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Estimation of narrow-sense heritability and genetic advance for yield and component traits in rice (*Oryza sativa* L.)

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Abstract
The present investigation aimed to estimate narrow-sense heritability and genetic advance as a percent of mean (GA%) for grain yield and its component traits in rice (*Oryza sativa* L.) using segregating generations. The experimental material consisted of four diverse crosses: NVSR 3169 × Gontra Bidhan 3, NVSR 3169 × Pusa 1509, Lal Kada Gold × DRR Dhan 62, and Lal Kada Gold × IR 55179-3B-11-3. Five generations (P_1, P_2, F_1, F_2, and F_3) were developed, but only F_2 and F_3 generations were considered for the estimation of heritability and GA%, as these represent segregating populations. The experiment was conducted during summer 2025 at the Regional Rice Research Station, Vyara, under Navsari Agricultural University. Observations were recorded on thirteen quantitative traits. Moderate to high estimates of narrow-sense heritability and GA% were observed for traits such as grain yield per plant, plant height, straw yield, and 100-grain weight, suggesting the involvement of additive gene action and the effectiveness of simple selection. These findings indicate that considerable improvement in yield and related traits is possible through direct selection in early segregating generations.

Keywords: Rice, narrow-sense heritability, genetic advance, grain yield, additive gene action, selection

Introduction
Rice (*Oryza sativa* L.) is a major cereal crop belonging to the tribe *Oryzeae* of the family *Gramineae*. It is a diploid species (2n = 2x = 24), self-pollinated in nature, and chasmogamous in floral structure. Its inflorescence is a panicle made up of spikelets, and the grain is classified as a caryopsis. Rice is cultivated in 116 countries and serves as a staple food for more than half of the global population. In 2023, global milled rice production reached 535.8 million metric tonnes, with more than 90% used for direct human consumption. In India, rice is grown over 47.83 million hectares with a production of 137.8 million tonnes, while in Gujarat, it covers an area of 9.68 lakh hectares producing 2.49 million tonnes (Anonymous, 2023a, 2023b) [3, 4].

Genetic improvement in rice depends on the presence of heritable variation and knowledge of gene action. Segregating generations, particularly F_2 and F_3, provide an opportunity to assess the variability created through recombination. Traits governed mainly by additive gene effects respond effectively to selection, especially when estimates of narrow-sense heritability and genetic advance are high. Narrow-sense heritability reflects the proportion of additive variance, while genetic advance as percent of mean (GA%) provides an estimate of the expected gain under selection pressure (Poehlman & Sleper, 1995; Johnson *et al.*, 1955) [12, 8]. Evaluation of these parameters in early generations helps in identifying traits with high selection efficiency. The present investigation was therefore carried out to estimate narrow-sense heritability and GA% for yield and its associated traits in F_2 and F_3 generations derived from four rice crosses.

Materials and Methods
The experiment was carried out during summer 2025 at the Regional Rice Research Station (RRRS), Vyara, under Navsari Agricultural University.

The experimental material comprised five generations (P_1, P_2, F_1, F_2, and F_3) from four rice crosses: NVSR 3169 × Gontra Bidhan 3, NVSR 3169 × Pusa 1509, Lal Kada Gold × DRR Dhan 62, and Lal Kada Gold × IR 55179-3B-11-3. However, only the F_2 and F_3 generations were utilized for estimating narrow-sense heritability and genetic advance, as these represent segregating populations where genetic variation is expressed.

The experiment was laid out in a Compact Family Block Design with three replications. Each plot consisted of four rows per generation with 20 cm inter-row and 15 cm intra-row spacing. Standard agronomic practices were followed. Data were recorded on forty randomly selected competitive plants from each plot of F_2 and F_3 generations for thirteen quantitative traits: days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of 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 (%).

