***Original Research Article***

**Genetic variability studies for yield, floral and quality traits in maintainer lines of rice (*Oryza sativa* L.)**

**ABSTRACT**

**Aim:** To study the variability, heritability and genetic advance for yield, floral and quality traits for selecting the efficient criteria for yield improvement.

**Study design:** Randomised block design

**Place and Duration of study:** Institute of Rice Research, ARI, Rajendranagar, Hyderabad, Telangana, during the kharif season in 2024.

**Methodology:** The study involved 28 maintainer lines and two checks. Sown in nursery and transplanted with spacing of 30 cm x15 cm after 25 days. Observations was recorded on days to 50% flowering, angle of the flower opening (°), stigma exertion (%), plant height (cm), panicle length (cm), number of productive tillers per plant, number of grains per panicle,1000 seed weight (g), grain yield per plant (g), kernel length (mm), kernel breadth (mm), kernel L/B ratio, hulling (%), milling (%), head rice recovery (%), head rice recovery and amylose content (%). Statistical analysis was conducted using INDOSTAT software for the analysis of variance for yield, floral and quality traits.

**Results:** Analysis of variance reveled that there was a significant variation (p < 0.01) among genotypes for all traits. Number of grains per panicle, 1000 seed weight, grain yield per plant shown highest PCV% and GCV % whereas moderate variation was exhibited by head rice recovery% and lowest variation exhibited by rest of the traits. High heritability was shown by all traits except panicle length. High heritability coupled with high genetic advance as percent mean was shown by number of productive tillers, number of grains per panicle, 1000 grain weight, grain yield, stigma length, kernel length, kernel breadth, kernel L/B ratio.

**Conclusion:**

The traits such as number of productive tillers, number of grains per panicle, 1000 grain weight, grain yield, stigma length, kernel length, kernel breadth, kernel L/B ratio showed high heritability with high genetic advance indicating that selection for these traits are effective.

**1.Introduction**

Rice (*Oryza sativa* L.) (2n=24) is a self-pollinated crop. Rice is the major staple food for nearly 50% of the world’s population. It is the predominant food crop in India in terms of area, production and production. At present all the varieties have reached the yield plateau. The development of hybrid rice varieties using male sterility, maintainer lines and fertility restoration systems has been one of the turning moments in rice history which helps to meet the food security. Whereas maintainer lines (B lines) are the key genotypes that are used to maintain the sterility and supply yield boosting genes to the female parent (A line) during new female line development in hybrid breeding. Maintainer lines (B lines) are mainly developed using B×B crossing method (Hossain et al.,2020). Hybrid rice breeders need to select new and better lines to develop new elite maintainers for CMS lines multiplication and as well hybrid rice production. Genetic variability plays a crucial role in crop improvement for selecting the elite maintainer lines for making rapid improvement in yield and other desirable characters as well as selecting the potential parent for hybridization programmes.

Greater the variability, there will be the greater chance for effective selection for desirable maintainer lines. The genotypic and phenotypic coefficient of variation helps in estimating the magnitude of genetic variation present in a population (Edukondalu et al., 2023).

Whereas, heritability (broad sense) is defined as the proportion of phenotypic variance comprising the sum of additive, dominance, and epistatic effects (Falconer,1996). Heritability is important parameter in quantitative genetics to determine the response to selection.

Heritability estimates give the measure of transmission of characters from one generation to another (Sabri et al., 2020). Knowledge of heritability of a trait helps in the selection of better maintainer lines. Genetic advance describes the degree of gain acquired in a trait under a particular selection pressure. High genetic advance along with high heritability offers the most effective condition for selection of a specific trait (Devi et al., 2022).

The present investigation was done in this context to know information on variability, heritability and genetic advance of the parameters towards yield and to identify superior maintainer line in respect of various floral and yield contributing traits.

**2.Materials and Methods**

The experimental material for the present investigation comprised of 28 genotypes along with 2 checks. The was done during Kharif season of 2024 in a randomized block design at the Institute of Rice Research, ARI, Rajendranagar, Hyderabad. All the genotypes were initially sown in a nursery bed. After twenty-five days after sowing, the seedlings were transplanted into the field with a spacing of 30 cm between the rows and 15 cm between the plants. Observations were recorded randomly on five plants for days to 50% flowering, angle of the flower opening (°), stigma exertion (%), plant height (cm), panicle length (cm), number of productive tillers per plant, number of grains per panicle,1000 seed weight, grain yield per plant.

