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**D Vineela**  
Master's Student, Department of  
Genetics and Plant Breeding,  
College of Agriculture, PJTAU,  
Rajendranagar, Hyderabad,  
Telangana, India

**G Shiva Prasad**  
Assistant Professor, Department  
of Genetics and Plant Breeding,  
Agricultural College, Huzurnagar,  
Suryapet

**K Sumalini**  
Professor, Department of Genetics  
and Plant Breeding, College of  
Agriculture, Rajendranagar,  
Hyderabad

**D Srinivasa Chary**  
Professor, Department of Statistics  
and Mathematics, College of  
Agricultural Engineering, Kandi

## Corresponding Author:

**D Vineela**  
Master's Student, Department of  
Genetics and Plant Breeding,  
College of Agriculture, PJTAU,  
Rajendranagar, Hyderabad,  
Telangana, India

## Genetic variability for yield and its components in alkalinity and inland salinity stress in rice (*Oryza sativa* L.)

**D Vineela, G Shiva Prasad, K Sumalini and D Srinivasa Chary**

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### Abstract

The present study consisted of fifty genotypes including four checks and were evaluated under naturally occurring alkalinity and inland salinity stress at ARS, Kampasagar during *kharif* 2025, to estimate genetic variability, heritability, and genetic advance for twelve agronomic traits. The experiment was laid out in an Alpha Lattice Design with two replications. Analysis of variance revealed highly significant variation among genotypes for all the traits studied, indicating the existence of substantial genetic variability within the experimental material and ample scope for improvement through selection. The phenotypic coefficient of variation was consistently higher than the genotypic coefficient of variation for all traits, though the narrow gap between the two indicated that the observed variability was predominantly genetic in nature with limited environmental influence. High genotypic and phenotypic coefficients of variation were recorded for seedling mortality, yellowing score, number of tillers per plant, number of productive tillers per plant and sterility percentage, while plant height, number of filled grains per panicle, and grain yield showed moderate variability, and days to 50% flowering, panicle length, number of grains per panicle, and test weight showed low variability. Seedling mortality, yellowing score, number of tillers per plant, number of productive tillers per plant, and number of filled grains per panicle, exhibited high heritability coupled with high genetic advance as a percentage of the mean, indicating the predominance of additive gene action and good scope for improvement of these traits through direct phenotypic selection. The results identified seedling mortality, yellowing score, number of tillers per plant, and number of productive tillers per plant as effective selection criteria for developing rice cultivars tolerant to combined alkalinity and inland salinity stress.

**Keywords:** Rice, genetic variability, GCV, PCV, heritability, genetic advance, alkalinity, inland salinity

### 1. Introduction

Rice (*Oryza sativa* L.) is the primary staple food for more than half of the world's population and plays a vital role in global food security. India is the world's leading rice producer and occupies an area of 51 mha with an annual production of approximately 150 mt and an average productivity of about 4.4 t/ha (USDA-FAS, 2025) <sup>[18]</sup>. Despite this impressive production, rice cultivation is increasingly challenged by salt-affected soils, which substantially reduce productivity in many rice growing regions. India alone possesses nearly 6.72 mha of salt-affected land, including about 2.95 mha of saline soils and 3.77 mha of sodic or alkaline soils, where rice is one of the major cultivated crops (FAO, 2024) <sup>[5]</sup>. Among these constraints, alkalinity stress is particularly severe because high soil pH and carbonate-bicarbonate accumulation adversely affect nutrient availability, ionic balance, and root growth, resulting in greater yield losses than salinity alone. However, compared with salinity, alkalinity has received relatively less attention in rice improvement programmes (Singh *et al.*, 2023) <sup>[16]</sup>.

The development of rice cultivars capable of performing well under these adverse conditions depends largely on the availability of sufficient genetic variability within the breeding material. Improving performance under such conditions requires a clear understanding of the genetic variability available within breeding material, since grain yield under stress is a complex quantitative trait governed by multiple genes and influenced by environmental factors, the assessment of genetic variability is an essential step in any crop improvement programme (Yadav *et al.*, 2024) <sup>[19]</sup>. Genetic parameters such as the genotypic coefficient of variation (GCV),

phenotypic coefficient of variation (PCV), heritability, and genetic advance expressed as a percentage of the mean (GAM) provide valuable information on the magnitude of genetic variation, the relative influence of genetic and environmental factors, and the expected response to selection (Praveena *et al.*, 2025) <sup>[15]</sup>.