Statistical Analysis

The narrow sense heritability was calculated by using the formula suggested by Warner (1952) as follows:

$$h^2(ns) = \frac{\frac{1}{2}D}{VF2} \times 100$$

Where,

h^2_{ns} = Heritability in narrow sense

VF_2 = Variance of F_2 generation

D = Additive genotypic variance

Estimation of Expected Genetic Advance under Selection

The expected genetic advance at 5% selection intensity was estimated by using formula suggested by Allard (1960).

Expected genetic advance = h^2 (ns) × K ×σp

Where,

h^2 (ns) = Heritability in narrow sense

σp = Phenotypic standard Deviation

K = Selection differential (K = 2.06 at 5% selection pressure) Expected genetic advance as per cent of mean was estimated by the following formula:

$$\text{Expected genetic advance as\% of mean} = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Mean of the character under study

Results and Discussion

The estimates of narrow-sense heritability and genetic advance as percent of mean (GA%) were calculated for thirteen agronomic and grain quality traits across four rice crosses evaluated in F_2 and F_3 generations. The values varied notably among crosses and traits, reflecting differences in genetic control and environmental influence.

In the cross NVSR 3169 × Gontra Bidhan 3, high heritability was recorded for plant height (64.18%), panicle length (61.19%), grains per panicle (60.11%), and 100-grain weight (83.18%), accompanied by high GA% for productive tillers per plant (35.18%), grain yield per plant (49.05%), and straw yield (80.9%). This suggests that additive gene action governs these traits and that selection can be highly effective. Conversely, low heritability and GA% for kernel length (20.44%, 2.58%) and harvest index (15.63%, 3.70%) indicate the influence of non-additive gene action or environmental effects.

In NVSR 3169 × Pusa 1509, high heritability was observed for plant height (80.36%), days to maturity (79.01%), kernel breadth (79.52%), and kernel length (64.87%), with moderate to high GA% for kernel breadth (21.54%) and L/B ratio (18.52%). These results suggest that selection for grain size and shape traits could be rewarding in this cross. Other traits like panicle length and grain yield were not estimated in this cross, and some traits showed moderate heritability, indicating partial additive control.

For the cross Lal Kada Gold × DRR Dhan 62, high heritability and GA% were observed for grain yield per plant (58.76%, 46.59%), 100-grain weight (84.94%, 19.77%), productive tillers per plant (59.47%, 45.77%), and harvest index (76.18%, 20.35%). These findings indicate that additive gene effects were predominant for these traits, and direct selection would be effective. Plant height and kernel length also showed favorable estimates, while traits like panicle length and grains per panicle had lower values, reducing selection efficiency.

Table 1: Estimates of narrow-sense heritability and genetic advance for days to flowering, maturity, plant height, productive tillers per plant, panicle length, grains per panicle, and 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 3169 × Gontra Bidhan 3)							
Heritability (ns)%	37.17	37.81	64.18	44.73	61.19	60.11	20.44
Genetic Advance%	1.28	1.75	13.87	35.18	13.22	33.86	2.58
Cross II (NVSR 3169 × Pusa 1509)							
Heritability (ns)%	31.22	79.01	80.36	33.79	18.91	35.15	64.87
Genetic Advance%	2.16	6.6	18.99	28.83	3.21	19.07	10.40
Cross III (Lal Kada Gold × DRR Dhan 62)							
Heritability (ns)%	-	-	77.54	59.47	-	32.89	61.14
Genetic Advance%	-	-	12.84	45.77	-	17.12	5.71
Cross IV (Lal Kada Gold × IR 55179-3B-11-3)							
Heritability (ns)%	79.64	65.41	71.58	45.26	19.58	21.54	64.41
Genetic Advance%	7.95	5.30	15.80	39.56	2.49	11.1	5.72

