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Heritability (h^2_b) Estimates for NaCl Tolerance in Wheat (*Triticum aestivum* L.)

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ABSTRACT

Root growth data of four-week-old seedlings of 98 wheat accessions grown in 0, 10 and 15 dSm^{-1} NaCl solutions were used to estimate broad sense heritabilities of salt tolerance. Estimates of broad sense heritabilities for absolute and relative root length were moderate in size (0.44 to 0.62) suggesting the scope for enhancing salt tolerance in wheat through selection and breeding.

Key Words: *Triticum aestivum* L.*;* Wheat; Salinity tolerance; Variation; Broad sense heritability

INTRODUCTION

Wheat is grown in arid and semi-arid regions of the world. Pakistan lies within the subtropical region and has semi-arid to arid climate. The spread of soil salinity in arid and semi-arid areas is posing a serious threat to crop production (Khan *et al*., 2001). The high rate of evapotranspirational loss of water under these environmental conditions results in the deposition of excess salts on the soils fraction in which the roots flourish. This stress like other abiotic soil stresses constitutes a major limiting factor, which hampers plant productivity throughout the world (Clark & Duncan, 1993). Breeding crop cultivars tolerant to these conditions is a possible alternative to the expensive engineering approach in solving the problem (Epstein *et al*., 1980; Shannon, 1984; McWilliam, 1986; Qureshi *et al*., 1990; Hollington, 1998).

Synthesis of crop material capable of giving economic yields in saline conditions, using conventional methods, is effective if variation in salinity tolerance is controlled by a significant genetic component. Although information on the occurrence of variability in different crop species for salt tolerance is well documented, the knowledge on the genetic basis of that variation is not frequently available. The genetic studies reported on citrus root stock (Furr & Ream, 1969), sorghum (Azhar & McNeilly, 1988, 1989), rice (Moeljopawiro & Ikehashi, 1981; Shannon *et al*., 1998), maize (Rao & McNeilly, 1999), *Triticeae* (Farooq & Azam, 2001; Xing *et al*., 2002), *Aegilops ovata* (Farooq, 2002), cotton (Azhar & Ahmad, 2000; Akhtar & Azhar, 2001; Noor *et al*., 2001), grasses and forages (Ashraf *et al*., 1986a, 1986b, 1987), and lucerne (Al-Khatib *et al*., 1994) provided evidence that salinity tolerance was genetically controlled. Based upon the estimates of heritability Nobel *et al*. (1984) made significant improvement in *Medicago sativa* for salinity tolerance after two generations of selection. Genetic variation showing high heritability is amenable to direct phenotypic selection, and only a few cycles of selection could result in significant improvement in salinity tolerance. An investigation of the response of wheat seedlings to increasing NaCl concentrations (Khan *et al*., 2003b) has revealed considerable variation in salinity tolerance in this species. The present paper examines the genetic basis of that variation.

MATERIALS AND METHODS

A hydroponic culture experiment was conducted in a greenhouse for screening the 98 available wheat accessions. Seed of accessions was sown in gravel. After two weeks of growth, the seedlings were transplanted in a tub filled with 200 liters of half strength Hoagland nutrient solution (Hoagland & Arnon, 1950). Besides NaCl free control, salinity was developed by adding NaCl and concentrations were adjusted to achieve 10 and 15 dSm^{-1}.

The indicator of response was a measurement of the longest root lengths of four-week-old seedlings. Based upon the measurements of root length, the responses of accessions were compared using values of absolute salt tolerance (Dewey, 1960), and relative salt tolerance (Maas, 1986). Relative salt tolerance of 98 accessions were computed according to the following formula:

$$\text{Relative salt tolerance (index of salt tolerance)} = \frac{\text{Mean value of a character in NaCl}}{\text{Mean value of a character in control}} \times 100$$

The root length data of 24 seedlings (6 from each of four replicates) of the 98 accessions assessed under each NaCl concentration and control were analysed using an analysis of variance which partitioned total variance into its components. The variance due to between-accessions and within-accessions were used to calculate broad-sense heritability using the formula given by Falconer and Mackay (1996). Between-accession variances comprised genetic and environmental components, whilst within-accession variance provided an estimate of environmental component, because wheat is predominantly a self-pollinated crop. The formula used to calculate the estimates of broad-sense heritability (h^2_B) is given below:

$$h^2_B = Vg/Vp$$

where,

Vg = genetic variance = (variance between-accessions – variance within-accessions)/24
Vp = phenotypic variance = [(variance between-accessions – variance within-accessions)/24] + variance within-accessions

It was assumed that the extent of the environmental components of intra-accession variation would be the same as that component for inter-accession variation. Failure to meet this assumption may inflate the heritability estimates.