Although rice germplasm possesses a rich reservoir of genetic diversity, much of its potential remains underutilized in crop improvement programmes. The effective utilization of this diversity depends on identifying traits that exhibit sufficient heritable genetic variation and can respond efficiently to selection. Such information is essential for broadening the genetic base, selecting suitable parental lines, and enhancing the efficiency of future breeding programmes. Therefore, the present study was undertaken to estimate genetic variability, heritability, and genetic advance for yield and its component traits in rice genotypes evaluated under alkalinity and inland salinity stress, with the objective of identifying promising traits for the

development of high-yielding and stress-tolerant rice cultivars.

## 2. Materials and Methods

### 2.1 Experimental site and soil characteristics

The field experiment was conducted at Agricultural Research Station, Kampasagar, during *kharif*, 2025. The experimental site was characterized by naturally occurring combined alkalinity and inland salinity, with a soil pH of 9.30, electrical conductivity (EC) of 4.68 dS m<sup>-1</sup>, and exchangeable sodium percentage (ESP) of 88.0, located at 17.05° N latitude and 79.26° E longitude

### 2.2 Plant material and experimental design

Fifty rice (*Oryza sativa* L.) genotypes from Kampasagar and Indian Rice Research Institute (IRRI) were evaluated in an alpha-lattice design with two replications and five incomplete blocks per replication with a spacing of 20 × 15 cm, a design suited to accommodating soil heterogeneity across the stress-affected field.

**Table 1:** List of rice genotypes evaluated at ARS, Kampasagar during kharif 2025

| S. No. | Genotype                           | S. No. | Genotype                     |
|--------|------------------------------------|--------|------------------------------|
| 1      | IRRI 147                           | 26     | KPS-64                       |
| 2      | SWARNA                             | 27     | KPS-65                       |
| 3      | IRRI 154                           | 28     | KPS-12534                    |
| 4      | Bhuthnath                          | 29     | KPS-12611                    |
| 5      | FL 478 (salinity tolerant check)   | 30     | KPS-12615                    |
| 6      | CSR 10                             | 31     | KPS-12631                    |
| 7      | ADT 45                             | 32     | KPS-12676                    |
| 8      | CSR 36 (alkalinity tolerant check) | 33     | KPS-12679                    |
| 9      | CSR 28                             | 34     | KPS-14368                    |
| 10     | CR Dhan 414                        | 35     | KPS-14411                    |
| 11     | MCM-152                            | 36     | KPS-14636                    |
| 12     | IR24LT <sub>2</sub> 933            | 37     | KPS-14751                    |
| 13     | IR19R1076                          | 38     | KPS-14809                    |
| 14     | IR20LT <sub>2</sub> 253            | 39     | KPS-14892                    |
| 15     | IRRI 185                           | 40     | KPS-14951                    |
| 16     | IR23LT <sub>12</sub> 96            | 41     | MCM-101                      |
| 17     | IR24LT <sub>2</sub> 377            | 42     | PUSA- 44 (susceptible check) |
| 18     | IR16T <sub>15</sub> 38             | 43     | RDR-1200                     |
| 19     | IR18T <sub>12</sub> 54             | 44     | RNR-35008                    |
| 20     | KPS-2874 (local check)             | 45     | RNR-11718                    |
| 21     | KPS-6251                           | 46     | KNM-7715                     |
| 22     | KPS-10642                          | 47     | KNM-12368                    |
| 23     | KPS-12673                          | 48     | JGL-28639                    |
| 24     | KPS-55                             | 49     | WGL-1537                     |
| 25     | KPS-59                             | 50     | WGL-1246                     |



