



# Characterization and Comparative Assessment of Ten Advanced Lines of Aus Rice (*Oryza sativa*)

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## Authors' contributions

This work was carried out in collaboration among all authors. Authors AAK, KS and MSRB designed the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Authors MH, SMKH and SMAG managed the analyses of the study. Authors RCK, MIH and MGM managed the literature searches. All authors read and approved the final manuscript.

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## ABSTRACT

The present study focuses on the characterization and comparative assessment of ten advanced lines of Aus rice (*Oryza sativa* L.), an ecotype known for its adaptability to adverse environmental conditions. The experiment was conducted at Sher-e-Bangla Agricultural University, Bangladesh, during the Aus season of 2017, using a Randomized Complete Block Design (RCBD) with three replications. Various agronomic traits, including plant height, panicle length, tiller number, and yield components, were recorded and analyzed to assess genetic variability. Significant genetic diversity was observed among the genotypes, with high heritability estimates for key traits, indicating their potential for selection in breeding programs. Correlation and path coefficient analyses revealed strong associations between plant height, panicle length, and grain yield, highlighting their importance in yield improvement strategies. The findings emphasize the genetic potential of Aus rice for breeding high-yielding, stress-tolerant varieties, contributing to global food security and sustainable rice production.

**Keywords:** *Aus rice; plant height; panicle length; tiller number; genetic diversity; rice production; randomized complete block design (RCBD).*

## 1. INTRODUCTION

Rice (*Oryza sativa* L.) is a staple food for over half of the global population, playing a pivotal role in food security and economic stability, particularly in Asia and Africa. Among the diverse rice ecotypes, the Aus group holds significant promise for enhancing rice productivity and resilience due to its unique genetic and phenotypic attributes. Aus rice, primarily cultivated in Bangladesh and Eastern India, is characterized by its adaptability to adverse conditions, including drought and low soil fertility. This resilience makes it a valuable genetic resource for breeding programs aimed at developing stress-tolerant rice varieties. Studies have highlighted the genetic diversity within Aus rice germplasm, underscoring its potential in rice improvement initiatives (Sar, et al., 2024). The genetic variability present in Aus rice is instrumental for breeding programs targeting yield enhancement and stress tolerance. Research has demonstrated significant variations in agronomic traits among Aus rice genotypes, indicating substantial potential for selection and improvement (Khan, et al., 2023). High heritability estimates for traits such as plant height and stem length suggest that these characteristics are predominantly controlled by genetic factors, making them reliable targets for selection in breeding programs. Recent breeding efforts have

focused on harnessing the genetic potential of Aus rice to develop high-yielding and resilient varieties. For instance, the evaluation of yield-attributing parameters in Aus rice has provided insights into enhancing productivity through targeted breeding strategies (Mahmud, et al., 2024). Additionally, studies have identified specific quantitative trait loci (QTLs) associated with agronomic, yield, and nutritional traits in Aus rice, facilitating marker-assisted selection in breeding programs (Calayugan, et al., 2024). The global rice research community continues to explore the genetic and phenotypic diversity of Aus rice to address challenges posed by climate change and increasing food demand. Collaborative efforts have led to the development of improved rice cultivars with enhanced resilience and productivity. For example, Rice Breeding Australia has made significant strides in delivering varieties that will shape the future of the rice industry. Similarly, public breeding programs in the United States have positively impacted rice yields under changing environmental conditions (Wang, 2024). In summary, the characterization and comparative assessment of advanced Aus rice lines are crucial for understanding their genetic potential and agronomic performance. Such studies provide a foundation for developing improved rice varieties that can contribute to global food security and agricultural sustainability.

## 2. MATERIALS AND METHODS

The present investigation was carried out during the Aus season of 2017 at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The detailed methodology is described below:

### 2.1 Experimental Site

The experiment was conducted at the university's experimental farm (latitude 23°41' N, longitude 90°22' E, elevation 8.6 m above sea level) from April to August 2017. The site belongs to the old Madhupur Tract (AEZ-28) with clay loam soil, a pH of 6.5, and organic carbon content of 0.84%. The climate is subtropical, with distinct seasons: winter (November–February), pre-monsoon (March–April), and monsoon (May–October).

