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Research Article

Study on gene action for sodic tolerance traits in rice (*Oryza sativa* L.)

P.Shanthi[1*], S.Jebaraj[2] and S.Geetha[3]

[3]National Pulses Research Centre, TNAU, Vamban.
[1]Agricultural Research Station, TNAU, Pattukkottai, 641 003.
[2]Agricultural College and Research Institute, TNAU, Madurai.
*Email: shanthi_pbg@yahoo.com

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Abstract:
Gene action studies were carried out on sodic tolerance physiological traits, yield and yield attributes from line x tester analysis by using 14 diverse parental lines and 54 hybrids. Analysis of variance revealed the importance of non-additive gene action in controlling all the characters studied. The significance of mean squares due to lines and testers indicated prevalence of additive type of gene action for most of the characters studied. BPT 5204, TRY (R) 2 and IR 36 among the lines and Pokkali and CT 9993 among the testers identified as best combiners for sodic talorance, yield and yield contributing characters. These parents could be exploited for development of salt tolerant high yielding varieties combined with more heterosis. Hybrids *viz.,* BPT5204xPokkali, IR36xCSR10, IR64xCSR10, BPT5204xN13, BPT5204xCT9993, W.PonnixMoroberekan, TRY(R)2xCSR10, CO43xPokkali and CO47x Pokkali were identified as the best hybrids for yield, yield attributing characters and sodic tolerant physiological characters. These hybrids could be utilized in heterosis breeding to exploit hybrid vigour.

Key words: sodicity, combining ability, gene action.

Introduction

Rice is the most important staple food for 40 percent of the world population. It is grown under a wide range of agro climatic conditions. A total of 800 million hectares of land throughout the world are salt affected either by salinity (397 million ha) or the associated condition of sodicity (434 million ha) In India alone, salt-affected soils have been estimated to occur in 8.6 million ha, of which about 3.0 million ha are coastal saline. Rice breeders are increasingly challenged in the new century to meet the rapidly growing food demands of an increasing human population. To increase the rice production there is the need to increase the rice growing areas. Hence the situation is arising to extend the rice cultivation into marginal lands where salinity levels in soils are above thresholds affecting rice growth and yield. Recently, the salt affected area is increasing due to the irrigation with salt affected water, high intensity of cropping pattern and more application of chemical fertilizers. Unfortunately, rice is one of the most salt-sensitive cereal crops. Growth and yield components of rice are severely affected by salinity (Akbar *et al.,* 1986). Hence there is an urgent need to develop the salt tolerant varieties in rice. The knowledge of combining ability analysis is useful to assess the nicking ability of parents and at the time elucidate the nature and magnitude of gene action involved for trait of interest especially the quantitative traits, which is important for successful development of crop varieties. Also, the correct choice of parents for hybridization is crucial for development of cultivars. Knowledge of the relative importance of additive and non-additive gene action is essential to identify breeding behaviour of different traits. Present investigation was carried out to study the gene action for sodicity tolerance in rice.

Material and Methods

The experimental material comprised nine lines (female parents) which are popular varieties in Tamil Nadu and five testers (male parents) of rice with diverse genetic base (salt tolerant varieties *viz.,* Pokkali, CSR 10 and N13 and drought tolerant varieties *viz.,* Moroberekan and CT9993). Their 45 hybrid combinations were recovered through Line x Tester mating design. The 45 F_1s along with their parents were raised under sodic soil condition during *Kharif,* 2008 at Anbil Dharmalingam Agricultural College and Research Institute, Trichy, Tamil Nadu, India. The experimental field soil pH is 9.5 and Exchangeable Sodium Percentage (ESP) is around 36. The seeds were sown in raised nursery bed. Twenty five days old seedlings were transplanted in the main field in a randomized block design and replicated thrice. Both the hybrids and parents were planted at a spacing of 20 x 15 cm apart, adopting three meters length plot. All the recommended cultural practices were adopted. Biometrical observations on sodic tolerance traits *viz.,* Days to 50 % flowering, spikelet fertility, chlorophyll a, chlorophyll b, total chlorophyll, chlorophyll a/b ratio, chlorophyll stability index, shoot Na, shoot K, shoot Na/K ratio, catalase, peroxidase and yield contributing traits *viz.,* Plant height, productive tillers per plant, panicle length, filled grains per panicle, hundred grain weight, single plant yield, harvest index, were recorded on randomly selected five plants per replication. The biometrical observations were recorded for yield and its component traits under sodic soil condition as per the Standard Evaluation System (SES) for rice (IRRI). The mean data were subjected to ANOVA and combining ability studies using the Line x Tester analysis (Kempthorne 1957).