**Plate 1:** Overview of salinity block

### 2.3 Observations

Data were recorded on five randomly selected plants for traits viz., plant height, Yellowing score, number of tillers per plant, number of productive tillers, panicle length, number of grains per panicle, number of filled grains per panicle, 1000 grain weight while, on plot basis for seedling mortality, days to 50% flowering, and grain yield. Sterility (%) was calculated as per the formula given below:

$$\text{Sterility (\%)} = \frac{\text{Total grains} - \text{Number of filled grains}}{\text{Total grains}} \times 100$$

In addition to this, alkalinity/salinity tolerance was scored using the Standard Evaluation System (SES) developed by the International Rice Research Institute (IRRI, 2013) <sup>[7]</sup>, on a 1–9 visual scale based on the extent of leaf tip burning, chlorosis, and growth reduction relative to unstressed controls, recorded at reproductive stage.

**Table 2:** Salt injury score under alkalinity and inland salinity stress (IRRI-SES 2013) <sup>[7]</sup>

| Salt injury score | Reaction to salinity | No. of genotypes | Genotypes                                                                                                                                                                                                                                                                       |
|-------------------|----------------------|------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1                 | Highly tolerant      | 0                | -                                                                                                                                                                                                                                                                               |
| 3                 | Tolerant             | 11               | CSR-28, Bhuthnath, KPS-12534, FL 478, KPS-12676, CSR-10, SWARNA, IR23LT <sub>12</sub> 96, KPS-14809, RDR-1200, CSR-36                                                                                                                                                           |
| 5                 | Moderately Tolerant  | 21               | RNR-11718, KNM-7715, IR24LT <sub>2</sub> 933, KPS-12615, IRRI 147, MCM-101, KPS-12673, KPS-12679, MCM-152, KPS-65, CR Dhan 414, KPS-2874, IR16T <sub>15</sub> 38, KPS-64, IR24LT <sub>2</sub> 377, IR19R1076, IRRI 154, IR20LT <sub>2</sub> 253, WGL-1537, KNM-12368, JGL-28639 |
| 7                 | Sensitive            | 11               | ADT-45, WGL-1246, KPS-10642, KPS-12631, KPS-14892, KPS-14951, KPS-14636, KPS-14411, RNR-35008, IRRI 185, KPS-55                                                                                                                                                                 |
| 9                 | Highly Sensitive     | 7                | KPS-14751, IR18T <sub>12</sub> 54, KPS-14368, KPS-12611, KPS-59, KPS-6251, PUSA-44                                                                                                                                                                                              |

## 2.4 Statistical analysis

The observations for each genotype were recorded from five randomly selected plants in each replication, and the mean values were used for further analysis. The recorded data were subjected to analysis of variance (ANOVA) following the procedure described by Patterson and Williams (1976) <sup>[13]</sup>. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to the method proposed by Burton and Devane (1953) <sup>[3]</sup>. Broad-sense heritability ( $H^2$ ) was computed following the approach of Hanson *et al.*, (1956) <sup>[6]</sup>. while genetic advance (GA) and genetic advance expressed as a percentage of the mean (GAM) were estimated using the method of Johnson *et al.* (1955) <sup>[8]</sup>. Heritability estimates were classified as low (<30%), moderate (30–60%), and high (>60%), whereas GAM values were categorized as low (<10%), moderate (10–20%), and high (>20%) as suggested by Johnson *et al.* (1955) <sup>[8]</sup>. All statistical analyses were performed using RStudio (Version 2026.05.0+218).

## 3. Results and Discussion

The success of any crop improvement programme depends on the availability of sufficient genetic variability within the breeding material, as selection can only be effective when heritable variation is present. The genotypic and phenotypic coefficients of variation (GCV and PCV) provide an estimate of the magnitude of genetic variability, whereas heritability and genetic advance as a percentage of the mean (GAM) indicate the extent to which this variability is genetically controlled and the expected response to selection. Traits exhibiting high heritability coupled with high GAM are generally governed by additive gene action and are therefore considered reliable targets for direct phenotypic selection. Analysis of variance (Table 3) revealed highly significant differences among the rice genotypes for all the twelve traits studied, indicating the presence of considerable genetic variability under combined alkalinity and inland salinity stress. This variability provided the basis for estimating GCV, PCV, heritability, and GAM, the results of which are presented in Table 4 and discussed for individual traits in the following sections.

