

Original Research Article

<https://doi.org/10.20546/ijcmas.2017.609.276>

Generation Mean Analysis for Yield and Salinity Tolerance in Rice (*Oryza sativa* L.)

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ABSTRACT

The experimental material consisted of six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) obtained from two crosses of rice using three parents laid out in a randomized block design with two replications to study the generation mean analysis for ten characters viz., days to flowering, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, total number of grains per panicle, 1000 grain weight and single plant yield. In ADT43 x FL478 a cross the characters like days to flowering, plant height, number of filled grains per panicle, total number of grains per panicle, spikelet fertility and 1000 grains weight were governed by dominance and dominance \times dominance gene effects, days to 50% flowering, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, total number of grains per panicle, 1000 grains weight and single plant yield were governed by additive and additive \times additive gene effects. The cross Improved White Ponni x FL478, characters like days to flowering, plant height, panicle length, number of productive tillers per plant, number of filled grains per panicle, total number of grains per panicle, spikelet fertility, 1000 grain weight and single plant yield were predominantly governed by additive and additive \times additive gene action. The complementary recessive epistasis was observed for the traits number of tillers per plant, number of productive tillers per plant and single plant yield in cross ADT43 x FL478. The presence of duplicate dominant epistasis was noticed for all the traits studied in cross Improved White Ponni x FL478.

Keywords

Generation mean analyses, Salinity, Complementary recessive epistasis, Duplicate dominant epistasis, Additive and dominance.

Article Info

Accepted:
23 August 2017
Available Online:
10 September 2017

Introduction

Rice is the major cereal food crop of the world and serves as the primary source of staple food for more than half of the global population and will continue to occupy the pivotal place in global food and livelihood security systems (Emani *et al.*, 2008). Rice is grown in more than 154 million hectares in the world in a wide range of ecosystems under varying temperatures and water regimes. India has the largest area under rice

(45 million hectares). The population of rice consumers is increasing at a rate of 1.8 per cent annually, as well as the population growth i.e., 1.5 per cent is increasing every year. Hence, the rice requirement by the year 2025 would be about 125 MT (Kumar *et al.*, 2009). A total of 800 million hectares of land throughout the world are salt affected either by salinity (397 million ha) or of sodicity (434 million ha). In Asia alone, 21.5 million

ha of land area is thought to be salt affected (of which 12 million ha is due to saline conditions and the remaining 9.5 million ha is due to alkaline/sodic conditions). In India, approximately 7.0 million ha of agricultural land is affected by varying degrees of salt related problems. The problems of soil sodicity, salinity and of poor quality water are likely to increase in near future. The estimates indicate that the salt affected soils will constitute nearly 16.2 m ha area in the country by 2050 (CSSRI-Vision 2050) without technological interventions, compared to the current estimate of 6.74 million ha. Growth and yield components of rice are severely affected by salinity (Akbar *et al.*, 1986). Hence, there is an urgent need to convert high yielding mega popular varieties as saline tolerant variety to meet out the alarming soil related problems for rice cultivation. Close observations on the yield performance of high yielding varieties have revealed that the realized yield in such varieties is showing a plateauing trend (Pingali, 1990). This situation warrants the development of innovative technologies to improve rice productivity under saline condition. The knowledge on generation mean analysis is useful to elucidate the nature and magnitude of gene action involved for traits of interest especially for quantitative traits, which is important for successful development of crop varieties. Generation mean analysis is a well-established biometrical technique to study the genetics and gene action and to infer the underlying gene action governing for quantitative traits in many crops including rice. In this paper an attempt has been made to assess the nature and magnitude of gene action for yield and yield related traits under salinity condition.

