Inheritance of important metric traits of wheat in salt stress environments

R. K. Rathore

Department of Genetic and Plant Breeding, College of Agriculture, Sumerpur, Rajasthan, India
Correspondence Author: R. K. Rathore

Abstract
Development of salinity tolerant genotypes is important for sustaining wheat productivity in suppressive soils. The generation mean analysis of three bread wheat crosses viz., Lok 1 x Raj 3880, Job 666 x Kharchia 65 and Raj 1972 x Kharchia 65 under normal and saline-sodic environment revealed presence of both additive and non-additive gene effects in the inheritance of grain yield per plant and other contributing characters under both the environments. Among the digenic interactions, all three types of epistatic effects were involved in the inheritance of characters studied. Only duplicate gene interaction was present, wherever available. Hence, intermating in early generations and intense selection in later generations could be successfully adopted for breeding wheat varieties having appreciable salinity tolerance level.

Keywords: wheat, salinity, inheritance

Introduction
Soil salinity is one of the major causes of low productivity in arid and semi-arid regions of the world [1]. Breeding for salinity tolerance is one of the rational approach of combating this problem. Salinity tolerance can be transferred from available genetic resources to high yielding and widely adapted wheat varieties only through a definite breeding programme. This would be possible if the nature of gene effects in the material is known. The study reported here was, therefore, taken up to investigate the gene effects controlling salinity tolerance using generation mean analysis and suggest appropriate breeding methlogy.

Materials and methods
The experimental material comprised six basic generation namely, P_1, P_2, F_1, F_2, BC_1 and BC_2 of the three bread wheat (*Triticum aestivum* L.) crosses viz., Lok 1 x Raj 3880, Job 666 x Kharchia 65 and Raj 1972 x Kharchia 65. Kharchia 65 and Job 666 have high degree of salinity tolerance, Lok 1 is semi-tolerant, and Raj 3880 and Raj 1972 are high yielding genotypes. These six generations were grown in Compact Family Block Design with three replication during *rabi* 2017-18 at Research Farm of ARSS, Sumerpur under normal (pH 8.17; Ece 1.02 dS/m) and saline sodic (pH 8.6; Ece 5.57 dS/m) soils. Each plot consisted of paired rows of, P_1, P_2, F_1, F_2, BC_1 and BC_2 and six rows of each F_2 generation. Each rows was 2 m long with 25 x10 cm spacing. Data on 10 competitive plants in non-segregating (P_1, P_2, and F_1) and 20 plants in segregating generations (BC_1, BC_2 and F_2) were recorded on six metric traits.
Individual scaling tests A, B, C and D proposed by Hayman and Mather [2] was first applied to determine adequacy of additive-dominance model. In the presence of digenic interactions, six-parameter model [3] was applied, while in the

absence, three parameter model [4] was used.

Results and discussion
The analysis of variance revealed significant differences among the generations for all the traits in both the environments expect for yield per spike in cross Job 666 x Kharchia 65 in normal as well as saline soils and Raj 1972 x Kharchia 65 in normal soils only. Further analysis was carried out only for crosses having significant differences.
The mean of six generations of three crosses in both the environments (Table 1) showed that both the parents of each cross differed for all traits expect Raj 1972 and Kharchia 65 having low differences for grains per spike and yield per spike. The mean values as expected were lower in saline soils than the normal soils. The F_2 means of all the characters reduced in comparison to F_1 and back crosses suggesting presence of dominance as well as epistatic interactions and affinity towards respective recurrent parent under both the environments except for yield per spike in Raj 1972 x Kharchia 65 in saline soil.
The scaling tests indicated inadequacy of additive-dominance model in 25 out of 33 cases. Thus, six-parameter model was used in these 25 cases and remaining 8 cases were subjected to three-parameter model. This revealed preponderance of non-allelic interactions in both the environments. Estimates of gene effects for the traits under study are presented in Table 2. The additive gene effects were highly significant for most of the character combinations. However, their magnitude in comparison with other gene effects was relatively low. The dominance gene effect were significant for tillers per plant in Job 666 x Kharchia 65 in normal soil; for spike length in Raj 1972 x Kharchia 65 in both the environments; for grains per spike in Raj 1972 x Kharchia 65 in saline soil; for yield per spike in both the crosses; and for grain yield per plant in crosses Job 666 x Kharchia 65 and Raj 1972 x Kharchia 65 in both the

