

Genetic Variability, Inbreeding Depression, and Inheritance Pattern in F₃ Segregating Generations of Ten Exotic Hybrid Rice in Bangladesh

Md.Tohid¹, M. Wazuddin², E. Mahmud³, N. M. Morshed⁴ and Ratna Rani^{*5}

¹ Additional Deputy Director, Department of Agriculture Extension, Bangladesh, Email: mtouhid2011@gmail.com

² Retired Professor, Department of Genetics and Plant Breeding, BAU, Bangladesh.

³ Senior Scientific Officer, Bangladesh Agricultural Research Institute, Email: eftekhamahmud@yahoo.com

⁴ Senior Scientific Officer, Bangladesh Sugar Crop Research Institute, Email: nizammoshedbsri@gmail.com

⁵ Department of Environmental Science, Patuakhali Science and Technology University (PSTU), Email: ratnapstu911@gmail.com

*Correspondence: ratnapstu911@gmail.com, Tel: +8801516517932

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Abstract: Hybrid rice technology offers a promising avenue for increasing productivity in Bangladesh, but the genetic potential of exotic hybrids and their segregating populations remains underexplored. This experiment aimed to evaluate the performance, level of inbreeding depression, relationships among different traits, and inheritance patterns of ten commercial hybrid rice varieties' F₃ generations through an augmented design with five blocks conducted at Bangladesh Agricultural University, Mymensingh, during July-December. Highly significant ($P \leq 0.01$) genotypic variations were observed for plant height and five-panicle weight, while effects of the blocks were non-significant, indicating strong genetic variation. The differences in average performance were highly significant, with the tallest plant being Taj-2 (91.9 cm), the shortest Shurma (79.7 cm), the highest tiller number in ACI-2 (7.34), and the lowest in Hira-99-5 (4.52). The weight of five panicles was highest in Shonar Bangla (16.79 g) and lowest in Krishan-2 (13.03 g). Maximum inbreeding depression was seen in grain yield for Tia (48.36%) and in tillers for Hira-99-5 (45.07%), while inbreeding depression below 9.93% was recorded in ACI-2 and Shurma, which showed greater stability than other genotypes. Correlation analysis demonstrated a significant positive relationship between effective tillers and total tillers across all genotypes, whereas five-panicle weight showed both positive and negative correlations with other traits. Genetic inheritance studies indicated various types of genetic control, including monogenic, digenic, and polygenic influences on plant height, and monogenic control with partial and complementary gene action for five-panicle weight. Genetic variability was notably high in the F₃ generation. ACI-2 and Shurma emerged as the most promising genotypes for hybrid rice breeding in Bangladesh.

Keywords: Hybrid rice; F₃ segregating population; Inbreeding depression; Inheritance pattern; Gene action.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the primary staples of over half of the world's population and is a vital component of food security, especially in South and Southeast Asia. But there are many hurdles in maintaining the productivity of rice against the increasing demands of a growing population, shrinking farmland areas, and variable climatic conditions. Enhancing yield potential while maintaining stability and grain quality requires efficient utilization of genetic variability and a clear understanding of inheritance mechanisms governing key agronomic traits. The

segregation of generations, especially F₂ and F₃, is important in the breeding process because it allows proper selection and genetic stabilization. The earlier segregating generations have higher phenotypic diversity owing to segregation and crossing-over, which makes it possible to select better genotypes. Earlier research has shown a considerable amount of diversity with medium to high heritability for yield attributes like productive tillers, grains per panicle, and yield per plant, thus suggesting great possibilities for phenotypic selection (Krishna et al., 2020; Saleem et al., 2010; Santhiya et al., 2024; Savitha and

Kumari, 2015). The significant genetic gain in favor of these characters is another piece of evidence for the dominance of additive gene effects and efficient early-generation selection (Harijan, 2021; Kumar et al., 2023; Madhuri et al., 2024).

Gene action with respect to the control of yield and the constituent factors may prove to be complicated and may comprise both additive and non-additive effects. It has been reported in several studies that while most of the yield contributing factors are controlled by additive gene actions, there is an influence of epistatic interactions as well as non-additive gene action, based on the genetic makeup of the genotype, as well as the environment (Bharali et al., 2025; Chacko et al., 2023; Nofal and Gaballah, 2024; Vignesh et al., 2025). Such complexity necessitates careful evaluation of inheritance patterns in segregating populations to design appropriate breeding strategies.

The utilization of exotic and hybrid rice varieties provides genetic variation and heterosis, characterized by a great deal of variation in terms of agronomic attributes as well as yields. Yet, the suitability of exotic or hybrid rice materials should be assessed properly before use, as their adaptation and stability depend upon the local conditions. There are several reports that demonstrate considerable variation among yield attributes, heritability, and genetic gains associated with them (Lipi et al., 2021; Sakran et al., 2022; Tabassum et al., 2023). Additionally, F_3 generations of genetically diverse parents have been found to be variable for stresses and stable yield (Laghari et al., 2025). Based on previous studies, it is clear that the phenotypic coefficient of variation (PCV) is usually higher than the genotypic coefficient of variation (GCV), which may be due to the effect of the environment on the expression of traits, despite the small difference between them. This points out that there is a genetic control of these traits. High heritability and genetic advance have also been found for plant height, number of grains per ear, and grain weight traits. These findings show that the traits are dominated by additive effects and high selection efficiency (Ferdous et al., 2023; Roy and Shil, 2020). Additionally, the occurrence of transgressive segregation highlights the potential for developing superior genotypes beyond parental performance (Lokaprakash and Mahadevappa, 1992).

