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# Assessment of Genetic Variability and Heritability in CMS Lines and their $F_1$'s of Rice (*Oryza sativa* L.)

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**ABSTRACT: Rice is the most important crop in India. Currently, it provides 43% of cereal output and 46% of food grain production. India has the greatest area among the countries that grow rice, with 49 million hectares, followed by China. India is the world's second-largest producer of rice, with an estimated 118.9 million tonnes annually, but there is still an opportunity for the development of high-yielding and stress-tolerant varieties to fulfill the demands of the planet's constantly growing population. The current study examined the degree of variability present among CMS lines of rice (*Oryza sativa* L.) and their hybrids in conducted in randomized block design during Kharif 2020 at Pilikothi Farm of Tilak Dhari Degree College Jaunpur (U.P.). For each replication of the twelve characters, the observations were made on five competing plants of a given genotype that were chosen at random from a plot. Twelve quantitative traits, including seedling height (cm), days to 50% flowering, flag leaf area ($cm^2$), plant height (cm), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, spikelet fertility (%), test weight (g), biological yield per plant (g), grain yield per plant (g), and harvest-index (%), were observed. Analysis of variance reveals significant genotype-to-genotype variation for each characteristic. For spikelets per panicle, the high estimations of PCV and GCV were calculated (PCV=21.20%, GCV=21.12%). For grain yield per plant, the high estimations of PCV with the modest GCV were noted (PCV=20.58%, GCV=19.40%). Estimates of broad sense heritability ranged from 53.25 percent (spikelet fertility%) to 99.25 percent (spikelets per panicle). Spikelets per panicle (99.25%), biological yield per plant (96.42%), flag leaf area (89.58%), grain yield per plant (88.91%), and plant height (87.55%) all showed strong heritability in the broad sense (>75%). For spikelets per panicle (43.35%), grain yield per plant (37.68%), biological yield per plant (34.97%), flag leaf area (30.93%), and panicle bearing tillers per plant (22.81%), the genetic advance in percent of mean was found to be high (>20%). For plant height, panicle length, and seedling height, moderate (>10–20%) estimates of genetic progress in percent of mean were noted. Hence the selection among these genotypes for these traits will be worthful in planning a breeding programme.**

**Keywords:** Rice, *Oryza sativa*, CMS, variability, heritability, coefficient of variation.

## INTRODUCTION

Rice is the most important crop in India. Currently, it provides 43% of cereal output and 46% of food grain production. Among the countries that cultivate rice, India has the largest area with 49 million hectares (Kharif rice accounting for 43.6 M ha and Rabi rice 5.4 Mha), followed by China. With 118.9 million tonnes produced, India is the second-largest producer of rice (Ministry of Agriculture and Farmers Welfare, 2020-21). The average output of rice in India is 4.1 metric tonnes per hectare (USDA report, 2022).

Since ancient times, rice (*Oryza sativa* L.) has been a significant staple crop in tropical and subtropical regions of the world, growing from 500 North in central Czechoslovakia on the equator to 350 South in Australia. From below sea level in the Kuttanadu district of Kerala (India) to as high as 2000 meters in the Himalayas, rice is produced with great success. The wild rice species (*Oryza glaberrima*) grows in tropical Africa, while the cultivated rice species (*Oryza sativa* L.) evolved in South Asia's tropics. One of India's oldest crops is rice (Vavilov, 1951).

The genus *Oryza* includes the annual grass known as rice (*Oryza sativa* L.). In the genus *Oryza*, there are 22 wild species (2n=24, 48), which correspond to 10 genetic kinds (AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ, and HHKK). Africa also cultivates *Oryza glaberrima* in large quantities in addition to *Oryza sativa* (Brar and Khush 1986).

