# Comprehensive Evaluation of Rice Genotypes for Salt Tolerance: *In vitro* Screening, Association Studies and Principal Component Analysis

**Balasubramanian M., S. Vennila**

## ABSTRACT

Rice is an important staple crop of most of the people around the world. The production of rice is affected mainly by salinity in coastal lines. In the present study correlation and path analysis and principal component analysis is done for eight yield attributing traits to find out the genotypes for saline tolerance and decide on what trait basis the selection could be done. Correlation analysis showed that essential yield- related traits are plant height, panicle length, total number of tillers per plant, number of productive tillers per plant, number of grains per plant, and 1000 seed weight as they are positively significantly correlated with grain yield. Path analysis showed that all the traits had positive indirect effect on each other's except days to 50% flowering and plant height indicating these two characters do not contribute much on yield. The highest positive direct effect on grain yield was obtained by number of grains per plant followed by 1000 seed weight and number of productive tillers per plant. Principal component analysis was performed for eight traits which showed PC1 and PC2 has eigen value greater than 1. The eigen value of PC1 and PC2 are 3.24 and 1.16 respectively. Percentage of variance for the two factors are 40.5% and 14.5% together accounting 55% of variability of the genotypes used for the study. The genotypes Kuzhi adichan, Kalanamak, Kalurundai samba, Vaikunda, Kalarpalai, Kottara samba, Illapai poo samba and Palkodai Valai which were tolerant to salinity and the genotypes ADT 37, ADT 39, ADT 42, ADT 43, ADT 45, ADT 47 which were susceptible to salinity were identified from PCA biplot and can be used for further breeding program.

**Keywords** Correlation analysis, Path analysis, Eigen value, Principal component analysis, PCA biplot.

## INTRODUCTION

Rice (*Oryza sativa*) an edible starchy grain which is an important crop of the family Poaceae. It serves as a staple crop for two third of the world's population (Mohammadi-Nejad *et al.* 2010). The daily calorie requirement of upto 70% for most of the people around the world is provided by rice. Due to unforeseen conditions in global climatic condition rice production is severely affected by abiotic conditions such as salinity, drought and flood. One of the main issues af-

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fecting rice production globally, particularly in coastal areas, is salinity (Reddy *et al.* 2017). When salinity is present during pollination and fertilization, it affects rice sterility as well as the growth and development of the plant as well as its ability to adapt to stress (Pearson George and Leon 1959). Muhammad and Tomosaburo (1977) found that salinity causes panicle sterility in only some rice varieties, suggesting some genetic control (Khatun *et al.* 1995). Salinity delays heading in rice, which negatively affects a number of yield components (Grattan *et al*. 2002). Salinity stress has an impact on a number of plant functions, including flowering stage, spikelet count, percentage of sterile florets, leaf size, shoot growth, shoot and root length, shoot dry weight and shoot fresh weight (Muhammad and Nudrat 2009, Hakim *et al.* 2010, Gupta and Bingru 2014). Salinity can cause osmotic stress akin to physiological drought, and elevated salt accumulation in soils makes it harder for plants to absorb water and nutrients (Verslues Paul *et al.* 2006). Elevated salinity diminishes the flowering stage's pollen viability, which ultimately impacts grain output (Khatun and Flowers 1995, Singh *et al.* 2004). The degree of salt tolerance and the concentration of salt determine how differently different genotypes grow in response to salinity (Eynard *et al.* 2005). Developing crops that are resistant of high salinity and comprehending the mechanisms underlying this stress can help boost food supply. Salinity tolerant crops can be developed by the improvement of known varieties. The primary step in any crop improvement program is to evaluate and characterize the available genotypes for genetic variability. Correlation study helps to understand the association between yield and yield attributes, which ultimately helps in the realization of higher crop productivity. Path analysis helps to measure the direct and indirect contributions of independent variables to the dependent ones. It splits the correlation coefficient into two components, i.e., direct and indirect effects. Correlation and path analysis will describe the extent of association between seed yield and its attributes and also indicate the relative importance of their direct and indirect effects. The knowledge of existing genetic variability among the genotypes for different characters and the estimation of character association is important to make the selection program effective (Mohanty *et al.* 2024). The widely held belief that genetic variety

exists in the genepool is a necessary condition for implementing a productive and worthwhile breeding strategy (Patel *et al.* 2022). Characterization of this existing variability and realignment of characters in them through selective breeding might go a long way in meeting the existing and emerging challenges that threaten the world food security (Vanaja and Babu 2006). Principal component analysis is one of the important tools used for identifying the plant characters that categorize the distinctiveness among the promising genotypes. Crop species vary on a regular basis, PCA aids in the removal of redundancy from data sets (Maji and Saibu 2012 and Ramakrishnan *et al.* 2014). In the present study correlation and path analysis and principal component analysis are done to evaluate the association of various characters to grain yield under salt stress in 50 genotypes of *O. sativa*.

