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Genetic Analysis of Salinity Tolerance in a Bread Wheat Cross

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ABSTRACT

Inheritance of salinity tolerance was determined in a cross between two spring bread wheat cultivars, "*Rovshan*" (P_1) a tolerant cultivar and "*Falat*" (P_2) a susceptible one. The parents, F_1, F_2 and backcross generations were studied under salinity conditions (EC= 12 dS m^{-1}) in a greenhouse. Eight characters namely: Heading Date (HD), Plant Height (PH), K^+, Na^+, K^+/Na^+ ratio, total Number of Tillers per plant (NT), Ratio of Fertile Tillers per plant (RFT) and total Chlorophyll Content (TC) were recorded to estimate means and variances pooled over replications, according to the weighted generation means analysis method. Generation means analysis of the data revealed that these characters show all types of gene actions (additive, dominance and epistasis) and suggest that complex epistatic effects are important in controlling salt tolerance characteristics. The highest broad sense heritability (0.87) was observed for K^+/Na^+, indicating the interference of a major gene in control of this trait. Regarding the existence of additive and non-additive effects in controlling traits in this cross, the recurrent selection followed by pedigree breeding may prove useful in improving salinity tolerance in wheat.

Keywords: Gene effects, Generation mean analysis, Heritability, Salinity, Wheat.

INTRODUCTION

Salinity of irrigation water and agricultural soils can probably be considered as the most important limiting factor of crop plants' growth in most areas of the world, adversely affecting about 7% of the world's total crop land area (Flowers *et al*., 1997; Flowers, 2004). Salinity influences seed sprouting by decreasing osmotic potential in the medium, by toxicity effect of ions including sodium and chlorine, and as well by a diminishing of necessary nutritive ions like calcium and potassium (Huang and Redmann, 1995). The reactions of various crops to salinity are different the differences being observed in various growth phases (Rehman, 1996). The problem of soil salinity is further increased due to the use of poor water quality for irrigation accompanied by poor drainage (Chinnusamy *et al.*, 2005). Adverse effects of salinity on plant growth may also be due to ion cytotoxicity (mainly due to Na^+, Cl^- and $SO_4^{=}$), and osmotic stress (Zhu, 2002; Ali *et al*., 2004). Saline soil can be defined as soil of an electrical conductivity of the saturated paste extract (ECe) of 4 dS m^{-1} (4 dS $m^{-1} \approx$ 40 mM NaCl) or more and while most crop plants show susceptibility to salinity even when *ECe* is less than 3.0 dS m^{-1} (Chinnusamy *et al*., 2005).

Iran suffers from a climate that is mostly arid and semi-arid. Water shortage here is a major obstacle to crop production, negatively affecting yield and grain quality. Tolerance to salinity stresses is a key topic of study for crop improvement, since seven percent of the land in Iran contains salt

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either in the irrigation water or in soil and that comprises about 12.5% of total area of the country (Zohary, 1973). Wheat (*Triticum aestivum* L.) is the most important and the most widely adapted food cereal in Iran, and the most efficient way to increase its yield is to improve salt tolerance in its genotypes. Biological methods of management, including an identification of plant mechanisms for salt tolerance and the breeding of new cultivars are some of the most effective strategies for reducing salinity problems and effects in Iranian agriculture. There are a number of possible mechanisms by which a cereal can tolerate high levels of salinity. As in wheat, salt tolerance is associated with low rates of transport of Na^+ to shoot, with high selectivity for K^+ over Na^+ (Munns *et al*., 2006; Chen *et al*., 2007). Bread wheat is affected by a low rate of Na^+ accumulation and an enhanced K^+/Na^+ discrimination, a character that is controlled by a locus on chromosome 4D (Dupcovsky *et al*.,1996). Tissue Na^+ concentration was used as a criterion for salinity tolerance but there was no consistent relationship between tissue Na^+ concentration and salinity tolerance in wheat (Genc *et al*., 2007). But in some investigations, close correlation was observed between Na^+ exclusion and salinity tolerance in bread wheat (Ashraf and O'leary, 1996; Poustini, 2004). Information on the genetic basis and knowledge about types of genes action in traits which contribute to salt tolerance would be helpful to breeders to develop and design breeding programs to improve this trait. Analysis of different species has suggested that the genetics of salt tolerance is complex. Research on the physiology of salt tolerance suggests that the overall trait is determined by a number of sub-traits, any of which might be determined by a number of genes with heterosis, dominance, and additive effects (Flowers, 2004). Previous work on wheat has revealed that salinity tolerance in this crop is controlled by additive and non-additive gene effects (Singh and Singh, 2000; Munns and James, 2003). Although the expression of salt tolerance in crop species is complex (Shannon *et al*., 1998) but assessment of plant material by an evaluation of important agronomic traits appear to be a practical method to determine salt injury (Nobel *et al*., 1984).

