



Research Article

Unveiling genetic basis of yield and salinity tolerance in rice (*Oryza sativa* L.) through insights from generation mean analysis

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Abstract

Rice (*Oryza sativa* L.) serves as a primary food source for over a billion people worldwide and is encountering challenges in yield due to the increasing global population and climate changes. Understanding the genetic variations that underlie complex traits is crucial for its enhancement and this can be accomplished through generation mean analysis. In this study, investigation was made to study the genetic mechanisms governing important quantitative traits, specifically yield and salinity tolerance in rice. The study involved six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) resulting from two crosses between three parents. The investigation specifically focused on generation mean analysis, assessing twelve traits includes days to flowering, plant height, total number of tillers, number of productive tillers, panicle length, flag leaf length, flag leaf width, number of filled grains per panicle, total number of grains per panicle, spikelet fertility, thousand-grain weight and single plant yield in the two crosses. In Cross I (ADT 45 × APD 19002), traits such as plant height, days to fifty percent flowering, total number of tillers and total number of grains per panicle exhibited opposing signs for dominance × dominance (I) and dominance (h), indicating a prevalence of duplicate epistasis. At the same time, additive and additive × additive gene effects influenced total number of tillers, plant height, total number of grains per panicle, number of filled grains per panicle and spikelet fertility. In Cross II (CO 54 × APD 19002), total number of tillers, plant height, flag leaf length, total number of grains per panicle, spikelet fertility and single plant yield suggested a predominance of duplicate epistasis. Further, the total number of grains per panicle, total number of tillers per plant, spikelet fertility and thousand-grain weight were primarily governed by additive and additive × additive gene effects. These observations show the feasibility of enhancement through selection in subsequent generations, emphasizing the necessity of integrating selection with salinity tolerance screening for the development of high-yield, salinity-tolerant rice varieties.

Keywords: Scaling test, genetic effects, salinity tolerance

INTRODUCTION

Rice (*Oryza sativa* L.) plays a crucial role as a primary food source for more than 3.5 billion people globally, especially in Asia and Africa. The world food basket relies heavily on rice as a cornerstone of food security. India has achieved self-reliance in food grain production and holds the second position in rice production trailing only China. India has also achieved the most prominent development

in rice export with more than 38 percent share in the global rice trade (Li *et al.*, 2024; Valera *et al.*, 2024). Global consumption has surpassed global production since the year 2021 and a deficit is projected over the next decade (Durand-Morat and Mulimbi, 2024). The estimated global demand for rice is expected to reach 944 million, an increase of 1.8 percent from the current level (FAO, 2018).

The rice production system faces continuous challenges due to dynamic climatic conditions such as heat waves, drought, unpredictable rain, flooding, increased sea level, and salinity, encompassing biotic and abiotic stresses. The primary objective and preliminary step in overcoming the major barriers to global rice production is breeding for high yields and resilience to abiotic and biotic stresses.

Among the abiotic stresses, such as drought, excessive salinity, cold and heat significantly impact grain production and quality threats to rice cultivation (Sarma *et al.*, 2023). In particular, salinity stress affects crop growth and yield, as well as extensive areas of irrigated land (Zhu, 2016). Soil salinity not only hinders agricultural productivity but also carries far-reaching consequences for global populations. Approximately 4.03 billion people and 800 million hectares of land worldwide are troubled by salt, either due to salinity or sodicity (Zaman *et al.*, 2018). Salinity is a widespread problem in both coastal and marginal inland environments, limiting rice production in 30% of rice growing area, encompassing 45 million hectares of irrigated land and 32 million hectares of dry land worldwide (FAO, 2018; Ravikiran *et al.*, 2018). In Asia alone, 21.5 million hectares grapple with these issues (Mohanty *et al.*, 2023). Notably, India faces challenges on nearly 7 million hectares of agricultural land are affected by varying degrees of salinity-related issues and this is expected to increase to 16.2 million hectares by 2050 (Liu *et al.*, 2020). The elevated salt levels disrupt water and nutrient absorption by the roots, causing an imbalance in the plant's metabolism, ultimately resulting in decreased plant growth, leading to a yield loss of up to 35% (Farooq *et al.*, 2015). Rice is highly susceptible to salinity stress (Chen *et al.*, 2021) which encounters the challenges as recent research unveils intricate patterns of salt tolerance during various developmental stages. While germination and vegetative stages exhibit heightened salt tolerance, vulnerability increases during the seedling and reproductive stages (Bundó *et al.*, 2022). Recent studies emphasize the necessity for tailored strategies to strengthen rice resilience against salinity stress. Moreover, high-yielding rice varieties showed a 12% reduction in yield under a salinity level of 3 dSm⁻¹, while a substantial 50% decline in yield was recorded at a salinity level of 6 dSm⁻¹ (Linh *et al.*, 2012), underscoring the need to develop innovative approaches for securing global food security in the face of a changing climate.