## MATERIALS AND METHODS

The present research work was carried out during the *kharif* 2022-2023 at Annamalai University, Department of Genetics and Plant Breeding, Annamalai Nagar, Tamil Nadu, India. The seed material for the present study was collected from various regions of Tamilnadu during 2021-2022. Totally 50 seed materials were collected from various agro climatic zones which includes indigenous rice varieties and commercial varieties. The collected germplasms were stored in the laboratory at 4°C. The list of genotypes used for the study were listed in the (Table 1).

The 50 rice genotypes were used for screening at the field condition and lab condition. Field was thoroughly prepared and levelled before sowing and before transplantation. During the season 50 rice genotypes were sown in the raised nursery beds. The experimental plot was laid out using Randomized Block Design (RBD) with 3 replications. Twenty-five days old seedlings were transplanted in the main field. All the standard agronomic practices recommended were followed to each plot and raised as a healthy crop and plant protection measures are done.

Evaluation of rice (*Oryza sativa* L.) genotypes for salt tolerance has become essential due to the increasing salinity stress in rice-growing areas. *In*

**Table 1.** List of genotypes used for the study.

| Sl. No. | Genotype | Sl. No. | Genotype |
|---|---|---|---|
| 1 | Kuzhi adichan | 26 | ADT37 |
| 2 | Tirupathi saram | 27 | ADT39 |
| 3 | Marathundi | 28 | ADT40 |
| 4 | Gobinth bhog | 29 | ADT41 |
| 5 | Mutrilum sannam | 30 | ADT42 |
| 6 | Samba mosanam | 31 | ADT43 |
| 7 | Anai komban | 32 | ADT44 |
| 8 | Vaikunda | 33 | ADT45 |
| 9 | Ottatam | 34 | ADT46 |
| 10 | Kalurundai samba | 35 | ADT47 |
| 11 | Illapai poo samba | 36 | ADT48 |
| 12 | Karuvachi | 37 | ADT49 |
| 13 | Chinnar | 38 | ADT50 |
| 14 | Kalajera | 39 | CO-50 |
| 15 | Kalanmak | 40 | CO-51 |
| 16 | Katti samba | 41 | BPT-5202 |
| 17 | Pal kodai valai | 42 | BPT-5204 |
| 18 | Anandanoor sanna | 43 | NLR - 3083 |
| 19 | Milagu samba | 44 | NLR - 3449 |
| 20 | Kottara samba | 45 | PS226 |
| 21 | Manjal ponni | 46 | AC-39000 |
| 22 | Kalarpalai | 47 | CR 1009 |
| 23 | Poong karr | 48 | AC 35534 |
| 24 | Kamban samba | 49 | TRY -1 (HTC) |
| 25 | ADT36 | 50 | IR64 (HSC) |

vitro screening methods, association studies and principal component analysis are widely used techniques for assessing salt tolerance in rice genotypes. *In vitro* screening provides a quick and efficient way to evaluate the response of rice plants to salt stress by exposing them to controlled salt concentrations. Association studies involve studying the correlation between genotypic variations and salt tolerance traits in a large population of rice genotypes, which helps identify the genetic markers associated with salt tolerance. Furthermore, principal component analysis is a statistical tool that allows for the identification of the most influential traits contributing to salt tolerance. By applying these three approaches in combination,

reliable and accurate evaluation of rice genotypes for salt tolerance can be achieved, leading to the development of improved salt-tolerant varieties and ultimately ensuring food security in areas affected by salinity stress.

### *In vitro* screening for salinity

All the 50 rice accessions were raised separately under normal and saline condition for seedling stage salinity tolerance using a hydroponic system under laboratory. The weather conditions that prevailed during the period were minimum temperature of 22˚C to 24˚C, maximum temperature of 30˚C to 31˚C, natural sunlight and relative humidity of 65% to 70%. The seeds were sterilized and placed in the germination paper and incubated at 27˚C for 48 hrs to germinate. One well pre-germinated seeds were sown per hole on storiform floats with a net bottom and it was suspended on the plastic tray with Yoshida nutrient solution (Yoshida and Parao 1976). The radical should be inserted through the nylon mesh so as to prevent the damage to the pre-germinated seeds. Yoshida nutrient solution was prepared by using various chemical reagents containing macro and micro nutrients as required (Table 2).

### Correlation and path analysis

Observations were recorded during the crop growth and at harvest time for the characters viz., Days to fifty per cent flowering, Plant height, Panicle length, Number of tillers per plant, Number of grains per panicle, Thousand seed weight and Grain yield and the data was subjected to statistical analysis. Statistical analyses for the above characters were done following Singh and Chaudhary (1977) for correlation coefficient and Dewey and Lu (1959) for path analysis.