Materials and Methods

The experimental materials comprised two recurrent parents namely, ADT 43 and Improved White Ponni (designated as

females) and one non recurrent donor parent for salinity tolerance FL478 were utilized. Two parents namely ADT43 and IWP and salinity tolerant donor FL478, sowing were taken staggeredly in the crossing block at 10 days interval in order to develop F₁s of the ADT43 x FL478 and IWP x FL478 cross combinations during August 2014 at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai. These parents were crossed and crossed seeds were collected. Single seedling was transplanted per hill following Randomized Block Design (RBD) with two replications in three meter row length with spacing a of 20 x 15 cm in the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai during *Kharif* 2016. Observations were recorded on ten randomly selected plants from the two F₁s in each replication for days to flowering, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, total number of grains per panicle, 1000 grain weight and single plant yield. The scoring for salinity level was evaluated based on standard evaluation system (SES) by IRRI in rice. Soil in the experimental field is slightly saline in nature with an EC of 2.30 dSm⁻¹ and PH around 9.5. However, irrigation water having the EC_{iw} of 5.40 dSm⁻¹ which is saline in nature.

This study was conducted at farmer's field of V. Vedapatti, Villathikulam taluk, Thoothukudi district, Tamil Nadu. Data were recorded on 10 randomly selected plants from parents and F₁, F₂, BC₁ and BC₂ utilized for the analysis.

Results and Discussion

Generation mean analysis, a first degree statistics, is a simple but useful technique for characterizing gene effects for a polygenic character (Hayman, 1958) and determines the

presence and absence of non-allelic interactions. The greatest merit of generation mean analysis is that it helps in the estimation of epistatic gene effects namely additive \times additive (i), additive \times dominance (j) and dominance \times dominance (l). The most commonly used design Line \times Tester analysis fails to detect the epistasis. The nature of gene action governing the inheritance of yield and its components was therefore studied using generation mean analysis.

The generation mean analysis was carried out in selected two crosses obtained from the hybridization programmes. The variation among the means of different generation in all the ten characters studied suggesting the usefulness of the estimation of additive, dominance and epistatic interaction. Significant differences among six generation means were noticed for days to 50 per cent flowering, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, total number of grains per panicle, 1000 grain weight and single plant yield.

The A, B and C scaling test for almost all the characters in the two crosses showed that at least one, two or all the three scales were found significant indicating the presence of non-allelic interaction in the inheritance of the characters under study. However the character panicle length of cross 1 showed non-significant values for all the three scales indicating the non-interacting mode of inheritance. Any one or both the scaling tests were found to be significant in all the traits indicating the presence of epistasis.

The type of epistasis was determined as complementary when dominance (h) and dominance \times dominance (l) gene effects have same sign and duplicate epistasis when the sign was different. Hence, the present study shows that significant additive and epistatic effects exist all the six generations. Although

their presence may vary from cross to cross. A or B or all the three scaling was found significant for all the traits except panicle length in cross 1 (Table 1).

Both the crosses exhibiting non-allelic interaction for inheritance of almost all the traits studied. In general, the interaction effect together i.e., additive \times additive (i) and dominance \times dominance (l) found in higher magnitude than the combined main effects of additive (d) and dominance (h) effects for all the traits in both the crosses.

Studies on gene effects in generation mean analysis revealed that additive gene effect (d) was significant in cross 1 for the traits days to flowering, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, total number of grains per panicle, 1000 grains weight and single plant yield (Table 2). These results indicated that there exist scope for direct selection for grain yield and its contributing traits. Additive effect for number of productive tillers per plant was reported by Robin (1997), Kalita and Upadhaya (2000b) and Kumar *et al.*, (2007). If additive gene action is present in self-pollinated crops like rice, the breeder can effectively select at various levels of inbreeding because additive gene effects are readily transmissible from one generation to another (Gravois and Mc New, 1993). In cross 2 significant additive effect was noticed for the days to flowering, plant height, panicle length, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, total number of grains per panicle, 1000 grains weight, spikelet fertility and single plant yield (Table 2). Anbumalarmathi (2005) reported additive gene effect for days to first flowering. As these parents were good for yield attributing as well as salinity tolerant traits, they could be exploited for development of salinity resistant / tolerant high yielding varieties.

