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Research Article

Comparative delineation of genetic variability and association among yield and its contributing traits under sodic and normal soil conditions in rice (*Oryza sativa* L.)

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Abstract
Genetic variability parameters were estimated in 150 diverse rice genotypes comprising landraces, improved varieties and Harvestplus lines at two environments *viz*., sodic and normal irrigated environments using Augmented Complete Block Design. The analysis of variance revealed significant differences among the test genotypes for all the traits. The analysis of mean performance of genotypes identified three genotypes outperformed all the check genotypes under sodicity conditions. The estimates of PCV, GCV, heritability and genetic advance as percent of mean inferred that most of the traits were governed by additive gene action and have good response to selection in both the environments. It was found that PCV and GCV had increased considerably for most of the traits under sodicity compared to normal irrigated environment. Correlation and path analysis revealed that the traits, number of productive tillers, panicle length, number of filled grains per panicle, panicle weight and hundred grain weight possessed high correlation and high direct effect on single plant yield indicating the importance of yield improvement through these traits.

Keywords: Germplasm, variability, correlation, path analysis

INTRODUCTION

Rice is one of the principal food crop that feeds majority of the people and satisfy their calorie needs. The crop was once considered luxury, has now become the most consumed food in India among the urban as well as rural community, being a backbone to Indian food security. Rice production also has increased exponentially with a total production of 53.5 million tonnes in 1961 to 79.9 million tonnes in 1981 and then to 122.27 million tonnes in 2020-21 (Anonymous 2022, FAOSTAT 2023). The credit to this massive increase in rice production is mainly due to the development of high yielding varieties during the green revolution phase of plant breeding (Somvanshi *et al.,* 2020).However, simultaneous increase in population demands higher food grain production, expecting to increase rice production by 70% mtonnes in 2050 (FAO 2013). The major decline in rice production is due to several biotic and abiotic stress factors. One among them is sodicity, which is a major and gradually increasing factor covering an area of 3.88 mha and expected to increase in the near future (IAB 2000).

Germplasm contains huge genetic variations that have been selected over the centuries to adapt itself to the natural climatic conditions. It serves as a reservoir for any trait that may be useful in development of varieties to augment crop production. Several studies were already done to evaluate germplasm lines for yield and contributing traits under sodicity (Khan and Abdullah 2003, Singh *et al.,* 2002).

Extensive knowledge on variability and interrelationship among yield and its contributing characters in a germplasm panel is of utmost importance for crop improvement. The estimates of genetic variability parameters indicate the extent of variability present in the population, while heritability and genetic advance as per cent of mean indicates the genetic control and the potential for improvement of these traits.

Hence, the present investigation is aimed to assess and compare the extent of variability and genetic control and association of yield and its contributing traits in sodic and normal irrigated environments.

MATERIALS AND METHODS

The present investigation was done using a set of 150 germplasm accessions consisting of landraces, improved varieties and Harvestplus lines (**Table 1**). The field experiment was carried out in Karur, Tamil Nadu, India (10º 57' 34'' N, 78º 00' 42'' E) as an irrigated crop (normal soil) and at Dept. of Genetics and Plant Breeding farm, Anbil Dharmalingam Agricultural College and Research Institute, Trichy (10º 45' 16'' N, 78º 36' 12'' E) as a sodic stress environment. The seeds were sown in raised nursery bed and transplanted to main field 27 days after sowing with a spacing of 20 × 20 cm. The experiment was laid out in Augmented complete block design with 144 test entries and 6 checks. All recommended package of practices were followed to maintain a healthy crop.

Different morphological and biometrical observations *viz*., Days to 50% flowering (Days), Plant height (cm), Number of tillers (No.), Number of productive tillers (No.), Flag leaf length (cm), Flag leaf breadth (cm), Panicle length (cm), Grains per panicle (No.), Filled grains per panicle (No.), Spikelet sterility (%), Panicle weight (g), Hundred grain weight (g) and Single plant yield (g) were recorded at crop maturity. All observations were recorded as per Standard Evaluation System (IRRI 2002).

Statistical analysis: The recorded observations were subjected to analysis of variance using "augmentedRCBD" package (Aravind *et al.,* 2021) in R software v4.1.2. The Genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV) and adjusted mean of the genotypes were also calculated using this R package. The adjusted mean of the genotypes were used for further analysis. Inter-relationship among yield and its contributing characters were calculated using correlation coefficient and path analysis using "corrplot" (Wei and Simko 2021) and "biotools" (da Silva *et al.,* 2017) package respectively in R software v4.3.0.

RESULTS AND DISCUSSION

Analysis of variance and per se performance of the genotypes: The ANOVA revealed significant difference between the genotypes for all the traits studied in both sodicity as well as normal irrigated environments. The genotypes exhibited wide range of variation for all the traits and are presented in **Table 2**. Dubey *et al.* (2022) also performed similar studies and inferred similar significant differences among the traits across environments.

