***Original Research Article***

***Assessment of Heritability and Genetic Advance in Segregating Generations of Rice (Oryza sativa L.) for Grain Yield and Yield Contributing Traits under Upland Conditions***

**ABSTRACT**

The study was conducted during the Kharif season of 2024 under upland conditions at the Regional Rice Research Station, N.A.U., Vyara, to evaluate narrow-sense heritability and genetic gain from the segregating generations of four distinct rice crosses, namely NVSR 2565 × NVSR 2272, NVSR 2565 × Dhanhar Black, Devli Kolam × NVSR 2272 and Devli Kolam × Dhanhar Black. For grain yield/ plant and most of the associated traits studied, medium to high per cent of genetic advance and narrow-sense heritability were observed across all four crosses. The predominance of additive gene effects likely contributed to these high values, suggesting that selection strategies could be effectively employed to enhance these favorable traits.

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

**INTRODUCTION**

Rice, often called the 'princess of cereals,' ranks as the second most important cereal crop globally in terms of annual production for human consumption, following maize. Over 90% of the world’s rice is cultivated and consumed in Asia, earning the region the title of the 'rice bowl' of the world (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, morning cereals, snack foods, beer, rice bran oil and fermented products. 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. A 50% increase in rice production is essential to address the rising demand and to secure food and nutritional needs for India's rapidly expanding population (Miah *et al*., 2013) [6].

Genetic variance is the key component in crop improvement, as it alone contributes to heritable changes passed on to the next 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. Genetic advance serves as an important indicator of selection efficiency, and narrow-sense heritability is crucial in selecting superior genotypes from segregating populations. Considering the pivotal role of grain yield and its associated traits in rice, a comprehensive evaluation of heritability and genetic advance was carried out for these key attributes.

**MATERIALS AND METHODS**

Four genetically diverse elite rice lines NVSR 2565, NVSR 2272, Devli Kolam and Dhanhar Black were chosen as experimental material, based on distinct variations in their morphological traits. At the Regional Rice Research Station (RRRS), Navsari Agricultural University (NAU), 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 carried out during the Kharif 2024 season under upland conditions at the RRRS, NAU, Vyara, involving all six generations of four rice crosses. The six generations P₁, P₂, F₁, F₂, B₁, and B₂ of each cross were sown in a compact family block design with three replications. The inter-row and intra-row spacings were maintained at 30 cm and 10 cm, respectively.

In each replication, ten plants were randomly selected from the P₁, P₂, and F₁ generations, forty plants from the F₂ generation and twenty plants from the B₁ and B₂ generations. Observations were recorded for the following traits: (1) days to flowering, (2) days to maturity, (3) plant height (cm), (4) productive tillers per plant, (5) panicle length (cm), (6) grains per panicle, (7) kernel length (mm), (8) kernel breadth (mm), (9) length to breadth (L/B) ratio, (10) 100 grain weight (g), (11) grain yield per plant (g), (12) straw yield per plant (g) and (13) harvest index (%).

**Estimation of narrow sense heritability**

Narrow-sense heritability was estimated following the method proposed by Warner (1952) [16], using the following formula:

$$h\_{\left(ns\right)}^{2}\left(\%\right)=\frac{\hat{σ}\_{A}^{2}}{\hat{σ}\_{P}^{2}}×100$$

Where,

|  |  |  |
| --- | --- | --- |
| $$h\_{\left(ns\right)}^{2}$$ | = | Heritability (narrow sense) |
| $$\hat{σ}\_{A}^{2}$$ | = | Additive component of genetic variance (d) |
| $$\hat{σ}\_{P}^{2}$$ | = | Total variance |

 The categorization of heritability percentage was carried out based on the classification proposed by Robinson et al. (1949) [12], as detailed below.

|  |  |  |
| --- | --- | --- |
| **Per cent range** |  | **Category** |
| 0 to 30  | : | Low |
| 30 to 60  | : | Medium |
| 60 & above | : | High |

1. **Assessment of expected genetic advance under selection**

 The expected genetic advance denotes the shift in the population mean toward superior performance following one cycle of selection. Its estimation was carried out according to the procedure outlined by Johnson et al. (1955) [4].

$$Expected genetic advance = k∙h^{2}\_{\left(ns\right)}∙\hat{σ}\_{P}$$

Where,

|  |  |  |
| --- | --- | --- |
| $$h^{2}\_{\left(ns\right)}$$ | : | Heritability (narrow-sense) |
| $$\hat{σ}\_{P}$$ | : | Phenotypic standard deviation |
| k | : | Selection differential |
| (k = 2.06 at 5 % selection pressure intensity) |

The expected genetic advance, expressed as a percentage of the population mean, was calculated using the following formula.

$$Expected genetic advance as \% of mean=\frac{GA}{\overline{X}}×100$$

Where,

|  |  |  |
| --- | --- | --- |
| GA | : | Genetic advance |
| $$\overline{X}$$ | : | Mean of the character under study |

 The classification of genetic advance as a percentage of the mean was carried out based on the criteria suggested by Johnson *et al.* (1955) [4].

|  |  |  |
| --- | --- | --- |
| **Per cent range** |  | **Category** |
| 0 to 10  | : | Low |
| 10 to 20  | : | Medium |
| 20 and above | : | High |

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 enhance the reliability of results and improve the mean genotypic performance of selected families compared to the base population, genetic advance was estimated using narrow-sense heritability, which proves to be more effective for selection within segregating populations in this study.

