INTERNATIONAL JOURNAL OF AGRICULTURE & BIOLOGY
1560–8530/2006/08–6–812–814
http://www.fspublishers.org

Genetic Study of Root Length in Spring Wheat (*Triticum aestivum* L.) Under Salinity

TAHIRA[1] AND ABDUS SALAM
Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad-38040, Pakistan
[1]Corresponding author's e-mail: drtahirawaqas@yahoo.com

ABSTRACT

A 6 × 6 diallel cross was conducted involving pre-screened 3 sensitive (18180-II, 18205-I, DN-18) and 3 tolerant (18194-II, DN-4, LU26S) wheat genotypes. Thirty-six genotypes were sown in a triplicated completely randomized design in hydroponic culture. The data for root length was recorded in three salinity levels i.e. control (1.5 dS m^{-1}), 10 and 15 dS m^{-1}. The results suggested that both additive and non-additive genes under saline and non-saline conditions affected total variation for root length. In control, additive and non-additive genes affected 25% and 79% of the total variation, whereas in 10 dS m^{-1} non-additive genes affects (56%) were greater than additive genes affects (33.5%). In, 15 dS m^{-1} both additive and non-additive genes contributing almost equally (34%). the genotype DN-4 under non-saline condition, while under saline condition the genotypes 18194-II under saline condition, DN-4 and LU-26S seemed to be good general combiner. The cross combinations with highest specific combining ability for root length were 18194-II × DN-4, 18180-II × 18205-I and LU26S × DN-18 under control, 10 dS m^{-1} and 15 dS m^{-1}, respectively. In reciprocals the crosses DN-18 × DN-4 and DN-4 × 18205-I appeared to be superior to the others under low and high salinity levels, respectively.

Key Words: Combining ability; Salinity tolerance; Root length; Spring wheat; Pakistan

INTRODUCTION

Keeping in view the increasing demand for more food supply needed for the growing population, development of research programmes aimed to exploring new genetic resources is being emphasized these days. Whereas soil salinity is a limiting factor in allowing exploitation of crops in many parts of the world and as an increasing phenomenon particularly in arid and semi-arid areas, it poses a great threat to the survival of human populations in those areas. The suggested biotic approach to this problem (Epstein *et al*., 1980; Shannon, 1984) that allows the use of salty areas for cultivation, in its essence requires improvement in the salinity tolerance of existing crop species so that they may be successfully grown in saline soils.

Significant improvement in salinity tolerance is to be effected through breeding program. Information from the various species examined for salt tolerance suggests that different genetic architectures may be controlling the character, from single major dominant/recessive gene, to polygenic control with mainly additive effects, but with some degree of dominance toward tolerance (Moeljopawiro & Ikehashri, 1981; Azhar & McNeilly, 1989; Gregorio & Senadhira, 1993; Ahsan *et al*., 1996), knowledge of the relative contribution of the genetic components, additive, dominance, epitasis and linkage controlling the variation for tolerance to salinity is an essential pre-requisite.

The present research work was an attempt to understand the genetic manipulations leading towards the progress in the process of evolution of salt tolerant wheat cultivars.

MATERIALS AND METHODS

The material comprised intra-specific crosses involving six diverse genotypes viz. 18180-II, 18205-I, DN-18 (sensitive), 18194-II, DN-4 and LU26S (tolerant). These 3 sensitive and 3 tolerant genotypes were crossed in all possible combinations i.e. 6 × 6 diallel fashion. The seeds of 36 genotypes were sown in iron trays filled with acid washed gravel. The young seedlings at the two-leaf stage were transferred to aerated half strength Hoagland solution (Hoagland & Arnon, 1950) in 3 large iron containers (118 × 88 × 30 cm) internally lined with polythene sheet. Seedlings of each genotype were held in position through foam-plugged holes made in thermopal sheets floating over 200 L culture solutions.

Each of the 36 genotypes was planted in triplicate in the two NaCl treatments i.e. 10 dS m^{-1}, 15 dS m^{-1} and one without salt (control). The appropriate salinity level in the two containers were developed after two days of transplanting the seedlings and completed in four equal NaCl doses. The pH of the solutions, ranging from 6.0 to 6.5, was maintained daily using 1 N HCl and/or NaOH solutions. The NaCl solutions in the containers were changed after every two weeks. After four weeks growth, root length (cm) of each genotype in each replication was measured. The data collected for root length under saline and non-saline conditions were subjected to analysis of

variance (Steel & Torrie, 1980). Then the data was further subjected to combining ability analysis by using Method 1 Model of Griffing (1956) as under:

General combining ability effects

$$gi = \frac{1}{2P}(X_{i.} + X_{.i}) - \frac{1}{P^2}X_{..}$$

Where

gi = General combining ability effects for line i

P = Number of parents/varieties

Xi. = Total of mean values of F_1's resulting from crossing jth line with ith lines.

X.i = Total of mean values of F_1's resulting from crossing ith line with jth lines.