**Table 2.** Mean value for saline analysis under laboratory condition.

| Genotype | SL | RL | TSL | G% | FSW | DSW | SV -1 | SES score |
|---|---|---|---|---|---|---|---|---|
| 1 | 15.39 | 25.3 | 40.69** | 89.51** | 0.103** | 0.104** | 3642.40** | 1 |
| 2 | 12.48 | 12.97 | 25.45 | 51.38 | 0.037 | 0.015 | 1311.13 | 3 |
| 3 | 8.55** | 16.71 | 25.27 | 53.58 | 0.026 | 0.021 | 1354.43 | 5 |
| 4 | 10.27 | 6.44** | 16.71 | 62.93 | 0.027 | 0.018 | 1052.18 | 7 |
| 5 | 11.6 | 13.71 | 25.31 | 63.63 | 0.023 | 0.023 | 1611.46 | 5 |
| 6 | 10.5 | 8.13* | 18.63 | 70.16 | 0.028 | 0.023 | 1316.76 | 5 |
| 7 | 11.71 | 14.52 | 26.23 | 51.5 | 0.027 | 0.009 | 1352.17 | 7 |
| 8 | 19.96 | 20.35 | 40.32** | 78.52 | 0.104** | 0.090** | 3171.6** | 3 |

**Table 2.** Continued.

| Genotype | SL | RL | TSL | G% | FSW | DSW | SV -1 | SES score |
|---|---|---|---|---|---|---|---|---|
| 9 | 12.35 | 18.62 | 30.97** | 72.5 | 0.098** | 0.053 | 2247.86* | 5 |
| 10 | 15.51 | 21.43 | 36.94** | 88.4** | 0.107** | 0.1 | 3263.37** | 1 |
| 11 | 9.37* | 9.45* | 18.83 | 62.4 | 0.071** | 0.060* | 1196.39 | 7 |
| 12 | 21.76 | 6.8** | 28.56* | 50.33 | 0.080** | 0.068* | 1450.26 | 7 |
| 13 | 9.56 | 13.78 | 23.34 | 68.13 | 0.020 | 0.015 | 1592.81 | 5 |
| 14 | 10.62 | 12.51 | 23.14 | 62.3 | 0.028 | 0.023 | 1451.62 | 5 |
| 15 | 18.36 | 9.11* | 27.47 | 91.41** | 0.129** | 0.103** | 2511.86** | 1 |
| 16 | 8.66** | 13.5 | 22.16 | 44.42 | 0.098** | 0.092 | 984.78 | 9 |
| 17 | 12.47 | 11.43 | 23.90 | 52.33 | 0.024 | 0.019 | 1259.11 | 7 |
| 18 | 10.00 | 13.93 | 23.94 | 54 | 0.019 | 0.019 | 1295.97 | 5 |
| 19 | 11.45 | 23.75 | 35.20** | 34 | 0.019 | 0.009 | 1196.06 | 5 |
| 20 | 11.19 | 13.02 | 24.22 | 47.5 | 0.026 | 0.018 | 1153.02 | 7 |
| 21 | 15.95 | 7.03** | 22.98 | 54 | 0.027 | 0.011 | 1242.78 | 7 |
| 22 | 10.47 | 18.03 | 28.5* | 90.70** | 0.105** | 0.103** | 2584.08** | 1 |
| 23 | 14.44 | 25.33 | 39.77** | 74.32 | 0.077** | 0.067* | 2958.21** | 1 |
| 24 | 9.81 | 12.21 | 22.02 | 66.39 | 0.021 | 0.016 | 1449.74 | 5 |
| 25 | 10.26 | 11.18 | 21.45 | 77.3 | 0.024 | 0.018 | 1664.98 | 5 |
| 26 | 8.12* | 9.51* | 17.63 | 80.33 | 0.016 | 0.020 | 1413.99 | 7 |
| 27 | 11.10 | 9.95* | 21.06 | 77.46 | 0.014 | 0.016 | 1631.99 | 7 |
| 28 | 9.90 | 6.60** | 16.51 | 55.66 | 0.032 | 0.02 | 903.42 | 9 |
| 29 | 13.53 | 8.21** | 21.74 | 74.33 | 0.019 | 0.017 | 1608.15 | 7 |
| 30 | 8.76* | 10.28 | 19.04 | 65.39 | 0.021 | 0.028 | 1281.17 | 7 |
| 31 | 8.61* | 12.15 | 22.76 | 74.68 | 0.020 | 0.006 | 1706.75 | 7 |
| 32 | 14.11 | 9.21 | 23.33 | 75.42 | 0.020 | 0.015 | 1748.88 | 7 |
| 33 | 12.48 | 13.12 | 25.60 | 35.45 | 0.021 | 0.028 | 907.26 | 9 |
| 34 | 13.83 | 8.64** | 22.48 | 57 | 0.025 | 0.019 | 1275.77 | 7 |
| 35 | 16.73 | 8.18** | 24.91 | 68.01 | 0.017 | 0.009 | 1686.65 | 7 |
| 36 | 13.89 | 12.01 | 25.91 | 71.87 | 0.02 | 0.017 | 1876.26 | 5 |
| 37 | 10.87 | 6.97** | 17.85 | 55.66 | 0.024 | 0.015 | 1001.25 | 7 |
| 38 | 9.90 | 6.60** | 16.51 | 76.33 | 0.032 | 0.02 | 1267.68 | 7 |
| 39 | 13.83 | 8.64** | 22.48 | 57 | 0.025 | 0.019 | 1275.77 | 7 |
| 40 | 12.96 | 14.55 | 27.52 | 77.69 | 0.013 | 0.009 | 2120.61* | 3 |
| 41 | 9.84 | 12.09 | 21.93 | 59.33 | 0.038 | 0.022 | 1315.91 | 9 |
| 42 | 10.00 | 12.10 | 22.11 | 74.33 | 0.019 | 0.017 | 1650.41 | 7 |
| 43 | 10.86 | 14.72 | 25.59 | 81.66* | 0.03 | 0.017 | 2082.66 | 5 |
| 44 | 10.85 | 14.16 | 25.01 | 74.51 | 0.028 | 0.013 | 1864.66 | 7 |
| 45 | 9.76 | 13.30 | 23.07 | 74.41 | 0.026 | 0.018 | 1707.71 | 7 |
| 46 | 10.53 | 11.07 | 21.61 | 75.29 | 0.024 | 0.011 | 1652.07 | 9 |
| 47 | 10.75 | 11.80 | 22.56 | 82.25* | 0.029 | 0.021 | 1853.34 | 5 |
| 48 | 10.23 | 10.82 | 21.06 | 70.33 | 0.026 | 0.016 | 1484.01 | 7 |
| 49 | 11.54 | 16.76 | 30.31** | 90.26** | 0.121** | 0.158** | 2544.36** | 1 |
| 50 | 8.49* | 13.43 | 21.93 | 33.6 | 0.031 | 0.091* | 736.97 | 9 |
| SE | 0.86 | 0.87 | 1.37 | 5.33 | 0.005 | 0.011 | 157.69 | |
| SEd | 1.22 | 1.24 | 1.94 | 7.53 | 0.008 | 0.015 | 223.01 | |
| CD (0.05) | 2.42 | 2.46 | 3.84 | 14.92 | 0.016 | 0.031 | 441.56 | |
| CD (0.01) | 3.22 | 3.27 | 5.11 | 19.82 | 0.02 | 0.04 | 586.52 | |
| | SL – Shoot length | RL – Root length | TSL – Total seedling length | G% - Germination percentage | FSW– Fresh seedling weight | DSW-Dry seedling weight | SV-1-Seedling vigour index 1 | |