Although there have been numerous studies related to the variation and inheritance of rice, these studies have largely involved single-generation or single-cross evaluation rather than an extensive study using various exotic hybrid-derived F_3 populations with a common experimental setup. Besides, a comprehensive investigation into aspects such as performance, inbreeding depression, correlation, and inheritance has not been adequately addressed. Therefore, the present study was undertaken to assess the performance of F_3 populations derived from exotic hybrids, estimate inbreeding depression, analyze correlations among important yield-related traits, and determine the inheritance patterns governing these traits. The study integrates phenotypic performance and genetic analysis to generate insights into variability and gene action in segregating populations. The findings are expected to

support effective selection strategies and enhance the utilization of exotic hybrid germplasm in rice improvement programs.

MATERIALS AND METHODS

Experimental Site and Environmental Conditions

The field experiment was carried out at the Genetics and Plant Breeding Field Laboratory, Bangladesh Agricultural University (BAU), Mymensingh, Bangladesh, during the Aman season (July - December). The location is covered by Agro-Ecological Zone (AEZ-9) with sandy loam soil and a pH of around 6.5. The weather in the study period had high temperature, humidity, and rainfall in the vegetative stage, although temperature and rainfall had declined in the maturity stage. Temperature, humidity, rainfall, and sunshine data were collected monthly.



Figure 1. Study area map

Plant Materials and Experimental Design

Ten segregating populations of F_3 generations generated from ten exotic commercial hybrids of rice, namely Shonar Bangla, Shurma, ACI-1, Tia, ACI-2, Taj-2, Hira-2, Shakti, Hira-99-5, and Krishan-2, and three check rice varieties, such as BRRI hybrid dhan 1, BR 11, and BRRI dhan 30, were employed. F_3 seeds were collected from the Department of Genetics and Plant Breeding, BAU, Mymensingh. Check varieties were provided by BRRI. This experiment was conducted using an augmented design comprising five blocks. Replication of the check varieties was done in every block, but the test varieties remained unreplicated and arranged randomly. The size of each plot consisted of 10 m² (2.5 m × 4 m). Design factors were considered as follows: checks (c), test varieties (v), blocks (b), entries in one block ($n = v/b$), plots in one block ($p = c + n$), and total plots ($N = b(c + n)$). Adjusted yield of test entries was determined based on the results obtained from checks.

Land Preparation and Fertilization

The field was prepared in wet conditions by ploughing using a power tiller, laddering, and puddling. The weeds and stubble were cleared before transplanting. Fertilizers were applied at the rates of cowdung 6 t ha⁻¹, urea 210 kg ha⁻¹, triple super phosphate (TSP) 125 kg ha⁻¹, Muriate of potash (MP) 70 kg ha⁻¹, gypsum 4 kg ha⁻¹, and zinc sulphate (ZnSO₄) 1 kg ha⁻¹. One-third of the urea, along

with full doses of other fertilizers, was applied during final land preparation, and the remaining urea was top-dressed in two equal splits at 22 and 42 days after transplanting.

Crop Establishment and Management

Seedbeds measuring 0.5 m × 6 m × 5 cm were provided with necessary inputs and drainage systems. The seeds were soaked in water for 14 hours and incubated for 48 hours for their germination, and then sown on 7th July. The water level was raised gradually to 5 cm, and weeds were manually removed. Transplantation was done on 4th August in rows spaced 20 cm × 20 cm with one seedling per hill. Transplantation was done, first of all, check varieties followed by random planting of test varieties. Intercultural operations like weed removal, irrigation, and gap filling were done during the seven days after transplantation. The standing water level was maintained between 4 and 6 cm. Urea was applied as top dressing at 22 and 42 days after transplantation. Incidence of pests and diseases was nil. Harvesting was done when 80% of the grains became mature.

Data Collection and Trait Measurement

Height of the plant, number of tillers per plant, number of effective tillers per plant, 5-panicle weight, and grain yield were observed from non-border plants. The height of the plant was noted from the soil surface to the tip of the panicle. The number of tillers and effective tillers per plant were observed. Five panicle weight was noted after appropriate drying, and grain yield was converted into t ha⁻¹. The minimum value, maximum value, and mean value were calculated for comparison of F₂ and F₃ populations. Data of the F₂ population were provided by Sobur, 2009.

