**Genetic variability, Heritability and Genetic advance for yield and it’s components traits in maintainer lines of rice (*Oryza sativa* L.)**

**ABSTRACT**

**Aim:** To study the variability, heritability and genetic advance for yield and its components traits for selecting better yield attributes for improvement of maintainer lines.

**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 were recorded on agromorphological characters. Statistical analysis was conducted using INDOSTAT software for the analysis of variance for variability, heritability and genetic advance.

**Results:** Analysis of variance reveled that there was a significant variation (p < 0.01) among genotypes for all traits. Number of grains per panicle (35.23%, 33.21%), 1000 seed weight (24.60%, 24.17%), grain yield per plant (27.41%, 26.44%) had shown highest PCV% and GCV % than the other traits under study. The results of heritability ranged from 32% in panicle length to 97% in days to 50% flowering. Higher heritability (> 80 %) was shown by all traits except panicle length. High heritability coupled with high genetic advance as percent mean (> 20 %) 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 than the other traits under study which is useful in the selection process.

**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 (> 80 %) with high genetic advance (> 20%) indicating that selection for these traits are effective for selection of better maintainer lines.

**Keywords:** Rice, Genetic variability, Heritability, Yield attributes or rice

**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. Of the annual world production is 787 million tonnes from 165 million hectares, whereas, largest rice producing countries are China, India, Bangladesh, Indonesia, Vietnam, Myanmar, Philippines, Cambodia and Pakistan. As Asia produces 524 million tonnes from 138.56 million hectares. While in India it is grown in about 46.28 million hectares with annual production of 132.5 million tonnes. In Telangana rice occupies an area of 14.51lakh ha with production of 12.41 million tonnes with productivity of 3395 kg/ hectare (India stat, 2023). 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. Whereas improvements directly related to the genetic variability. It plays an important role in crop breeding for selecting the elite traits for making rapid improvement in yield as well as is 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). Which helps in the selection of traits by comparing within the population.

While “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 its components traits to identify superior maintainer lines.

**2.Materials and Methods**

**2.1 Material and Planting**

The experimental material for the present investigation comprised of 28 genotypes along with 2 checks. The experiment 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.

**2.2 Data collection**

**Chart 1: Recorded observations on morphological traits, floral traits and quality traits of rice**

**Morphological traits: Floral traits Quality traits**

Days to 50% flowering Angle of flower opening Hulling%

Plant height stigma exertion Milling%

Panicle length stigma length Head rice recovery%

Number of productive tillers per plant kernel length

Number of grains per panicle kernel breadth

1000- grain weight kernel L/B ratio

Grain yield per plant Amylose content

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 (%) 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. Amylose content was estimated by chemical method. Statistical analysis was conducted using INDOSTAT software for the analysis of variance for variance for variability, heritability and genetic advance.

**2.3 Statistical analysis**

**2.3.1. 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

**2.3.2 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

**2.4. Heritability and genetic advance (PRASAD, 2014)**

**2.4.1. 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%

**2.4.2 Genetic advance (Expected) (PRASAD, 2014)**

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

Genetic advance as per cent of mean= (GA/Grand mean) ×100

The range of genetic advance as per cent of mean was classified as suggested by Johnson et al. (1955).

 Low: less than 10%

 Moderate: 10–20%

 High: more than 20%

**3. Results and Discussion**

**3.1 Analysis of variance (ANOVA)**

“The analysis of variance for the randomized block design for yield, and its components were statistically tested and found to be significant for all evaluated traits such as 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, Kernel length (mm), Kernel breadth (mm), Kernel L/B ratio, Hulling (%), Milling (%), Head rice recovery (%), Amylose content (%). Indicating the presence of sufficient variation among the traits, 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. A higher coefficient of variation indicates a higher degree of variability among the observations. A lower coefficient of variation indicates a lower degree of variability among the observations. The PCV is an estimate of how much variation there is in a given trait among individuals within a population. This measure is used to detect the differences in performance between individuals in a population.

The GCV is an estimate of the degree of variability among individuals due to genetic factors. This measure is used to detect the differences in performance between individuals due to genetic factors. In general; the PCV will be much higher than the GCV because the environment which can have a much larger effect on the expression of a trait than the genes. However, it is important to note that the environment can also interact with the genetic factors to influence the expression of a trait, so the PCV and GCV may be similar in such cases. Tables 2 provide the information on mean, genotypic variation, phenotypic variation, PCV%, GCV%, heritability, and genetic advance in percent as mean for yield and its components traits.