Hybrid rice technology seems to be the most practical and flexible genetic method being investigated to crack the yield barrier in rice. Currently, two methods—three-line systems and two-line systems—are used for hybrid rice breeding. The cytoplasmic genetic male sterility (CGMS) mechanism is utilized in the three-line breeding technique. The first person to make large-scale hybrid seed production feasible was Yuan Long Ping, known as the "Father of Hybrid Rice." From a male sterile plant of wild rice (*Oryza sativa* L. f. spontanea), the first CMS line that was utilized to create a commercial rice hybrid was created in China. Since then, a number of CMS lines have been created using diversely cultivated and wild accessions. The hybrid rice breeding that was initiated in China in the 1970s led to a great improvement in rice productivity.

The secret to any crop development effort is genetic diversity. Breeders now have the chance to mix desired genes into fresh genotypes to improve the yield and stability of economically significant agricultural plants. Germplasm is the most valuable natural source of relevant traits for creating genotypes with high-yielding input responsiveness and resistance to a variety of biotic and abiotic stressors.

Multiple lines' evaluations for various genetic factors give us a new tool to use for the crossing programme. Highly heterotic parents for creating hybrids with excellent yields are the ideal requirements in a hybrid rice breeding programme. Increased grain production would be efficiently supported by the capabilities of features that are strongly related to yield components. Heritability is described by Falconer and Mackay (1996) as the measurement of the relationship between breeding values and phenotypic values. Heritability, which expresses the dependability of phenotype as a reference to its breeding value, thus plays a predictive role in breeding.

In light of the foregoing information, the current study was carried out to shed light on the genetic diversity, heritability, and genetic advancement of CMS rice lines and their $F_1$s.

## MATERIALS AND METHODS

The current investigation was carried out at Tilak Dhari Post Graduate College's Pilikothi Farm in Jaunpur (U.P.). The soil type of the experimental area is defined as sandy loam, and it is located in the sub-tropical region of the Indo-Gangetic plain. This location is 83 metres above mean sea level and is situated between 25.74°N latitude and 82.69°E longitude. District Jaunpur experiences a semi-arid environment with hot summers and chilly winters. 83.10 cm of rain falls on average each year.

Three CMS lines with "wild abortive" (WA) cytoplasm were used as the experimental material for this study, along with 15 different rice genotypes as testers (males). The rice section of the Department of Genetics and Plant Breeding at the A.N.D. University of Agriculture & Technology, Kumarganj, Ayodhya, selected these distinct superior genotypes from their genetic stock collection. In order to produce 45 F1s, the crosses were created using a "line x tester" mating scheme (Kempthorne, 1957).

A randomized block design with three replications was used to examine the final group of 45 F1s and their 18 parents in Kharif, 2020. On the 21st of June 2020, the seeds for each entry were seeded in separate plots, and 30 days later, on the 20th of July 2020, mature seedlings were transplanted, one seedling per hill, in single-row plots measuring 3 meters in length with inter- and intra-row spacing of 20 and 15 cm, respectively. To cultivate a high-quality crop, all suggested cultural practices were followed.

For each replication of the twelve characters, the observations were made on five competing plants of a given genotype that were chosen at random from a plot. Twelve quantitative traits, including seedling height (cm), days to 50% flowering, flag leaf area ($cm^2$), plant height (cm), panicle bearing tillers per plant, panicle length (cm), spikelets per panicle, spikelet fertility (%), test weight (g), biological yield per plant (g), grain yield per plant (g), and harvest-index (%), were observed. For statistical analysis, the mean values of data made on five plants from each plot were used, are as follows: Analysis of variance suggested by Panse and Sukhatme (1967), Coefficient of variation suggested by Burton and de Vane (1953), heritability in a broad sense ($h^2b$) as suggested by Hanson *et al*. (1956) and genetic advance as suggested by Johnson *et al*. (1955).