Generation means analysis can determine types of genes action and also estimate their effects and genetic components in a cross. This technique helps in an understanding of the performance of the parents selected and the potential of the resulting populations to be employed either for heterosis exploitation or pedigree selection (Singh and Chaudhary, 1985). In a previous study, generation means analysis indicated that a simple genetic model (including additive and dominance effects) is sufficient for Na^+ and K^+/Na^+ ratio determination in a cross between *Shorawaki* and *Niknejad* cultivars (Dehdari *et al*., 2007). In addition, Dehdari *et al*. (2005) have also evaluated six cultivars along with their crosses in response to salinity stress and have introduced *Roshan*× *Alvand*, *Roshan*× *Kharchia* and their reciprocal crosses as the highest salt-tolerant crosses. In an experiment conducted on salt tolerance inheritance in barley, generation mean analysis revealed that dominance and epistasis gene action contribute to control of K+, Na+ and K+/Na+ (Farshadfar *et al.,* 2008). To obtain more precise estimates of gene effects of wheat cultivars under salinity conditions, salinity tolerant and sensitive wheat cultivars were selected to produce F_1, F_2, and backcross generations, which were then analyzed for gene effects controlling agronomic traits.

MATERIALS AND METHODS

Plant Materials

"*Roshan*" (P_1) a tolerant and "*Falat*" (P_2) a sensitive spring bread wheat were employed in this work for salinity studies (Poustini and Siosemardeh, 2004). F_1 and parents were used to produce F_2 and backcross generations.

Evaluation of Agronomic Traits

The six populations were evaluated under greenhouse conditions using a completely randomized design. For each parent and backcross 20 pots, for F_1 4 pots and for F_2 population 50 pots were used where a number of four seeds were sown in each of the 20-cm-diameter pots of approximately 2.5 kg of soil. In order for the plant vernalization, to be met the pots were taken outside and exposed to cold weather during winter. They were returned to the greenhouse after 7 weeks for salinity treatments, to be applied. The needed NaCl to get *EC* to 12 dS m-1 was computed according to Richard (1954), the salt being added to the soil through irrigation water in three applications. Twenty pots of each set of parents were taken with no salinity treatment (EC= 2 dS m^{-1}) as control (normal condition). To maintain soil salinity at a constant level of *EC= 12* during the growth period, pots were irrigated with distilled water, allowing for no leaching.

The data on heading date, plant height, total number of tillers per plant, number of fertile tillers per plants, and days to heading time were recorded in any one of the plants of each generation. The concentrations of Na^+ and K^+ ions in each plant part were measured at flowering in the 5 upper leaves by means of flame photometer. Na^+ and K^+ contents as wellas potasium to sodium ratios K^+/Na^+were also assessed. Total chlorophyll (according to Arnon (1949)) was measured using spectrophotometry. Generation means and variances were determined for plants within each experimental unit. The parental, F_1, F_2, BC_1, and BC_2 means (a total of six generations) were analyzed to estimate parameters for the genetic model containing additive and dominance effects (Mather and Jinks, 1982), the overall mean for each trait being estimated as follows:

$$y=m+\alpha[d]+\beta[b]+\alpha^2[i]+2\alpha\beta[j]+\beta^2[l]$$

where *y, m, d, h, i, l* and *j* represent mean for one generation, mean of all generations, sum of additive effects, sum of dominance effects, sum of additive×additive, sum of additive ×dominant and sum of dominant×dominant interactions, respectively. α, β, 2α β, α^2 , β^2 are the coefficients for the additive, dominant effects and their interactions in the model, respectively. Computer software MINITAB version 14 was employed in the analysis.