**Table 3:** Analysis of variance (ANOVA) for yield and its components

| Source of Variation | d.f | Mean sum of squares |         |          |           |          |         |         |          |           |           |         |             |
|---------------------|-----|---------------------|---------|----------|-----------|----------|---------|---------|----------|-----------|-----------|---------|-------------|
|                     |     | SM                  | YS      | DFF      | PH        | NOT      | NPT     | PL      | NGP      | NFG       | SP        | TW      | GY          |
| Replication         | 1   | 40.781              | 0.354   | 12.461   | 267.912   | 0.176    | 2.161   | 1.510   | 14.372   | 76.650    | 98.996    | 1.488   | 61157.29    |
| Treatment           | 49  | 349.958**           | 6.734** | 98.013** | 240.887** | 14.030** | 6.599** | 8.684** | 43.861** | 128.120** | 210.518** | 4.797** | 303835.14** |
| Block               | 8   | 257.452             | 2.175   | 40.310   | 99.238    | 14.468   | 3.713   | 5.981   | 17.772   | 34.085    | 51.964    | 3.183   | 354309.65   |
| Error               | 41  | 17.522              | 0.788   | 19.190   | 43.303    | 2.385    | 0.960   | 2.396   | 4.198    | 20.372    | 63.899    | 0.886   | 64238.36    |

\*\*Significant at 1% level; \* Significant at 5% level;

S. No. Serial number, d.f: degrees of freedom, SM: Seedling mortality (%), YS: Yellowing score, DFF: Days to 50% flowering, PH: Plant height, NOT: Number of tillers per plant, NPT: Number of productive tillers per plant, PL: Panicle length, NGP: Number of grains per panicle, NFG: Number of filled grains per panicle, SP: Sterility percentage (%), TW: 1000 grain weight, GY: Grain yield kg per ha.

## 3.1 Genotypic and Phenotypic Coefficients of Variation

In the present investigation, high values of GCV and PCV were observed for seedling mortality (42.84%, 45.04%), yellowing score (31.13%, 35.02%), number of productive tillers (32.85%, 38.04%), sterility percentage (31.23%, 42.72%), and number of tillers (23.16%, 27.49%), indicating the presence of considerable inherent variability among the genotypes for these traits. Moderate estimates of GCV and PCV were recorded for plant height (10.23%, 12.27%), number of filled grains per panicle (16.47%, 19.01%), and grain yield (11.01%, 13.65%). Low estimates of GCV and PCV were observed for days to 50% flowering, panicle length, number of grains per panicle, and test weight, indicating comparatively limited inherent variability and reduced scope for improvement through direct selection for these

traits within the genotypes evaluated.

Across all twelve traits, PCV values were higher than or close to the corresponding GCV values, and the differences between them were consistently small. This narrow gap indicated that the observed variability was predominantly due to genotypic differences rather than environmental influence, a notable finding given that the trial was conducted under considerable alkalinity-salinity stress, and consistent with the pattern reported for yield related rice traits by Chacko *et al.* (2023) <sup>[4]</sup>, where a narrow PCV-GCV gap similarly indicated that genetic rather than environmental factors were the primary drivers of trait expression given by Kalaiselvan *et al.* (2019) <sup>[9]</sup> and Surjaye *et al.* (2022) <sup>[17]</sup> under sodic and stress field conditions respectively.

