

Abstract

Wheat, a grass available in wild and domestic species, belongs to the family of *Poaceae* and the tribe of *Triticum*. The success of its breeding procedures depends on the amount of genetic diversity in the desired population. Familiarizing with the genetic distance between individuals or populations and being aware of the kinship relationships of the species in the breeding program can provide the possibility of organizing heritable reserves and effective sampling of genotypes and optimal use of such diversity. Indicators available in the ITS region of the ribosomal genes along with the markers of the Chloroplast_intragenic suppression regions (IGS) are the major markers used for studying genetic diversity and phylogenetic relationships. Moreover, in order to determine the ability of IGS and ITS markers in evaluating different wheat cultivars of Sistan bread, to realize the genetic distance and variety among wheat cultivars in this kind of bread, and to identify valuable commercial cultivars and use them in breeding programs, fifteen varieties and genotypes of wild and domestic species of wheat are evaluated in three genotype levels of diploid, tetraploid, and hexaploid. After sequencing the ITS and IGS regions and analyzing the sequences by NCBI blasting software, the ClustalW algorithm in MEGA6 software is used to match the sequences. The results of evaluating the genetic indices using Dnasp software, it is found that among all cultivars and genotypes examined in the ITS region, the highest content of C + G (63.7%) is reported in speltoides. Also, IGS marker in speltoides is 45.7%. The results of studying the nucleotide substitution based on the Tamura-Nei pattern indicate that in both regions of IGS and ITS, the highest rate of substitution is transient and is related to Pyrimidine base. The numerical values of dN /dS for all cultivars in the ITS and IGS regions are 0.13 and 0.57, respectively, indicating the net selection process during the evolution period. The highest genetic distance between the pair of ITS sequences is reported between Shabrang and ofogh cultivars, yet in IGS, it is reported between Dandan Shotori and speltoides. The greatest inter-group variation in the ITS region (0.656) occurs on hexaploid and tetraploid genotypes and in the IGS region, it is reported on the genotypic levels of tetraploid and diploid (0.273). Molecular variance, analyzed by GenAlex software, shows that in the ITS region between the genotypic group and in the populations it is 9 and 91%, respectively, while in IGS, among the genotypic groups and in the populations, it is 26 and 74 %, respectively. By plotting the phylogenetic tree and the pcoA chart, it is also found that the ITS marker, with a greater diversity and genetic distance than the IGS marker, can differentiate various cultivars of wheat species.

Key words: Diversity, Genetic similarity, IGS, ITS



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