RESULTS

Due to the significant adverse effects of two NaCl concentrations on root lengths of the accessions, the variances due to 10 and 15 dSm^{-1} were also reduced as compared to those in the control (Table I). Analysis of variance of the absolute and relative data showed that the mean squares from two salinity levels were highly significant ($p \leq 0.01$). Increase in NaCl concentration resulted decrease in between-accession mean squares, and in within-accession mean squares, consequently estimates of broad sense heritabilities (Table II).

At 10 and 15 dSm^{-1} NaCl, estimated genetic variances for the absolute root length were 14.20, 7.15, and estimates of h^2_B were 0.59, and 0.54, respectively. Genetic variances for relative root length were 312.69, 532.07, and estimates of h^2_B were 0.59, and 0.44, respectively. Variation in root length in control solution also had a significant genetic basis with an estimated h^2_B value of 0.62.

DISCUSSION

Availability of differing accession-responses to salinity may be good, if it is genetically controlled. The estimates of broad sense heritabilities as shown in Table II are moderate. Previous estimates of broad sense heritabilities for salinity tolerance in other crop species showed considerable differences. In alfalfa the estimate of h^2_{BS} was 0.5 (Allen *et al*., 1985), whilst in seven grass and four forage species estimates ranged from 0.23 to 0.77, and 0.31 to 0.62, respectively (Ashraf *et al*., 1986b, 1987). In sorghum the estimates of broad sense heritabilities were 0.73 under low salinity level (50 mM) and 0.38 under 200 mM NaCl stress (Azhar & McNeilly, 1989). In cotton estimates of h^2_B were 0.93 under control and 0.83 under NaCl stress (Akhtar & Azhar, 2001), and in *Zea mays,* these ranged from 0.62 to 0.82 (Rao & McNeilly, 1999; Khan *et al*., 2003a). Based upon these estimates of heritabilities, these workers suggested that significant advance in salinity tolerance in these species may be possible using high selection pressures. Clearly the estimates of h^2_B for salt tolerance in wheat under two NaCl concentration generally agree with those reported in wheat and other species, and suggest that variation for salinity tolerance in wheat germplasm, on the basis of root length, for the most part, is genetically determined. These estimates suggest that prospects of improving the character through selection and breeding are considerable, provided the genetic system controlling the variation is affected by the genes with additive effects.

Table I. Mean squares of absolute and relative root lengths of 98 wheat accessions grown in control and two NaCl concentrations

Sources of variation	Absolute root length		Relative root length	
	Between accessions	Within accessions	Between accessions	Within accessions
Degrees of freedom	97	2254	97	2254
Control	398.02**	9.98		
10 dSm^{-1}	350.68**	9.85	7723.82**	219.38
15 dSm^{-1}	177.59**	6.01	2225.25**	112.44
Expected mean squares	$\delta^2_w + 24\delta^2_b$	δ^2_w	$\delta^2_w + 24\delta^2_b$	δ^2_w

** = $p \leq 0.01$

Table II. Components of variance and broad sense heritability (h^2_B) of NaCl tolerance at seedling stage

Component	Absolute root length			Relative root length	
	Control	10 dSm^{-1}	15 dSm^{-1}	10 dSm^{-1}	15 dSm^{-1}
δ^2_b =Vg	16.17	14.20	7.15	312.69	88.03
$\delta^2_b + \delta^2_w$ = Vp	26.15	24.05	13.16	532.07	200.47
h^2_B = Vg/Vp	0.62	0.59	0.54	0.59	0.44

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