A weighted least square analysis (Mather and Jinks, 1982) was performed on the generation means. Six parameters, *viz*., *m* (average effect), *d* (additive), *h* (dominance), *i* (additive× additive), *j* (additive×dominance) and *l* (dominance×dominance) were estimated after testing adequacy of the three parameter models through joint scaling test. Further models of increasing complexity were fit if the chi square value was significant. The best-fitted model was the one which had the significant estimates of all parameters along with a non-significant chi square value. Broad-sense heritability was estimated according to:

$$h^2_{bs} = \frac{V_{f_2} - \frac{(V_{p_1} + V_{p_2} + V_{f_1})}{3}}{V_{f_2}}$$

Where, V_{F2}, V_{F1}, V_{p1} and V_{p2} are variance of F_2, F_1, Parent 1 and Parent 2.

RESULTS AND DISCUSSION

Relationship between Studied Traits

To determine the degree of association among the characteristics, Pearson's coefficients were used. Table 1 shows that significant positive correlation exists between K+/Na+ ratio (salinity tolerance index) and: total chlorophyll, number of total tillers per plant as well as plant height and K+, indicating that increase in K+/Na+ caused increase in chlorophyll, increase in duration of vegetative growth and so producing more tillers along with increase in height . This result is in consistence with the results reported by Semikhodskii *et al.*

Table 1. Correlation (r) between studied traits.

Traits	HD *a*	PH *b*	K+	Na+	K+/Na+ c	NT *d*	RFT *e*	TC *f*
TC	0.087	0.393**	0.236*	-0.123	0.334**	0.292**	0.239**	1
RFT	0.038	0.017	0.103	-0.172*	-0.09	-0.492**	1	
NT	-0.162*	0.287**	0.145	-0.303*	0.375**	1		
K/Na	0.101	0.362**	0.216*	-0.624**	1			
Na+	0.008	-0.412**	0.102	1				
K+	0.115	-0.026	1					
PH	-0.241*	1						
HD	1							

[a] Heading Date; [b] Plant Height; [c] K/Na ratio; [d] Total Number of Tillers per plant; [e] Ratio of Fertile Tillers per plants, [f] Total Chlorophyll.
* and **, Significant at 0.05 and 0.01 levels, respectively.

(1997). As the photosynthesis process is affected by salinity (Udovenk, 1977) the level of chlorophyll accumulation may also be used as a criterion for salinity tolerance. The significant negative correlation found between K+/Na+ and Na+ concentrations indicates that increase in Na+ will decrease K+/Na+ ratio. This is in consistence with results reported by Poustini and Siosemardeh (2004), Dehdari *et al.* (2005), and Farshadfar *et al*. (2008). The ratio of fertile tillers (stems with spike), was significantly and negatively in correlation with total number of tillers, indicating that increase in total number of tillers will reduce the ability of the plant for spike production. No significant correlation was observed between ion ratio of K+/Na+ and heading date. Moreover, a negative correlation was observed between Na+ content, and the number of fertile tillers, total number of tillers and plant height supporting the idea that Na+ reduces the growth of wheat (Poustini and Siosemardeh, 2004; Salam *et al*., 1999; Rashid *et al*., 1999).

Comparison of Parents in Normal and Salinity Conditions

Analysis of traits for parents in two normal and salt stress conditions revealed that there is a significant difference between control and salt stress treatments for all the studied characteristics, except for heading date. This result suggests that heading date is probably affected by vernalization and photoperiodic genetic systems. Salt stress decreased the mean values of all traits except Na^+ concentration (Table 2). This result is in agreement with reports of other studies (Poustini and Siosemardeh, 2004; Dehdari *et al*., 2005).

In general, *Roshan* (P_1) was significantly different from *Falat* (P_2) in all the traits under study except for K^+, reflecting a

Table 2. Difference between parents' means for the studied traits in normal and in saline conditions.

Stress	Parents	HD [a]	PH [b]	K^+	Na^+	K^+/Na^+ [c]	NT [d]	RFT [e]	TC [f]
Normal	Roshan	35a	46.5a	3.08b	0.98b	9.44ab	9.11a	0.91a	0.00441a
	Falat	25.2b	35.8b	4.18ab	0.711b	10.56a	10.14a	0.80a	0.00567a
	mean	30.1	40.15	3.60	0..819	9.82	9.12	0.85	0.00504
Salinity	Roshan	33.66a	40.9ab	5.13a	0.759b	8.95b	8.76a	0.22b	0.00248b
	Falat	24.5b	25.33c	4.94a	1.320a	5.12c	5.07b	0.13c	0.00207c
	mean	29.08	32.11	5.05	1.0395	6.43	6.35	0.175	0.002275
Salinity-Normal		-1.02	-8.04*	1.45^{ns}	0.265*	-3.38**	-2.87*	-0.675*	-0.002765*

[a] Heading Date; [b] Plant Height; [c] K/Na ratio; [d] Total Number of Tillers per plant; [e] Ratio of Fertile Tillers per plants, [f] Total Chlorophyll.
* and **, Significant at 0.05 and 0.01 levels, respectively.