The mean performance of test genotypes were compared with that of the checks to study their comparative performance in sodic and normal irrigated environment. The range of SPY was observed from 2.91g (TG127) to 32.39g (TG160) under sodicity (**Table 3**). Similarly, under irrigated environment, the SPY was observed from 12.25 (TG162) to 51.78 (TG139). Frequency distribution of the traits differed considerably between sodic and irrigated conditions (**Fig. 1**). The genotypes exhibited normal distribution for the traits *viz*., DFF, PH, FLL, PL and FPP under sodicity, and for the traits *viz*., PH, NT, NPT, FLL, FLB, PL and HGW under normal irrigated environment. Similarly, skewed distribution was observed for the traits NT, NPT, FLB, SS, PW, HGW and SPY under sodicity and DFF, FPP, SS, PW and SPY under normal irrigated environment. The traits, SS, PW and SPY followed skewed distribution in both sodic as well as normal irrigated environments. These results clearly indicate the difference in susceptibility reaction of test and check genotypes in stress and non-stress environment.

Three genotypes (TG160, TG169 and TG190) outperformed all the check genotypes under sodicity, whereas in irrigated condition only one genotype, TG139 out yielded the check entries. The genotypes (TG160, TG169 and TG190) that performed well under sodicity also had higher yield under normal conditions, but the check genotypes showed comparatively higher yield under irrigated conditions and higher reduction under sodicity. The reduction in number of filled grains per panicle as a result of spikelet sterility in the check genotypes resulted in higher reduction in SPY. However, these genotypes (TG160, TG169 and TG190) exhibited minimal reduction for these traits, whereas, the trait mean value for other traits were almost comparable to that of the irrigated environment. This may be due to several anatomical and physiological mechanisms of these genotypes facilitating them to outperform the check genotypes under sodicity. Geetha *et al.* (2022) studied several anatomical and physiological features of salt tolerant and susceptible genotypes. They indicated clear difference in Na^+/K^+ homeostasis, stomatal size, stomatal density, trichome length and density through Scanning Electron Microscope (SEM) with energy dispersive X-ray spectroscopy (EDAX).

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Table 1. List of genotypes used in the present study

Code	Name	Code	Name	Code	Name	Code	Name	Code	Name
TG1	*Mapillai Samba*	TG22	IR 36	TG48	*Kalarkar*	TG70	*Karthi samba*	TG95	*Jeeragasamba*
TG2	CK 275	TG25	*Sorna kuruvai*	TG50	*Sornavari*	TG72	*Aarkadu kichili*	TG96	RP BIO 226
TG3	*Senkar*	TG26	*Rasacadam*	TG51	RPHP 134	TG74	ARB 65	TG98	IG 5(EC 729642-121698)
TG4	*Murugankar*	TG31	*Chinthamani*	TG53	IR 68144-2B-2-2-3-1-127)	TG76	*Matta kuruvai*	TG100	IG 7(EC 729598-121648)
TG5	CHIR 6	TG32	*Togai Samba*	TG54	PTB 19	TG77	*Karuthakar*	TG102	*Varakkal*
TG6	CHIR5	TG33	*Malayalathan Samba*	TG55	IG 67 (EC 729050-120988)	TG80	IG 66(EC 729047-120985)	TG103	*Mattaikar*
TG7	*Kudai Vazhai*	TG34	RPHP 125	TG56	RPHP 59	TG81	CB 07701-252	TG104	IG 53(EC 728752-117719)
TG8	CHIR 8	TG35	CK 143	TG57	RPHP 103	TG82	*Thooyamalli*	TG105	IG 6(EC 729592-121642)
TG9	*Kuruvai Kalanjiyam*	TG36	*Kattikar*	TG58	*Kodaikulathan*	TG83	RPHP 93	TG106	*Katta samba*
TG11	CSR36	TG37	*Shenmolagi*	TG59	RPHP 68	TG85	RPHP 104	TG107	RH2-SM-1-2-1
TG12	*Vellaichithiraikar*	TG39	*Kattu ponni*	TG60	*Rama kuruvaikar*	TG86	RPHP 102	TG108	*Red sirumani*
TG13	*Pokkali samba*	TG40	Pusa 44	TG61	FL478	TG88	ASD19	TG109	*Vadivel*
TG14	Jothi	TG41	*Godavari Samba*	TG63	IG 71 (EC 728651-117588)	TG89	IR 83294-66-2-2-3-2	TG110	*Norungan*
TG15	*Palkachaka*	TG42	*Earapalli Samba*	TG66	*Seevanasamba*	TG90	CSR27	TG111	TRY3
TG17	*Sivapuchithiraikar*	TG43	RPHP 129	TG67	RPHP 106	TG91	IG 23(EC 729391-121419)	TG112	IG 35(EC 728858-117843)
TG18	CHIR 11	TG44	*Mangam samba*	TG68	IG 63 (EC 728711-117674)	TG92	IG 49(EC 729102-121052)	TG113	IG 45(EC 7287698-117736)
TG20	*Kalvalai*	TG46	IG 4 (EC 729639-121695)	TG69	RPHP 48	TG94	CSR23	TG114	RPHP 159

Table 1. Continued..