## Principal component analysis

The majority of the reported genotype changes were found to be attributed to certain plant features, which were found using Principal component analysis. For eight quantitative traits, the mean values of 50 genotypes were employed. Principal components are generally estimated from correlation matrix or covariance

matrix. The data was analyzed using STAR software.

## RESULTS AND DISCUSSION

Mean value for saline under laboratory condition is given in Table 2. All the genotypes showed varied response at seedling stage towards saline stress. The genotypes were scored from 1 (highly tolerant) to 9 (highly susceptible) (Rajabi Dehnavi et al. 2020). The resistant checks, TRY - 1 not show any symptoms under saline conditions and had normal growth and development (Rahman et al. 2016). While, the susceptible checks ADT – 40, ADT – 46, CO – 50 and BPT – 5202 showed whitish leaf tips, drying and rolling of leaves, and death of seedlings (Negrao et al. 2017). The genotypes like Kuzhi adichan, Kalanamak, Kalurundai samba kalarpalai and Kottara samba, (score of 1 and highly tolerant) also showed normal growth and development as resistant checks at seedling stage. The tolerant genotypes maintain ion homeostasis by ion uptake and compartmentalization of excess ions in the vacuole or older tissues (Hasegawa 2013). In addition to ion homeostasis, the tolerant genotypes accumulate large amount of osmolytes like proline, glycine betaine, polyols, and sugars to maintain the osmotic balance (Saxena et al. 2013).

The results of the present study indicated genotypic correlation coefficient and phenotypic correlation coefficient were similar. Phenotypic and genotypic correlation analysis for eight characters of rice under salinity is given in Table 3. The grain yield was positively correlated with all the characters like panicle length, number of tillers per plant, number of productive tillers per plant, number of grains per plant and 1000 seed weight whereas days to 50% flowering and plant height are not significantly correlated with grain yield per plant at genotypic levels. This can be improved by selecting early maturing lines. The grain yield per plant had no significant correlation with days to 50% flowering (Islam et al. 2016). The associations between yield and plant height were revealed by Faysal et al. (2022). Phenotypic correlation was found significant between grain yield with all the characters except days to 50% flowering. Days to 50% flowering was correlated significantly only with panicle length at genotypic levels whereas at phenotypic levels it was correlated with plant height, panicle length, number of tillers per plant, number of grains per plant and 1000 seed weight. All the other characters were not