Rice remains intertwined with the global food security imperatives and there exists an overwhelming need that combat saline conditions without compromising yield. The development of plant varieties capable of enduring elevated salinity levels poses a considerable challenge. This arises due to the complex ways in which crops respond to salinity stress, involving both osmotic and ionic stress factors (Pareek *et al.*, 2020). Achieving salinity tolerance entails the concerted responses of various stress-responsive elements, including quantitative trait loci (QTL)

genes, and enzymes that are activated at different stages in response to salt stress (Singh *et al.*, 2024). Despite high-yielding varieties reaching a plateau in realized yield, it is imperative to advance innovative technologies for enhancing rice productivity in saline environments (Muthuvijayaragavan and Murugan 2017; Krishnamurthy, *et al.*, 2024). A comprehensive understanding of the genetics and gene actions influencing quantitative traits in rice is crucial for successful variety development. Consequently, plant breeders must concentrate on selecting superior genotypes, which is a pivotal factor in genetic improvement within a breeding program. This selection process depends on the genetic values of progeny performance, aiming to produce genetically improved crop cultures capable of withstanding both biotic and abiotic stress conditions (Samy *et al.*, 2024). According to Falconer (1996), the breeding value of genotypes is linked to the gene action of the traits they control. A more comprehensive understanding of gene action can be obtained through various genetic analyses. The current study assesses the gene action for yield and yield-related traits under salinity conditions using generation mean analysis. This well-established biometrical technique reveals the nature and extent of gene interaction which includes additive × additive (i), dominance × dominance (l) and additive × dominance (j) influencing these traits. This method helps breeders to choose the appropriate breeding approach for the development of a climate-resilient variety for enhancing rice cultivation in challenging environments.

MATERIALS AND METHODS

The experimental setup featured two main female parents, ADT 45 (IR 50/ADT 37, short duration) and CO 54 (CB 04110 / CB 05501, short duration) and one non-recurrent donor parent, APD 19002 (IWP/CB 53 MAS14065, early-medium, salinity tolerant) were collected from Department of Rice, Tamil Nadu Agricultural University. A crossing block was raised and the planting of these parents was done at staggered seven-day intervals to develop F₁ hybrids (ADT 45 × APD 19002 and CO 54 × APD 19002) during January 2022. A portion of hybrid seeds was planted during summer, 2022. The true F₁ plants were confirmed using molecular marker of their respective parents. These F₁ plants were then backcrossed with P₁ and P₂ parental lines to develop B₁ and B₂ generations. The F₂, B₁ and B₂ generations were developed during Rabi 2022 at the Department of Rice, Centre for Plant Breeding and Genetics, TNAU, Coimbatore. Evaluation of two crosses from each population (P₁, P₂, F₁, F₂, B₁, B₂) were raised in a salinity spot field with the spacing of 20 × 20 cm, following standard agronomical practices, to analyze gene action for yield and yield-related traits. The soil in the experimental field exhibited slight salinity, with an electrical conductivity (EC) of 0.19 dSm⁻¹, Exchangeable Sodium Percentage (ESP) around 36.7 and a pH of around 9.1. However, the irrigation water had an electrical conductivity (EC) of 2.21 dSm⁻¹, pH around 9.37