environments. Additive x additive gene effects were also present but other digenic interactions also played major role in both the environments. Additive x additive and additive x dominance digenic interactions were significant for tiller per plant in cross Job 666 x Kharchia 65 in normal soil and for yield per spike in Raj 1972 x Kharchia 65 in saline soils. For spike length and grain yield per plant either one or more interaction effects were significant for crosses Lok 1 x Raj3880 and Job 666 x Kharchia 65. All the three types of digenic gene interactions were significant and for yield per spike in cross Lok 1 x Raj 3880; and also for grain yield per plant in crosses Job 666 x Kharchia 65 and Raj 1972 x Kharchia 65 in both the environment. Additive x additive gene interaction was significant for grains per spike in saline environment only. Biological yield per plant was influenced by all the three interaction types in Job 666 x Kharchia 65 but had significant additive x dominance interaction for Raj 1972 x Kharchia 65

in saline environment only. Only duplicate type of epistasis was observed in the present investigation, which would hinder progress of selection. This complexity of inheritance obtained for the traits used in the study are in agreement with the findings of various workers. Additive and dominance gene effects in wheat were reported by Singh and Rana [5] and Singh [6], whereas epistatic effects were obtained by Singh et al. [7], Amawate and Behl [8] and Walia et al. [9].

Keeping in view the presence of both additive and non-additive gene actions as well as duplicate type of epistasis in the inheritance of the traits used in the present study, simple selection procedures will definitely prove to be less effective. Under such a situation exploitation of both fixable and non-fixable variations through intermating in early segregating generations followed by inter selection in later generations would help in exploiting both types of gene effects.

Table 1: Per se performance of yield and its contributing characters under normal (N) and saline (S) soils

Character/Cross	$\overline{P_1}$	$\overline{P_2}$	$\overline{F_1}$	$\overline{F_2}$	$\overline{BC_1}$	$\overline{BC_2}$
Tillers/plant						
C_1N	9.07±0.48	7.53±0.37	8.13±0.54	7.87±0.30	9.27±0.38	7.60±0.51
S	6.93±0.30	5.67±0.33	6.60±0.43	6.27±0.44	7.17±0.51	5.40±0.22
C_2N	11.67±0.51	16.53±0.48	14.20±0.58	12.57±0.34	11.77±0.44	15.90±0.58
S	9.60±0.28	13.80±0.31	12.60±0.24	11.93±0.41	9.90±0.37	13.17±0.52
C_3N	12.93±0.35	16.33±0.41	14.13±0.39	13.50±0.61	12.83±0.34	16.03±0.43
S	9.73±0.39	13.60±0.31	13.13±0.24	11.83±0.54	10.30±0.40	13.40±0.55
Spike length						
(cm) C_1N	10.48±0.17	12.75±0.11	12.33±0.14	11.73±0.24	10.97±0.19	11.93±0.24
S	10.42±025	11.52±0.15	12.13±0.21	11.15±0.20	10.29±0.17	11.76±0.19
C_2N	11.29±0.14	9.75±0.15	11.81±0.19	11.40±0.20	11.20±0.22	10.41±0.19
S	10.73±0.20	9.67±0.20	10.82±0.15	10.53±0.18	10.55±0.21	9.66±0.18
C_3N	11.65±0.19	10.28±0.22	12.00±0.15	10.68±0.25	11.45±0.19	10.62±0.21
S	11.41±0.25	9.93±0.19	11.61±0.17	10.39±0.20	11.28±0.20	10.11±0.18
No. of grains/ Spike						
C_1N	49.47±1.79	54.93±1.71	53.27±1.56	50.07±1.03	48.60±1.62	53.83±1.76
S	48.00±1.67	50.20±1.77	49.20±1.45	46.90±1.10	47.80±1.46	49.50±1.88
C_2N	59.40±2.27	53.00±1.66	60.73±1.90	58.60±2.11	58.87±1.71	54.60±1.40
S	56.67±2.27	51.80±1.81	58.20±1.91	54.20±1.60	57.13±1.97	49.83±1.69
C_3N	52.47±1.96	51.80±2.13	53.60±1.53	51.70±1.70	52.07±1.86	51.60±1.41
S	48.80±1.74	50.73±1.93	49.80±1.46	45.30±0.91	49.40±1.61	50.77±2.03
Yield/spike (g)						
C_1N	3.41±0.12	3.82±0.13	4.41±0.13	4.37±0.13	3.75±0.11	3.06±0.17
S	2.94±0.09	2.09±0.08	2.59±0.18	3.02±0.15	1.85±0.08	2.87±0.11
C_3S	2.63±0.06	2.98±0.09	2.84±0.09	3.72±0.11	2.65±0.13	3.64±0.10
Biological yield/plant (g)						
C_1N	30.40±2.92	40.27±2.00	42.20±1.93	36.77±1.62	32.63±1.97	37.50±2.14
S	28.20±2.57	36.60±1.71	40.53±3.08	34.50±2.04	29.03±1.52	35.90±2.84
C_2N	43.00±1.58	75.20±2.49	70.67±2.68	66.20±1.94	44.47±3.02	74.77±3.52
S	41.27±2.08	72.53±3.20	64.20±2.63	52.40±2.91	38.10±1.97	70.50±3.40
C_3N	52.27±2.71	74.07±2.26	68.20±3.01	59.20±3.21	53.67±2.92	72.37±3.48
S	39.33±2.47	70.20±2.85	61.60±1.76	53.50±2.90	36.67±1.83	71.13±3.41
Grain yield/plant						
C_1N	13.12±0.56	18.56±0.55	20.45±0.66	16.65±0.39	13.16±0.45	17.21±0.78
S	11.78±0.62	17.20±0.51	18.44±0.48	15.25±0.43	12.18±0.58	17.20±0.75
C_2N	17.28±0.58	25.36±0.51	32.86±0.43	29.80±0.52	17.42±0.77	25.88±0.83
S	15.61±0.55	22.00±0.64	31.40±0.47	25.96±0.81	14.87±0.57	23.04±0.80

