Use of wild-wheat resources

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Wild wheats still flourish over a small corner of southeastern Europe and much of the Mideast. They are found from the Balkan Peninsula to Transcaucasia and southward in both arcs of the Fertile Crescent, to the Persian Gulf on the east and the Dead Sea on the west. From these wheats Stone Age man domesticated the types that fed emerging Near Eastern civilizations and, in time, gave rise to our durum and bread wheats.

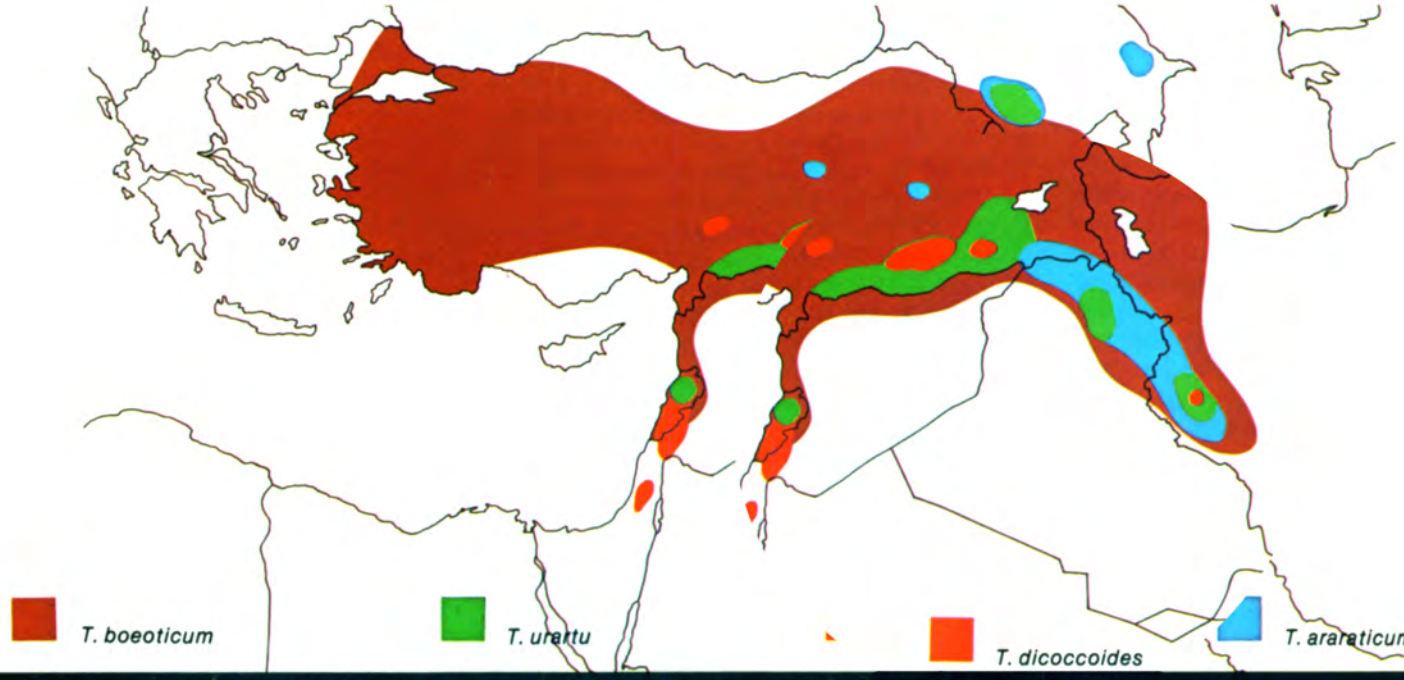
As a result of selection by man during 10,000 years or more, the domesticated wheats have acquired a stockpile of genes that ensure high productivity under cultivation. But this is built on a very narrow genetic base. By comparison, wild progenitors from which our wheats have come, have acquired a larger reservoir of genes as a result of adaptation to a great diversity of environments during the evolutionary time scale. This pool in the wild populations has remained largely unavailable, or at least unused by wheat breeders. However, University of California plant scientists have begun to draw on its diverse germplasm. Studies into the ancestry and distribution of wild and cultivated wheats provide new perspectives on the accessibility of wild gene resources for improving the cultivated crop by conventional breeding methods, and have opened the door to using new methods based on the mode of evolution.

UCR collection

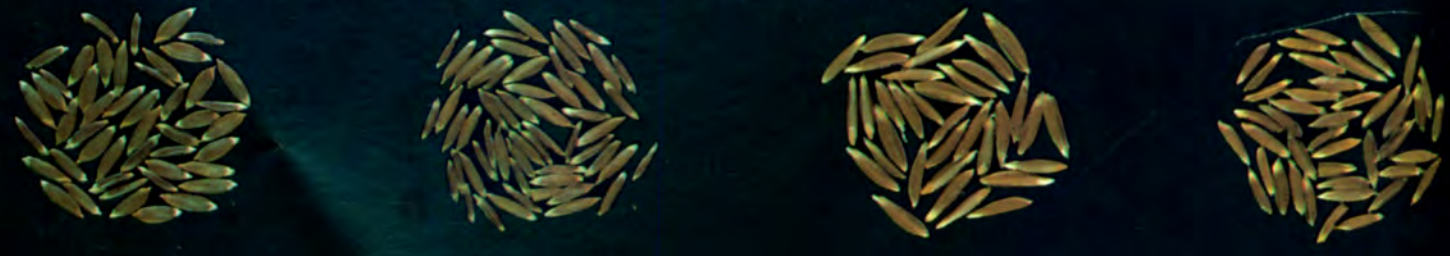
More than 2200 accessions (table 1) of wild wheats *(Triticum)* and their near relatives, including species of *Aegilops*, have been assembled at the University of California at Riverside (UCR) by collecting seed from single plants and massed seed from individual populations. A first expedition was made in 1965 through southern Turkey to the Iranian border. It returned across the Anatolian Plateau with collections of most *Triticum* and *Aegilops* species known to occur in Turkey. Through subsequent donations and exchange this collection includes all known species of *Aegilops*.