Table.1 Scaling test of quantitative traits of two crosses for salinity tolerance in rice

Crosses/scales	Cross 1 (ADT43 x FL478)	Cross 2 (IWP x FL478)
Days to flowering		
A	4.90*±0.93	-16.17*±1.09
B	5.33*±0.76	20.52*±0.88
C	23.51*±1.75	-18.05*±1.88
Plant height		
A	10.56*± 1.20	-20.30*± 1.07
B	-11.88*± 0.96	34.25*± 1.05
C	38.75*± 1.60	-16.01*±4.36
Panicle length		
A	0.88 ± 1.64	-7.87*± 0.64
B	9.46 ± 1.22	5.17*± 0.68
C	1.02 ± 0.96	-5.98*± 1.23
Number of tillers per plant		
A	-1.48*± 0.61	-0.37±0.68
B	1.73*± 0.77	3.90*±0.73
C	1.15 ± 1.13	2.73*±1.34
Number of productive tillers per plant		
A	0.20 ± 0.48	0.74 ± 0.49
B	0.65± 0.45	2.56*± 0.46
C	1.73*± 0.75	1.26 ±0.86
Number of filled grains per panicle		
A	43.20*±6.15	-9.82±8.99
B	-33.98*±6.93	96.02*±9.28
C	-84.38*±14.79	25.00 ±16.97
Total number of grains per panicle		
A	6.37 ± 8.81	-61.19*± 9.96
B	-30.30*± 9.76	86.87*± 9.24
C	-109.93*±17.59	82.16*± 17.29
Spikelet fertility		
A	17.27*±2.73	14.53*±2.46
B	-4.71*±2.17	9.25*±2.44
C	-5.38±4.57	-16.44*±5.18
1000 grains weight		
A	-2.65*±0.46	1.89*±0.51
B	-20.44*±0.46	-15.05*±0.39
C	-10.75*±0.97	-7.21*±0.69
Single plant yield		
A	3.69*±1.60	6.48*±2.10
B	-41.83*±1.68	2.58±2.87
C	-33.91*±3.84	-1.21±4.59

*Significant at 5% level

Table.2 Genetic components of generation mean for quantitative traits for Salinity tolerance in rice

Genetic effects	Cross 1 (ADT43 x FL478)	Cross 2 (IWP x FL478)
Days to flowering		
m	92.39*±0.34	96.95*±0.37
(d)	-1.34*±0.44	-9.62*±0.55
(h)	-21.60*±1.73	24.27*±1.95
(i)	-13.28*±1.64	22.40*±1.87
(j)	-0.21 ±0.50	-18.34*±0.61
(l)	3.05±2.48	-26.75*±2.90
Plant height		
m	100.97*± 0.29	99.68*± 1.05
(d)	0.26 ± 0.59	-22.45*± 0.58
(h)	-29.79*± 1.76	33.48*±4.40
(i)	-40.08*±1.68	29.96*±4.36
(j)	11.22*±0.73	-27.27*±0.67
(l)	41.40*±2.88	-43.91*±4.94
Panicle length		
m	11.79 ± 7.75	23.23*±0.20
(d)	-0.13 ± 0.22	-4.82*±0.28
(h)	29.69 ± 23.21	6.83*±1.10
(i)	-	3.28*±1.01
(j)	-	-6.52*±0.39
(l)	-	-0.58*±1.68
Number of tillers per plant		
m	13.52*± 0.19	13.22*± 0.24
(d)	-2.08*± 0.33	-2.36*± 0.29
(h)	0.317 ± 1.10	0.12 ± 1.22
(i)	-0.90 ± 1.02	0.80 ± 1.13
(j)	-1.605*± 0.43	-2.13*± 0.44
(l)	0.658 ± 1.77	-4.33*± 1.79
Number of productive tillers per plant		
m	11.42*± 0.12	11.14*± 0.12
(d)	-0.60*± 0.23	-1.26*± 0.19
(h)	0.04 ± 0.74	2.59*± 0.72
(i)	-0.88 ± 0.69	2.04*± 0.64
(j)	-0.22 ± 0.30	-0.91*± 0.27
(l)	0.03 ± 1.19	-5.34*± 1.15
Number of filled grains per panicle		
m	134.88*± 3.33	184.95*± 3.30
(d)	14.44*± 3.72	-48.82*± 4.91
(h)	91.45*± 15.61	48.00 ± 17.32
(i)	93.60*± 15.29	61.20*± 16.49
(j)	38.59*± 4.35	-52.92*± 5.58
(l)	-102.82*± 21.00	-147.40*± 25.97
Total number of grains per panicle		
m	179.63*±3.48	260.14*±3.42
(d)	19.66*±4.91	-45.68*±5.09
(h)	71.77*±17.89	-59.78*±17.88
(i)	86.00*±17.07	-56.48*±17.08
(j)	18.33*±5.80	-74.03*±6.21
(l)	-62.07*±26.39	30.80*±26.73

