



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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NAAS Rating (2026): 5.20
www.agronomyjournals.com
2026; SP-9(5): 285-288
Received: 11-02-2026
Accepted: 15-03-2026

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Skewness and kurtosis studies for yield and nutritional traits in Rice (*Oryza sativa* L.) F₂ population

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DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i5Sd.5573>

Abstract

Improvement programs for rice are nowadays not only oriented towards increasing the grain yield but also towards improving its nutritional qualities. In the current study, the variability and distribution pattern of certain yield and nutritional features have been assessed in F₂ progenies obtained through crossing between lines CO54 and *Chinkinkar*. The population under assessment has been evaluated for 17 quantitative traits including grain yield-related parameters, grain morphological features and grain nutritional composition. Wide variation among F₂ segregants has been established concerning all traits which shows successful creation of valuable recombinants via the combination of CO54 and *Chinkinkar* lines. High variances have been obtained especially for number of total and filled grains per panicle and plant height, which means that there is considerable genetic variation in respect of these traits. Analysis of distribution patterns revealed both positive and negative skewness which suggests involvement of additive and non-additive gene action in inheritance. Majority of traits showed platykurtic distribution and, hence, they can be classified as polygenic ones possessing rather broad genetic base. There has also been identified considerable variation for iron, zinc and protein contents in grain which demonstrates the value of this population in bio-fortification breeding.

Keywords: Skewness, kurtosis, bio-fortification, F₂ population, rice

Introduction

Rice (*Oryza sativa* L.) serves as the main source of sustenance for a significant percentage of the world's population and provides an important source of calories, especially in Asia. Although it is an important staple food, milled rice grains have relatively low amounts of micronutrients like iron and zinc. The lack of these micronutrients poses a serious nutritional problem in developing nations where rice comprises the bulk of their diet. Hence, the breeding of nutritious rice varieties has become highly prioritized (Yadav *et al.*, 2025) ^[1].

Genetic enhancement using traditional breeding techniques is among the most cost-effective methods for improving the nutritive value of cereal grains. The efficiency of the breeding program is greatly influenced by the genetic diversity available in the breeding stock. Generations of segregation such as F₂ offer tremendous potential for selection due to their high degree of recombination and segregation. The evaluation of frequency distribution parameter characteristics like skewness and kurtosis aids in understanding the mode of inheritance and the genetic behavior of the quantitative characters (Sheshaiah *et al.*, 2028) ^[9]. Skewness will help in understanding the degree of asymmetry in the distribution of the character and gives an idea about the gene action involved, while kurtosis will help understand the distribution of the genes involved and estimate the number of genes responsible for the character (Riyanto *et al.*, 2024) ^[7].

Chinkinkar is characterized by its red grain color and higher micronutrient content, especially that of iron and zinc. On the other hand, CO54 is a high-yielding variety, showing good agronomic characteristics (Deepika *et al.*, 2025) ^[1]. Hybridization between such genetically dissimilar parents could produce better recombinants that would combine both high yield potential and nutritional value. Therefore, the current study has been conducted to analyze variability and distribution patterns for yield and nutrition-related traits in the F₂ population derived from crossing between CO54 and *Chinkinkar*.

Materials and Methods

This experiment was conducted at the experimental farm of the Department of Plant Breeding and Genetics, Tamil Nadu Rice Research Institute, Aduthurai, Tamil Nadu. The selection of parents is based on the documented performance data (Table 1&2). Based on these performances and crossing, two mapping populations were made in the year 2023. The F₂ population derived from crossing of CO54 × *Chinkinkar* was raised. Seedlings of 26 days old were transferred to the main field with spacing of 30 cm × 30 cm. Total number of potential F₂ segregates of CO54 × *Chinkinkar* cross was found out to be 238. Recommended practices for agronomics and disease management were followed.

Observation of various characters were made from selected plants in each of the cross combinations and tagging of each randomly selected individual plant was done prior to anthesis. All of the seventeen characters including days to maturity (DM), plant height (PH), number of productive tillers per plant (NPT), flag leaf length (FL), flag leaf width (FW), kernel length (KL), kernel breadth (KB), length-to-breadth ratio (LBR), panicle length (PL), panicle weight (PW), number of branches per panicle (NB), filled grains (FG), total number of grains per panicle (TGP), single plant yield (SPY), Fe content in brown rice (FEB), Zn content in brown rice (ZNB), protein content in brown rice (PCB) were studied at Quality Laboratory in Tamil Nadu Rice Research Institute using ED-XRF.

