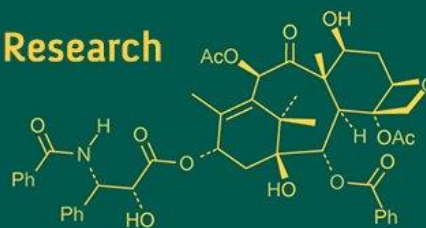


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Genetic architecture and frequency distribution of yield and nutritional traits in ADT56 x *Kalanamak* derived F₂ population of Rice (*Oryza sativa* L.)

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Abstract

In the present study, frequency distribution and descriptive statistical parameters were analysed for seventeen yield and grain nutritional traits in ADT56 X *Kalanamak* of F₂ population of rice. Significant variability was observed across all traits. The total grains per panicle (3214.50), filled grains (2235.30) and plant height (320.10) exhibiting the highest variance. Skewness values ranged from -1.26 to 1.21 indicating involvement of both additive and non-additive gene actions. Kurtosis values suggested that most traits followed a platykurtic distribution, reflecting polygenic inheritance. Traits such as single plant yield and grain zinc content showed positive skewness suggesting the potential for selection in advanced generation. The results demonstrate that the F₂ population provides a valuable resource for identifying superior recombinants and designing efficient breeding strategies.

Keywords: F₂ population, frequency distribution, skewness, kurtosis, yield and nutritional traits

Introduction

Rice (*Oryza sativa* L.) is a staple food crop supporting more than half of the world's population. Rice is the primary food crop and energy source for almost half of the world's population. This crop is economically significant not only in Southeast Asia but globally. People who only eat rice suffer from concealed hunger or vitamin deficiencies. The most common deficiencies are those in zinc and iron, which affect around 2 billion people and result in about 0.8 million fatalities each year (WHO, 2002).

From the past few years of breeding efforts resulted in development of bio-fortified crops including rice with increasing bio available zinc in rice endosperm is an important target of bio-fortification efforts. In order to identify the genes responsible for high grain iron, zinc and protein mechanism, and development of mapping population and QTL mapping is prerequisite. Although there are several mapping populations, segregating mapping population like F₂ are quick and easy to develop as they permit mapping the QTLs (Singh and Singh, 2015) ^[17]. Several studies on character association have used homozygous genotypes or variations. Correlation studies in segregating populations can yield more significant results as they focus on individual plant observations. Early generation testing can be used to select individuals in segregating populations (Singh *et al.*, 2020) ^[16].

Consumers are concerned about the physical quality of rice, as it is ingested whole. When purchasing rice, buyers consider its length, shape, homogeneity, and appearance. The consumer examines the rice's cooking quality, flavor, and nutritional value. Enhancing the length and form of rice is a key goal in generating new types. To improve the physical quality of rice, crosses between selected parents can increase gene diversity and heritability of the desired characteristic (Riyanto *et al.*, 2024) ^[14].

Landraces may have varying levels of minerals, vitamins and other essential nutrients (Rathna Priya *et al.*, 2019) ^[13]. In most of the landraces, grain Fe content ranges from 7.8 to 19 mgkg⁻¹, Zn from 13.3 to 32 mgkg⁻¹ and protein content from 6.9 to 12.4% (Kamupang *et al.*, 2017) ^[5]. The genotypes having more grain yield ranged from 22.31g to 29.93g (*Kalanamak* and ADT56) and the genotypes more than 12.00 mg kg⁻¹ of Fe, 24 mg kg⁻¹ of Zn and 10% of protein content are considered as nutritional rich varieties for Fe, Zn and protein content

respectively (Deepika *et al.*, 2023) ^[3]. Enhancing yield potential grain quality and nutritional traits remains a key objective in modern rice breeding programs. The success of breeding depends largely on the availability of genetic variability and the understanding of gene action governing important traits (Das *et al.* 2021) ^[2]. The F₂ generation is highly informative due to maximum segregation and recombination, allowing the expression of diverse phenotypes. Frequency distribution analysis provides insights into inheritance pattern of quantitative traits. The skewness and kurtosis are particularly useful in understanding gene action and genetic architecture.

