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# Assessing genetic variability in rice (*Oryza sativa* L.) under sodic soil following generation mean analysis

**Priyanka Gupta, OP Verma, RL Verma, Rahul Kumar Gupta, Krishna Pratap Singh and Priyansh Singh**

## Abstract
The experiment was conducted in on Main Experimental Station of A.N.D. University of Agriculture & Technology, Narendra Nagar (Kumarganj), Ayodhya during *kharif* season 2019 to estimate genetic variability in rice four cross combination including six generations *viz.*, parents ($P_1$, $P_2$), the $F_1$s, $F_2$s, and back crosses with both the parents ($B_1$ and $B_2$) of crosses Swarna *Sub-1* x CSR-10, Sambha *Sub-1* x CSR-10, Pusa Sugandha -5 x CSR-10, Pusa Sugandha -5 x NDR-2064 with respect to yield and quality traits. Observation was recorded on twenty characters. The estimates of high genotypic and phenotypic variances in cross I for the characters like days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, plant height (cm), number of effective tillers/plant, flag leaf area ($cm^2$), number of spikelet's/panicle, protein content (%), in cross I, while in cross II, high GCV and PCV was recorded for days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, plant height (cm), number of effective tillers/plant, flag leaf area ($cm^2$), number of spikelet's/panicle, protein content (%) and grain yield/plant. Cross III shows high GCV and PCV for chlorophyll a, chlorophyll b, carotene, total chlorophyll, plant height (cm), number of effective tillers/plant, grains/panicle, flag leaf area ($cm^2$), number of spikelet's/panicle, grain size (l: b ratio), protein content (%). In cross IV high GCV was recorded for chlorophyll a, chlorophyll b, carotene, total chlorophyll, , flag leaf area ($cm^2$), number of spikelet's/panicle, grains/panicle, grain size (l: b ratio), grain yield/plant (g) and PCV was recorded for trait days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, , flag leaf area ($cm^2$), biological yield/plant (g), number of spikelet's/panicle, grains/panicle, spikelet fertility (%), grain size (l: b ratio) and grain yield/plant (g). Therefore, all the cross (F1, F2, B1 and B2) combinations can be used further for selecting the novel recombinants for improvement under sodic soil for sustainability.

**Keywords:** Rice (*Oryza sativa* L.), genetic variability GCV and PCV

## Introduction
Rice (*Oryza sativa* L.), belonging to family Gramineae (Poaceae), has a chromosome number of 2n = 24. It is one of the major food crops of the developing world and form the staple diet of about half of the world's population. Asia is the leader in rice production accounting for about 90% of the world's production. About 75% of the world's supply is consumed by the people in Asian countries and thus, rice is of immense importance to food security of Asia. The demand for quality rice is expected to increase with continuous increase in global population. Production of rice is not increasing rapidly because of more affected part of cultivation by biotic and abiotic stress, in all the abiotic stress salinity plays a major role in yield loss. Mainly Salt affected areas have increased day by day because of excessive use of irrigation water with improper drainage coupled with the poor-quality irrigation water. Development of varieties for underutilized soil is the only option to increase the production. Thus, adoption of high yielding and resistant varieties of rice to various stress environment and underutilized land such as salt affected soil would be an important strategy to meet this challenge. The presence of desirable variability in different generation of selected germplasm enables breeders to recombine favourable phenotypes of different traits to develop improved genotypes capable of producing high and stable yield. Therefore, it becomes imperative to evaluate the available germplasm and assess the existing genetic variability for yield attributing and quality trait. Various workers have observed significant contributions in this context *viz.*, for grains/panicle and number of spikelets/panicle (Devi *et al.*, 2020) Protein content of milled rice is 6-7 per cent, rice however, compares favourably with other cereals in amino acid content. The biological value of protein is high, the fat content of rice is low (2.0-2.5%) and much of the fat is lost during milling. Rice grain contains as much B group vitamin

as wheat. Milled rice losses valuable proteins, vitamins and minerals in the milling process during which embryo and aleurone layer are removed and much of the loss of nutrients can avoided through parboiling process. The by-products of rice milling are used for a variety of purposes. Rice being the staple food for more than 70 percent of our national population along with the source of livelihood for 120-150 million rural household. It is a backbone to the Indian agriculture. This study was therefore, conducted to select potential cross combination of different generation of selected genotype and to identify the most important yield attributed and quality characters for breeding programmes by exploiting the genotypic variance, phenotypic variance, genotypic coefficient of variance, phenotypic coefficient of variance analysis of quality and yield related attributes of four cross combination of generation mean.