Table 3. Analysis of variance for the studied traits.

S. O. V.	HD [a]	PH [b]	K^+	Na^+	K^+/Na^+ [c]	NT [d]	RFT [e]	TC [f]
Generation	325.72**	1320.60**	1.08^{ns}	4.24**	311.97**	40.10**	0.117*	0.000036**
Error	52.81	58.38	0..95	0.3	44.7	9.12	0.04	0.0000011

[a] Heading Date; [b] Plant Height; [c] K/Na ratio; [d] Total Number of Tillers per plant; [e] Ratio of Fertile Tillers per plants, [f] Total Chlorophyll.
* and **, Significant at 0.05 and 0.01 levels, respectively.

higher tolerance of P_1 under salinity conditions than P_2 as also reported in a previous study (Poustini and Siosemardeh, 2004). The interaction between salinity and genotype was not significant.

Generation Means Analysis

Significant differences were found among the generation means for all the traits except for K^+, which revealed the presence of genetic diversity between generation means for this attribute (Table 3). In conclusion the results of estimated parameters for the genetic models revealed that all the recorded characteristics, except the number of fertile tillers per plant, were explained by both additive and non-additive (dominant and epistasis) effects. Moreover, for all the traits the mean for F_1s was inclined to that of one of the parents, indicating the importance of dominant gene effect on the traits (Table 4). Transgressive segregation was observed for K^+/Na^+ ratio, indicating the contribution of both parental genes for tolerance (Table 4) and also demonstrating the polygenic nature of salinity tolerance in the varieties employed.

The generation variance and broad sense heritability (h^2_{bs}) for the studied traits are presented in Table 5. Broad sense heritability of traits was observed between 0.065 and 0.87. The highest heritability observed for K^+/Na^+, indicated that a major gene is probably responsible for the control of the trait. In previous studies the *Kna1* gene that enhanced K^+/Na^+ discrimination by low rates of Na^+ accumulation was reported on chromosome 4D (Dubcovsky *et al*., 1996; Munns *et al*., 2006). As heritability is very important in choosing the breeding approach and in estimating selection response, the K^+/Na^+ ratio was taken as a suitable characteristic for evaluation of salinity tolerance (Munns *et al*., 2003; Asch *et al*., 2000; Poustini and Siosehmardeh, 2004). This result is in consistence with results reported by Dvorak and Gorham (1992), and Dehdari *et al*. (2007). The

Table 4. Means and standard deviations for the studied traits in different generations.

Generation	HD [a]	PH [b]	K^+	Na+	K^+/Na^+ [c]	NT [d]	RFT [e]	TC [f]
P_1	33.66±4.38	40.90±7.91	5.13±0.43	0.76±0.62	8.95±580	8.76±1.92	0.22±0.09	0.00248 ±0.0010
P_2	24.50±5.30	25.33±8.09	4.94±0.77	1.32±0.51	5.12±3.10	5.07±3.11	0.13±0.13	0.00207 ±0.0009
F_1	24.12±4.22	46.13±7.90	4.82±0.48	0.55±0.04	7.10±1.23	5.37±1.99	0.26±0.23	0.0069± 0.00018
F_2	22.52±7.88	42.59±13.4	4.73±0.90	0.58±0.48	11.0±8.31	6.26±3.34	0.21±0.19	0.00275 ±0.0010
BC_1	28.30±8.18	36.56±7.48	5.12±1.5	0.59±0.43	10.71±6.9	6.02±2.52	0.224±22	0.00305 ±0.0013
BC_2	21.7±6.98	36.11±7.18	4.8±1.01	1.18±0.7	5.32±4.82	5.57±2.58	0.213±0.26	0.00217 ±0.0009

[a] Heading Date; [b] Plant Height; [c] K/Na ratio; [d] Total Number of Tillers per plant; [e] Ratio of Fertile Tillers per plants, [f] Total Chlorophyll.
* and **, Significant at 0.05 and 0.01 levels, respectively.

