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Research Article

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Genetic analyses of advanced breeding lines of rice for yield-attributing traits and salinity stress tolerance

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ABSTRACT

The development of advanced rice breeding lines and their evaluation for yield-attributes and salinity stress tolerance offers a significant opportunity to identify high-yielding salt-tolerant genotypes exhibiting desired traits. The present study aimed to examine the morpho-genetic variability of thirty-six advanced breeding lines of rice, with a focus on features that contribute to yield and salinity stress tolerance. Three replications of a randomized complete block design were used in the first experiment. Significant variability was observed among the lines for the studied quantitative traits. Based on yield attributing traits, the advanced breeding lines *viz*., Line 10, Line 21, Line 22, Line 23, Line 24 and Line 25 showed better performances in terms of earliness and yield. In yield-related variables such as the number of effective tillers per plant, plant height, and grain yield per plant exhibited high heritability coupled with high genetic advance as percentage of mean. The results of PCA biplot showed that the PC1 and PC2 accounted for the greatest variability of advanced Line 10, Line 11, Line 18, Line 21, Line 22, Line 23, Line 24, Line 25, Nerica 10, Begunipata, and Binadhan-14 with significant influence of the studied traits. Cluster analysis reflected that the high-yielding genotypes were placed in cluster II and VI. Highest genetic distance was observed among the genotypes of cluster III and cluster VI. In the second experiment, four advanced breeding lines along with salt tolerant and susceptible checks were assessed for salinity tolerance at the reproductive stage. The plants were cultivated in a large plastic-tub filled with field soil. During the late booting stage, saline (EC=10 dS/m) irrigation water was applied to the plants and continued for three weeks. While Lines 10 and 12 demonstrated a reduced decline, salt stress caused a significant loss in yield and yield-attributing characteristics in all genotypes. Line 10 and Line 12 which showed a reasonable degree of salt tolerance as well as early maturity were placed in the respective quadrant of the biplot. Stress tolerance indices also reflecting the better salt tolerance phenomena of the advanced Line 10 and Line 12. Considering all of the traits, Line 10 and Line12 could be selected as desired advanced rice lines for the development of early, high-yielding and salt tolerant rice varieties.

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KEYWORDS: Advanced lines, Yield-attributes, Phenotypic variability, Genetic parameters, Diversity analysis, Principal component analysis, Salt stress

INTRODUCTION

After corn, rice (*Oryza sativa* L.) is the second primarily grown grain worldwide. Approximately 95% of all grains consumed in Bangladesh are derived from rice, making it the most essential meal crop (Chowdhury *et al*., 2023). Because of the world population's rapid expansion and rising food need, rice became more and more in demand every day (Ashraf, 2023). It is projected that the world's population will continue to grow and will reach nearly 9.3 billion by 2050. In order to feed this larger, we need to produce 60% more food while the expansion of arable land is expected to rise by only 70 million hectares or roughly 5% (FAO, 2009; UN, 2012). Based to some calculations, climate change could cause a 40% decrease in the production of rice by the turn of the 20th century (Anderson, 2023). The main cereal crop of Bangladesh, boro rice being the supplier for the 14% of total paddy output, is harvested in the early monsoon, and during this time the northeastern portion of the country frequently faces flash flooding (BBS, 2015; Ahmed, 2024). Because of a shortfall of 0.88 million metric tons of boro rice in the Haor districts, almost 62% of families currently face food insecurity. Consequently, the nation lost $ 450 million in 2017 (Parvez *et al*., 2022; Hossain *et al*., 2023). In their rice-mustard-rice cropping system, farmers may be able to plant boro rice on time with the assistance of oilseed and short-duration rice cultivars through minimizing the danger of losses from flash floods (Opu, 2017). Therefore, one of Bangladesh's top breeding priorities is producing rice varieties with high yields as well as with early-maturity in order to feed the region's expanding population to escape the sudden flash floods as well as to fit them in aman-mustard-boro cropping pattern.

With 36 million metric tons of milled rice harvested from 11.70 million hectares in the 2021-2022 crop year, Bangladesh ranked third globally in rice production. Despite this improvement, Bangladesh's agricultural industry has been negatively impacted by the country's shifting climate, and abiotic stresses like salt and drought are a constant danger to rice yield and sustainability (Hussain *et al.*, 2016; Shelley *et al.*, 2016). Plants cannot thrive in saline-prone soils due to an imbalance in metabolic activities when stressed by salt (Shrivastava & Kumar, 2015). Saline soil is defined by an intrusion of sodium ions, primarily sulfate and chloride anions, on the soil's surface due to human or natural activity, resulting in a high level of electrical conductivity of greater than 4 dS/m (Ali *et al.*, 2013; Hussain *et al.*, 2017). Very little agricultural production takes place on the 1.056 million hectares of offshore farmland, out of 2.85 million hectares, that are damaged by seawater (SRDI, 2010). The commercial production of boro rice, rabi (winter) crops, and aus during kharif-1 (March-July) season is restricted by increased salinity induction during the dry season. As consequence, the introduction of potential rice cultivars that are seasonally specific and salt tolerant may boost cropping intensity refraining the areas from being fallow during the rabi season (Hakim *et al.*, 2014; Rahman *et al.*, 2016).

The quantity and type of genetic diversity influence a complicated attribute like grain yield, which is regulated by numerous genes (Ashraf *et al.*, 2020). For any breeding effort to be successful, a thorough understanding of the genetic diversity for the traits under consideration is necessary. It is essential to understand the genetic factors of different yield and yield-contributing traits to facilitate designing an efficient breeding strategy. This is because this information not only serves as a foundation for selection but also offers important insights into the choice of parents to be hybridized (Datta *et al.*, 2005). Therefore, in order to find striking genotypes with an appropriate trait combination, a number of selection criteria must be applied. Additionally, identifying the genetic variety within a genotype group helps produce better recombinants. On the other hand, one effective method for determining a set of breeding lines that leads to maximal diversity is principal component analysis (PCA) (Gireesh *et al.*, 2017; Basavaraj *et al.*, 2022). In rice breeding, there is strong selection pressure, which reduces rice's genetic variability (Viana *et al.*, 2019). Significantly, in the subsequent years that have followed, breeders' interest has grown in the development of genetic diversity in rice. One potential method for obtaining genetic variation or bringing desirable traits to a new population is cross-breeding. Notably, we have developed many promising rice lines through cross-and-mutation breeding approaches. Therefore, it would be worthwhile to investigate these advanced lines for phenotypic diversity, yield potential and salinity stress tolerance. Identification of potential lines might be useful for developing early, high-yielding and salt tolerant rice varieties. Considering the above facts in mind, the present investigation was thus aimed to (i) characterize the advanced breeding lines of rice for yield and yield-attributing traits, (ii) estimate the nature and magnitude of genetic diversity of the advanced lines of rice based on morphological traits, and (iii) evaluate four advanced breeding lines (Line 8, Line 10, Line 11, and Line 12) of rice for salinity stress tolerance.

MATERIALS AND METHODS

Experiment 1: Field Evaluation of the Advanced Lines of Rice for Yield and Yield Attributing Traits

Plant materials, experimental site and season

Thirty-six diverse genotypes of rice (twenty early maturing and five high-yielding advanced (F_6 generation) breeding lines selected from different cross combinations, two early and one late maturing cultivated varieties, two salt tolerant varieties, two drought tolerant varieties, two advanced mutant lines, one black and one begunipata rice genotypes) were used in this investigation as plant materials (Supplementary Table S1). The seeds of the advanced breeding lines/varieties/genotypes were received from Bangladesh Rice Research Institute (BRRI), and Bangladesh Institute of Nuclear Agriculture (BINA), the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU). The study was carried out at the Department of Genetics & Plant Breeding's Farm Research Laboratory, BAU, Mymensingh-2202, Bangladesh, during Boro season (December 2022 to May 2023). Medium-high land in Agro-Ecological Zone-9 (Old Brahmaputra Flood Plain) comprised the topography of the trial area. The pH range of the soil was 6.5 to 6.7, with a sandy loam texture.

Land preparation

After a series of ploughing, cross-ploughing, and laddering operations to introduce the soil into proper tilth and leveling, the trial field was ready. The suggested dosages for different chemical fertilizers (50% Urea @246 kg/ha, Triple Super Phosphate @150 kg/ha, Muriate of Potash @123 kg/ha, Gypsum @75 kg/ha, and Zinc sulphate @6 kg/ha) and Cowdung @5 ton/ha were applied during the final stage of land preparation. Two installments were made to apply the remaining 50% Urea. Two weeks following transplantation, the half of the Urea was administered. One week prior to flowering, the remaining half of the Urea was applied as top dressing.

Experimental design, layout and seedling transplanting

The experiment was conducted in a randomized complete block design (RCBD) with three replications. Each individual plot was 2 m in length and 2.2 m in width. The spacing was given as 20 cm between plants and 25 cm between rows and 50 cm between plots. Two seedlings were transplanted in each hill.

Intercultural operations

To ensure that the rice plants grew more effectively, several agronomic approaches, including irrigation and weeding were carried out in accordance with conventional cultivation techniques. Additional intercultural operations were carried out whenever necessary. Insecticide Virtako @1.5 g/10 L water was applied to prevent rice stem borer. Proper care was taken to prevent the infestation of nematode and rice yellow stem borer.

Data collection

Data on yield and associated variables that influence yield, including days to first flowering (DFF), days to maturity (DM), no. of effective tillers per plant (NET/P), plant height (PH), panicle length (PL), 100-seed weight (100-SW) and grain yield per plant (GY/P), respectively were collected from five randomly selected plants per genotype from each replication.

Estimation of genetic parameters

Utilizing genetic characteristics, the following formulas recommended by biometricians, such as phenotypic and genotypic variance, heritability in broad sense, phenotypic and genotypic coefficient of variations, genetic advance and genetic advance as percentage of mean were calculated separately (Johnson *et al.*, 1955; Allard, 1960; Singh & Chaudhary, 1977). According to Deshmukh *et al.* (1986), the PCV and GCV estimates were categorized as low, <10%, moderate, 10-20%, high, >20%. Johnson *et al.* (1955) classified the heritability in the broad sense (h^2b) as low, 0-30%; medium, 31-60%; high, >60%, and the GA% as low <10%; moderate, 10-20%; and high, >20%.

