



## Genetic and Cytogenetic Characterization of Local Rice (*Oryza sativa* L.) Varieties from Chalan Beel

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### ABSTRACT

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An experiment was conducted in the Agronomy Field Laboratory, along with a laboratory experiment at the Farming System Engineering Laboratory, Department of Agronomy and Agricultural Extension, University of Rajshahi, from mid-May to mid-November 2024. Eight rice genotypes were analyzed to understand their genetic variation, heritability (broad sense), genetic advance, and karyotype details. The study design followed Randomized Complete Block Design (RCBD), and each treatment was repeated three times, evaluating agronomic traits like plant height, leaf number, tiller number, effective tillers per meter<sup>2</sup>, panicle length, grains per plant, filled grains, 1000-grain weight, straw yield, yield of grain, and biological yield. Significant variation was observed across most traits. Grain yield exhibited the highest genotypic (GCV) and phenotypic coefficient of variation (PCV), followed by plant height, while grain per plant and 1000-grain weight showed the lowest. For each trait, the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV), indicating a measurable environmental influence on trait expression. Heritability was observed to be high in the case of 1000-grain weight, followed by panicle length and grain yield, whereas the height of the plant showed the highest genetic advance. For karyotype analysis, metaphase plate photomicrographs, camera-lucida drawings, and idiograms were used to assess total chromosome length (TCL), arm ratio, centromeric position, TF%, and karyotype formulae. The highest TCL with the lowest TF% was observed in SADA VAULA, while the lowest TCL with the highest TF% was recorded in BINA-7. The combination of high heritability and genetic advance for traits like plant height and grain yield indicates the predominance of additive gene action and suggests good potential for improvement through direct selection.

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## Introduction

Rice (*Oryza sativa* L.) is a staple crop and a major food source for over half of the global population, providing more than 21% of the world's caloric intake (Ishfaq et al., 2023). In Asia, where almost 90% of the rice in the world is both produced and eaten, it forms an integral part of both diet and culture (Fadah et al., 2024). With increasing global food demand and the effects of climate change, maintaining rice productivity and diversity has become a central focus for food security initiatives (Zheng et al., 2024). Bangladesh, where rice is central to agriculture, nutrition, and economic stability, is no exception to this reliance. It accounts for nearly 70% of caloric intake in Bangladesh, underscoring its critical role in the nation's food system (Sarma et al., 2024).

Chalan Beel, one of the largest inland wetlands in Bangladesh, has historically been home to a rich diversity of deep-water rice varieties. However, many of these traditional varieties are now either extinct or facing a decline in adaptability and yield performance due to changing environmental conditions and other stress factors. This decline has significant implications for local food security and the livelihoods of farmers in these flood-prone regions. The development and conservation of local rice varieties that can withstand submergence stress through mechanisms such as elongation of leaf sheath, leaf lamina, and internodes, or submergence tolerance, is vital for sustaining rice production in these areas (Pradhan et al., 2024).

A comprehensive understanding of the genetic fidelity and variability among local rice varieties is essential for the effective management and enhancement of these genotypes. Genetic fidelity, referring to the genetic uniformity and stability among plant varieties, can be assessed through morphological, cytogenetic, biochemical, and molecular analyses (Tyagi et al., 2021). This knowledge aids in the selection of parental lines for breeding programs aimed at improving yield and resilience.

Genetic variability, which denotes the differences in genetic makeup among individuals within a population, is a crucial factor in plant breeding as it determines the capacity for adaptation and selection. Morphological traits, such as plant height and tiller number, often serve as preliminary indicators of genetic diversity due to their ease of observation (Rahul et al., 2024). Understanding how heritable these traits are and their genetic advance allows breeders to estimate selection outcomes and develop new high-yielding varieties (Dwivedi et al., 2020). Moreover, the correlation between traits and their direct and indirect effects, assessed through path analysis, provides valuable insights into complex trait interactions.

Given the importance of preserving and optimizing rice varieties suited for the Chalan Beel region, this study was conducted to investigate the nature and magnitude of variability among selected rice genotypes or varieties. Estimate genotypic and phenotypic variability. Assess heritability and genetic advance under selection. Analyze genetic distance and relationships among rice genotypes through karyotype analysis. This research aims to inform breeding strategies that can enhance the resilience and yield of rice varieties adapted to flood-prone ecosystems, thereby contributing to sustainable agricultural practices and food security in Bangladesh.

## Materials and Methods

### Experimental Site and Conditions

The study took place at the Agronomy Field Laboratory, part of the Department of Agronomy and Agricultural Extension. This site is located at 24°22'36" N latitude and 88°38'27" E longitude, with an elevation of 20 meters, in the High Ganges River Floodplain area (AEZ-11). The soil at the location was flat, well-drained sandy loam, and had a pH level of 8.1. The region experiences a sub-tropical region known for hot temperatures, high humidity, and heavy rainfall during the kharif season (May-November). The highest recorded rainfall (353.4 mm) occurred in July, with an average monthly rainfall of 123.8 mm. The temperature ranged from 24°C (minimum) to 37.72°C (maximum). The study utilized eight rice cultivars along with three check varieties commonly grown in the lowland areas of Chalan Beel.

### Experimental Design and Data Collection

The experiment was arranged as a Randomized Complete Block Design (RCBD), repeated three times, where eight genotypes were randomly assigned across plots (10m<sup>2</sup> each). Approximately 110-120g of seed per plot was sown using the broadcasting method. Standard cultural practices, including irrigation, fertilization, and weeding, were applied as required throughout the growing

season. Harvesting took place in mid-November 2024 when crops matured. Data collection involved measuring plant height, leaf number, tiller count, effective tillers m<sup>-2</sup>, panicle length, filled grains, 1000-grain weight, straw yield, grain yield, and biological yield. Three plants per plot were randomly selected for measurements, and with three replications, a total of nine plants per cultivar were evaluated. Grain and straw yields were converted to t/ha for analysis.