Code	Name	Code	Name	Code	Name	Code	Name
TG115	IG 43(EC 728788-117759)	TG134	IG 9(EC 729682-121739)	TG159	*Sembala*	TG182	ARB 59
TG116	RPHP 27	TG135	RPHP 161	TG160	IG 72(EC 728650-117587)	TG183	RPHP 163
TG117	IG 65(EC 729024-120958)	TG136	IG 8(EC 729601-121651)	TG161	*Panamarasamba*	TG184	IG 18(EC 728892-117880)
TG118	*Ponmani samba*	TG139	CO43	TG162	IR 64	TG185	RPHP 36
TG120	*Thattan samba*	TG141	IG 44(EC 728762-117729)	TG163	*Mikuruvai*	TG186	IG 28(EC 728920-117914)
TG121	IG 74(EC 728622-117517)	TG142	Sasyasree	TG164	*Thillainayagam*	TG187	*Vadakathi samba*
TG122	*Kaliyan samba*	TG143	IG 46	TG165	ARB 64	TG188	RPHP 80
TG123	IG 2(EC 729808-121874)	TG144	Apo	TG166	RPHP 140	TG189	IG 41(EC 728800-117776)
TG124	IG 29(EC 728925-117920)	TG145	IG 60(EC 728730-117695)	TG168	*Haladichudi*	TG190	IG 26(IC 0590943-121899)
TG126	*Kallimadayan*	TG147	IG 58(EC 728725-117689)	TG169	IG 24(EC 728751-117718)	TG191	IG 15(IC 728910-117901)
TG127	IG 10	TG149	RH2-SM-2-23	TG170	RPHP 42	TG192	*Nootri pathu*
TG128	IG 75(EC 728587-117420)	TG151	IG 32(EC 728838-117823)	TG172	IG 25(EC 729728-121785)	TG231	*Kalanamak*
TG129	IG 38(EC 728742-117707)	TG152	RPHP 47	TG173	IG 73(EC 728627-117527)	TG249	TRY4
TG130	IG 39(EC 728779-117750)	TG153	BPT5204	TG174	IG 51(EC 728772-117742)	TG250	TRY5
TG131	RPHP 90	TG154	IG 48	TG175	*Vellai kudaivazhai*		
TG132	IG 33(EC 728938-117935)	TG156	IG 12(EC 729626-12168)	TG176	*Kodai*		
TG133	IG 42(EC 728798-117774)	TG157	*Karungan*	TG181	IG 52(EC 728756-117723)		

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Table 2. Analysis of variance for the biometrical traits under sodic and normal irrigated environments

ANOVA - Sodicity

Source	Df	Mean.Sq											
		DFF	PH	NT	NPT	FLL	FLB	PL	FPP	SS	PW	HGW	SPY
Treatment (ignoring Blocks)	149	105.56**	381.93**	12.02*	8.74**	70.83*	0.06*	16.24**	1365.67**	111.77*	0.62**	0.12**	32.89**
Treatment: Check	5	498.77**	554.82*	39.45**	37.89**	48.24^{ns}	0.1*	7.02^{ns}	4838.9**	193.07*	1.13**	0.27**	113.4**
Treatment: Test	143	92.43**	317.68*	11.14*	7.78**	71.49*	0.06*	12.62*	1250.03**	104.98*	0.6**	0.12**	27.05**
Treatment: Test vs. Check	1	17.02^{ns}	8704.99**	0.95^{ns}	0.11^{ns}	90.47^{ns}	0.24**	579.79**	536.68*	676.37**	0.21^{ns}	0.07*	464.52**
Block (eliminating Treatments)	3	16.11*	529.7*	4.62^{ns}	7.73**	19.04^{ns}	0.02^{ns}	2.4^{ns}	26.62^{ns}	25.83^{ns}	0^{ns}	0.01^{ns}	11.6^{ns}
Residuals	15	4.61	122.83	4.76	1.14	26.11	0.03	4.35	68.53	43.41	0.06	0.01	4.47

ANOVA - Normal Irrigated

Source	Df	Mean.Sq											
		DFF	PH	NT	NPT	FLL	FLB	PL	FPP	SS	PW	HGW	SPY
Treatment (ignoring Blocks)	149	126.83**	496.31**	16.15**	10.91*	104.95**	0.06**	16.41**	2813.99**	19.91**	0.63**	0.14**	69.42**
Treatment: Check	5	706.5**	1443.85**	60.65**	13.42^{ns}	128.15**	0.16**	8.3^{ns}	7619.57**	68.07**	1.24**	0.32**	289.86**
Treatment: Test	143	105.89**	410.65**	13.5*	10.69*	94.64**	0.05**	10.76*	2623.47**	17.94*	0.61**	0.13**	53.06**
Treatment: Test vs. Check	1	222.89**	8008.24**	172.18**	30.45*	1463.79**	0.43**	865.88**	6031.23**	60.55**	0.22*	0.26**	1307.15**
Block (eliminating Treatments)	3	4.78^{ns}	10.19^{ns}	4.08^{ns}	1.49^{ns}	0.49^{ns}	0.01^{ns}	19.17*	378.02^{ns}	1.71^{ns}	0.17*	0.01^{ns}	7.67^{ns}
Residuals	15	9.41	112.36	5.43	5.04	16.46	0.01	4.53	172.63	6.74	0.04	0.01	7.53

^{ns} P > 0.05; * P <= 0.05; ** P <= 0.01

DFF- Days to 50% flowering, PH- Plant Height, NT- No. of tillers, NPT- No. of productive tillers, FLL- Flag leaf length, FLB- Flag leaf breadth, PL- Panicle length, FPP- No. of filled grains per panicle, SS- Spikelet sterility %, PW- Panicle weight, HGW- Hundred grain weight, SPY- Single plant yield