C$_3$N	22.79±0.42	26.40±0.51	33.06±0.73	27.54±0.64	19.24±0.72	25.50±0.72
S	18.74±0.37	25.66±0.68	30.11±0.62	25.64±0.56	16.85±0.66	23.34±0.73

C$_1$= Lok 1 x Raj 3880, C$_2$= Job 666 x Kharchia 65 and C$_3$= Raj 1972 x Kharchia 65

Table 2: Estimates of Gene action for yield and its components under normal (N) and saline (S) soils

Character / Cross	$\hat{m}$	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{j}$	$\hat{l}$
Tillers/plant						
C$_1$N	6.03±1.78	0.77*±0.31	5.23±4.63	-	-	-
S	6.26±0.43	1.76**±0.55	0.36±2.12	0.06±2.07	1.13±0.59	0.60±2.98
C$_2$N	12.56±0.34	-4.13**±0.72	5.16*±2.11	5.06*±2.00	-1.70*±0.80	-3.79±3.49
S	11.93±0.41	-3.26**±0.63	-0.70±2.11	-1.60±2.08	-1.16±0.67	4.06±3.10
C$_3$N	10.90±2.67	-1.70**±0.27	7.17±5.92	-	-	-
S	11.83±0.53	-3.09**±0.68	1.53±2.56	0.06±2.53	-1.16±0.72	2.13±3.53
Spike length(cm)						
C$_1$N	11.72±0.24	-0.95**±0.30	-0.38±1.15	-1.10±1.14	0.17±0.32	3.20*±1.59
S	11.15±0.20	-1.46**±0.25	0.64±0.98	-0.15±0.95	-0.90**±0.29	2.65±1.40
C$_2$N	11.40±0.19	0.79**±0.29	-1.11±1.00	-2.40*±0.97	0.02±0.30	3.86**±1.47
S	10.52±0.17	0.89**±0.27	-1.07±0.91	-1.69±0.89	0.36±0.30	3.32*±1.36
C$_3$N	10.68±0.24	0.82**±0.28	2.42*±1.16	1.39±1.14	0.14±0.32	0.41±1.57
S	10.38±0.19	1.16**±0.27	2.16*±0.99	1.21±0.96	0.42±0.31	0.57±1.41
No. of grains/spike						
C$_1$N	47.60±6.43	-2.73*±1.23	4.20±7.02	-	-	-
S	42.10±6.58	-1.10±1.22	12.10±7.20	-	-	-
C$_2$N	63.67±9.62	3.20*±1.41	-17.33±1.92	-	-	-
S	54.20±1.60	7.36**±2.59	1.09±8.58	-2.86±8.24	4.86±2.97	13.80±13.44
C$_3$N	51.60±8.37	0.33±1.45	-1.60±2.05	-	-	-
S	45.30±0.91	-1.36±2.58	19.16**±6.63	19.33**±6.33	-0.39±2.89	-20.33±11.65
Yield/spike(g)						
C$_1$N	4.36±0.13	0.69**±0.19	-3.04**±0.68	-3.84**±0.66	0.89**±0.21	6.28**±1.01
S	3.01±0.15	-1.02**±0.13	-2.54**±0.68	-2.61**±0.66	-1.44**±0.14	3.37**±0.89
C$_3$S	3.75±0.11	-0.98**±0.16	-2.27**±0.57	-2.30**±0.56	-0.81**±0.17	1.02±0.84
Biological yield/plant(gm)						
C$_1$N	42.13±8.88	-4.93*±1.77	-21.53±22.43	-	-	-
S	34.50±2.04	-6.96*±3.22	0.00±1.95	-8.13±6.40	-2.66±3.57	24.13±16.75
C$_2$N	66.20±1.93	-30.30**±4.63	-14.76±12.46	-26.33*±12.08	-14.20**±4.86	47.39*±21.01
S	52.40±2.90	-32.40**±3.92	14.89±14.44	7.59±4.04	-16.76**±4.36	17.40±10.60
C$_3$N	47.90±15.82	-10.90**±1.77	24.90±7.93	-	-	-