### Data Analysis

Different statistical analyses were applied to the data gathered on yield-contributing, developmental, and physiological traits, as outlined below-

#### Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by (Johnson et al., 1955)

$$\sigma_g^2 = \frac{GMS - EMS}{r} \text{ with } (n-1)df$$

Where, GMS = Genotypic mean square, EMS = Error mean square, r = Number of replications.

Phenotypic variance,  $\sigma_p^2 = \sigma_g^2 + EMS$ .

Where,  $\sigma_g^2$  = Genotypic variance, EMS = Error mean square.

#### Coefficient of variation (CV)

The CV, in percentage form relative to the mean, was worked out as follows:

$$CV (\%) = \frac{\sigma_e \times 100}{\bar{x}}$$

Where,  $\sigma_e^2$  = Error mean sum of square,  $\bar{x}$  = Population mean of observations.

#### Calculating the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Genotypic and phenotypic coefficient of variations were estimated according to (R. K. Singh & Chaudhary, 1985)

$$\text{Genotypic coefficient of variation, GCV } (\%) = \frac{\sigma_g \times 100}{\bar{x}}$$

Where,  $\sigma_g$  = Genotypic standard deviation  $\bar{x}$  = Population mean.

Similarly, the PCV was estimated by applying the formula below-

$$\text{Phenotypic coefficient of variation, PCV } (\%) = \frac{\sigma_p \times 100}{\bar{x}}$$

Where,  $\sigma_p$  = Phenotypic standard deviation,  $\bar{x}$  = Population mean.

The GCV and PCV values are ranked as low, medium, and high (Shivasubramanian & Menon, 1973) and are mentioned below:

- <10% - Low
- 10-20% - Moderate
- > 20% - High

### Estimation of heritability

The heritability in a broad sense ( $h^2_b$ ) was estimated following the formula given by Hanson et al., (1956); Johnson et al., (1955).

$$\text{Heritability, } h^2_b = \frac{\sigma^2_g \times 100}{\sigma^2_p}$$

Where,  $\sigma^2_g$  = Genotypic variance; and  $\sigma^2_p$  = Phenotypic variance.

### Estimation of genetic advance (GA)

The genetic advance was estimated by applying the formula proposed by Johnson et al., (1955).

$$\text{Genetic advance, GA} = h^2_b \cdot i \cdot \sigma_p$$

Where,  $h^2_b$  = Heritability in a broad sense (decimal),  $i$  = Selection differential, the value of which is 2.06 at 5% selection intensity,  $\sigma_p$  = Phenotypic standard deviation.

### Calculating genetic advance as a percentage of the mean

The genetic advance as a percentage of the mean was calculated using the formula suggested by Comstock & Robinson, (1952), shown below-

$$\text{GA (\% mean)} = \frac{GA}{\bar{x}} \times 100$$

Where, GA = Genetic advance,  $\bar{x}$  = Population mean.

Genetic advance as a percent of the mean was classified as low, moderate, and high (Johnson et al., 1955) and values are given below:

- <10% - Low
- 10-20% - Moderate
- > 20% - High

### Pre-treatment, fixation, and preservation of root tips:

Root tips collected between 7:30 a.m. and 9:30 a.m. contained the maximum number of dividing cells. After the root tips had grown between 1 and 1.5 cm, they were collected with fine forceps, then poured into the root tip area with the help of a needle and pre-treated in 0.05% colchicine for 1-2 hours at 26-32°C. The root tips were then fixed by placing them in 1:3 aceto-alcohol at room temperature. Following 48 hours of fixation, the root tips were transferred to 75% ethanol and stored in the fridge until used in the lab.

### Staining of root tips and preparation of slides

The root tip cells were stained with 0.5% Haematoxylin following a stepwise process. After removal from 75% ethanol, they were washed with distilled water, hydrolyzed in 50% HCl, and rinsed again. Next, they were treated with 2% iron alum, followed by another wash, and then stained with Haematoxylin for five minutes. Finally, they underwent a thorough wash to remove excess stains. This staining process helped enhance chromosome visibility, ensuring accurate karyotype analysis under a microscope. For slide preparation, the stained root tip was placed on a clean slide, and the meristematic zone was carefully cut with a sharp blade and squashed in a drop of 0.5% acetocarmine. The cells were then

covered with a cover glass, and the slide was gently warmed over an alcohol flame. Gentle pressure was applied to the cover glass, followed by tapering. The slide was wrapped in blotting paper before being observed under a microscope. Selected metaphase plates were photographed using a microscope, and chromosomes were measured from camera lucida drawings. Idiograms of chromosome complements were prepared. Photomicrographs of metaphase plates, along with camera lucida drawings and idiograms for each cultivar.

### The technique of chromosome analysis

Chromosomes from three metaphase plates of each cultivar were measured using a stage micrometer, and the chromosomal sizes were converted to microns ( $\mu$ ). The chromosomes were classified based on the centromere position and the proportion between the short arm and the long arm. Chromosomes having an arm ratio under 0.50 were labeled sub-terminal (st), and those with ratios from 0.51 to 0.75 were labeled sub-median (sm), and those with an arm ratio above 0.75 as median (m), following the classification by KB, (1983). Additionally, chromosomes were grouped according to chromatin length as follows: large (L) for lengths above 2.95  $\mu$ , medium (M) for lengths between 2.40  $\mu$  and 2.94  $\mu$ , relatively short (S1) for lengths between 1.85  $\mu$  and 2.39  $\mu$ , and short (S2) for lengths below 1.84  $\mu$ . The chromosome formula for each cultivar was derived, and chromosome pair idiograms were arranged by total length in descending order, with the short arms pointing up and the centromeres aligned on the same plane. Huziwar, (1962) method was followed to find the total frequency (TF%), using the formula shown below:

$$\text{TF\%} = \frac{\text{Total sum of short arm}}{\text{Total sum of chromosome length}} \times 100$$

