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# Genetic Variability and Association Analysis for Yield and its Components in Alkaline and Inland Saline Stress in Rice (*Oryza sativa* L.)

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## ABSTRACT

The experiment was conducted at Agricultural Research Station, Kampasagar, Nalgonda, Telangana, India during the *rabi* season (December, 2020 to May, 2021) to identify suitable lines tolerant to alkalinity and inland salinity stress in rice. Analysis of variance evinced plenteous quantum of variability in all the 36 genotypes investigated. Phenotypic coefficients of variation were higher than genotypic coefficients demonstrating the effect of the prevalent stress environment. High estimates of genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance as percent mean was observed for the traits, seedling mortality, number of filled grains panicle$^{-1}$ and sterility %. These findings suggested the preponderance of additive gene action for these characters. The remaining traits were mostly under the influence of non-additive gene effects as they recorded low to moderate estimates of genetic advance. Studies from association analysis showed that number of productive tillers hill$^{-1}$ and number of filled grains panicle$^{-1}$ had a positive significant correlation with yield whereas, seedling mortality and sterility % had a negative significant association with yield. Path analysis revealed that traits number of productive tillers hill$^{-1}$, number of grains panicle$^{-1}$ and 1000 grain weight had a positive direct effect on yield. Hence primacy should be given to the above-mentioned traits to develop alkalinity and inland saline tolerant and high yielding rice cultivars. Lines CT 118911, Sahel 177, M 202 and KPS 10654 were found to be promising entries and can be used tolerant parents in the breeding programme. Three principal components combined could explain 68.86% of the total variation.

**KEYWORDS:** Rice, Alkalinity and inland salinity, variability, correlation, PCA

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***Data Availability Statement:*** Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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## 1. INTRODUCTION

Salinity is the major abiotic stress after drought in rice-growing areas of the world. Nearly 6.73 million hectares of land in India are saline (Krishnamurthy et al., 2014). The area under salinization is increasing due to various reasons including low precipitation, high surface evaporation, weathering of native rocks, excessive irrigation with saline water from bore wells, and poor cultural practices (Shrivastava and Kumar, 2015). Though irrigated lands are further expected to suffer from secondary inland salinization, it has been estimated that more than 50% of the arable land will be salinized by the year 2050 (Jamil et al., 2011). Soil salinity is known to influence about 20% of the earth's land and is relatively more widespread in arid and semi-arid climates compared to humid regions. For rice, salinity is next only to drought in limiting its productivity. Indeed, frequent occurrences of the combination of drought, due to declining water resources, and salinity, often due to poor irrigation management have created a situation where rice ecosystem are now highly vulnerable to climate change (Singh et al., 2021). Salt stress affects rice at two stages of growth i.e., seedling and reproductive stages, although many studies have documented that rice crop is resistant to salinity at the germination stage and then becomes very sensitive during the seedling stage (2–3 leaves). The effect of saline soil and alkaline soil on plants is not identical. Both of them produce ionic and osmotic stress, but alkaline soil leads to a high pH environment. High pH will affect both plants and soil, so alkaline stress is more harmful to plants than salt stress. Generally, salt affects the growth of crop plants by limiting the absorption of water through the root which ultimately affects the metabolic processes of the plant (Singh et al., 2021). It has an immediate effect on cell growth and enlargement, as high concentration of salt can be very toxic (Gregorio et al., 1997). Ion toxicity is the primary cause while osmotic stress and oxidative damage are secondary causes of salt damage. (Munns and Tester, 2008). The stress has strong effects on rice plants over its entire crop duration resulting in low seed germination rate, seedling growth retardation, seedling mortality, low biomass accumulation, reduction in the main root length and lateral root numbers, reduction in tillering ability, a lesser number of spikelets panicle$^{-1}$, greater spikelet sterility %, reduced panicle weight and thus a significant reduction in yield.

Salinity is a complex quantitative trait with low heritability and phenotypic responses of plants to salinity are greatly influenced by the environment (Tack et al., 2015). One of the easiest and cheapest ways to address the problem of salinity is to develop a tolerant variety. The existence of genetic variability for salt tolerance within the species is pivotal for the crop improvement programs concerning salinity stress because it tells whether these variations are heritable or nonheritable. The presence of sufficient genetic variability, the knowledge of the nature of association among different characters, and the relative contribution of different characters to yield is a prerequisite to any breeding program. The heritability and genetic advance are important selection parameters and are more helpful in predicting the genetic gain under effective selection (Bisne et al., 2009). Therefore, the present investigation was undertaken to estimate the genetic parameters, character association, and path coefficients in a set of 36 genotypes to be used as breeding materials for developing high-yielding alkalinity and inland salinity tolerant varieties.