Cluster analysis

Using statistical software Minitab version18, a cluster analysis based on Ward's approach (Ward Jr., 1963) was carried out to group the genotypes according to their morphological attributes. The method used squared Euclidean distance of the distance metric and standardized variables. The following formula was used to calculate the squared distance (D^2) for each pair of genotype combinations:

$$D^2ij = ((Xi\text{-}Xj)S^{-1}(Xi\text{-}Xj))$$

Where, D^2ij = the square distance between any two groups i and j, Xi and Xj = the vectors for the values for genotypes ith and j th genotypes, and S^{-1} = the inverse of pooled variance covariance matrix within groups.

Experiment 2: Screening of Advanced Lines for Salinity Tolerance at the Reproductive Stage

Experimental materials

Six rice genotypes-four early maturing advanced (F_5 generation) breeding lines (Line 8, Line 10, Line 11 and Line 12), one high-yielding early rice variety (Binadhan-16), and one saline (8 dS/m) & submergence (15 days) tolerant rice variety (Binadhan-23) were used as plant materials. The seeds of the selected advanced lines were developed by the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU) and the seeds of the selected rice varieties were collected from Bangladesh Institute of Nuclear Agriculture (BINA).

Experimental site, season, and design

The experiment was conducted at the net house of the Farm Research Laboratory of the Department of Genetics & Plant Breeding, BAU, Mymensingh-2202, Bangladesh, during the Aman season (July to October 2022) of rice cultivation. It used a RCBD with three replications and two treatments: control and salt stress (EC=10 dS/m).

Seedling transplantation and imposition of salt stress

Plastic tubs (135 cm × 90 cm × 24 cm) filled with field soil were used to perform the experiment. At first the soils were thoroughly mixed with the suggested doses of cow dung @5000 kg/ha and inorganic fertilizers (Urea @200 kg/ha, TSP @123 kg/ha, MP @98 kg/ha, Gypsum @86 kg/ha, Zinc sulphate @5 kg/ha, and Boron @7 kg/ha). Importantly, one-third amount of Urea was used along with other fertilizers during the final stages of the plastic-tub soil preparation. The second and third doses of urea were applied following top dressing method during the active tillering and panicle initiation stages, respectively. Twenty-five-day old seedlings were transplanted in the plastic tub. Plant to plant and row to row spacing were kept 20 cm and 25 cm, respectively while transplanting two seedlings per hill on 27th July, 2022. Following the procedure outlined by Ahmadizadeh *et al.* (2016), leaf clipping of each genotype was carried out at the conclusion of rice growth stage 4 (heading stage), which is just before the fresh panicle evolves from the flag leaf. For the following three weeks, the soil was irrigated with saline water (10dS/m, one centimeter above the surface level (Figure 1). After three weeks of salt stress treatment, the tubs were irrigated with normal irrigation water. Following harvesting, data were recorded for different yield-attributing traits.

Intercultural operations

The experimental plots were kept free from weeds whenever necessary pulling up without harming the rice plants. Insecticide

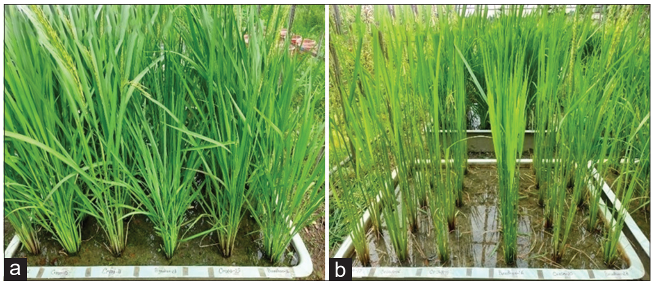

Figure 1: Experimental setting for salinity screening at the reproductive stage (a) control (b) salinity stress

Virtako @1.5 g/10 L water was applied to prevent rice stem borer. Proper care was taken to prevent the infestation of nematode and rice yellow stem borer.

Data collection on yield related traits

Information on yield and traits that contribute to yield, including DM, NET/P, PH, PL, no. of filled grains/panicle (NFG/P), no. of unfilled grains/panicle (NUG/P), spikelet fertility (SF%), 100-SW, and grain yield per panicle (GY/P), respectively were collected from five randomly selected plants per genotype for each replication.

Statistical analysis

The recorded data for the different parameters were compiled and appropriately tabulated for statistical analyses. MINITAB version 18 (Minitab Inc., State College, Pennsylvania) following RCBD design for the both experiments performed all statistical analyses. At the 5% probability level, the Tukey's multiple comparison tests were employed to ascertain if there was a significant variation in the treatment means. The MINITAB 18 was also used to perform principal component analysis.

Stress tolerance indices

The subsequent equations were applied to determine the stress tolerance indices on grain yield per panicle:

Geometric Mean Productivity (GMP) = $\sqrt{Y_p \times Y_s}$ (Fernandez, 1992)

Mean Productivity (MP) = $\left(Y_s + Y_p\right)/2$ (Rosielle & Hamblin, 1981)

Stress Susceptibility Index (SSI) = $\dfrac{1 - Y_s / Y_p}{1 - \overline{Y}_s / \overline{Y}_p}$ (Fischer & Maurer, 1978)

Stress Tolerance index (STI) = $\dfrac{(Y_s)(Y_p)}{(Y_p^{\,2})}$ (Fernandez, 1992)

Tolerance Index (TOL) = $Y_p - Y_s$ (Rosielle & Hamblin, 1981)

Yield Stability Index (YSI) = $\dfrac{Y_s}{\overline{Y}_s}$ (Bouslama & Schapaugh, 1984)

Where, Ys & Yp, and $\bar{Y}$s &$\bar{Y}$p indicate seed yield and mean seed yield of the genotypes under stress and normal condition, respectively.

RESULTS

Analysis of Variance (ANOVA) for Yield and Yield Contributing Traits of the Thirty Six Advanced Lines of Rice

The thirty-six genotypes under study have their yield and yield-related variables examined using ANOVA results reported in Supplementary Table S2. For the seven variables under investigation, the results revealed a highly significant ($p<0.001$) variation in the genotypes (advanced lines, mutants, and varieties), suggesting a high level of genetic variability among the genotypes.

Mean Performances for Yield and Yield Contributing Traits of Thirty-six Advanced Lines

The mean performance of the advanced lines for attributes that contribute to yield was displayed in the results of Table 1. The least number of days (92.67 days) for the first flowering was specified by the advanced Line 15, whereas the advanced Line 22 stipulated the highest possible number of days for first flowering (127.67 days). The genotypes that matured earlier were advanced Line 12 and Nerica 10, as they required minimum number of days (132.33 days) to mature, whereas advanced Line 22 required maximum number of days (156.67 days) to mature. The highest NET/P (21.51) was recorded in the advanced Line 10 while the lowest NET/P (8.91) was recorded in Begunipata. The minimum PH was found in the advanced Line 11 (56.39 cm), and the maximum PH (94.40 cm) was recorded in advanced Line 22. Line 24 had the highest PL (30.60 cm) and the lowest PL (20.14 cm) was recorded in Binadhan-14. The highest 100-SW was recorded in advanced Line 22 (2.92 g); however, the lowest (1.76 g) was recorded in advanced Line 16. The highest GY/P was observed in the advanced Line 25 (42.65 g) the lowest GY/P was recorded in Begunipata (21.94 g) (Table 1).

Estimation of Genetic Parameters

Data on phenotypic and genotypic variances, PCV and GCV, heritability, GA, and GA% of the seven traits under study are shown in Table 2. The traits those had high phenotypic and genotypic variance values were PH (93.12 and 78.51%, respectively), GY/P (42.94 and 36.24%, respectively), DFF (42.21 and 41.81%, respectively) and DM (30.00 and 29.62%, respectively), whereas the remaining characters showed very modest phenotypic and genotypic variance values *viz.*, NET/P (9.48 and 7.20%, respectively), PL (5.65 and 3.79%, respectively) and 100-SW (0.08 and 0.06%, respectively). The attributes exhibiting a significant degree of PCV (>20%) were NET/P and GY/P (21.37 and 20.41%, respectively) whereas PH and 100-SW showed medium (10%-20%) PCV values (12.89 and 12.75%, respectively). However, medium (10%-20%) GCV values were obtained in GY/P (18.75%), NET/P (18.62%), PH (11.84%) and 100-SW (10.86%), respectively. For all traits, the PCV values exceeded the GCV values. Meanwhile, the lowest PCV and GCV values have been obtained for PL (9.72 and 7.91%, respectively), DFF (6.35 and 6.35%, respectively), and DM (3.97 and 3.95%, respectively). In general, over 60% of the variables under study had a high h^2b; however, DFF had the highest heritability (99.06%), while PL had the lowest (67.13%). The range of genetic advances was from 0.43 to 16.76. Genetic advance as a percentage of mean varied between 8.08 (DM) to 35.49% (GY/P) (Table 2).