Results and discussion

Analysis of variance for combining ability revealed highly significant differences among the hybrids with respect to all the characters studied. The significance of mean squares due to lines and testers indicated prevalence of additive type of gene action for most of the characters. The significance of mean squares due to line x tester for all the characters indicated the presence of epistasis for most of the characters. This also showed that the lines contributed much to the observed variability for all the characters than that of testers revealing wide diversity among the lines and testers.

The preponderance of SCA variances for all the characters suggested that significant role of non-additive gene action which resulted from dominance, epistasis and other interaction effects. Importance of non-additive gene for expression of different traits have also been reported by Thirumeni *et al*. (2003) and Pradhan *et al.* (2006), days to 50 per cent flowering, plant height, productive tillers per plant, harvest index, and single plant (Singh *et al.* (2005)), 100 grain weight and panicle length (Sanjeev Kumar *et al*. (2005)), filled grains per panicle (Manonmani and Fazlullah Khan (2003)), spikelet fertility (Priya (2003)) Chlorophyll content, Na content and Na/K ratio (Thirumeni (1998) and Natarajan *et al.* (2005)), K content (Mohmood *et al*. (2002)) and chlorophyll stability index (Ganesh *et al*. (2004) and Anbumalarmathi *et al.* (2005)) recorded non additive gene action. The predominance of non additive gene action for all the characters indicated that their genetic improvement under salt stress environment was tedious. Similar findings were reported by Mishra (1990) and Mohamood *et al*. (2002) for salt tolerant traits. Heterosis breeding programme is suggested for exploitation of the non-additive gene action. The predominant *sca* effects in self-pollinated crops indicate that the major portion of the variability is due to additive x additive effects or divergence among progenies in the same parental array, therefore, selection should be delayed to later generations (Pradhan *et al.*(2006).

The lines IR36 and BPT5204 excelled others by having significant *gca* effects for 15 characters followed by IR64 for 12 characters out of 19 characters studied including yield. Among the testers, the tester Pokkali was superior to others by showing significant *gca* effects for 15 characters followed by CT9993 for 11 characters out of 19 characters studied

Based on the duration, the line ADT 43 and the tester Moroberekan could be utilized for developing varieties with less duration and for development of dwarf plants the lines IR36 and CO47 and the testers CSR10 and CT9993 could be utilized. Similarly IR36, BPT5204 and IR64 among lines and Pokkali and CT 9993 among testers were the good combiners for yield attributing as well as salt tolerant traits including yield. Hence, these parents could be exploited for development of salt tolerant high yielding varieties combined with more heterosis. As *gca* effect is generally associated with additive gene action in inheritance, the lines and testers with high *gca* effects may be utilized in hybridization programme to improve the salt tolerant traits through transgressive breeding.

The negative *sca* effects were considered for days to 50 % flowering, plant height, chlorophyll a/b ratio, shoot Na and shoot Na/K ratio. The hybrid IR64xCSR10 exhibited superior *sca* effects for 14 characters and negative *sca* effects for days to 50 % flowering, chlorophyll a/b ratio, shoot Na and shoot Na/K ratio followed by W.PonnixMoroberekan registered high *sca* effects for 13 characters and negative *sca* effects for days to 50% flowering, chlorophyll a/b ratio and shoot Na and shoot Na/K followed by IR36xCSR10 which has recorded high *sca* effect for 14 characters and negative *sca* effects for days to 50 per cent flowering, shoot Na and shoot Na/K ratio and BPT5204xPokkali for 13 characters and negative *sca* effects for shoot Na and shoot Na/K ratio.Hence, the hybrids *viz*., IR64xCSR10, W.PonnixMoroberekan, IR36xCSR10, BPT5204xPokkali were the best hybrids for development under salt affected soils based on their *sca* effects

In respect to yield, the high magnitude of *sca* effects of these hybrids resulted from the combinations of parental lines having *gca* effects of high/high (BPT5204xPokkali); high/ medium (BPT5204xCT9993); high /low (IR64xCSR10); medium/medium (CO43XCT9993); medium / low (CO47xCSR10); low / low (W.PonnixMoroberekan). In the case of high/high, high/medium general combiners are involved for high *sca* effects, there are possibilities of complementary epistatic effects acting in the direction of additive effects of the good combiners (Haque *et al.,* 1988). The crosses would be utilized for yield improvement through single plant selection in segregating generations. But in the crosses showing high *sca* effects due to high/low and medium/low general combiners, simple pedigree breeding would not be effective to improve the characters. The expression of high positive *sca* effects may be due to interaction between dominant alleles from good combiners and recessive allele from poor combiners expected to produce desirable segregants in the subsequent generations (Lingham, 1961 and Dubey, 1975). Population improvement *i.e.,* mass selection with concurrent random mating in early segregating generation (Redden and Jensen, 1974) could be perspective breeding procedure for yield improvement in rice. The crosses showing high *sca* effects involving low/low general combiners indicate the non-additive genetic effects and these crosses and these combination could be exploited for heterosis breeding programme (Singh *et al.,* 2007).