## RESULTS AND DISCUSSION

**Analysis of variance for the design of experiment.** Analysis of variance was carried out concerning twelve characters to test the significance of differences between various treatments (genotypes) *viz*., three CMS rice lines, 15 testers, and 45 $F_1$s as depicted in Table 1. The mean squares due to treatments (genotypes), parents, crosses and crosses vs parents were highly significant for all the characters indicating the presence of sufficient variability in the experimental materials. The mean squares due to lines (p) were highly significant for most of the traits except plant height (13.53), panicle bearing tillers per plant (0.65), panicle length (1.54), spikelets fertility % (2.52), harvest index (4.58) and grain yield per plant (4.04) and also the mean squares due to the line (p) vs tester (p) were significant for all the traits except seedling height (0.55), panicle bearing tillers per plant (0.03) and test weight (0.81).Previously, a similar pattern of variances was also observed by Jayasudha and Sharma (2010).

**Coefficients of variation.** The phenotypic (PCV) and genotypic (GCV) coefficients of variation for the twelve characters have been presented in Table 2. In general, the magnitude of the phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits. The high estimates (>20%) of PCV along with GCV were estimated for spikelets per panicle (PCV=21.20%, GCV=21.12%). The high estimates of PCV with moderate GCV were recorded for grain yield per plant (PCV=20.58%, GCV=19.40%). The moderate estimates (10-20%) of PCV and GCV were recorded for biological yield per plant (PCV=17.61%, GCV=17.29%), flag leaf area (PCV=16.76% and GCV=15.86%) and panicle bearing tillers per plant (PCV=15.02%, GCV=12.90%). The remaining characters exhibited low estimates (<10%) of PCV or

GCV. These are in agreement with the earlier reports of Anis *et al*. (2016); Manjunatha and Kumara (2019).

**Heritability and genetic advance.** Heritability and response to selection, often known as genetic progress, are inversely correlated. The best environment for selection is one with high genetic progress and high heritability estimates. Therefore, the value of heritability rises when it is used to determine genetic progress, which is the level of improvement in a feature attained under specific selection pressure. Genetic advancement is thus another crucial selection factor that aids the breeder in a selection programme. Furthermore, to research plant breeding, it is necessary to use relatively large populations because the majority of essential agronomical variables, such as grain yield, have a complicated genetic inheritance.

**Table 1: Analysis of variance including parents and crosses for 12 traits in rice.**

| Characters | Replications | Treatments | Error |
|---|---|---|---|
| df | 2 | 62 | 124 |
| Seedling height cm | 1.16 | 5.43** | 0.94 |
| Days to 50% flowering | 19.94 | 33.58** | 5.31 |
| Flag leaf area (cm²) | 5.79 | 35.51** | 1.33 |
| Plant height (cm) | 1.89 | 185.55** | 8.39 |
| Panicle bearing tillers per plant | 8.14 | 8.50** | 0.9 |
| Panicle length (cm) | 9.05 | 11.14** | 1.88 |
| Spikelets per panicle | 32.79 | 2558.13** | 6.43 |
| Spikelets fertility (%) | 33.14 | 12.63** | 2.85 |
| Biological yield per plant (g) | 70 | 235.63** | 2.88 |
| Harvest index (%) | 22.22 | 20.42** | 3.5 |
| Test weight (g) | 4.52 | 7.47** | 1.01 |
| Grain yield per plant (g) | 34.7 | 54.77** | 2.19 |

*,**Significant at 5% and 1% probability levels, respectively

**Table 2: Estimates of coefficient of variation, heritability ($h^2b$), and genetic advance in % of mean for 12 traits in rice.**