## 2. MATERIALS AND METHODS

The experiment was conducted with 36 genotypes (Table 1) in randomized block design with three replications at Agricultural Research Station, Kampasagar, Nalgonda, Telangana, India during the *rabi* season (December, 2020 to May, 2021). The latitude is 16.8509° N and longitude is 79.4724° E and the field is an in-situ stress block for alkalinity and inland salinity stress with a pH of 9.30, E.C of 4.68 dSm$^{-1,}$ and ESP value is 88.0. Seeds were sown in the nursery and 30-day old seedlings were transplanted in the main field which is a stress block. FL 478 was used as salinity check, CSR 23 and CSR 36 were used as alkalinity checks and Pusa 44 as susceptible check. All the recommended package of practices, and necessary plant protection measures were followed to ensure a normal crop. Data on 10 traits *viz.* seedling mortality (SM), days to 50% flowering (DFF), plant height (PH), panicle length (PL), number of productive tillers hill$^{-1}$ (NPT), number of grains panicle$^{-1}$ (NGP), number of filled grains panicle$^{-1}$ (NFG), sterility % (SP), 1000 grain weight (TW), yield (kg ha$^{-1}$) were recorded on 5 random plants per genotype in each replication. The days to 50% flowering and yield (kg ha$^{-1}$) were recorded on a whole plot basis.

The analysis of variance and their significance for all the traits were worked out as suggested by Panse and Sukhatme (1964). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula given by Burton and Devane (1953). Heritability in broad sense $h^2$ and genetic advance as percent of mean were estimated as per Hanson (1956) and Johnson (1955). The path and correlation coefficient analysis were done following the method given by Dewey and Lu (1959). These were done using Indostat version 9.1 software. Principal component analysis was done using the PAST software v 4.03.

## 3. RESULTS AND DISCUSSION

### 3.1. *Genetic parameters*

Analysis of variance revealed significant differences for all

Table 1: Details of experimental material (genotypes) used in the study

| Sl. No. | Genotype | Sl. No. | Genotype | Sl. No. | Genotype | Sl. No. | Genotype |
|---|---|---|---|---|---|---|---|
| 1. | FL478 | 10. | IRRI154 | 19. | KPS10633 | 28. | KPS10667 |
| 2. | Pusa44 | 11. | GSRIR2 | 20. | KPS10640 | 29. | KPS10669 |
| 3. | CSR23 | 12. | CT11891 | 21. | KPS10642 | 30. | KPS10672 |
| 4. | CSR36 | 13. | IR13F167 | 22. | KPS10651 | 31. | KPS10676 |
| 5. | RNR11718 | 14. | Sahel177 | 23. | KPS10654 | 32. | KPS10683 |
| 6. | KPS2874 | 15. | Jasmine85 | 24. | KPS10656 | 33. | KPS10316 |
| 7. | IR69726 | 16. | M202 | 25. | KPS10657 | 34. | KPS10319 |
| 8. | IR77186 | 17. | KPS10628 | 26. | KPS10658 | 35. | KPS10321 |
| 9. | NSICRC240 | 18. | KPS10631 | 27. | KPS10661 | 36. | KPS10329 |

the traits indicating that sufficient variability existed in the material used in the study (Table 2). Means were calculated for the estimation of genetic parameters for all the traits (Table 3). Box-plots were drawn with the mean data (Figure 1). In descriptive statistics a box plot or boxplot (box and whisker plot) is a type of chart used for explanatory analysis. Box plots are useful as they provide a visual summary of the data enabling researchers to quickly identify mean values, the dispersion of the data set, and signs of skewness (McLeod, 2019). In the box plots the center thick lines show the median values; box limits indicate the 25th and 75th percentiles, whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles, outliers are represented by dots; and the cross sign in the box represent sample means. The trait plant height had a mean of 94.2 cm and was least in Sahel 177 (78.3 cm) to high in IR13F 167 (111.3