Estimation of Fe, Zn and Protein Content

Each plant was harvested individually and subjected to analysis for their nutritional content of grains. The required number of seeds was removed from the husk and ground by using a non-metallic dehusker (Krishi International 810 dehusker) in the grain quality lab at Tamil Nadu Rice Research Institute, Aduthurai, Tamil Nadu. The seeds were polished for 30-45 seconds and cleaned with the help of tissue paper. Only intact grains without any damage and free from any debris were used for analysis. The content of iron and zinc in brown rice was estimated through an energy-dispersive x-ray fluorescence spectrometer (ED-XRF) (Hitachi X-supreme) according to Harvest Plus protocol (Maganti *et al.*, 2020, Yadav *et al.*, 2025 and Deepika *et al.*, 2025) ^[4, 11, 1]. Brown rice samples (5 grams each) were measured and placed into the sample cups. The iron and zinc content in the grains was expressed in milligram per kilogram (mg/kg) or parts per million (ppm).

The measurement of protein concentration in grains using NIR spectroscopy was done by irradiating the samples to specific wavelengths of absorbance (900-2500nm). The grain samples were prepared by cleaning off all contaminants, dust, and broken grains. The samples were then reduced to powder form through the use of the laboratory mill. The samples were introduced into the sample chamber, and the NIR spectrometer irradiated near-infrared light onto the samples.

Results and Discussion

The segregating generation obtained by crossing CO54 with *Chinkinkar* showed high variations for all the characters, which suggested that there was proper recombination among the parent lines. The duration from planting to harvesting for the F₂ generation was observed to be from 110.30 days to 156.80 days, with the average being 130.33 days. This indicated that there were some early and late maturing plants in the segregating generation. The height of the plants had a broad range, which was from 103.20 cm to 198.60 cm, with the average being 151.22 cm.

A wide range of variability was also noted for grain and panicle characteristics. Kernel length ranged from 5.10 to 7.60 mm, while kernel width ranged from 1.40 to 2.60 mm. Variability was noted for the ratio of kernel length to width, ranging from 2.17 to 4.33, indicating that diverse kernels were present among segregants. Panicle length and panicle weight ranged from 17.20 to 37.50 cm and 1.45 to 5.08 g,

There were large variations in relation to the yield attributes in the population studied. The number of filled grains in the panicle ranged from 51.20 to 283.30, whereas the total grains per panicle ranged from 100.40 to 439.00. Individual yield had variation from 7.60 g to 52.60 g.

Large variations were also found in the nutritional characteristics of brown rice. For example, the iron content varied between 8.10 and 16.70 mg kg⁻¹, whereas the zinc content varied between 17.53 and 39.35 mg kg⁻¹. The protein content also varied from 5.80% to 11.73%. These large variations observed in the traits of micronutrients indicated that the cross can be exploited in breeding programs for nutritional improvement.

The variations found within the segregants suggest that there was enough genetic variation present to conduct phenotypic selections. Such a situation had also been noted previously in rice segregating populations by Riyanto *et al.*, and Priyanka, *et al.*

Variability analysis

The analysis of variance parameters showed that there were high variances in the segregants for almost all the characteristics studied. The characteristic with the highest variance was the number of grains per panicle (5657.79), while the number of filled grains per panicle (3320.41) and plant height (417.07) were second and third, respectively.

Variability was high regarding the number of grains and the yield associated traits, showing great potential for identifying good plants during the initial generations of segregation. Wide variability was also exhibited by the nutritional parameters, suggesting the possibility of identifying good strains with increased contents of the micronutrients. High levels of variability are highly desirable within breeding programs since the chances of getting transgressive segregants are increased (Piyari *et al.*, 2023) ^[6].