Table 2: Estimates of narrow-sense 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 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 3169 × Gontra Bidhan 3)						
Heritability (ns)%	33.6	63.8	83.18	53.54	86.3	15.63
Genetic Advance%	5.39	13.41	16.98	49.05	80.9	3.7
Cross II (NVSR 3169 × Pusa 1509)						
Heritability (ns)%	79.52	57.23	-	-	14.29	66.17
Genetic Advance%	21.54	18.52	-	-	11.43	27.85
Cross III (Lal Kada Gold × DRR Dhan 62)						
Heritability (ns)%	42.18	31.68	84.94	58.76	46.03	76.18
Genetic Advance%	6.4	5.26	19.77	46.59	31.03	20.35
Cross IV (Lal Kada Gold × IR 55179-3B-11-3)						
Heritability (ns)%	55.03	58.25	-	14.04	45.73	62.97
Genetic Advance%	8.99	12.81	-	13.73	41.09	13.98

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

In Lal Kada Gold × IR 55179-3B-11-3, days to flowering (79.64%), plant height (71.58%), and kernel length (64.41%) exhibited high heritability, while moderate to high GA% was recorded for straw yield (41.09%), 100-grain weight (13.73%), and L/B ratio (12.81%). These values indicate the presence of additive gene action in certain traits. However, grain yield per plant showed low heritability (14.04%) and moderate GA% (13.73%), reflecting strong environmental influence and the need for modified selection strategies.

Evaluation of narrow-sense heritability and GA% across thirteen traits in the four rice crosses indicated varying degrees of additive genetic control. Traits such as plant height, productive tillers, 100-grain weight, and grain yield showed high h^2_n and GA%, indicating predominance of additive gene action and scope for direct selection. A visual comparison of heritability and genetic advance across crosses for key traits is illustrated in Figure 1."