Table 3. Descriptive statistics, skewness and kurtosis of the biometrical traits in both environments

Descriptive Statistics - Sodicity

Trait	Mean	Min	Max	Skewness	Kurtosis
DFF	92.29	69.83	115.67	0.24^{ns}	2.31*
PH	106.97	52.03	160.69	-0.21^{ns}	2.49^{ns}
NT	11.96	6.4	24.53	1.09**	4.07*
NPT	9.32	4.06	18.06	0.72**	3.1^{ns}
FLL	31.55	10.58	51.78	0.14^{ns}	2.73^{ns}
FLB	1.31	0.78	2.08	0.47*	3.15^{ns}
PL	16.22	7.22	28.12	0.04^{ns}	3.26^{ns}
FPP	110.51	34.42	241.16	0.1^{ns}	3.35^{ns}
SS	28.82	9.01	71.47	0.73**	3.93*
PW	2.35	1.03	4.54	0.4*	2.47^{ns}
HGW	2.1	0.94	2.88	-0.52*	3.9*
SPY	14.66	2.91	32.39	0.62**	3.2^{ns}

Descriptive Statistics- Normal Irrigated

Trait	Mean	Min	Max	Skewness	Kurtosis
DFF	94.34	72	120	0.41*	2.55^{ns}
PH	143.61	90.41	187.54	-0.17^{ns}	2.6^{ns}
NT	19.07	9.99	27.3	-0.15^{ns}	2.59^{ns}
NPT	14.4	6.4	22.4	0.06^{ns}	3.04^{ns}
FLL	41.6	21.52	66.28	0.09^{ns}	2.46^{ns}
FLB	1.61	1.02	2.22	0.25^{ns}	2.92^{ns}
PL	17.86	8.3	28.64	0.18^{ns}	2.59^{ns}
FPP	161.9	67.86	299.44	0.43*	2.62^{ns}
SS	8.26	1.04	22.48	0.48*	3.25^{ns}
PW	2.91	1.38	5.36	0.57**	3.32^{ns}
HGW	2.1	0.94	2.9	-0.34^{ns}	3.52^{ns}
SPY	26.43	12.25	51.78	0.81**	3.88*