Table 1: Mean performances of the thirty six genotypes of rice for yield and yield contributing traits grown under field conditions

Genotype	DFF	DM	NET/P	PH (cm)	PL (cm)	100-SW (g)	GY/P (g)
BRRI dhan28	102.33^{F-I}	134.67^{H-L}	10.45^{FG}	73.01^{F-K}	23.04^{D-G}	2.18^{D-I}	22.83^{LM}
BRRI dhan67	103.67^{E-G}	137.33^{D-G}	10.35^{GH}	73.92^{E-K}	23.15^{D-G}	2.28^{C-H}	23.66^{K-M}
BRRI dhan89	110.33^{B}	132.67^{LM}	12.35^{C-H}	76.17^{C-J}	24.27^{C-G}	2.00^{F-I}	24.73^{J-M}
Binadhan-10	101.67^{G-J}	138.33^{C-F}	15.72^{B-D}	74.64^{D-K}	24.50^{B-G}	2.66^{A-D}	40.75^{AB}
Binadhan-14	99.33^{K-N}	137.33^{D-G}	10.27^{GH}	60.31^{LM}	20.14^{G}	2.22^{C-I}	22.78^{LM}
Binadhan-17	103.33^{E-H}	138.33^{C-F}	18.58^{AB}	63.40^{K-M}	22.12^{E-G}	1.93^{HI}	36.25^{A-H}
Begunipata	101.33^{H-K}	132.67^{LM}	8.91^{H}	60.23^{LM}	21.39^{FG}	2.48^{A-F}	21.94^{M}
Black rice	108.33^{BC}	138.67^{C-E}	15.67^{B-E}	82.30^{A-G}	26.02^{B-E}	2.38^{B-H}	37.06^{A-F}
GR Line 1	104.67^{DE}	137.33^{D-G}	15.32^{B-F}	69.80^{H-L}	24.08^{D-G}	2.08^{E-I}	31.88^{C-K}
EM Line 1	104.33^{D-F}	137.33^{D-G}	16.11^{B-D}	68.62^{I-M}	25.30^{B-F}	2.16^{E-I}	34.63^{A-I}
Nerica 10	99.67^{J-M}	132.33^{M}	18.58^{AB}	85.34^{A-F}	25.17^{B-F}	2.24^{C-I}	41.60^{A}
Line 1	94.67^{Q-S}	135.67^{G-J}	12.81^{C-H}	71.46^{G-L}	23.39^{D-G}	2.08^{E-I}	26.70^{I-M}
Line 2	98.33^{L-N}	138.33^{C-F}	16.44^{B-D}	77.85^{C-J}	25.51^{B-F}	2.11^{E-I}	34.69^{A-I}
Line 3	93.33^{RS}	135.33^{G-K}	16.40^{B-D}	65.79^{J-M}	24.45^{C-G}	1.99^{G-I}	32.64^{B-J}
Line 4	94.67^{Q-S}	136.67^{E-H}	12.35^{C-H}	81.88^{B-H}	25.40^{B-F}	2.24^{C-I}	27.68^{I-M}
Line 5	103.67^{E-G}	135.67^{G-J}	10.80^{E-H}	91.95^{AB}	26.02^{B-E}	2.22^{C-I}	23.96^{K-M}
Line 6	108.33^{BC}	136.33^{F-I}	13.81^{C-H}	87.37^{A-C}	24.81^{B-F}	2.17^{E-I}	28.51^{G-M}
Line 7	102.67^{E-H}	138.33^{C-F}	13.52^{C-H}	83.78^{A-G}	24.47^{C-G}	2.34^{B-H}	31.64^{C-K}
Line 8	97.67^{M-O}	134.33^{I-M}	17.14^{A-C}	68.21^{I-M}	23.49^{D-G}	2.15^{E-I}	36.83^{A-G}
Line 9	101.67^{G-J}	135.67^{G-J}	11.95^{D-H}	62.91^{K-M}	22.83^{D-G}	2.42^{B-G}	28.93^{F-M}
Line 10	99.33^{K-N}	133.67^{J-M}	21.51^{A}	73.98^{E-K}	23.16^{D-G}	1.97^{G-I}	42.15^{A}
Line 11	93.33^{RS}	133.33^{K-M}	13.88^{B-G}	56.39^{M}	21.37^{FG}	2.36^{B-H}	32.67^{B-J}
Line 12	95.67^{O-Q}	132.33^{M}	16.34^{B-D}	71.67^{G-L}	24.31^{C-G}	2.36^{B-H}	38.43^{A-D}
Line 13	97.67^{M-O}	139.33^{CD}	12.91^{C-H}	86.79^{A-D}	25.88^{B-E}	2.29^{C-H}	29.52^{E-M}
Line 14	102.33^{F-I}	135.33^{G-K}	15.11^{B-G}	66.25^{J-M}	24.34^{C-G}	2.18^{D-I}	32.82^{B-J}
Line 15	92.67^{S}	135.67^{G-J}	15.05^{B-G}	79.58^{B-I}	23.75^{D-G}	1.78^{I}	26.83^{I-M}
Line 16	100.33^{I-L}	140.33^{C}	16.79^{B-D}	66.92^{J-M}	21.91^{E-G}	1.76^{I}	29.54^{E-M}
Line 17	95.33^{P-R}	136.33^{F-I}	14.77^{B-G}	77.18^{C-J}	23.88^{D-G}	2.08^{E-I}	30.72^{D-L}
Line 18	101.67^{G-J}	138.33^{C-F}	10.52^{FG}	74.87^{D-K}	23.65^{D-G}	2.78^{AB}	29.15^{F-M}
Line 19	97.33^{N-P}	136.00^{G-I}	12.41^{C-H}	74.99^{C-K}	24.31^{C-G}	2.28^{C-H}	28.18^{H-M}
Line 20	101.67^{G-J}	135.33^{G-K}	13.93^{B-G}	72.41^{G-L}	23.59^{D-G}	1.90^{H-I}	26.36^{I-M}
Line 21	108.33^{BC}	150.33^{B}	16.15^{B-D}	77.65^{C-J}	28.54^{A-C}	2.43^{B-G}	39.00^{A-D}
Line 22	127.67^{A}	156.67^{A}	12.96^{C-H}	94.40^{A}	25.76^{B-F}	2.92^{A}	37.82^{A-E}
Line 23	106.33^{CD}	149.33^{B}	14.72^{B-G}	85.86^{A-E}	28.88^{AB}	2.68^{A-C}	39.43^{A-C}
Line 24	109.33^{B}	150.67^{B}	16.27^{B-D}	83.82^{A-G}	30.60^{A}	2.53^{A-E}	40.85^{AB}
Line 25	103.33^{E-H}	136.67^{E-H}	18.46^{AB}	73.47^{E-K}	26.96^{A-D}	2.32^{B-H}	42.65^{A}
Mean	101.84	137.86	14.41	74.87	24.46	2.25	32.11
Range	92.67-127.67	132.33-156.67	8.91-21.51	56.39-94.40	20.14-30.60	1.76-2.92	21.94-42.65
SE	0.36	0.35	0.87	2.21	0.79	0.09	1.50
CV (%)	0.62	0.44	10.48	5.11	5.57	6.69	8.06
Tukey's value	2.06	2.00	4.94	12.51	4.46	0.49	8.47

Here, DFF=days to first flowering, DM=days to maturity, NET/P=no. of effective tillers/plant, PH=plant height (cm), PL=panicle length (cm), 100-SW=100-seed weight (g), GY/P=grain yield/plant (g), SE=standard error; CV=coefficient of variation

Significantly, High GA% and high heritability were noted for GY/P, NET/P, and PH.

Principal Component Analysis (PCA)

In order to look into the contributors to the principal component, the morphological values in PC1 and PC2 were assessed. The best characteristics of PCs are considered to be superior Eigen values (>1) (Table 3). Regarding the seven quantitative variables examined, PC1 and PC2 were accounted for roughly 69.7% of the variation observed across the thirty-six rice genotypes. While DM had the highest positive loading (0.480), the first principal component (PC1) explained the highest variation (43.4%) of the data, followed by PL (0.450), DFF (0.418), PH (0.394), GY/P (0.336), 100-SW (0.333), and NET/P (0.116) (Table 3). The PC2 accounted for 26.3% variation whereby 100-SW (0.345), DFF (0.220), PH (cm) (0.129) and DM (0.115) exhibited positive coefficients while the NET/P (-0.713), GY/P (-0.531) and PL (-0.113) exhibited negative coefficient values (Table 3).

Trait-specific genotypic relationship through biplot

By calculating the angle of the trait vector from the origin, biplot analysis offers a visual comparison of genotypes and a correlation between traits depending on different traits. To display the locations of the variables, the coefficients of PC1 and PC2 were projected in two dimensions (Figure 2). The biplot revealed that the PC1 scores of Line 11, Binadhan-14, and Line 21 were entirely distinct from those of Line 22, Line 23, and Line 24 that were being evaluated in the field. Similarly, PC2 scores of Line 10, Line 25 and Nerica 10 were completely separated from those of Line 18 and Begunipata. These variations are due to the highest vector length (from the origin) of the trait DM followed by PL, DFF and GY/P, respectively.

Cluster Analysis

Cluster analysis was employed to evaluate the total genetic divergence resulting from a number of yield and yield contributing characteristics. Although genotypes from the same cluster performed similarly, they differed greatly from different cluster groups. Based on the magnitude of diversity, thirty-six rice genotypes were grouped into six clusters (Table 4). The distribution pattern showed that cluster III contained the fewest genotypes (3 genotypes), covering 8.33% of the total genotypes tested, while cluster I had the greatest number of genotypes (11 genotypes), covering 30.56% of the total genotypes studied. Nine genotypes and five genotypes, respectively, from clusters IV and II represented 25.00 and 13.89% of all genotypes examined. Four genotypes altogether from Clusters V and VI made up 11.10% of all the genotypes that were analyzed (Table 4).

