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Correlation analysis of polygenic traits of rice under salinity stress

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Abstract

Salinity is a major issue affecting rice production. To address this emerging issue, an experiment was conducted using a Completely Randomized Design (CRD) with three replicates under three salt treatments: 1.2 dS/m, 8 dS/m, and 12 dS/m Data were recorded for the traits like plant height (PH), tiller per plant (TPP), panicle length (PL), total spike length (TSL), grain per panicle (GPP), days to flowering (DTF), 1000 grain weight (TGW), root length (RL), root dry weight (RDW), and shoot dry weight (SDW). Recorded data was subjected to Analysis of Variances (ANOVA) study which shows that a significant amount of variation was present among the recorded data. A correlation study also revealed that grain per panicle showed a significantly positive correlation with thousand grain weight (0.79**), panicle length (0.29**), tiller per plant (0.30**), root length (0.21**) while it showed negatively significant correlation root dry weight (-0.42**) under normal condition. Under salinity condition (T1) grain per panicle showed a significantly positive correlation day to flowering (0.63**), thousand grain weight (0.85**), panicle length (0.33**), tiller per plant (0.33**), shoot dry weight (0.50**) with it showed negatively significant correlation with root dry weight (-0.48**). Under salinity level (T2) grain per panicle showed passively significant correlation with panicle length (0.32**), tiller per plant (0.34**), root length (0.36**) indicating potential pathways for improving yield in rice. The G10 (NIAB IRRI-9), G5 (PAK-386) and G13 (KSK-434) were found to be salt tolerant genotypes because they performed better for most of the traits under study while G4 (KISSAN BASMATI), G15 (PAK 2021) and G25 (K-134) were found to be salt susceptible genotypes as they performed significantly poor for most of study traits. The best performing germplasm under salt stress can be a desirable genotype for future breeding programs and early selection criteria for generating high yielding according to the findings.

Keywords: Breeding program, Food, Polygenic traits, Rice genotypes, Salinity stress

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Introduction

It is predicted that by 2028, the global population will reach 8.0 billion. To feed this population by 2025, the world's food output must increase. Abiotic stressors including drought, salt, heat, cold, and other conditions are projected to cause yield losses of 18%, 20%, 40%, 15%, and 8%, respectively (Ashraf & Foolad, 2005). Unfortunately, the impact of these stresses on agricultural output is becoming more severe, threatening the security of the global food supply (Savvides et al., 2016). The principal abiotic stressor inhibiting good crop growth is salinity. By 2050, the world's population is predicted to reach nine billion, necessitating a 25% increase in current rice output (Senguttuvel et al., 2022). Therefore, it is necessary to reverse any sluggish or low-yielding tendencies. Salinity due to various kinds of salt affects the root system. Salinity results in uneven, stunted development of agricultural plants, patchy seed germination and emergence, and decreased crop quality and production. Soil salinity, which is largely inherited because of surroundings with extreme temperatures and inadequate precipitation, puts crops at risk constantly (Musavizadeh et al., 2021). Hot, dry climates cause quick evaporation, which promotes salt to accumulate on the surface of the soil. Other salinity-causing factors include exploiting saline ground water, using canal water, coastal floods, seawater interruptions, poor farming techniques, and the decomposition of pepper-bearing minerals because of chemical and physical processes (Hussain et al., 2018). Water from irrigation systems with 100 mg L^{-1} of total dissolution material will add 0.136 tons of salts to the soil each canal of water delivered per acre (Rahman et al., 2021). When 100 mm of irrigation with 500 g of salt L^{-1} is used, each acre of land gets 500 kg of salt (Mustafa & Akhtar, 2019). Even though salinity offers a severe threat to sustainable agriculture and is a major factor in low yields, very little research has been done to determine the country's true salinity situation.

Under salt stress, glycophytic plants display a variety of negative effects, such as metal uptake, osmotic consequences, nutritional imbalance, and other metabolic disorders, which reduce the plants' overall photosynthetic activity, development, and fertility cycle (Zaman & Qureshi, 2018; Aftab, 2021; Syed et al., 2021; Iqbal & Qureshi, 2021). The majority of saline soils have greater levels of Na+ and Cl^- ions. When these two ions stack up in large quantities inside plant cells, they become highly poisonous because they damage or break the cells, which prevents development and results in a 4% drop in crop yield (Läuchli & Grattan, 2007; Jan et al., 2018; Hussain et al., 2022; Shaheen et al., 2023). Other detrimental impacts of salinity include decreased leaf growth, which eventually reduces photosynthetic area and total biomass, and reduced germination percentage and seedling establishment (Ahmad et al., 2010). Various negative impacts of soil salinity on growth and development of plants may also be seen at the physiological and biochemical levels (Liu et al., 2022). In one sense, it lowers yield, and in another, it lowers the nutritional and calorie value of the agricultural goods (Razzaq et al., 2020).