Statistical Analysis

ANOVA analysis was done for all the traits. Evaluation for homozygosity in relation to the F₂ population has been done on the basis of minimum, maximum, and mean values of the F₃ populations. Inbreeding depression percentage was calculated by using height of plants, tillers per plant, effective tillers, and yield as follows:

$$\text{Inbreeding depression} = \frac{\text{Mean } F_2 - \text{Mean } F_3}{\text{Mean } F_2} \times 100$$

Correlation coefficient among plant height, tillers per plant, effective tillers, and 5-panicle weight has been calculated taking into account the block effects using the following formula: $R_j = B_j - M$;

Where R_j is the block effect, B_j is the mean of checks in the jth block, and M is the grand mean of checks. The analysis was performed using PLABTAT software. The inheritance pattern has been worked out based on adjusted means. Frequency distribution has been prepared using MS Excel, in which a uniform class interval is taken from the minimum and maximum value, and a bar diagram has been drawn to interpret the segregation pattern. For comparison, F₂ data were analyzed alongside F₃ populations.

RESULTS AND DISCUSSIONS

Ten F₃ segregating populations derived from exotic hybrid rice, along with three check varieties (BRRI hybrid dhan 1, BR 11, and BRRI dhan 30), were evaluated based on four quantitative traits: plant height, number of tillers plant⁻¹, effective tillers plant⁻¹, and five-panicle weight. These traits were used to compare F₂ and F₃ performance, estimate inbreeding depression, assess trait associations through correlation analysis, and determine inheritance patterns. The results are presented and discussed below.

Analysis of Variance for Check Varieties

Analysis of Variance (ANOVA) showed highly significant variation between the three checks for the traits under study (Table 1). Genotype mean squares were highly significant (p ≤ 0.01) for plant height and five panicle weights, while no significant variation was found for the number of tillers plant⁻¹ and effective tillers plant⁻¹. Block effects were non-significant for all traits, indicating uniform experimental conditions across blocks. The extremely small coefficient of variation (CV) values (1.93% to 8.94%) validate high precision in experiments.

Table 1. Analysis of variance for check varieties

Source	df	Plant height (cm)	No. of tillers plant ⁻¹	Effective tillers plant ⁻¹	5-panicle wt. (g)
Replication	4	13.28	0.22	0.22	0.36
Genotype	2	16.24**	0.24 NS	0.17 NS	9.63**
Error	8	7.82	0.43	0.38	0.168
CV (%)		3.11	8.35	8.94	1.93

Note: ** indicates significance at 1% level; NS = non-significant.

Table 2. Summary of Traits for F₃ Seeds of Different Hybrids

Genotypes	Value	Plant Height (cm) F ₂ *	F ₃	No. of Tillers plant ⁻¹ F ₂ *	F ₃	Effective Tillers plant ⁻¹ F ₂ *	F ₃	5 Panicle wt. (g) F ₂ *	F ₃
F ₃ Seeds of Shonar Bangla hybrid	MIN	62.11	57	5.41	2	5.65	2	9.64	7.05
	MAX	104.11	105	11.41	12	10.65	12	23.64	27.01
	MEAN	80.06	85.88	8.01	5.8	7.18	5.24	17.4	16.79
F ₃ Seeds of Shurma hybrid	MIN	63.87	63	4.95	3	4.93	3	10.04	6.19
	MAX	106.87	93	11.95	12	10.93	12	24.24	22.44

	MEAN	88.24	79.66	7.77	6.32	7.17	5.78	16.51	13.19
F ₃ Seeds of ACI-1 hybrid	MIN	71.11	67	5.41	3	5.65	2	8.66	7.35
	MAX	107.11	104	11.41	10	10.65	9	16.74	24.41
	MEAN	90.04	85.68	7.83	5.98	7.47	5.5	13.85	13.81
F ₃ Seeds of Tia hybrid	MIN	85.04	66	3.68	3	3.63	2	11.4	7.55
	MAX	108.04	118	10.68	8	8.63	8	28.6	22.4
	MEAN	95.66	85.24	7.34	5	6.69	4.84	20.33	14.32
F ₃ Seeds of ACI-2 hybrid	MIN	65.87	63	4.95	3	4.93	3	10.04	8.24
	MAX	106.87	100	10.95	16	9.93	16	29.74	23.1
	MEAN	84	82.88	8.15	7.34	7.57	7	19.9	13.5
F ₃ Seeds of Taj-2 hybrid	MIN	67.77	73	3.88	3	3.96	3	9.94	5.07
	MAX	99.77	106	10.88	11	9.96	9	28.14	35.9
	MEAN	85.3	91.9	7.25	6.18	7.02	5.96	19.84	15.27
F ₃ Seeds of Hira-2 hybrid	MIN	69.11	72	5.41	4	3.83	3	11.47	5.54
	MAX	104.11	102	12.41	11	10.83	9	26.67	40.53
	MEAN	85.91	87.22	7.83	5.76	7.09	5.6	21.61	15.4
F ₃ Seeds of Shakti hybrid	MIN	77.04	64	4.68	3	4.63	2	11.4	4.38
	MAX	98.04	102	10.68	11	9.63	10	25.6	18.83
	MEAN	86.48	86.06	7.54	5.54	7.18	5.2	21	13.21
F ₃ Seeds of Hira-99-5 hybrid	MIN	68.11	74	5.41	3	4.83	2	11.47	9.08
	MAX	97.11	105	13.41	9	9.83	9	25.47	31.55
	MEAN	83.26	89.7	8.23	4.52	7.25	4.44	19.88	15.46
F ₃ Seeds of Krishan-2 hybrid	MIN	62.11	73	5.41	2	5.65	2	10.64	7.3
	MAX	109.11	96	12.41	13	11.65	13	27.84	20.13
	MEAN	89.04	86.04	8.78	5.66	8.58	5.6	21.21	13.03