Table 2: Estimation of genetic parameters of yield and yield contributing traits

Traits	PV (σ^2P)	GV (σ^2G)	PCV (%)	GCV (%)	h^2b (%)	GA	GA (%)
DFF	42.21	41.81	6.38	6.35	99.06	13.26	13.02
DM	30.00	29.62	3.97	3.95	98.75	11.14	8.08
NET/P	9.48	7.20	21.37	18.62	75.94	4.82	33.42
PH (cm)	93.12	78.51	12.89	11.84	84.31	16.76	22.39
PL (cm)	5.65	3.79	9.72	7.91	67.13	3.18	13.44
100-SW (g)	0.08	0.06	12.75	10.86	72.54	0.43	19.06
GY/P (g)	42.94	36.24	20.41	18.75	84.40	11.39	35.49

Here, DFF=days to first flowering, DM=days to maturity, NET/P=no. of effective tillers/plant, PH (cm)=plant height (cm), PL (cm)=panicle length (cm), 100-SW (g)=100-seed weight (g), GY/P (g)=grain yield/plant (g), GV=genotypic variances, PV=phenotypic variances, h^2b=heritability in broad sense, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, GA=genetic advance, GA %=genetic advance in percentage of mean

Table 3: Principal components (PCs) for seven morphological traits in thirty-six studied advanced lines of rice from principal component analysis (PCA)

Variable	PC1	PC2
DFF	0.418	0.220
DM	0.480	0.115
NET/P	0.116	-0.713
PH (cm)	0.394	0.129
PL (cm)	0.450	-0.113
100-SW (g)	0.333	0.345
GY/P (g)	0.336	-0.531
Eigen value	3.037	1.839
Proportion	0.434	0.263
Cumulative	0.434	0.697

Here, DFF=days to first flowering; DM=days to maturity; NET/P=no. of effective tillers/plant; PH=plant height (cm); PL=panicle length (cm); 100-SW=100-seed weight (g); and GY/P=grain yield/plant (g)

Dendrogram

The rice genotypes under study were categorized into six separate clusters according to the Dendrogram (Figure 3).The height of the Dendrogram indicates the order in which clusters are joined. The smaller the height of Dendrogram, the rows are more similar. The higher the height of Dendrogram indicates the higher the variations of the rows. Cluster V is the smallest in height and has only four genotypes which indicates lowest amount of variation with 76.64% similarity in this cluster. Cluster III and II show Dendrogram medium in height and have three and five different genotypes, respectively in each cluster which indicates very low amount of variation with 70.06 and 68.42% similarity, respectively in these clusters. Cluster IV is quite high in Dendrogram height and the rows are linked moderately to each other, also has nine different genotypes in the cluster which indicates moderate amount of variation with 60.57% similarity in this cluster. Cluster I is very high in Dendrogram height and the rows are linked highly to each other, also has eleven different genotypes in each cluster which indicates high amount of variation with 44.66% similarity in this cluster. Among all the six clusters, cluster VI is the highest one having four genotypes which indicates more variation with 40.58% similarity than other clusters.

Intra- and inter- cluster distances

Figure 4 displayed the intra-and inter-cluster distances between the six clusters and indicated the extent of group divergence. Clusters III and VI (38.42), III and V (29.59), IV and VI (28.14), I and VI (26.25), and II and III (25.97) were determined to have the highest inter-cluster distances. The optimum intra-cluster distance was found in cluster VI (18.33), followed by cluster I (11.85) and cluster III (9.23).

Table 4: Number, percentage and name of the genotypes of rice in different clusters for yield and yield contributing traits

Cluster number	Number of genotypes	Salient features	Percentage (%)	Name of genotypes
I	11	No specific salient feature was found	30.56	BRRI dhan28, BRRI dhan67, BRRI dhan89, Line 20, Line 19, Line 18, Line 17, Line 15, Line 4, Line 2 and Line 1
II	5	More effective tiller number/plant, maximum grain yield/plant	13.89	Binadhan-10, Black rice, Nerica 10, Line 25, Line 12 and Line 10
III	3	Early flowering, early maturing, less effective tiller number/plant, short plant height, short panicle length, minimum grain yield/plant	8.33	Binadhan-14, Begunipata and Line 11
IV	9	Minimum 100-seed weight	25.00	Binadhan-17, GR Line 1, EM Line 1, Line 16, Line 14, Line 12, Line 9, Line 8 and Line 3
V	4	Tall plant height	11.10	Line 13, Line 7, Line 6 and Line 5
VI	4	Late flowering, late maturing, long panicle length, maximum 100-seed weight	11.10	Line 24, Line 23, Line 22 and Line 21

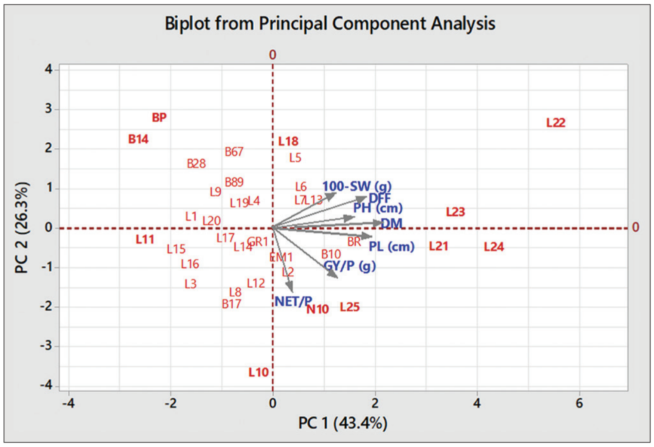

Figure 2: Biplot from principal component analysis of morphological traits of thirty six rice genotypes in the field. Here, DFF=days to first flowering, DM=days to maturity, NET/P=no. of effective tillers/plant, PH (cm)=plant height (cm), PL (cm)=panicle length (cm), 100-SW (g)=100-seed weight (g), GY/P (g)=grain yield/plant (g), B28=BRRI dhan28, B67=BRRI dhan67, B89=BRRI dhan89, B10=Binadhan-10, B14=Binadhan-14, B17=Binadhan-17, BP=Begunipata, BR=Black rice, GR1=GR Line 1, EM1=EM Line 1, N10=Nerica 10, L1=Line 1, L2=Line 2, L3=Line 3, L4=Line 4, L5=Line 5, L6=Line 6, L7=Line 7, L8=Line 8, L9=Line 9, L10=Line 10, L11=Line 11, L12=Line 12, L13=Line 13, L14=Line 14, L15=Line 15, L16=Line 16, L17=Line 17, L18=Line 18, L19=Line 19, 20=Line 20, L21=Line 21, L22=Line 22, L23=Line 23, L24=Line 24 and L25=Line 25, respectively

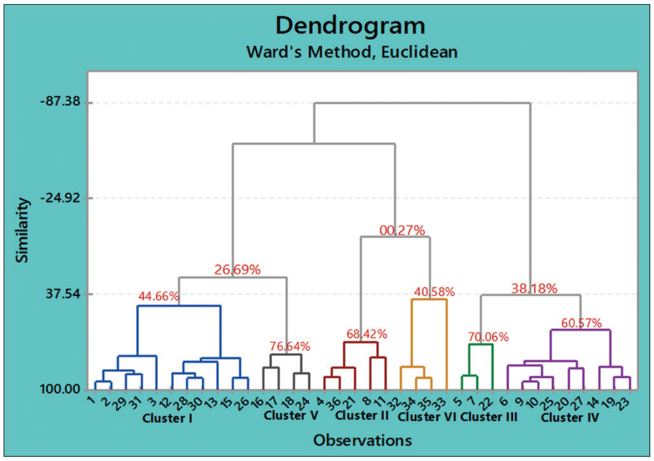

Figure 3: Dendrogram based on summarized data on differentiation among thirty six rice genotypes according to Ward's method. Here, 1=BRRI dhan28, 2=BRRI dhan67, 3=BRRI dhan89, 4=Binadhan-10, 5=Binadhan-14, 6=Binadhan-17, 7=Begunipata, 8=Black rice, 9=GR Line 1, 10=EM Line 1, 11=Nerica 10, 12=Line 1, 13=Line 2, 14=Line 3, 15=Line 4, 16=Line 5, 17=Line 6, 18=Line 7, 19=Line 8, 20=Line 9, 21=Line 10, 22=Line 11, 23=Line 12, 24=Line 13, 25=Line 14, 26=Line 15, 27=Line 16, 28=Line 17, 29=Line 18, 30=Line 19, 31=Line 20, 32=Line 21, 33=Line 22, 34=Line 23, 35=Line 24 and 36=Line 25, respectively

Characterization of individual cluster by cluster means

Table 5 displays the cluster mean for the examined attributes associated with the yield of the studied rice genotypes. All of the early flowering genotypes were grouped into cluster III (98 days), whereas all of the late flowering genotypes were found in cluster VI (112.92 days), according to the results of the cluster mean performance (Tables 4 and 5). Early maturing genotypes were assembled into cluster III (134.44 days) while cluster VI had late maturing (151.75 days) genotypes followed by the cluster V (137.42 days) (Tables 4 and 5). Considering NET/P, genotypes with less effective tillers (11.02) were assigned to cluster III, whereas genotypes with more effective tillers (17.99) were assigned to cluster II, then cluster IV (15.97) (Tables 4 and 5). In regarding to PH, tall genotypes (87.47 cm) were shown in cluster V, followed by cluster VI (85.43 cm), while short genotypes (58.97 cm) were put into cluster III (Tables 4 and 5). The shortest panicle produced by the studied genotypes was grouped into cluster III (20.97 cm) while genotypes having longest PL (28.45 cm) were included in cluster VI (Table 4 and 5). The maximum 100-SW was found in cluster VI (2.64 g) while cluster IV showed the minimum 100-SW (2.12 g) for this trait (Table 4 and 5). In case of GY/P (g), cluster II was comprised of genotypes with a higher GY/P of 40.84 g, whereas cluster III was made up of genotypes with a lower GY/P of 25.80 g (Tables 4 and 5).

Effect of Salt Stress at the Reproductive Stage on Yield and Yield-Attributing Traits

Analysis of variance for yield and yield attributing traits under salinity

When genotype (G), treatment (T), and G × T were taken into account, the findings of the analysis of variance showed extremely significant variation for all tested traits (Supplementary Table S3).

Days to maturity (DM)

Under control conditions, the average range of DM was 110.33 days to 98.33 days for the genotypes. Line 12 and Binadhan-23 have minimum and maximum requirements for the number of days to mature (98.33 days and 110.33 days, respectively). For most of the genotypes under investigation, DM was significantly reduced as a result of salt stress. The data indicated that Binadhan-23 had the largest decline (3.63%), whereas Line 12 had a noteworthy increase (5.08%) (Table 6).

No. of effective tillers/plant (NET/P)

The maximum NET/P value was observed in Binadhan-16 (13) and minimum number was found in Line 8 (7.33) under control condition. When compared to control, the NET/P was significantly lower after imposition salt stress. Line 12 had the biggest drop (37.95%) and Line 10 had the lowest drop (23.67%) (Table 6).