### 2.2 Experimental Materials

The experimental materials consisted of seeds from ten advanced Aus rice lines collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University. The pedigrees of these lines are provided in Table 1.

### 2.3 Experimental Design and Layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three

replications. The field was divided into 30 plots (26 m × 29 m total area), each measuring 6 m × 2 m. The ten lines were randomly assigned to the plots in each block.

### 2.4 Seed Germination and Seedling Raising

Seeds were soaked for 24 hours, followed by incubation for 72 hours for sprouting. The seedbed was prepared with puddling, and germinated seeds were sown on April 11, 2017. Proper protection against birds and pests was ensured.

### 2.5 Main Field Preparation and Fertilizer Application

The main field was prepared by ploughing 3–4 times, followed by laddering. Fertilizers were applied as per BRRI (Bangladesh Rice Research Institute) recommendations (2014). The doses and methods of fertilizer application are shown in Table 2.

### 2.6 Transplanting and Intercultural Operations

Twenty-five-day-old seedlings were transplanted on May 5, 2017, maintaining a 20 cm row-to-row and 10 cm plant-to-plant distance.

**Table 1. Ten advanced Aus rice lines collected from the Department of Genetics and Plant Breeding**

Lines	Pedigree	Source
L1	21 x 29 S6P1P1S2	Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University
L2	21 x 29 S6P6P4S1	
L3	21 x 29 S6P1P1S1	
L4	21 x 29 S6P2P4S2	
L5	21 x 29 S6P1S3	
L6	21 x 28 S5P4P2	
L7	21 x 28 S5P1P2S2	
L8	21 x 28 S5P1P2S3	
L9	21 x 28 S5P7P6S1	
L10	21 x 29 S6P2P4S2	

**Table 2. Fertilizer Dose and Application Method**

Fertilizer	Dose (per ha)	Basal (%)	1st Installment (%)	2nd Installment (%)	3rd Installment (%)
Cow dung	6 ton	100	--	--	--
Urea	135 kg	--	33.33	33.33	33.33
TSP	55 kg	100	--	--	--
MoP	85 kg	50	16.67	16.67	16.67

- Gap Filling: Done within seven days of transplanting.
- Irrigation and Drainage: Early-stage water depth was maintained at 2 cm to promote tillering, increasing to 10–12 cm at later stages. The field was dried 15 days before harvest.
- Weeding: Hand weeding was carried out at 25 and 40 days after transplanting.
- Plant Protection: Diazinon 50EC and Furadan 5G were applied to control pests like rice stem borer and yellow stem borer. Cupravit 80 WP was used against bacterial leaf blight.
- Grain Count and 1000-Seed Weight: The number of filled and unfilled grains was recorded. A random sample of 1000 healthy seeds was weighed at 12% moisture content.
- Dry Weight (g/m<sup>2</sup>) and Yield Per Plant (g): Weighed after drying the seeds and adjusted to 12% moisture content.
- Yield Per Hectare (t/ha): Converted per plant yield data into yield per hectare.

### 3. RESULTS AND DISCUSSION

The Table 3 presents the ANOVA results for fourteen traits, showing the mean sum of squares for replication, genotype, and error. Significant genotypic variation was observed for all traits ( $P < 0.05$  or  $P < 0.01$ ), indicating genetic diversity among the genotypes. Similar findings have been reported in previous studies on Aus rice genotypic variation (Khan, et al., 2023).

Traits such as plant height, panicle length, and yield per plant exhibited highly significant genotypic effects, emphasizing their importance in the differentiation of the studied lines. These traits have been recognized as key factors in distinguishing rice genotypes and enhancing yield potential (Courtney, et al., 2021).

The results align with earlier research indicating that substantial genetic variation exists within Aus rice germplasm, which can be utilized for future breeding programs (Sar, et al., 2024).

## 2.7 Harvesting and Yield Measurement

The rice was harvested manually at full maturity. Threshing and cleaning were done to separate grains. Various growth and yield-related parameters were measured, including plant height, total tiller and effective tiller, panicle length, primary and secondary branch, grain weight, dry weight, and yield per hectare.