Spikelet fertility		
m	74.42*±0.73	71.04*±0.76
(d)	-0.57±1.04	-4.79*±0.83
(h)	22.25*±4.00	35.05*±4.07
(i)	17.94*±3.59	40.23*±3.50
(j)	10.99*±1.38	2.63*±0.97
(l)	-30.51*±6.19	-64.03*±6.17
1000 grains weight		
m	20.35*±0.15	18.32*±0.09
(d)	2.77*±0.18	0.87*±0.24
(h)	-10.92*±0.82	-7.40*±0.69
(i)	-12.35*±0.74	-5.94*±0.63
(j)	8.89*±0.20	8.47*±0.25
(l)	35.45*±1.23	19.11*±1.21
Single plant yield		
m	31.77*±0.82	38.36*±0.84
(d)	5.85*±0.89	-12.17*±1.26
(h)	0.39±3.88	9.21*±4.50
(i)	-4.22±3.75	10.27*±4.23
(j)	22.76*±0.96	1.95±1.54
(l)	42.36*±5.26	-19.34*±6.82

*Significant at 5% level

(m) = mid parental value, (d) = additive effect, (h) = dominance effect, (i) = additive x additive, (j) = additive x dominance and (l) = dominance x dominance

These results were in conformity earlier findings of Geetha *et al.*, (2006) and Shanthy *et al.*, (2011) under salinity. These parents could be utilized as potential donors in the hybridization programme which might result in identification of superior segregants through transgressive breeding with favourable genes for yield, its component traits as well as salinity tolerance.

The dominance gene effect (h) was significant in cross 1 for the days to flowering, plant height, number of filled grains per panicle, total number of grains per panicle, spikelet fertility and 1000 grains weight whereas in the case of cross 2 it was observed significant effect for the traits days to flowering, plant height, panicle length, number of productive tillers per plant, number of filled grains per panicle, total number of grains per panicle, spikelet fertility, 1000 grain weight and single plant yield. The dominant effect was non-significant in both the crosses for the trait number of tillers whereas number of productive tillers and single plant yield in

cross 1 alone (Table 2). Dominance gene effect for number of productive tillers plant was earlier reported by Koodalingam (1994), Kumar *et al.*, (2007), Patil *et al.*, (2003) and Priya (2003). There was a linear relationship between these two cross combinations for the traits depicting the importance of dominance gene action. The result was in good accordance with the earlier reports of Rogbell and Subbaraman (1997), Deepasankar *et al.*, (2008) and Verma *et al.*, (2010) under saline-sodic soils.

The additive × additive (i) interaction effect was significant in cross1 for the traits days to flowering, plant height, number of filled grains per panicle, total number of grains per panicle, spikelet fertility and 1000 grain weight but in the case of cross 2 the significant effect was noticed for the traits days to flowering, plant height, panicle length, number of productive tillers per plant, number of filled grains per panicle, total number of grains per panicle, spikelet fertility, 1000 grain weight and single plant

yield (Table 2). These results were in conformity with Vaithilingam (1995) for the trait number of productive tillers per plant, Robin (1997) for the trait number of grains per panicle, Kumar *et al.*, (2007), and Robin (1997), Yogameenakshi (2002). Hence, the selection to be postponed to later generations after obtaining homozygosity for most of the alleles. Rogbell (1995), Deepasankar *et al.*, (2008); Kumar *et al.*, (2010) observed similar findings for days to 50 per cent flowering in rice evaluated under saline soils.

