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EVOLUTION AND POPULATION ECOLOGICAL GENETICS OF WILD BARLEY, *HORDEUM SPONTANEUM*, IN THE FERTILE CRESCENT

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Wild barley, *Hordeum spontaneum*, the progenitor of cultivated barley, *H. vulgare*, is extensively distributed in the Fertile Crescent in diverse ecological habitats. Israel may be its center of origin and genetic diversity.

The genetic diversity and structure of *H. spontaneum* populations from three countries — Israel, Turkey and Iran — were compared and contrasted. The analysis is based on electrophoretically discernible allozymic variation in proteins encoded by 27 shared loci in 2125 individuals representing 52 populations. The results indicate that: (*a*) *H. spontaneum* in the Fertile Crescent is genetically highly variable; (*b*) genetic differentiation of populations includes some clinical, but primarily regional and local patterns, often displaying sharp geographic differentiation over short distances; (*c*) the average relative genetic differentiation was 54% within populations, 39% among populations, and 8% among the three countries; (*d*) allele distribution is characterized by a high proportion of unique alleles (51%), and a high proportion of common alleles that are either locally or sporadically distributed; (*e*) discriminant analysis by allele frequencies successfully clustered wild barley of each of the three countries (96% correct classification); (*f*) a substantial portion of the patterns of allozyme variation in the wild gene pool was significantly correlated with the environment and was ecologically predictable, chiefly by a combination of humidity and temperature variables; and (*g*) natural populations of wild barley are, on the average, more variable than two composite crosses and land races of cultivated barley. The spatial patterns and environmental correlates and predictors of genetic variation of *H. spontaneum* populations in the Fertile Crescent indicate that genetic variation is both rich and partly adaptive and predictable by ecology and allozyme markers. Consequently, conservation and utilization programs should optimize sampling strategies by following the ecological-genetic factors and allozyme markers as effectively predictive guidelines. The rich genetic variation of wild barley provides the basis for its aggressive competition and widespread distribution into desert habitats.