Table 3. Inbreeding depression (%) in F₃ over F₂ for four characters

Derivatives	Plant height	No. of tillers plant ⁻¹	Effective tillers plant ⁻¹	Yield (t ha ⁻¹)
Shonar Bangla	-7.26	27.59	27.02	12.16
Shurma	9.72	18.66	19.39	4.73
ACI-1	4.84	23.63	26.37	8.16
Tia	10.89	31.88	27.65	48.36
ACI-2	1.33	9.93	7.52	34.56
Taj-2	-7.73	14.75	15.09	46.52
Hira-2	-1.52	26.44	21.02	38.70
Shakti	0.49	22.41	27.58	41.58
Hira-99-5	-7.73	45.07	38.75	44.19
Krishan-2	3.37	35.53	34.73	40.60

Table 4. correlation coefficients among four traits across ten F₃ populations

Genotype	PH × PW	PH × TT	PH × ET	TT × ET	PW × TT	PW × ET
Shonar Bangla	0.68**	0.12	0.10	0.85**	-0.42*	-0.39*
Shurma	0.72**	0.08	0.05	0.81**	-0.36*	-0.34*
ACI-1	0.21	0.09	-0.33*	0.79**	-0.61**	-0.58**
Tia	0.66**	0.11	0.09	0.83**	-0.40*	-0.37*
ACI-2	0.70**	0.06	0.04	0.87**	-0.38*	-0.35*
Taj-2	0.18	0.07	0.05	0.78**	-0.65**	-0.60**
Hira-2	0.22	0.10	0.08	0.80**	-0.63**	-0.59**
Shakti	0.29	0.55**	0.52**	0.82**	-0.41*	-0.39*
Hira-99-5	0.69**	-0.31*	0.06	0.84**	-0.37*	-0.35*
Krishan-2	0.73**	0.58**	0.54**	0.86**	-0.43*	-0.41*

Note: PH = plant height; PW = five-panicle weight; TT = total tillers plant⁻¹; ET = effective tillers plant⁻¹, * p < 0.05, ** p < 0.01.

Population Performance

The mean performance of F₃ populations indicated that their performance was generally lower than that of F₂

populations in almost all traits, signifying an increase in homozygosity. The plant height varied from 79.7 cm for Shurma derivatives to 91.9 cm for Taj-2 derivatives. In the case of the number of tillers per plant and effective tillers

per plant, the maximum means were found in ACI-2 derivatives (7.34 and 7.00), while the minimum values were found in Hira-99-5 derivatives (4.52 and 4.44, respectively). In relation to the five-panicle weight, the maximum means were in the Shonar Bangla derivatives (16.79 g) and the minimum in Krishan-2 derivatives (13.03 g). A summary of these trait performances in the F₃ generation is presented in Table 2. From the above observations, it is clear that the decline in the mean values from F₂ to F₃ indicates heterozygosity loss and allele fixation in the segregating populations (Aanathi, 2018).

Inbreeding Depression

The inbreeding depression (ID) is calculated as a percentage of decline in the mean performance of the F₃ generation compared with F₂. It is expressed in Table 3 as a percent reduction in plant height and other traits. The highest ID in terms of plant height was observed in Tia derivatives (10.89%), and negative values in Taj-2 and Hira-99-5 derivatives (-7.73%), which means increased plant height in F₃. Numbers of tillers plant⁻¹ and effective tillers plant⁻¹ had the highest ID in Hira-99-5 derivatives (45.07% and 38.75%, respectively), but the lowest ID occurred in ACI-2 derivatives (9.93% and 7.52%, respectively). For yield (t ha⁻¹), the highest ID was observed in Tia derivatives (48.36%), while the lowest ID (%) occurred in Shurma derivatives (4.73%). Thus, the presence of high inbreeding depression in tillering and yield traits in several crosses may be indicative of dominance and epistasis of gene action, implying the existence of opportunities for heterosis exploitation through hybridization (Ganapati et al., 2020).

