an increasing population must be met by agricultural food production. In order to meet the rising demand and guarantee food and nutritional security for India's constantly growing population, rice production must be raised by 50 % (Miah *et al*., 2013) [6].

Only the genetic component of variance matters in crop development since it is the only one that can be passed on to the following generation. Because the breeder can utilise the heritability estimates as a helpful guide. Although it indicates the proportion of variance that is heritable, its estimate in conjunction with genetic advance is more helpful in forecasting the outcome of choosing the optimal genotypes. To create an effective breeding strategy, one must have a thorough understanding of how quantitative traits are inherited as well as knowledge of the heritability of grain yield and its constituent attributes. Furthermore, genetic advance is necessary to determine the efficacy of selection and narrow sense heritability plays a significant part in the selection of elite genotypes from segregating populations. Given these facts, the most significant variables are rice grain yield and its contributing traits; therefore, an assessment of heritability and genetic advance for yield and its contributing traits was conducted.

# MATERIALS AND METHODS

The experimental material was comprised of four diverse elite lines of rice *viz*., NVSR 2565, NVSR 2272, Devli kolam and Dhanhar black, which were selected on the basis of variation in their morphological traits. At the Regional Rice Research Station, Navsari Agricultural University, Vyara, four distinct crosses - NVSR 2565 × NVSR 2272, NVSR 2565 × Dhanhar black, Devli kolam × NVSR 2272 and Devli kolam × Dhanhar black were produced by crossing four separate parents in the summer of 2023. F1s were produced in 2023's summer. During *kharif* 2023, F1s were selfed and backcrossed to create F2s and backcrossed seeds, respectively.

The evaluation trial was conducted with all six generations of four crosses during *kharif* 2024 in upland condition at Regional Rice Research Station, Navsari Agricultural University, Vyara. Six generations *viz*., P1, P2, F1, F2, B1 and B2 of four different crosses were sown during *kharif* 2024 in compact family block design with three replications. Inter and intra row spacing was 30 cm and 10 cm, respectively.

Ten plants from each of the P1, P2 and F1, 40 plants from F2 and 20 plants from each of the B1 and B2 generations were randomly selected per replication and observations were recorded for the characters *viz*., days to flowering, days to maturity, plant height (cm), productive tillers per plant, panicle length (cm), grains per panicle, kernel length (mm), kernel breadth (mm), L/B ratio, 100 grain weight (g), grain yield per plant (g), straw yield per plant (g) and harvest index (%).

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]. Low heritability (0 - 30%), Moderate heritability (30 - 60%) and 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) [4]. Low genetic advance (0 - 10%), Moderate genetic advance (10 - 20%) and High genetic advance (> 20%).

A trait with a high heritability should be very straightforward to select for since the genotype and phenotype would closely coincide because the environment would have a much lower influence on phenotype. In order to determine more dependable results and an improvement in the mean genotypic value of chosen families over that of the base population, the genetic advance was computed based on narrow sense heritability, which may be more useful in the selection of segregating populations in the current study.

# RESULTS AND DISCUSSION

Only the genetic component of variation matters in crop improvement because it is passed down to the subsequent generation. The success of using phenotypic performance to guide genotype selection is indicated by heritability. Determining heritability and genetic gain under selection may help achieve this. The success of selection is governed by the degree to which the desired character is transmitted to the offspring’s of the selected parents. According to Burton (1952) [1], the art of plant breeding could become a science if quantitative character inheritance were understood. Thus, a strong tool for choosing the breeding program can be a trustworthy estimate of heritability.

Tables 1 and 2 present the findings of genetic advance and narrow sense heritability for thirteen distinct traits examined in four rice crosses. The majority of the traits in all four crosses had narrow sense heritability ranging from high to moderate. For both days to flowering and days to maturity, all four crosses showed high narrow sense heritability.

**Table 1:** Estimates of heritability and genetic advance for days to flowering, days to maturity, plant height, productive tillers per plant, panicle length, grains per panicle and kernel length in four crosses of rice

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Particulars** | **Estimates (%)** | | | | | | |
| **Days to flowering** | **Days to maturity** | **Plant height (cm)** | **Productive tillers per plant** | **Panicle length (cm)** | **Grains per panicle** | **Kernel length (mm)** |
| **Cross I (NVSR 2565 × NVSR 2272)** | | | | | | | |
| **Heritability (ns) %** | 152.46 | 130.71 | - | 44.58 | 40.91 | - | 46.88 |
| **Genetic Advance %** | 24.89 | 14.39 | - | 6.76 | 1.78 | - | 15.14 |
| **Cross II (NVSR 2565 × Dhanhar black)** | | | | | | | |
| **Heritability (ns) %** | 128.50 | 134.84 | 93.38 | 111.27 | 108.54 | 59.58 | 32.95 |
| **Genetic Advance %** | 19.46 | 14.70 | 40.99 | 91.09 | 46.19 | 53.07 | 10.68 |
| **Cross III (Devli kolam × NVSR 2272)** | | | | | | | |
| **Heritability (ns) %** | 155.86 | 161.36 | - | 50.77 | - | 139.69 | 2.78 |
| **Genetic Advance %** | 26.58 | 18.61 | - | 38.95 | - | 143.40 | 0.71 |
| **Cross IV (Devli kolam × Dhanhar black)** | | | | | | | |
| **Heritability (ns) %** | 122.66 | 130.67 | 54.57 | 177.21 | 84.45 | 18.71 | 42.70 |
| **Genetic Advance %** | 17.31 | 13.21 | 16.51 | 143.57 | 25.77 | 14.98 | 4.02 |