### Measured Parameters:

- Plant Height (cm): Measured from the ground to the tip of the main panicle.
- Total Tiller and Effective Tiller Count: Counted at maturity; effective tillers bear panicles.
- Panicle Length (cm): Measured from the base of the panicle to the tip of the panicle.
- Primary and Secondary Branch Count: Total number of branches per panicle recorded at maturity.

**Table 3. Analysis of variance (ANOVA) for fourteen traits in Aus rice**

Characters/Variety	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 9	Error (r-1) (g-1) = 18
Stem length (cm)	55.76	1,302.77**	28.20
Plant height (cm)	81.06	1,428.56**	28.49
Total no. tiller per plant	3.86	3.35*	1.20
No. of effective tiller per plant	2.55	3.57**	0.76
Panicle length (cm)	3.93	21.06**	2.14
No. of primary branches per panicle	2.86	10.38**	0.77
No. of secondary branches per panicle	56.71	65.61**	11.56
Total no. of spikelets per panicle	113.15	467.50**	67.22
No. of filled grain of main tiller	226.02	908.87**	128.25
No. of unfilled grain of main tiller	2.71	599.80**	115.30
1000 seed weight (g)	0.61	9.29**	1.37
Dry weight (g) in 1 sqm	2,254.90	34,004.49**	826.53
Yield per plant (g)	3.90	92.05**	12.86
Yield per ha (Ton)	0.31	3.27**	0.08

\*= Significant at the 0.05 level

\*\* = Significant at the 0.01 level.

These findings validate the genetic variation present in the advanced Aus rice genotypes and reinforce the potential for selecting high-performing lines for further improvement.

The Table 4 summarizes the observed range, mean values, and coefficients of variation (CV) for fourteen traits across ten rice genotypes. Traits such as unfilled grains per panicle exhibited the highest CV (44.68%), indicating substantial variability among the genotypes. In contrast, plant height and panicle length showed lower CV values, signifying greater stability. Understanding this variability is crucial for identifying lines with desirable traits for breeding programs.

Similar findings have been reported in previous studies. For instance, research on Italian rice germplasm observed high phenotypic variation in traits like yield, with coefficients of variation ranging from 5.9% to 45.4% G Mongiano, et al. 2020.

Another study on upland rice genotypes found significant variability in the number of filled grains per panicle and yield per plant, highlighting the importance of these traits in selection processes Tuhina-Khatun M et al 2015.

Additionally, an analysis of agronomic traits in rice reported coefficients of variation ranging from 2.88% to 19.20%, with lower CVs observed for traits like plant height and thousand-grain weight Calayugan, M.I.C et al, 2020.

These studies underscore the importance of assessing trait variability to inform effective

selection and breeding strategies in rice cultivation.

The Table 5 compares the mean performance of ten advanced Aus rice genotypes across fourteen traits, revealing significant differences in stem length, plant height, panicle length, tiller number, and yield per hectare among the genotypes. For instance, genotype G1 demonstrated a superior yield per plant (18.75 g), while genotype G2 excelled in total tillers and dry weight (434 g). These findings underscore the variability in agronomic performance and highlight the potential of specific lines for further development.

Similar studies have reported significant variations in agronomic traits among Aus rice genotypes. For example, research evaluating 50 F<sub>5</sub> Aus rice accessions found notable differences in traits such as plant height, panicle length, and grain yield, emphasizing the genetic diversity within these genotypes (Khan, et al., 2023).

Another study assessing the genetic diversity within Aus rice germplasm identified significant loci associated with essential agronomic traits, with genes like GLT1, PUP4, and SAC1 emerging as key players in yield determination (Sar, P. et al 2024).

These findings are crucial for breeding programs aiming to enhance specific traits in Aus rice. The observed variability provides a foundation for selecting and developing genotypes with desirable characteristics, such as higher yield or increased tiller number, to improve overall crop performance.

