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ELECTROPHORETIC-SYSTEMATIC STUDIES
IN AEGILOPS.

John Giles Waines, Ph. D.
University of California, Riverside, 1969

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Chairman: Professor B. Lennart Johnson

Alcohol extracts of seed proteins of 137 accessions, including material of the diploids Aegilops mutica, Ae. bicornis, Ae. sharonensis, Ae. longissima, Ae. speltoides, Ae. squarrosa, Ae. uniaristata, Ae. comosa, Ae. caudata and Ae. umbellulata and the tetraploids Ae. variabilis, Ae. kotschy, Ae. triuncialis, Ae. columnaris, Ae. biuncialis, Ae. ovata and Ae. triaristata and hexaploid Ae. triaristata are investigated using the techniques of disc electrophoresis. All these species show different and characteristic protein patterns. There is pattern variation among accessions of the same species. This intraspecific pattern variation is considerable for diploid species, less marked for tetraploid species and almost absent in the hexaploid species. The decrease of intraspecific variability with increase of ploidy suggests that only a few biotypes of each diploid hybridised to form a tetraploid species and that still fewer tetraploid and diploid biotypes hybridised to form a hexaploid.

The electrophoretic patterns support diploid species affinities based on morphology and genome analysis, but the positions of Ae. mutica and Ae. caudata are not clear. The patterns of Ae. squarrosa, Ae. uniaristata and Ae. comosa suggest divergence from a common ancestor. The patterns of Ae. speltoides, Ae. longissima and Ae. bicornis also suggest divergence from a common ancestor, while those of Ae. sharonensis indicate that this species originated from introgression between Ae. longissima and Ae. bicornis. This is the only example of clear evidence for introgression of protein characters in all the species studied.

Karyotype data suggest that Ae. umbellulata is the common parent in all of these polyploid species. The protein patterns support this hypothesis. Patterns of Ae. variabilis and Ae. kotschy indicate that Ae. speltoides, or perhaps Ae. longissima or Ae. sharonensis, is the donor of the second genomes. Ae. caudata is confirmed as the second genome donor of Ae. triuncialis. M-group genome parents are suggested for Ae. triaristata (4x) and Ae. columnaris. The second ancestor of Ae. biuncialis requires further study. The patterns of Ae. ovata indicate that Ae. squarrosa is the donor of these protein characters. The pattern of hexaploid Ae. triaristata combines that of tetraploid Ae. triaristata with that of Ae. uniaristata.

It is not possible to separate the role played by polyploidy involving different parental types from that played by introgressive hybridisation at the polyploid level, once the raw polyploids have arisen. However, the relative uniformity of the patterns within each polyploid species suggests that introgression of protein characters at the polyploid level is not common.

The electrophoretic pattern of a synthetic amphiploid (Ae. caudata x Ae. umbellulata) contains two extra protein bands which are not present in the patterns of the parents. Several explanations of this phenomenon are discussed. The success of the Aegilops polyploids in colonising large areas is attributed to the fixation of a superior polyploid hybrid vigour, which may include the production of polyploid proteins, from among the vast number of possible combinations of the variable diploid species.

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