Table 2: Analysis of variance of 36 rice genotypes for yield and its related traits under for alkaline and inland saline stress

| Source of variation | d.f | Mean sum of squares | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | SM | DFF | PH | PL | NPT | NGP | NFG | SP | TW | Yield (kg ha$^{-1}$) |
| Replication | 2 | 13.481 | 54.065 | 42.954 | 7.148 | 0.944 | 95.071 | 60.731 | 1.410 | 1.366 | 5958.371 |
| Genotypes | 35 | 264.073$^{**}$ | 33.978$^{*}$ | 185.597$^{**}$ | 3.806$^{*}$ | 1.838$^{**}$ | 427.606$^{**}$ | 283.539$^{**}$ | 495.550$^{**}$ | 35.145$^{**}$ | 642548.400$^{**}$ |
| Error | 70 | 9.548 | 19.246 | 15.849 | 2.336 | 0.364 | 68.048 | 51.131 | 49.715 | 0.476 | 42684.700 |
| Total | 107 | 92.877 | 24.715 | 71.880 | 2.907 | 0.857 | 186.166 | 127.332 | 194.646 | 11.833 | 238215.300 |

*: Indicates significance at 5 percent probability level; **: Indicates significance at 1 percent probability level; d.f: degrees of freedom

Table 3: Estimation of genetic variability parameters for yield, yield components

| Sl. No. | Trat | Mean | Range | PCV (%) | GCV (%) | h$^2$ | GAPM |
|---|---|---|---|---|---|---|---|
| 1. | SM | 27.4 | 10.3-60.3 | 35.5 | 33.6 | 89.9 | 65.7 |
| 2. | DFF | 100.9 | 93.3-108 | 4.9 | 2.2 | 20.3 | 2.0 |
| 3. | PH | 94.2 | 78.3-111.3 | 9.0 | 8.0 | 78.1 | 14.5 |
| 4. | PL | 21.3 | 18.2-24.3 | 7.9 | 3.0 | 17.3 | 3.0 |
| 5. | NPT | 5.4 | 3.9-6.9 | 17.0 | 12.9 | 57.5 | 20.2 |
| 6. | NGP | 61.6 | 33.3-80.0 | 22.3 | 17.8 | 63.8 | 29.3 |
| 7. | NFG | 42.6 | 21.3-61.3 | 26.6 | 20.7 | 60.2 | 33.1 |
| 8. | SP | 29.9 | 12.2-56.1 | 47.1 | 40.8 | 74.9 | 72.7 |
| 9. | TW | 19.7 | 15.6-25.9 | 17.6 | 17.2 | 96.0 | 34.8 |
| 10. | Yield (kg ha$^{-1}$) | 3075 | 1825-4097 | 16.0 | 14.5 | 82.4 | 27.2 |

PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; h$^2$: heritability; GAPM: GA as percent of mean (at 5%)