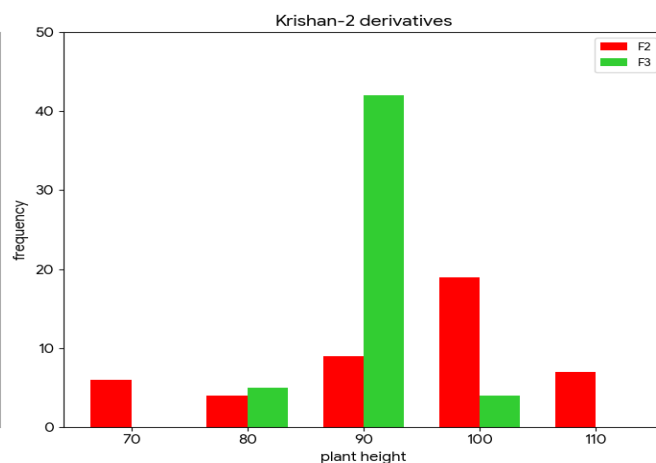
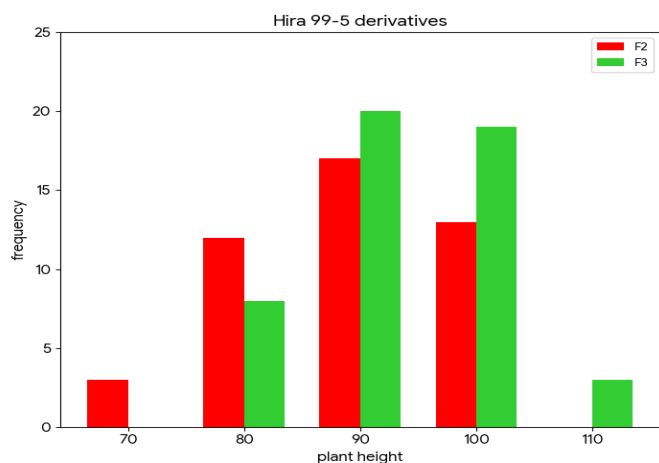
Correlation Coefficients

Correlation coefficients were estimated to determine the relationships among plant height, number of tillers plant⁻¹, effective tillers per plant⁻¹, and five-panicle weight across the F₃ populations. The genotype-wise correlation coefficients are presented in Table 4, while the major significant trends are summarized below.

Five-panicle weight showed a positive and significant correlation with plant height in Shonar Bangla, Shurma, Tia, ACI-2, Hira-99-5, and Krishan-2 derivatives. In contrast, it exhibited a negative association with the number of tillers plant⁻¹ and effective tillers plant⁻¹ in most genotypes, particularly in ACI-1, Taj-2, and Hira-2 derivatives (Sakran et al., 2022). Effective tillers plant⁻¹ consistently showed a positive and significant correlation with total tillers plant⁻¹ across all genotypes, indicating that total tiller production largely determines the number of productive tillers. In ACI-1 derivatives, effective tillers plant⁻¹ also showed a negative association with plant height, whereas in Shakti and Krishan-2 derivatives, both tillers plant⁻¹ and effective tillers plant⁻¹ were positively and significantly correlated with plant height. In Hira-99-5 derivatives, plant height showed a negative association with tiller plant⁻¹, while in most other genotypes, no significant relationship was observed between these traits. Overall, the relationships among traits were genotype-dependent, reflecting differential genetic control and interaction among yield components. These findings indicate that improvement in panicle weight may be achieved through indirect selection for plant height in some genetic backgrounds; however, the negative association with tillering traits suggests a potential trade-off. Therefore, careful selection strategies are required to achieve a balanced improvement of yield-contributing characters.

Estimation of Inheritance Patterns

Inheritance patterns of the populations were analyzed for four different characters, including plant height, number of tillers plant⁻¹, effective tillers plant⁻¹, and five-panicle weight. The raw data were corrected for any effect of blocks, and the means obtained were then classified into frequency distributions through the use of the frequency function in MS Excel. The class intervals used depended on the minimum and maximum values attained by each trait. Inheritance patterns were inferred from the shape, symmetry, and modality of the resulting frequency distributions.