## Materials and Methods

The present investigation was conducted during *Kharif*, 2018 and 2019 on Main Experimental Station of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya-224229 (U.P.), and *rabi* season 2018 at Research Farm of National Rice Research Institute (ICAR-NRRI), Cuttack, Odisha, India. Five genetically diverse genotypes are used in four cross combination *viz*., (Swarna *Sub-1* x CSR-10), (Sambha *Sub-1* x CSR-10), (Pusa Sugandha -5 x CSR-10) and (Pusa Sugandha -5 x NDR2064) crossed to generate six generations *viz*., parents ($P_1$, $P_2$), the $F_1$s, $F_2$s, and back crosses with both the parents ($B_1$ and $B_2$) following generation mean analysis. The experiment was evaluated in compact family Block Design with three replications during *Kharif* 2019. Each plot was consisting of a double row of 3-meter-long beds with intra row spacing spaced 20 cm apart. Seed to seed distance within a row was kept 15 cm. Similar planting distance was maintained for P1, P2, F1's, F2's, B1 and B2. The desired observation was recorded on ten randomly selected plants of parents, 10 plants from F1's, 15 plants from B1, B2 population and 30 plants from F2 generation. The soil type of the experimental site was sandy loam, low in organic carbon, nitrogen, and phosphorus and rich in potash (EC-3.2dSm-1; ESP-45% and pH-9.2).Data were collected on 20 characters germination percentage, days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, days of maturity, plant height (cm), number of effective tillers/plant, panicle length (cm), flag leaf area ($cm^2$), biological yield/plant (g), number of spikelets/panicle, grains/panicle, spikelet fertility (%), grain size (L: B ratio), test weight (g), harvest index (%), protein content (%), grain yield/plant (g). Analysis of variance was done following procedure of Singh and Chaudhary (1985). The genetic parameters, including the genotypic and phenotypic variance, genotypic and phenotypic coefficient of variance, were calculated using the formula given by Burton and De Vane (1953) [1]. And Johnson *et al.* (1955) [5].

## Results and Discussion

The analysis of variance for four cross combination have been depicted in table-1. The analysis of variance was carried out for twenty characters of four cross families in Compact Family Block Design under sodic soil. Significance of data was tested by 'F' test. Variances for differences between progenies within families are calculated for both genotypic and phenotypic. The analysis of variance of Compact Family Block Design for differences between families (crosses) for twenty characters of four crosses (Swarna *Sub-1* x CSR-10), (Sambha *Sub-1* x CSR-10), (Pusa Sugandha -5 x CSR-10) and (Pusa Sugandha -5 x NDR2064) was calculated. The mean squares for differences between four crosses families were either significant for all the twenty characters under study. The mean sum of squares due to replications were significant in case of chlorophyll content (cross II) and plant height (cross IV). The analysis of variance of Compact Family Block Design for differences among progenies within family is presented in Table-1. The mean sum of squares due to replications were found non-significant for all the characters in all the crosses except chlorophyll content in cross II and plant height in cross IV. The mean sum of squares due to differences among generations or progenies within each cross family were significant or highly significant in all the characters except germination percentage and chlorophyll b in cross I, chlorophyll a and chlorophyll b in cross III**.**