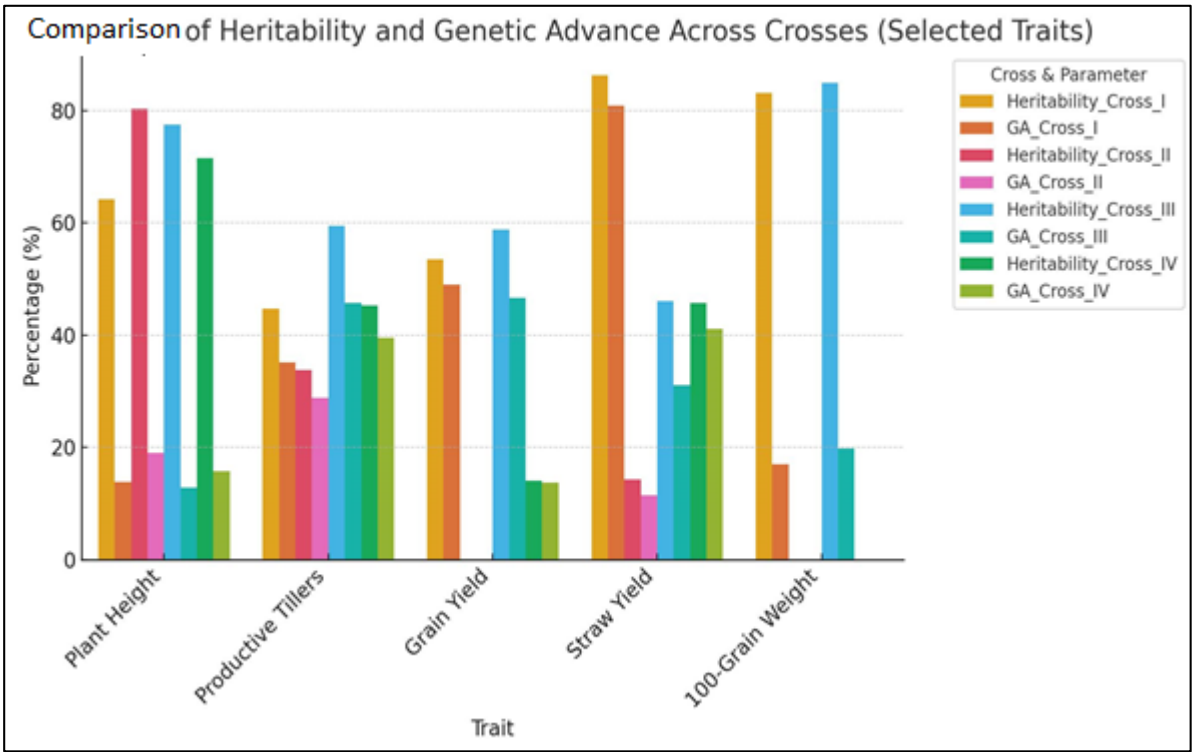

Fig 1: Combined bar chart comparing narrow-sense heritability (h^2_n) and genetic advance as percent of mean (GA%) across four rice crosses (NVSR 3169 × Gontra Bidhan 3, NVSR 3169 × Pusa 1509, Lal Kada Gold × DRR Dhan 62, and Lal Kada Gold × IR 55179-3B-11-3) for five key agronomic traits. Each group of bars shows the heritability and GA% for a given trait across the four crosses.

In contrast, traits with low estimates may require recurrent selection or heterosis breeding to exploit non-additive gene effects. These results corroborate previous findings by Patel *et al.* (2022) [11], Harijan *et al.* (2021) [7], and Satasiya *et al.* (2022) [14], who reported similar genetic patterns for yield and its components in rice, confirming that additive gene action plays a significant role in governing key agronomic traits. The observed predominance of additive gene action for key traits such as plant height, productive tillers, 100-grain weight, and grain yield aligns with the findings of these studies. In addition, similar patterns were also reported by Akinwale *et al.* (2011) [2] and Ahmed *et al.* (2016) [1] for kernel dimensions and yield attributes, supporting the efficacy of early generation selection. Traits like harvest

index and panicle length, which showed lower heritability and GA% in the present study, also showed complex inheritance in previous reports by Divya *et al.* (2014) [6] and Lingaiah *et al.* (2023) [9]. These comparisons confirm that while several agronomic traits are governed by additive effects and suitable for direct selection, others may require delayed selection, recurrent breeding, or heterosis exploitation to capture their full genetic potential.

Heritability and Genetic Advance (GA%)

Heritability in the narrow sense (h^2_n) provides an estimate of the proportion of total phenotypic variation that is attributed to additive genetic variance. This parameter is of particular importance in plant breeding, as it reflects the potential of a trait to respond to selection. However, heritability alone does not predict the genetic gain; hence, it is interpreted together with the genetic advance as percent of mean (GA%), which indicates the expected progress from selection in the following generation.

In the present investigation, h^2_n and GA% were estimated for thirteen traits across F_2 and F_3 generations in four rice crosses. The magnitude of heritability estimates varied across traits and crosses, reflecting differential genetic control. According to the classification proposed by Robinson *et al.* (1949), traits were grouped into low (<30%), moderate (30-60%), and high (>60%) heritability, while GA% was interpreted based on Johnson *et al.* (1955) [8] as low (0-10%), moderate (10-20%), and high (>20%).

Traits such as plant height, 100-grain weight, productive tillers per plant, and grain yield per plant frequently exhibited high h^2_n coupled with high GA% across multiple crosses, suggesting a predominant role of additive gene action. Such traits are largely governed by fixable genetic effects, making them amenable to early generation selection and offering good scope for genetic improvement through direct phenotypic selection.

In contrast, traits such as days to flowering, days to maturity and panicle length often exhibited moderate heritability or lower GA% in certain crosses. These findings suggest a more complex genetic architecture involving non-additive gene effects or environmental interactions, where conventional selection methods may be less effective. For these traits, alternative strategies like delayed selection, recurrent selection, or biparental mating might be more suitable to accumulate favorable alleles.

Grain quality traits such as kernel length, kernel breadth, and L:B ratio exhibited a wide range of heritability and GA% values across crosses. In some combinations, moderate to high heritability accompanied by low GA% indicates the presence of additive effects partially masked by environmental influence or dominance effects. These traits may respond to selection but require more precise phenotyping or replicated testing to reduce environmental noise.

