

TRIPLE TEST CROSS ANALYSIS FOR SALINITY TOLERANCE IN WHEAT

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Triple test cross analysis applied to study additive, dominance and epistatic components of genetic variation for five seedling traits namely shoot length, fresh shoot weight, root length, fresh root weight and root/shoot ratio at two salinity levels 0 (control) and 10 dSm⁻¹ in wheat. The results revealed that the epistatic component is an important element for salinity tolerance at seedling stage in wheat. Both additive and dominance gene effects were involved in the inheritance of shoot length, fresh shoot weight, root length fresh root weight and root/shoot ratio. Complete dominance was indicated for shoot length, fresh root weight and root/shoot ratio and partial dominance was observed for other traits at control and over dominance was observed for shoot length, fresh shoot weight and root/shoot ratio, complete dominance for fresh root weight and partial dominance for root length at 10 dSm⁻¹ salinity level. Significant epistasis was observed for all the traits except shoot length at both the salinity treatments.

Keywords: Wheat, salinity, genetic studies, triple test cross

INTRODUCTION

Soil salinity is a major environmental factor causing decreased yield of crops grown in irrigated systems in arid and semi arid regions (Downton, 1978). Khan *et al.* (2001) reported that 357.3 m ha of land in Australia, 211.7 m ha in North and Central Asia, 129.2 mha in South America, 87.6 m ha in South Asia, 80.5 m ha in Africa, 50.8 m ha in Europe, 20.0 m ha in Southeast Asia, 15.7 m ha in North America and 2.0 m ha in Mexico and Central America is affected by salinity. Thus no continent on the earth appears completely free from salt affected soils and a total about 950 mha of land is salt affected world wide (Flowers and Yeo, 1995). According to an estimate, about 5.7 mha of arable land have been affected by salinity in Pakistan (Mujtaba *et al.*, 2003). Variability for salt tolerance, within and between species has been found in many cultivated crops and their wild relatives (Maas, 1993). Some progress has been made through the use of simple breeding programs and a few cultivars possessing useful degree of salt tolerance have been developed, but the rate of progress is very slow. A better understanding of the genetic basis of desirable traits involved in the manifestation of improved salt tolerance might accelerate pace of progress (Fooland and Jones, 1992). The available evidence from the various species studied for salt tolerance, like sorghum (Azhar and McNilley, 1988). Pearl millet (Kebebew and McNilley, 1995) and tomato (Fooland and Jones, 1992) suggests that both additive and dominance gene effects are important for salt tolerance. The triple test cross (TTC) analysis (Kearsey and Jinks, 1968) provides estimates of epistatic variation, in addition

variation with equal efficiency when epistasis is absent. The assumptions for TTC are not demanding and the model is independent of gene correlation, mating system and allelic frequency.

MATERIALS AND METHODS

Wheat varieties KRL-1-4 and Alexandria with differing responses to NaCl salinity stress were used to study the genetic basis of salinity tolerance based on seedling traits viz., shoot length, shoot fresh weight (g) root length (cm), root fresh weight and root shoot ratio following triple test cross (TTC) design Kearsey and Jinks (1968).

KRL-1-4 and Alexandria were crossed to development F₁ and F₂ population. Twenty five randomly selected males from the F₂ populations were crossed to three testers. P₁ (KRL-1-4), P₂ (Alexandria) and F₁ (KRL-1-4-X Alexandria).

Each male, therefore, had three progenies, total of 75 triple test cross progenies were produced.

The responses of 40 day old seedling of the 75, TTC progenies along with three testers (P₁, P₂ and F₁) were examined in control and 10 dSm⁻¹ NaCl prepared in half strength Hoagland solution (Hoagland and Arnon, 1950). The experiment was set up in three replication arranged in a complete randomized design in a glass house with natural temperature (11-16°C) and photoperiod (about 10 hours). Data after 40 days old five seedlings per replication of each TTC family per treatment were measured. Mean values for shoot length, fresh shoot weight, root length, root fresh weight and root/shoot ratio for five seedling per replicate of each family along with three testers grown

in control and 10 dSm⁻¹ NaCl was used to examine the genetic basis for salt tolerance.