^{ns} P > 0.05; * P <= 0.05; ** P <= 0.01

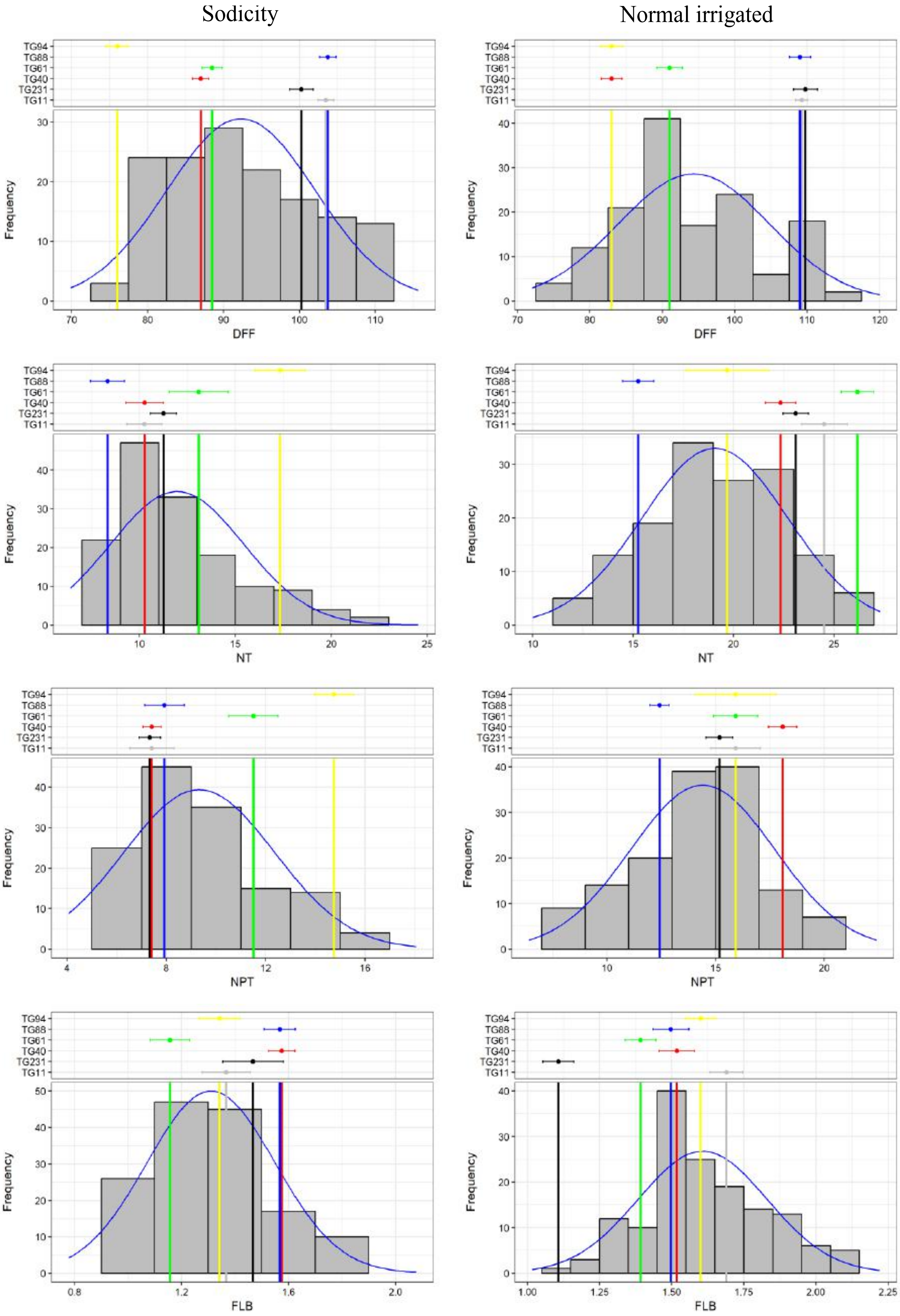
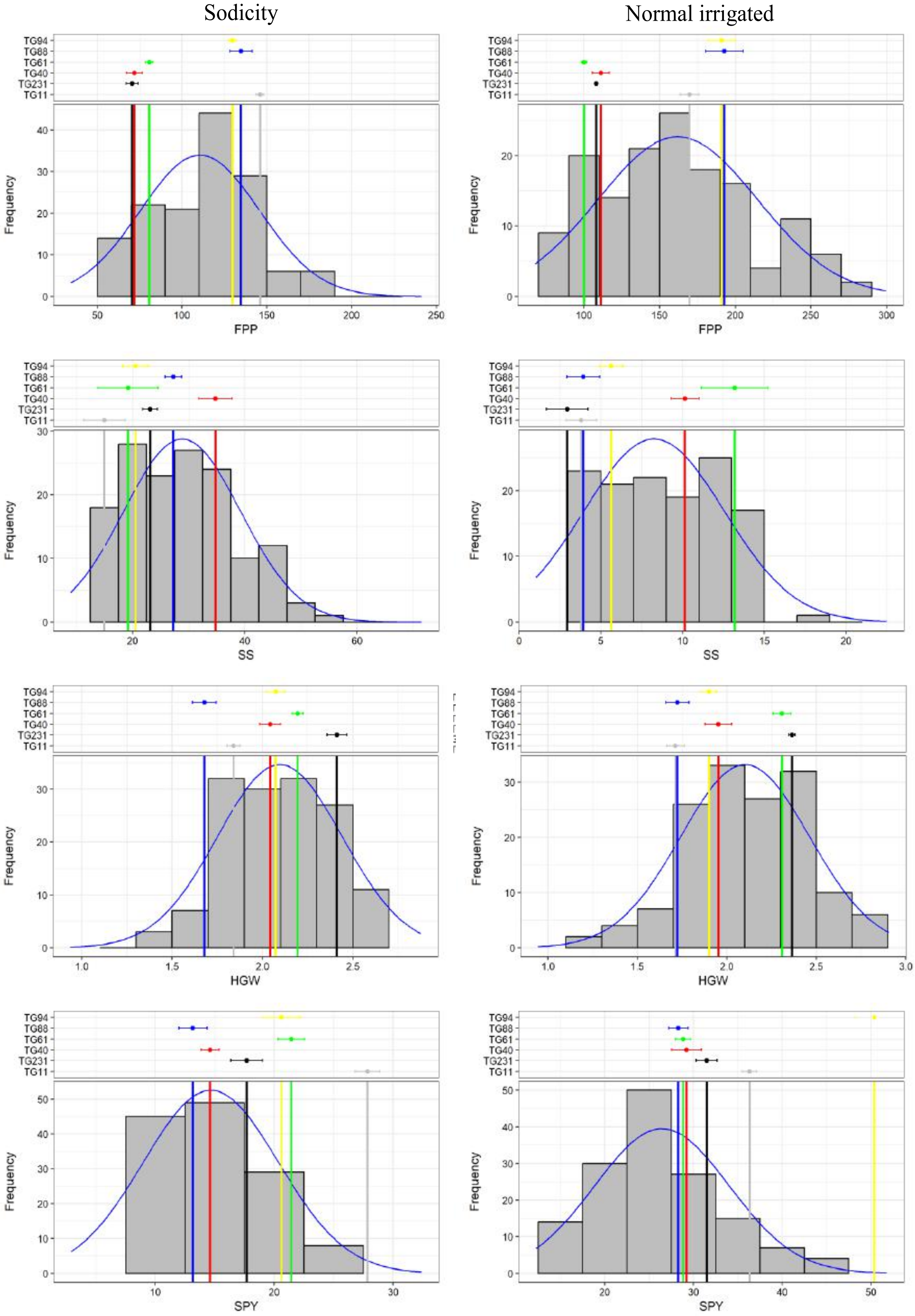


Fig. 1. Difference in Frequency distribution of biometrical traits in both environments

Fig. 1. Continued..