Plant height (PH)

Significant differences existed in PH between the genotypes that were being studied. Under the control treatment, Line 8 had the highest PH (91.22 cm), while Binadhan-23 had the lowest PH (64.77 cm).Comparing the infusion of salt stress to

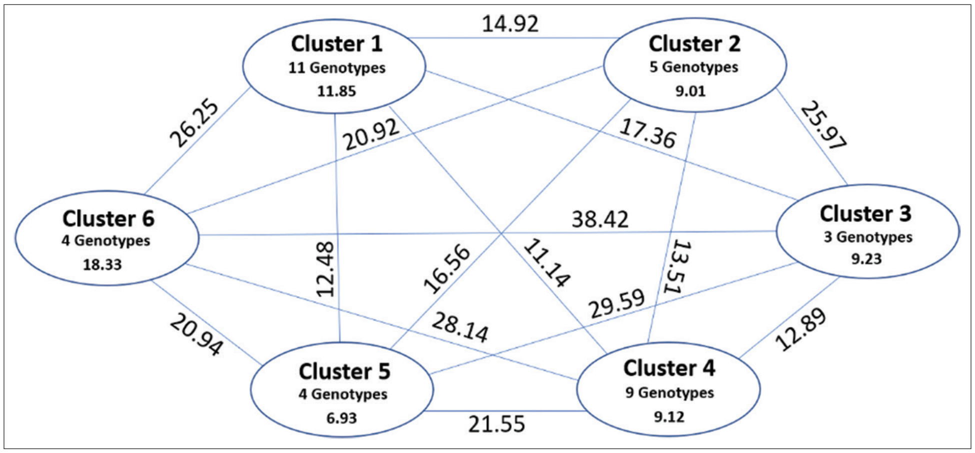

Figure 4: Thirty-six rice genotypes were divided into six clusters based on Euclidean values for the inter-and intra-cluster distances (D^2)

Table 5: Cluster mean values for seven characteristics associated with the studied rice genotypes

Traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
DFF	99.33	102.47	98.00	100.37	103.08	112.92
DM	136.09	135.93	134.44	136.26	137.42	151.75
NET/P	12.86	17.99	11.02	15.97	12.76	15.03
PH (cm)	75.76	77.94	58.97	67.06	87.47	85.43
PL (cm)	23.99	25.16	20.97	23.65	25.29	28.45
100-SW (g)	2.16	2.32	2.35	2.12	2.25	2.64
GY/P (g)	27.41	40.84	25.80	33.55	28.46	39.28

Here, DFF=days to first flowering, DM=days to maturity, NET/P=no. of effective tillers/plant, PH (cm)=plant height (cm), PL (cm)=panicle length (cm), 100-SW (g)=100-seed weight (g), GY/P (g)=grain yield/plant (g).

the control, the PH significantly decreased. Line 11 exhibited the largest reduction of 23.67%, whereas Binadhan-16 had a lowest decrease of 10.94% (Table 6).

Panicle length (PL)

Under both control and salt stress conditions, there was a notable degree of variation found in the PL genotypes. The highest PL under control condition was discovered in Line 12 (26.97 cm), whilst the lowest was recorded in Binadhan-16 (20.24 cm) under control condition. When rice plants were exposed to salt stress, their PL (cm) significantly decreased; Binadhan-23 showed the most drop (12.31%) followed by the lowest drop (3.60%) of Line 10 (Table 6).

No. of filled grains/panicle (NFG/P)

Line 8 (165.11) had the highest NFG/P under control, whereas Binadhan-23 (55.32) had the lowest. The NFG/P significantly increased as a result of salt stress. The highest damage is noted in Line 11 (70.02%) and Binadhan-2319.61%) had the lowest damage (Table 6).

No. of unfilled grains/panicle (NUG/P)

There was a notable difference in the NUG/P between the genotypes under both salt stress and control conditions. Binadhan-23 (6.03) had the lowest NUG/P, while Line 8 (55.57) had the most. In comparison to the control, salt stress caused a considerable induction of the NUG/P. The induction in Binadhan-23 was the greatest at 538.12% followed by the lowest induction (67.11%) of Line 8 (Table 6).

Spikelet fertility (SF%)

The SF (%) ranged from 74.50 to 91.24, indicating a notable variation. Under control conditions, Line 18 displayed the lowest value (74.50) for SF, while Binadhan-16 displayed the greatest value (91.24) for SF (%). SF (%) decreased significantly for all genotypes under study in response to salt stress. Line 11 had the highest reduction (68.68%) and Binadhan-23 had the lowest reduction (40.63%) (Table 6).

100-seed weight (100-SW)

The genotypes examined in this study showed a notable variance in 100-SW. On average, under the control condition, 100-SW was lowest in Line 10 (2.33 g) and highest in Binadhan-16 (2.56 g). Significant decrease in 100-SW was triggered by salt stress. The line that showed the maximum reduction was Binadhan-23 (21.58%) and Line 12 had the lowest reduction (5.71%) (Table 6).

Grain yield/panicle (GY/P)

A sharp variation was observed in GY/P among the advanced lines and varieties. Under control conditions, Binadhan-23 (1.33 g) had the lowest GY/P and Line 8 (3.88 g) had the highest. GY/P significantly decreased under salt stress across all genotypes; Line 8 had the largest decrease (73.84%), whereas the lowest decrease (36.96%) was recorded in Binadhan-23 (Table 6).

Principal Component Analysis (PCA)

Two principal components (PC) with Eigen values greater than unity were found by principal component analysis of all the morphological and biochemical parameters in the six rice genotypes under salt-stressed and unstressed conditions

Table 6: Mean performances of six rice genotypes based on different morphological traits related to yield grown under control and salt stress (10 dS/m) conditions at the reproductive stage

Genotype name	Treatment	DM	NET/P	PH (cm)	PL (cm)	NFG/P	NUG/P	SF (%)	100-SW (g)	GY/P (g)
Line 8	Control	106.33^{B}	7.33^{B-E}	91.22^{AB}	23.69^{B-D}	165.11^{A}	55.57^{D}	74.50^{B}	2.35^{AB}	3.88^{A}
	Salt	103.33^{C}	5.33^{E}	95.94^{A}	22.32^{C-E}	55.36^{DE}	92.87^{C}	37.29^{D}	1.85^{D}	1.02^{EF}
Line 10	Control	103.33^{C}	10.00^{AB}	90.53^{AB}	22.98^{B-D}	114.55^{BC}	37.96^{F}	75.10^{B}	2.33^{AB}	2.67^{B}
	Salt	102.33^{C}	7.67^{B-E}	72.39^{CD}	22.15^{DE}	58.55^{DE}	95.25^{B}	38.02^{D}	2.13^{BC}	1.25^{DE}
Line 11	Control	103.33^{C}	8.33^{B-E}	80.70^{BC}	21.57^{DE}	107.23^{C}	36.17^{F}	74.77^{B}	2.34^{AB}	2.51^{B}
	Salt	101.67^{C}	6.33^{C-E}	61.59^{DE}	20.30^{E}	32.15^{E}	104.60^{A}	23.42^{E}	2.05^{CD}	0.66^{G}
Line 12	Control	98.33^{D}	9.67^{A-C}	89.65^{AB}	26.97^{A}	152.60^{AB}	30.38^{G}	83.19^{AB}	2.45^{A}	3.74^{A}
	Salt	103.33^{C}	6.00^{DE}	71.32^{CD}	24.85^{A-C}	55.25^{DE}	91.05^{C}	37.76^{D}	2.31^{AB}	1.28^{DE}
Binadhan-16	Control	106.33^{B}	13.00^{A}	68.69^{CD}	20.24^{E}	79.12^{CD}	7.50^{H}	91.24^{A}	2.56^{A}	2.03^{C}
	Salt	103.33^{C}	9.00^{B-D}	61.18^{DE}	21.88^{DE}	36.89^{DE}	39.62^{E}	47.22^{CD}	2.40^{A}	0.89^{FG}
Binadhan-23	Control	110.33^{A}	9.33^{B-D}	64.77^{DE}	25.17^{AB}	55.32^{DE}	6.03^{H}	89.35^{A}	2.41^{A}	1.33^{D}
	Salt	106.33^{B}	6.67^{B-E}	54.86^{E}	22.07^{DE}	44.47^{DE}	38.50^{E}	53.05^{C}	1.89^{CD}	0.84^{FG}

Different letters in the same column show significant difference at 5% level of probability following Tukey's method. Here, DM=days to maturity, NET/P=no. of effective tillers/plant, PH (cm)=plant height (cm), PL (cm)=panicle length (cm), NFG/P=no. of filled grains/panicle, NUG/P=no. of unfilled grains/panicle, SF (%)=spikelet fertility (%), 100-SW (g)=100-seed weight (g), GY/P (g)=grain yield/panicle (g)

(Table 7). Of the overall variation in the datasets, PC1 and PC2 were taken into account 72.4%. The greater contributions of SF% (0.453), GY/P (g) (0.414), NFG/P (0.389), 100-SW (g) (0.368), NET/P (0.327), PL (cm) (0.221), PH (cm) (0.208), DM (0.057) towards the positive direction, and NUG/P (-0.367) towards the negative direction are responsible for 46.8% of the total variation, which was explained by PC1 (Table 7 and Figure 5). The larger negative loading of PH (-0.488) and higher positive loadings of DM (0.440), NET/P (0.323), 100-SW (g) (0.180), and SF (%) (0.174) were the primary respondents to the second component, which explained 25.6% of the overall variation (Table 7 and Figure 5).