**Table 4.2:** Analysis of variance for differences between progenies (generations) within families (crosses) for a cross I, II, III and IV in sodic soil

| Characters D.F. | Cross I | | | Cross II | | | Cross III | | | Cross IV | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Replications | Progenies | Error | Replications | Progenies | Error | Replications | Progenies | Error | Replications | Progenies | Error |
| | 2 | 5 | 10 | 2 | 5 | 10 | 2 | 5 | 10 | 2 | 5 | 10 |
| Germination percentage | 2.06 | 3.66 | 2.12 | 2.39 | 3.96** | 1.06 | 0.06 | 15.12** | 3.59 | 0.06 | 23.02** | 2.99 |
| Days to 50% flowering | 0.50 | 290.77** | 3.17 | 1.72 | 379.12** | 2.46 | 2.06 | 121.82** | 2.19 | 6.22 | 36.46** | 1.62 |
| Chlorophyll a | 0.020 | 0.399** | 0.149 | 0.304 | 0.385** | 0.048 | 0.473 | 0.230 | 0.104 | 0.029 | 0.411** | 0.064 |
| Chlorophyll b | 0.005 | 0.055 | 0.026 | 0.004 | 0.068** | 0.015 | 0.082 | 0.082 | 0.039 | 0.002 | 0.104** | 0.011 |
| Carotene | 0.013 | 0.080** | 0.013 | 0.026 | 0.059** | 0.009 | 0.047 | 0.060** | 0.015 | 0.012 | 0.123** | 0.014 |
| Total chlorophyll | 0.05 | 0.66** | 0.22 | 0.36 | 0.50** | 0.08 | 0.92 | 0.52** | 0.14 | 0.02 | 0.84** | 0.10 |
| Days of Maturity | 0.50 | 270.50** | 3.30 | 1.17 | 372.67** | 2.03 | 1.56 | 111.56** | 4.36 | 0.39 | 34.09** | 2.32 |
| Plant height(cm) | 0.78 | 209.00** | 2.47 | 0.85 | 199.66** | 1.37 | 4.99 | 391.05** | 2.88 | 1.42 | 102.83** | 2.87 |
| Number of effective tillers/plant | 2.08 | 3.71** | 0.60 | 0.11 | 3.59** | 0.12 | 0.07 | 4.56** | 0.13 | 0.08 | 1.33** | 0.13 |
| Panicle length (cm) | 0.80 | 7.35** | 0.24 | 0.18 | 6.04** | 0.17 | 1.94 | 12.39** | 0.34 | 1.62 | 1.85** | 0.24 |
| Flag leaf area (cm2) | 2.04 | 25.19** | 0.38 | 7.42 | 55.05** | 0.88 | 18.78 | 96.41** | 1.06 | 5.89 | 42.66** | 2.15 |
| Biological yield/plant (g) | 20.24 | 9.98* | 4.90 | 13.08 | 29.02** | 3.81 | 6.21 | 45.15** | 5.89 | 1.68 | 47.20** | 7.81 |
| Number of spikelets/panicle | 87.35 | 4479.68** | 53.34 | 128.75 | 5805.42** | 27.41 | 68.20 | 947.25** | 8.71 | 485.52 | 911.63** | 310.44 |
| Grains/panicle | 94.06 | 4606.47** | 41.16 | 43.57 | 5025.00** | 16.88 | 48.84 | 740.77** | 7.92 | 62.52 | 1129.02** | 19.76 |
| Spikelet fertility (%) | 12.59 | 25.33** | 2.91 | 6.17 | 17.40** | 5.96 | 7.90 | 10.62** | 2.67 | 53.73 | 143.26** | 64.74 |
| Grain size (L: B ratio) | 0.009 | 0.047** | 0.003 | 0.011 | 0.185** | 0.011 | 0.129 | 3.679** | 0.031 | 0.008 | 2.028** | 0.011 |
| Test weight (g) | 0.26 | 1.04** | 0.11 | 0.17 | 1.16** | 0.12 | 0.04 | 9.34** | 0.19 | 0.52 | 4.65** | 0.44 |
| Harvest index (%) | 4.97 | 29.64** | 1.22 | 2.94 | 45.66** | 2.81 | 6.59 | 34.70** | 1.24 | 0.65 | 16.01** | 4.67 |
| Protein content (%) | 0.00 | 5.63** | 0.07 | 0.05 | 5.23** | 0.07 | 0.00 | 4.46** | 0.07 | 0.20 | 0.55** | 0.14 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Grain yield/plant (g) | 7.18 | 5.47** | 0.76 | 4.57 | 13.60** | 0.82 | 1.06 | 6.34** | 0.77 | 0.67 | 10.88** | 1.42 |

*, ** significant at 5% and 1% level of probability, respectively.

