

P075

Genetic variation of *Aegilops cylindrica* Host. from Iran, based on RAPD-PCR and HMW glutenin subunits diversity

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Genetic variation of 28 populations of *Aegilops cylindrica* Host., collected from different parts of Iran, were determined with random amplified polymorphic DNA (RAPD) and diversity of high molecular weight (HMW) subunits of glutenin by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) method. The diversity within and between populations for the three-band HMW glutenin subunits pattern were extremely low. Out of 15 screened primers of RAPD, 14 primers generated 133 reproducible fragments of which 92 fragments were polymorphic (69%). Genetic similarity calculated from the RAPD data ranged from 0.41 to 0.84. A dendrogram was prepared on the basis of a similarity matrix using the unweighted pair group method with arithmetic averages (UPGMA) algorithm and separated the 28 populations into two groups. Confusion among the population can be happened because of weedy characteristic of *A. cylindrica*, that as a result the possibility of transportation and cross fertilization between populations across Iran can be high.

P076

Phylogenetic relationships among *Aegilops-Triticum* species based on sequence data of chloroplast DNA

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This study analyzes intra-and interspecific variation in chloroplast DNA (cpDNA) in diploid and polyploid *Aegilops-Triticum* species. The analysis focused on DNA sequence variation in noncoding regions of cpDNA, which included base-pair substitutions, 50 insertion/deletion loci, 7 microsatellite loci, and inversions. Nine of 13 diploid *Aegilops-Triticum* species were successfully identified and genotyped using these data. Sixty-two haplotypes were detected in 115 accessions of these diploid species. Because of the large number of characters examined, novel deep relationships within and among *Aegilops-Triticum* species could be identified and evaluated. Phylogenetic trees for the genus *Aegilops-Triticum* were constructed with *Hordeum vulgare* and *Dasypyrum villosum* as outgroups, and the results were compared to previous studies. These data support the following inferences: (1) *Aegilops* and *Triticum* should be merged; (2) groups D, T, M, N, U, and section *Sitopsis* (except *Ae. speltooides*) underwent speciation concurrently, but most diploid species evolved independently; (3) *Ae. mutica* does not occupy a basal position in *Aegilops-Triticum*; (4) *Ae. speltooides* is in a basal position and differs significantly from other *Sitopsis* species; (5) *Ae. caudata* is polyphyletic in all trees; (6) the genus *Aegilops* is paraphyletic with *Secale*, 7) origin of polyploid species generally follow those reported previously including several di- or polyphyletic origin; 8) *T. dicoccoides* and *T. araraticum* formed a cluster and this, further, formed a cluster with *Ae. speltooides*.

P077

Analysis of genetic diversity in wild diploid wheat *Triticum boeoticum* from West of Iran using RAPD, AFLP and SSR markers

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The application of RAPDs, AFLPs, and SSRs to examine genetic relationships in the 36 populations of *Triticum boeoticum* from west of Iran was investigated. A total of 224 (135 polymorphic), 979 (429 polymorphic) and 246 (145 polymorphic) bands were detected using 14 RAPD primers, 17 primer combinations of AFLP and 17 well distributed, mapped SSR markers, respectively. The polymorphic information content (PIC) value was high for SSRs (0.81) but low for RAPD (0.45) and AFLP (0.56) reflecting the hypervariability of the first system. While the highest marker index (MI) value was for AFLPs (14.19) reflecting the high multiplex ratio of this system. The correlation coefficients of similarity were statistically significant for all three marker systems used but these correlations were higher for RAPDs and AFLPs comparing than those obtained with the other comparings, indicates that these two methods may selectively screen similar regions of the genome. The UPGMA cluster plots separated the 36 populations into three major groups based on their RAPD fragment similarities, and into two major groups based on their AFLP and SSR genotypic similarities. These different marker systems should provide different levels of information which is important in management of germplasm resources.

Keywords: AFLPs, genetic diversity, RAPDs, SSRs, *Triticum boeoticum*

Abbreviations: AFLP, amplified fragment length polymorphism; MI, marker index; PCR, polymerase chain reaction; PIC, polymorphism information content; RAPD, random amplified polymorphic DNA; SSR, simple sequence repeat; UPGMA, un-weighted pair-group method with an arithmetic average

P078

Genetic diversity of high-molecular-weight glutenin subunit compositions in hexaploid wheat

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The high-molecular-weight (HMW) glutenin subunit composition of seed storage protein of 40 syntetic lines (sented of meczic) and 40 cultivars of hexaploid wheat (*Triticum aestivum*) have been examined by using sodium dodecyl sulfate polyacrylamide gel electrophoresis system. 15 different alleles were found that 2* allele in Glu-A1, 7+8 allele in Glu-B1 loci and 5+10 in Glu-D1 had high frequency. 2***+12 subunit, was reported firstly in Pakistan, was observed in 7 line. 26 different glutenin subunit patterns were observed for 15 alleles. The high variation detected in the glutenin subunits could be useful for variety identification.

Key words: genetic diversity, HMW-GS, bread wheat, SDS-PAGE.