Rice is a staple food for over half of the world's population, serving as a primary source of carbohydrates and essential nutrients (Ibrahim et al., 2016; Ali et al., 2019; Mehmood et al., 2021; Hassan et al., 2022; Roheen et al., 2023). Rice is tolerant to salinity stress throughout the germination, physiological development, and mature stages, but it is particularly sensitive during the early seedling (2-3 leaf stage), pollination, and fertilization phases (Mondal & Borromeo, 2016; Ali, 2024). Salinity affects growth parameters such as root length (RL), root dry weight (RDW) and shoot dry weight (SDW), number of tillers per plant (TPP), day to flowering, spikelet numbers, 1000-grain weight, and overall productivity. Salinity also delays development in different rice varieties (Jamil et al., 2012). The maximum permissible salinity for rice crops is 3 dSm^{-1}. The production rate of rice decreases by 12% for every 1 dSm^{-1} increase over this level of concentration (Bashir, 2024; Gupta & Huang, 2014). At EC 10 dS m^{-1}, rice seedlings perish (Asch et al., 2000). If the EC level hits 3.5 dS m^{-1} during the germination of seeds, yield loss might approach 90%. In waterlogged soil cultivated on EC of 8–10 dS m^{-1} at 25°C, the majority of rice genotypes suffer serious damage; sensitivity ones suffer harm even at 2 dS m^{-1} (El-Mouhamady et al., 2010). Salinity has an impact on rice's fragrance and kernel characteristics as well as its antioxidant and osmo-protectant systems (Singh et al., 2020). Because rice is the only crop that can survive flooding circumstances, it is the only one that can be grown in tropical areas. The capability of plants to endure the harmful consequences of salt varies among genotypes but is also influenced by the physiological age of the plant (Shaheen & Hood-Nowotny, 2005). Evaluation of morphological traits that influence salinity and crop productivity interaction is necessary to address the salinity problem. The development and productivity of the rice crop have been impacted by plant spacing and the timing of salt stress (Badawy et al., 2021; Ahmed et al., 2024). When treated to salt during the blooming stage of rice development rather than to the vegetative growth stage, grain production is significantly reduced. Although pollen viability is a crucial characteristic that has been demonstrated to influence the final rice yield, pollens are extremely vulnerable to salt and ionic toxicity (Mohammadinezhad et al., 2010).

The global human population is growing at an alarming rate. To accommodate the rapidly rising population's need for food, further efforts are thus needed to boost global food production by 38% by 2025 and 50% by 2050. As a result, it is crucial to cultivate stress-tolerant kinds of crops in the saline-prone area through intensive crop farming (Abdallah et al., 2016). There are many techniques for eliminating crop species and types that can tolerate salt. In this regard, a set of three tests was conducted to compare the salt tolerance of rice genotypes that were aromatic and those that weren't. This study's main goal was (1) To find rice genotypes that are both sensitive and tolerant to salt. (2) To determine how salinity affects the different stages of rice development and yield characteristics. (3) To ascertain how salinity levels affect the performance of different rice genotypes.

Materials and Methods

The experiment was conducted at the Department of Plant Breeding and Genetics (PBG), The Islamia University of Bahawalpur (IUB) during the rice growing season 2021. Thirty-five rice genotypes were obtained from the Rice Research Institute, Kala Shah Kaku Lahore. These genotypes are listed in Table 1. The genotypes were initially grown in petri dishes with moist filter paper. Three-week-old seedlings were transplanted into pots (20 cm × 25 cm) loaded with dirt. The experiment was conducted using Complete Randomized Design (CRD) in plastic pots with three repeats. Three treatments were applied to these pots; one set is under non-stress condition T0 (1.2 dS/m) while other two were 8dS/m (T1) and 12 dS/m (T2) salt stress. Basal nutrient solution in the amount of 1L was applied to each pot. One week after BNS spraying, seeds were planted in each container. At the stage of two leaves (20 days after emergence, or 20 DAE), salinity treatments were given to three treatments: (1) control (non-salinized), in which soils in the pots were kept moist (60–80% water-holding capacity) throughout; (2) salinity stress (S), in which 1.5L 200 mM NaCl per pot was added on 20 DAE after adding 1L 100 mM NaCl per pot on 20 DAE, and (3) salinity stress (S).