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 (35.23, 33.21) had shown highest values for PCV% and GCV% than the 1000 seed weight (24.60, 24.17) and grain yield per plant (27.41, 26.44) while they also come under higher variability range. The results from these traits clearly showing the negligible influence of environment on them and providing chance of existence of high genetic variability. Hence, selection based on number of grains per panicle, 1000- grain weight and grain yield per plant will be effective which can help in selection of the better maintainers based on these traits 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.

Whereas high moderate PCV% and GCV % was shown by number of productive tillers per plant (14.99, 12.24), compare to grain dimensions such kernel length (12.92, 12.56), kernel breadth (11.95, 11.12), kernel L/B ratio (12.82, 11.3.4) as followed by stigma length (11.62, 10.77). This indicates the existence of moderate variability for these traits indicating the presence moderate variability which can be exploited for improvement through selection in advanced generation.

Contrasting to the stigma length other floral traits angle of flower opening (8.06, 7.25) and stigma exertion% had shown lowest PCV% and GCV % (8.93, 7.10) and morphological traits such as days to 50% flowering (7.91, 7.80), plant height (8.49, 7.57), panicle length (8.19, 4.67), exhibited lowest percentage of coefficient of variations and quality trait hulling% (3.79, 3.29) lowest variation than the milling% (8.59, 8.23) and amylose content (6.73, 5.39). In contrasting to other quality traits head rice recovery (10.44, 9.45) exhibited low PCV% and moderate GCV%. Due to low coefficient of variance in these traits leads to less variability in these traits so, there is little scope for selection 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. Days to 50% flowering (97%) had shown higher heritability than the 1000 seed weight (96). Whereas grain dimensions such as kernel length (94%) higher heritability than the other grain dimension such as kernel breadth (86%), kernel L/B ratio (78%). “Grain yield per plant” (93%) has exhibited higher heritability than the other quality parameters except kernel length with 94%. Whereas, Milling% (91%), has shown higher value of heritability compared to head rice recovery% (82%) and hulling% (75%). Number of grains per panicle (88%) high value of heritability than angle of the flower opening (80%), plant height (79%), number of productive tillers per plant (66%), amylose content (64%). stigma exertion% (63%) exhibited lowest value of heritability than other traits under study.

High heritability helps in making selection of superior traits on the the basis of phenotypic performance. These traits can be selected for improvement of maintainer lines. Similar findings were reported earlier by Nath *et al.* (2016), Lakshmi *et al*. (2020), Barde *et al.* (2021), Sadhana *et al.* (2022).

However, GCV, PCV, ECV and heritability results shown considerable amount of genetic variation in the traits under study which permit parental selection for the development of better maintainer line, but does not show any indication to the amount of genetic progress for selecting the high heritable traits. To achieve more effective character selection, heritability supplemented with genetic advance is more suitable than heritability alone.

**3.4 Genetic advance**

The estimation of genetic advances helps to understand the types of gene action involved in the expressions. Madishetty *et al*. (2023). Genetic advance as percent of mean was high for number of grains for panicle (64.47) than the grain yield per plant (52.55), in contrasting to this grain yield per plant (52.55) has shown higher value than thousand grain weight (48.94) whereas number of productive tillers (20.06), stigma length (20.59), kernel length (25.16), kernel breadth (21.33), kernel L/B ratio (20.67) had shown border values of high genetic advance compare to other traits of high genetic advance.

 While moderate genetic gain as percent of mean was shown by quality traits such as head rice recovery% (17.65) and milling% (16.23) whereas low genetic advance was shown by amylose content (8.89) and hulling% (5.87) and floral traits such as angle of flower opening (13.43), stigma exertion% (11.63) moderate genetic advance contrasting to the stigma length (20.59) exhibited high genetic advance whereas low genetic advance was shown by panicle length (5.48) compare to other traits under study. Whereas days to 50% flowering (15.87) along with plant height (13.90) exhibited moderate genetic advance.