Skewness indicates the asymmetry of trait distribution and reflects dominance or epistatic interactions, whereas kurtosis provides information about the number of genes controlling a trait. Traits showing normal distribution governed by multiple genes, while deviations suggest complex inheritance.

Therefore, the present investigation was undertaken to analyze distribution patterns, and gene behavior of yield and its nutritional component traits in F₂ population of ADT56 X *Kalanamak* cross.

Materials and Methods

The current investigation was carried out in the experimental field of Department of Plant Breeding and Genetics, Tamil Nadu Rice Research Institute, Aduthurai, Tamil Nadu. Based on documented results, (Table 1 & 2) the parents were chosen based on yield and grain iron and zinc content and crossed and developed mapping populations during 2023. The F₂ generations resulting from the cross between ADT56 x *Kalanamak*, were grown. Twenty six days old seedlings were transplanted in to the main field with a spacing of 30 cm x 30 cm. A total of 222 possible F₂ segregants of ADT56 x *Kalanamak* cross were identified and labeled for further assessment. The recommended agronomic practices and crop protection measures were followed during the crop growth period. Each F₂ plant was harvested separately. Observations were recorded from selected plants of each of the cross combinations and each of the randomly selected individual plant was tagged before anthesis. Data on all the seventeen characters namely 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; LBR-length-to-breadth ratio, PL- Panicle Length, PW-Panicle Weight, 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 and ZNB-Zn content in brown rice and PCB- Protein content in brown rice were analyzed at Tamil Nadu Rice Research Institute, quality lab, with ED-XRF. The recorded data was subjected to statistical analysis mean, variance, Skewness and Kurtosis using R studio software.

Estimation of grain Fe and Zn content

Each individual plants are harvested separately and analyzed the grain nutritional content. Required amount of seeds were de-husked and milled using non-metallic de-husker (Krishi international 810 de-husker) at the grain quality laboratory, Tamil Nadu Rice Research Institute, Aduthurai, Tamil Nadu. Samples were polished for 30-45 sec and cleaned using tissue paper. Only full, undamaged grains free from

debris were analysed. The grain iron and zinc content in brown rice samples were estimated using a non-destructive, energy-dispersive x-ray fluorescence spectrometry (ED-XRF) instrument (Hitachi X-supreme) following Harvest plus guidelines (Stangoulis *et al.*, 2007 and Deepika *et al.* 2025) ^[19, 4]. Each sample of brown rice (5g) was weighed and transferred to sample cups. The sample cups were gently shaken for uniform distribution of samples and then set aside for analysis. The concentration of grain iron and zinc was expressed in milligram per kilogram (mg kg⁻¹) or parts per million (ppm) of grains.

Estimating grain protein content using Near-Infrared (NIR) spectroscopy involves scanning samples to absorbance at specific wavelengths (900-2500nm). Grain samples are cleaned to remove impurities, dust and damaged kernels. Samples grind into fine flour using a laboratory mill. Samples are placed on a sample compartment and NIR analyzer passes near-infrared light on the samples and device measure the reflected or absorbed light, which is affected by molecular bonds.

Results and Discussion

per se performance of the genotypes

Each individual F₂ plants were recorded significant variation for all studied traits. The Days to maturity ranged from 102 to 159 days with mean of 133 days followed by plant height 90.78 to 165.58 cm with an average mean of 128.81cm, the number of productive tillers per plants was ranged from 6.8 to 38.82 with grand mean of 20.48. On the other hand, the panicle weight has recorded with 1.44g to 5.3g including the mean of 2.85g and the number of filled grains per panicle ranged from 73.50 to 284 with mean of 177.28, likewise the total number of grains per panicle noted 101.80 to 469.60 with grand mean of 242.31. The single plant yield had observed 9.20g to 53.40g with grand mean of 27.26g. The nutritional traits like grain iron, zinc and protein content were ranged 8.60 - 16.90 with mean of 12.32 and 17.41-36.75 with average mean of 25.03 mg kg⁻¹ followed by protein content of 7.21 to 11.54 with the mean of 8.80% respectively. The same results were recorded by Lakshmi *et al.* (2017) ^[8], Khandappagol *et al.* (2019) ^[6] and Riyanto *et al.* (2024) ^[11].