Table 1 List of the genotypes used in this experiment

Code	Genotypes Name	Code	Genotypes Name
G1	Basmati-1122	G19	Chenab Basmati
G2	PK-1121	G20	KSK-111
G3	NIAB-2013	G21	Bas-370 E
G4	Kissan Basmati	G22	Bas-385 E

G5	Pk-386	G23	Bas- 2000 E
G6	Basmati-515	G24	BAS-2000GIR3P7
G7	Supper Basmati-19	G25	K-134
G8	Supper Gold-19	G26	IRRI-6
G9	KS-282	G27	Taroti
G10	NIAB-IRRI-9	G28	3370
G11	IRRI-6	G29	4040
G12	KSK-133	G30	3920
G13	KSK-434	G31	4270
G14	GSR-6	G32	Bas-370G2
G15	PK 2021	G33	Bas-315G3
G16	Shaheen Basmati-05	G34	Bas-198G3
G17	Naib Basmati 2016	G35	KSK-133G1R3P2
G18	PK-386		

At maturity, the data were recorded for following traits which include plant height (PH), tiller per plant (TPP), panicle length (PL), total spike length (TSL), grain per panicle (GPP), days to flowering (DTF), 1000 grain weight (GW), root length (RL), root dry weight (RDW), and shoot dry weight (SDW). Data was collected from five plants per replication for each genotype and treatment, and the average was calculated. Tillers that produce panicles with or without full grains were regarded as productive tillers. They were separately tallied for every treatment, including the control. Each panicle contained around 100 grains, which were manually counted, weighed (g) using an electronic balance (AND Model: GR 200 Japan), and then multiplied by 10. For root dry weight, twenty five-day old seedlings were uprooted from the soil at the end of experiment, washed with distilled water to remove dust soil particles and placed them on dry polythene sheets to dry out free surface moisture. Dried plant materials were stored in paper bags and oven dried at 80°C for 72 hours and allowed to cool in a dry environment (in a paper bag to keep moisture out) and then weighed on an electronic balance (Model: GR 200 Japan).Depending on their morphological characteristics, the panicle development stages may be divided into several phases, and the number of days between sowing and blooming can be calculated depending on the phase of panicle development.

In order to assess the variation across different genotypes (Steel & Torrie, 1960) technique was utilized for statistical analysis to compute variance from data obtained for each attribute. The analysis of variance was calculated using Statistics 8.1.0 software. To determine the linear relationship between each morphological and physiological factors, Karl Pearson's correlation coefficient (Pearson, 1920) was computed using the following formula:

$$r_{xy} = \frac{\sum(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum(x_i - \bar{x})^2 \sum(y_i - \bar{y})^2}}$$

Where is the Pearson’s correlation coefficient, X and Y are the variables for which the correlation has been estimated, and n is the number of observations. Using XLSTAT software, the diverse genotypes were chosen based on Principal Component Analysis (Fahad et al., 2017). Using the criterion given by Eigen values, the statistically significant main components were chosen (Beena et al., 2021).

Results and Discussion

The analysis of variance showed that variation was present among the studied genotypes and among the interaction between genotypes and environment as mentioned in Table 2.

Table 2 Mean sum of squares (MSS) of analysis of variance (ANOVA) for studied attributes

S.O. V	df	PH	TPP	SL	RL	RDW	SDW	DTF	PL	GPP	GW
Treatment	2	256.6261**	11.83**	198245.8**	60.6**	0.01**	0.03**	15801.95**	330.53**	87988.61**	1684.77**
Genotypes	34	1343.927**	59.23**	58.63**	0.69**	0.001**	0.004**	100.8**	12.14**	536.9**	875.67**
G*T	68	0.70087**	0.07**	73.87**	0.72**	0.001**	0.004**	68.56**	0.002**	183.24**	109.27**
Error	210	24.08364	6.33	339.15	0.74	0.002	0.005	241.67	2.37	196.52	218.17
Total	314										

** highly significant (0.01); * significant (0.05); sources of variation (S.O.V), degree of freedom (df), plant height (PH), tiller per plant (TPP), panicle length (PL), total spike length (TSL), grain per panicle (GPP), days to flowering (DTF), 1000 grain weight (GW), root length (RL), root dry weight (RDW), and shoot dry weight (SDW)

Mean performance

Under normal conditions, plant height varies from 74.8 cm to 123.0 cm. The genotype G4 showing the highest plant height, followed by G5 (122.2 cm) and G6 (121 cm), and genotype G32 showing the lowest plant height, followed by G33 (76.1 cm) and G35 (74.8 cm) as exhibited in Fig. 1. Plant height in T1 varies from 73.7 cm to 121.9 cm. The genotype G4 has the highest plants, followed by G5 (121.1 cm) and G6 (120.0 cm), and genotype G32 have the shortest plants, which are G33 (75.0 cm) and G35 (85.0 cm) respectively as represented in Fig. 2. The plant height varies from 71.5 cm to 120.2 cm under T2 stress conditions. The genotype G3 (120.2 cm) had the highest-growing plants, followed by G5 (119.4 cm) and G6 (120.0 cm), whereas genotype G (71.5 cm) had the shortest plants, followed by G24 (82.2 cm) and G33 (72.8 cm) as displayed in Fig. 3. Plant height can be reduced by oxidative damage, which can impair normal development processes and alter cellular structures and activities. The plant's height shrank while it was under stress. Similar findings were also made by (Razzaq et al., 2020), who found that salt stress drastically reduces rice plant height.