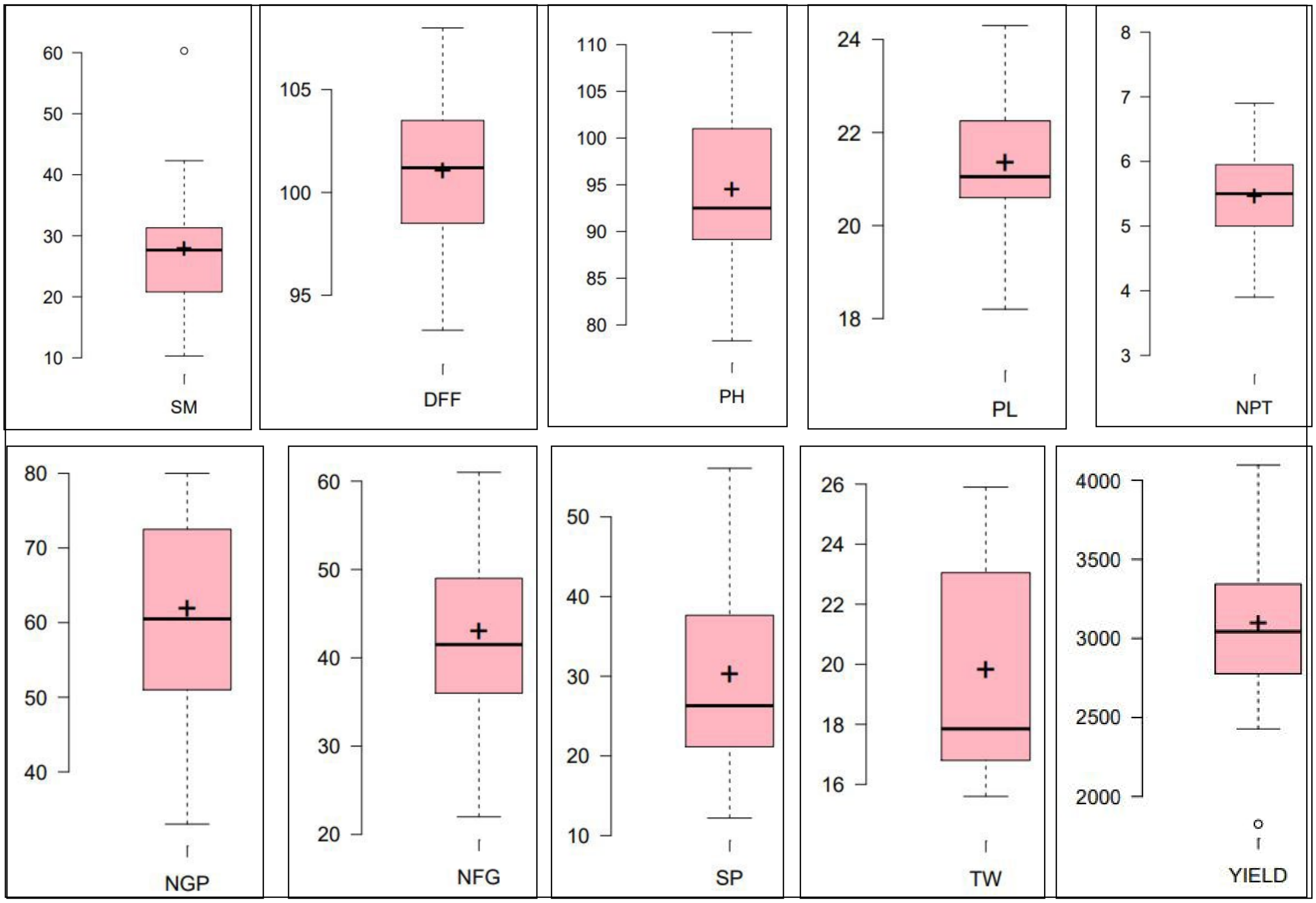

Figure 1: Box plots of yield and its related traits for the 36 genotypes under study; (Plus sign: -Mean value; dots: -Outliers; SM- Seedling mortality, DFF-Days to 50 % flowering, PH- Plant height, PL- Panicle length, NPT- Number of productive tillers hill$^{-1}$, NGP-Number of grains panicle$^{-1}$, NFP- Number of filled grains panicle$^{-1}$, SP- Sterility %, TW-1000 grain weight.

cm), while panicle length ranged had a mean value of 21.3 cm from 18.2 cm (KPS 10651) to 24.3 cm (Sahel 177), while mean for number of filled grains panicle$^{-1}$ was 42.6 ranging from 21.3 (Pusa 44) to 61.3 (KPS 2874), number of productive tillers hill$^{-1}$ mean was 5.4 ranging from 3.9 (KPS 10661 and KPS 10667) to 6.9 (Sahel 177), sterility % mean was 29.9% least in M 202 line (12.2% ) and highest in Pusa 44 (56.1% ), while the mean for 1000 grain weight was 19.7 g and ranged from 15.6 g (KPS 10628) to 25.9 g (FL 478). The characters seedling mortality, number of filled grains panicle$^{-1}$, and sterility % recorded high values of GCV and PCV indicating the presence of ample variation for these traits in the lines studied. In general, PCV is more GCV indicating environmental effect on the phenotypic expression. But negative selection should be attempted for seedling mortality and sterility percentage as they are of negative significance to the yield improvement program. Moderate values of GCV and PCV were observed for number of productive tillers hill$^{-1}$ (12.9 and 17.0), number of grains panicle$^{-1}$ (17.7 and 22.2) 1000 grain weight (17.2 and 17.5) and yield (kg ha$^{-1}$) (14.5, and 16.0). Low estimates of GCV and PCV were observed for days to 50% flowering (2.1, and 4.9), plant height (8.0, and 9.0), and panicle length (3.3 and 7.9) indicating a lack of inherent variability and limited scope for improvement through selection for these traits among the genotypes. Similar results of GCV and PCV were reported by Islam et al. (2007) for panicle length, Hasan-ud-daula and Sarker (2020) for sterility %, days to 50% flowering, number of grains panicle$^{-1}$, and number of filled grains panicle$^{-1}$, Sumanth et al. (2017) for 1000 grain weight. High heritability estimates were observed for seedling mortality (89.9), plant height (78.1), number of grains panicle$^{-1}$ (63.8), number of filled grains panicle$^{-1}$ (60.2), sterility (74.9), 1000 grain weight (96.0), and yield (82.4) suggesting that these traits are under genetic control, i.e., less environmental influence. High heritability alone is not enough to make sufficient improvement through selection in advanced generations unless accompanied by a substantial amount of genetic advance. The efficacy of heritability is increased with the estimation of genetic advance, which indicates the degree of gain in a trait obtained under particular selection pressure. High heritability coupled with high genetic advance was observed for seedling mortality, number of grains panicle$^{-1}$, number of filled grains panicle$^{-1}$, sterility %, test weight, and yield (kg ha$^{-1}$). Direct selection of these characters based on phenotypic values would be effective due to the accumulation of more additive genes along with negative selection for seedling mortality and sterility %, while aiming for yield improvement. These results of high heritability coupled with high gentic advance were observed for the trait number of grains per panicle by Sameera et al. (2016), Saha et al. (2019) for number of grains panicle$^{-1}$, number of filled grains panicle$^{-1}$ , 1000 grain weight, yield (kg ha$^{-1}$), and Hasan-ud-daula and Sarker (2020) for sterility %.