Skewness and Kurtosis analysis

The skewness values indicate the nature of gene actions governing various traits. The skewness values in this study ranged between -0.57 and 1.06. Majority of the characteristics showed positive skewness, namely days to maturity, flag leaf width, panicle length, total number of grains in panicle, yield per plant, and nutritive traits. Of the characters analyzed, the content of zinc had the maximum positive skewness (1.06), whereas the ratio of length to breadth had the second highest value (0.63). Positive skewness is often an indication of complementary gene action and can be improved through selective breeding. However, kernel breadth displayed negative skewness alone (-0.57), suggesting that the dominance gene action was common in this character. The presence of positive and negative skewness in traits indicated that additive as well as non-additive gene effects played roles in determining the inheritance of traits. Such observations have been noted earlier in rice by Kaur *et al.* (2024) ^[3], Sahu *et al.* (2023) ^[8] Nikhitha *et al.* (2020) ^[5], Sheshaiah *et al.* (2018) ^[9].

A study on kurtosis was performed to examine the nature of trait distribution among the segregating population. The majority of

the characters had negative kurtosis, implying that their distributions were platykurtic. Platykurtic distribution usually implies that there were many genes with minor contributions that controlled the traits. Characteristics like filled grains/panicle (-1.00), maturity period (-0.71), productive tillers (-0.62), and grain width (-0.63) displayed wider and flatter distribution patterns, demonstrating the existence of variation within the segregants. Moreover, iron content and protein content had negative kurtosis values, thus signifying that the population was ideal for improving nutrition.

Table 1: Parents used for development of CO54 x Chinkinkar F2 population

Parents	Genotype	Parentage	Features	Source
P ₁	CO54	CB04110/CB 05501	White Medium slender rice. Moderately resistant to Blast, Sheath rot, Brown Spot and BPH	Coimbatore, TNAU
P ₂	Chinkinkar	Landrace	Short duration, grain colour-red long bold, low gel consistency. Zn (26.4 mg kg ⁻¹) and Fe (16.10 mg kg ⁻¹)	TRRI, Aduthurai

Table 2: Descriptive statistics of CO54 X Chinkinkar cross

Parameters	DM	PH	NPT	FL	FW	KL	KB	L/B	PL	PW	NB	FG	TGP	SPY	FEB	ZNB	PCB
Mean	130.33	151.22	20.17	47.85	1.30	6.19	2.12	2.99	24.83	2.97	11.28	170.95	240.35	25.26	11.76	24.54	9.06
Maxi	156.80	198.60	38.40	75.20	1.80	7.60	2.60	4.33	37.50	5.08	17.20	283.30	439.00	52.60	16.70	39.35	11.73
Mini	110.30	103.20	5.20	28.30	1.10	5.10	1.40	2.17	17.20	1.45	5.30	51.20	100.40	7.60	8.10	17.53	5.80
Standard Deviation	11.29	20.42	6.47	10.41	0.16	0.44	0.30	0.46	4.47	0.71	2.16	57.62	75.22	8.93	1.93	4.37	1.07
Standard Error	0.78	1.42	0.45	0.72	0.01	0.03	0.02	0.03	0.31	0.05	0.15	4.01	5.23	0.62	0.13	0.30	0.07
Variance	127.42	417.07	41.84	108.42	0.03	0.20	0.09	0.21	19.98	0.51	4.65	3320.41	5657.79	79.77	3.73	19.11	1.14
Skewness	0.32	0.23	0.18	0.25	0.51	0.20	-0.57	0.63	0.47	0.20	0.09	0.13	0.47	0.42	0.39	1.06	0.48
Kurtosis	-0.71	-0.43	-0.62	-0.66	-0.42	-0.07	-0.63	0.08	-0.44	-0.42	-0.33	-1.00	-0.33	-0.32	-0.32	0.83	-0.12

DM - Days to maturity, PH - Plant Height, NPT –number of productive tillers per plant, FL – Flag leaf length, FW – Flag leaf width, KL – Kernel Length, KB- Kernel Breadth, LB – Length to Breadth ratio, NB – Number of branches per panicle, FG – Filled Grains, UFG – Unfilled Grains, TGP – Total number of Grains per Panicle, SPY – Single Plant Yield; FEB- Fe content in brown rice ZNB- F Zn content in brown rice: PCB- Protein content in brown rice