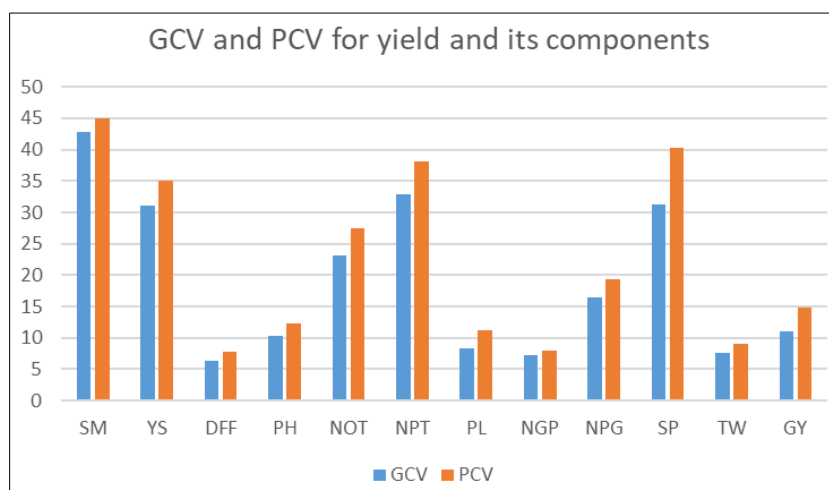


**Fig 1:** Graphical representation of GCV and PCV for yield and yield attributing traits and grain quality traits

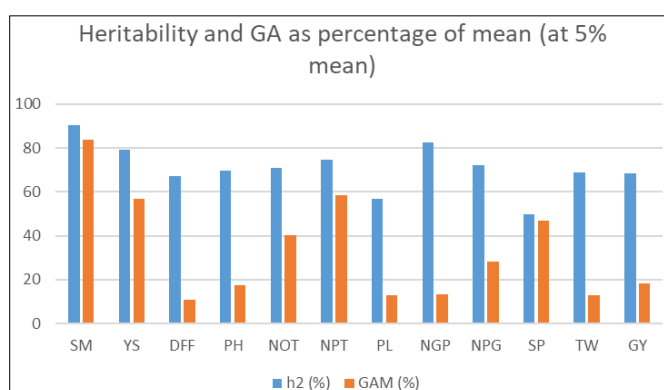


**Fig 2:** Graphical representation of Heritability in broad sense and Genetic advance as percentage of mean for yield and yield attributing traits and grain quality traits

### 3.2 Heritability and Genetic Advance

Heritability estimates varied from moderate to high across the twelve traits studied, ranging from 53.43% (sterility percentage) to 90.46% (seedling mortality), with half of the traits recording values above 70%, indicating that phenotypic expression was under fairly strong genetic control even under the imposed stress. However, heritability alone is a less reliable indicator of selection response, since broad-sense heritability incorporates both additive and non-additive genetic variance; a trait may show high heritability while remaining largely governed by non-additive effects, in which case genetic advance stays low despite the high heritability estimate. The combined use of heritability with genetic advance as percentage of mean (GAM) therefore provides a more dependable basis for identifying traits amenable to direct selection.

Genetic advance as percentage of mean was high (>20%) for seedling mortality (83.93%), sterility percentage (47.02%), number of productive tillers (58.46%), yellowing score (57.01%), number of tillers (40.18%), and number of filled grains per panicle (28.41%). Among these, seedling mortality, yellowing score, number of tillers per plant, number of productive tillers per plant, and number of filled grains per panicle also recorded high heritability, indicating preponderance of additive gene action, and direct phenotypic selection should be effective for their

improvement. Sterility percentage, despite recording only moderate heritability, showed high genetic advance as percentage of mean, suggesting that selection gains for this trait, while still attainable, may be comparatively less predictable due to a greater relative influence of non-additive and environmental effects. This was in agreement with that of Bindu *et al.* (2024) [2], who recorded high heritability coupled with high genetic advance for seedling mortality percentage, Karthikeyan *et al.* (2019) [10] and Praveena *et al.* (2025) [15] for tiller related traits, Mahantashivayogayya *et al.* (2016) [11] and Prashanth *et al.* (2020) [14] for filled grains per panicle, Manohara *et al.* (2020) [12] for sterility percentage.

High heritability coupled with moderate genetic advance is generally attributed to a comparatively narrow genetic base for the traits within the panel evaluated, or to a partial influence of non-additive gene action, rather than to environmental variance alone, since heritability itself remained high. A comparable pattern for days to 50% flowering was reported by Akshay *et al.* (2022) [1], who similarly found high heritability with only moderate genetic advance and attributed it to the joint involvement of additive and non-additive gene effects. For traits in this category, improvement is likely to require intermating of superior segregants or recurrent selection over several generations, since the moderate genetic advance indicates that gains from a single cycle of direct selection alone would be limited.