Higher heritability coupled with high genetic advance as percent mean exhibited by 1000 grain weight, grain yield. In contrasting to this Grain yield had shown higher values of heritability and genetic advance than the number of productive tillers. Number of grains per panicles also exhibited higher values compare to the plant height, days to 50% flowering. Whereas plant height and days to 50% flowering shown high heritability with moderate genetic advance. The stigma length had shown higher values of genetic advance than other floral traits such as angle of flower opening, stigma exertion% which exhibited high heritability with moderate genetic advance. Grain dimensions such as kernel length, kernel breadth, kernel L/B ratio exhibited high genetic advance with high heritability. Other quality traits such as milling%, head rice recovery% had shown moderate genetic advance with high heritability contrasting to this hulling% and amylose content exhibited high heritability with low genetic advance. High heritability connected with high genetic advance for these traits resulted due to the actions of additive gene. These traits are well-suited for improvement through direct selection methods, such as simple or progeny selection. Focusing on such traits increases the likelihood of accumulating additive genes, which in turn contributes to continued improvement in performance. Similar findings were reported earlier by Kumar *et al.* (2020), Jamal and Sunian (2023).

Compare to other trait panicle length had shown moderate heritability with low genetic advance indicating the role of both additive and non-additive gene effects for controlling the characters and selection for this trait may be less effective due accumulation of non-additive gen. 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 and its components 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\*\*\* | 13.484 |
| **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 (%)** | 2.961 | 64.413\*\*\* | 6.339 |
| **14** | **Kernel length (mm)** | 0.005 | 1.164\*\*\* | 0.033 |
| **15** | **Kernel breadth (mm)** |  0.000 | 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 and it’s components 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)**  | 28.68 | 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 and its components traits in maintainer lines of rice.**