**Table 4.9:** Genotypic variance of four cross in 20 observation

| Traits | Cross I | Cross II | Cross III | Cross IV |
|---|---|---|---|---|
| Germination percentage | 0.51 | 0.97 | 3.84 | 6.68 |
| Days to 50% flowering | 95.87 | 125.56 | 39.88 | 11.61 |
| Chlorophyll a | 0.08 | 0.11 | 0.04 | 0.12 |
| Chlorophyll b | 0.01 | 0.02 | 0.01 | 0.03 |
| Carotene | 0.02 | 0.02 | 0.02 | 0.04 |
| Total chlorophyll | 0.15 | 0.14 | 0.13 | 0.25 |
| Days of Maturity | 89.07 | 123.54 | 35.73 | 10.59 |
| Plant height(cm) | 68.84 | 66.10 | 129.39 | 33.32 |
| Number of effective tillers/plant | 1.04 | 1.16 | 1.48 | 0.40 |
| Panicle length (cm) | 2.37 | 1.96 | 4.02 | 0.54 |
| Flag leaf area (cm2) | 8.27 | 18.06 | 31.78 | 13.50 |
| Biological yield/plant (g) | 1.69 | 8.40 | 13.09 | 13.13 |
| Number of spikelets/panicle | 1475.45 | 1926.00 | 313.85 | 200.40 |
| Grains/panicle | 1521.77 | 1669.37 | 244.28 | 369.75 |
| Spikelet fertility (%) | 7.47 | 3.81 | 2.65 | 26.17 |
| Grain size (L: B ratio) | 0.01 | 0.06 | 1.22 | 0.67 |
| Test weight (g) | 0.31 | 0.35 | 3.05 | 1.40 |
| Harvest index (%) | 9.47 | 14.28 | 11.15 | 3.78 |
| Protein percentage | 1.85 | 1.72 | 1.46 | 0.14 |
| Grain yield/plant (g) | 1.57 | 4.26 | 1.85 | 3.15 |

**Table 4.9:** Phenotypic variance of four cross in 20 observation

| Traits | Cross I | Cross II | Cross III | Cross IV |
|---|---|---|---|---|
| Germination percentage | 2.63 | 2.02 | 7.43 | 9.67 |
| Days to 50% flowering | 99.03 | 128.01 | 42.07 | 13.23 |
| Chlorophyll a | 0.23 | 0.16 | 0.15 | 0.18 |
| Chlorophyll b | 0.04 | 0.03 | 0.05 | 0.04 |
| Carotene | 0.04 | 0.03 | 0.03 | 0.05 |
| Total chlorophyll | 0.37 | 0.22 | 0.27 | 0.35 |
| Days of Maturity | 92.37 | 125.58 | 40.09 | 12.91 |
| Plant height(cm) | 71.31 | 67.47 | 132.27 | 36.19 |
| Number of effective tillers/plant | 1.63 | 1.28 | 1.61 | 0.53 |
| Panicle length (cm) | 2.61 | 2.13 | 4.35 | 0.77 |
| Flag leaf area (cm2) | 8.65 | 18.94 | 32.84 | 15.65 |
| Biological yield/plant (g) | 6.59 | 12.21 | 18.98 | 20.94 |
| Number of spikelet's/panicle | 1528.79 | 1953.41 | 321.55 | 510.84 |
| Grains/panicle | 1562.93 | 1686.25 | 252.20 | 389.51 |
| Spikelet fertility (%) | 10.38 | 9.77 | 5.32 | 90.91 |
| Grain size (L: B ratio) | 0.02 | 0.07 | 1.25 | 0.68 |
| Test weight (g) | 0.42 | 0.47 | 3.24 | 1.84 |
| Harvest index (%) | 10.69 | 17.09 | 12.39 | 8.45 |
| Protein percentage | 1.93 | 1.79 | 1.54 | 0.28 |
| Grain yield/plant (g) | 2.33 | 5.08 | 2.63 | 4.57 |