X.. = Grand total of all mean values in the table

Specific combining ability effects

$$S_{ij} = \frac{1}{2}(X_{ij} + X_{ji}) - \frac{1}{2P}(X_{i.} + X_{.i} + X_{j.} + X_{.j}) + \frac{1}{P^2}X_{..}$$

Where

Sij = Specific combining ability between ith and jth lines

Xij = Mean values of the F_1 resulting from crossing the ith and jth lines

Xji = Mean values of the F_1 resulting from crossing the jth and ith lines.

Xi. = Total of mean values of F1's resulting from jth line with ith inbred

X.i = Reciprocal value of Xi.

X.j = Total values for the F_1's resulting from crossing ith line with jth line

Xj. = Value of reciprocal F_1's of X.j.

X.. = Grand total of the observation.

Reciprocal effects

$$rij = \tfrac{1}{2}(Xij - Xji)$$

Where

rij = Reciprocal effects of ith and jth varieties/lines

Xij = Mean values for the F_1 resulting from crossing the ith and jth line

Xji = Reciprocal values of F_1 resulting from Xij.

RESULTS AND DISCUSSION

The total genetic variability was partitioned into three components i.e. general combining ability, specific combining ability and reciprocal effects. The mean squares due to general combining ability (GCA), specific combining ability (SCA) and reciprocal effects were obtained from combining ability analysis of root length data as suggested by Griffing (1956) and are given in Table I. The results showed that differences between general combining ability of parents were significant ($p \geq 0.01$) in control (non-saline), low and high salinity levels. The specific combinations were revealed to be significant ($p \geq 0.01$) in non-saline and high salinity level, whilst these were non-significant ($p > 0.05$) under low salinity level, whereas reciprocal effects were significant ($p \geq 0.01$) in high salinity level only and non-significant ($p > 0.05$) in non-saline and low salinity level. The mean squares due to GCA were greater than that due to SCA under control and two salinities. This indicates the pervasiveness of additive gene effects in the genetic control of salt tolerance for root length.

Table I. Mean squares of general (GCA), specific combing ability (SCA) and reciprocals of root length in 6 parent diallel cross of wheat

Source of variation	DF	Control	10 dS m^{-1}	15 dS m^{-1}
GCA	5	17.630**	5.293**	11.114**
SCA	15	6.178**	1.399NS	2.098**
Reciprocals	15	0.577NS	0.586NS	2.246**
Error	70	0.867	0.423	0.832

The relative sizes of variances due to the three components of variation and their magnitude is calculated in percentages (Table II). The values revealed that additive gene effects under both the salinity levels affected 34% of the total variation for salt tolerance and the genes acting non-additively contributed 58% in 10 dS m^{-1} and 33% in 15 dS m^{-1}. Whereas the additive genes and non-additive genes affected 25% and 79% of the total variation, respectively under normal conditions i.e. control or non-saline. These results are in agreement with the earlier finding of Rao and McNeilly (1999). They examined genetic basis of salt tolerance in selected salt tolerant and sensitive maize material and reported that salinity tolerance is under the control of genes with additive and non additive effects.

General and specific combining ability and reciprocal effects for salt tolerance are presented in (Table III a, b & c) under control, 10 dS m^{-1} and 15 dS m^{-1} of salinity levels. DN-4 showed the highest general combining ability for root length under non-saline conditions. The genotype 18194-II and DN-18 also showed considerable general combining ability. The genotypes 18194-II, DN-4 and LU26S were good general combiner under salinity. The genotypes 18194-II and LU26S exhibited highest general combining abilities under 10 dS m^{-1} and 15 dS m^{-1}, respectively.

The performances of the parents in cross combinations for root length reveals that only five crosses under control and low salinity and three crosses under high salinity had high values showing good specific combining ability. The cross combinations with highest specific combining ability for root length were 18194-II × DN-4, 18180-II × 18205-I and LU26S × DN-18 under control, 10 dS m^{-1} and 15 dS m^{-1}, respectively. In reciprocals the crosses DN-18 × DN-4 and DN-4 × 18205-I appeared to be superior to the others beneath low and high salinity levels, respectively. Similar conclusions were also illustrated by Ratanadilok *et al.* (1978).

According to Griffing (1956), high GCA effects are mostly due to additive gene effects/additive ×additive interaction effects. Keeping this in sight, in a breeding program designed for improvement of salinity tolerance in

Table II. Estimates of variance components for salt tolerance due to GCA, SCA and reciprocal effects and their percentages (in parentheses) under control and two salinities

Salinity level	GCA (σ^2_g)	SCA (σ^2_s)	Reciprocals (σ^2_r)	σ_e^2	σ_A^2	σ_D^2
Control	0.97 (24.78)*	3.08 (78.92)*	$^{-0.14}$(-3.70)*	0.87	1.94	3.08
10 dS m^{-1}	0.33 (33.54)	0.57 (58.11)	0.08 (8.35)	0.42	0.66	0.57
15 dS m^{-1}	0.75 (34.35)	0.74 (33.46)	0.71 (32.19)	0.83	1.50	0.74

* Values given in parenthesis are the percentage of the total genetic variance

Table III. General combining ability (diagonal), specific combining ability (above diagonal) and reciprocal effects (below diagonal) for root length of wheat grown in control and two salinities