Skewness and Kurtosis analysis

The segregating population of ADT56 X *Kalanamak* exhibited a wide range of variation. The highest variance was recorded for Total number of grains per panicle 3214.50 and Filled grains were recorded as 2235.30 followed by Plant height observed has 320.10. The days to maturity recorded the variance of 140.3 and the single plant yield recorded as 56.90.

In F₂ population of ADT56 X *Kalanamak*, significant positive skewness was observed for most of the traits (Table 2). Skewness values were ranged from -1.26 to 1.21. The positive skewness was observed for length to breadth ratio (1.21), grain zinc content in brown rice (0.76), filled grains (0.72), protein content in brown rice (0.38), panicle length (0.32), and single plant yield (0.27). Characters observed with positive skewness indicate that more proportion of individuals present in low end of distribution but transgressive segregants were also obtained for these traits. Hence selection of single plants with grain zinc and protein content from the transgressive segregants will improve the positively skewed traits which implies that can helpful for

selection cross combination and development of bio-fortified rice varieties.

Significant negative skewness was observed for days to maturity (-0.33) and kernel breadth (-1.23). However negative skewness observed for days to maturity, selection may be done from lower end of distribution to obtain early type segregants. Sufficient variability was available for most of the traits in this population, superior segregants with high yield along grain zinc and protein content could be isolated for developing a bio-fortified rice varieties.

Frequency distribution of yield and nutritional traits were represented in Figure 1. Regarding kurtosis, even though significant leptokurtic nature of distribution was observed

for length to breadth ratio, wide range of distribution was recorded for these traits.

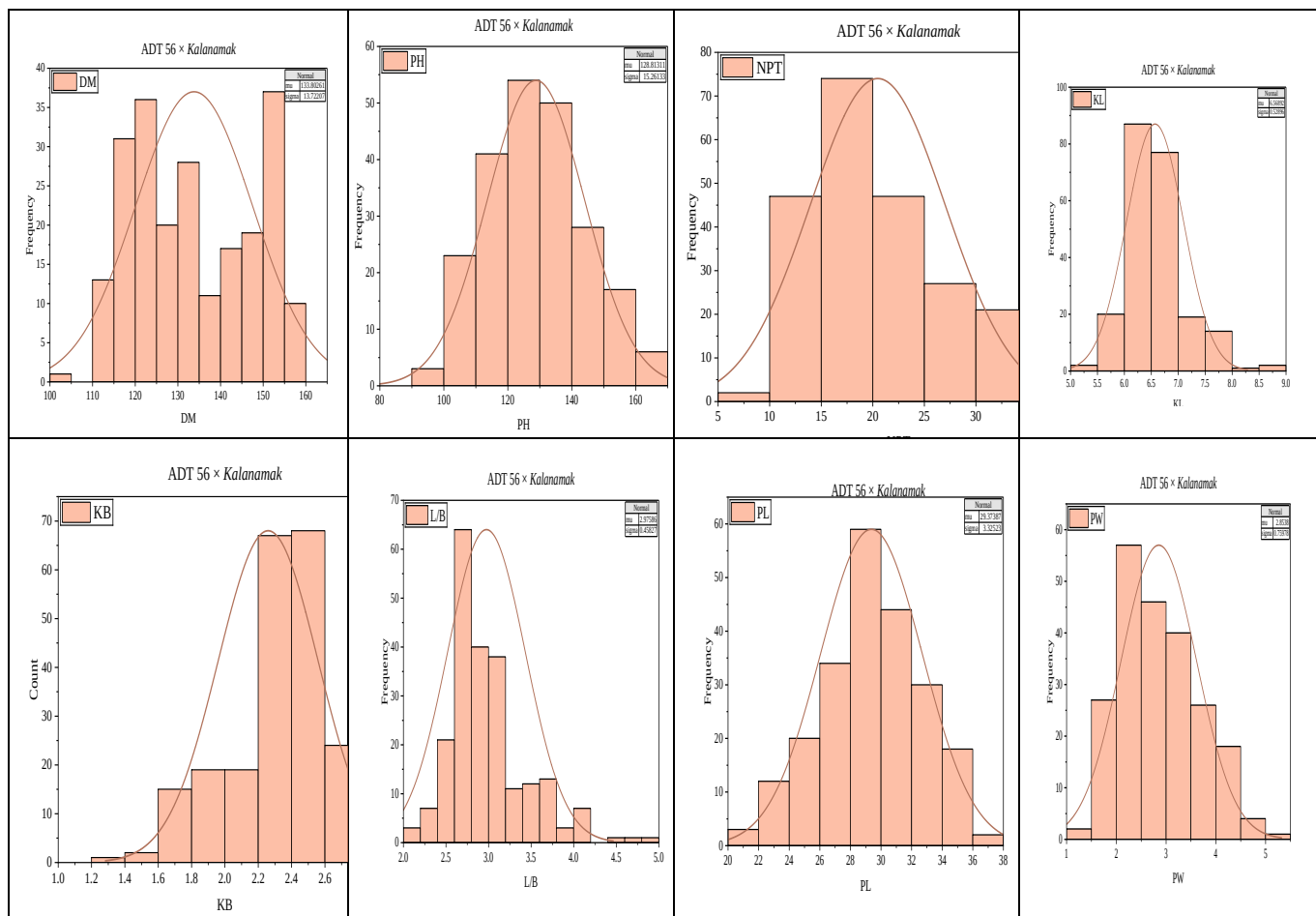
Mostly of these traits like zinc content in brown rice (-0.87), iron content in brown rice (-0.54), number of productive tillers (-0.46) and protein content in brown rice (-0.45) were showed negative kurtosis (platykurtic) with uniform distribution indicating polygenic inheritance. The traits like single yield per plant (0.51) followed by days to maturity (0.23) and filled grains (0.19) were recorded mesokurtic with normal distribution. The results were confirmed with Prabhu *et al.* (2015)^[12], Patel *et al.* (2020)^[11], Bhadru *et al.* (2021)^[1] Manoj kumar *et al.* (2022)^[7], Sowmiya *et al.* (2023)^[18] and Sahu *et al.* (2023)^[15].