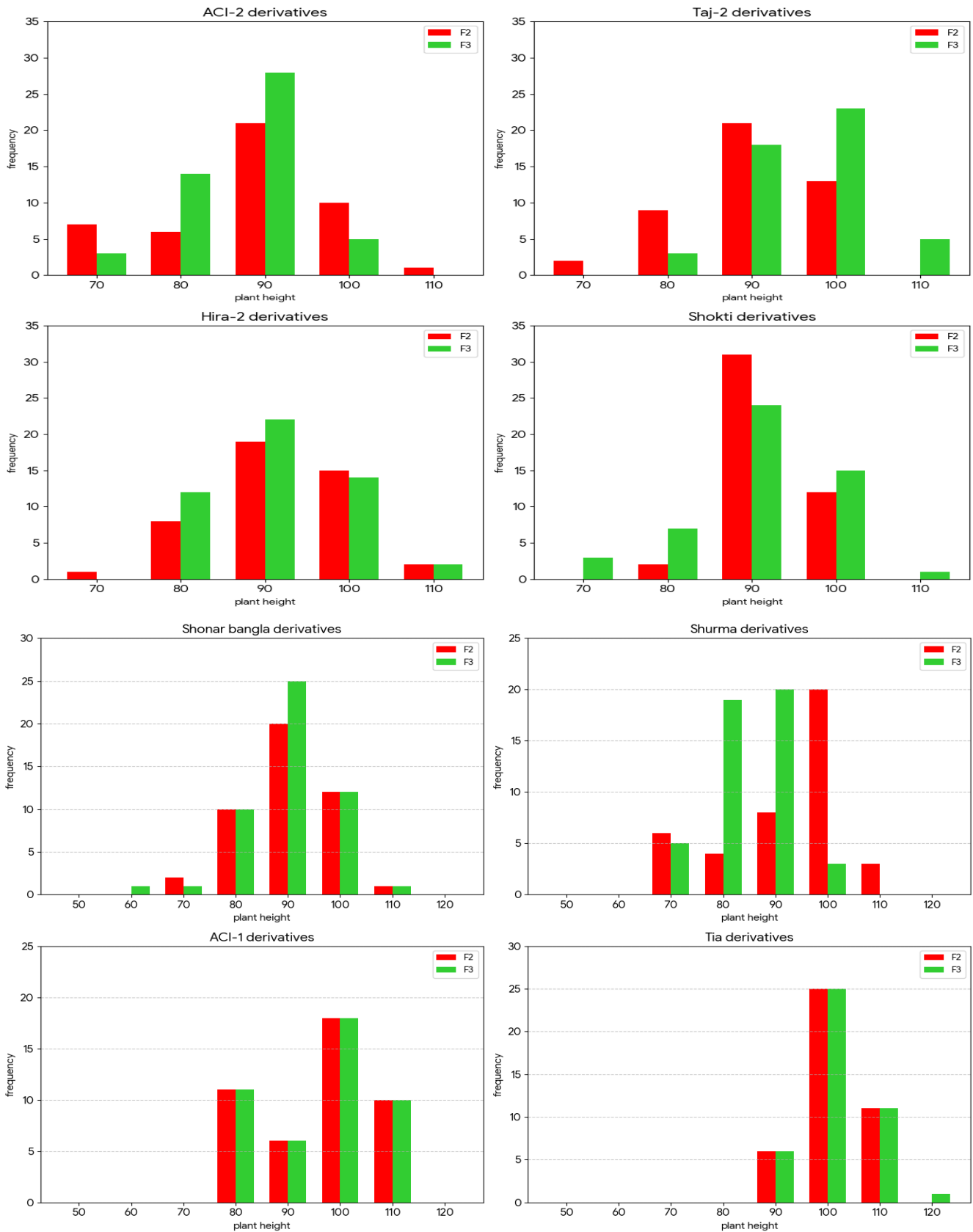


Figure 2. Frequency distribution of plant height in F₂ and F₃ populations of Krishan-2 derivatives showing monogenic inheritance (class interval = 5 cm). The unimodal distribution in F₃ indicates fixation of a major gene effect.