Taken together, seedling mortality and number of productive tillers per plant emerge as the most promising traits for direct selection toward alkalinity-salinity tolerance in this germplasm, combining high exploitable genetic variability, high heritability, and high genetic advance. Sterility percentage, though showing only moderate heritability, recorded high genotypic variability and genetic advance, and as an established physiological indicator of salt/alkali injury (Singh *et al.*, 2023; Karthikeyan *et al.*, 2019) [16, 10] remains biologically relevant for early-stage tolerance screening. Grain yield, despite moderate genetic advance, recorded high heritability and remains the ultimate target trait for selection, its improvement best achieved indirectly through selection on strongly heritable component and tolerance-indicator traits such as seedling mortality and sterility percentage rather than through direct selection alone.

**Table 4:** Genetic variability, heritability and genetic advance as per cent of mean for yield, yield components and grain quality characters in rice genotypes

| TRAITS                             | Mean    | Minimum | Maximum | GCV   | PCV   | h <sup>2</sup> (%) | GAM (%) |
|------------------------------------|---------|---------|---------|-------|-------|--------------------|---------|
| Seedling mortality                 | 30.10   | 3.81    | 78.28   | 42.84 | 45.04 | 90.46              | 83.93   |
| Yellowing score                    | 5.54    | 2.59    | 9.00    | 31.13 | 35.02 | 79.04              | 57.01   |
| Days 50% flowering                 | 98.97   | 83.9    | 116.35  | 6.34  | 7.73  | 67.25              | 10.72   |
| Plant height                       | 97.15   | 72.42   | 124.16  | 10.23 | 12.27 | 69.53              | 17.57   |
| Number of tillers per plant        | 10.42   | 3.55    | 14.55   | 23.16 | 27.49 | 70.94              | 40.18   |
| Number of productive tillers/plant | 5.11    | 0.55    | 7.85    | 32.85 | 38.04 | 74.61              | 58.46   |
| Panicle length                     | 21.1    | 15.90   | 25.35   | 8.40  | 11.15 | 56.75              | 13.04   |
| Number of grains/panicle           | 62.25   | 55.02   | 68.69   | 7.15  | 7.88  | 82.53              | 13.39   |
| Number of filled grains/panicle    | 44.59   | 21.98   | 58.71   | 16.47 | 19.01 | 72.56              | 28.41   |
| Sterility percentage               | 28.66   | 14.11   | 56.01   | 31.23 | 42.72 | 53.43              | 47.02   |
| 1000 grain weight                  | 18.53   | 14.85   | 21.66   | 7.55  | 9.10  | 68.82              | 12.90   |
| Grain yield                        | 3091.31 | 2066    | 4008    | 11.01 | 13.65 | 65.09              | 18.30   |

GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation;

h<sup>2</sup>bs = Heritability in broad sense; GAM = Genetic advance in percentage of mean

#### 4. Conclusion

The present investigation revealed substantial genetic variability among the fifty rice genotypes evaluated under combined alkalinity and inland salinity stress. High genotypic and phenotypic coefficients of variation were observed for seedling mortality, yellowing score, number of tillers per plant, number of productive tillers per plant, and sterility percentage, indicating considerable exploitable genetic variability for these traits. Seedling mortality, yellowing score, number of tillers per plant, number of productive tillers per plant, and number of filled grains per panicle exhibited high heritability coupled with high genetic advance as a percentage of the mean, suggesting the predominance of additive gene action and highlighting their suitability for improvement through direct phenotypic selection. In contrast, days to 50% flowering, number of grains per panicle, test weight, grain yield, and plant height recorded high heritability but only moderate genetic advance, indicating a comparatively lower expected response to a single cycle of direct selection despite strong genetic control. Improvement of these traits may therefore benefit from intermating of superior segregants or recurrent selection over successive generations to enhance exploitable variability before selection gains can be maximized. Among the evaluated traits, seedling mortality, yellowing score, number of tillers per plant, and number of productive tillers per plant emerged as particularly useful indicators of stress tolerance because of their high genetic variability and close association with plant performance under stress, despite sterility percentage showing only moderate heritability. These traits may therefore serve as reliable early-generation selection criteria for developing high-yielding rice cultivars adapted to combined alkalinity and inland salinity conditions.

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