**Table 4. Range, mean, CV (%) of 14 traits in Aus rice**

Parameters	Range		Mean	CV (%)
	Min	Max		
Stem length (cm)	67.67	120.20	87.02	6.10
Plant height (cm)	98.27	158.60	119.91	4.45
Total no. tiller per plant	9.38	12.33	10.74	10.22
No. of effective tiller per plant	8.68	12.10	10.09	8.66
Panicle length (cm)	23.77	31.00	26.45	5.54
No. of primary branches per panicle	7.90	12.87	10.04	8.78
No. of secondary branches per panicle	23.97	36.10	28.40	11.97
Total no. of spikelets per panicle	120.21	153.87	133.80	6.13
No. of filled grain of main tiller	92.73	137.17	112.62	10.06
No. of unfilled grain of main tiller	9.17	58.47	24.03	44.68
1000 seed weight (g)	20.50	26.00	23.11	5.07
Dry weight (g) in 1 sqm	196.33	434.33	322.82	8.91
Yield per plant (g)	8.60	24.77	16.39	21.89
Yield per ha (Ton)	1.96	4.34	3.25	8.74

*Min: minimum*

*Max: maximum*

*CV (%): coefficient of variation*

Table 5. Mean performance of 14 characters of 10 Aus rice

Genotype	Stem length (cm)	Plant height (cm)	Total no. tiller per plant	No. of effective tiller per plant	Panicle length (cm)	No. of primary branches per panicle	No. of secondary branches per panicle	Total no. of spikelets per panicle	No. of filled grain of main tiller	No. of unfilled grain of main tiller	1000 seed weight (g)	Dry weight (g) in 1 sqm	Yield per plant (g)	Yield per ha (Ton)
G1	74.66	105.05	9.38	8.68	25.42	9.38	25.15	125.55	108.09	18.32	25.67	394.33	18.75	3.94
G2	67.67	98.27	11.13	10.43	24.57	7.90	23.97	122.60	98.40	25.67	21.33	434.00	18.53	4.34
G3	74.30	111.17	11.17	10.23	25.03	9.63	27.57	122.37	96.17	23.87	26.00	390.33	20.47	3.90
G4	70.40	103.70	11.97	11.33	25.23	8.23	24.70	126.47	92.73	34.13	23.33	417.67	19.60	4.18
G5	71.64	104.07	9.67	9.13	23.77	8.60	24.34	120.21	105.17	15.38	24.00	434.33	20.40	4.34
G6	88.53	119.50	11.63	10.63	25.03	10.70	27.63	141.50	129.50	12.70	22.30	196.33	9.93	1.96
G7	109.93	141.40	10.40	9.83	29.87	12.87	33.40	149.90	124.37	25.63	22.00	206.40	11.97	2.06
G8	117.67	149.80	9.53	8.87	31.00	12.70	36.10	153.87	137.17	17.00	22.60	206.92	10.83	2.25
G9	120.20	158.60	10.17	9.60	29.73	11.77	35.13	144.37	136.17	9.17	20.50	200.50	8.60	2.00
G10	75.23	107.50	12.33	12.10	24.80	8.57	26.03	131.15	98.40	58.47	23.33	347.33	24.77	3.47

This Table 6 provides estimates of genetic and phenotypic parameters, including genotypic variance ( $\sigma^2_g$ ), phenotypic variance ( $\sigma^2_p$ ), heritability in the broad sense ( $h^2_b$ ), and genetic advance (GA) for various traits in Aus rice genotypes. High heritability values were observed for traits such as stem length (93.77%) and plant height (94.25%), coupled with substantial genetic advance, suggesting the predominance of additive genetic effects. This indicates the potential for effective selection to improve these traits in Aus rice breeding programs.

High heritability, especially when accompanied by significant genetic advance, suggests that the observed trait variations are primarily due to genetic factors rather than environmental influences. This combination is indicative of additive gene action, which is favorable for selection in breeding programs. For instance, a study on upland rice reported high heritability and genetic advance for traits like leaf chlorophyll content and number of productive tillers per plant, highlighting the effectiveness of selection for these traits (Tuhina-Khatun, 2015).

Similarly, research evaluating natural variation in photosynthetic and morphological traits in indica rice demonstrated significant heritability and genetic advance, emphasizing the potential for selection to enhance these characteristics (Acevedo-Siaca, et al., 2021).