The plant tiller measures between 74.8 and 123.0 in the current study. The genotype G4 has the highest tiller, followed by G5 (122.2) and G6 (119.2), and genotype G32 having the lowest tiller, which is then followed by G33 (76.1) and G35 (84.2) as exhibited in Fig. 1 under normal condition. Plant tiller in T1 ranged from 70.5 to 120.5 in this study. The genotype G4 having the highest tiller (120.5), followed by G5 (121.1) and G6 (118.0), and genotype G32 having the lowest tiller (70.4), which was then followed by genotypes G33 (75.0) and G35 (85.0) as represented in Fig. 2. The plant tiller varies from 71.5 to 120.0 under T2 stress conditions. The genotype G4 had the highest plant tiller (120.0), followed by G5 (119.4) and G6 (117.5), while the genotype G32 had the lowest plant tiller (71.5), followed by G24 (82.9) and G33 (72.8) as displayed in Fig. 3. The plant tiller reduced under conditions of stress. Long-term, high salt stress in rice results in decreased plant vigor, which eventually lowers plant productivity. Similar findings were also published by Umego et al. (2020), who claim that salt stress has a major impact on rice plant tiller.

Under normal conditions, total spike lengths range between 129.5 cm and 14.3 cm. The genotype G4 shows the maximum total spike length, followed by G10 (140.0 cm) and G12 (139.3 cm), and genotype G7 shows the minimum total spike length, followed by G1 (131.7 cm) and G17 (130.0 cm) as exhibited in Fig. 1. Total spike length in T1 is between 115.1 cm and 138.4 cm. The genotype G26 (138.4 cm) has the longest total spike length, followed by G24 (135.4 cm) and G25 (137.4 cm), and genotype G15 (115.1) having the shortest total spike length, followed by G14 (118.1) and G3 (117.5) as represented in Fig. 2. The overall spike length varies from 45.5 cm to 69.3 cm under T2 stress settings. The genotype G14 had the longest total spike length (69.3), followed by G1 (66.9 cm) and G30 (66.1 cm), whereas genotype G9 had the shortest total spike length (45.9 cm), followed by G5 (51.1 cm) and G33 (49.3 cm) as displayed in Fig. 3. Under stressful circumstances, the overall spike length reduced. Poor plant vigor brought on by prolonged, increased salt stress in rice ultimately results in a reduction in (Zhang et al., 2023).

Root length ranges from 2.4 cm to 4.8 cm. The genotype G27 (4.8) showing the longest roots, followed by G15 (4.3 cm) and G17 (4.1 cm), and G29 (2.4 cm), followed by G21 (2.5 cm) and G7 (2.7 cm) as exhibited in Fig. 1 under normal condition. The largest root length in T1 is genotype G31 (3.8 cm), followed by G34 (3.7 cm) and G35 (3.6 cm), while the smallest root length was genotype G23 (2.0 cm), followed by G32 (1.8 cm) and G23 (2.1 cm) as represented in Fig. 2. The root length ranges from 1.0 cm to 2.9 cm under T2 stress conditions. The genotype G26 (2.9 cm) recorded the longest root length, followed by G19 (2.6 cm) and G13 (2.4 cm) as displayed in Fig. 3. When under stress, the root's length is reduced. In rice, prolonged high salt stress results in decreased plant vigor, which ultimately shortens plant length (Jahan et al., 2020).

In non-stressed conditions, root dry weight varies from 0.03 g to 0.24 g. The genotype G33 (0.24 g) showing the highest root dry weight, followed by genotypes G34 (0.13 g) and G22 (0.06 g), and G30 (0.03 g) showing the lowest root dry weight, followed by genotypes G23 (0.04 g) and G8 (0.05 g) as exhibited in Fig. 1. In T1, root dry weight varies from 0.01 g to 0.06 g. The genotype G31 (0.06 g) has the highest root dry weight, followed by G35 (0.05 g) and G34 (0.06 g), and genotype G4 (0.01 g) having the lowest root dry weight, followed by G5 (0.02) and G1 (0.02) as represented in Fig. 2. The root length varies from 0.01 g to 0.05 g under T2 stress conditions. G13 (0.05 g) had the highest root dry weight, followed by G4 (0.04 g) and G5 (0.02 g) as displayed in Fig. 3. Under stress, the dry weight of the roots decreased. Poor plant vigor brought on by prolonged high salt stress in rice affects plant dry weight in the end (Jahan et al., 2020).

