increasing of NaCl concentration leads to the decrease in the relative water content of wheat flag leaf **(Aldesuquy *et al.*, 1997).** The genetic modification of plants to allow growth and yield under unfavorable conditions is an important component of the solution to problems of environmental stresses in breeding programs.

Traditional methods of plant breeding have made a significant contribution to crop improvement, but they have been slow in targeting complex traits like grain yield, grain quality, drought or salinity resistance. To meet the great need to increase food production necessitated by population growth, and the higher standards of living expected in most of the developing countries, biotechnology brings novel and powerful tools to assist and complement the breeding efforts.

Protein and isozyme electrophoreses markers have been used in many crops to some extent. The major limitation of these two procedures is the lack of enough polymorphisms among closely related cultivars **(Beckmann and Soller, 1993).** For these reasons, DNA- based genetic markers have been recently integrated into several plant systems and are playing a very important role in molecular genetics and plant breeding **(Beckmann and Soller, 1990 and 1993).** Protein and isozyme electrophoreses markers have been used in many crops to some extent. The major limitation of these two procedures is the lack of enough polymorphisms among closely related cultivars **(Beckmann and Soller, 1993).** For these reasons, DNA- based genetic markers have been recently integrated into several plant systems and are playing a very important role in molecular genetics and plant breeding **(Beckmann and Soller, 1990 and 1993).** Protein and isozyme electrophoreses markers have been used in many crops to some extent. The major limitation of these two procedures is the lack of enough polymorphisms among closely related cultivars **(Beckmann and Soller, 1993).** For these reasons, DNA- based genetic markers have been recently integrated into several plant systems and are playing a very important role in molecular genetics and plant breeding **(Beckmann and Soller, 1990 and 1993).**

Bulked segregent analysis (BSA) of F_2 plants was developed by **(Michelmore *et al.*, 1991)** as a simpler alternative to isogenic line analysis where the highest and lowest extremes of F_2 population are bulked for the detection of PCR- based markers.

One of the most popular techniques in biotechnology and molecular biology is randomly amplified polymorphic DNA (RAPD) which was demonstrated by **(Williams *et al.*, 1990)** and called AB- PCR (Arbitrarily primer PCR) by **(Welsh and McClelland, 1990)**. In this technique, a single species of primer (10-base, with at least 60 GC% contents) binds to the genomic DNA at different sites opposite strands of the DNA template **(Berhan, 2001)**. This technique is a useful method for generating molecular markers **(Williams *et al.*, 1990; Welsh and McClelland, 1990)**. It has been applied to construct linkage maps **(Williams *et al.*, 1990)**, to identify varieties **(He *et al.*, 1992)** and to assess genetic diversity **(Koller *et al.*, 1993; Igbar and Raybum, 1994; Abdel-Twab *et al.*, 1998b; 1998c; 2001)**. As an added advantage, it is characterized by its low technical input and small quantity of plant DNA needed for the analysis **(Debner *et al.*, 1996; Hernandez *et al.*, 1999; Cao *et al.*, 1999 and Manabe *et al.*, 1999)**.

Simple sequence repeats (SSRs), also called Microsatellites or second generation markers are subsets of the tandemly repeated DNA family represented by extremely short nucleotide sequence repeats from 1-5 base pairs (bp) that are abundantly present and interspersed in eukaryotic genomes **(Ma *et al.*, 1996 and Hakki *et al.*, 2001)**. The positive features that characterize SSRs, such as the random distribution throughout the genome, the large allelic variation, and the ease of use, have made SSRs the preferred markers for mapping of genomes and evolutionary genetic studies **(Bruford and Wayne, 1993 and Boweock *et al.*, 1994)**. SSRs have been reported to be highly polymorphic and thus highly informative in plants. Providing many different alleles for each marker, even among closely related individuals **(Akkaya *et al.*, 1992 and Saghai- Maroof *et al.*, 1994)**. Moreover, SSRs are inherited co-dominantly showing simple Mendelian segregation and they are

abundant and uniformly dispersed in genomes (**Weber, 1990; Wang *et al.*, 1994 and Akkaya *et al.*, 1995**).

The objectives of this study are:

1. To study the effect of salinity on three cultivars of bread wheat ***Triticum aestivum*** **L.** and the r (F_1) and (F_2) progenies.
2. To choose the most tolerant and the most sensitive genotypes for salinity stress for some yield- related traits.
3. To detect some molecular markers associated with salinity tolerance using RAPD-PCR and SSR-PCR techniques by the use of bulked sergeant analysis (BSA).