" - " represent negative value

**Table 2:** Estimates of heritability and genetic advance for kernel breadth, L/B ratio, 100 grain weight, grain yield per plant, straw yield per plant and harvest index in four crosses of rice

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Particulars** | **Estimates (%)** | | | | | |
| **Kernel breadth (mm)** | **L/B ratio** | **100 Grain weight (g)** | **Grain yield per plant (g)** | **Straw yield per plant (g)** | **Harvest index (%)** |
| **Cross I (NVSR 2565 × NVSR 2272)** | | | | | | |
| **Heritability (ns) %** | 83.33 | 125.00 | - | - | - | 54.60 |
| **Genetic Advance %** | 16.25 | 33.89 | - | - | - | 25.59 |
| **Cross II (NVSR 2565 × Dhanhar black)** | | | | | | |
| **Heritability (ns) %** | 106.04 | 155.34 | - | - | 38.64 | NS |
| **Genetic Advance %** | 24.29 | 52.22 | - | - | 2.11 | NS |
| **Cross III (Devli kolam × NVSR 2272)** | | | | | | |
| **Heritability (ns) %** | - | NS | - | 66.56 | - | - |
| **Genetic Advance %** | - | NS | - | 52.91 | - | - |
| **Cross IV (Devli kolam × Dhanhar black)** | | | | | | |
| **Heritability (ns) %** | 10.78 | 39.44 | - | 11.44 | 26.01 | 66.54 |
| **Genetic Advance %** | 7.14 | 28.63 | - | 15.17 | 1.66 | 55.01 |

" - " represent negative value, NS – Non-significant cross

Plant height in cross II, productive tiller per plant in crosses II and IV, panicle length in crosses II and IV, grains per panicle in cross III, kernel breadth in crosses I and II, L/B ratio in crosses I and II, grain yield per plant in cross III, and harvest index in cross IV were noted as high values as well. These results are in correspondence with Nugraha *et al.* (2016) [7], Priyanka *et al.* (2019) [11], Harijan *et al.* (2021) [3], Singh *et al.* (2021) [14], Patel *et al.* (2022) [10], Satasiya *et al.* (2022) [13] and Patel (2024) [8].Moderate narrow sense heritability was observed for plant height in cross IV; productive tillers per plant in cross I and III; panicle length in cross I; grains per panicle in cross II; kernel length in cross I, II and IV; L/B ratio in cross IV; straw yield per plant in cross II and harvest index in cross I. Higher estimates of narrow sense heritability suggest that these traits were less influenced by the environment and that their phenotypes accurately reflect their genotypes. As a result, they were crucial in selecting superior genotypes based on the phenotypic performance of these matric traits. However, in cases where heritability is lower, pedigree, sib, or progeny tests can be used to improve genetics. The material under investigation exhibited a majority of non-additive variance for yield and yield characteristics, as evidenced by the moderate estimates of heritability.

In present investigation, the estimates of genetic advance were recorded high for plant height in cross II; productive tiller per plant in cross II, III and IV; panicle length in cross II and IV; grains per panicle in cross II and III; kernel breadth in cross II; L/B ratio in cross I, II and IV; grain yield per plant in cross III and harvest index in cross I and IV. Moderate genetic advance was recorded for days to flowering and days to maturity in all crosses; plant height in cross IV; grains per panicle in cross IV; kernel length in cross I and II; kernel breadth in cross I and grain yield per plant in cross IV. However, Low estimates of genetic advance were recorded for productive tillers per plant and panicle length in cross I; kernel length in cross III and IV; kernel breadth in cross IV and straw yield per plant in cross II and IV. Similar results were also reported by Khaled Salem *et al.* (2015) [5], Priyanka *et al.* (2019) [11], Gupta *et al.* (2020) [2],Patel and Patel (2020) [9], Harijan *et al.* (2021) [3], Singh *et al.* (2021) [14], Patel et al. (2022) [10] and Patel (2024) [8].

The present investigation revealed that the high heritability coupled with high genetic advance was observed for plant height in cross II; productive tillers per plant in cross II and IV; panicle length in cross II and IV; grains per panicle in cross III; kernel breadth in cross II; L/B ratio in cross I and II; grain yield per plant in cross III and harvest index in cross IV, which indicated the governance of additive gene action and selection for improvement of these traits would be rewarding. Days to flowering, days to maturity, and kernel breadth in cross I showed high heritability and moderate to low genetic advance, indicating the significance of environmental influence and non-additive gene action. Therefore, it would be advantageous to improve these traits through heterosis breeding. For variables such as productive tillers per plant in cross III, grains per panicle in cross II, L/B ratio in cross IV, and harvest index in cross I, low to moderate heritability combined with significant genetic advance demonstrates the impact of additive gene action in addition to environmental influence. Selection techniques would therefore be helpful in enhancing these traits.

**CONCLUSION**

Pedigree or progeny tests can be used to improve lower heritability, but higher estimates of heritability indicate that these traits were relatively less affected by the environment and that their phenotype is a good reflection of genotype. As a result, they are crucial in selecting a superior genotype based on the phenotypic performance of these matric traits. In all four crosses studied, the majority of the characters showed moderate to high genetic advancement and moderate to high heritability (narrow-sense) estimations. The combination of strong genetic advancement and high heritability was probably caused by additive gene effects. Therefore, adopting selections in subsequent generations can further improve characters with high heritability and high genetic advance.

**DISCLAIMER (ARTIFICIAL INTELLIGENCE)**

Author(s) hereby declare that generative AI technologies such as Large Language Models, etc. have been used during writing or editing of manuscripts. This explanation will include the name, version, model, and source of the generative AI technology and as well as all input prompts provided to the generative AI technology.

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