Table 7: Principal components (PCs) for nine morphological traits in six rice genotypes from principal component analysis (PCA)

Variable	PC1	PC2
DM	0.057	0.440
NET/P	0.327	0.323
PH (cm)	0.208	-0.488
PL (cm)	0.221	-0.256
NFG/P	0.389	-0.337
NUG/P	-0.367	-0.368
SF (%)	0.453	0.174
100-Sw (g)	0.368	0.180
GY/P (g)	0.414	-0.293
Eigen value	4.211	2.303
Proportion	0.468	0.256
Cumulative	0.468	0.724

Here, DM=days to maturity, NET/P=no. of effective tillers/plant, PH (cm)=plant height (cm), PL (cm)=panicle length (cm), NFG/P=no. of filled grains/panicle, NUG/P=no. of unfilled grains/panicle, SF (%)=spikelet fertility (%), 100-SW (g)=100-seed weight (g), GY/P (g)=grain yield/panicle (g)

Trait-specific genotypic relationship through biplot

The positions of the variables were displayed via the two-dimensional projection of PC1 and PC2 coefficients (Figure 5). The biplot revealed a perfect separation between the PC1 scores of Line 11 under the salt stress treatment and those of Line 12 under the control treatment. A larger negative coefficient of the traits: NUG/P compared to the positive coefficients of the traits of SF (%), GY/P (g), NFG/P, 100-SW (g), NET/P, PL (cm), PH (cm), and DM, respectively, was the cause of the variation between Line 11 under salinity treatment and Line 12 under control condition (Figure 5). Similar to how the PC2 scores of Line 12 under control completely separated from those of Binadhan-23 under control treatments, this difference was caused by higher positive coefficients of the traits DM, NET/P, 100-SW (g), and SF (%) in comparison to higher negative coefficients of the traits PH (cm), NUG/P, NFG/P, GY/P (g), and PL (cm), respectively.

Stress Tolerance Indices

Stress tolerance indices, including MP, GMP, SSI, TOL, STI, and YSI, were computed based on the grain yield per panicle and are displayed in Table 8. Considering the performance of the genotypes under both normal and salt-stressed circumstances, these selection criteria are recommended for genotype selection, accounting for plant production. Line 12 recorded the maximum MP (2.51) and Binadhan-23 had the lowest MP (1.09) (Table 8). The genotype Line-12 (2.19) yielded the highest GMP, and it was preceded by Binadhan-23 (1.06) (Table 8). Line 8 showed the highest SSI (1.17) value whereas the lowest SSI (0.58) value of Binadhan-23 (Table 8). Advanced Line 8 had the highest TOL value (5.31) and Binadhan-23 had the lowest value (0.49) (Table 8). Line 12 showed the maximum STI (0.66) value whereas the minimum STI value (0.15) was recorded in Binadhan-23 (Table 8). Binadhan-23 had the highest YSI (0.63), however, the lowest YSI (0.26) was recorded in Line 8 and Line 11 (Table 8).

DISCUSSION

Mean Performances for Yield and Yield Contributing Traits of Thirty-six Advanced Lines

One of the top priorities for sustainable rice production in Bangladesh's flood-prone lowland areas is the introduction of early maturing rice varieties, which would boost cropping intensity and safeguard rice fields from natural disasters

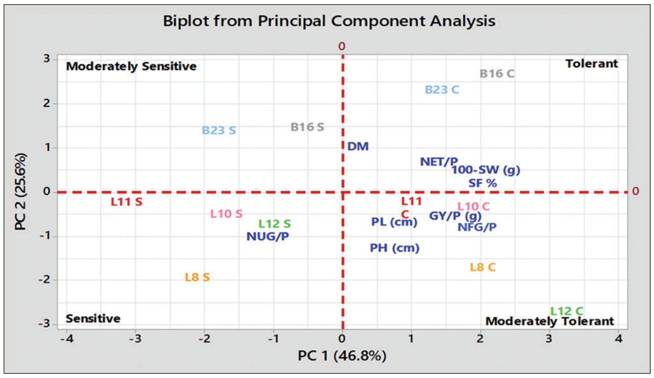

Figure 5: Biplot from principal component analysis of morphological traits of six rice varieties under control and salt stress (10 dS/m) condition at the reproductive stage. Here, DM=days to maturity; NET/P=no. of effective tillers/plant; PH (cm)=plant height (cm); PL (cm)=panicle length (cm); NFG/P=no. of filled grains/panicle; NUG/P=no. of unfilled grains/panicle; SF (%)=spikelet fertility (%); 100-SW (g)=100-seed weight (g); and GY/P (g)=grain yield/panicle (g); B16=Binadhan-16; B23=Binadhan-23; L8=Line 8; L10=Line 10; L11=Line 11; L12=Line 12. 'C' and 'S' indicate treatment under control and salt stress (10 dS/m) conditions, respectively

Table 8: Stress tolerance indices in six rice genotypes, estimated from grain yield/panicle obtained in control and salt stress (10 dS/m) condition

Genotype name	MP	GMP	SSI	TOL	STI	YSI
Line 8	2.45	1.99	1.17	2.87	0.54	0.26
Line 10	1.96	1.83	0.84	1.42	0.46	0.47
Line 11	1.59	1.29	1.16	1.85	0.23	0.26
Line 12	2.51	2.19	1.04	2.46	0.66	0.34
Binadhan-16	1.46	1.34	0.89	1.14	0.25	0.44
Binadhan-23	1.09	1.06	0.58	0.49	0.15	0.63

Here, MP=mean productivity, GMP=geometric mean productivity, SSI=stress Susceptibility Index, TOL=tolerance Index, STI=stress tolerance index and YSI=yield stability index

(Chowdhury *et al.*, 2023). To assess the field performance of the chosen advanced lines, parents, check varieties, and mutant lines, the study selected seven quantitative traits. A substantial ($p<0.001$) difference was found using analysis of variance between the parents, check varieties, and mutant lines and the chosen advanced lines. Of the studied advanced rice lines, advanced Line 15 was the early flowering genotype, followed by advanced Line 1, Line 3, Line 4, Line 11 and Line 22 (Table 1). One trait that is thought to be beneficial for rice improvement is early flowering, which denotes a short life cycle (Oladosu *et al.*, 2014). In addition, advanced Line 12 and Nerica 10 were the most early maturing genotypes whereas Line 12 required approximately less than one week to mature contrast to parent Binadhan-10 as well as other released varieties (Table 1).

A significant feature linked to higher production is the number of effective tillers per plant. In comparison to the parents, nearly all advanced lines had moderate NET/P, which indicated an insignificant rise or decrease. Advanced Line 8, Line 10, Line 21, Line 22, Line 23, Line 24 and Line 25, respectively showed higher to moderate NET/P as well as they resulted into higher yields (Table 1). Recent theories on rice ideotype breeding predict that modest NET/P will result in higher yields since high tiller counts lead to tiller abortions, low grain filling percentages, and eventually low yields (Chowdhury *et al.*, 2023). Because it has a direct impact on how well carbon assimilation is used to enhance plant products, PH is important in rice breeding. Most high-yielding genotypes in the current study have low to medium PH.

Panicle length, which is connected with the quantity of grains per panicle, is also positively correlated with grain yield (Chowdhury *et al.*, 2023). In the current investigation, Line 21, Line 23, Line 24 and Line 25 contributed to higher yield for having long PL (Table 1).The final yield per unit area is largely influenced by the weight of 100 seeds. Advanced Line 18, Line 21, Line 22, Line 23, Line 24, Binadhan-10 and Begunipata showed a similar trend towards higher yield based on 100-SW(Table 1). The total yield is the result of the sum of the contributions made by each panicle grain yield and each plant's individual yield (Oladosu *et al.*, 2014). Therefore, a significant selection criterion for the total GY might be effectively employed to measure high yield per plant. GY was an outcome of numerous characters interacting with one another. The genetic divergence in the material emerged by the variation in each character's yield-related contribution. Line 10 became the early matured high yielding advanced line considering highest NET/P. On the other hand, advanced Line 21, Line 22, Line 23, Line 24, and Line 25 were the high yielding group (39.00, 37.82, 39.43, 40.85 and 42.65 g/plant, respectively) influenced by the yield increasing parameters *viz.*, NET/P, PH, PL and 100-SW(Table 1). The results agreed with the findings of the others (Oladosu *et al.*, 2014; Andrew-Peter-Leon *et al.*, 2021; Chowdhury *et al.*, 2023).

Genetic Parameters

Plant breeders use a large number of resources to select the most desired lines based on a large range of variation. The variance study's findings showed that the phenotypic variance consistently outweighed the genotypic variance, indicating the effects of the environment on these traits (Table 2). It is clear that the genotypes themselves, with a minor influence from the environment, are the primary determinants of character expression. Additionally, these results were supported by the results of Chowdhury *et al.* (2023). It may be possible for selection to enhance attributes with higher PCV and GCV. As might be predicted, PCV was marginally greater than GCV for each attribute. A small difference between PCV and GCV indicates that all qualities are not highly expressed in the environment (Chowdhury *et al.*, 2023). According to Deshmukh *et al.* (1986) and Takele *et al.* (2022), PCV and GCV were primarily classified as high >20%, medium 10-20%, and low<10%. According to this classification, high PCV estimates were noted for NET/P and GY/P, respectively suggested that genetic control influenced these characteristics. The degree of environmental influences can be inferred from the extent of the variations between GCV and PCV. Greater genetic influence is indicated by smaller differences, while larger differences suggest that environmental influences play a significant role in trait variation. Traits such as DFF, DM, PH, and GY/P show slight variations between PCV and GCV, indicating that these traits are more genetically determined and less impacted by environmental variables. This suggests that rather than environmental factors, genetic variations among the individuals under study are primarily responsible for the observed variability in these qualities.

Three groups are identified by heritability *viz.*, highly heritable (>60%), medium heritable (60-30%), and low heritable (<30%) (Robinson *et al.*, 1949; Takele *et al.*, 2022). Although a high heritability does not always imply a high GA for a given trait, it does show how well phenotypic features are selected for. However, selective processes would be more useful and successful if heritability values and genetic advancements were combined (Chowdhury *et al.*, 2023). The study's estimated h^2b magnitude ranged from 67.13% for PL to 99.06% for DFF. Since additive gene expression frequently causes genetic variance, the high heritability of all the variables examined in this study indicates that future breeding programs can expect these characters to improve and benefit from selection more than other characters.