and ESP of 49.06, indicating higher salinity and sodicity. The experiment was conducted at ADAC & RI, Trichy during *Rabi* 2023. Data collection involved selecting 10 plants randomly from parents and 50 random plants in B_1 and B_2 generations, and from an F_2 population of 250 plants. Observations were made to assess various traits, including days to flowering (DFF), plant height (PH), Total number of tillers (TNT), number of productive tillers (NPT), panicle length (PL), Flag leaf length (FLL), Flag leaf width (FLW), Number of filled grains per panicle (NFGpP), total number of grains per panicle (TNGpP), spikelet fertility (SF), thousand-grain weight (TGW) and single plant yield (SPY) for analysis. These observations aimed to provide a comprehensive understanding of the gene action controlling the expression of traits within these cross combinations and generations.

Statistical analysis: Generation mean analysis, following the methods outlined by Hayman (1960) and Jinks and Jones (1958), was conducted in two stages. The initial stage involved testing for epistasis to determine the presence of any inter-allelic interactions. Subsequently, an analysis was performed to estimate gene effects, variances and identify the type of epistasis present. A, B, C and D Scaling test was done as given by Mather (1949). The standard error of A, B, C and D was calculated by taking the square root of the respective variances, and 't' values were determined by dividing the values of A, B, C and D by their corresponding standard errors. The significance of any of these four scales indicated the presence of epistasis. All statistical analyses were carried out using TNAU STAT software (Manivannan, 2014).

RESULTS AND DISCUSSION

The complexity of analyzing individual genes in a comprehensive whole-genome analysis is inclined by the influence of numerous genes and varied environmental factors. This study aimed to evaluate the nature and extent of allelic and non-allelic interactions in rice, focusing on yield and related traits under salinity tolerance. A key objective was to partition genetic variability into broad components. The assessment of the adequacy of the additive dominance model or the determination of the presence or absence of epistasis is conducted through a scaling test. Furthermore, generation mean analysis is a valuable and straightforward method for characterizing gene effects in polygenic traits (Hayman, 1960). This methodology is crucial for detecting the presence or absence of non-allelic interactions. A significant advantage of gene interaction analysis is its ability to estimate various epistatic gene effects, including additive \times additive (i), dominance \times dominance (l), and additive \times dominance (j). In this study, generation mean analysis was employed to investigate the underlying gene action influencing the inheritance patterns of yield and its component traits.

Mean performance: The analysis focused on two specific crosses (ADT 45 \times APD 19002 and CO 54 \times APD 19002) derived from hybridization programs. The observed

variation among the means across various generations for all twelve traits emphasizes the importance of estimating additive, dominance and epistatic interactions. Significant distinctions were evident among the means of six generations, particularly in traits such as days to 50 percent flowering, number of tillers, plant height, number of productive tillers, panicle length, flag leaf width, flag leaf length, number of filled grains per panicle, total number of grains per panicle, thousand-grain weight, spikelet fertility and single plant yield (**Table 1**). The agronomic attributes including number of productive tillers, grains per panicle, plant height, thousand grain weight, spikelet fertility and these attributes are influenced by genetic expression and inheritance (Hua *et al.*, 2002). Similar findings by Ganapati *et al.* (2020), Solanke *et al.* (2019), Yogameenakshi *et al.* (2019) also support the presence of epistasis for yield and yield-related traits in rice. The inheritance of traits related to both yield and salinity tolerance in rice is quite complex. Therefore, when non-allelic epistasis was detected in certain crosses, a six-parameter model was used to understand how genes act in influencing these traits.

Scaling test: The A, B, C, and D scaling tests conducted across most traits in the two crosses yielded significant results, indicating the presence of non-allelic interactions in the inheritance patterns of these traits. However, for the trait days to 50% flowering in Cross I and flag leaf width in Cross II, all four scales displayed non-significant values, suggesting a non-interacting mode of inheritance. For all other traits, either one or both scaling tests produced significant results, indicating the presence of epistasis. Both crosses exhibited non-allelic interactions in the inheritance of nearly all the traits under examination (**Table 2**). Generally, the interaction effects, specifically dominance \times dominance (l) and additive \times additive (i), were found to be of higher magnitude compared to the cumulative main effects of dominance (h) and additive (d) for all traits in both crosses.