## Result and Discussion

The experimental data were collected and analyzed to study genetic variability and selection response for yield and yield-contributing phenological and physiological traits. The analysis of variance (ANOVA) for different advanced lines regarding morphological traits, as shown in Table 2, revealed highly significant differences among the genotypes for eleven traits: plant height, leaf number, tiller number, effective tiller  $m^{-2}$ , panicle length, grains per plant, filled grains, 1000-grain weight, straw yield, grain yield, and biological yield. It suggests that the genotypes vary widely in their genetic traits. The observed variability aligns with previous studies, Mousa et al., (2024) and Ukwu et al., (2025) that reported significant phenotypic differences in rice, indicating a broad genetic base in the studied genotypes. Although all genotypes showed significant differences, some studies have reported non-significant variation in certain cases, as observed by Duan et al., (2021), suggesting that individual grain characteristics play a crucial role in yield improvement. The ANOVA results confirmed highly significant variations among the genotypes for yield and its components. Additionally, univariate statistical analysis provided an opportunity to categorize the genotypes based on their performance in various traits. The range, standard error (SE), and mean performances of the eight rice genotypes for their respective traits are summarized in Tables 3 and 4.

Table 1. List of the eight rice cultivars used in the experiment with their source.

Code no.	Genotype	Source
G-01	AJOLDIGHA	SINGRA, NATORE
G-02	DIGHA	SINGRA, NATORE
G-03	DUDSOR	SINGRA, NATORE
G-04	SADA VAULA	SINGRA, NATORE
G-05	SORSORI	SINGRA, NATORE
G-06	BINA-7	BRRI, GAZIPUR
G-07	BRRI-39	BRRI, GAZIPUR
G-08	SHORNA	LOCAL MARKET, RAJSHAHI

Table 2. ANOVA (Mean Square) results for yield and its related traits

Source of Variation	df	Mean Square										
		PH	LN	TN	ETPM	PL	GPPL	FG	TGW	SY	GY	BY
Replication	2	1130.73	58.78	1.92	1210.07	6.48	1872.7	426.32	0.06	6.43	1.48	14.07
Genotype	7	2140.93	42.2	3.72	398.375	26.42	340.56	204.51	4.25	3.27	5.38	10.58
Error	14	186.405	7.348	0.24	151.259	0.81	234.09	53.29	0.04	0.8	0.19	1.759

df=Degrees of freedom, PH=Plant height, LN=Leaf number, TN=Tiller number, ETPM=Effective tiller per meter<sup>2</sup>, PL=Panicle length, GPPL=Grain per plant, FG=Filled grain, TGW=1000-grain weight, SY=Straw yield, GY=Grain yield, and BY=Biological yield.

Table 3. Mean values of genotypes for yield and yield-related characteristics

Genotypes	PH	LN	TN	ETPM	PL	GPPL	FG	TGW	SY	GY	BY
AJOLDIGHA	121.82cd	26.52bcd	4.31f	84.42c	18.5cde	152.2ab	136bc	22.8c	5.41c	2.37d	7.78c
DIGHA	146.97ab	31.18ab	6.62bc	101.42bc	22.1b	165.1ab	144.6ab	23.2b	6.86bc	3.11cd	9.97bc
DUDSOR	143.39bc	29.65ab	7.82a	123a	25.2a	173.5a	151.2a	22.8c	8.96a	4.07b	13.03a
SADAVAULA	137.89bc	28.03bc	6.98ab	111.96ab	23.7a	169.3a	145.9ab	24.3a	7.6ab	3.38bc	10.98ab
SORSORI	169.45a	33.71a	6.06cd	94.2bc	19.5c	158.1ab	141.7ab	23.9a	6.5bc	2.64cd	9.14bc
BINA 7	94.28d	23.98cd	5.45def	100.3bc	17.7de	148.4ab	134.3bc	21.3d	6.79bc	5.6a	12.39a
BRRI 39	90.4d	22.95d	5.91cde	105.91ab	18.9cd	156.9ab	138.4b	21.4d	7.17b	5.74a	12.91a
SHORNA	127.15bc	24.76cd	5.08ef	99.94bc	17.1e	142.2b	124.4c	21.3d	6.23bc	5.13a	11.36ab
Mean	128.92	27.59	6.03	102.64	20.34	158.21	139.56	22.6	6.94	4.01	10.95
SE	7.79	1.57	0.28	7.1	0.52	8.83	8.72	0.11	0.52	0.25	0.77

PH=Plant height, LN=Leaf number, TN=Tiller number, ETPM=Effective tiller per meter<sup>2</sup>, PL=Panicle length, GPPL=Grain per plant, FG=Filled grain, TGW=1000-grain weight, SY=Straw yield, GY=Grain yield, BY=Biological yield and SE=Standard error. Means followed by same letter(s) or no letter in a column do not differ significantly at a 5% level of probability.

Table 4. Range, mean, and standard error (SE) with coefficient of variation (CV) for eleven characters of eight genotypes.

Characters	Maximum	Minimum	Mean ±SE	CV%
Plant height	169.45	90.4	128.92±7.79	10.6
Leaf number	33.71	22.95	27.59±1.57	9.83
Tiller number	7.82	4.31	6.03±0.28	8.12
Effective tiller/ m <sup>2</sup>	123	84.42	102.64±7.1	12
Panicle length	25.2	17.1	20.34±0.52	4.42
Grains per plant	173.5	142.2	158.21±8.83	9.67
Filled grain	151.2	124.4	139.56±8.72	5.23
1000 grain weight (g)	24.3	21.3	22.63±0.11	0.92
Straw yield (t/ha)	8.96	5.41	6.94±0.52	12.9
Grain yield (t/ha)	5.74	2.37	4.01± 0.25	10.7
Biological yield (t/ha)	13.03	7.78	10.95 ± 0.77	12.1