**Fig 2: Estimates of GCV and PCV % of for yield and components traits in maintainer lines of rice.**

 **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 for improvement of maintainer lines.

**Disclaimer (Artificial intelligence)**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

**Reference**

1. Allard, R.W. 1960. Principles of plant breeding. Published by John Wiley and Sons Inc. New York, USA. 485.
2. Barde, M.A., Mohammed, M.S., Oyekunle, M., Usman, I.S and Shaahu, A. 2021. Estimation of genetic variability, heritability and genetic advance in rice (*Oryza sativa l*) genotypes. *Int. J. Res. Sci. Innov. Appl. Sci.* *4*: 5-90. [Estimation-of-Genetic-Variability-Heritability-and-Genetic-Advance-in-Rice-Oryza-sativa-L-Genotypes.pdf](https://www.researchgate.net/profile/M-Mohammed-4/publication/349215251_Estimation_of_Genetic_Variability_Heritability_and_Genetic_Advance_in_Rice_Oryza_sativa_L_Genotypes/links/60255b6f299bf1cc26bcb3ac/Estimation-of-Genetic-Variability-Heritability-and-Genetic-Advance-in-Rice-Oryza-sativa-L-Genotypes.pdf)
3. Burton, G.W., 1952. Quantitative inheritance in grasses. Proceeding on 6th International Grassland Congress Journal 1: 277–283.
4. Burton, G.W and Devane, E.M. 1953. Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*. 51: 515-518.
5. Chouhan, Y.N., Singh, S.K., Chakrawarty, V.K., Elahi, T., Chandanan, S and Gautam, R. 2024. Genetic assessment of fertility restorer rice lines for yield and yield contributing traits. *Plant Archives. (09725210)*: *24*(2). 10.51470/PLANTARCHIVES.2024.v24.no.2.119.
6. Devi, K.R., Chandra, B.S., Venkanna, V and Hari, Y. 2019. Variability, correlation and path studies for yield and quality traits for upland rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry.* 8 (6): 676-685. [Variability-correlation-and-path-studies-for-yield-and-quality-traits-in-irrigated-upland-rice-Oryza-sativa-L.pdf](https://www.researchgate.net/profile/K-Devi-6/publication/338188370_Variability_correlation_and_path_studies_for_yield_and_quality_traits_in_irrigated_upland_rice_Oryza_sativa_L/links/61e5584b9a753545e2d97340/Variability-correlation-and-path-studies-for-yield-and-quality-traits-in-irrigated-upland-rice-Oryza-sativa-L.pdf)
7. Devi, K.R., Hari, Y., Chandra, B.S and Prasad, K.R. 2022. Genetic association, variability and path studies for yield components and quality traits of high yielding rice (*Oryza sativa* L.) genotypes. *International Journal of Bio-resource and Stress Management*. *13*(1): 81-92. HTTPS://DOI.ORG/10.23910/1.2022.2297
8. Edukondalu, B., Reddy, V.R., Rani, T.S., Kumari, C.A and Soundharya, B. 2017. Studies on variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*. *6*(10): 2369-2376. https://doi.org/10.20546/ijcmas.2017.610.279
9. Edukondalu, B., Reddy, V.R., Rani, T.S., Kumari, A and Soundharya, B. 2023. Study of genetic variability for yield and yield attributes and bran oil content in maintainer lines of rice (*Oryza sativa* L.). *International Journal of Bio-resource and Stress Management*. *14*(7): 978-985.HTTPS://DOI.ORG/10.23910/1.2023.3418
10. Falconer, D.S., 1981. Introduction to quantitative genetics. Oliver Boyd, 340.
11. Falconer, D.S., Mackay, T.F.C. 1996. An Introduction to Quantitative Genetics (4th Edn.). Prentice Hall, London, 480.
12. Hari, R.K.B., Satyanarayana, P.V., Babu, D.R., Chamundeswari, N., Rao, V.S and Raju, S.K. 2018. Genetic variability estimates for yield and yield components traits and quality traits in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*. 7 (5): 551-559. https://doi.org/10.20546/ijcmas.2018.705.xx
13. Hossain, M.S., Ivy, N.A., Raihan, M.S., Kayesh, E and Maniruzzaman, S. 2020. Genetic variability, correlation and path analysis of floral, yield and its component traits of maintainer lines of rice (*Oryza sativa* L.). *Bangladesh Rice Journal*. *24*(1): 1-9. https://doi.org/10.3329/brj.v24i1.53235
14. Hossain, M.S., Ivy, N.A., Maniruzzaman, S., Raihan, M.S., Ruma, A.S., Akter, A., Hasan, M.R., Kulsum, M.U., Uddin, M.N and Kabir, K.F. 2023. Genetic Variability of Floral and Agronomic Characteristics that Influence Outcrossing Rate Percentage of Cytoplasmic Male Sterile Rice. *Asian J. Adv. Agric. Res*. *22*(1): 46-57. DOI: 10.9734/AJAAR/2023/v22i1433.
15. Islam, M.Z., Mian, M.A.K., Ivy, N.A., Aktar, N and Rahman, M.M. 2019. Genetic variability, correlation and path analysis for yield and its component traits in restorer lines of rice. *Bangladesh Journal of Agriculture Research*. 44 (2): 291-301. <https://doi.org/10.3329/bjar.v44i2.41819>.
16. Jamal, M.S and Sunian, E. 2023. Genetic Studies for Selected Agronomic Traits in 19 Maintainer Genotypes of Rice (*Oryza sativa* L.). *Int. J. Environ. Clim. Change*. *13*(12): 77-88. DOI: 10.9734/IJECC/2023/v13i123663.