In the context of Aus rice, evaluating genetic parameters is essential for identifying traits amenable to improvement through selection. The observed high heritability and genetic advance for stem length and plant height in this study suggest that these traits are primarily controlled by additive genetic factors. Consequently, selecting for these traits in breeding programs could lead to significant genetic gains and the development of superior Aus rice varieties.

In summary, the combination of high heritability and substantial genetic advance for specific traits indicates that selection can be effectively applied to enhance these characteristics in Aus rice breeding programs. Focusing on such traits will facilitate the development of improved genotypes with desirable agronomic performance.

This Table 7 presents the correlation coefficients between various agronomic traits and yield at

both genotypic and phenotypic levels. Traits such as plant height ( $r_{G} = 0.99$ ) and panicle length ( $r_{G} = 0.98$ ) exhibit strong positive genotypic correlations with yield, indicating their direct contribution to yield enhancement. Identifying these key traits is crucial for developing effective selection strategies in rice breeding programs.

Strong positive correlations between plant height and yield have been documented in previous studies. For instance, research on rainfed lowland early rice genotypes reported significant genotypic and phenotypic correlations between plant height and grain yield, suggesting that taller plants may possess attributes contributing to higher yields (Tiwari, et al., 2019, Jayasudha & Sharma, 2010).

Similarly, panicle length has been identified as a critical trait influencing yield. A study evaluating 50 traditional and 45 improved rice genotypes found that panicle length had a significant positive correlation with grain yield, emphasizing its importance in selection criteria for yield improvement.

Understanding these relationships enables breeders to focus on traits with the most substantial impact on yield. By selecting for characteristics such as increased plant height and panicle length, it is possible to develop rice varieties with enhanced yield potential. This targeted approach streamlines the breeding process, making it more efficient and effective in achieving desired agronomic outcomes.

In summary, the strong positive correlations of plant height and panicle length with yield at the genotypic level highlight their significance in rice breeding programs. Prioritizing these traits in selection strategies can lead to the development of high-yielding Aus rice varieties, thereby contributing to improved food security and agricultural sustainability.

This Table 8 presents the path coefficient analysis, dissecting the direct and indirect contributions of various traits to yield. Panicle length demonstrated the strongest direct positive effect (0.525) on yield, while traits like stem length showed indirect effects through other traits. These findings offer insights into the underlying relationships between traits and yield, guiding the selection of key traits for breeding.

**Table 6. Estimation of genetic parameters for fourteen characters in Aus rice**

Parameters	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$	PCV	GCV	ECV	$h^2$	GA (5%)	GA (% mean)
Stem length (cm)	453.07	424.86	28.21	24.46	23.69	6.10	93.77	41.12	47.25
Plant height (cm)	495.19	466.69	28.50	18.56	18.02	4.45	94.25	43.20	36.03
Total no. tiller per plant	1.92	0.72	1.20	12.91	7.89	10.22	37.34	1.07	9.93
No. of effective tiller per plant	1.70	0.94	0.76	12.93	9.59	8.66	55.10	1.48	14.67
Panicle length (cm)	8.45	6.31	2.15	10.99	9.50	5.54	74.61	4.47	16.90
No. of primary branches per panicle	3.98	3.20	0.78	19.88	17.84	8.78	80.51	3.31	32.97
No. of secondary branches per panicle	29.58	18.02	11.56	19.15	14.94	11.97	60.91	6.82	24.03
Total no. of spikelets per panicle	200.65	133.43	67.23	10.59	8.63	6.13	66.50	19.40	14.50
No. of filled grain of main tiller	388.46	260.20	128.26	17.50	14.32	10.06	66.98	27.20	24.15
No. of unfilled grain of main tiller	276.81	161.50	115.31	69.23	52.88	44.68	58.34	20.00	83.20
1000 seed weight (g)	4.01	2.64	1.37	8.67	7.04	5.07	65.84	2.72	11.76
Dry weight (g) in 1 sqm	11885.85	11059.32	826.53	33.77	32.58	8.91	93.05	208.97	64.73
Yield per plant (g)	39.26	26.39	12.87	38.24	31.36	21.89	67.23	8.68	52.96
Yield per ha (Ton)	1.15	1.07	0.08	32.99	31.81	8.74	92.98	2.05	63.19