The shoot dry weight ranges from 0.05 g to 0.13 g. The genotype G10 (0.24 g) showing the highest shoot dry weight, followed by G2 (0.12 g) and G4 (0.11 g), and genotype G7 (0.05 g), followed by G8 (0.07 g) and G33, showing the lowest shoot dry weight (0.08 g) as exhibited in Fig. 1 in normal environment. Shoot dry weight in T1 varies from 0.03 g to 0.11 g. The genotype G4 (0.11 g) having the highest shoot dry weight followed by G11 (0.10 g) and G34 (0.11 g), and genotype G9 (0.03 g) having the lowest shoot dry weight (0.02 g) as represented in Fig. 2. The shoot length varies from 0.02 g to 0.07 g under T2 stress conditions. The genotype G12 (0.07 g) recorded the highest shoot dry weight, followed by genotypes G14 (0.06 g) and G18 (0.05 g). Under stressful conditions, the dry weight of the shoot decreased. In rice, extended increased salinity stress results in decreased plant vigor, which eventually lowers shoot dry weight (Hussain et al., 2024; Singh et al., 2020).

Under normal conditions, the Days to Flower vary from 84.0 to 92. The genotype G31 (92.0) shows the most Days to Flower, followed by genotypes G22 (90.0) and G17 (91.0), and genotype G33 (84.0) showing the least Days to Flower, followed by genotypes G6 (85.0) and G3 (87.00) as exhibited in Fig. 1. Days to flowering in T1 vary from 78.1 to 123.5. The genotype G35 (123.5) has the highest days to flowering, followed by G25 (115.0) and G1 (113.7), while genotype G14 (71.8) has the lowest Days to flowering, followed by genotypes G22 (78.8) and G3 (77.0) as represented in Fig. 2. Days until blooming under T2 stress conditions range from 50.6 to 82.4. The genotype with the highest number of days to flowering was G28

(82.4), followed by G25 (81.4), and G35 (80.1) as displayed in Fig. 3.

The panicle length ranges from 22.6 cm to 27.1 cm. The with genotype G15 showing the greatest panicle length (27.1), followed by genotypes G14 (27.00 cm) and G15 (27.1 cm), and genotype G33 showing the smallest panicle length (22.6), followed by genotypes G5 (22.9 cm) and G35 (84.4 cm) as exhibited in Fig. 1 in non-stressed condition. In T1 panicles range in length from 22 cm to 26.6 cm. The genotype G15 has the longest panicles (26.6 cm), followed by G13 (25.7 cm) and G14 (26.5 cm), and genotype G33 having the shortest panicles (22.0), followed by G5 (22.4), and genotype G85 (22.2 cm). The panicle length varies from 19.3 cm to 23.8 cm under T2 stress conditions. The genotype G15 had the longest panicles (23.8 cm), followed by G13 (23.0 cm) and G14 (23.7 cm), whereas genotype G33 had the shortest panicles (19.3 cm), followed by G8 (19.5 cm) and G5 (19.6 cm) as displayed in Fig. 3. Long-term high salt stress in rice results in weak plants, which eventually shorten panicles (Gupta & Huang, 2014).

Under normal conditions, the grain per panicle ranges from 71.00 to 124.00 in the current study. The genotype G1 showing the highest grain per panicle, followed by genotypes G12 (121.7) and G35 (123.3), and genotype G3 showing the lowest grain per panicle, which was observed before genotypes G14 (80.5) and G23 (78.5) as exhibited in Fig. 1. The largest grain per panicle in T1 is genotype G21 (121.5), followed by G12 (115.5) and G14 (118.8), whereas the least grain per panicle was seen in genotype G34 (71.00), followed by G27 (73.0), and G3 (78.8) as represented in Fig. 2. The grain per panicle in T2 stress conditions range from 40.8 to 59.4. G1 genotype had the longest grain-to-panicle ratio (59.4), followed by G17 (55.0) and G27 (55.0) (58.2). Long-term high salt stress in rice results in weak plants, which eventually diminish the amount of grain produced per panicle (Huang et al., 2023).

