

Genetic diversity in some *Aegilops* species in Jordan as revealed by RAPDs

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Genetic diversity among 31 *Aegilops* accessions collected from 18 locations in Jordan was estimated using random amplified polymorphic DNA (RAPD). Using a set of five random decamer primers, 581 data points were scored over all accessions. The data points corresponded to a total of 47 loci for which 52 markers were polymorphic. A genetic similarity matrix based on Dice coefficients was constructed using the RAPD data to assess the genetic relatedness. The mean similarity indices associated with the 31 accessions ranged from 0.24 to 0.94 for all accessions with a mean of 0.55. The resulting phenograms indicated that clusters of the same species have common genomes, but clusters were not associated with collection site. The clustering trend was also associated with ploidy level. There was an average of 95% reproducibility of results using two to three replications of five primers. Under stringent reaction conditions RAPD patterns were highly reproducible. There was agreement between classical classification and that based on RAPD analysis.