$\sigma^2_p$ : Phenotypic variance,  $\sigma^2_g$ : Genotypic variance,  $\sigma^2_e$ : Environmental variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, ECV: Environmental coefficient of variation,  $h^2$ : Heritability, GA (5%): Genetic advance (5%) and GA (% mean) : Genetic advance (% mean)

**Table 7. Genotypic (G) and phenotypic (P) correlation with yield**

		SL	PH	TTP	ETP	PL	PBP	SBP	SPP	FG	UFG	TSW	DW	YPP
PH	G	0.99**												
	P	0.99**												
TTP	G	-0.51**	-0.50**											
	P	-0.30	-0.26											
ETP	G	-0.46*	-0.44*	0.97**										
	P	-0.29	-0.26	0.94**										
PL	G	0.98**	0.97**	-0.58**	-0.49**									
	P	0.89**	0.88**	-0.29	-0.28									
PBP	G	0.97**	0.95**	-0.63**	-0.58**	0.92**								
	P	0.88**	0.86**	-0.23	-0.27	0.88**								
SBP	G	0.98**	0.97**	-0.62**	-0.54**	0.96**	0.91**							
	P	0.84**	0.86**	-0.16	-0.16	0.83**	0.84**							
SPP	G	0.81**	0.98**	-0.30	-0.25	0.99**	0.86**	0.98**						
	P	0.79**	0.75**	-0.13	-0.14	0.74**	0.78**	0.80**						
FG	G	0.83**	0.86**	-0.74**	-0.59**	0.94**	0.99**	0.98**	0.97**					
	P	0.72**	0.71**	-0.20	-0.34	0.57**	0.72**	0.67**	0.76**					
UFG	G	-0.47**	-0.48**	0.84**	0.92**	-0.42*	-0.54**	-0.49**	-0.26	-0.74**				
	P	-0.32	-0.31	0.53**	0.60**	-0.14	-0.28	-0.18	-0.20	-0.41*				
TSW	G	-0.61**	-0.59**	-0.17	-0.22	-0.59**	-0.45*	-0.59**	-0.65**	-0.58**	0.26			
	P	-0.46*	-0.43*	-0.00	-0.00	-0.31	-0.22	-0.29	-0.42*	-0.47**	0.01			
DW	G	-0.92**	-0.90**	0.20	0.19	-0.84**	-0.95**	-0.98**	-0.85**	-0.99**	0.37*	0.60**		
	P	-0.84**	-0.82**	0.089	0.12	-0.68**	-0.81**	-0.67**	-0.78**	-0.80**	0.26	0.45*		
YPP	G	-0.92**	-0.90**	0.37*	0.47**	-0.84**	-0.93**	-0.90**	-0.87**	-0.72**	0.70**	0.77**	0.95**	
	P	-0.72**	-0.70**	0.36*	0.37*	-0.59**	-0.66**	-0.61**	-0.73**	-0.65**	0.70**	0.39*	0.72**	
YPH	G	-0.91**	-0.89**	0.16	0.16	-0.82**	-0.94**	-0.96**	-0.84**	-0.98**	0.37*	0.60**	0.98**	0.94**
	P	-0.83**	-0.81**	0.08	0.11	-0.67**	-0.80**	-0.66**	-0.77**	-0.79**	0.25	0.47**	0.89**	0.72**

\*\* = Significant at 1%

\* = Significant at 5%

SL = Stem length (cm), PH = Plant height (cm), TTP = Total no. tiller per plant, ETP = No. of effective tiller per plant, PL = Panicle length (cm), PBP = No. of primary branches per panicle, SBP = No. of secondary branches per panicle, SPP = Total no. of spikelets per panicle, FG = No. of filled grain of main tiller, UFG = No. of unfilled grain of main tiller, TSW = 1000 seed weight (g), DW = Dry weight (g) in 1 sqm, YPP Yield per plant (g) and YPH = Yield per ha (Ton)

Table 8. Direct (bold) and indirect effects of different traits at genotypic level on yield