Significant differences among the genotypes were observed for various agronomic traits. Plant height ranged from 90.40 cm to 169.45 cm, with a mean of 128.92 cm, where the tallest plants were found in SORSORI, followed by DIGHA, DUDSOR, SADA VAULA, SHORNA, and AJOLDIGHA, while the shortest was in BRRI-39. Leaf numbers varied from 22.95 to 33.71, averaging 27.59, with the highest recorded in SORSORI, followed by DIGHA and DUDSOR, while the lowest was in BRRI-39. Tiller number ranged from 4.31 to 7.82, with the maximum in DUDSOR, followed by SADA VAULA and DIGHA, and

the minimum in AJOLDIGHA. Effective tillers per square meter ranged from 84.42 to 123.00, with the highest in DUDSOR, followed by SADA VAULA and BRRI-39, while the lowest was in AJOLDIGHA. Panicle length varied between 17.1 cm and 25.2 cm, averaging 20.34 cm, with the longest in DUDSOR, followed by SADA VAULA, and the shortest in SHORNA. The highest number of grains per plant (173.50) was recorded in DUDSOR, followed by SADA VAULA and DIGHA, while the lowest (142.20) was in SHORNA, with a mean of 158.21. A similar trend was observed for filled grains,

where DUDSOR exhibited the highest count, followed by SADA VAULA and DIGHA, while SHORNA had the lowest. The 1000-grain weight ranged from 21.3g to 24.3g, averaging 22.63g, with the maximum in SADA VAULA, followed by SORSORI and DIGHA, while the minimum was in BINA-7. Straw yield showed variation from 5.41 t ha<sup>-1</sup> to 8.96 t ha<sup>-1</sup>, with the highest in DUDSOR, followed by SADA VAULA and BIRRI-39, while the lowest was in AJOLDIGHA, with a mean of 6.94 t ha<sup>-1</sup>. Grain yield varied from 2.37 t ha<sup>-1</sup> to 5.74 t ha<sup>-1</sup>, where the highest was observed in BIRRI-39, followed by BINA-7 and SHORNA, while the lowest was recorded in AJOLDIGHA, with a mean of 4.01 t ha<sup>-1</sup>. Biological yield ranged from 7.78 t ha<sup>-1</sup> to 13.03 t ha<sup>-1</sup>, with the highest in DUDSOR, followed by BIRRI-39 and BINA-7, while the lowest was in AJOLDIGHA, with an average of 10.95 t ha<sup>-1</sup>.

#### Estimation of Genetic Parameters of Rice Genotypes

All yield-contributing traits were analyzed for genotypic and phenotypic variance, heritability, GCV, PCV, genetic advance, and GA (%), as shown in Table 5.

#### Variability Parameters

A considerable degree of variability was observed among the eight rice genotypes across ten yield-contributing traits and overall grain yield. The analysis of variance (Table 5) revealed highly significant differences for all studied traits, indicating the presence of substantial genetic diversity among the genotypes. Such significant variation in key agronomic traits suggests their strong potential for use in selection and improvement programs within rice breeding.

The phenotypic variance consistently exceeded the genotypic variance across all traits, indicating that environmental factors played a considerable role in the expression of these characteristics. Similar findings were reported by El-Aty et al., (2024) and Habib et al., (2024). The coefficient of variation analysis showed that the estimates of PCV were higher than the corresponding GCV for all traits (Table 5), demonstrating environmental interaction. These findings agree with those reported by Y. Singh et al., (2025), who observed a similar pattern in rice, reinforcing the idea that environmental interactions contribute to variations in plant traits.

Among the traits studied, grain yield had the largest GCV and PCV values (32.8% and 34.6%, respectively), followed by plant height (19.79% and 22.45%), tiller

number (17.86% and 19.62%), biological yield (15.66% and 19.79%), panicle length (14.37% and 15.03%), straw yield (13.05% and 18.39%), leaf number (12.36% and 15.79%), and effective tillers (8.84% and 14.89%). These traits' high GCV and PCV values point to the chance of improving yield through selective breeding.

In contrast, grains per plant (3.77% and 10.38%), filled grains (5.09% and 7.29%), and 1000-grain weight (5.23% and 5.30%) exhibited low GCV and PCV values. Low PCV and GCV estimates for days to maturity have also been reported by Siva Reddy et al., (2023).

#### Heritability

Heritability values indicate the accuracy of phenotypic traits, and high heritability supports better selection of those traits. The heritability estimates for the traits in this study were high, varying from 61.25% to 97.22%. The highest heritability value was found in the 1000-grain weight (97.22%), followed by panicle length (91.34%), grain yield (90.10%), tiller number (82.86%), plant height (77.75%), biological yield (62.55%), and leaf number (61.25%). Moderate heritability was recorded for straw yield (50.31%), filled grain (48.61%), and effective tillers per square meter (35.26%). The lowest was observed for grains per plant (13.16%) (Table 5).

These traits are less influenced by environmental factors, as indicated by their high heritability. Therefore, plant breeders can safely select individuals based on their phenotypic expression using simple selection methods (Caradus, 2024).

#### Genetic Advance

Genetic advance shows the likely improvement from selection. When used with heritability, it gives a better measure of selection value (Johnson et al., 1955). In this study, the highest genetic advance was observed for plant height (46.36%), while the lowest was recorded for straw yield (1.32%) (Table 5).

Among the traits, grain yield recorded the highest genetic advance percentage (64.09%), with plant height (35.96%), tiller number (33.5%), panicle length (28.27%), and biological yield (25.48%) following. The lowest percentage was observed in grains per plant (2.81%). Demeke et al., (2023) also found the number of filled grains per panicle had the largest genetic advance, whereas grain width showed the greatest genetic advance as a percentage of the average.