**RESULTS AND DISCUSSION**

Crop improvement relies on genetic variation, as it is the only component transmitted to future generations. The success of using phenotypic performance to guide genotype selection is indicated by heritability. Determining heritability and genetic gain under selection is instrumental in achieving improvement. The success of selection is primarily influenced by how efficiently the desired traits are transmitted to the progeny of selected individuals. As stated by 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 traits in all 4 crosses had heritability (narrow sense) ranging from high to medium. 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 (1) Days to Flowering, (2) Days to Maturity, (3) Plant Height, (4) Productive Tillers per Plant, (5) Panicle Length, (6) Grains per Panicle and (7) Kernel Length in Four Rice Crosses

|  |  |
| --- | --- |
| **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 (8) kernel breadth, (9) L/B ratio, (10) 100 grain weight, (11) grain yield per plant, (12) straw yield per plant and (13) harvest index in four rice crosses

|  |  |
| --- | --- |
| **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

Notably high values were recorded for plant height in Cross II; number of productive tillers per plant in Crosses II and IV; panicle length in Crosses II and IV; grains per panicle in Cross III; kernel breadth and L/B ratio in Crosses I and II; grain yield per plant in Cross III; and harvest index in Cross IV. 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 levels of narrow-sense heritability were recorded for plant height in Cross IV; number of productive tillers per plant in Crosses I and III; panicle length in Cross I; number of grains per panicle in Cross II; kernel length in Crosses I, II, and IV; L/B ratio in Cross IV; straw yield per plant in Cross II; and harvest index in Cross I. The relatively higher estimates of narrow-sense heritability for these traits suggest minimal environmental influence and indicate that the phenotypic performance of these traits closely reflects their underlying genotypic potential. Therefore, such traits hold significant importance for the selection of superior genotypes based on phenotypic expression. Conversely, in cases where heritability estimates are low, the implementation of alternative breeding strategies such as pedigree selection, sib selection, or progeny testing may be required to achieve genetic improvement. The predominance of moderate heritability values for yield and its associated traits further indicates that non-additive gene action plays a major role in the inheritance of these characters within the genetic material under investigation.

In the present investigation, high estimates of genetic advance were observed for plant height in Cross II; number of productive tillers per plant in Crosses II, III, and IV; panicle length in Crosses II and IV; number of grains per panicle in Crosses II and III; kernel breadth in Cross II; L/B ratio in Crosses I, II, and IV; grain yield per plant in Cross III; and harvest index in Crosses I and IV. Moderate genetic advance was recorded for days to flowering and days to maturity across all crosses, plant height in Cross IV, grains per panicle in Cross IV, kernel length in Crosses I and II, kernel breadth in Cross I, and grain yield per plant in Cross IV. Conversely, low estimates of genetic advance were noted for number of productive tillers per plant and panicle length in Cross I, kernel length in Crosses III and IV, kernel breadth in Cross IV, and straw yield per plant in Crosses II and IV. These results were akin to the results of 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 high heritability coupled with high genetic advance was observed for plant height in Cross II; number of productive tillers per plant in Crosses II and IV; panicle length in Crosses II and IV; number of grains per panicle in Cross III; kernel breadth in Cross II; L/B ratio in Crosses I and II; grain yield per plant in Cross III; and harvest index in Cross IV. These results suggest the predominance of additive gene action, indicating that selection for the improvement of these traits would be highly effective. In contrast, traits such as days to flowering, days to maturity, and kernel breadth in Cross I exhibited high heritability but moderate to low genetic advance, implying a greater influence of environmental factors and the involvement of 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**

Traits exhibiting low heritability can be improved through approaches such as pedigree selection or progeny testing. However, higher heritability estimates indicate that environmental influence is minimal, and the phenotypic expression reliably represents the genotypic value. This makes such traits particularly useful for selecting superior genotypes based on phenotype alone. In the current study, most traits across the four rice crosses demonstrated moderate to high levels of narrow-sense heritability and genetic advance. The occurrence of high genetic advance in conjunction with high heritability suggests the involvement of additive genetic effects. Therefore, selection in subsequent generations is likely to be effective in enhancing these traits, making them ideal targets for breeding programs

**IMPORTANCE FOR THE SCIENTIFIC COMMUNITY**

In Asia, rice is a significant staple crop. Research on rice always includes genetic enhancement in rice types. Improved rice varieties with stable features can be obtained by using a scientific approach to correlate desired phenotypic differences with the associated genetic background. In this sense, this effort is beneficial.

**DISCLAIMER (ARTIFICIAL INTELLIGENCE)**

Author(s) hereby declare that generative AI technologies such as Large Language Models, etc. have not been used during writing or editing of manuscripts.

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