According to Kaul and Garg (1982), GA for a particular trait is an indication for the expected genetic progress under the suitable selection procedure. GA% is divided into three categories as low, moderate, and high, corresponding to values of < 10%, 10-20%, and > 20%, respectively (Johnson *et al.*, 1955; Takele *et al.*, 2022). For GY/P (h^2b=84.40, GAM=35.49), NET/P (h^2b=75.94, GAM=33.42) and PH (h^2b=84.31, GAM=22.39), there was a high GA% and heritability. It suggests that there is a greater chance to enhance certain features through natural selection and highlights the significance additive genes play in expressing these traits. On the contrary, DFF, DM, PL, and 100-SW showed non-additive genetic effects and an insufficient range to advance such traits through a straightforward selection procedure due to high heritability with low GA%. So, estimating the subsequent impact of selection upon choosing the greatest individual would be more feasible with heritability estimates combined with GA than with heritability alone (Johnson *et al.*, 1955). However, selecting progeny through hybridization can be a successful process (Chowdhury *et al.*, 2023).

Principal Component Analysis

Using PCA analysis to assess morphological variation across several crops revealed genetic relationships among genotypes. Every coefficient of proper vectors in PCA indicates the extent to which each original variable contributes to the overall variance, making it useful for measuring the independent effects of a given feature (Sanni *et al.*, 2012). The present investigation identified two PCs that accounted for 69.70% of the variance overall. The first component, which mostly explained variation in DFF, DM, NET/P, PH, PL, 100-SW, and GY/P, respectively was responsible for 43.40% of the variation overall. Meanwhile, 26.30% of the variability was attributed to the second component, which primarily affected DFF, DM, PH, and 100-SW (Table 3). The bulk of the heterogeneity observed in rice germplasm collections was also explained by two PCs, according to Maji and Shaibu (2012). Comparable results were reported earlier by Chowdhury *et al.* (2023).

Biplots were a great way to visualize qualities in connection to one another, show how different traits relate to one another, and choose genotypes or combinations of genotypes that could be presented as the most advantageous ones (Peterson *et al.*, 2005). Based on the PCA biplot, it was found that the variables DFF, DM, PL, and GY/P, as well as the genotypes advanced Line 10, Line 11, Line 18, Line 21, Line 22, Line 23, Line 24, and Line 25, were distributed and distant from the source, with substantial genetic variability between the PC1 and PC2 (Figure 2). As determined by measuring the acute angle between these qualities, the attributes GY/P demonstrated strong positive associations with the traits NET/P and PL. The outcomes supported the conclusions of Sharma *et al.* (2016) and Khan *et al.* (2023), who reported that genotypes and characteristics closer to the origin and one another indicated a minimal amount of divergence.

Estimation of Nature and Magnitude of Genetic Diversity for Yield Attributing Traits

Genetic diversity has been considered as an important factor in all breeding programs. To create high-yielding progenies through hybridization, genetic diversity is also a necessary initial requirement. Different genotypes in a population can be classified and distinguished from one another using divergent genetic study between genotypes of rice determined on physical characteristics (Franco *et al.*, 2001). This genetic divergence investigation is also necessary to choose a range of genotypes in order to enhance rice varieties through breeding (Shahidullah *et al.*, 2010). Therefore, using seven morphological features, thirty-six rice genotypes were successfully grouped into six groups for improved handling of the heterogeneous genotype and greater heterotic vigor in the progeny that follow crossing due to improved selection (Table 4). This study demonstrated how well morphological or quantitative traits can classify genotypes of rice. Cluster V showed highest similarity followed by cluster III, cluster II, cluster IV, cluster I and cluster VI, respectively. Highest similarity leads to less variation whereas less similarity leads to high variation. Cluster VI, cluster II and cluster III can be beneficial for selecting breeding lines having early flowering and maturity, long panicle, high 100-SW, high NET, and high GY/P (Figure 3).

The average distances between clusters were found to be larger than the average distances within clusters, suggesting that there may be more genetic variation among the 36 rice genotypes (Figure 4) (Debata *et al.*, 2020; Mondal *et al.*, 2024). Increased inter and intra-cluster distances are positively correlated with increased genotype variability both inside and within the clusters, respectively (Sheeba *et al.*, 2023). In order to realize greater genetic advance, selection of genotypes with a high degree of divergence belonging to clusters VI, I, and III (Figure 4) would synthesize more desirable segregants in recombination breeding program (Sheeba *et al.*, 2023). However, cluster V (6.93) exhibited the least intra-cluster distance, suggesting that constant selection may have led to homogeneity and reduced genotype variation (Rajesh *et al.*, 2010; Mandavi *et al.*, 2023). The genotypes with the greatest genetic distance between clusters III and VI (Figure 4) would cross to produce maximum heterosis (Khodadadi *et al.*, 2011; Mondal *et al.*, 2024). Combining the superior genotypes of the aforementioned different cluster pairs for example, Binadhan-14, Begunipata, and Line 11 from cluster III with Line 24, Line 23, Line 22, and Line 21 from cluster VII may result in attractive transgressive segregants that can be used to create high-yielding rice varieties (Sheeba *et al.*, 2023). On the other hand, clusters I and IV have the smallest inter-cluster distance (11.14), suggesting a close interaction between them that would prevent these clusters from producing the expected outcomes (Mandavi *et al.*, 2023). In a future breeding program, highly correlated qualities may be used to choose genotypes from various clusters as parents (Nisar *et al.*, 2017).

The superiority of the cluster was evaluated by computing the cluster-wise mean values of seven distinct features, which may be taken into consideration for improving different characters. Cluster II and cluster VI were better suited for selecting high yielding advanced lines comprising more NET/P, long PL, maximum 100-SW and maximum GY/P because of the high cluster mean values for that traits. Clusters III was important for the selection of early maturing advanced lines since its cluster mean values were high for DM (Table 5). The outcomes of this inquiry were consistent with the findings of the previous research (Palaniyappan *et al.*, 2020). Hence, for the improvement of these characters *viz.*, DM and GY/P, genotypes from cluster II, cluster III and cluster IV could serve as a potential source of resources.

Effect of Salt Stress on Yield and Yield-Attributing Traits at the Reproductive Stage

Plant morphology, physiology, and biochemistry are all negatively impacted by the complex process of salinity stress (Dustgeer *et al.*, 2021; Sultan *et al.*, 2021).From seed germination to flowering and fruiting settings, salt's effects resulted in significant yield losses. These included reductions in plant height, biomass, productive tiller number, grain yield, filled grain per panicle, grain weight, grain quality, harvest index, and photosynthetic activity. Additionally, salt increased the uptake of Na^+ and Cl^- to the shoot (El Sabagh *et al.*, 2021; Alkahtani & Dwiningsih, 2023). Osmotic and ionic stress are brought on by salt stress, and it also increases the generation of reactive oxygen species (ROS), which harm important components including DNA, proteins, and cellular membranes (Hassan *et al.*, 2020, 2021; Hossain *et al.*, 2021; Sultan *et al.*, 2021; Batool *et al.*, 2022). Osmotic and ionic stress are brought on by salt stress, and it also increases the generation of ROS, which harm important components including DNA, proteins, and cellular membranes (Chen *et al.*, 2021; Singh *et al.*, 2021; Yao *et al.*, 2022). In our investigation, we found that when salt stress was applied, yield-related features such as DM, NET/P, PH, PL, NFG/P, SF%, 100-SW, and GY/P greatly decreased while NUG/P significantly increased (Table 6). Others have also documented similar trends in yield and yield-attributing characteristics in rice in response to salt stress (Vispo *et al.*, 2015; Ahmadizadeh *et al.*, 2016; Gerona *et al.*, 2019; Khatun *et al.*, 2024). There are several possible reasons for the production decrease, including excessive Na^+ and Cl^- accumulation in floral parts, disruptions to pollen and stigma, and insufficient nutrients and glucose translocation to the panicles (Hussain *et al.*, 2017). Binadhan-23 had the lowest reduction (36.96%) in GY/P followed by Line 10. In our study, Line 10 showed less reduction for GY/P, DM, NET/P, PL and SF (%) under salt stress among the studied genotypes which recognized it as an early maturing salt tolerant high yielding line. Similarly, Line 12 recognized as salt tolerant high yielding line demonstrating less reduction in NFG/P, 100-SW, GY/P. The phenological characteristics of the rice plants' panicles under controlled and salt stress conditions align well with the qualities that contribute to yield (Figure 6). Panicle sterility is considered to be of great concern impacting head rice rate and chalkiness under salt stress throughout the rice reproductive stage (Razzaq *et al.*, 2020; Xiao *et al.*, 2022; Yao *et al.*, 2022).

Principal Component Analysis

Modern data analysis relies heavily on PCA, which is typically used to examine the relative contributions of various features and their dissemination patterns within a population's observed variance. This scenario involved the selection of a criterion to determine the minimum acceptable limit for the parameters of the relevant vectors. The overall variance observed was found to be significantly influenced by traits whose coefficient value was larger than 0.3, but traits whose value was less than 0.3 were not considered to have significant effects. In contrast to SF (%), GY/P (g), NFG/P, 100-SW (g), and NET/P were the most significant variables responsible for the variation whereas PC1 was inversely linked with NUG/P, according to PCA analysis (Table 7). According to the findings, in saline conditions, plants with higher NUG/P have lower SF (%), GY/P (g), and 100-SW (g). Rahman *et al.* (2020) discovered that PC1 had a positive association with GY/P (g), SF (%), NFG/P, DM, and 100-SW (g), and a negative correlation with NUG/P. The positive and negative values of the characteristics were also used to

Figure 6: Phenological appearances of mature panicles after imposition of salt stress (10 dS/m) at the reproductive stage. Here, L8=Line 8, L10=Line 10, L11=Line 11, L12=Line 12, B16=Binadhan-16 and B23=Binadhan-23

distinguish the genotypes in PC2. Negative numbers simply reveal the direction of the link between the component and the variable. So, In PC2, the negative direction of variation was better explained by greater values of PH and NUG/P. Khatun *et al.* (2024) also reported similar tendencies in their data.