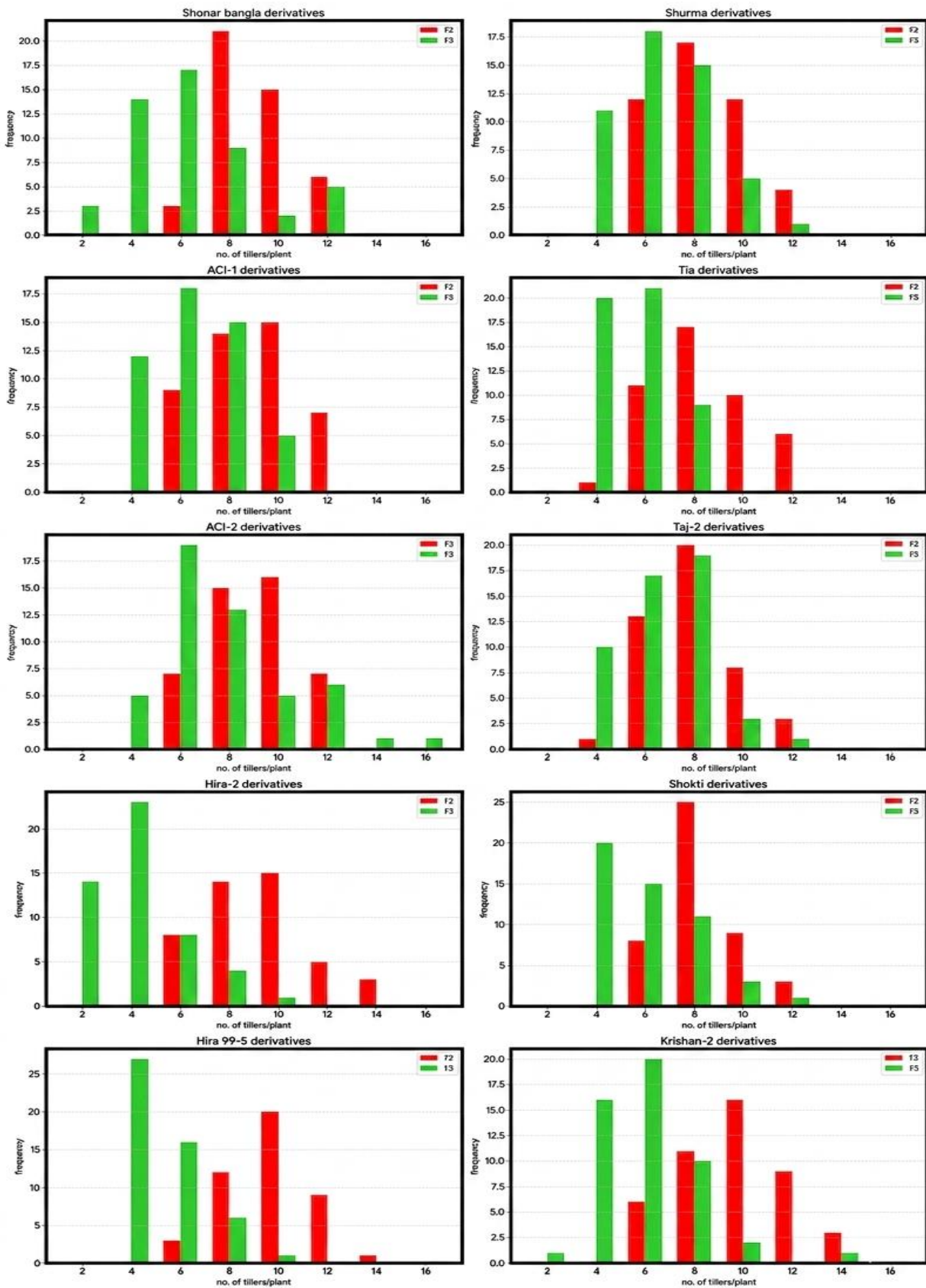


Figure 3. Distribution pattern of the number of tillers per plant in F₂ and F₃ generations of rice derivatives.

Plant height

In the case of F₃ populations, the traits in Krishan-2 were controlled by one gene; Tia, ACI-1, ACI-2, Taj-2, Hira-2, and Shakti derivatives were controlled by one gene with partial effect from another gene; Shurma and Hira-99-5 by two genes; and Shonar Bangla derivatives were polygenic. A comparison of F₂ and F₃ segregations revealed that the traits in Tia and Shakti derivatives were altered from digenic to monogenic mode of inheritance, while

Hira-2 derivatives were altered from monogenic to digenic. ACI-1, ACI-2, and Taj-2 continued to be controlled by one gene with partial effect; Shurma and Krishan-2 became two-gene with partial effect, while Shonar Bangla and Hira-99-5 derivatives continued to be polygenic. These insights align with (Kahani and Hittalmani, 2016; Nanda et al., 2025). An example for monogenic segregation pattern can be seen in Figure 2.