These genotypes were also evaluated for sodicity tolerance under hydroponics condition. The susceptibility reaction of all these outperforming genotypes showed that they are susceptible to sodicity stress at seedling stage (Unpublished). These results were in accordance with Singh *et al.* (2021) who stated that tolerance mechanism of rice genotypes are different at seedling and reproductive stages. Hence, the results suggest that, these genotypes (TG160, TG169 and TG190) outperforming at reproductive stage does not express tolerance at seedling stage.

Genetic variability parameters: The genetic variability parameters including GCV, PCV, heritability and genetic advance as percent of mean were presented in **Fig. 2**. The estimates of PCV was higher than GCV for all the traits in both the environments and were found to be from moderate to high. The traits, NT, NPT, FLL, FPP, SS, PW and SPY showed high PCV and GCV values under sodicity. These results were in accordance with Selvarani *et al.* (2022) for NPT and SPY. Singh and Verma (2021) also reported high PCV and GCV values for SPY in a comparatively high sodic environment. The trait PL in the current study showed high PCV and moderate GCV as against other traits. Similarly, under normal irrigated environment FLL, FPP, SS, PW and SPY showed high PCV and GCV. However, higher PCV and moderate GCV were observed for NPT. This difference in variability among these yield contributing traits in stress and non-stress environments may be attributed to the effect of sodicity on the tested genotypes.

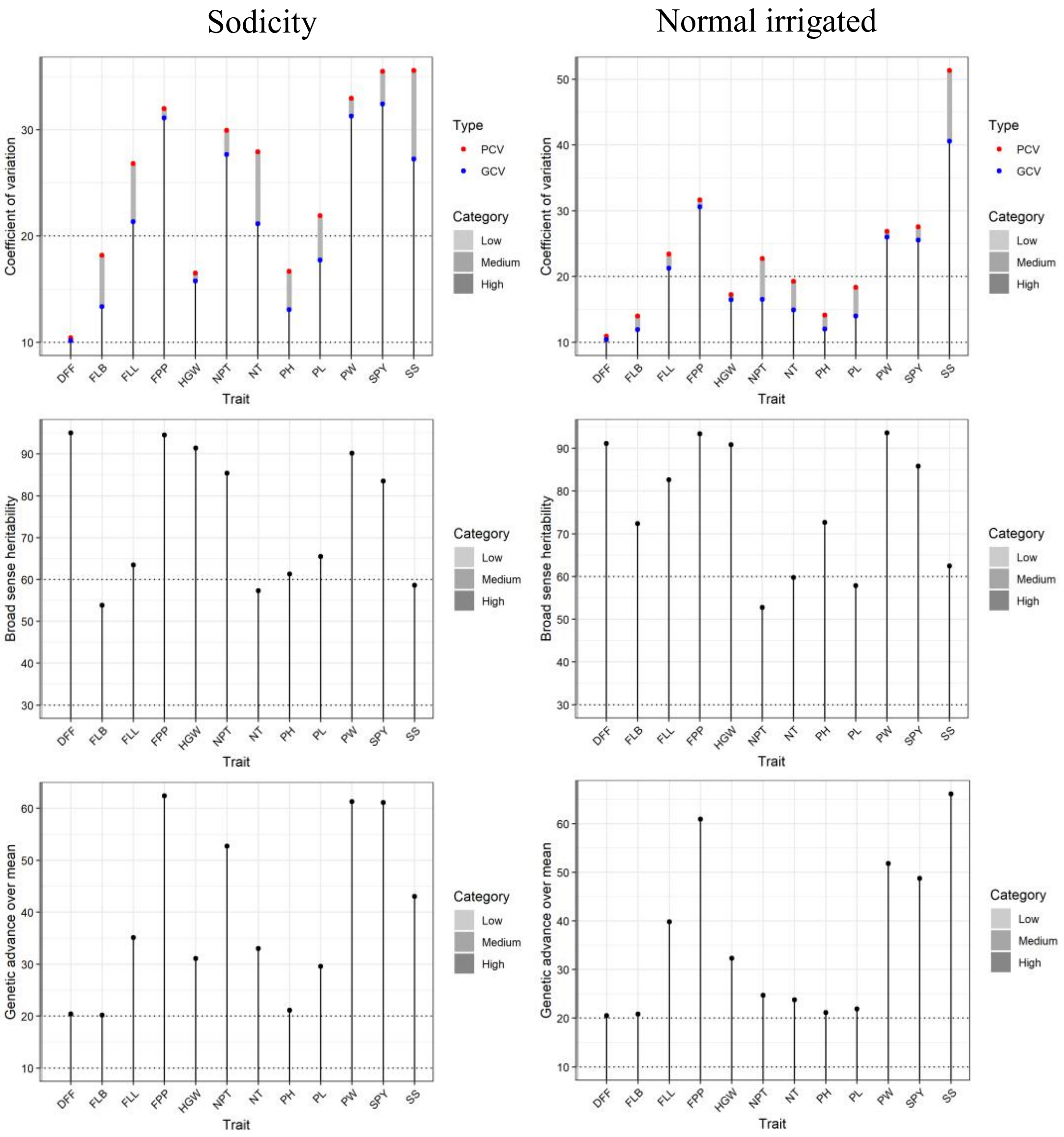
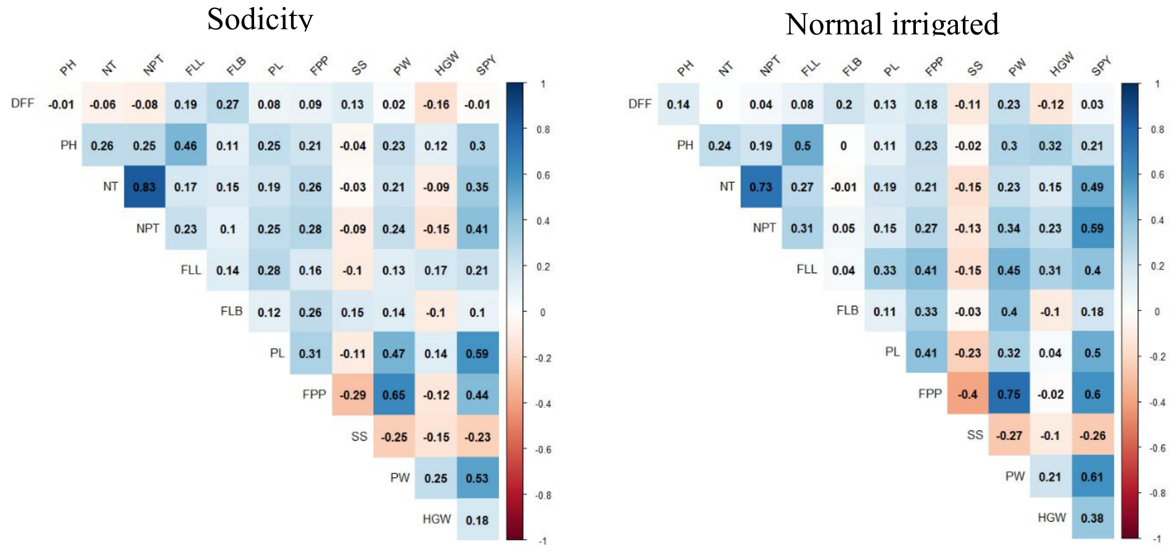