Data was recorded on quality parameters such as kernel length (mm), kernel breadth (mm), kernel L/B ratio, hulling (%), milling (%), head rice recovery (%), head rice recovery and amylose content (%) from genotype was recorded. Observations on hulling% and milling% were taken with the help of Satake Company make laboratory huller and polisher. Kernel length and kernel width of 10 hulled rice were measured by means of dial micrometer and length and breadth ratio was computed. Amyose content was estimated by chemical method. Statistical analysis was conducted using INDOSTAT software for the analysis of variance for yield, floral and quality traits.

**2.2 Statistical analysis**

**2.2.1. Variance**

The treatment means for all the characters were subjected to analysis of variance techniques on the basis ofmodel proposed by Panse and Sukhatme (1961).

The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane, 1953) Genotypic variance (σ²g) = (Mean sum of squares due to treatments-Mean sum of squares due to

error)/Number of replications

Phenotypic variance (σ²p) = (σ²g) + (σ²e)

Where, (σ²e) = Error variance

**2.2.2 Genotypic and phenotypic coefficients of variance**

Genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer, (1981).

Genotypic coefficient of variation= (Genotypic standard deviation/Mean) ×100

Phenotypic coefficient of variation= (Phenotypic standard deviation/Mean) ×100

Categorization of the range of variation was done as per Sivasubramanian and Madhavamenon (1973).

Less 10% - low

10 -20 - moderate

More than 20%: high

**2.3. Heritability and genetic advance**

**2.3.1. Heritability**

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population.

Heritability (h²) in the broad sense was calculated according to the formula given by Allard (1960).

h²=σ²g /σ²p

Where, h²=Heritability in broad sense

σ²g =Genotypic variance

σ²p =Phenotypic variance (σ²g) + (σ²e)

σ²e =Environmental variance

As suggested by Johnson et al. (1955) (h²) estimates were categorized as:

Low: 0–30%

Medium: 30–60%

High: Above 60%

**2.3.2 Genetic advance (Expected)**

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

GA=K.h²(b). σp

Where, GA=Expected genetic advance

K=Selection differential, the value of which is 2.06 at 5% selection intensity

σp =Phenotypic standard deviation

h² (b)=Heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent for mean was computed

**3. Results and Discussion**

**3.1 Analysis of variance (ANOVA)**

The 28 maintainer lines along with 2 checks for all 17 characters showed highly significant variance, indicating the presence of sufficient variation among the genotypes, thereby providing an opportunity for effective selection (Table 1). The analysis of variance yields genotypic, phenotypic and environment variance which form the basis for the calculation of respective coefficients of variation.

**3.2 GENETIC VARIABILITY**

The presence of variability for any character is very important for the improvement of a crop through breeding. Tables 2 provide the information on mean, range, genotypic variation, phenotypic variation, PCV%, GCV%, heritability, and genetic advance in percent of mean for yield, floral and quality traits. The extent of influence of environment on any character indicates the magnitude of the difference between the genotypic and phenotypic coefficient of variation, so the PCV will be higher than GCV.

However, the phenotypic co-efficient of variation ranged from 35.23 to 3.79 whereas genotypic co-efficient of variation ranged from 33.21 to 3.29. Number of grains per panicle, 1000 seed weight, grain yield per plant had shown highest PCV% and GCV %. Indicating the negligible influence of environment and existence of high genetic variability. Hence, selection on the based on these traits can be effective. Similar findings were reported earlier by Umarani *et al.* (2017) for number of grains per panicle, Pratap *et al.* (2018) for grain yield and Islam *et al.* (2019) for 1000- seed weight.

Moderate PCV% and GCV % was shown by number of productive tillers per plant, stigma length, kernel length, kernel breadth, kernel L/B ratio. This indicates the low existence of moderate variability for these traits which could be exploited for improvement through selection in advanced generation.

whereas, lowest PCV% and GCV % was exhibited by traits days to 50% flowering, plant height, panicle length, angle of flower opening, stigma exertion%, hulling%, milling% and amylose content. While head rice recovery exhibited low PCV% and moderate GCV%. Low variability had shown and therefore, there is little scope for improvement of these traits.