S	53.50±2.90	-34.76**±3.86	7.83±4.19	0.99±3.96	19.03**±4.30	16.73±20.03
Grain yield/plant						
C$_1$N	16.65±0.39	-4.04**±0.90	-1.24±2.51	-5.85*±2.39	1.32±0.98	17.69**±4.22
S	15.25±0.43	-5.05**±0.94	1.71±2.63	-2.23±2.56	-2.30*±1.02	9.94*±4.35
C$_2$N	29.80±0.52	-8.46**±1.12	-21.05**±3.13	-32.59**±3.07	-4.42**±1.19	54.35**±5.11
S	25.96±0.81	-8.17**±0.98	-15.43**±3.85	-28.03**±3.80	-4.97**±1.07	52.62**±5.26
C$_3$N	27.54±0.64	-6.26**±1.01	-12.21**±3.37	-20.68**±3.27	-4.45**±1.07	46.51**±5.07
S	25.64±0.55	-6.49**±0.98	-14.27**±3.06	-22.18**±2.98	-3.03**±1.05	46.42**±4.76

*,** significant at 5 and 1 % levels, respectively, C$_1$= Lok 1 x Raj 3880, C$_2$= Job 666 x Kharchia 65 and C$_3$= Raj 1972 x Kharchia 65

References

1. Rabie RK, Matter MK, Khanis AMK, Mostagha MM. Effect of salinity and moisture content of soil on growth, nutrient uptake and yield of wheat plant. Soils sci. and Plant Nutr. 1985;31:545.

2. Haymean BI, Mather K. The description of genetic interaction in continuous variation. Biometrics. 1955;11:69-82.

3. Hayman BI. The separation of epistatic from additive and dominance variation in generation means. Heredity. 1958;12:371-390.

4. Jinks JL, Jones RM. Estimation of components of heterosis. Genetics. 1958;43:223-234.

5. Singh KN, Rana RS. Influence of soil alkalinity and salinity on estimates of heterosis and gene effects governing some quantitative traits in bread wheat. Indian J. Genet. 1987;47:76-78.

6. Singh KN. Gene effects of some quantitative characters in wheat under salt stress conditions. Annals of Agric. Res. 1989;10:1-4.

7. Singh R, Rana RS, Chaudhary MS. Nature of gene effects in the inheritance of grain yield and its components in bread wheat under normal and sodic soils. (Abstract) Proc. Golden Jubilee Symp. On Genetic Research and Education: Current Trends and the Next Fifty Years. Vol. 1, Feb. 12-15, 1991, Indian Society of Genetics and Plant Breeding, New Delhi, 1991, 216.

8. Amawate JS, Behl PN. Genetical analysis of some quantitative components of yield in bread wheat. Indian J. Genet. 1995;55:120-125.

9. Walia DP, Tashi Dawa, Plaha P, Chaudhary HK. Gene effects controlling grain yield and its components in bread wheat. Agric. Sci. Digest (Karnal). 1995;15:129-131.