Table 5. The variance of generations and broad sense heritability (h^2_{bs}) for the studied traits.

Generation	HD [a]	PH [b]	K^+	Na^+	K^+/Na^+ [c]	NT [d]	RFT [e]	TC [f]
P1	19.18	62.56	0.1849	0..3844	33.64	3.68	0.0081	8.836e-7
P2	28.09	65.44	0.5929	0.2601	9.61	9.67	0.0169	1.02e-7
F1	17.8	62.41	0.2304	0.0016	1.52	3.96	0.0529	3.24e-8
F2	62.09	181.98	0.810	0.2304	69.05	11.15	0.0361	1.081e-6
BC1	66.91	55.95	2.250	0.1849	47.61	6.35	0.0488	1.69e-6
BC2	48.72	51.55	1.020	0.49	23.23	6.65	0.0676	9.80e-7
VE	21.69	63.47	0.32	.0.2153	15.63	5.77	0.023	3.23e-7
VG	41.21	118.5	0.48	0.016	54.12	5.38	0.0122	7.58e-7
h^2_{bs}	0.52	0.65	0.58	0.065	0.87	0.48	0.37	0.70

[a] Heading Date; [b] Plant Height; [c] K/Na ratio; [d] Total Number of Tillers per plant; [e] Ratio of Fertile Tillers per plants, [f] Total Chlorophyll.

genetically low estimate of broad sense heritability for Na^+ (Table 5) indicates that environment in which the plants are tested exerts a larger effect on this trait than the genotype (Farshadfar *et al.,* 2008). The other traits demonstrated moderate (0.2-0.5) to high (0.5 <) heritability,exhibiting that selection may be effective for the improvement of salt tolerance (Farshadfar *et al.,* 2008). A four parametric model was estimated for K^+/Na^+, reflecting aditive, dominance and additive×additive components as the major contributors to variation of K^+/Na^+in this cross. In addition, a significant effect of interaction components (i, j, l) for PH, K^+/Na^+, NT, Na^+ and TC indicates the evidence of non-allelic interaction in these traits(Adeniji *et al*.,2007). Negative additive×additive interaction [i] for K^+/Na^+, PH and NT in this cross indicates the potential for a reduction of these traits along with a fixation of additive effects in the subsequent generations (Singh and Narayanan, 2000). Genetic variation of Na^+ between generation means in this cross was explained by a five parametric model (Table 6). This model shows that Na^+ concentration in tissue is affected by non-additive epecially dominance [h] effects, hence F_1 mean trend being towards the lower parent (*Roshan*) (Table 4). As decrease in Na^+ concentration will inrease K^+/Na^+ ratio, this can be the genetical basis for the negative and high significant correlation between $Na^+$and K^+/Na^+ (Table 1). *Roshan* cultivar has a low rate of Na^+ accumulation and an enhanced K^+/Na^+ discrimination as well as high selectivity, in comparison with *Falat* (Poustini and Siosemardah, 2004; Dehdari *et al*., 2005), therefore the results obtained in this expriment being in complete agreement with their obtained results.

For fertile tillers per plant three parameters of the genetic model [m], additive [d] and dominance [h] were shown to be the best fit of the observed to the expected generation means. It means that for this trait epistasis was not making a significant contribution to the differences among the generation means. A four parameter model including [m], [d], [h] and dominance×dominance [l] was fitted for heading date and total chlorophyll (TC). These results show that non-additive effect is more important in controlling HD. For chlorophyll, model [h] and [l] showed significant effects on controlling chlorophyll concentration and therefore the mean of F_1 trend towards parents of higher TC. The genetic analysis also revealed that additive×additive [i] and additive×domina nce [j] components affected K^+/Na^+ and total number of tillers per plant. Plant height was the only trait affected by six parameters. The [h] and [l] components showed values in the opposite direction for HD, PH, Na^+ and TC, indicating the presence of duplicate epistasis in these traits (Adeniji *et al.*, 2007; Farshadfar *et al.,* 2008). This complementary interaction increases the variation between the generations and in segregating populations.

Table 6. Estimation of genetic components of the mean for the studied traits.

