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## Evaluation of genetic variability, heritability and genetic advance in selected landraces of rice (*Oryza sativa* L.)

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### Abstract

In the present experiment 24 landraces of rice from Telangana, Karnataka, and Chhattisgarh were used to conduct the research work. In *Kharif* (2022), the research work was conducted through a Randomized Block Design (RBD) with three replications at the research farm of the M.S. Swaminathan School of Agriculture (MSSSoA) at Centurion University of Technology and Management (CUTM), Paralakhemundi, Odisha. Total 15 quantitative parameters were recorded in order to evaluate genetic variability, heritability, and genetic advance. The analysis of the experimental data showed that the genotypes have a lot of variation. The investigation's findings revealed that characters such as the number of tillers per plant, the number of effective tillers per plant, the number of filled grains, the number of unfilled grains, and the grain yield per plant, all had high estimates of GCV and PCV. The plant height showed low levels of GCV and PCV, and the traits 1000-seed weight, number of tillers per plant, number of effective tillers per plant, number of grains per plant, kernel length, number of filled grains, grain yield per plant and number of unfilled grains all showed high heritability along with high genetic advance as mean percentage. For grain breadth, low genetic progress and low heritability were observed.

**Keywords:** Genetic advance, heritability, PCV, variability, landrace rice

### Introduction

Asian rice (*Oryza sativa* L.) is a member of the Gramineae family and the Oryzoidea subfamily. Over a third of the world's population is fed by rice, an important staple grain that has been grown for over 10,000 years and may grow to a height of 2 to 6 feet. If we research the rice's health advantages, it also has some positive effects.

Rice is a food that is high in calories and low in cholesterol. It is high in carbohydrates, protein, and healthy fats, supports cardiovascular health, lowers blood pressure, prevents cancer, treats skin conditions, and prevents cancer disease. There is also vitamin B6, calcium, magnesium, and iron. Recent analysis by the United States Department of Agriculture indicates (USDA), (Siddiq *et al.*, 2021) <sup>[8]</sup> around 20% of all food calories worldwide come from rice. More over 70% of Asians eat rice, making it a staple meal in human diets and a vital component of Indian traditional cuisine. For these people, rice has come to represent a grain of life. About 49 percent of the calories we consume as humans come from rice, wheat, and maize, with rice making up 23 percent, wheat making up 17 percent, and maize making up 9 percent. Thus, rice accounts for the majority of calories consumed by the entire world's population and are crucial for both economic growth and food security. The two major varieties of Asian rice that are grown are split into two groups: Japonica and Indica. Among the two groups physiological, morphological and genetic differences exist. Contrarily, rice is very diverse, and there are many cultivars that are intermediates between these groups and don't exactly fit into this classification.

With 90% of the world's rice land, Asia is referred to as the "Rice Bowl" of the world. According to (Anuj *et al.*, 2020) <sup>[1]</sup> Rice is one of the most significant crops in India, which is the largest country in the world by land area and comes in second place in terms of production and consumption just behind China. Because rice requires a lot of water to grow, it is only grown in India during the monsoon. For any the breeding effort to be successful, the population's genetic variety must be high. Any crop's base population should come from the Germplasm since it offers a wide range of variety. There is a wealth of information in nature that can be used to inform the selection of the best parents for various breeding programmes by plant breeders. This information includes the sort and degree of genetic difference.

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Transgressive segregation is more likely to occur when the parents are more different. Larger likelihood of obtaining good recombinants due to a higher degree of segregating generation diversity. The availability of so many different rice options may also be contributing to its widespread global growth.

### Materials and Methods

The M.S. Swaminathan School of Agriculture (MSSSoA) at Centurion University of Technology and Management (CUTM), Paralakhemundi, Odisha, is where the current experiment was carried out.

The farm is 182.9 m above sea level and is situated at coordinates 23.39 N latitude and 87.42 E longitudes. 24 different rice Germplasm samples from Telangana, Chhattisgarh, and Karnataka make up the experimental material (Table No.1). These lines were planted using a three-replication randomized block design (RBD). Weeds were kept out of the test plots. Weeding by hand was done as necessary. The crop was grown in accordance with the suggested set of procedures. From each genotype in each replication, five plants were randomly chosen to record observations on the days to 50% flowering, days to maturity, plant height (cm), total number of effective tillers per plant, panicle length (mm), number of grains/panicle, kernel length (mm), kernel breadth (mm), L/B ratio, 1000-seed weight (g), grain yield per plant, grain length, grain breadth, number of filled grains/panicle, and number of unfilled grains/panicle. The heritability in the broad sense ( $h^2$ ) was used to estimate PCV and GCV, and genetic advance, or the projected genetic gain,

### Result and Discussion

Since all of the characteristics' mean sums of squares due to genotypes were significant according to the analysis of variance ( $P > 0.05$  and  $P > 0.01$ ), it was clear that the material under examination had a high degree of genetic diversity. This implied that there were genetic variations between the genotypes that were inborn. For all the traits under examination, the phenotypic coefficient of variation was noticeably larger than the genotypic coefficient of variance as is customary. Certain show how these qualities are influenced by environmental factors. To make inferences regarding these characteristics, PCV and GCV were categorized as low (below 10%), medium (10%–20%), and high (beyond 20%).