Table 5. Components of genotypic and phenotypic variation, heritability, and genetic advance for yield and yield contributing characters of Rice

Components	PH	LN	TN	ETPM	PL	GPPL	FG	TGW	SY	GY	BY
$\sigma^2_g$	651.5	11.6	1.16	82.37	8.54	35.49	50.41	1.4	0.82	1.73	2.94
$\sigma^2_p$	837.9	19	1.4	233.6	9.35	269.6	103.7	1.44	1.63	1.92	4.7
GCV (%)	19.79	12.4	17.9	8.84	14.4	3.77	5.09	5.23	13.1	32.8	15.7
PCV (%)	22.45	15.8	19.6	14.89	15	10.38	7.29	5.3	18.4	34.6	19.8
$h^2_b$	77.75	61.3	82.9	35.26	91.3	13.16	48.61	97.2	50.3	90.1	62.6
GA% (i=5%)	46.36	5.49	2.02	11.1	5.75	4.45	10.2	2.4	1.32	2.57	2.79
GA% of mean	35.96	19.9	33.5	10.81	28.3	2.81	7.31	10.6	19	64.1	25.5
CV (%)	10.59	9.83	8.12	11.98	4.42	9.67	5.23	0.92	12.9	10.7	12.1
$\bar{X}$	128.9	27.6	6.03	102.6	20.3	158.2	139.6	22.6	6.94	4.01	11

PH=Plant height, LN=Leaf number, TN=Tiller number, ETPM=Effective tiller per meter<sup>2</sup>, PL=Panicle length, GPPL=Grain per plant, FG=Filled grain, TWG=1000-grain weight, SY=Straw yield, GY=Grain yield, BY=Biological yield,  $\sigma^2_g$ =Genotypic variances,  $\sigma^2_p$ =Phenotypic variances, GCV=Genotypic co-efficient of variation, PCV=Phenotypic co-efficient of variation,  $h^2_b$ = Broad sense heritability, GA=Genetic advance and CV=Coefficient of variation.

Understanding genetic variation, heritability, and genetic advance helps estimate the genetic improvement expected in the following generations when traits are selected. In general, Additive genes typically control traits that have high heritability and genetic advance (Gowsika et al., 2025) and are able to be improved through easy selection approaches (Sinha et al., 2021).

Traits with high heritability and high genetic advance are likely controlled by additive genes, which helps improve their performance. In this study, plant height showed both high heritability and genetic advance. Other traits had moderate to high heritability but only moderate or low genetic advance, meaning they can be improved by breeding from the best plants in the segregating groups, as reported by Saleem et al., (2023) and Yeshitila et al., (2023).

### **Karyotype Analysis**

The karyotype study was carried out on root tip cells (RTCs) of eight cultivars of *Oryza sativa* L., with results presented in Tables 6 and 7. The diploid chromosome number for the eight cultivars of *Oryza sativa* L. was observed to be  $2n = 24$ .

#### **AJOLDIGHA:**

The genotype had a diploid chromosome number of  $2n = 24$ , comprising six metacentric, four submetacentric, and two sub-terminal chromosome pairs. Chromosome lengths ranged from 1.74  $\mu\text{m}$  to 2.24  $\mu\text{m}$ , with a total chromatin length (TCL) of 24.07  $\mu\text{m}$  and a total form percentage (TF%) of 40.01. The karyotype formula in this cultivar was as follows:

$$5S_1^m + 3S_1^{sm} + 2S_1^{st} + S_2^m + S_2^{sm}$$

#### **DIGHA:**

The cultivar had a diploid chromosome number of  $2n = 24$ , comprising four metacentric, five submetacentric, and three sub-terminal chromosome pairs. Chromosome lengths ranged from 2.00  $\mu\text{m}$  to 2.64  $\mu\text{m}$ , with a total chromatin length (TCL) of 27.22  $\mu\text{m}$  and a total form percentage (TF%) of 40.08. The karyotype formula in this cultivar was as follows:

$$3M^m + M^{sm} + S_1^m + 4S_1^{sm} + 3S_1^{st}$$

#### **DUDSOR:**

The cultivar had a diploid chromosome number of  $2n = 24$ , consisting of six metacentric, three submetacentric, and three sub-terminal chromosome pairs. Chromosome lengths ranged from 1.93  $\mu\text{m}$  to 2.60  $\mu\text{m}$ , with a total chromatin length (TCL) of 26.67  $\mu\text{m}$  and a total form percentage (TF%) of 41.21. The karyotype formula in this cultivar was as follows:

$$M^m + 5S_1^m + 3S_1^{sm} + 3S_1^{st}$$

#### **SADA VAULA:**

The cultivar had a diploid chromosome number of  $2n = 24$ , comprising seven submetacentric and five sub-terminal chromosome pairs. Chromosome lengths ranged from 2.17  $\mu\text{m}$  to 2.52  $\mu\text{m}$ , with a total chromatin length (TCL) of 28.12  $\mu\text{m}$  and a total form percentage (TF%) of 33.43. The karyotype formula in this cultivar was as follows:

$$3M^{sm} + M^{st} + 4S_1^{sm} + 4S_1^{st}$$

#### **SORSORI:**

The cultivar had a diploid chromosome number of  $2n = 24$ , consisting of six metacentric, five submetacentric, and one sub-terminal chromosome pair. Chromosome lengths ranged from 1.71  $\mu\text{m}$  to 2.66  $\mu\text{m}$ , with a total chromatin length (TCL) of 27.07  $\mu\text{m}$  and a total form percentage (TF%) of 42.3. The karyotype formula in this cultivar was as follows:

$$M^m + 2M^{sm} + 5S_1^m + 2S_1^{sm} + S_1^{st} + S_2^{sm}$$

#### **BINA 7:**

The cultivar had a diploid chromosome number of  $2n = 24$ , comprising nine metacentric, two submetacentric, and one sub-terminal chromosome pair. Chromosome lengths ranged from 1.47  $\mu\text{m}$  to 2.51  $\mu\text{m}$ , with a total chromatin length (TCL) of 23.91  $\mu\text{m}$  and a total form percentage (TF%) of 44.58. The karyotype formula in this cultivar was as follows:

$$M^m + 4S_1^m + 2S_1^{sm} + 4S_2^m + S_2^{st}$$

#### **BRR1 39:**

The cultivar had a diploid chromosome number of  $2n = 24$ , consisting of five metacentric, four submetacentric, and three sub-terminal chromosome pairs. Chromosome lengths ranged from 1.82  $\mu\text{m}$  to 2.53  $\mu\text{m}$ , with a total chromatin length (TCL) of 25.06  $\mu\text{m}$  and a total form percentage (TF%) of 39.07. The karyotype formula in this cultivar was as follows:

$$M^{sm} + 4S_1^m + 3S_1^{sm} + 2S_1^{st} + S_2^m + S_2^{st}$$

#### **SHORNA:**

The cultivar had a diploid chromosome number of  $2n = 24$ , comprising three metacentric and nine submetacentric chromosome pairs. Chromosome lengths ranged from 1.68  $\mu\text{m}$  to 2.93  $\mu\text{m}$ , with a total chromatin length (TCL) of 26.33  $\mu\text{m}$  and a total form percentage (TF%) of 41.09. The karyotype formula in this cultivar was as follows:

$$M^m + 2M^{sm} + 2S_1^m + 3S_1^{sm} + 4S_2^{sm}$$

In the present study, all eight cultivars of *Oryza sativa* L. exhibited a diploid chromosome number of  $2n = 24$ . Chromosome lengths varied among the cultivars, with SHORNA having the longest chromosome (2.93  $\mu\text{m}$ ) and BINA-7 the shortest (1.47  $\mu\text{m}$ ). Total chromatin length (TCL) ranged from 23.91  $\mu\text{m}$  in BINA-7 to 28.12  $\mu\text{m}$  in SADA VAULA, while total form percentage (TF%) varied from 33.43% in SADA VAULA to 44.58% in BINA-7. Medium-sized chromosomes were present in all cultivars except AJOLDIGHA, and relatively short ( $S_1$ ) chromosomes were found in all eight cultivars, with short ( $S_2$ ) chromosomes detected in five cultivars: AJOLDIGHA, SORSORI, BINA-7, BRR1-39, and SHORNA. Submetacentric chromosomes were observed in all cultivars, with the highest number in SHORNA and the lowest in BINA-7. Metacentric chromosomes were absent only in SADA VAULA, while BINA-7 had the highest number and SHORNA the lowest. Sub-terminal chromosomes were present in all cultivars except SHORNA, with the highest count in SADA VAULA and the lowest in SORSORI and BINA-7.

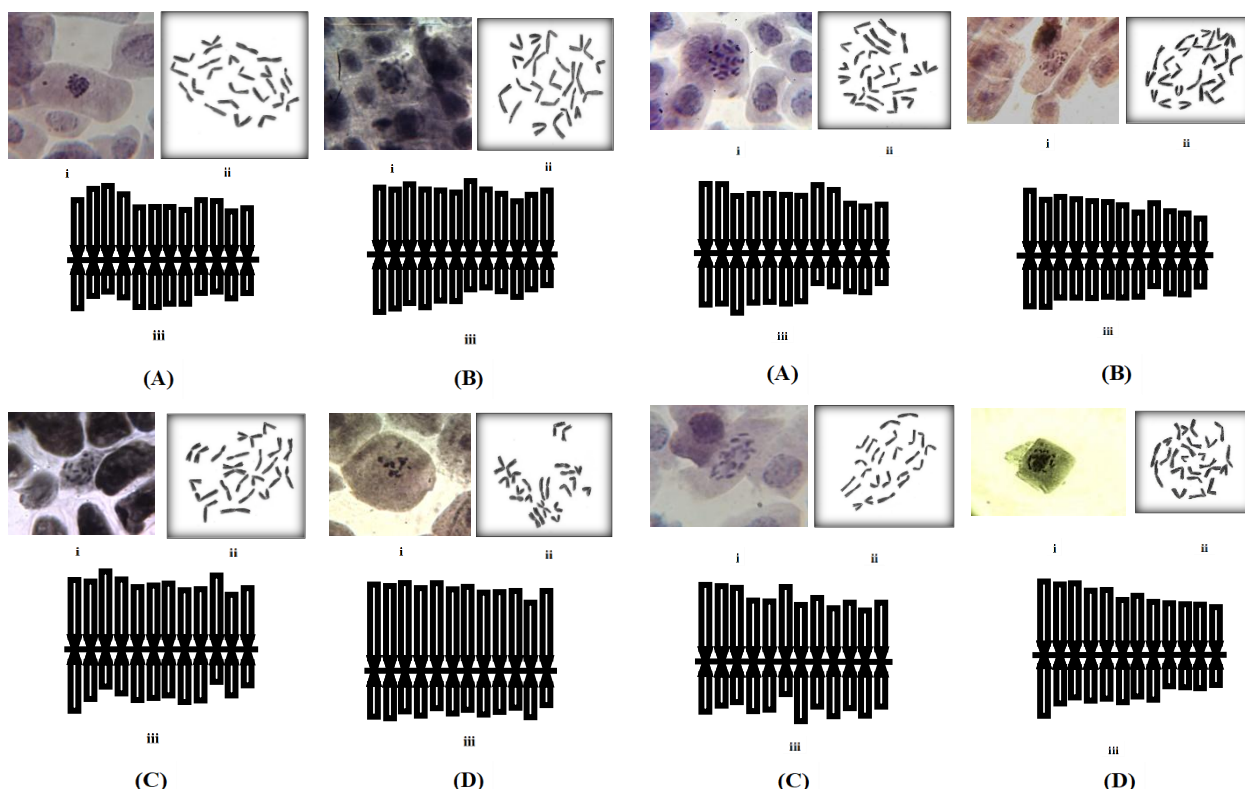


Figure 1. Representative karyotypes of four rice cultivars: (A) AJOLDIGHA, (B) DIGHA, (C) DUDSOR, (D) SADA VAULA. For each cultivar, (i) shows the photomicrograph of chromosomes, (ii) the corresponding camera-lucida drawing (scale bar = 1  $\mu$ m), and (iii) the idiogram.

Figure 2. Representative karyotypes of four rice cultivars: (A) SORSORI, (B) BINA 7, (C) BRRI-39, (D) SHORNA. For each cultivar, (i) shows the photomicrograph of chromosomes, (ii) the corresponding camera-lucida drawing (scale bar = 1  $\mu$ m), and (iii) the idiogram.

Table 6. Chromosome length, arm ratio, centromeric position and chromosome types of AJOLDIGHA, DIGHA, DUDSOR, SADAVAULA varieties of rice.