Evaluation of narrow-sense heritability and GA% across thirteen traits in the four rice crosses indicated varying degrees of additive genetic control. Traits such as plant height, productive tillers, 100-grain weight, and grain yield showed high h^2_n and GA%, indicating predominance of additive gene action and scope for direct selection.

Traits like panicle length, days to flowering, and kernel dimensions exhibited moderate to low h^2_n or GA%, reflecting more complex inheritance. These traits may benefit from advanced breeding strategies like recurrent selection or selection in later generations to capture hidden variability.

Overall, traits with both high heritability and high genetic advance offer the greatest promise for efficient selection in rice improvement programs. Cross-specific patterns in narrow-sense heritability are further represented in a heatmap (Figure 2).

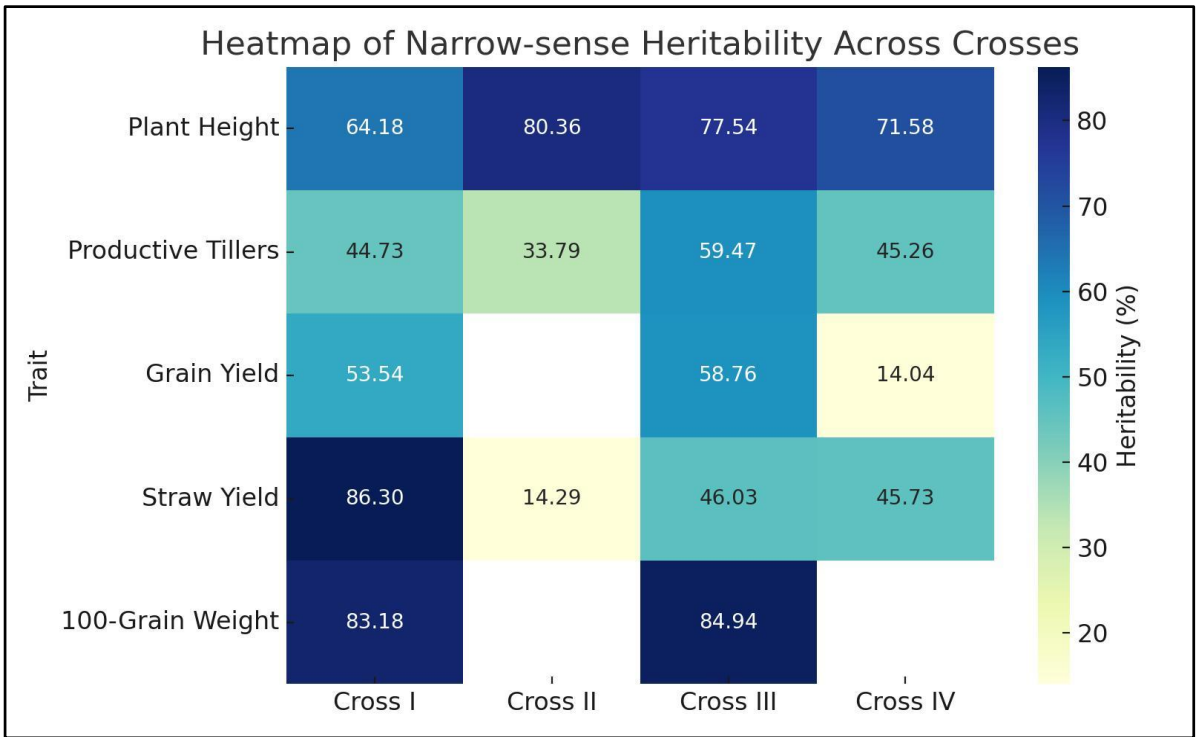

Fig 2: Heatmap representation of narrow-sense heritability (h^2_n) across selected traits and four rice crosses. Darker shades indicate higher heritability estimates, suggesting stronger additive genetic control and greater potential for genetic gain through selection.