### *3.2. Correlation analysis*

Results from correlation analysis (Table 4) showed traits such as seedling mortality and sterility percentage showed a significant negative correlation with yield (kg ha$^{-1}$) whereas number of productive tillers hill$^{-1}$ and number of filled grains panicle$^{-1}$ showed positive significant associations with yield (kg ha$^{-1}$). The number of productive tillers hill$^{-1}$ had a positive significant association with number of filled grains panicle$^{-1}$ (0.2341$^{*}$), yield (kg ha$^{-1}$) (0.5171$^{*}$), and a negative significant association with seedling mortality (-0.4366$^{*}$) and sterility % (-0.4127$^{*}$). So, selecting genotypes with more productive panicles increases the number of filled grains and thus increases the yield. These findings are in accordance with the findings of Muthuvijayaragavan and Murugan (2020) for number of productive tillers hill$^{-1}$.

The trait number of filled grains panicle$^{-1}$ had a significant positive association with yield (kg ha$^{-1}$) (0.5413$^{*}$), number of productive tillers hill$^{-1}$ (0.2341$^{*}$), and number of grains panicle$^{-1}$ (0.6014$^{*}$) while with traits sterility % (-0.5519$^{*}$) and 1000 grain weight (-0.2420$^{*}$) it has shown a negative significant association. Hasan-Ud-Daula and Sarker (2020) also reported similar findings for number of filled grains panicle$^{-1}$ with yield (kg ha$^{-1}$). Plant height exhibited a negative correlation with yield (-0.0237), panicle length (-0.1399), number of productive tillers hill$^{-1}$ (-0.0158) indicating that selection of dwarf lines that are resistant to lodging increases the yield through the production of more panicles.

Table 4: Phenotypic correlations for yield and yield components in 36 genotypes under study

| Trait | SM | DFF | PH | PL | NPT | NGP | NFG | SP | TW | Yield (kg ha$^{-1}$) |
|---|---|---|---|---|---|---|---|---|---|---|
| SM | 1.0000 | 0.2728$^{**}$ | -0.0689 | -0.0958 | -0.4366$^{**}$ | 0.0860 | -0.3657$^{**}$ | 0.5946$^{**}$ | -0.2559$^{**}$ | -0.6391$^{**}$ |
| DFF | 0.2728$^{**}$ | 1.0000 | 0.1022 | -0.1206 | 0.0141 | 0.0984 | -0.0121 | 0.1110 | -0.0722 | -0.1522 |
| PH | -0.0689 | 0.1022 | 1.0000 | -0.1399 | -0.0158 | 0.1548 | 0.1302 | -0.0178 | -0.1773 | -0.0237 |
| PL | -0.0958 | -0.1206 | -0.1399 | 1.0000 | -0.0135 | 0.0141 | 0.0453 | -0.0321 | 0.1574 | -0.0420 |
| NPT | -0.4366$^{**}$ | 0.0141 | -0.0158 | -0.0135 | 1.0000 | -0.1149 | 0.2341$^{*}$ | -0.4127$^{**}$ | 0.1700 | 0.5171$^{**}$ |
| NGP | 0.0860 | 0.0984 | 0.1548 | 0.0141 | -0.1149 | 1.0000 | 0.6014$^{**}$ | 0.3150$^{**}$ | -0.5805$^{**}$ | 0.1748 |
| NFP | -0.3657$^{**}$ | -0.0121 | 0.1302 | 0.0453 | 0.2341$^{*}$ | 0.6014$^{**}$ | 1.0000 | -0.5519$^{**}$ | -0.2420$^{*}$ | 0.5413$^{**}$ |
| SP | 0.5946$^{**}$ | 0.1110 | -0.0178 | -0.0321 | -0.4127$^{**}$ | 0.3150$^{**}$ | -0.5519$^{**}$ | 1.0000 | -0.3109$^{**}$ | -0.5060$^{**}$ |
| TW | -0.2559$^{**}$ | -0.0722 | -0.1773 | 0.1574 | 0.1700 | -0.5805$^{**}$ | -0.2420$^{*}$ | -0.3109$^{**}$ | 1.0000 | 0.0341 |