Table 1: Parents used for development of F₂ population

Parents	Genotype	Parentage	Features	Source
P1	ADT56	WGL1437/MDU5	Short duration, good cooking & eating quality. Moderately resistant to leaf blast, grain discoloration, stem borer and leaf folder	TRRI, Aduthurai
P2	Kalanamak	Landrace	Short duration, finest quality, resistant to blast. Cooked rice is fluffy, soft, non-sticky, sweet and easily digestible with relatively longer shelf-life. It had 15.6 mg/kg of Fe. It is famous for taste, palatability and aroma.	TRRI, Aduthurai

Table 2: Descriptive statistics of ADT56 X Kalanamak cross

Parameters	DM	PH	NPT	FL	FW	KL	KB	L/B	PL	PW	FG	UFG	TGP	SPY	FEB	ZNB	PCB
Mean	133.80	128.81	20.48	39.22	1.54	6.57	2.26	2.98	29.37	2.85	177.28	65.03	242.31	27.26	12.32	25.03	8.80
Maxi	159.38	165.58	38.82	67.23	2.50	8.50	2.90	4.83	37.30	5.30	284.10	193.30	469.60	53.40	16.90	36.75	11.54
Mini	102.75	90.78	6.83	25.42	0.70	5.40	1.20	2.07	21.40	1.44	73.50	7.80	101.80	9.20	8.60	17.47	7.21
Variance	140.3	320.10	38.50	91.20	0.05	0.15	0.07	0.18	8.86	0.42	2235.30	889.50	3214.50	56.90	3.10	13.60	-0.30
Skewness	0.24	-0.33	0.23	0.25	0.05	0.35**	-1.26	1.21**	0.32	0.13	0.72**	0.21	0.20	0.27	0.21	0.76**	0.38
Kurtosis	0.23	-0.62	-0.46	-0.01	-0.45	-0.04	-0.12	1.21	-0.40	-0.43	0.19	-0.23	-0.27	0.51	-0.54	-0.87	-0.45