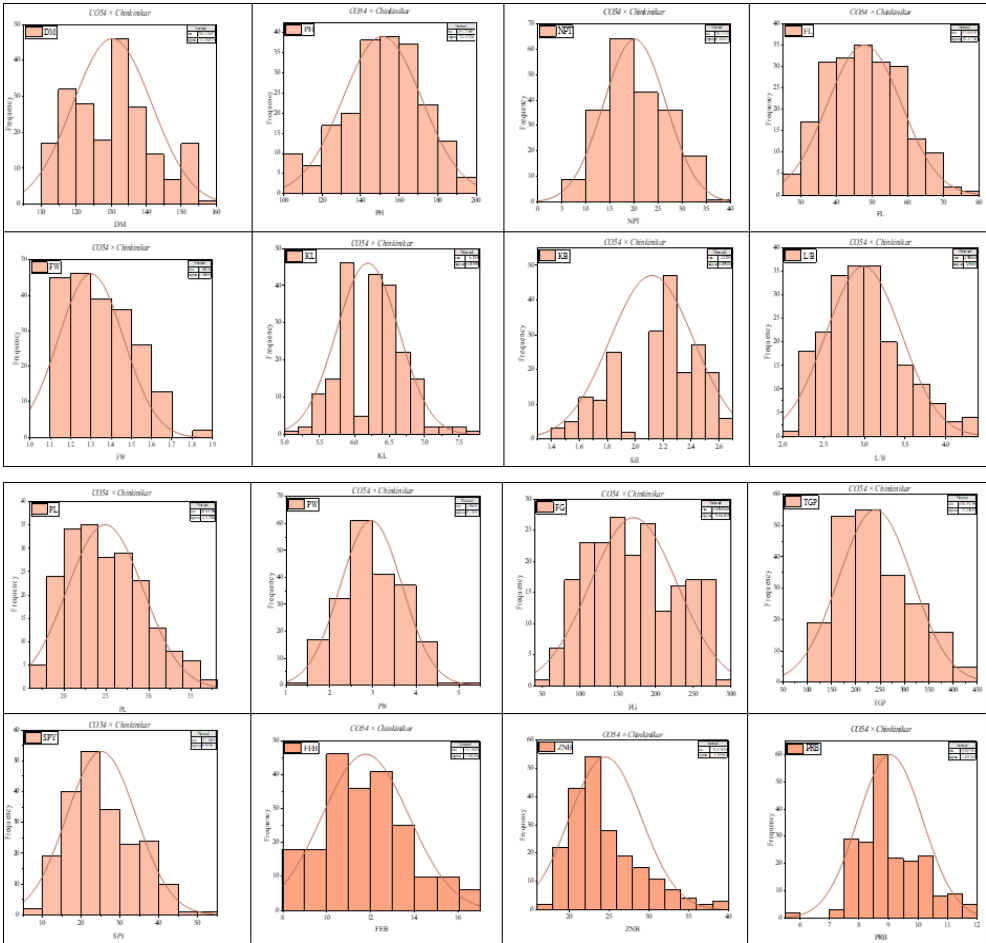


Fig 1: Distribution pattern of yield and nutritional characters in CO54 X Chinkinkar of F2 segregating generation of rice

Conclusion

There was considerable variation in yield and nutritional traits in the F₂ population obtained from the cross between CO54 and *Chinkinkar*, suggesting considerable scope for selection and further genetic improvement. The high variance found in the traits like total grains per panicle, filled grains, and plant height indicated the possibility of considerable genetic variation among the segregants. Skewness and kurtosis test results pointed out the influence of both additive and non-additive genetic effects on most of the traits, which have a polygenic mode of inheritance. Traits like grain iron, zinc and protein contents were encouraging in terms of their variation, indicating the scope of this population to develop nutritionally rich rice varieties.

Acknowledgements

All authors offered equal suggestions and contributions on original draft preparations.

Conflict of Interests

The authors declare that they have no conflict of interest.

Author's Contributions

All authors listed have made a substantial, direct and intellectual contribution to the work and approved it for publication.

Ethical approval

None

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