$^{*}p$=0.05; $^{**}p$=0.01; P: Phenotypic path coefficients; Phenotypic Residual Effect=0.6270

Seedling mortality showed a negative significant association with yield (-0.6391$^{*}$), number of productive tillers hill$^{-1}$ (-0.4366$^{*}$), number of filled grains panicle$^{-1}$ (-0.3657$^{*}$), and 1000 grain weight (-0.2559$^{*}$) stating that selection of genotypes with low seedling mortality would increase the yield through production of more panicles and a higher% of filled grains in panicle and increasing the 1000 grain weight. These results are in line with the findings of Touhiduzzaman et al. (2016) and Hasan-Ud-Daula and Sarker (2020). Sterility % had a negative significant association with yield (kg ha$^{-1}$) (-0.5060$^{*}$), number of productive tillers hill$^{-1}$ (-0.4127$^{*}$), number of filled grains panicle$^{-1}$ (-0.5519$^{*}$) and 1000 grain weight (-0.3109$^{*}$) indicating that, for increasing the of the yield, selection should be done for lines having low sterility %. Ghazy et al. (2020) reported a similar finding for sterility % having a negative significant association with yield (kg ha$^{-1}$).

### *3.3. Path coefficient analysis*

An estimate of simple correlation would not provide the true contribution of the characters towards the yield and by apportioning the correlations, path analysis allows separating these correlations into the direct effect and indirect effects for better interpretation of cause and effect (Table 5). Path coefficient analysis revealed a positive direct effect of number of productive tillers hill$^{-1}$ (0.2749), number of grains panicle$^{-1}$ (0.5647) and 1000 grain weight (0.0032)

Table 5: Phenotypic path coefficient analysis for yield and its components in 36 genotypes under study

| Trait | SM | DFF | PH | PL | NPT | NGP | NFG | SP | TW | Yield (kg ha$^{-1}$) |
|---|---|---|---|---|---|---|---|---|---|---|
| SM | -0.3715 | -0.1013 | 0.0256 | 0.0356 | 0.1622 | -0.0319 | 0.1358 | -0.2209 | 0.0951 | -0.6391 |
| DFF | -0.0166 | -0.0608 | -0.0062 | 0.0073 | -0.0009 | -0.0060 | 0.0007 | -0.0068 | 0.0044 | -0.1522 |
| PH | 0.0081 | -0.0120 | -0.1179 | 0.0165 | 0.0019 | -0.0182 | -0.0153 | 0.0021 | 0.0209 | -0.0237 |
| PL | 0.0106 | 0.0133 | 0.0155 | -0.1106 | 0.0015 | -0.0016 | -0.0050 | 0.0035 | -0.0174 | -0.0420 |
| NPT | -0.1200 | 0.0039 | -0.0043 | -0.0037 | 0.2749 | -0.0316 | 0.0643 | -0.1134 | 0.0467 | 0.5171 |
| NGP | 0.0486 | 0.0556 | 0.0874 | 0.0079 | -0.0649 | 0.5647 | 0.3396 | 0.1779 | -0.3278 | 0.1748 |
| NFP | 0.0893 | 0.0030 | -0.0318 | -0.0111 | -0.0571 | -0.1468 | -0.2442 | 0.1348 | 0.0591 | 0.5413 |
| SP | -0.2867 | -0.0535 | 0.0086 | 0.0155 | 0.1990 | -0.1519 | 0.2661 | -0.4821 | 0.1499 | -0.5060 |
| TW | -0.0016 | -0.0006 | -0.0011 | 0.0007 | 0.0009 | -0.0036 | -0.0015 | -0.0010 | 0.0032 | 0.0341 |

on yield (kg ha$^{-1}$). These findings are in line with the findings of Muthuvijayaragavan and Murugan (2020). Panicle length and number of filled grains panicle$^{-1}$ had positive indirect effects on yield through plant height (0.0155), number of grains panicle$^{-1}$ (0.0874), 1000 grain weight (0.0005) and number of productive tillers hill$^{-1}$ (0.0643), number of grains panicle$^{-1}$ (0.3396) respectively. Sterility % had a negative direct effect (-0.3715) as well as a significant negative correlation with yield (kg ha$^{-1}$) (-0.6391$^{*}$). Therefore, it is logical to select genotypes having low sterility % for the improvement of yield.