	Effect via													r <sub>g</sub> with yield
	SL	PH	TTP	ETP	PL	PBP	SBP	SPP	FG	UFG	TSW	DW	YPP	
SL	<b>-0.049</b>	0.046	0.152	-0.141	-0.299	0.556	0.004	0.120	-0.164	0.100	0.160	-0.980	-0.423	-0.91**
PH	-0.049	<b>0.046</b>	0.149	-0.137	-0.293	0.541	0.004	0.116	-0.158	0.100	0.150	-0.950	-0.417	-0.89**
TTP	0.025	-0.023	<b>-0.293</b>	0.316	0.176	-0.362	-0.003	-0.036	0.117	-0.180	0.050	0.210	0.173	0.16
ETP	0.023	-0.021	-0.303	<b>0.306</b>	0.150	-0.330	-0.002	-0.030	0.094	-0.200	0.060	0.200	0.218	0.16
PL	-0.049	0.045	0.171	-0.152	<b>-0.302</b>	0.525	0.004	0.118	-0.149	0.090	0.150	-0.880	-0.387	-0.82**
PBP	-0.048	0.044	0.187	-0.178	-0.279	<b>0.568</b>	0.004	0.120	-0.157	0.120	0.120	-1.010	-0.431	-0.94**
SBP	-0.053	0.049	0.184	-0.168	-0.321	0.578	<b>0.004</b>	0.116	-0.156	0.100	0.150	-1.040	-0.414	-0.96**
SPP	-0.050	0.045	0.088	-0.077	-0.302	0.577	0.004	<b>0.118</b>	-0.154	0.060	0.170	-1.120	-0.401	-0.94**
FG	-0.051	0.046	0.217	-0.182	-0.285	0.565	0.004	0.115	<b>-0.158</b>	0.160	0.150	-1.050	-0.517	-0.98**
UFG	0.020	-0.020	-0.250	0.280	0.130	-0.310	0.000	-0.030	0.120	<b>-0.210</b>	-0.070	0.400	0.322	0.37*
TSW	0.030	-0.030	0.050	-0.070	0.180	-0.260	0.000	-0.080	0.090	-0.060	<b>-0.260</b>	0.640	0.356	0.60**
DW	0.050	-0.040	-0.060	0.060	0.250	-0.540	0.000	-0.120	0.160	-0.080	-0.150	<b>1.050</b>	0.439	0.98**
YPP	0.050	-0.040	-0.110	0.150	0.250	-0.530	0.000	-0.100	0.180	-0.150	-0.200	1.000	<b>0.460</b>	0.94**

Residual effect: 0.036

\*\*: Significant at 1%

\*: Significant at 5%.

SL = Stem length (cm), PH = Plant height (cm), TTP = Total no. tiller per plant, ETP = No. of effective tiller per plant, PL = Panicle length (cm), PBP = No. of primary branches per panicle, SBP = No. of secondary branches per panicle, SPP = Total no. of spikelets per panicle, FG = No. of filled grain of main tiller, UFG = No. of unfilled grain of main tiller, TSW = 1000 seed weight (g), DW = Dry weight (g) in 1 sqm, YPP Yield per plant (g) and YPH = Yield per ha (Ton)

Path coefficient analysis is a valuable tool in plant breeding, as it partitions the correlation coefficients into direct and indirect effects, thereby identifying traits that have a significant impact on yield. For instance, a study on rice genotypes found that panicle density had the largest positive direct effect on rice yield, even at low seeding rates (Gravios & Helms, 1992), (Manoj, et al., 2023).

In the context of Aus rice, understanding the direct and indirect effects of traits like panicle length and stem length on yield can inform breeding programs. By focusing on traits with strong direct effects and considering the indirect effects mediated through other traits, breeders can develop varieties with enhanced yield potential.

#### 4. CONCLUSION

The study underscores the substantial genetic variability among the ten advanced Aus rice genotypes, demonstrating their potential for yield improvement through selection and breeding programs. Traits such as plant height, panicle length, and grain yield exhibited high heritability and significant correlations, making them ideal targets for genetic enhancement. The results support the utilization of Aus rice germplasm for the development of climate-resilient, high-yielding rice varieties. Future research should focus on integrating molecular breeding techniques to accelerate the selection of superior genotypes, ensuring sustainable rice production in the face of climate change.

#### DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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