**Table 4.9:** Genotypic coefficient of variance of four cross GCV (%)

| Traits | Cross I | Cross II | Cross III | Cross IV |
|---|---|---|---|---|
| Germination percentage | 0.91 | 1.30 | 2.54 | 3.34 |
| Days to 50% flowering | 10.51 | 12.22 | 7.00 | 3.78 |
| Chlorophyll a | 13.58 | 15.34 | 11.86 | 19.68 |
| Chlorophyll b | 14.62 | 19.80 | 24.40 | 35.53 |
| Carotene | 23.37 | 19.40 | 22.63 | 35.16 |
| Total chlorophyll | 13.72 | 13.16 | 16.01 | 22.35 |
| Days of Maturity | 7.70 | 9.14 | 5.00 | 2.72 |
| Plant height(cm) | 10.38 | 10.10 | 13.42 | 6.81 |
| Number of effective tillers/plant | 10.81 | 10.74 | 11.72 | 6.10 |
| panicle length (cm) | 7.24 | 6.61 | 9.02 | 3.30 |
| Flag leaf area (cm2) | 11.72 | 15.49 | 19.05 | 12.42 |
| Biological yield/plant (g) | 2.90 | 6.56 | 8.77 | 8.79 |
| Number of spikelets/panicle | 30.54 | 30.90 | 17.08 | 13.67 |
| Grains/panicle | 33.68 | 31.96 | 17.50 | 21.53 |

| | | | | |
|---|---|---|---|---|
| Spikelet fertility (%) | 2.99 | 2.18 | 1.89 | 5.94 |
| Grain size (L: B ratio) | 4.63 | 8.19 | 25.90 | 19.26 |
| Test weight (g) | 2.52 | 2.61 | 7.72 | 5.24 |
| Harvest index (%) | 7.55 | 9.37 | 8.30 | 4.83 |
| Protein percentage | 15.09 | 14.50 | 12.07 | 3.67 |
| Grain yield/plant (g) | 6.86 | 11.58 | 8.24 | 10.74 |

**Table 4.9:** phenotypic coefficient of variance of four cross PCV (%)

| Traits | Cross I | Cross II | Cross III | Cross IV |
|---|---|---|---|---|
| Germination percentage | 2.07 | 1.88 | 3.53 | 4.02 |
| Days to 50% flowering | 10.68 | 12.34 | 7.19 | 4.03 |
| Chlorophyll a | 22.65 | 18.31 | 22.12 | 24.52 |
| Chlorophyll b | 28.08 | 26.81 | 46.75 | 41.58 |
| Carotene | 29.56 | 23.93 | 32.22 | 41.40 |
| Total chlorophyll | 21.62 | 16.54 | 23.31 | 26.47 |
| Days of Maturity | 7.85 | 9.21 | 5.30 | 3.01 |
| Plant height(cm) | 10.56 | 10.20 | 13.57 | 7.10 |
| Number of effective tillers/plant | 13.56 | 11.28 | 12.23 | 7.04 |
| Panicle length (cm) | 7.60 | 6.89 | 9.39 | 3.96 |
| Flag leaf area (cm2) | 11.99 | 15.86 | 19.37 | 13.37 |
| Biological yield/plant (g) | 5.73 | 7.91 | 10.56 | 11.10 |
| Number of spikelet's/panicle | 31.08 | 31.11 | 17.31 | 21.82 |
| Grains/panicle | 34.14 | 32.12 | 17.78 | 22.10 |
| Spikelet fertility (%) | 3.53 | 3.49 | 2.68 | 11.06 |
| Grain size (L: B ratio) | 5.02 | 8.95 | 26.22 | 19.41 |
| Test weight (g) | 2.92 | 3.04 | 7.96 | 6.00 |
| Harvest index (%) | 8.02 | 10.25 | 8.75 | 7.22 |
| Protein percentage | 15.38 | 14.78 | 12.37 | 5.28 |
| Grain yield/plant (g) | 8.37 | 12.64 | 9.81 | 12.94 |