Trait	m	[d]	[h]	[i]	[j]	[l]	χ^2
HD [a]	9.16±0.91**	4.89±0.84**	-17.76±4.04**	-	-	12.73±4.33**	4.2364
PH [b]	58.12±5.29**	7.78±2.28**	-50.14±14.78**	-25.01±4.77**	-14.68±5.99**	38.14±10.95**	0.00
K^+	3.758±0.067**	-0.0215±0.09^{ns}	---	0.241±0.124^{ns}	-	-	1.86
Na^+	0.25±0.32	-0.400±0.097**	2.35±0.94**	1.22±0.305**	-	-1.57±0.61*	3.30
K/Na [c]	14.41±1.39**	3.25±0.718**	-7.43±1.87**	-6.797±1.79**	-	-	4.895
NT [d]	9.21±1.17**	1.84±0.39**	-5.77±1.72**	-2.27±1.26	-2.79±1.36*	-	0.0517
RFT [e]	0.17±0.018**	-0.038±0.017*	0.091±0.04**	-	-	-	3.4347
TC [f]	0.002±1e-4**	-0.00019±1e-4	0.0028±5e-4**	-	-	-0.0034±4e-4**	3.690

[a] Heading Date; [b] Plant Height; [c] K/Na ratio; [d] Total Number of Tillers per plant; [e] Ratio of Fertile Tillers per plants, [f] Total Chlorophyll.

* and **, Significant at 0.05 and 0.01 levels, respectively.

ns: Non-significant at 0.05.

It also indicates that two heterozygous loci together exert a less effect than the summed effects of two separate loci (Mather and Jinks, 1982). As the difference between generation means was not significant for K^+, no model was estimated for this trait (Table 3).

A detailed genetic analysis based on individual population using generation mean analysis would be an important step forward to fully elucidate the gene effect (i.e. when non-additive gene effect plays a major role). Generation mean analysis of the data revealed additive and non-additive types of gene effects in most of the traits involving salt tolerance. These large parameter models suggest that complex epistatic effects are important in controlling salinity tolerance characteristics. The magnitude and significance of the estimates for [i], [j] and [l] indicated that epistatic genes are important in the basic mechanism of traits involved in salt tolerance inheritance in the wheat crosses studied. Hayman (1960) has indicated when epistasis is of major importance in the inheritance of a trait, then it is impossible to obtain unbiased estimates of pooled additive or dominance effects. However these effects of genes could be important in heterosis. Also, regarding the existence of additive and non-additive effects in controlling traits in this cross, the recurrent selection followed by pedigree breeding or a selective diallel mating system may sound useful in improving salinity tolerance in wheat (Dehdari *et al.,* 2007).The development of appropriate markers linked with tolerance genes would greatly enhance the feasibility of such a strategy.

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تجزیه ژنتیکی تحمل شوری در گندم نان

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چکیده

وراثت تحمل به شوری در گندم نان با استفاده از یک تلاقی بین دو رقم روشن (متحمل به شوری) و فلات (حساس به شوری) مورد مطالعه قرار گرفت. نسلهای والدین، F_1، F_2 وتلاقی های برگشتی (BC_1 وBC_2) در گلخانه تحت شرایط شوری ($EC= 12\ ds\ m^{-1}$) مورد ارزیابی قرار گرفتند و صفات تاریخ خوشه دهی، ارتفاع، نسبت K^+/Na^+، K^+، Na^+، تعداد کل پنجه در گیاه، نسبت پنجه های بارور در گیاه و مقدار کل کلروفیل اندازه گیری شد. برای مطالعه وراثت صفات تحت مطالعه و برآورد اثرات ژنتیکی از تکنیک تجزیه میانگین نسل استفاده شد. تجزیه میانگین نسل نشان داد که در این تلاقی انواع اعمال ژن (افزایشی، غالبیت و اپیستاتیک) در کنترل صفات مرتبط با شوری وجود داشته و اثرات پیچیده اپیستاتیک اهمیت زیادی دارند. نسبت K^+/Na^+ دارای وراثت پذیری عمومی بالا (۰/۸۷) بود که نشان دهنده دخالت یک زن اصلی در کنترل این صفت است. با توجه به وجود اثرات افزایشی و غیر افزایشی در کنترل صفات تحت مطالعه در این تلاقی ، انتخاب دوره ای می تواند در اصلاح تحمل شوری در گندم مفید باشد.