The 1000 grain weight ranges from 72.3 g to 115.3 g in the present study. The genotype G12 (115.3 g) shows the highest 1000 grain weight followed by genotypes G25 (114.6g) and G2 (104.5 g), and genotype G14 (72.3 g) showing the lowest 1000 grain weight followed by genotypes G3 (75.6 g) and G10 (74 g) as exhibited in Fig. 1. The 1000 grain weight in T1 varies from 70.2 g to 112.8 g. The genotype G1 (112.8 g) having the highest 1000 grain weight followed by genotypes G2 (109.5 g) and G12 (110.5 g), and genotype G23 (70.2 g) having the lowest 1000 grain weight followed by genotypes G14 (73.2 g) and G3 (75.5 g) as represented in Fig. 2. The 1000 grain weight ranges from 68.7 to 108.6 under T2 stress conditions. The genotype G1 (108.6 g) achieved the highest 1000 grain weight, followed by genotypes G2 (105.3 g) and G12 (107.8 g) as displayed in Fig. 3. Under pressure, the 1000 grain weight was decreased. Similar findings were also published by (Liu et al., 2022) who claim that salt stress has a considerable impact on rice's 1000 grain weight.

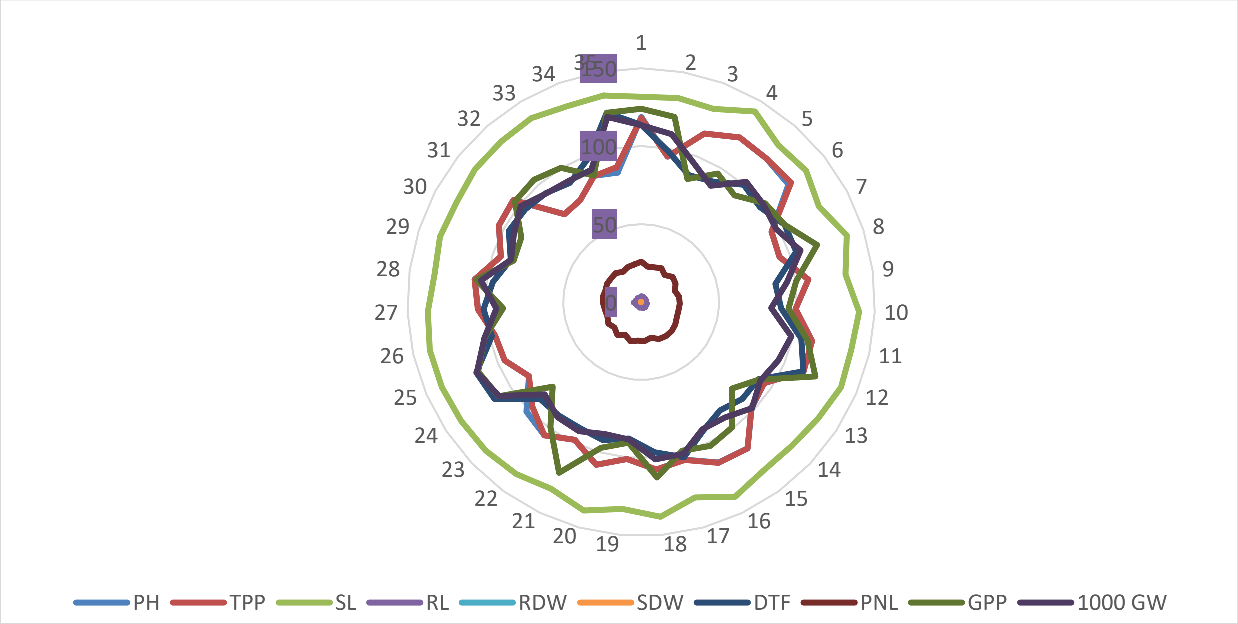

Fig. 1 Mean performance of genotypes under non-stressed conditions

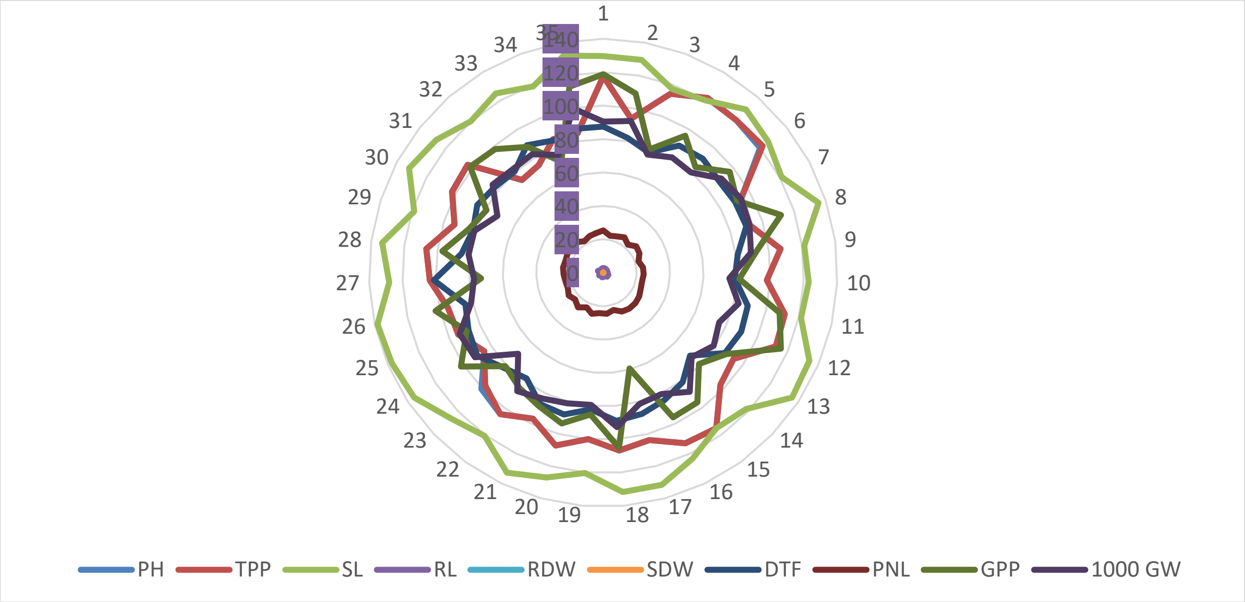

