

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 *Dasyphyrum 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. speltoides*) underwent speciation concurrently, but most diploid species evolved independently; (3) *Ae. mutica* does not occupy a basal position in *Aegilops-Triticum*; (4) *Ae. speltoides* 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. speltoides*.