Similar findings were reported earlier by Rajkumar and Ibrahim (2015) for plant height, Hari *et al.* (2018) for panicle length, Saha *et al.* (2019) for days to 50% flowering, Rashid *et al.* (2017) for number of productive tillers per plant, Mahalingam et al. (2013) for stigma exertion% and angle of flower opening, Hossain *et al.* (2023) for stigma length, Suman *et al.* (2020) for hulling% and milling%, Edukondalu *et al.* (2017) for head rice recovery%, Devi *et al*. (2022) for kernel length, kernel breadth, kernel L/B ratio and amylose content.

**3.3 Heritability**

The results of heritability ranged from 32% in panicle length to 97% in days to 50% flowering, whereas, panicle length showed moderate heritability and other traits showed high heritability such as days to 50% flowering (97%), 1000 seed weight(96), kernel length (94%), grain yield per plant (93%), milling% (91%), number of grains per panicle (88%), kernel breadth (86%), head rice recovery% (82%), angle of the flower opening (80%), plant height (79%), kernel L/B ratio(78%), hulling% (75%), number of productive tillers per plant (66%), amylose content (64%), stigma exertion% (63%). Similar findings were reported earlier by Nath *et al.* (2016), Lakshmi *et al*. (2020), Barde *et al.* (2021), Sadhana *et al.* (2022).

However, high heritability values will helpful in making selection of superior genotypes based on the phenotypic performance, it does not show any indication to the amount of genetic progress for selecting the best individual which is possible by using the estimate of genetic advance.

**3.4 Genetic advance**

Genetic advance as percent of mean was high for number of productive tillers, number of grains for panicle, thousand grain weight, grain yield per plant, stigma length, kernel length, kernel breadth, kernel l/b. While moderate genetic gain as percent of mean was shown by days to 50% flowering, plant height, angle of flower opening, stigma exertion%, milling%, head rice recovery% and low genetic advance was shown by panicle length, hulling%, amylose content.

High heritability coupled with high genetic advance as percent mean shown by number of productive tillers, number of grains per panicle, 1000 grain weight, grain yield, stigma length, kernel length, kernel breadth, kernel L/B ratio indicating that the high heritability is due to additive gene effects and selection may be effective for these characters. Similar findings were reported earlier by Kumar *et al.* (2020), Jamal and Sunian (2023).

Whereas high heritability with moderate genetic advance were shown by plant height, panicle length, angle of flower opening, stigma exertion% milling% and head rice recovery%, moderate heritability with low genetic advance were observed in panicle length and indicating the role of both additive and non-additive gene effects for controlling the characters and selection for this trait may be ineffective. Similar findings were reported earlier by Devi *et al*. (2019), Noatia *et* *al.* (2022), Chouhan *et al.* (2024).

**Table:1 Analysis of variance for yield attributes, floral and quality traits in maintainer lines of rice.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **GENOTYPES** | **Mean Sum of Squares** | | |
| **SI.NO.** | **Replications**  **(df =1)** | **Treatments**  **(df =29)** | **Error**  **(df = 29)** |
| **1** | **Days to 50% flowering** | 2.017 | 114.037\*\*\* | 1.499 |
| **2** | **Plant height (cm)** | 6.521 | 118.101\*\*\* | 1.499 |
| **3** | **Panicle length (cm)** | 9.457 | 5.108\* | 2.064 |
| **4** | **Number of productive tillers** | 1.667 | 9.944\*\*\* | 1.988 |
| **5** | **Number of grains per panicle** | 361.131 | 9746.753\*\*\* | 576.815 |
| **6** | **1000 grain weight (g)** | 0.434 | 37.478\*\*\* | 0.652 |
| **7** | **Grain yield / plant (g)** | 11.80 | 119.369\*\*\* | 4.298 |
| **8** | **Angle of flowering (°)** | 2.860 | 11.913\*\*\* | 1.258 |
| **9** | **Stigma exertion (%)** | 4.532 | 75.659\*\*\* | 17.040 |
| **10** | **Stigma length (μm)** | 9798.689 | 27987.040\*\*\* | 2103.040 |
| **11** | **Hulling (%)** | 10.626 | 15.974\*\*\* | 2.258 |
| **12** | **Milling (%)** | 3.169 | 64.209\*\*\* | 2.801 |
| **13** | **Head rice recovery (%)** | 3.961 | 64.209\*\*\* | 2.801 |
| **14** | **Kernel length (mm)** | 0.005 | 1.164\*\*\* | 0.03 |
| **15** | **Kernel breadth (mm)** | 0.0001 | 0.097\*\*\* | 0.007 |
| **16** | **Kernel L/B ratio** | 0.001 | 0.294\*\*\* | 0.036 |
| **17** | **Amylose content (%)** | 0.131 | 4.292\*\*\* | 0.940 |