**Table 3.** Phenotypic and genotypic correlation analysis.

|  | Correlation coefficient | DFPF | PH | PL | NTPP | NPTPP | NGPP | 1000 SW | GY |
|---|---|---|---|---|---|---|---|---|---|
| DFPF | $r_g$ | 1** | 0.1791 | 0.373 ** | 0.180 | -0.010 | 0.210 | 0.209 | 0.035 |
|  | $r_p$ | 1** | 0.1791 * | 0.3733 ** | 0.18 * | -0.0098 | 0.2106 ** | 0.2088 * | 0.0353 |
| PH (cm) | $r_g$ | 0.179 | 1** | 0.5131 ** | 0.3618 ** | 0.1643 | 0.3078 * | 0.4904 ** | 0.2262 |
|  | $r_p$ | 0.179* | 1** | 0.5122 ** | 0.3596 ** | 0.1633 * | 0.3078 ** | 0.4887 ** | 0.2257 ** |
| PL | $r_g$ | 0.373** | 0.513** | 1** | 0.4802 ** | 0.2947 * | 0.5044 ** | 0.3317 * | 0.3535 * |
|  | $r_p$ | 0.373** | 0.5122 | 1** | 0.478 ** | 0.2922 ** | 0.5032 ** | 0.3302 ** | 0.3523 ** |
| NTPP | $r_g$ | 0.180 | 0.361** | 0.480** | 1** | 0.3465 * | 0.4133 ** | 0.4214 ** | 0.3924 ** |
|  | $r_p$ | 0.18* | 0.356** | 0.478** | 1** | 0.3441 ** | 0.4104 ** | 0.417 ** | 0.389 ** |
| NPTPP | $r_g$ | -0.010 | 0.164 | 0.294* | 0.346* | 1** | 0.1818 | 0.209 | 0.3897 ** |
|  | $r_p$ | -0.009 | 0.163* | 0.292** | 0.344** | 1** | 0.1813 * | 0.2077 * | 0.3863 ** |
| NGPP | $r_g$ | 0.210 | 0.307* | 0.504** | 0.413** | 0.818 | 1** | 0.1636 | 0.4695 ** |
|  | $r_p$ | 0.210* | 0.307** | 0.503** | 0.410** | 0.181* | 1** | 0.163 * | 0.4686 ** |
| 1000 SW | $r_g$ | 0.209 | 0.49** | 0.331* | 0.421** | 0.209 | 0.163 | 1** | 0.3578 * |
|  | $r_p$ | 0.208* | 0.488** | 0.503** | 0.410** | 0.181* | 1** | 0.163* | 0.356 ** |
| GY | $r_g$ | 0.035 | 0.226 | 0.353* | 0.392* | 0.389* | 0.469** | 0.357** | 1** |
|  | $r_p$ | 0.035 | 0.225** | 0.352** | 0.389** | 0.386** | 0.468** | 0.356** | 1** |

DFPF- Days to fifty per cent flowering  PH- Plant height  PL- Panicle length
NTPP- Number of tillers per plant  NPTPP- Number of productive  GY – Grain yield
NGPP- Number of grains per plant        tillers per plant
1000 SW – 1000 Seed weight

**Table 4.** Path coefficient analysis of direct (diagonal) and indirect effects of various traits on grain yield.

|  |  | DFPF | PH | PL | NTPP | NPTPP | NGPP | 1000 SW |
|---|---|---|---|---|---|---|---|---|
| DFPF | Genotypic | **-0.11735** | -0.01752 | 0.02506 | 0.01187 | -0.00239 | 0.07922 | 0.05642 |
|  | Phenotypic | **-0.11738** | -0.01731 | 0.02544 | 0.01182 | -0.00230 | 0.07910 | 0.05593 |
| PH | Genotypic | -0.02102 | **-0.09778** | 0.03438 | 0.02374 | 0.03901 | 0.11578 | 0.13206 |
|  | Phenotypic | -0.02102 | **-0.09665** | 0.03491 | 0.02362 | 0.03834 | 0.11561 | 0.13090 |
| PL | Genotypic | -0.04388 | -0.05017 | **0.06702** | 0.03152 | 0.06996 | 0.18971 | 0.08934 |
|  | Phenotypic | -0.04382 | -0.04951 | **0.06815** | 0.03139 | 0.06861 | 0.18900 | 0.08847 |
| NTPP | Genotypic | -0.02122 | -0.03537 | 0.03218 | **0.06564** | 0.08227 | 0.15545 | 0.11348 |
|  | Phenotypic | -0.02113 | -0.03476 | 0.03258 | **0.06568** | 0.08079 | 0.15414 | 0.11170 |
| NPTPP | Genotypic | 0.00118 | -0.01607 | 0.01975 | 0.02275 | **0.23741** | 0.06839 | 0.05628 |
|  | Phenotypic | 0.00115 | -0.01578 | 0.01991 | 0.02260 | **0.23479** | 0.06810 | 0.05563 |
| NGPP | Genotypic | -0.02471 | -0.03010 | 0.03380 | 0.02713 | 0.04316 | **0.37614** | 0.04405 |
|  | Phenotypic | -0.02472 | -0.02975 | 0.03429 | 0.02695 | 0.04257 | **0.37559** | 0.04366 |
| 1000 SW | Genotypic | -0.02458 | -0.04795 | 0.02223 | 0.02766 | 0.04961 | 0.06152 | **0.26931** |
|  | Phenotypic | -0.02451 | -0.04723 | 0.02251 | 0.02739 | 0.04877 | 0.06122 | **0.26786** |

