Phylogeny of *Aegilops* and *Triticum* Inferred from Sequence Data of cpDNA

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Abstract: This study analyzes intra- and interspecific chloroplast DNA sequence variation of diploid and polyploid species belonging to the *Triticum-Aegilops* complex. Particularly informative data were obtained from noncoding regions of cpDNA including base pair substitutions, insertion/deletions (indels) (50 loci pooled), microsatellites (7 loci pooled), and an inversion. Nine out of thirteen diploid *Triticum-Aegilops* species were successfully identified and genotyped using these data. Sixty-two haplotypes were detected in 115 accessions of 13 diploid species. Because of the large number of characters examined, novel deep relationships within and among diploid *Triticum-Aegilops* species could be evaluated. Phylogenetic trees for the genus *Triticum-Aegilops* were rooted with *Hordeum vulgare* and *Dasypyrum villosum* as outgroups and the results were compared to previous studies. The following inferences were made: (1) *Aegilops* species should be included in *Triticum*; (2) groups D, T, M, N, U and subsection Emarginata of section Sitopsis underwent speciation concurrently, but most diploid species evolved independently; (3) *Ae. mutica* does not occupy a basal position in *Triticum-Aegilops*; (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 and includes *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*.