\*\*\*, \* significance at 1% and 5% level of probability

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table: 2 Variability studies for yield, quality and floral traits in maintainer lines of rice.** | | | | | | | | |
| **SI.NO.** | **GENOTYPES** | **Mean** | **Phenotypic variation** | **Genotypic variation** | **PCV (%)** | **GCV (%)** | **Heritability in broad sense (h2) (%)** | **Genetic advance as % mean** |
| **1** | **Days to 50% flowering** | 96.08 | 57.76 | 56.26 | 7.91 | 7.80 | 97 | 15.87 |
| **2** | **Plant height (cm)** | 95.516 | 65.79 | 52.30 | 8.49 | 7.57 | 79 | 13.90 |
| **3** | **Panicle length (cm)** | 23.95 | 3.85 | 1.25 | 8.19 | 4.67 | 32 | 5.48 |
| **4** | **Number of productive tillers** | 16.28 | 5.96 | 3.97 | 14.99 | 12.24 | 66 | 20.60 |
| **5** | **Number of grains per panicle** | 203.88 | 5161.78 | 4584.96 | 35.23 | 33.21 | 88 | 64.47 |
| **6** | **1000 grain weight (g)** | 17.74 | 19.06 | 18.41 | 24.60 | 24.17 | 96 | 48.94 |
| **7** | **Grain yield / plant (g)** | 82.68 | 61.83 | 57.53 | 27.41 | 26.44 | 93 | 52.55 |
| **8** | **Angle of flowering (°)** | 31.83 | 6.58 | 5.32 | 8.06 | 7.25 | 80 | 13.43 |
| **9** | **Stigma exertion (%)** | 76.21 | 46.35 | 29.30 | 8.93 | 7.10 | 63 | 11.63 |
| **10** | **Stigma length (μm)** | 1055.47 | 15045.38 | 12941.66 | 11.62 | 10.77 | 86 | 20.59 |
| **11** | **Hulling (%)** | 79.60 | 9.11 | 6.85 | 3.79 | 3.29 | 75 | 5.87 |
| **12** | **Milling (%)** | 67.32 | 33.50 | 30.70 | 8.59 | 8.23 | 91 | 16.23 |
| **13** | **Head rice recovery (%)** | 56.96 | 35.37 | 29.03 | 10.44 | 9.45 | 82 | 17.65 |
| **14** | **Kernel length (mm)** | 5.98 | 0.59 | 0.56 | 12.92 | 12.56 | 94 | 25.16 |
| **15** | **Kernel breadth (mm)** | 1.90 | 0.05 | 0.04 | 11.95 | 11.12 | 86 | 21.33 |
| **16** | **Kernel L/B ratio** | 3.16 | 0.16 | 0.12 | 12.82 | 11.34 | 78 | 20.67 |
| **17** | **Amylose content (%)** | 24 | 2.61 | 1.67 | 6.73 | 5.39 | 64 | 8.89 |

**Fig 1: Estimates of heritability and genetic advance as % of mean for yield, floral and quality traits**

**Fig 2: Estimates of GCV and PCV % of for yield, floral and quality traits.**

**Conclusion:**

The significant results are obtained by analysing the ANOVA confirms that there was a genetic variation among genotypes for all evaluated traits, providing a robust foundation for selection. High heritability coupled with high genetic advance as percent mean was recorded for number of productive tillers, number of grains per panicle, 1000 grain weight, grain yield, stigma length, kernel length, kernel breadth, kernel L/B ratio, indicated importance of characters and selection for these traits may be effective. Collectively, these findings highlights that these specific traits can be utilised by breeders for further breeding programmes through both direct and indirect selection strategies.

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