The dominance \times dominance (l) interaction effect had significant effect in cross 1 for the traits plant height, number of filled grains per panicle, total number of grains per panicle, spikelet fertility, 1000 grain weight and single plant yield whereas in the case of cross 2 the traits viz., days to flowering, plant height, panicle length, number of tillers, number of productive tillers per plant, number of filled grains per panicle, total number of grains per panicle, spikelet fertility, 1000 grain weight and single plant yield were observed significant (l) effect (Table 2). Similar results were earlier reported for number of productive tillers (Koodalingam, 1994 and Vaithilingam, 1995); number of grains per panicle (Robin, 1997), 1000 grain weight (Mahalingam, 2003) and for grain yield (Kumar *et al.*, 2007).

These results were in confirmation with the findings of Thirumeni *et al.*, (1998); Liang-jun (2006) and Kumar *et al.*, (2010) under saline situation. Hence, in those crosses, postponement of selections to later generations to tag promising segregants possessing tolerance to salinity would be of ideal and practical method. These results were in conformity with earlier findings of Geetha *et al.*, (2006); Karthikeyan and Anbuselvam (2006). To obtain desirable early segregants, the appropriate breeding method would be bi-parental mating or reciprocal recurrent

selection method. Hence, bi-parental mating followed by recurrent selection method might be considered to obtain an array of desirable segregants. Similar findings were reported by Mishra (1995); Thirumeni *et al.*, (2003) and Karthikeyan *et al.*, (2009).

The dominance (h) and dominance \times dominance (l) had opposite sign for all the traits in cross 1 except for the traits number of tillers per plant, number of productive tillers per plant and single plant yield (Table 2). It indicated the presence of complementary recessive epistasis. These results are in conformity with the findings of Chauhan (1993) in rice. In the case of good \times good general combiners there are possibilities of complementary epistatic interaction acting in the direction of additive effects of the good combiners. The crosses would be utilized for yield improvement through single plant selection in segregating generations. This finding was in good accordance with earlier reports of Rogbell (1995); Karthikeyan and Anbuselvam (2006). In the cross 2 the predominance of duplicate epistasis was noticed from opposite sign of (h) and (l) for the expression of all the traits studied.

It could be noted that the presence of additive, dominance, additive \times additive and dominance \times dominance interaction effects were present along with either duplicate dominant epistasis or complementary recessive epistasis for grain yield and most of its contributing traits. Hence, selection in the early segregating generations may not give desirable recombinants. Therefore selection may be delayed to later segregating generations when the dominance and epistasis disappear and resorting to intermating of segregants followed by recurrent selection.

Simple selection procedures or pedigree breeding method is sufficient to harness additive gene action. But the presence of

dominance gene action in most of the characters warrants postponement of selection to later generations after effecting crosses. Heterosis breeding procedures are effective in harnessing dominance gene action to the full extent.

Both additive and dominance gene actions play major role in several characters. In such circumstances biparental mating design or reciprocal recurrent selection can be followed for further recombination of alleles to produce desirable segregants. These methods can also be well adopted in order to harness the epistatic interactions by way of breaking the undesirable linkages. Diallel selective mating system proposed by Jensen (1970) could also be followed to break such undesirable linkages between two or more genes and to produce desirable recombinants.

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How to cite this article:

Muthuvijayaragavan, R. and Murugan, E. 2017. Generation Mean Analysis for Yield and Salinity Tolerance in Rice (*Oryza sativa* L.). *Int.J.Curr.Microbiol.App.Sci*. 6(9): 2249-2257.
doi: <https://doi.org/10.20546/ijcmas.2017.609.276>