| | Range | | | Variance | | Coefficient of Variation | | Heritability ($h^2b$) (%) | GA 5% | GA% mean 5% | GA 1% | GAM 1% |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Mean | Min | Max | var (g) | var (p) | GCV (%) | PCV (%) | | | | | |
| **Seedling height cm** | 18.63 | 16.39 | 23.10 | 1.50 | 2.44 | 6.57 | 8.38 | 61.43 | 1.98 | 10.61 | 2.53 | 13.59 |
| **Days to 50% flowering** | 93.66 | 87.33 | 102.67 | 9.42 | 14.73 | 3.28 | 4.10 | 63.94 | 5.06 | 5.40 | 6.48 | 6.92 |
| **Flag leaf area (cm²)** | 21.28 | 15.60 | 27.99 | 11.40 | 12.72 | 15.86 | 16.76 | 89.58 | 6.58 | 30.93 | 8.44 | 39.63 |
| **Plant height (cm)** | 94.75 | 78.48 | 114.89 | 59.05 | 67.44 | 8.11 | 8.67 | 87.55 | 14.81 | 15.63 | 18.98 | 20.03 |
| **Panicle bearing tillers per plant** | 12.34 | 8.87 | 16.55 | 2.53 | 3.44 | 12.90 | 15.02 | 73.71 | 2.81 | 22.81 | 3.61 | 29.23 |
| **Panicle length (cm)** | 22.63 | 18.28 | 26.67 | 3.09 | 4.97 | 7.77 | 9.85 | 62.20 | 2.86 | 12.62 | 3.66 | 16.17 |
| **Spikelet's per panicle** | 138.06 | 103.67 | 226.08 | 850.57 | 856.99 | 21.12 | 21.20 | 99.25 | 59.85 | 43.35 | 76.71 | 55.56 |
| **Spikelets fertility (%)** | 88.26 | 82.02 | 91.91 | 3.25 | 6.11 | 2.04 | 2.80 | 53.25 | 2.71 | 3.07 | 3.47 | 3.94 |
| **Biological yield per plant (g)** | 50.95 | 39.80 | 76.03 | 77.58 | 80.46 | 17.29 | 17.61 | 96.42 | 17.82 | 34.97 | 22.83 | 44.82 |
| **Harvest index (%)** | 42.01 | 35.76 | 47.78 | 5.64 | 9.14 | 5.65 | 7.20 | 61.68 | 3.84 | 9.14 | 4.92 | 11.72 |
| **Test weight (g)** | 23.41 | 20.24 | 27.42 | 2.15 | 3.17 | 6.27 | 7.60 | 68.02 | 2.49 | 10.65 | 3.20 | 13.65 |
| **Grain yield per plant (g)** | 21.58 | 16.73 | 31.85 | 17.53 | 19.71 | 19.40 | 20.58 | 88.91 | 8.13 | 37.68 | 10.42 | 48.29 |

The estimates of heritability in broad sense ($h^2_b$) and genetic advance in % of mean estimated for all the twelve characters have been presented in Table 2. Broad sense heritability estimates ranged from 53.25 % (spikelet fertility %) to 99.25% (spikelets per panicle). The high heritability in broad sense (>75%) was recorded for spikelets per panicle (99.25%), biological yield per plant (96.42%), flag leaf area (89.58%), grain yield per plant (88.91%), and plant height (87.55%). The remaining characters possessed a moderate broad sense of heritability (50 to 75%). The genetic advance in percent of mean was found to be high (>20%) for spikelets per panicle (43.35%), grain yield per plant (37.68%), biological yield per plant (34.97%), flag leaf area (30.93%) and panicle bearing tillers per plant (22.81%). Moderate (>10-20%) estimates of genetic advance in percent of mean were observed for plant height, panicle length, and seedling height. The rest of the traits exhibited low estimates (<10%) of broad-sense heritability. Most of these results showed a similarity with the previous reports of Akter *et al.* (2010); Choudhary *et al.* (2021).

## CONCLUSION

In any breeding programme planned to improve a trait, it is crucial to have a better understating of the variability and heritability of a population. Because it provides an idea about the breeding schemes to be adopted for the improvement of particular traits. In this sense, the characters spikelets per panicle, biological yield per plant, flag leaf area, grain yield per plant, and plant height had high estimates of heritability and genetic advance indicating additive gene action. So, selection will be rewarding for the improvement of these traits in a breeding programme planned in CMS rice.

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**Conflict of Interest.** None.

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