Data based on 225 values, each being the mean of five plants and corresponding variances of these sets of five plants. Jinks and Perkins (1970) analysis was applied to detect epistasis and to test and estimate additive and dominance components of genetic variation.

For the test of epistasis, twenty five values of $L_{1i} + L_{2i} - 2L_{3i}$, for 0 to 25 were obtained for each of three replicates. After summing over the replicates, the sum of twenty-five for squared deviations of $L_{1i} - L_{2i} - 2L_{3i}$ from zero for 25 degree of freedom, that is, sum of squares due to epistasis, was obtained. Sum of squares due to replicate error, that is, the error for testing the significance of apistasis, was obtained by the mean variance with the L_{1i} , L_{2i} and L_{3i} type of families at both the salinity levels for 50 degree of freedom.

The epistasis of sum of squares of 25 degree of freedom could be partitioned into J and L1 degree of freedom, testing for J+I type epistasis (additive x additive interaction) and an item for 24 degree of freedom testing for j and l types of epistasis (additive x dominance and dominance x dominance), respectively. Similarly, the sum of squares due to replicates error of 50 degree of freedom could be sub divided into two items, namely replicates and epistasis x replicates, respectively for 2 and 48 degree of freedom.

RESULTS AND DISCUSSION

Significant epistasis was recorded for all the traits except shoot length at both salinity levels. Further partitioning the epistasis into j+l types revealed that j+l type epistasis was significant ($P < 0.01$) for all the character at both the salinity levels except shoot length at salinity level and for fresh shoot weight j+l type was non-significant at 10 dSm⁻¹ salinity level.

The analysis of variance of mean squares for sums ($L_{1i} + L_{2i}$) and differences ($L_{1i} - L_{2i}$) provides direct tests of significance for additive and dominance component. Both the items sums and differences were significant for shoot length and root length, and non significant for fresh root weight and root/shoot ratio at both the

salinity levels. But both items were significant for fresh shoot weight at control and non significant at 10 dsm⁻¹, (Table 2) the component of D (additive) and H (dominance) were significant for shoot length and root length and non significant for fresh root weight and root/shoot ratio at both salinity levels. But both additive and dominance components were significant for fresh shoot weight at control and non-significant at 10 dsm⁻¹ salinity level (Table 2). But since, there was an evidence of significance epistasis for D and H were biased except shoot length by epistasis to an unknown extent at both the salinity treatments. Relative magnitude of D and H components indicated the predominance of former for root length at both salinity treatments, and for fresh shoot weight and fresh root weight at control.

Non additive type of gene action was predominant for shoot length and root/shoot ratio at both salinity levels, for fresh shoot weight and fresh root weight at 10 dsm⁻¹.

By and large, the epistasis formed an important part of the genetic architecture of the material, in the present study therefore, this component (epistasis) warrants its detection, estimation and consideration in the formation of suitable breeding program for the manipulation of such traits in wheat. If the presence of epistasis is overlooked as is the case with various reports using design assuming absence of epistasis, one would not only lose the information about the implication of epistasis, but would also obtained biased estimates of additive and dominance components of genetic variation and would lead to faulty breeding procedure.

The reciprocal recurrent selection as suggested by Comstock *et al.* (1949) would be effective for the improvement of these traits in wheat.

Similar finding were reported by Singh (1976) for plant height, spikelets per spike, grains per spike and yield per plant in wheat, similar findings were also reported for ear length, ear height and number of kernels row in maize Duane and Hallauer (1997) and for 100-seed weight in adzuki bean by Chaudhary *et al.* (1992) and for 100 seed weight in wheat by Malhotra (1983) in urdbean by Barush and Pandey (1983) in mungbean.

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