DFPF- Days to fifty per cent flow- PH- Plant height　　　　　　　　PL- Panicle length
ering　　　　　　　　　　　　NPTPP- Number of productive tillers　GY – Grain yield
NTPP- Number of tillers per plant　per plant
NGPP- Number of grains per plant　1000 SW – 1000 seed weight

significant with days to 50% flowering. The plant height was correlated genotypically with panicle length, number of tillers per plant, number of grains per plant and 1000 seed weight and phenotypically significant with all the traits. The report is also similar to the findings of Soujanya *et al.* (2020) and Srijan *et al.* (2016) which showed significant and positive associations between panicle length and plant height. The panicle length and number of tillers per plant was significantly correlated with all the traits at both phenotypic and genotypic levels. The number of productive tillers per plant is negatively correlated with days to 50% flowering at genotypic and phenotypic levels whereas it was not significant with 1000 seed weight at genotypic level. All other characters were significantly correlated with number of productive tillers per plant. The genotypic correlation was not significant between number of grains per plant and 1000 seed weight. The close relation of phenotypic and genotypic correlation coefficients is studied from the correlation study which indicates the masking effect of environment on character association. In the current study the yield attributing characters like number of tillers per plant, number of tillers per plant, number of grains per plant and 1000 seed weight had positive significant association at genotypic and phenotypic levels. These traits would be efficient for enhancing the yield, and the yield of rice in future

breeding programs would be increased. The correlation response in specific characters might lead to the selection of the predicted characters, and knowing the relationship between qualities would assist in the appropriate selection process (Goncalves *et al.* 2017). Generally, one or two desired traits could be selected at the same time, so a deep understanding of the effect of these traits on other characters was required. For example, yield improvement could be achieved by the genotype development with long panicle length and high number of panicles. Moreover, knowledge about the correlation between various characters with grain yield per plant, which is the most important target character, is required. By using this knowledge, this critical trait could be obtained by selecting easily observable traits. Our research results confirmed that essential yield- related traits are plant height, panicle length, the total number of tillers per plant, number of productive tillers per plant, number of grains per plant, and 1000 seed weight and they could be used as selection standards for rice grain yield enhancement.

**Path coefficient analysis**

Knowledge of the association among phenotypic characters and their effect on yield would be essential for selecting desired lines to be integrated with a breeding program and for releasing new varieties

**Table 5.** Eigen value, contribution of variability and factor loadings for the Principal Component axes.

|  | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 |
|---|---|---|---|---|---|---|---|---|
| Eigen value | 3.239217 | 1.156857 | 0.940538 | 0.750557 | 0.657584 | 0.559769 | 0.371391 | 0.324086 |
| Variance percent | 40.49022 | 14.46071 | 11.75673 | 9.381965 | 8.219805 | 6.99711 | 4.642386 | 4.051079 |
| Cumulative variance percent | 40.49022 | 54.95093 | 66.70765 | 76.08962 | 84.30942 | 91.306 | 95.94892 | 100 |
| Standard deviation | 1.7998 | 1.0756 | 0.9698 | 0.86635 | 0.8109 | 0.74818 | 0.60942 | 0.56929 |
| Proportion of variance | 0.4049 | 0.1446 | 0.1176 | 0.09382 | 0.0822 | 0.06997 | 0.04642 | 0.04051 |
| Cumulative proportion | 0.4049 | 0.5495 | 0.6671 | 0.7609 | 0.8431 | 0.91307 | 0.95949 | 1.000005 |
| DFF | 0.208214 | 0.645454 | -0.30179 | 0.512899 | -0.297 | 0.13085 | 0.130333 | 0.252137 |
| PH | 0.366888 | 0.256249 | 0.404559 | -0.32343 | 0.446661 | 0.254773 | 0.177833 | 0.485196 |
| PL | 0.435126 | 0.201379 | -0.19315 | 0.015522 | 0.369648 | 0.085149 | -0.64744 | -0.41169 |
| NTPP | 0.408822 | -0.09693 | 0.04385 | 0.081421 | -0.01901 | -0.86566 | -0.05038 | 0.250289 |
| NPTPP | 0.276329 | -0.51633 | 0.036479 | 0.649585 | 0.329273 | 0.213209 | 0.278039 | -0.05064 |
| NGPP | 0.36869 | -0.05143 | -0.55085 | -0.42177 | -0.00763 | 0.002016 | 0.553939 | -0.27054 |
| 1000 SW | 0.350641 | 0.115709 | 0.621422 | 0.015227 | -0.44705 | 0.041319 | 0.155691 | -0.50146 |
| GY | 0.361014 | -0.43028 | -0.12288 | -0.1593 | -0.51667 | 0.337901 | -0.34824 | 0.376373 |