Fig. 2 Mean performance of genotypes under stressed T1 conditions

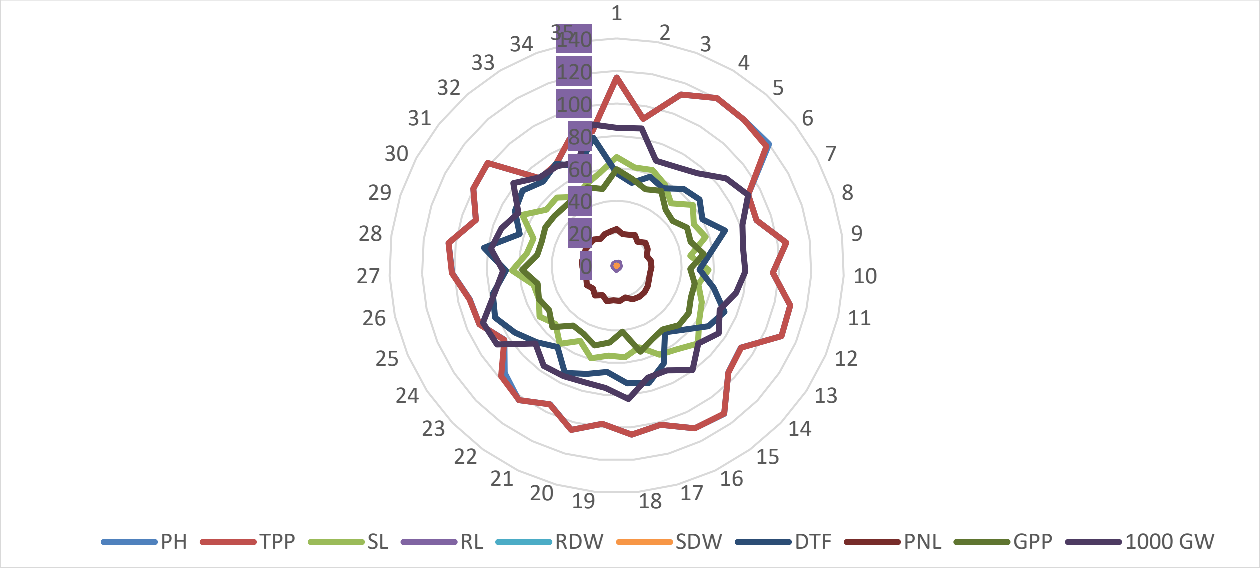

Fig. 3 Mean performance of genotypes under stressed T2 conditions

Correlation analysis

The strength of the relationship between two variables is indicated by the correlation coefficient. It is particularly significant in plant breeding since it may provide an analytical association that can be used in practice and because it provides information about the connections between various desired features. It provides a fundamental understanding of the relationships between numerous yield-contributing qualities, which helps plant breeders choose varieties with desirable characteristics. This investigation may help enhance tactics for the selection of necessary varieties with chosen qualities by providing evidence of the association between rice properties under stress and non-stress situations. Table 3 showed the correlation analysis for the normal (N), T1 and T2 stress situations. In this investigation, under both control and stress settings, the simple correlation coefficient of plant height showed a strongly negative association with the number of tillers (Ranawake et al., 2014) reported a similar outcome as well.