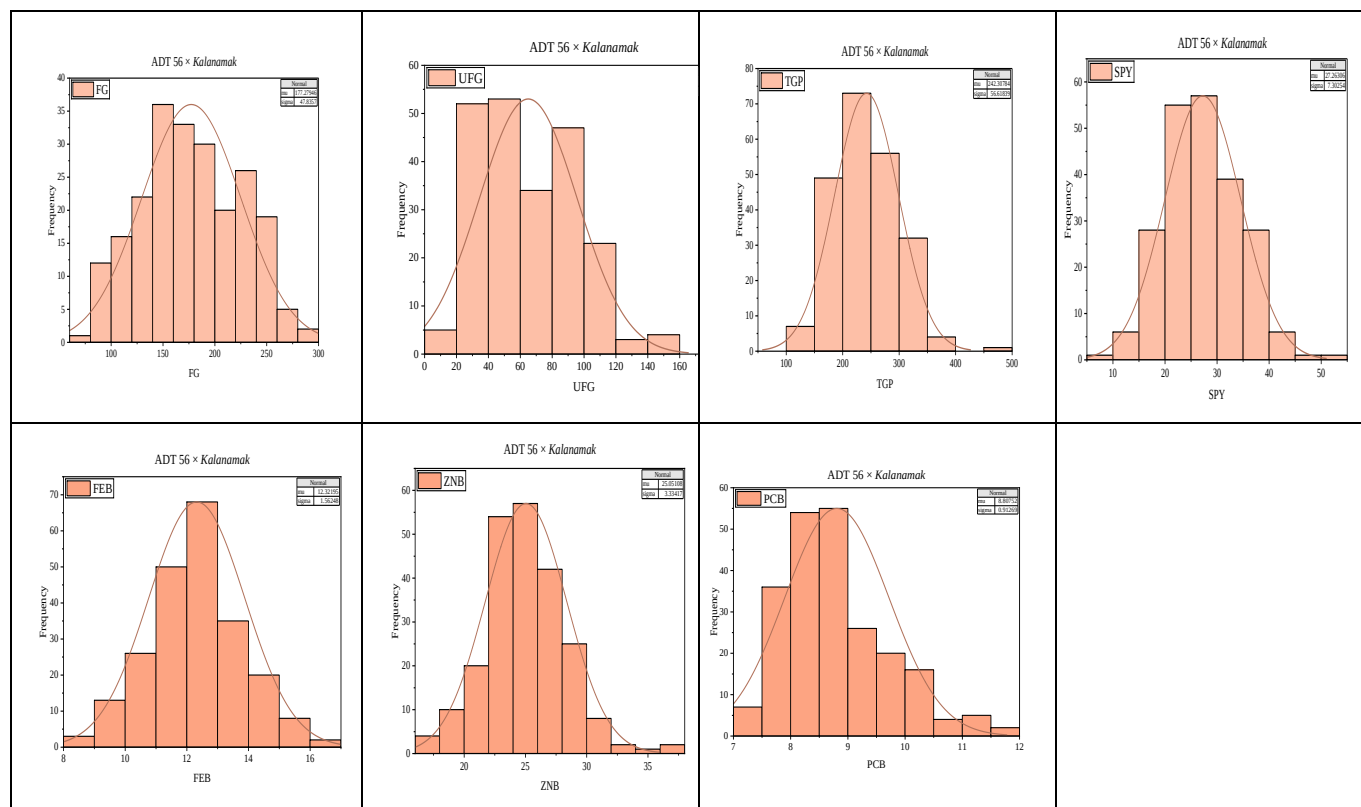


Fig 1: Distribution pattern of various characters in ADT56 X *Kalanamak* of F_2 segregating generation of rice

Conclusion

The F_2 population exhibited wide variation. Most traits showed polygenic inheritance with both additive and non-additive gene effects. Yield and nutritional traits demonstrated promising variability, indicating potential for improvement. The study highlights the importance of early-generation analysis in selecting superior genotypes and improving breeding efficiency.

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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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