Assessment of genetic divergence among wheat (*Triticum aestivum*) genotypes using random amplified polymorphic DNA (RAPD) analysis

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Abstract: The degree of genetic divergence was estimated in 7 wheat (*Triticum aestivum* L.) genotypes from diverse locations of Pakistan using Random Amplified Polymorphic DNA (RAPD) methodology. A total of 160 DNA fragments were amplified with 20 random decamer primers with an average of 8 bands per primer. Genetic similarity matrix ranged from 84.0% to 93.0%, which indicated a narrow genetic base among the genotypes. The maximum similarity, 93.0%, was observed between WC-65 and SARC-1. The local variety, PARC-N2, showed the lowest similarity with the exotic types studied. It is suggested that RAPD analysis can be used for the characterization and grouping of wheat genotypes and the results will be helpful to wheat breeders.

Key words: genetic diversity, RAPD, wheat genotypes.

Abbreviations: RAPD, random amplified polymorphic DNA; RFLP, restriction fragment length polymorphism; UPGMA, unweighted pair group of arithmetic means.

Introduction

Being a staple food, wheat occupies an important place in the crop husbandry of Pakistan. Soil salinity is a major constraint in food production because it limits crop yield and restricts the use of land previously uncultivated. United Nations Environment Protection Program estimates that approximately 20% of agricultural land and 50% of cropland in the world is salt stressed (Flowers & Yeo, 1995). Although for the last few years the situation of wheat production in Pakistan is satisfactory, due to its increasing demand – as a result of increasing population – continuous enhancement of the wheat productivity is highly desirable. For the last few years, the yield improvement in wheat varieties has not been substantial; a narrow genetic base of the germplasm used has been considered as the major reason. Knowledge of diversity patterns allows the plant breeders (i) to understand better the evolutionary relationships among accessions; (ii) to sample germplasm in a more systematic fashion; and (iii) to develop the strategies leading to incorporation of useful diversity in their breeding programs (Bretting & Widrlechner, 1995). The information about genetic diversity and relatedness in the available germplasm and among elite breeding material is a fundamental element in plant breeding. The future success in wheat improvement depends upon the availability of genetic variability. Traditionally, assessment of genetic diversity has been based on the differences in morphological and agronomic traits in different crops (Gizlice et al., 1996; Sneller, 1997).

Restriction fragment length polymorphism (RFLP) and isozyme markers have been used for the diversity studies and genetic mapping of different crops (Messmer et al., 1992; Trujillo et al., 1995; Paull et al., 1998). But their use remained limited as they revealed low level of polymorphism and the isozyme expression was found to be highly influenced by the environmental conditions (Hernendez et al., 2001). However, the PCR-based DNA marker techniques seem to provide the means for generating useful information on polymorphism, genetic relatedness and diversity. The PCR-based random amplified polymorphic DNA (RAPD) markers (Williams et al., 1990) are dominant markers and extensively used in the genetic mapping (Chalmers et al., 2001) and identification of markers linked with different traits (Bai et al., 2003; Galova et

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