The PCV and GCV showed high tiller density (32.389 and 32.008), effective tiller density (44.712 and 43.85), filled grain density (44.677 and 44.308), unfilled grain density (46.666 and 46.084), and grain yield per plant, respectively (31.583 and 30.324). (Singh *et al.*, 2018; Tefera *et al.*, 2018; Rajendra *et al.*, 2017 and Dhakal *et al.*, 2020) [9, 13, 6, 3] all reported similar findings for the rice crop. The 1000-seed weight (19.702) and the number of grains/panicle had moderate GCV (19.939). (Tefera *et al.*, 2018; Singh *et al.*, 2018; Dhakal *et al.*, 2020; Srujan *et al.*, 2019; Sameer *et al.*, 2016 and Bhargavi *et al.*, 2021) [13, 9, 3, 10, 11, 2] all found similar findings.

Grain length (17.723 and 10.593), kernel length (12.38 and 11.677), and kernel breadth (14.454 and 11.371) all had moderate PCV and GCV values, with L/B ratio coming in second (17.741 and 12.335). Days to maturity (10.280 and 9.446), panicle length (11.554 and 9.079), and grain breadth showed moderate PCV with low GCV, respectively (13.982 and 8.111). In the past, (Lakshmi *et al.*, 2015; Singh *et al.*,

2018; Srujan *et al.*, 2019 and Dhakal *et al.* 2020) [5, 9, 10, 3] reported findings of a similar nature. For plant height, lower PCV and GCV predictions were noted (8.223 and 8.123). The current finding agreed with earlier Bhargavi *et al.*, 2021) [2].

Heritability is a helpful quantitative metric that takes into account how environment and heredity interact to determine how a feature manifests all the features under consideration had their heritability for the broad sense evaluated, and the results are shown in Table No. 2. The observed range is (33.65 to 98.358%). High heritability (above 70%) was found in the current study for the following traits: days to maturity (85.633), 1000-seed weight (96.192), plant height (97.593), tillers per plant (97.658), effective tillers per plant (96.181), grains per panicle (83.278), kernel length (88.979), filled grains (98.358), unfilled grains (97.519), and grain yield per plant (92.185).

Earlier studies by (Padamaja *et al.*, 2008; Bhargavi *et al.*, 2021; and Venkata *et al.*, 2021) [5, 2, 16] reported similar findings. Panicle length (61.744) and kernel breadth, two features with moderate heritability (50 to 705%), were observed (61.888) In the past, (Singh *et al.*, 2018; Sriram *et al.*, 2017; and Dhakal *et al.*, 2020) [9, 8, 3] reported findings of a similar nature. High heritability and high genetic progress as percentage of mean suggest that these traits are mostly governed by additive gene action, suggesting that mass selection and progeny selection are viable methods for improving these traits.

Grain yield per plant (59.977) was the factor with the highest genetic advance percent of mean, followed by 1000-seed weight (>20%), tillers per plant (65.159), effective tillers per plant (88.59), grains per plant (37.482), kernel length (22.691), filled grains per panicle (90.523), and unfilled grains per panicle (93.747). These results were in agreement with the reports by (Bhargavi *et al.*, 2020; Singh *et al.*, 2018; Rajendra *et al.*, 2017; Umarani *et al.*, 2017) [2, 9, 7, 14]

However, for the traits Days to maturity (18.007), Panicle length (14.696), Plant height (16.531), Grain length (13.043), Kernel breadth (18.427), and L/B ratio, only moderate genetic improvement (10–20%) was seen (17.668).

Earlier reports of similar findings were from (Islam *et al.*, 2019; Dhakal *et al.*, 2020; and Srujan *et al.* 2019) [4, 3, 10]. For the trait grain breadth, low genetic progress as a percentage of the mean was observed.

High genetic gain is not always correlated with high heritability. Genetic progress and heritability are important selection criteria. Heritability estimations that are combined with genetic progress are typically more accurate at predicting the gain subject to selection. Breeders should exercise caution when making selections based on heritability because it generally indicates both additive and non-additive gene action. Additive gene action controls traits with high heritability and high genetic advance, which can be enhanced using a straightforward selection method.

Characters with high heritability and little to no genetic progress can be made better by combining superior population data obtained by combination breeding. In the current collection of data, high heritability along with genetic progress was recorded as a percentage for 1000-seed weight, number of tillers per plant, number of effective tillers per plant, number of grains per plant, kernel length, number of filled grains, number of unfilled grains, and grain yield per plant. This indicates that these traits are under the control of additive gene action. Days to maturity and plant height were

traits with high heritability and moderate genetic progress that were regulated by non-additive gene action.