Conclusion

The present investigation demonstrated substantial variability in narrow-sense heritability (h^2_n) and genetic advance as percent of mean (GA%) among thirteen quantitative traits across four diverse rice crosses. Traits including grain yield per plant, plant height, productive tillers per plant, straw yield per plant, and 100-grain weight consistently showed moderate to high estimates of narrow-sense heritability coupled with high genetic advance, indicating a predominance of additive gene action. These findings suggest that such traits are primarily governed by fixable genetic effects and hence, direct selection can be effectively practiced during early segregating generations.

The effectiveness of direct phenotypic selection for these traits is underscored by the substantial expected genetic gain, making them prime targets for immediate improvement through conventional breeding methods. Conversely, traits such as kernel length, panicle length, harvest index, and certain quality parameters displayed comparatively lower estimates of heritability and genetic advance. This lower magnitude reflects the complexity of genetic inheritance involving significant non-additive gene effects, such as dominance and epistasis, and indicates a substantial influence of environmental factors. Consequently, direct selection in early generations for these traits would likely be less effective due to the masking effect of non-additive gene action and environmental fluctuations. Thus, these traits necessitate alternative breeding approaches to enhance genetic progress. Breeding strategies such as recurrent selection, biparental mating, population improvement schemes, or hybrid breeding are recommended to effectively exploit the non-additive genetic variance inherent in these traits.

Furthermore, substantial cross-specific variability was observed in genetic parameters, reinforcing the necessity for trait-specific and cross-specific breeding strategies. For instance, the cross NVSR 3169 × Gontra Bidhan 3 exhibited high heritability and GA% for productive tillers, grain yield, and straw yield, making it particularly suitable for direct phenotypic selection. Similarly, crosses such as Lal Kada Gold × DRR Dhan 62 demonstrated favorable genetic parameters for traits like grain yield, productive tillers, 100-grain weight, and harvest index, emphasizing their potential for significant genetic improvement through early generation selection. In contrast, the cross NVSR 3169 × Pusa 1509 displayed mixed results, with grain size traits exhibiting promising heritability but other traits showing moderate or low genetic parameters, suggesting a selective and more nuanced breeding strategy is required.

The clear delineation of traits based on genetic parameters highlights the importance of interpreting heritability alongside genetic advance rather than in isolation. Traits combining both high heritability and high genetic advance consistently emerged as ideal candidates for simple and direct phenotypic selection, while traits with moderate or discordant values suggest partial additive control influenced by environment, thereby requiring more strategic selection approaches and rigorous evaluation methodologies to enhance selection efficiency.

Overall, this comprehensive trait-wise and cross-specific genetic analysis provides critical and actionable insights for rice breeders. It outlines a clear framework for optimizing selection decisions, prioritizing breeding objectives, and effectively harnessing genetic variation to achieve substantial yield gains and agronomic improvements. By distinctly differentiating between additive and non-additive gene effects across diverse traits and genetic backgrounds, these findings significantly enhance the precision, efficiency, and success rate of rice improvement programs.

Author's Contributions

Naresh Chaudhary, V. P. Patel, R. K. Patel, V. B. Patel, and Kaushal Modha designed the study. Naresh Chaudhary, Hemali Pandya, V. B. Rana, Soumyanetra Saha, Vishwa Gohil, D. P. Patel, and M. R. Prajapati collected the data. Naresh Chaudhary, Vishwa Gohil and K. G. Baria organized the data, performed the statistical analysis and prepared the manuscript.

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Disclaimer (AI)

The authors declare that generative AI technologies, including OpenAI ChatGPT (GPT-5 model), were used during the writing and editing of this manuscript to assist in language refinement and formatting. All intellectual and analytical contributions are the authors' own, and the AI was used solely as a tool for improving readability.

Competing Interests

The authors declare that no competing interests exist.

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