The results revealed a wide range of variability among individual cross I, II, III and IV in sodic soil condition for yield attributing and quality trait. The phenotypic variance ($\sigma$2P) of most of the traits was higher than the genotypic variance ($\sigma$2G), similarly, the phenotypic coefficient of variation (PCV) was also higher than genotypic coefficient of variation (GCV). The highest GCV was recorded in cross I for days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, plant height (cm), number of effective tillers/plant, flag leaf area ($cm^2$), number of spikelets/panicle, grains/panicle, protein content (%) while in cross II highest genotypic variance and genotypic coefficient of variance was recorded for all the above cross I characters also including grain yield/plant (g). The highest GCV was recorded in cross III for chlorophyll a, chlorophyll b, carotene, total chlorophyll, plant height (cm), number of effective tillers/plant, flag leaf area ($cm^2$), number of spikelets/panicle, grains/panicle, protein content (%) and in cross IV show highest genotypic variance and genotypic coefficient of variance for chlorophyll a, chlorophyll b, carotene, total chlorophyll, , flag leaf area ($cm^2$), number of spikelets/panicle, grains/panicle, grain size (L: B ratio), grain yield/plant (g), Seneega *et al.* (2019) [11]. The highest PCV was recorded in cross I for days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, plant height (cm), number of effective tillers/plant, flag leaf area ($cm^2$), number of spikelets/panicle, grains/panicle, protein content (%) and in cross II highest phenotypic variance and phenotypic coefficient of variance was recorded for all the traits in above cross I and also including, harvest index (%), grain yield/plant (g). The highest PCV was recorded in cross III for days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, plant height (cm), number of effective tillers/plant, flag leaf area ($cm^2$), number of spikelets/panicle, grains/panicle, spikelet fertility (%), protein content (%) and in cross IV show highest phenotypic variance and phenotypic coefficient of variance for days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, , flag leaf area ($cm^2$), biological yield/plant (g), number of spikelet's/panicle, grains/panicle, spikelet fertility (%), grain size (L: B ratio) and grain yield/plant (g).

## Discussion

The genetic analysis of quantitative traits is a prerequisite for plant breeding programmes, which can lead to a systemic method of design and to the appropriate planning of plant breeding strategies. Very wide range of variation in mean performance of different cross combinations and their derivatives was observed for all the 20 characters under study. The comparison of mean performance of all the 6 generations (P1, P2, F1, F2, B1, B2) and difference between parent are more means they are more diverse parent used in the crossing programme, Devi *et al.* (2017) [2] for 20 traits using least significant differences revealed existence of very high level of variability in the germplasm collections evaluated in the present study. The current study suggests that the PCV was higher than the GCV for all traits (Tiwari *et al.*, 2019) [13]. This was also the case for all the traits observed in another study (Osman *et al.*, 2012) [7], which reported that the environmental effect on any trait is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation; large differences reflect a large environmental effect, whereas small differences reveal a high genetic influence. In this study, the small differences between the PCV and GCV for most of the traits, such as days to 50% flowering, flag leaf area, grains/panicle, protein content (%) represented some degree of environmental influence on the phenotypic expression of these characters. Rani *et al.* (2016) [9], (Habib *et al.*, 2005) [4], Saravanan and Senthil (1997) [10]. It also suggests that selection based on these characters would be effective for future crossing programmes. The other traits, which showed a higher difference between PCV and GCV, indicated that the environmental effect on the expression of those traits is higher

and that selection based on these characters is not effective for further yield improvement. The highest PCV was recorded for grains/penicle and number of spikelets/paniclein (Devi *et al.*, 2020) [3] Cross I, and II while in cross III and IV highest PCV is for chlorophyll b and carotene. High GCV and PCV for flag leaf area and number of spikelet/penicle were also recorded by the following researchers (Mazid *et al*., 2013) [6], Pandey *et al.* (2010) [8] and Devi *et al*. (2017). These results are similar to those of (Tiwari *et al*., 2019) and (Devi *et al*., 2020).

**Conclusions**

The present study shows that all the four cross combinations were diverse from each other and parents used in this crossing possessed diverse genetic back ground, which shows very high level of genetic variance. It reflects that all the cross (F1, F2 B1, B2) combinations can be used further for selecting the desirable / novel recombinants for rice improvement under sodic soil.

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