### Conclusion

For all the characters under consideration, mean squares owing to genotypes were found to be highly significant, indicating that there was more variability among the rice genotypes. The genotypes of Ranikanda and Ambaimohiria displayed significant grain yield per plant. The genotypes Balududima, which has the shortest duration, and

Sunderamani, Dadiga, and Easakarawada, which had the highest number of filled grains per panicle, would be employed in future breeding programmes. The number of tillers per plant, the number of productive tillers per plant, the number of filled grains and the number of unfilled grains exhibited strong GCV, PCV, heritability, and genetic advance percent mean. These traits are used in upcoming breeding programmes since they are less influenced by the environment.

**Table 1:** List of Rice Land races

| Sl. No. | Genotype         | Source                |
|---------|------------------|-----------------------|
| 1       | Kukudumundu      | Telangana             |
| 2       | Karamgurvay      | Telangana             |
| 3       | Kistompeta gold  | Telangana             |
| 4       | Haladichudi      | Telangana, Karimnagar |
| 5       | Dadiga           | Telangana             |
| 6       | Balududima       | Telangana             |
| 7       | Basumathi        | Telangana             |
| 8       | Baruavanahi      | Kartanaka             |
| 9       | Ranikanda        | Kartanaka             |
| 10      | Kandasagara      | Kartanaka             |
| 11      | Thoda            | Telangana             |
| 12      | Kalagera         | Kartanaka             |
| 13      | Kakirakalu       | Telangana             |
| 14      | Kalamucch        | Karnataka             |
| 15      | Jivapuli         | Telanagna             |
| 16      | Ambaimohiria     | Telangana             |
| 17      | Kodisha          | Chhattisgarh          |
| 18      | Pedhasudhivanja  | Chhattisgarh          |
| 19      | Ottesuri         | Chhattisgarh          |
| 20      | Chinnasudhivanja | Chhattisgarh          |
| 21      | Sudhivanja       | Chhattisgarh          |
| 22      | Porasuvanje      | Chhattisgarh          |
| 23      | Sudi             | Chhattisgarh          |
| 24      | Easakarawada     | Chhattisgarh          |

**Table 2:** Estimation of components of variance and genetic parameters for 15 characters in selected landraces of rice

| Characters                     | Range  |        | Mean   | Coefficient of variation |       | Heritability (bs) | GA     | GA% Mean |
|--------------------------------|--------|--------|--------|--------------------------|-------|-------------------|--------|----------|
|                                | Min    | Max    |        | PCV                      | GCV   |                   |        |          |
| Days to maturity               | 51.33  | 72.33  | 63.03  | 10.21                    | 9.45  | 85.63             | 11.35  | 18.01    |
| 1000-seed weight (g)           | 16.69  | 38.34  | 26.10  | 20.09                    | 19.70 | 96.19             | 10.39  | 39.81    |
| Panicle length (cm)            | 21.35  | 29.48  | 25.26  | 11.55                    | 9.08  | 61.74             | 3.71   | 14.7     |
| Plant height (cm)              | 106.55 | 142.72 | 126.7  | 8.22                     | 8.12  | 97.59             | 20.94  | 16.53    |
| No. of tillers/plant           | 13.08  | 54.45  | 31.76  | 32.39                    | 32.01 | 97.66             | 20.69  | 65.16    |
| Grain length (cm)              | 5.95   | 10.56  | 8.51   | 17.72                    | 10.59 | 35.73             | 1.11   | 13.04    |
| Grain breadth (cm)             | 2.28   | 3.29   | 2.82   | 13.98                    | 8.11  | 33.65             | 0.27   | 9.69     |
| No. of effective tillers/plant | 7.48   | 36.08  | 18.59  | 44.71                    | 43.85 | 96.18             | 16.47  | 88.59    |
| No. of grains/panicle          | 19.28  | 38.77  | 28.39  | 21.85                    | 19.94 | 83.28             | 10.64  | 37.48    |
| Kernel length (cm)             | 4.38   | 7.93   | 6.24   | 12.38                    | 11.68 | 88.98             | 1.42   | 22.69    |
| Kernel breadth (cm)            | 2.44   | 3.77   | 3.05   | 14.45                    | 11.37 | 61.89             | 0.56   | 18.43    |
| No. of filled grains           | 32.54  | 256.71 | 114.12 | 44.68                    | 44.31 | 98.36             | 103.31 | 90.52    |
| No. of unfilled grains         | 9.76   | 44.75  | 21.92  | 46.67                    | 46.08 | 97.52             | 20.55  | 93.75    |
| L/B ratio                      | 1.51   | 2.72   | 2.02   | 17.74                    | 12.34 | 48.35             | 0.36   | 17.67    |
| Grain yield/plant (g)          | 10.24  | 48.58  | 35.82  | 31.58                    | 30.32 | 92.19             | 21.48  | 59.98    |

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