Genetic effect: Analyzing of gene effects using generation mean analysis, it was identified that the additive gene effect (d) displayed a negative significance in cross I for morphology traits such as total number of tillers, plant height, flag leaf width, flag leaf length total number of grains per panicle, number of filled grains per panicle and single plant yield. These findings imply the potential for direct selection as a strategy to enhance grain yield and its associated traits. Previous studies have also documented additive effects on the number of tillers, number of filled grains per panicle and single plant yield (Kacharabhai, 2015). In contrast, in Cross II, a significant positive additive effect was observed for the total number of grains per panicle, while a negative significant effect was observed in plant height, total number of tillers, flag spikelet fertility, leaf length, thousand-grain weight and single plant yield (**Table 3**). The manifestation of additive gene effects in self-pollinated crops like rice is advantageous for breeders since these effects can reliably be inherited across the generations, thereby facilitating

Table 1. Mean and standard errors for yield and yield attributing traits of rice

Generation	P ₁		P ₂		F ₁		F ₂		B1		B2	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
DFF	77.3±0.4	80.6±0.64	83±0.56	88.8±1.05	85.7±1.55	85±0.26	83.55±0.29	87.22±0.29	84.7±2.04	85±0.3	86.8±1.1	89.1±0.72
PH	71.8±2.19	91.1±2.13	79±1.79	78.8±0.55	83.4±2±1.14	80.1±1.16	73.03±0.51	79.86±0.6	81.4±2.96	87±1.74	80.1±2.46	83.1±1.79
NPT	13.2±1.35	14.9±1.39	12±0.76	14.4±0.96	15.3±1.14	18.6±1.44	10.7±0.2	12.46±0.31	12.2±1.59	15.6±1.06	12.4±1.03	11.5±0.91
TNT	16.65±0.68	21.75±0.68	19.7±0.79	20±0.28	21.93±0.53	15±0.63	17.84±0.15	18.91±0.18	20.54±0.54	22.31±0.59	20.76±0.71	20.5±0.58
PL	15.5±1.49	16±1.22	14.3±0.78	16.4±0.98	17.8±1.25	19.8±1.41	13.7±0.22	15.49±0.32	15±1.58	16.2±0.92	14.7±0.92	13.9±0.81
FLL	16.25±1.37	23.9±1.59	19.43±0.83	21.2±0.69	23.69±1.06	18.4±1.07	18.32±0.23	21.76±0.26	20.45±1.3	24.37±0.59	20.72±0.95	22.91±1.08
FLW	0.99±0.04	1.15±0.05	1.12±0.04	1.09±0.09	1.22±0.03	2.68±1.37	1.11±0.02	1.57±0.11	1.17±0.04	1.41±0.03	1.22±0.06	1.34±0.04
NGpP	173±3.79	165.6±10.57	177±4.43	179.4±4.21	224.6±7.73	247±7.75	185.44±2.65	214.13±2.53	201.8±6.99	194.9±7.12	206.3±6.28	197.3±6.21
TNFGP	153.9±5.3	140.4±5.61	157.9±4.72	154.8±4.69	212.7±7.34	225.3±7.72	154.19±2.36	172.36±2.61	169.3±6.59	174.5±7.76	176.6±8.16	180.2±8.73
SF	88.76±1.32	85.95±2.6	89.16±1.03	86.22±1.13	94.71±0.67	91.21±1.08	83.2±0.5	80.26±0.59	83.89±1.51	89.36±1.25	85.23±1.63	90.9±1.71
TGW	1.4±0.01	1.69±0.05	1.49±0.02	1.48±0.04	1.56±0.05	1.69±0.05	2.14±0.7	1.38±0.01	1.52±0.05	1.61±0.04	1.48±0.08	1.6±0.08
SPGY	16.86±1.77	25.74±1.29	25.22±1.03	25.77±1.65	36.7±5.06	30.01±3.04	18.39±0.51	17.79±0.73	26.59±3.52	28.18±1.46	22.82±3.61	30.74±3.06

Cross I- ADT 45 x APD 19002, Cross II- CO 54 x APD 19002.