### *3.4. Principal component analysis*

PCA (Principal component analysis) measures the importance and contribution of each component to total variance. Each coefficient of vectors indicates the degree of contribution of every original variable with which each principal component (PCs) is associated. The higher the coefficients, regardless of the sign, the more effective they will be in discriminating between accessions.

Principal component analysis has shown the genetic diversity of the experimental material under study. The cumulative variances of 68.86% by the first three axes with eigen values of >1.0 (Table 6) indicates that the identified traits within the axes exhibited great influence on the phenotype of experimental material under study. Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers (Figure 2). It depicted the gradual decline of eigen values across the different principal components. A scatter plot

Table 6: Principal component analysis for 10 characters and the variation accounted due to the stress

| | PC 1 | PC 2 | PC 3 | PC 4 | PC 5 | PC 6 | PC 7 | PC 8 | PC 9 | PC 10 |
|---|---|---|---|---|---|---|---|---|---|---|
| Eigenvalue | 3.39 | 2.32 | 1.17 | 0.91 | 0.83 | 0.58 | 0.36 | 0.26 | 0.16 | 0.00 |
| % variance | 33.93 | 23.22 | 11.71 | 9.13 | 8.32 | 5.79 | 3.62 | 2.64 | 1.60 | 0.04 |
| Cumulative variance | 33.93 | 57.15 | 68.86 | 77.99 | 86.31 | 92.10 | 95.72 | 98.36 | 99.96 | 100.00 |
| SM | -0.473 | 0.052 | 0.017 | 0.140 | -0.167 | -0.136 | -0.277 | 0.727 | 0.301 | -0.101 |
| DFF | -0.198 | 0.149 | 0.475 | 0.731 | -0.167 | -0.058 | 0.134 | -0.339 | 0.124 | 0.015 |
| PH | 0.004 | 0.260 | 0.551 | -0.170 | 0.710 | 0.233 | 0.004 | 0.169 | 0.109 | 0.012 |
| PL | 0.010 | -0.255 | -0.510 | 0.504 | 0.593 | 0.026 | -0.198 | -0.061 | 0.160 | 0.000 |
| NPT | 0.407 | -0.040 | 0.096 | 0.308 | -0.210 | 0.623 | -0.305 | 0.298 | -0.339 | -0.005 |
| NGP | -0.058 | 0.577 | -0.322 | 0.133 | 0.068 | 0.072 | 0.389 | 0.112 | -0.261 | -0.548 |
| NFG | 0.334 | 0.431 | -0.078 | 0.168 | 0.063 | -0.477 | -0.025 | 0.239 | -0.209 | 0.580 |
| SP | -0.462 | 0.091 | -0.233 | -0.026 | -0.032 | 0.502 | 0.343 | 0.012 | -0.021 | 0.593 |
| TW | 0.145 | -0.533 | 0.150 | 0.146 | 0.081 | -0.138 | 0.667 | 0.402 | -0.139 | -0.017 |
| YIELD | 0.471 | 0.171 | -0.121 | -0.001 | -0.168 | 0.180 | 0.244 | 0.064 | 0.781 | 0.018 |

SM: Seedling mortality; DFF: Days to 50% flowering; PH: Plant height; PL: Panicle length; NPT: Number of productive tillers hill$^{-1}$; NGP: Number of grains panicle$^{-1}$; NFP: Number of filled grains panicle$^{-1}$; SP: Sterility %; TW:1000 grain weight