Fig. 2. Genetic variability parameters for sodicity and normal irrigated environments

Heritability and genetic advance: Heritability and genetic advance estimates depicted in **Fig. 2** indicate the nature of gene action for the concerned trait. The heritability estimates under sodicity showed that all the observed traits showed high heritability coupled with high genetic advance except NT, FLB and SS. These traits had moderate heritability coupled with high genetic advance as per cent of mean. Moderate heritability of these traits might be due to high environmental influence and selection may be effective in this case also (Singh and Narayanan, 2017). Similarly, under normal irrigated environment, all the observed traits showed high heritability coupled with high genetic advance except NT, NPT and PL, which showed moderate heritability and high genetic advance. Hence, the observed traits in both the environments may result in efficient selection and crop improvement. Similar findings under sodic soils were reported by Kalaiselvan *et al.* (2019), Yadav *et al.* (2022) and Singh and Verma (2021).

Correlation and path coefficients: The correlation coefficients in **Fig. 3** indicated the relationship between two dependent variables. Single plant yield exhibited significant and positive correlation with PH, NT, NPT, FLL, PL, FPP, PW and HGW under sodicity. These results were in accordance with Sharma *et al.* (2022) for PH and NPT, Rajasekar *et al.* (2021) for NT, NPT, FLL, PW and HGW and Shrivastav *et al.* (2020) for PL and FPP. On the other hand, SS exhibited negative and significant correlation with SPY. Similarly, Single plant yield had significant and positive association with all the above traits along with FLB under normal irrigated environment. SS also exhibited negative and significant correlation with SPY similar to that of the sodic environment. However, the magnitude of correlation under sodicity was low in all the correlated traits except PH and PL as compared to that of the normal irrigated environment. Path coefficient analysis was performed to analyse the direct and indirect effects of different yield contributing traits on the dependent variable SPY (**Table 4**). Path analysis under sodicity revealed positive and highest direct effect of PL towards SPY followed by NPT, FPP, HGW and PW. Similar higher direct effects of NPT, HGW and PW were reported by Rajasekar *et al.* (2021) and of NPT, PL and FPP were reported by Singh *et al.* (2022). The indirect effects of some traits also had higher effects on SPY. The trait NT had highest indirect effect on SPY *via* NPT, followed by FPP and PW having indirect effect on SPY *via* PL. Path analysis performed for normal environment revealed highest and positive direct effect of FPP on SPY followed by HGW, NPT, PL and PW. The Residue effect in both the environment indicates that there might be other traits that influence SPY, which needs to be further studied.

Sodicity is one of the most important abiotic stresses that affect rice production and area under sodicity is counting to be increased. The present study revealed significant differences in distribution of some traits *viz*., DFF, NT, NPT, FPP, SS, HGW and SPY under both irrigated and sodic environments. The genetic variability estimates for all the traits revealed high variability and additive gene action indicating high response to selection in both the environments. It was found that PCV and GCV had increased considerably for most of the traits under sodicity as compared to normal soil environment. Inter-relationships of different traits indicate that NPT, PL, FPP, PW and HGW possessed high correlation and high direct effect on single plant yield indicating the importance of yield improvement through these traits.