Table 2. Scaling test of genetic parameters for yield and yield attributing traits in rice

Scale	A		B		C		D	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
DFF	6.4±4.38	4.4±0.91**	4.9±2.75	4.4±1.8*	2.51±3.38	9.48±1.76**	-4.39±2.39	0.34±0.97
PH	7.58±6.41	2.8±4.24	-2.22±5.35	7.3±3.79	-25.53±4.17**	-10.67±4**	-15.45±3.98**	-10.38±2.77**
NPT	-4.1±3.64	-2.3±2.91	-2.5±2.48	-10±2.51**	-12.82±2.87**	-16.66±3.56**	-3.11±1.94	-2.18±1.53
TNT	2.5±1.38	7.87±1.5**	-0.11±1.7	6±1.35**	-8.86±1.61**	3.88±1.64*	-5.62±0.94**	-4.99±0.9**
PL	-3.3±3.71	-3.4±2.62	-2.7±2.36	-8.4±2.36**	-10.61±3.14**	-10.04±3.47**	-2.3±1.88	0.88±1.38
FLL	0.96±3.12	6.44±2.25**	-1.68±2.33	6.22±2.51*	-9.78±2.82**	5.15±2.94	-4.53±1.67**	-3.75±1.34**
FLW	0.13±0.1	-1.01±1.37	0.1±0.13	-1.09±1.38	-0.1±0.11	-1.34±2.78	-0.16±0.08*	0.38±0.23
NGpP	6±16.42	-22.8±19.35	11±15.4	-31.8±15.23*	-57.43±19.64**	17.52±21.72	-37.22±10.79**	36.06±10.71**
TNFGP	-28±15.99	-16.7±18.22	-17.4±18.51	-19.7±19.65	-120.44±18.83**	-56.38±20.02**	-37.52±11.5**	-9.99±12.79
SF	-15.68±3.36**	1.55±3.77	-13.4±3.48**	4.38±3.76	-34.55±2.93**	-33.54±4.27**	-2.73±2.43	-19.74±2.42**
TGW	0.08±0.11	-0.15±0.1	-0.08±0.17	0.03±0.18	2.55±2.79	-1.02±0.13**	1.28±1.39	-0.45±0.09**
SPGY	-0.38±8.84	0.61±4.41	-16.28±8.87	5.7±7.03	-41.91±10.52**	-40.37±7.06**	-12.63±5.14*	-23.34±3.69**

selection at various inbreeding levels. The notable additive effects observed in both crosses underscore the potential utility of these parents in breeding programs, especially for developing high-yielding varieties resilient to salinity. The identified parents, recognized for their positive contributions to yield and salinity tolerance, can serve as valuable contributors to hybridization programs. This strategy could potentially lead to the discovery of superior individuals via transgressive breeding, possessing favorable genes for yield, its component traits and salinity tolerance. These findings align with earlier research on the number of grains per panicle (Singh, 2019, Solanke *et al.*, 2019), flag leaf length (Das *et al.*, 2022) and spikelet fertility (Ganapati *et al.*, 2020) in similar conditions, emphasizing the promising role of these parental lines in upcoming breeding initiatives.

In cross I, the dominance gene effect (h) exhibited positive significance for traits such as days to flowering, plant height, total number of tillers, flag leaf length, flag leaf width, number of filled grains per panicle and total number of grains per panicle. In Cross II, positive and significant dominance effects were observed for plant height, total number of tillers, flag leaf length, spikelet fertility, thousand-grain weight and single plant yield. Conversely, a negative dominance effect for the total number of grains per panicle was noted (Table 3). Previous studies have documented dominance gene effects for the number of grains per panicle (Verma *et al.*, 2010). The direct correlation observed between these two crosses for various traits highlights the significant importance of dominance gene action. These results are consistent with earlier findings in saline-sodic soils reported by Muthuvijayaragavan and Murugan (2017), Verma *et al.*, (2010), Kargbo *et al.*, (2019).