NCV	NC	Pairs of Chromosomes	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
AJOLDIGHA	24	Long arm( $\mu$ m)	1.2	1.5	1.53	1.4	1.1	1.1	1.1	1	1.2	1.2	1	1.1
		Short arm( $\mu$ m)	1	0.7	0.64	0.8	1	1	0.9	0.9	0.7	0.6	0.8	0.7
		Total length	2.2	2.2	2.17	2.1	2.1	2.1	2	1.9	1.9	1.9	1.8	1.7
		Arm ratio SA/LA	0.8	0.5	0.42	0.6	0.9	0.9	0.8	0.9	0.6	0.5	0.8	0.6
		Centromeric position	m	st	st	sm	m	m	m	m	Sm	sm	m	sm
		Types	S1	S1	S1	S1	S1	S1	S1	S1	S1	S1	S1	S2
DIGHA	24	Long arm( $\mu$ m)	1.4	1.4	1.49	1.4	1.4	1.3	1.6	1.4	1.3	1.1	1.3	1.4
		Short arm( $\mu$ m)	1.2	1.1	1.02	1.1	1	1	0.7	0.7	0.8	0.9	0.7	0.6
		Total length	2.6	2.5	2.51	2.5	2.3	2.3	2.3	2.1	2.1	2	2	2
		Arm ratio SA/LA	0.9	0.8	0.69	0.8	0.7	0.8	0.5	0.5	0.6	0.8	0.6	0.5
		Centromeric position	m	m	sm	m	sm	sm	st	st	Sm	m	sm	st
		Types	M	M	M	M	S1	S1	S1	S1	S1	S1	S1	S1
DUDSOR	24	Long arm( $\mu$ m)	1.4	1.4	1.56	1.4	1.2	1.3	1.3	1.2	1.2	1.5	1.1	1.2
		Short arm( $\mu$ m)	1.2	1	0.73	0.9	1	1	0.9	1	1	0.6	0.9	0.7
		Total length	2.6	2.3	2.29	2.3	2.2	2.2	2.2	2.2	2.2	2.1	2	1.9
		Arm ratio SA/LA	0.9	0.7	0.47	0.6	0.8	0.8	0.7	0.9	0.9	0.4	0.8	0.6
		Centromeric position	m	sm	st	sm	m	m	sm	m	M	st	m	st
		Types	M	S1	S1	S1	S1	S1	S1	S1	S1	S1	S1	S1
SADAVAULA	24	Long arm( $\mu$ m)	1.7	1.6	1.67	1.6	1.7	1.6	1.6	1.5	1.5	1.5	1.3	1.5
		Short arm( $\mu$ m)	0.9	0.9	0.76	0.8	0.7	0.8	0.7	0.8	0.8	0.7	0.9	0.6
		Total length	2.5	2.5	2.43	2.4	2.4	2.4	2.3	2.3	2.3	2.2	2.2	2.2
		Arm ratio SA/LA	0.5	0.6	0.46	0.5	0.4	0.5	0.5	0.6	0.5	0.5	0.7	0.4
		Centromeric position	sm	sm	st	sm	st	sm	st	sm	Sm	st	sm	st
		Types	M	M	M	M	S1	S1	S1	S1	S1	S1	S1	S1

NCV: Name of the cultivar/variety; NC: No. of chromosomes

Table 7. Chromosome length, arm ratio, centromeric position and chromosome types of SORSORI, BINA 7, BRRI 39, SHORNA varieties of rice.

NCV	NC	Pairs of Chromosomes	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	
SORSORI	24	Long arm(μm)	1.5	1.5	1.27	1.3	1.3	1.3	1.3	1.5	1.4	1.1	1	1.1	
		Short arm(μm)	1.1	1.1	1.29	1.1	1.1	1.1	1	0.6	0.7	0.8	0.8	0.6	
		Total length	2.7	2.6	2.56	2.4	2.4	2.4	2.3	2.2	2.1	1.9	1.9	1.7	
		Arm ratio SA/LA	0.7	0.7	1.02	0.8	0.8	0.8	0.8	0.4	0.5	0.8	0.8	0.6	
		Centromeric position	sm	sm	m	m	m	m	m	m	st	Sm	sm	m	sm
		Types	M	M	M	S1	S1	S1	S1	S1	S1	S1	S1	S1	S2
BINA 7	24	Long arm(μm)	1.4	1.2	1.27	1.2	1.2	1.2	1.1	0.9	1.1	1	0.9	0.8	
		Short arm(μm)	1.1	1.1	0.91	0.9	0.9	0.9	0.9	0.9	0.9	0.7	0.8	0.8	0.7
		Total length	2.5	2.3	2.18	2.1	2.1	2.1	2	1.8	1.8	1.8	1.8	1.5	
		Arm ratio SA/LA	0.8	0.9	0.72	0.7	0.8	0.8	0.8	1	0.6	0.9	0.9	0.8	
		Centromeric position	m	m	sm	sm	m	m	m	m	m	St	m	m	m
		Types	M	S1	S1	S1	S1	S1	S1	S1	S2	S2	S2	S2	S2
BRRI 39	24	Long arm(μm)	1.5	1.5	1.47	1.2	1.2	1.5	1.1	1.3	1.1	1.2	1	1.2	
		Short arm(μm)	1	0.9	0.8	1	1	0.6	0.9	0.6	0.8	0.7	0.8	0.6	
		Total length	2.5	2.4	2.27	2.2	2.2	2.1	2.1	1.9	1.9	1.9	1.8	1.8	
		Arm ratio SA/LA	0.7	0.6	0.54	0.8	0.8	0.4	0.8	0.5	0.8	0.6	0.8	0.5	
		Centromeric position	sm	sm	sm	m	m	st	m	st	M	sm	m	st	
		Types	M	S1	S1	S1	S1	S1	S1	S1	S1	S1	S1	S2	S2
SHORNA	24	Long arm(μm)	1.6	1.5	1.56	1.4	1.4	1.2	1.3	1.2	1.1	1.1	1.1	1	
		Short arm(μm)	1.3	1	0.91	1	1	1	0.9	1	0.7	0.7	0.7	0.6	
		Total length	2.9	2.6	2.47	2.4	2.4	2.2	2.2	2.1	1.8	1.8	1.8	1.7	
		Arm ratio SA/LA	0.8	0.7	0.58	0.7	0.7	0.9	0.7	0.8	0.6	0.6	0.7	0.6	
		Centromeric position	m	sm	sm	sm	sm	m	sm	m	sm	sm	sm	sm	sm
		Types	M	M	M	S1	S1	S1	S1	S1	S2	S2	S2	S2	S2

NCV: Name of the cultivar/variety; NC: No. of chromosomes

Table 8. Range of chromosome length, total chromatin length, TF%, and karyotypic formulae in eight cultivars of *Oryza sativa* L.