PH- Plant height  
NPTPP-Number of productive tillers per plant  
1000 SW – 1000 Seed weight  
PL- Panicle length  
GY – Grain yield  
NTPP- Number of tillers per plant  
NGPP- Number of grains per plant

(Dhavaleshvar *et al.* 2019). The correlation between two factors could be divided into indirect and direct impact through other factors based on path coefficient analysis. The direct and indirect impacts among yield and yield-related components could be positive or negative, but the direct impact of that particular character and indirect impact via other components could be pointed out. Therefore, the determination of the path coefficient is crucial, so the correlation of these impacts could be observed partially and revealed the root and relationship that exist between yield-related elements and yield. In the present study, path coefficient analysis was carried out for eight traits to find their correlation with grain yield per plant under saline conditions (Table 4). Among the characters studied panicle length, number of tillers per plant, number of productive tillers per plant, number of grains per plant and 1000 seed weight had direct positive effect on grain yield per plant. The highest positive direct effect on grain yield was obtained by number of grains per plant followed by 1000 seed weight and number of productive tillers per plant. Positive direct effects of various traits on grain yield reported in the present research agree with the findings of Yadav *et al.* (2010) for the number of tillers per plant, Faysal *et al.* (2022) for test weight, Saleh *et al.* (2020) for 1000 grain weight. The negative effect was obtained

by days to 50% flowering and plant height. These two characters do not have any effect on improving grain yield. Our findings are against the findings of Muthuvijayaragavan and Murugan (2017) where they reported a negative direct effect of panicle length, number of tillers per plant and number of productive tillers per plant on grain yield per plant respectively.

The highest positive indirect effect on grain yield per plant via days to 50% flowering is number of grains per plant whereas the lowest indirect effect was by number of tillers per plant. The negative indirect effect on grain yield via days to 50% flowering is plant height and number of productive tillers per plant. The plant height on grain yield had positive indirect effect in the order number of 1000 seed weight, number of grains per plant, number of productive tillers per plant, panicle length and number of tillers per plant. It has indirect negative effect on days to 50% flowering. All the traits had positive indirect effect on each other's except days to 50% flowering and plant height indicating these two characters do not contribute much to yield. The highest positive indirect effect on grain yield via panicle length, number of tillers per plant, number of productive tillers per plant and 1000 seed weight, number of grains per plant. Number of grains per plant had highest positive indirect effect

via 1000 seed weight. Our results agreed with that of Reetisana *et al.* (2022) and Aarthi *et al.* (2019) which revealed that days to 50% flowering had a negative indirect impact on grain yield per plant via panicle length. Saleh *et al.* (2020) also reported that the indirect impact of plant height on grain yield via panicle length which was negative.

In this research, the indirect and direct effects of yield contributing factors and yield were calculated. The relation-ship between the effect and a causal factor was similar to its direct effect, so the true relationship was explained and plant breeder could be selected directly through these traits. However, the positive correlation could be caused by indirect effects in the case of the direct effect were negligible or negative. In the present study, in the selection process, the other factors were involved simultaneously. Besides, some restrictions could be used to limit the unexpected indirect effects in order to utilize the direct effect when the direct effect was strong and positive but the correlation was negative. For improvement of grain yield, based on the correlation and coefficient data, test weight, number of productive tillers per plant, number of grains per plant, number of productive tillers per plant and panicle length were essential factors, which should be considered as selection criteria. Overall, among the genotypes used, grain yield per plant showed a highly significant and positive correlation with its component traits like test weight, number of productive tillers per plant, number of grains per plant, number of productive tillers per plant and panicle length while it exhibited a strong negative correlation with plant height and days to 50% flowering. Therefore, a separated but simultaneous selection for enhancement of these traits could be executed. The results also revealed that the total number of tillers per plant had maximum positive direct effects as well as indirect effects on other traits, which suggested that selection based on this trait for grain yield would be most effective strategy. Additionally, the role of number of panicles had maximum positive effect on grain yield that could be used for selection (Balasubramanian and Vennila 2022).

**Principal component analysis**

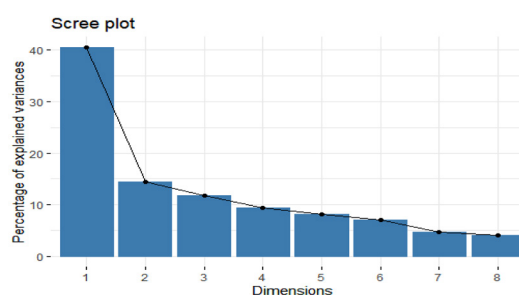The main purpose of principal component analysis is