Days to flowering were closely associated with grain per panicle under both normal and salt-stressed environments. Similar findings were reported by (Prasath et al., 2020), who found that under both normal and salt-stress circumstances, grain weight was substantially and inversely correlated with days to flowering. Under both control and stress situations, panicle weight was substantially and adversely linked with day to blooming. These outcomes also agreed with those of (Yu et al., 2019). Under control, T1 and T2 stress conditions, panicle length, plant height, and thousand grain weights are all positively linked with plant length. Similar findings from (Chaturvedi et al., 2017) studies on rice under salt stress were also reported. Under control, T1 and T2 stress conditions, the relationship between root dry weight and plant tiller is positive. Similar findings were published by Prasath et al. (2020) who found that root length is positively connected with plant tiller under control, T1 and T2 stress conditions. Under control, T1 and T2 stress conditions, shoot dry weight is positively connected with days to flowering along with dry root weight and plant tiller. These results were in agreement with those of (Yu et al., 2019). According to Prasath et al. (2020), root length is closely associated with plant height under control, T1 and T2 stress conditions, as well as root dry weight and plant tiller. Under both control and stress settings, shoot dry weight was substantially and positively linked with day to blooming, root dry weight, and root length. These outcomes also agreed with those of (Yu et al., 2019). Under both normal and salt stress circumstances, total spike length was positively linked with days to blooming, grain per panicle, and plant length. Previously scientists (Prasath et al., 2020) reported a similar outcome as well. Other characters' contributions were insufficient to be regarded significant, and several scientists presented opposing conclusions considering the available evidence.

Table 3 Correlation analysis of thirty-five rice genotypes under normal and salt stress conditions

		DTF	GPP	GW	PH	PL	PT	RDW	RL	SDW
GPP	N	0.04**								
	T1	0.63**								
	T2	0.13**								
TGW	N	-0.01**	0.79**							
	T1	0.55**	0.86**							
	T2	-0.05**	-0.05							
PH	N	-0.01**	-0.08	-0.07						
	T1	-0.06**	0.05	0.03						
	T2	-0.34**	0.02	0.01						
PL	N	0.02	-0.09	-0.26	0.29**					
	T1	-0.25	-0.01	0.003	0.33**					
	T2	-0.29	-0.01	0.02	0.32**					
TPP	N	-0.03**	-0.05	-0.05	0.99**	0.3				
	T1	-0.05**	0.05	0.04	0.99**	0.33**				
	T2	-0.34**	0.01	0.01	0.99	0.32				
RDW	N	0.35**	-0.11	-0.09	-0.43**	-0.27	-0.42**			
	T1	0.18**	0.06	-0.05	-0.49**	0.11	-0.48**			
	T2	0.04**	-0.04	-0.16	0.01	0.14	0.01			
RL	N	0.16	-0.03	-0.05	0.33**	0.21	0.33**	0.21**	0.13	
	T1	0.17	-0.03	-0.15	0.004**	0.09	0.009**	0.12**	0.15	
	T2	0.01	-0.05	-0.09	0.06**	0.14	0.06**	0.36**	0.11	
SDW	N	0.04**	-0.06	-0.14	-0.23	-0.28	-0.23	0.53**	0.04**	
	T1	0.37**	0.26	0.16	-0.19	0.06	-0.17	0.20**	0.50**	0.3
	T2	0.23**	0.01	-0.1	-0.01	0.07	-0.05	0.31**	0.08**	0.14
TSL	N	0.26**	0.11**	0.1	-0.07	0.009**	-0.08	0.06	-0.04	0.1
	T1	0.63**	0.49**	0.29	-0.14	0.330*	-0.13	0.27	0.11	-0.08
	T2	0.31**	0.21**	0.01	0.25	0.59**	0.25	0.02	0.18	0.07

N = Normal, T1 = Salinity level treatment 1, T2 = Salinity level treatment 2, PH = Plant height, TPP = Tiller per plant, PL = Panicle length, TSL = Total spike length, GPP = Grain per panicle, DTF = Days to flowering, TGW = Thousand grain weight, RL = Root length, RDW = Root dry weight, SDW = Shoot dry weigh

Conclusion

The experiment comprised of two salinity stress levels, and one normal level to screen the 35 rice genotypes against salt stress. Analysis of Variances (ANOVA) results for studied attributes including plant height (PH), tiller per plant (TPP), panicle length (PL), total spike length (TSL), grain per panicle (GPP), day to flowering (DTF), thousand grain weight (TGW), root length (RL), root dry weight (RDW), and shoot dry weight (SDW) under normal and two salinity stress levels showed highly significant variation due to the presence of germplasm diversity. In this study, plant height showed significant negative association with tiller plant-1 simple correlation under normal and salt conditions. Grain per panicle was positively correlated with days to flowering under normal and salt stress conditions and Grain weight was negatively and significantly associated with days to flowering under normal and salt stress conditions. The G10 (NIAB IRRI-9), G5 (PAK-386) and G13 (KSK-434) were found to be salt tolerant genotypes because of better performance in most of the studied traits. The high yielding and salt-tolerant rice genotypes would be developed for long-term food security using the salt-tolerant genotypes in subsequent rice breeding programs.

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