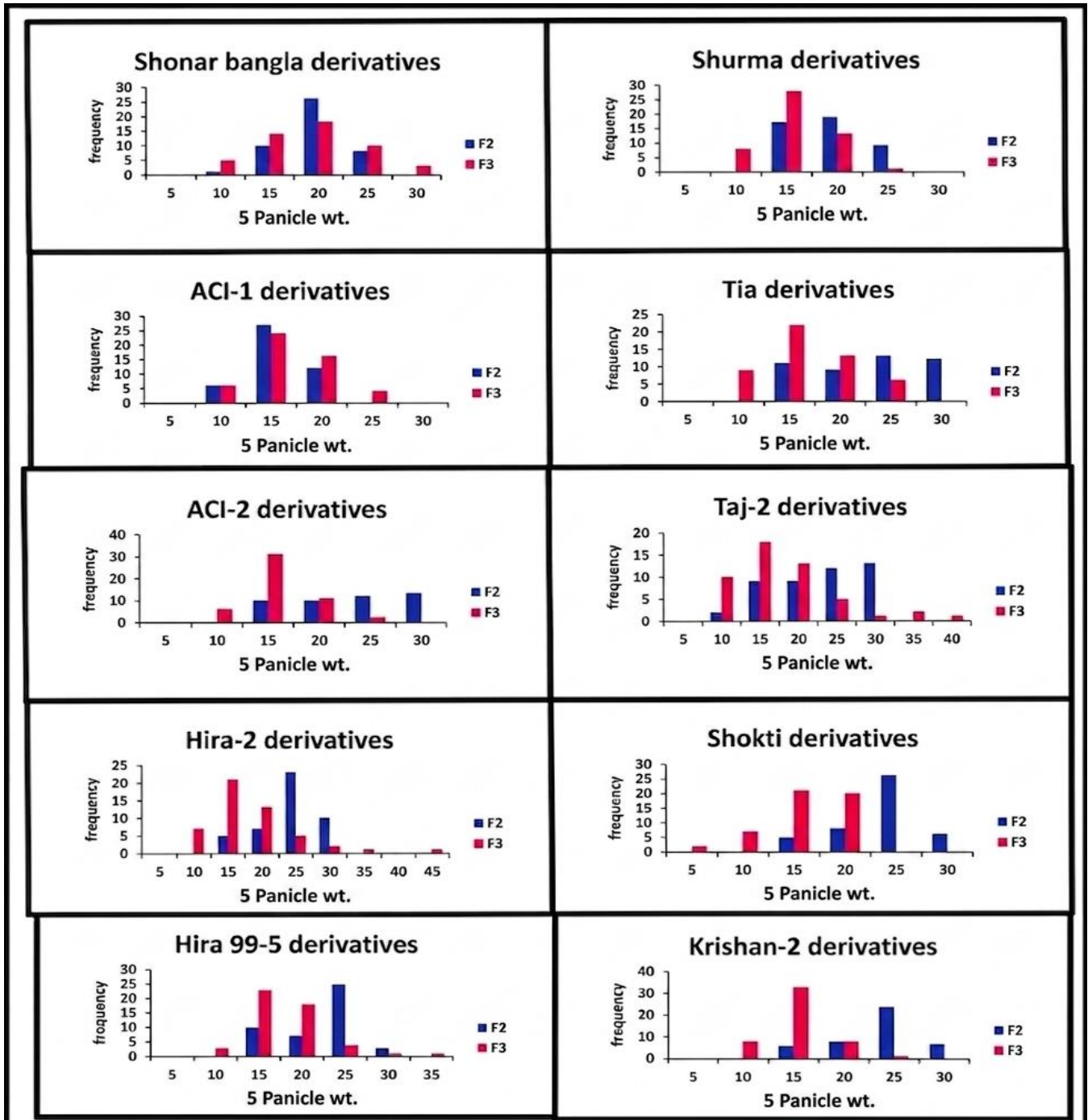


Figure 4. Frequency distribution of five-panicle weight in F₂ and F₃ segregating rice populations of different derivatives, showing inheritance patterns.

Number of tillers plant⁻¹

In F₃, the number of tillers plant⁻¹ was monogenic in Tia derivatives and controlled by a single gene with a partial effect in ACI-1 derivatives. All other genotypes (Shonar Bangla, Shurma, ACI-2, Shakti, Hira-2, Taj-2, Krishan-2, Hira-99-5) showed polygenic control. Relative to F₂, Hira-99-5 changed from polygenic to monogenic; Shurma from polygenic to digenic; Shonar Bangla, ACI-1, ACI-2, and Shakti from polygenic to single-gene with partial effect; Hira-2 from polygenic to two-gene with partial effect; while Tia, Taj-2, and Krishan-2 remained polygenic. Similar findings were reported by Nirubana et al., 2019, and Viswabharathy et al., 2025, indicating that the productivity of tiller plants usually shows polygenic inheritance, with an unbalanced distribution pattern that is a result of complicated interactions between genes and the necessity for careful selection within segregating generations. The segregating patterns and inheritance of tiller numbers per plant are illustrated in Figure 3.

Effective Tillers plant

Tillers plant in F₃ was found to be regulated by two genes in the case of Hira-2 derivatives, one gene having incomplete dominance in the case of Shurma and Tia derivatives, while polygenes were involved in Shonar Bangla, ACI-1, ACI-2, Shakti, Taj-2, Krishan-2, and Hira-99-5 derivatives. Compared to F₂, there was a change from polygenic inheritance to monogenic inheritance in Taj-2, Shakti, and Hira-99-5 derivatives; from polygenic inheritance to digenic inheritance in the ACI-1 derivative. Complementary gene action was seen in the case of Shurma, Tia, and ACI-2 derivatives based on F₂-to-F₃ distribution shifts. In addition to these, the changes in the action of genes across generations also illustrate the dynamic process involved in the segregation and recombination processes in the early generations of rice populations (Tareque et al., 2025).

Five-panicle weight

Five panicle weights in F₃ were determined by one gene with partial dominance in Shurma, ACI-1, Tia, ACI-2, Shakti, and Krishan-2 derivatives; polygenic in Shonar Bangla, Taj-2, Hira-2, and Hira-99-5 derivatives. Compared to F₂, Shurma and ACI-1 changed from polygenic to monogenic; Hira-99-5 from polygenic to digenic; Shonar Bangla, Hira-2, Shakti, and Krishan-2 from polygenic to single-gene with partial effect. Complementary gene action was evident in Tia, ACI-2, and Taj-2 derivatives. These observations are corroborated by (Priyanka et al., 2019). As shown in Figure 4, the distribution patterns of five-panicle weight in F₂ and F₃ generations.

CONCLUSION AND RECOMMENDATION

Genetic variations have been found to exist in large numbers among the examined populations with respect to traits such as height of plants, number of tillers plant⁻¹, effective tillers plant⁻¹, and weight of five panicles.

Significant variations among the genotypes and variations in inbreeding depression and correlation patterns have established that the desired genetic variations existed among them. Monogenic, digenic, and mostly polygenic control over various characters was found based on the inheritance pattern analysis, where yield-related traits have mostly been found under complex gene control. It seems that all those genotypes that were selected as populations under study have not shown good performance, together with genetic stability and desired correlations. The combination of simple and complex modes of inheritance implies that there is adequate scope for selection in improving the segregating populations. It is advised that more effort be devoted to taking the selected superior F₃ populations into further generations (F₄-F₆). The use of molecular markers in conjunction with selection and QTL analysis will assist in identifying the genes associated with yield-related traits. Yield stability can be tested across different environments using multi-environment trials. Selection of the superior genotypes should be based on yield potential, low inbreeding depression, and correlation among traits. Polygenic traits can be improved through either recurrent or pedigree selection, whereas genotypes with a simpler mode of inheritance can be used in directed breeding programs and for gene introgression. It is advisable that superior exotic hybrid germplasms be introduced for rice breeding purposes.

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Conflict of Interest

There are no conflicts of interest declared by the authors.

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