17. Kumar, A., Kumar, S., Singh, S., Prasad, J., Jeena, AS and Upreti, MC. 2020. Genetic variability, heritability and genetic advance studies for quantitative and quality traits in Basmati rice. (*Oryza sativa. L*). *Journal of Pharmacognosy and Phytochemistry*. 9(4): 2065-2068. https://www.phytojournal.com/archives/2020/vol9issue4/PartAB/9-4-42-531.pdf
18. Lakshmi, M.S., Suneetha, Y and Srinivas, T. 2020. Genetic variability, correlation and path analysis for grain yield and yield components in rice genotypes. *Journal of Pharmacognosy and Phytochemistry.* 10 (1): 1369-1372. [Genetic variability, correlation and path analysis for grain yield and yield components in rice genotypes](https://www.researchgate.net/profile/Suneetha-Yadla/publication/362057494_Genetic_variability_correlation_and_path_analysis_for_grain_yield_and_yield_components_in_rice_genotypes/links/62d63f56daa38132ab59909d/Genetic-variability-correlation-and-path-analysis-for-grain-yield-and-yield-components-in-rice-genotypes.pdf).
19. Madishetty, A. R., Lal, G. M., & Adarsh K. (2023). Genetic Variability and Correlation Studies for Yield and Yield Related Traits in Rice (Oryza sativa L.). International Journal of Plant & Soil Science, 35(20), 1165–1176. <https://doi.org/10.9734/ijpss/2023/v35i203914> .
20. Mahalingam, A., Saraswathi, R., Ramalingam, J and Jayaraj, T. 2013. Genetics of floral traits in cytoplasmic male sterile (CMS) and Restorer lines of hybrid rice (Oryza sativaL.). *Pak. J.Bot.,* 45(6):1897-1904. [cabidigitallibrary.org/doi/full/10.5555/20133428756](https://www.cabidigitallibrary.org/doi/full/10.5555/20133428756)
21. Nath, A., Chowdhury, B.S., Dasgupta, T and Santra, C.K. 2016. Evaluation of elite WA CMS lines of rice: characterization and variability analysis with special reference to floral traits. *IOSR J. of Agric. and Veterinary Sci*. 9(5): 1-05. DOI: 10.9790/2380-0905020105
22. Noatia, P., Sao, A., Tiwari, A., Nair, S.K and Gauraha, D. 2021. Genetic dissection of yield determinants in advance breeding lines (ABLs) of rice (*Oryza sativa* L.) under irrigated condition of Chhattisgarh, India. *International Journal of Plant & Soil Science*. *33*(20): 119-131. DOI: 10.9734/IJPSS/2021/v33i2030638
23. Pratap, A., Bisen, P., Loitongbam, B., Sandhya and Singh, P.K. 2018. Assessment of genetic variability for yield and yield components in rice (*Oryza sativa* L.*)* germplasms. *International Journal of Bio Resource and Stress Management.* 9 (1): 087-092. HTTPS://DOI.ORG/10.23910/IJBSM/2018.9.1.3C0818
24. Rajkumar, S and Ibrahim, S.M. 2015. Genetic variability in CMS lines of rice *(Oryza sativa* L.) genotypes that influence outcrossing rate percentage. *Indian Journal of Agricultural Research.* 49 (2): 165-169. 10.5958/0976-058X.2015.00024.4.
25. Rashid, M.M., Nuruzzaman, M., Hassan, L and Begum, S. N. 2017. Genetic variability analysis for various yield attributing traits in rice genotypes*. Journal of m Bangladesh Agriculture University.* 15 (1): 15-19.  <https://doi.org/10.3329/jbau.v15i1.33525>
26. Sabri, R.S., Rafii, M.Y., Ismail, M.R., Yusuff, O., Chukwu, S.C and Hasan, N.A. 2020. Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast resistant rice lines tested in four environments. *Agronomy*. *10*(8): 1098.  [**https://doi.org/10.3390/agronomy10081098**](https://doi.org/10.3390/agronomy10081098)
27. Sadhana, P., Raju, C.D., Rao, L.V and Kuna, A. 2022. Studies on variability, correlation and path coefficient analysis for yield and quality traits in rice (*Oryza sativa* L.) genotypes. *Electronic journal of plant breeding*. *13*(2): 670-678. <https://doi.org/10.37992/2022.1302.084>
28. Saha, S.R., Hassan, L., Haque, A., Islam, M.M and Rasel, M. 2019. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *Journal of Bangladesh Agricultural University*. 17 (1): 26–32. <https://doi.org/10.3329/jbau.v17i1.40659>
29. Sivasubramanian, S., Madhavamenon, P. 1973. Combining ability in rice. *Madras Agricultural Journal.* 60: 419–421.
30. Suman, K., Madhubabu, P., Rathod, R., Rao, S.D., Rojarani, A., Prashant, S., Subbarao, L.V., Ravindrababu, V and Neeraja, C.N. 2020. Variation of grain quality characters and marker-trait association in rice (*Oryza sativa* L.). *Journal of Genetics*. 99 (5): 1-12. https://doi.org/10.1007/s12041-019-1164-4
31. Umarani, E., Radhika, K., Padma, V and Subbarao, L.V. 2017. Variability, heritability and genetic advance for agro-morphological and grain quality parameters in landraces of rice (*Oryza sativa* L.). [BD14cccc27.pmd](https://environmentandecology.com/wp-content/uploads/2025/03/MS16-1-7.pdf).
32. PRASAD K. L., (2014) STUDIES ON GENETIC DIVERGENCE AND CHARACTERIZATION OF BORO RICE (Oryza sativa L.) GENOTYPES, (M.SC Unpublished Thesis submitted to ACHARYA N. G. RANGA AGRICULTURAL UNIVERSITY)