Sodicity

	PH	NT	NPT	FLL	FLB	PL	FPP	SS	PW	HGW	SPY
DFF	-0.01	-0.06	-0.08	0.19	0.27	0.08	0.09	0.13	0.02	-0.16	-0.01
PH		0.26	0.25	0.46	0.11	0.25	0.21	-0.04	0.23	0.12	0.3
NT			0.83	0.17	0.15	0.19	0.26	-0.03	0.21	-0.09	0.35
NPT				0.23	0.1	0.25	0.28	-0.09	0.24	-0.15	0.41
FLL					0.14	0.28	0.16	-0.1	0.13	0.17	0.21
FLB						0.12	0.26	0.15	0.14	-0.1	0.1
PL							0.31	-0.11	0.47	0.14	0.59
FPP								-0.29	0.65	-0.12	0.44
SS									-0.25	-0.15	-0.23
PW										0.25	0.53
HGW											0.18

Normal irrigated

	PH	NT	NPT	FLL	FLB	PL	FPP	SS	PW	HGW	SPY
DFF	0.14	0	0.04	0.08	0.2	0.13	0.18	-0.11	0.23	-0.12	0.03
PH		0.24	0.19	0.5	0	0.11	0.23	-0.02	0.3	0.32	0.21
NT			0.73	0.27	-0.01	0.19	0.21	-0.15	0.23	0.15	0.49
NPT				0.31	0.05	0.15	0.27	-0.13	0.34	0.23	0.59
FLL					0.04	0.33	0.41	-0.15	0.45	0.31	0.4
FLB						0.11	0.33	-0.03	0.4	-0.1	0.18
PL							0.41	-0.23	0.32	0.04	0.5
FPP								-0.4	0.75	-0.02	0.6
SS									-0.27	-0.1	-0.26
PW										0.21	0.61
HGW											0.38

Fig. 3. Correlation coefficient for different biometrical traits under sodicity and normal irrigated environments

Table 4. Direct and indirect effects of different yield contributing traits on SPY under sodic and normal irrigated environments

SODICITY	DFF	PH	NT	NPT	FLL	FLB	PL	FPP	SS	PW	HGW
DFF	0.007	-0.001	-0.001	-0.019	-0.012	-0.003	0.030	0.014	-0.010	0.003	-0.022
PH	0.000	0.091	0.004	0.059	-0.030	-0.001	0.098	0.031	0.003	0.029	0.016
NT	0.000	0.024	0.015	0.197	-0.011	-0.002	0.077	0.039	0.002	0.026	-0.013
NPT	-0.001	0.023	0.012	0.237	-0.015	-0.001	0.098	0.043	0.007	0.030	-0.020
FLL	0.001	0.042	0.003	0.054	-0.065	-0.001	0.109	0.024	0.007	0.016	0.024
FLB	0.002	0.010	0.002	0.024	-0.009	-0.010	0.046	0.039	-0.011	0.018	-0.014
PL	0.001	0.023	0.003	0.059	-0.018	-0.001	0.396	0.047	0.008	0.059	0.019
FPP	0.001	0.019	0.004	0.067	-0.010	-0.003	0.123	0.151	0.021	0.083	-0.017
SS	0.001	-0.003	0.000	-0.022	0.007	-0.002	-0.043	-0.044	-0.072	-0.032	-0.020
PW	0.000	0.021	0.003	0.056	-0.008	-0.001	0.185	0.098	0.018	0.127	0.034
HGW	-0.001	0.011	-0.001	-0.035	-0.011	0.001	0.054	-0.018	0.011	0.032	0.137
Residual effect: 0.687											
NORMAL IRRIGATED	**DFF**	**PH**	**NT**	**NPT**	**FLL**	**FLB**	**PL**	**FPP**	**SS**	**PW**	**HGW**
DFF	-0.052	-0.011	0.000	0.010	-0.006	0.002	0.037	0.067	-0.006	0.029	-0.038
PH	-0.007	-0.078	0.026	0.057	-0.034	0.000	0.030	0.084	-0.001	0.037	0.100
NT	0.000	-0.019	0.107	0.218	-0.018	0.000	0.053	0.079	-0.008	0.028	0.047
NPT	-0.002	-0.015	0.078	0.299	-0.021	0.001	0.042	0.101	-0.007	0.042	0.073
FLL	-0.004	-0.038	0.028	0.092	-0.068	0.000	0.093	0.154	-0.008	0.056	0.096
FLB	-0.011	0.000	-0.001	0.015	-0.003	0.010	0.031	0.124	-0.002	0.050	-0.032
PL	-0.007	-0.009	0.020	0.045	-0.023	0.001	0.278	0.152	-0.012	0.039	0.011
FPP	-0.009	-0.018	0.023	0.081	-0.028	0.003	0.114	0.371	-0.021	0.093	-0.006
SS	0.006	0.002	-0.016	-0.038	0.010	0.000	-0.064	-0.148	0.053	-0.033	-0.032
PW	-0.012	-0.023	0.024	0.101	-0.031	0.004	0.088	0.279	-0.014	0.125	0.065
HGW	0.006	-0.025	0.016	0.070	-0.021	-0.001	0.010	-0.007	-0.005	0.026	0.313
Residual effect: 0.521											

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