**Fig.1.** Screen plot showing eigen value and cumulative variability with their respective PCs.

reducing the dimension of a large dataset, increasing interpretability but at the same time minimizing information loss (Patel *et al.* 2022). Eigen vector values, percentage of variance and the cumulative percentage are presented in Table 5. In the present study PC1 and PC2 has eigen value greater than 1. The eigen value of PC1 and PC2 are 3.24 and 1.16 respectively. Percentage of variance for the two factors are 40.5% and 14.5% together accounting 55 % of variability of the genotypes used for the study. Similar type of finding also reported by Shaibu and Uguru (2017) and Salem *et al.* (2021). Rotated component matrix showed that PC1 exhibited highest variability 40.5% with highly loaded character viz panicle length, number of tillers per plant, number of grains per plant, 1000 seed weight and grain yield. It shows that PC1 is mainly dependent on panicle length and number tillers per plant. PC2 exhibited variance of 14.5 % with highly loaded for days to 50% flowering. Similar type of finding also reported by Sanni *et al.* (2012), Radhamani *et al.* (2015) and Lakshmi *et al.* (2019). The Principal component analysis revealed a wide range of scores for the eight quantitative traits, indicating a significant degree of variation. The analysis explained the variance structure through a few linear combination of the variables, proportion of variability. Thus, an accurate image of the component qualities that are providing the most variability is obtained based on factor loadings. Scree plots are graphs that display the eigen values in order of greatest to smallest as well as the percentage of variability in terms of primary component and eigen value. PC 1 showed 40.5% variability with eigen value 3.24 and then the graph gradually declines for another PC. Steep curve followed by bend and then straight found for
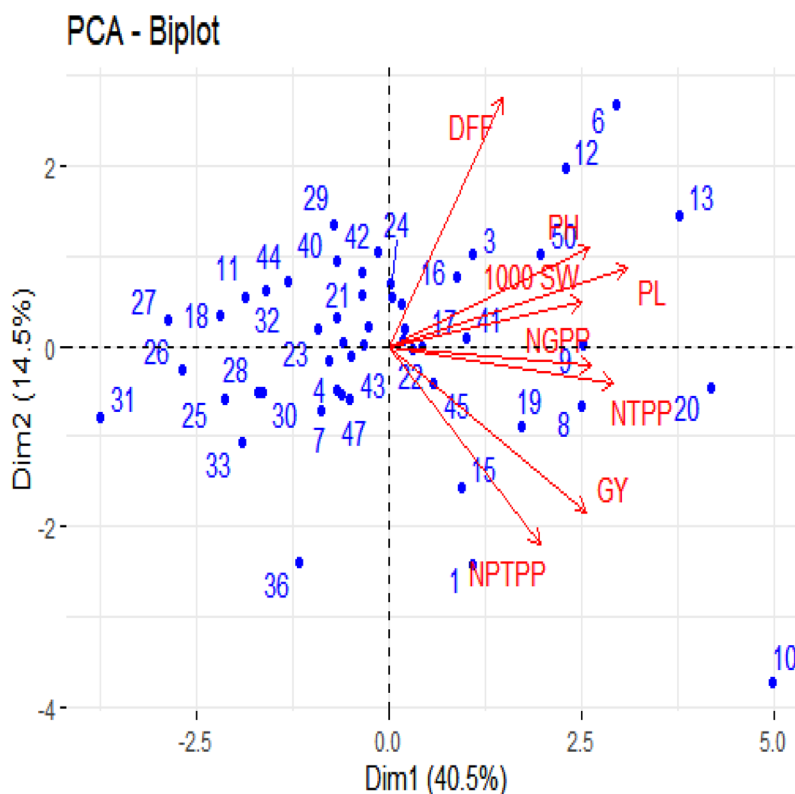
**Fig. 2.** Biplot analysis for 50 germplasm of rice with 2 PCs.

different PCs. The graph (Fig. 1) provided a concise explanation of the variability, which peaked for PC1. The distribution and kind of diversity for both the genotypes and the variables were described by the biplot diagram (Fig. 2) that shows the relationship between PCs 1 and 2. Nearly every genotype and variable showed a great degree of variance, as the loading plot illustrated. Ravi *et al.* (2018) observed similar reports.

The Biplot diagram (Fig. 2) revealed significant heterogeneity among genotypes and between parameters. In this regard, the study will be useful in finding the variability-contributing characteristics and selecting appropriate genotypes for breeding and use in crop development for yield-related traits. The results of the Biplot analysis are shown in Fig. 2. The results indicated that the two PCs were separated into two clusters. The result of box plot revealed that cluster 1 was mainly characterized by plant height, number of tillers per plant and number of productive tillers per plant. The cluster 1 consisted of genotypes Kuzhi adichan, Kalanamak, Kalurundai samba, Vaikunda, Kalarpalai, Kottara samba, Illapai poo samba and Pal kodai valai. The cluster was characterized by 1000 seed weight and grain yield. The cluster 2 consists of genotypes ADT 37, ADT 39, ADT 42, ADT 43, ADT 45, ADT 47. Since the present study is done under salt stress condition we must select genotypes from 1st cluster for parents for saline breeding and genotypes from 2nd cluster as yield improvement. In the present study PCA revealed high level of genetic variation among the accession and the variable contributing the diversity. So, the result will be useful in choosing the parent in hybridization program for saline tolerance rice variety with higher yield performance.

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