It's interesting to note that in our analysis, the PC1 successfully distinguished between the stressed and non-stressed samples. The non-stressed samples with the tolerant check Binadhan-23 and the susceptible check Binadhan-16 were positioned in the same biplot quadrant at the furthest distance from one another (Figure 5). The genotypes in the upper-right corner of the biplot were considered to be highly salinity tolerant genotypes because they displayed the greatest values for the positively linked characteristics for PC1 and PC2. The genotypes situated in the upper left and lower right corners of the graph, corresponding to moderate values for PC1 and PC2, were classified as moderately sensitive to salt and moderately tolerant to salt, respectively. On the contrary, genotypes classified as salt sensitive are those with low values of positively linked features, which are located in the lower left quadrant of the biplot. With the use of 74 rice genotypes, Kakar *et al.* (2019) also classified similar four primary groupings. For both stressed and non-stressed samples, the advanced Line 10 and Line 12, which demonstrated a respectable level of salt tolerance as well as early maturity, were positioned in line with the resistant check Binadhan-23 and the early maturing check Binadhan-16 in the corresponding quadrant of the biplot (Figure 5). Khatun *et al.* (2024) also observed similar findings. Line 12 and Line 10 would be therefore classified as highly salt tolerant genotypes. This result aligned with the findings of the study carried out by Rahman *et al.* (2020).

Stress Tolerance Indices in Rice Genotypes Estimated from Grain Yield/Panicle

In line with the morphological and biochemical characteristics that confer salt tolerance in rice, stress tolerance indices effectively distinguished between tolerant and sensitive cultivars. Stress tolerance indices SSI, TOL, STI and YSI values estimated from GY/P and which ranges of 0.58-1.17; 0.49-2.87; 0.15-0.66; and 0.26-0.63, respectively (Table 8). Girma *et al.* (2017) used 15 rice genotypes produced under stress and non-stress settings to find similar ranges. Line 12 had the highest values for STI and YSI in both the stress and control conditions based on the stress tolerance indices. Line 10 showed the maximum values for STI and YSI and the minimal values for SSI and TOL in both stressed and non-stressed conditions (Table 8). According to Khan and Kabir (2014) and Krishnamurthy *et al.* (2016), among the stress tolerance markers, a smaller value of TOL and SSI for a particular genotype suggests that the genotype is more stable under stress and in non-stressful conditions. Selection procedures favor genotypes that have high yield under stressors. On the other hand, in comparison to genotypes with lower values (Rosielle & Hamblin, 1981; Bouslama & Schapaugh, 1984; Anshori *et al.*, 2018), bigger values of STI and YSI indicate a genotype that is comparatively more resistant to salt stress (Girma *et al.*, 2017). Therefore, among the studied advanced lines, Line 10 and Line 12 were recognized as the most tolerant and high-yielding rice lines under control and salt stress condition. Further molecular study could be required through the effective evaluation of these genotypes. The outcomes completely matched those of and Rahman *et al.* (2020) and Khatun *et al.* (2024).

CONCLUSION

Among the selected advanced lines, Line 10 performed as an early-maturing and high-yielding line maintaining higher DM, GY/P and NET/P whereas advanced Line 21, Line 22, Line 23, Line 24, and Line 25 also performed as high-yielding lines for their higher GY/P accompanying high PH, high PL and maximum 100-SW. The current study found that the characteristics GY/P, NET/P, and PH had significant heritability and GA%, respectively. Therefore these traits can be enhanced by using straightforward or progeny selection techniques. Two PCs explained 69.70% of the total variation where GY/P showed positive association with DFF, DM, NET/P, PH, PL and 100-SW, respectively. Advanced Line 10, Line 11, Line 18, Line 21, Line 22, Line 23, Line 24, Line 25 and Nerica 10, Begunipata, Binadhan-14, respectively showed greatest variability for the significant influences of the evaluated traits. Cluster II and cluster VI were better suited for selecting high yielding advanced lines comprising more NET/P, long PL, maximum 100-SW and maximum GY/P whereas considering the maturity duration, cluster III was better as compared to other clusters. Hybridization between the superior genotypes of cluster III such as Binadhan-14, Begunipata, Line 11 and the genotypes of cluster VII such as Line 24, Line 23, Line 22, and Line 21 may provide desirable transgressive segregants for higher grain yield.

Salinity caused a considerable loss in yield and yield-related traits (*viz.*, DM, NET/P, PH, PL, NFG/P, SF (%), 100-SW, and GY/P), although salt intrusion circumstances produced a notable increase in NUG/P. Hence, Line 10, Line 12 performed as early maturing salt tolerant lines for their considerable less reduction in yield attributing traits. PC1 and PC2 accounted for 46.8 and 25.6% of the overall variation, respectively, whereas PCA explained 72.4% of the variation. For both stressed and unstressed samples, Line 10 and Line 12, which demonstrated a respectable level of salt tolerance as well as early maturity, were positioned according to the resistant check Binadhan-23 and the early maturing check Binadhan-16 in the corresponding quadrant of the biplot. The SSI and TOL stress tolerance indices demonstrated higher values for the sensitive genotype Line 8, but the YSI and STI indices demonstrated higher values for the tolerant genotypes, Line 10 and Line 12. In light of all the characteristics, Line 10 and Line 12 represent the ideal advanced rice lines for the selection of a subsequent breeding program aimed at developing them into early maturing, high-yielding and salt-tolerant rice types. Additional molecular research ought to be carried out to isolate the gene(s) or QTLs conferring higher yield and salinity stress tolerance.

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SUPPLEMENTARY TABLES

Table S1: A list of plant materials used for this study

S. No.	Name of the genotypes/varieties	Salient features	Source
1	BRRI dhan28	High-yielding and early maturing variety	BRRI
2	BRRI dhan67	High-yielding and salt tolerant variety	BRRI
3	BRRI dhan89	High-yielding variety	BRRI
4	Binadhan-10	Salt tolerant variety	BINA
5	Binadhan-14	Potential high-yielding and early maturing variety	BINA
6	Binadhan-17	High-yielding drought tolerant variety	BINA
7	Begunipata	Purple colored leaf	GPB, BAU
8	Black rice	Seed coat black in color	GPB, BAU
9	GR Line 1	Advanced mutant line developed through gamma irradiation	GPB, BAU
10	EM Line 1	Advanced mutant line developed through EMS mutagenesis	GPB, BAU
11	Nerica 10	Drought tolerant line	BRRI
12	Line 1	Advanced line selected for earliness	GPB, BAU
13	Line 2	Advanced line selected for earliness	GPB, BAU
14	Line 3	Advanced line selected for earliness	GPB, BAU
15	Line 4	Advanced line selected for earliness	GPB, BAU
16	Line 5	Advanced line selected for earliness	GPB, BAU
17	Line 6	Advanced line selected for earliness	GPB, BAU
18	Line 7	Advanced line selected for earliness	GPB, BAU
19	Line 8	Advanced line selected for earliness	GPB, BAU
20	Line 9	Advanced line selected for earliness	GPB, BAU
21	Line 10	Advanced line selected for earliness	GPB, BAU
22	Line 11	Advanced line selected for earliness	GPB, BAU
23	Line 12	Advanced line selected for earliness	GPB, BAU
24	Line 13	Advanced line selected for earliness	GPB, BAU
25	Line 14	Advanced line selected for earliness	GPB, BAU
26	Line 15	Advanced line selected for earliness	GPB, BAU
27	Line 16	Advanced line selected for earliness	GPB, BAU
28	Line 17	Advanced line selected for earliness	GPB, BAU
29	Line 18	Advanced line selected for earliness	GPB, BAU
30	Line 19	Advanced line selected for earliness	GPB, BAU
31	Line 20	Advanced line selected for earliness	GPB, BAU
32	Line 21	Advanced line selected for higher yield	GPB, BAU
33	Line 22	Advanced line selected for higher yield	GPB, BAU
34	Line 23	Advanced line selected for higher yield	GPB, BAU
35	Line 24	Advanced line selected for higher yield	GPB, BAU
36	Line 25	Advanced line selected for higher yield	GPB, BAU

Table S2: Analysis of variance for yield and yield contributing traits of the thirty six genotypes of rice in the field

Source of Variation	DFF	DM	NET/P	PH (cm)	PL (cm)	100-SW (g)	GY/P (g)
Replication (R)	0.176	0.528	1.68	11.39	0.125	0.005	10.05
Genotype (G)	125.84***	89.25***	23.89***	250.14***	13.23***	0.202***	115.41***
Error	0.395	0.375	2.28	14.61	1.85	0.023	6.70

*, ** and *** indicate that values are significant at 5%, 1% and 0.1% level of probability, respectively. Here, DFF=days to first flowering, DM=days to maturity, NET/P=no. of effective tillers/plant, PH (cm)=plant height (cm), PL (cm)=panicle length (cm), 100-SW (g)=100-seed weight (g), GY/P (g)=grain yield/plant (g)

Table S3: Analysis of variance (ANOVA) for morphological characters of six rice genotypes grown under control and salt stress (10 dS/m) conditions at the reproductive stage

Source of Variation	DM	NET/P	PH (cm)	PL (cm)	NFG/P	NUG/P	SF (%)	100-SW (g)	GY/P (g)
Replication	0.028	0.528	38.71	0.125	215.50	0.300	17.30	0.004	0.028
Genotype (G)	40.56***	15.18***	915.94***	20.32***	3629.40***	3371.60***	433.30***	0.128***	1.94***
Treatment (T)	14.69***	69.44***	1165.42***	12.42***	38263.70***	20783.10***	15837.90***	0.815***	26.17***
G x T	15.89***	1.11^{NS}	128.95***	3.81**	2003.80***	382.30***	56.70**	0.042**	1.14***
Error	0.360	1.47	19.73	0.830	217.90	0.500	15.60	0.008	0.009

*, **, *** and NS indicate that values are significant at 5%, 1%, 0.1% level of probability and non-significant, respectively. Here, DM=days to maturity, NET/P=no. of effective tillers/plant, PH (cm)=plant height (cm), PL (cm)=panicle length (cm), NFG/P=no. of filled grains/panicle, NUG/P=no. of unfilled grains/panicle, SF (%)=spikelet fertility (%), 100-SW (g)=100-seed weight (g), and GY/P (g)=grain yield/panicle (g), respectively