**Original Research Article**

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

### 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 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.

**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, P 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, M.A.R 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 A 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, M.I.C. 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 (**D.R. 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.

**Materials and method**

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**.

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

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

**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 plowing 3–4 times, followed by laddering. Fertilizers were applied as per BRRI recommendations (2014). The doses and methods of fertilizer application are shown in **Table 2**.

**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 |

**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.

* **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.

**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, tiller count, panicle length, grain 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 to the tip of the panicle.
* **Primary and Secondary Branch Count**: Total number of branches per panicle recorded at maturity.
* **Grain Count and 1000-Seed Weight**: The number of filled and unfilled grains was recorded. A random sample of 1000 seeds was weighed at 12% moisture content.
* **Dry Weight (g/m²) and Yield Per Plant (g)**: Weighed after drying the seeds and adjusted to 12% moisture content.
* **Yield Per Hectare (t/ha)**: Converted from plant yield data.

**Result and Discussion**

This table 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 substantial genetic diversity among the genotypes. Similar findings have been reported in previous studies on Aus rice genotypic variation. (Khan MAR 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 E 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, P et al 2024

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.

**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.

This table 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.

**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

This table 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 F₅ 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 MAR,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 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 provides estimates of genetic and phenotypic parameters, including genotypic variance (σ²g), phenotypic variance (σ²p), heritability in the broad sense (h²b), 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 M, 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, L. G., 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.

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

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Parameters** | **σ2p** | **σ2g** | **σ2 e** | **PCV** | **GCV** | **ECV** | **h2** | **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 |

σ2p: Phenotypic variance, σ2g: Genotypic variance, σ2 e: Environmental variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, ECV: Environmental coefficient of variation, h2: Heritability, GA (5%): Genetic advance (5%) and GA (% mean) : Genetic advance (% mean)

This table presents the correlation coefficients between various agronomic traits and yield at both genotypic and phenotypic levels. Traits such as plant height (r<sub>G</sub> = 0.99) and panicle length (r<sub>G</sub> = 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 D.N., et al 2019)

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.

**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).

This table 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.

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 and Helmes, 1992)

Similarly, research on cowpea revealed that traits such as biomass and harvest index had high positive direct effects on seed yield, highlighting their importance in selection strategies.( Lenka and Misra, 1973)

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.

In summary, path coefficient analysis provides a comprehensive understanding of how different traits contribute to yield. By identifying traits with significant direct effects, such as panicle length, and understanding the indirect effects mediated through other traits, breeding programs can be more effectively designed to improve yield in Aus rice.

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

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Effect via | | | | | | | | |  |  |  |  | rg with yield |
| SL | PH | TTP | ETP | PL | PBP | SBP | SPP | FG | UFG | TSW | DW | YPP |
| SL | **-0.049** | 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 | **0.046** | 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 | **-0.293** | 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 | **0.306** | 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 | **-0.302** | 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 | **0.568** | 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 | **0.004** | 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 | **0.118** | -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 | **-0.158** | 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 | **-0.210** | -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 | **-0.260** | 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 | **1.050** | 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 | **0.460** | 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).

### 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.

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