Name of the cultivars	2n	Range of chromosome length (μm)	Total chromatin length (μm)	TF%	Karyotypic formulae (K.F.)			
					L	M	S <sub>1</sub>	S <sub>2</sub>
AJOLDIGHA	24	1.74 - 2.24	24.07	40.01	-	-	5S <sub>1</sub> <sup>m</sup> + 3S <sub>1</sub> <sup>sm</sup> + 2S <sub>1</sub> <sup>st</sup>	S <sub>2</sub> <sup>m</sup> + S <sub>2</sub> <sup>sm</sup>
DIGHA	24	2.00 - 2.64	27.22	40.08	-	3M <sup>m</sup> + M <sup>sm</sup>	S <sub>1</sub> <sup>m</sup> + 4S <sub>1</sub> <sup>sm</sup> + 3S <sub>1</sub> <sup>st</sup>	-
DUDSOR	24	1.93 - 2.60	26.67	41.21	-	M <sup>m</sup>	5S <sub>1</sub> <sup>m</sup> + 3S <sub>1</sub> <sup>sm</sup> + 3S <sub>1</sub> <sup>st</sup>	-
SADAVAUVA	24	2.17 - 2.52	28.12	33.43	-	3M <sup>sm</sup> + M <sup>st</sup>	4S <sub>1</sub> <sup>sm</sup> + 4S <sub>1</sub> <sup>st</sup>	-
SORSORI	24	1.71 - 2.66	27.07	42.3	-	M <sup>m</sup> + 2M <sup>sm</sup>	5S <sub>1</sub> <sup>m</sup> + 2S <sub>1</sub> <sup>sm</sup> + S <sub>1</sub> <sup>st</sup>	S <sub>2</sub> <sup>sm</sup>
BINA 7	24	1.47 - 2.51	23.91	44.58	-	M <sup>m</sup>	4S <sub>1</sub> <sup>m</sup> + 2S <sub>1</sub> <sup>sm</sup>	4S <sub>2</sub> <sup>m</sup> + S <sub>2</sub> <sup>st</sup>
BRRI 39	24	1.82 - 2.53	25.06	39.07	-	M <sup>sm</sup>	4S <sub>1</sub> <sup>m</sup> + 3S <sub>1</sub> <sup>sm</sup> + 2S <sub>1</sub> <sup>st</sup>	S <sub>2</sub> <sup>m</sup> + S <sub>2</sub> <sup>st</sup>
SHORNA	24	1.68 - 2.93	26.33	41.09	-	M <sup>m</sup> + 2M <sup>sm</sup>	2S <sub>1</sub> <sup>m</sup> + 3S <sub>1</sub> <sup>sm</sup>	4S <sub>2</sub> <sup>sm</sup>

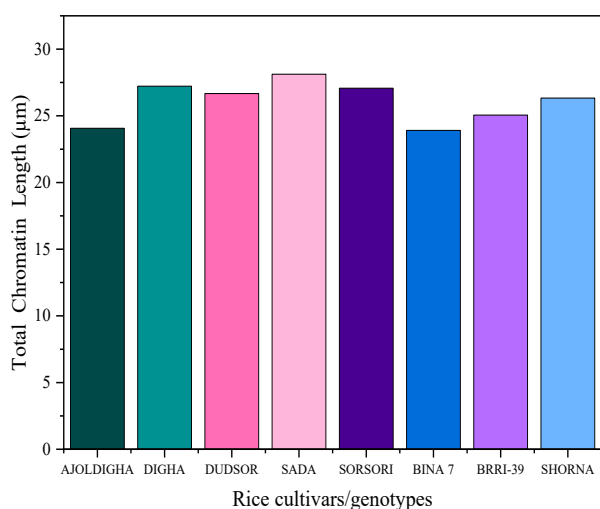


Figure 3. Total chromatin length (TCL) in μm of eight cultivars of Rice (*Oryza sativa* L.)

These findings highlight structural chromosomal diversity among the studied cultivars, and the colchicine-based root tip preparation method enabled successful visualization of metaphase chromosomes despite initial staining difficulties.

### Conclusion

This study successfully revealed substantial genetic diversity among the eight local rice cultivars from Chalan Beel, both at the morphological and chromosomal levels by examining genetic differences, heritability, and cytogenetic features of eight locally grown rice (*Oryza sativa* L.) varieties from Chalan Beel. Significant differences were found among the varieties for important growth, physiological, and yield traits. Among them, genotypes DUDSOR, BRRI-39, BINA-7, SHORNA, and SADA VAULA showed higher biological yield and good agronomic qualities.

The fact that PCV was greater than GCV suggested that the environment affects trait expression. High heritability was found for 1000-grain weight, panicle length, and grain yield, indicating strong genetic influence. Plant height showed both high heritability and genetic advance, which points to additive gene effects. Karyotype analysis confirmed a chromosome number of  $2n = 24$  across all genotypes, with variations in chromosome length and total chromatin length. These findings provide valuable insights for rice breeding programs aimed at selecting high-yielding and genetically stable cultivars. Further research integrating molecular markers and genomic tools could enhance genetic improvement strategies for rice cultivation in the Chalan Beel region and other similar agroecological zones.

## Declarations

The authors declare no competing interests

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