It is concluded from the present experiments results, that there is the possibility to breed more sodic tolerance with agronomically adapted high yielding rice varieties than the existing tolerant varieties either through heterosis breeding or through recombinant breeding with selection in later generation can help to develop agronomically adaptable high yielding sodic tolerant rice varieties.

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Table 1: Analysis of variance for combining ability of morphological characters

		Mean Squares								
Sources of variation	**d. f**	**Days to 50 per cent flowering**	**Plant height (cm)**	**Productive tillers per plant**	**Panicle length (cm)**	**Filled grains per panicle**	**Spikelet fertility (%)**	**Hundred grain weight (g)**	**Single plant yield (g)**	**Harvest Index (%)**
Replication	2	0.75	9.68	0.21	0.01	0.01	3.86	0.004	0.186	0.0001
Parents	13	334.95**	1625.29**	1.29**	13.70**	142.53**	142.53**	0.106**	13.27**	0.005**
Crosses	44	229.70**	245.35**	10.86**	15.78**	95.02**	95.02**	0.06**	101.34**	0.007**
Parents x Crosses	1	32.17**	96.77**	96.77 **	37.76**	286.58**	286.58**	0.17**	1015.11**	0.004**
Lines	8	595.84**	350.77**	19.3 **	23.63**	124.25**	124.25**	0.22**	182.79**	0.007**
Testers	4	811.99**	3698.44**	18.64**	15.64**	47.33**	47.33**	0.002**	165.52**	0.015**
Lines x Testers	32	65.39**	134.09**	7.78**	9.37*	60.08**	60.08**	0.032**	72.96**	0.005**
Error	116	1.25	4.93	0.4	0.5	1.78	1.78	0.001	0.79	0.0002

** Significant at 1% level

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Table 2: Analysis of variance for combining ability of physiological traits

Source of variation	d. f	*Mean Squares* Chlorophyll a	Chlorophyll b	Total chlorophyll	Chlorophyll a/b ratio	Chlorophyll Stability Index	Shoot Na	Shoot K	Shoot Na/K ratio	Catalase	Peroxidase
Replication	2	0.001	0.005	0.01	0.01	0.51	0.03	0.04	0.0003	0.05	0.04
Parents	13	0.02**	0.06**	0.15**	0.10**	189.39**	1.09**	0.21**	0.07**	0.74**	3.85**
Crosses	44	0.07**	0.18**	0.46**	0.16**	232.13**	2.90**	0.86**	0.14**	0.03**	6.12**
Parents x Crosses	1	0.65**	1.43**	2.46**	0.07**	85.55**	3.74**	3.15**	0.06**	0.98**	9.19**
Lines	8	0.19**	0.49**	1.27**	0.40**	450.62**	6.63**	1.31**	0.33**	1.85**	17.40**
Testers	4	0.10**	0.17**	0.51**	0.10**	328.49**	3.17**	2.28**	0.19**	0.88**	9.44**
Lines x Testers	32	0.04**	0.10**	0.25**	0.11**	165.47**	1.93**	0.57**	0.09**	0.77**	7.11**
Error	116	0.001	0.002	0.002	0.003	0.17	0.02	0.01	0.001	0.02	0.04

** Significant at 1% level

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Table.3. Parents identified based on high *per se* and high *gca* effects performance