The additive \times additive (i) interaction effect was demonstrated in cross I, which was positively significant for traits including the total number of tillers, plant height, flag leaf length, total number of grains per panicle, number of filled grains per panicle and single plant. Similarly, in Cross II, traits such as plant height, total number of tillers, flag leaf length, spikelet fertility, thousand-grain weight and single plant yield displayed positive significance, however, the total number of grains per panicle exhibited negative significance (Table 3). These results align with previous studies focusing on traits like plant height, flag leaf length, flag leaf width, total number of grains per panicle and single plant yield. Consequently, the selection process is recommended to be deferred to later generations after achieving homozygosity for most alleles. Similar outcomes have been reported in studies evaluating rice under saline soils by researchers such as (Das *et al.*, 2022, Muthuvijayaragavan and Murugan 2017, Mohammadi *et al.*, 2014, Solanke *et al.*, 2019).

In cross I, the dominance \times dominance (l) interaction effect was significantly negative for traits such as days to fifty percent flowering, plant height, total number of

tillers, total number of grains per panicle and spikelet fertility. Conversely, in Cross II, significant (l) effects were observed for traits such as days to flowering, plant height, total number of tillers, flag leaf length, total number of grains per panicle, thousand grain weight, spikelet fertility and single plant yield (Table 3). Prior research has reported similar findings for various traits, encompassing the number of productive tillers, number of grains per panicle, thousand-grain weight and single plant yield. These results are consistent with findings under saline conditions documented by researchers like Kacharabhai (2015), Rahman *et al.*, (2022), Muthuvijayaragavan and Murugan (2017), Thirumeni *et al.*, (2001). It is recommended to delay selections to subsequent generations to identify segregants tolerant to salinity as an ideal and practical method (Geetha *et al.*, 2006). To acquire desirable early segregants, a suitable breeding method could be bi-parental mating or reciprocal recurrent selection. Therefore, bi-parental mating followed by recurrent selection might be considered to obtain a range of desirable segregants, as supported by Ganapati *et al.*, (2020), Karthikeyan and Anbuselvam (2006) and Ray and Islam (2008).

In cross I, dominance (h) and dominance \times dominance (l) had exhibiting the contrasting signs for the traits such as plant height, days to fifty percent flowering, total number of tillers and total number of grains per panicle suggesting a prevalence of duplicate epistasis. Similarly, in Cross II, plant height, total number of tillers, flag leaf length, total number of grains per panicle, spikelet fertility and single plant yield suggest a prevalence of duplicate epistasis with the findings of Kacharabhai (2015), Singh (2019) and Ganapati *et al.*, (2020). This implies the need to defer the selection process to subsequent generations for these traits in crop improvement, aligning with earlier reports by Muthuvijayaragavan and Murugan (2017), Ganapati *et al.*, (2020), Singh (2019) and Solanke *et al.*, (2019).

Investigation of result depicted that, additive, dominance, additive \times additive, and dominance \times dominance interaction effects in relation to grain yield and other key traits. Notably, dominance and dominance \times dominance interaction effects were detected, indicating duplicate dominant epistasis. However, early selection in segregating generations may not yield the desired recombinants. To address this, postponing selection until later segregating generations, when dominance and epistasis effects diminish. Employing inter-mating of segregants followed by recurrent selection is advisable. For harnessing additive gene action, simple selection procedures or the pedigree breeding method sufficient. However, when dominant gene action is prevalent in most traits, delaying selection until later generations after crosses are made becomes necessary. Heterosis breeding procedures effectively influence dominance gene action, with both additive and dominance gene actions significantly impacting various traits. In such

Table 3. Estimation of genetic parameters for yield and yield contributing traits in rice