(a)Control

Parent	LU26S	DN-18	18194-II	DN-4	18180-II	18205-I
LU26S	**-2.116**	1.347	-0.502	-2.733	1.669	-0.680
DN-18	-1.383	**0.419**	-0.555	0.963	0.883	-1.133
18194-II	-0.200	-0.616	**0.452**	$^{2.597}$	-1.65	-0.250
DN-4	0.766	0.333	-0.333	**1.555**	-0.997	2.236
18180-II	0.001	0.683	-0.583	0.001	**-0.286**	2.322
18205-I	-0.416	0.001	0.083	0.166	0.416	**-0.019**

S.E. (g i) = 0.245 S.E. (s ij) = 0.559 S.E. (r ij) = 0.658

(b) 10 dS m^{-1}

Parent	LU26S	DN-18	18194-II	DN-4	18180-II	18205-I
LU26S	**0.246**	0.328	-0.301	-0.179	0.050	-1.393
DN-18	-0.133	**-0.720**	-1.035	-1.246	0.550	-0.260
18194-II	-0.666	0.533	**1.043**	0.623	-0.379	0.525
DN-4	0.400	1.366	-0.333	**0.321**	-0.357	-0.185
18180-II	0.333	-0.466	0.466	-0.266	**-0.309**	0.662
18205-I	0.183	0.450	-0.666	0.366	0.283	**-0.581**

S.E. (g i) = 0.171 S.E. (s ij) = 0.391 S.E. (r ij) = 0.460

(c) 15 dS m^{-1}

Parent	LU26S	DN-18	18194-II	DN-4	18180-II	18205-I
LU26S	**1.303**	1.529	-0.445	0.365	-0.089	0.924
DN-18	0.050	**-1.326**	0.151	-1.637	0.307	-0.495
18194-II	-0.166	-1.933	**0.298**	0.804	-0.650	-1.550
DN-4	-0.983	-2.110	0.116	**0.737**	0.710	0.340
18180-II	-0.533	-0.866	-1.000	1.166	**-0.390**	-0.381
18205-I	-0.350	-0.166	1.000	1.600	0.716	**-0.621**

S.E. (g i) = 0.240 S.E. (s ij) = 0.548 S.E. (r ij) = 0.645

wheat, the good general combiners could be utilized by the breeder. Singh (2002) reported that the SCA effects do not contribute actually in the improvement of self pollinated crops normally, excluding where profitable utilization of heterosis is practicable. The SCA represents the dominance and epistatic interaction, which can be related with heterosis. However, in self-pollinated crops like wheat, the additive × additive type of interaction component is fixable in later generations. The crosses18194-II× DN-4 and LU26S × DN-18 are important because the parent of the crosses have already been declared as a good combiner and the genotypes 18194-II, DN-4 and LU26S could be utilized widely in hybridization programme to hasten the pace of genetic improvement of salt tolerance in bread wheat.

REFERENCES

Ahsan, M., D. Wright and D. Vrik, 1996. Genetic analysis of salt tolerance in spring wheat (*Triticum aestivum* L.). *Cereal Res. Comm*., 24: 353–60

Azhar, F.M. and T. McNeilly, 1989. The response of four sorghum accessions/cultivars to salinity during plant development. *J. Agron. Crop Sci*., 163: 33–43

Epstein, E., J.D. Norlyn, D.W. Rush, R.W. Kingsbury, D.B. Kelley, G.A. Cunningham and A.F. Wrona, 1980. Saline culture of crops: A genetic approach. *Sci.,* 210: 399–404

Gregorio, G.B. and D. Senadhira, 1993. Genetic analysis of salinity tolerance in rice. *Theor. Appl. Gen*., 86: 333–8

Griffing, B., 1956. Concept of general and specific combining ability in relation to diallel crossing system. *Australian J. Biol.,* 9: 463–93

Hoagland, D.R. and D.I. Arnon, 1950. *The Water Culture Method for Growing Plants Without Soil*. Agriculture Experimental State University of California Circular No. 347

Moeljopawiro, S. and H. Ikehashi, 1981. Inheritance of salt tolerance in rice. *Euphytica*, 30: 291–300

Rao, S.A. and T. McNeilly, 1999. Genetic basis of variation for salt tolerance in maize (*Zea mays* L.). *Euphytica*, 108: 145–50.

Ratanadilok, N., V. Marcarian and C. Schmalzel. 1978. Salt tolerance in grain sorghum. *Agron. Abst*., 70:160.

Shannon, M.C., 1984. Breeding, selection and genetics of salt tolerance. *In:* Staples, R.C. and G.A. Toenniessen (eds.), *Salinity Tolerance in Plants-Strategies for Crop Improvement,* PP: 231–54. John Wiley and Sons, New York, USA

Singh, H., 2002. Genetic architecture of yield and its associated traits in bread wheat. PhD Thesis, Rajasthan Agriculture Univ., Bikaner, Rajasthan, India.

Steel, R.G.D. and J.H. Torrie, 1980. *Principles and Procedures of Statistics: A Biometrical Approach*. McGraw Hill Book Co., New York, USA

(Received 08 August 2006; Accepted 02 October 2006)