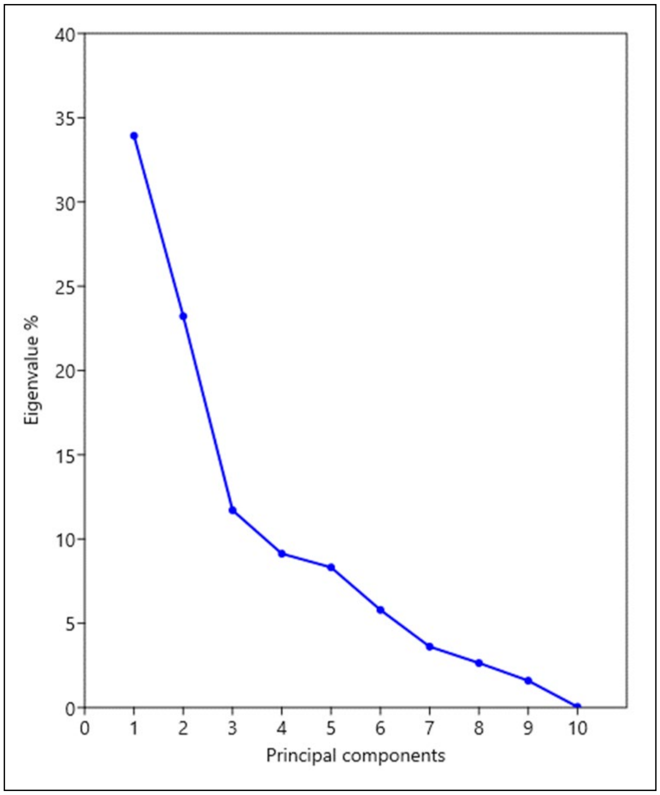

Figure 2: Scree plot showing eigen value variation between different principal components

was drawn between PC1 and PC2 depicted a clear pattern of grouping genotypes in the factor plane (Figure 3). The variables that are on the same quarter are very close to each other signify that there are positive correlations between them. The genotypes and the traits lying in the same quarter representing the possibility of selection of genotypes for the specific traits. Thus, these biplot diagrams can be used to select the genotypes while searching to improve a specific trait.

The different morphological traits contribute for total variation calculated for each component. In principal component 1, three traits yield (0.471), number of productive tillers hill$^{-1}$ (0.407) and number of filled grains panicle$^{-1}$ (0.334) contributed 33.93% to the total variation. In principal component 2, seven traits number of grains panicle$^{-1}$ (0.577), number of filled grains panicle$^{-1}$ (0.431), plant height (0.260), yield (0.171), days to 50% flowering (0.149), sterility % (0.091), and seedling mortality (0.052) contributed 23.22% to the total variation. In principal component 3, five traits plant height (0.551), days to 50% flowering (0.475), 1000 grain weight (0.150), number of productive tillers hill$^{-1}$ (0.096) and seedling mortality (0.017) contributed to 11.71% to the total variation.

From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other PCs. So, selection of lines from this PC will be useful. Those principal components having more than one eigen value that showed more variation among the rice genotypes for the selection of the diverse parents.

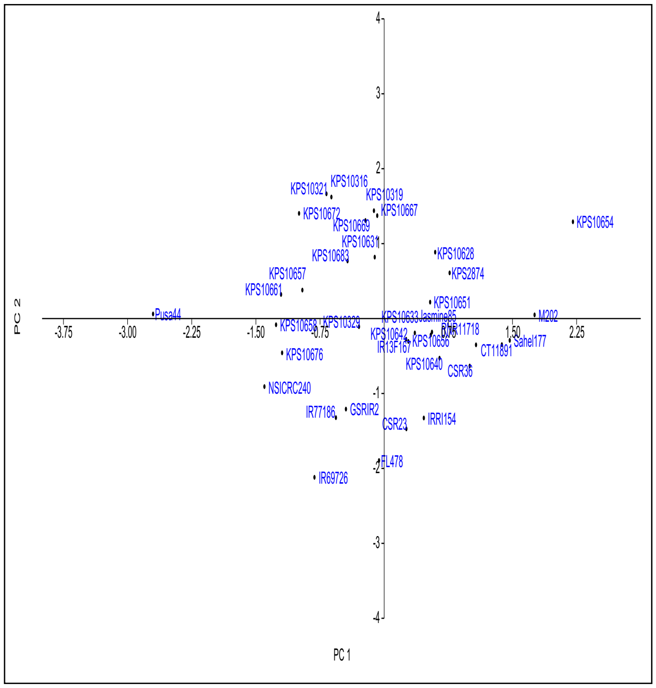

Figure 3: Bi-plot of PC1 against PC2 showing variations among rice genotypes

Similar results of 3 PCs having eigen value >1 was obtained by Surapaneni et al., 2016 while studying the diversity analysis in rice breeding lines for yield and its components. Four PCs were observed by Shoba et al., 2019 whereas five principal components were observed by Ibrahim et al., 2019.

## 4. CONCLUSION

The number of productive tillers hill$^{-1}$, the number of grains panicle$^{-1}$, the number of filled grains panicle$^{-1}$, seedling mortality (%), and sterility percentage (%) were identified as the most reliable traits for yield improvement in the study. Lines CT 118911, Sahel 177, M 202, and KPS 10654 exhibited better performance with early flowering and high responsiveness to stress, coupled with lower mortality. Consequently, they were considered suitable lines for parental roles in a hybridization program.

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