Genetic parameter	m		d		[h]	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
DFF	71.36±4.8**	85.38±2.03**	-2.85±0.34**	-4.1±0.61**	34.42±14.23*	7.73±5.54
PH	44.51±8.08**	64.18±5.64**	-3.6±1.41*	6.15±1.1**	75.16±23.83**	46.78±16.09**
NPT	6.38±3.96	10.29±3.17**	0.6±0.77	0.25±0.84	8.55±11.79	0.37±9.2
TNT	6.93±1.95**	10.89±1.84**	-1.53±0.52**	0.88±0.37*	28.64±5.72**	27.97±5.32**
PL	10.29±3.85**	17.96±2.87**	0.6±0.84	-0.2±0.78	6.12±11.44	-11.73±8.24
FLL	8.78±3.44*	15.04±2.81**	-1.59±0.8	1.35±0.87	23.25±10.17*	23.53±8.18**
FLW	0.73±0.16**	1.88±0.47**	-0.07±0.03*	0.03±0.05	1.05±0.47*	-2.06±1.68
NGpP	100.57±21.78**	244.62±22.16**	-2±2.92	-6.9±5.69	215.47±61.37**	-124.35±63*
TNFGP	80.86±23.28**	127.62±25.84**	-2±3.55	-7.2±3.66	161.47±66.97*	81.25±74.33
SF	83.5±4.94**	46.61±5.05**	-0.2±0.84	-0.13±1.42	-12.41±14.15	89.99±14.25**
TGW	4±2.79	0.69±0.19**	-0.05±0.01**	0.1±0.03**	-5±5.59	1.77±0.56**
SPGY	-4.21±10.34	-20.92±7.45**	-4.18±1.02**	-0.02±1.05	49.5±31.09	103.91±21.6**
Epistasis (Cross I)	Duplicate	duplicate	-	duplicate	-	-
Epistasis (Cross II)	-	duplicate	-	duplicate	-	duplicate

Table 3. Contd...

Genetic parameter	[i]		[j]		[l]	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross2
DFF	8.79±4.78	-0.68±1.94	0.75±2.34	0±0.99	-20.09±9.87*	-8.12±3.58*
PH	30.89±7.96**	20.77±5.53**	4.9±4.1	-2.25±2.72	-36.25±15.93*	-30.87±10.74**
NPT	6.22±3.88	4.36±3.05	-0.8±2.05	3.85±1.63*	0.38±8.11	7.94±6.62
TNT	11.25±1.88**	9.99±1.81**	1.31±1.03	0.94±0.9	-13.64±3.9**	-23.86±3.68**
PL	4.61±3.75	-1.76±2.76	-0.3±2.01	2.5±1.45	1.39±7.95	13.56±6*
FLL	9.06±3.35**	7.51±2.68**	1.32±1.8	0.11±1.51	-8.34±7.02	-20.17±5.74**
FLW	0.33±0.16*	-0.76±0.47	0.02±0.08	0.04±0.07	-0.56±0.32	2.86±2.79
NGpP	74.43±21.58**	-72.12±21.42**	-2.5±9.84	4.5±11.02	-91.43±42.41*	126.72±43.57**
TNFGP	75.04±23**	19.98±25.58	-5.3±11.08	1.5±12.24	-29.64±45.99	16.42±50.82
SF	5.46±4.87	39.47±4.85**	-1.14±2.37	-1.41±2.55	23.62±9.36*	-45.4±9.49**
TGW	-2.55±2.79	0.9±0.19**	0.08±0.09	-0.09±0.1	2.56±2.81	-0.77±0.39*
SPGY	25.25±10.29*	46.67±7.38**	7.95±5.14	-2.55±3.55	-8.59±22.74	-52.98±15.29**
Epistasis (Cross I)	-	duplicate	-	-	-	-
Epistasis (Cross II)	-	duplicate	-	duplicate	duplicate	duplicate

scenarios, using biparental mating designs is proposed to further recombine alleles, leading to the production of desirable segregants. These methods effectively address epistatic interactions by disrupting undesirable gene linkages and facilitating the production of favorable recombinants. The findings suggest that enhancing traits in subsequent generations through selection, while assessing salinity tolerance can lead to the development of high-yielding rice varieties resilient to salinity conditions

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