Characters	*Per se* performance	*gca* effects	*Per se* and *gca* effects
*Days to 50% flowering	IR36, ADT43 CSR10, CT9993	ADT43 Moroberekan	ADT43
*Plant height (cm)	ADT43, IR64, IR36, CSR10	CO 47, IR36 CSR10, CT9993	IR36, CSR10
Productive tillers per plant	BPT5204, TRY (R)2	IR36, IR64 N13 ,Moroberekan	-
Panicle length (cm)	IR64, CO43 Pokkali	BPT5204, CO 47 Pokkali, CT9993	Pokkali
Filled grains per panicle	BPT5204, IR64	BPT5204, IR36 Pokkali, CT9993	BPT5204
Spikelet fertility (%)	TRY1, TRY(R)2 Pokkali, N13 and CSR10	TRY(R)2, BPT5204 Pokkali , CSR10	TRY(R)2, Pokkali , CSR10
Hundred grain weight (g)	CO47, TRY1 Pokkali	TRY(R)2 ,TRY1 N13	TRY1
Single plant yield (g)	BPT5204, IR64 and IR36	BPT5204, IR36 Pokkali	BPT5204, IR36
Harvest index (%)	BPT5204, TRY (R)2, CO43, CSR10, CT9993 and N13	BPT5204, IR36 Pokkali, CT9993	BPT5204, CT9993
Chlorophyll a	BPT5204, IR64 Pokkali and Moroberekan	TRY(R)2, IR36 Pokkali, CT9993	Pokkali
Chlorophyll b	BPT5204, IR64 Pokkali and CSR10	TRY(R)2 , IR36 Pokkali, N13	Pokkali
Total chlorophyll	BPT5204, CO47, IR64 Pokkali and CSR10	TRY(R)2, BPT5204 Pokkali, CT9993	BPT5204, Pokkali
*Chlorophyll a/b	BPT5204, CO47, IR64 Pokkali and CSR10	TRY(R)2, IR64 Pokkali, N13	IR64, Pokkali
Chlorophyll stability index	TRY(R)2, TRY1, BPT5204, Pokklai and N13	TRY(R)2, BPT5204 Pokkali, CT9993	TRY(R)2, Pokklai
*Shoot Na	BPT5204,TRY1 Pokkali, CSR10	TRY(R)2, IR36 Pokkali, CT9993	Pokkali
Shoot K	Pokkali, N13 and Moroberekan	BPT5204, TRY(R)2 Pokkali	Pokkali
*Shoot Na/K	IR64, BPT5204 CSR10 and Pokkali	TRY(R)2, BPT5204 Pokkali, CT9993	BPT5204, Pokkali
Catalase	BPT5204, IR64 Pokkali	BPT5204, TRY(R)2 Pokkali , CT9993	BPT5204, Pokkali
Peroxidase	IR64, BPT5204 Pokkali, CSR10	BPT5204, CO47 Pokkali, CT9993	BPT5204, Pokkali

* less *per se* performance and negative *gca* effects.

Table 4. Superior hybrids identified based on high *sca* effects and *per se* performance

Characters	*Per se* performance	*sca* effects
*Days to 50% flowering	IR64xCSR10 IR36xCSR10	W.PonnixMoroberekan BPT5204xCSR10
*Plant height (cm)	W.PonnixCSR10 CO47xCSR10	W.PonnixCSR10 ADT43xN13
Productive tillers per plant	IR36xPokkali CO43xPokkali	CO47xCSR10, IR36xPokkali W.PonnixMoroberekan
Panicle length (cm)	BPT5204xPokkali, BPT5204xN13 BPT5204xCT9993	W.PonnixMoroberekan IR64xCSR10
Filled grains per panicle	BPT5204xPokkali, BPT5204xCT9993	W.PonnixMoroberekan IR36xCSR10
Spikelet fertility (%)	TRY(R)2 xPokkali BPT5204xPokkali	W.PonnixMoroberekan CO47xCSR10
Hundred grain weight (g)	TRY(R)2 xMoroberekan, CO43xN13	BPT5204xCT9993 CO43xN13
Single plant yield (g)	BPT5204xPokkali IR36xPokkali	IR64xCSR10 TRY2xCSR10 IR36xCSR10
Harvest index (%)	BPT5204xPokkali IR36xPokkali	IR36xCSR10 CO47xCSR10
Chlorophyll a	IR36xPokkali IR36xCSR10	IR64xCSR10, CO43xPokkali W.PonnixN13
Chlorophyll b	BPT5204xPokkali IR64xCSR10	CO43xCT9993, W.PonnixN13 W.PonnixMoroberekan
Total chlorophyll	IR36xPokkali, BPT5204xPokkali	W.PonnixMoroberekan ADT43xCT9993
*Chlorophyll a/b	CO47xN13 TRY1xCT9993	CO47xCSR10 W.PonnixMoroberekan
Chlorophyll stability index	BPT5204xPokkali BPT5204xCT9993	IR64xCSR10 CO47xPokkali
*Shoot Na	TRY(R)2 xCSR10 TRY(R)2 xPokkali	W.PonnixMoroberekan CO47xCSR10
Shoot K	TRY(R)2 xPokkali BPT5204xPokkali	BPT5204xPokkali BPT5204xCT9993
*Shoot Na/K	TRY(R)2 xPokkali BPT5204xPokkali	W.PonnixMoroberekan TRY(R)2 xCSR10
Catalase	BPT5204xPokkali IR36xPokkali	ADT43xCT9993 ADT43xMoroberekan
Peroxidase	BPT5204xPokkali TRY(R)2 xCSR10	IR36xCSR10 ADT43xCT9993