UCR expeditions in 1972 and 1973 focused on the Fertile Crescent where the greatest diversification of wheat species seems to have occurred. The diploid (14-chromosome) *Triticum boeoticum*, which is prevalent in all wild wheat areas, was found in abundance in ungrazed sites at elevations of 600 to 1200 meters in southeastern Turkey, somewhat higher in the Zagros foothills of northeastern Iraq, and at 1100 to 1900 meters in western Iran. In the Mt. Hermon area of Lebanon it was found at 1000 meters. This diploid is thought to be one of the parents of the wild tetraploid (28-chromosome) wheats from which the cultivated durum wheats were domesticated.

More significantly, another diploid wheat, *T. urartu*, previously known only as a restricted Armenian endemic,



The map shows the areas in which wild wheats grow. Seeds of the wild wheats are pictured below.



was widely found throughout the Fertile Crescent. In Turkey it grew luxuriantly in the volcanic soil of the Upper Mesopotamian Province at 600 meters elevation; in the Bekaa Valley of Lebanon it formed large pure stands. At higher elevations, *T. urartu* occurred in mixed stands with *T. boeoticum* and the tetraploid *T. dicoccoides* in southeastern Turkey, and with *T. boeoticum* and the tetraploid *T. araraticum* in Iraq and Iran. It may be the other parent of the tetraploid wheats.

Clues to the ancestors

The diploid species, which are reproductively isolated from one another, comprise populations with marked morphological variation, wide climatic tolerance, and adaptation to diverse habitats. These populations also vary genetically in cold and drought tolerance, resistance to pests and diseases, and in seed protein content and quality.

The tetraploid wheats are more restricted in geographic distribution. Within species they are more uniform than the diploids in morphology and seed albumin proteins. Natural selection for greater fertility in the evolving tetraploid wheats may have led to the emergence of two distinct sets of chromosomes, namely genomes A and B, as a result of differentiation of similar (homoeologous) chromosomes contributed by the two parents.

Chromosomes of the A genome pair well with those of *T. boeoticum* and *T. urartu*, and with those of various related diploid species, especially of the genus *Aegilops*. In contrast, chromosomes of the B genome pair little, or not at all, with those of any known diploid species. Consequently, as a result of recombinations between the pairing chromosomes, genes from the diploid wheats and *Aegilops* species can readily be transferred to the A, but not to the B genome by conventional breeding.

The main reason why the B genome chromosomes do not pair with homeologous chromosomes is that a gene, *Ph*, on the long arm of chromosome 5B, inhibits such pairing. However, removal of this long arm allows homeologous chromosomes to pair. Pairing also is allowed by the presence of the gene, *ph*— a mutant of the *Ph* gene induced in an experimental hexaploid wheat.

The uniformity of the populations found by the UCR expeditions in the tetraploid *T. dicoccoides* points to its probable origin from one or a very few hybrids between its two parental diploid species. Such an origin suggests that initially, genetic variability consisted of genes from only a few diploid individuals, and that it was isolated from the total gene resources of the wild diploid populations by the sterility of diploid x tetraploid crosses. Subsequent selection of the tetraploids under domestication further reduced their native genetic diversity.

The hexaploid (42 chromosome) bread wheat *T. aestivum* is thought to have originated around 8,000 years ago as a result of hybridization between a cultivated tetraploid and the wild diploid *Aegilops squarrosa*. Bread wheat carries the A and B genomes as well as the squarrosa genome D, but because it originated from only one or a very few hybrids, it would be expected to carry little, if any, of the genetic variability of the parental species or from the wild diploid wheats. With embryo culture, genes can be transferred to the A and D genomes by conventional means, but not to the B genome.

Putting wild wheats to work

Our studies involve the transfer of the *ph* mutant into California cultivars of durum and bread wheat, to permit the introduction of desirable genes from diploid parents or other wild relatives directly into the A, B, and D genomes. This objective also requires the systematic screening of the *Triticum-Aegilops* collection for traits desirable for transfer.

Consequently, we are screening the UCR collection for seed protein concentrations. There is a considerable range in protein content (table 2), although all wild and primitive types have higher values than many commercial wheats. These values support the idea that man's selection in wheat for high yield and good semolina or bread making quality was achieved by increasing the content of starch relative to that of protein. The collection also is being screened for genotypes with high lysine and threonine, essential amino acids now present at undesirably low levels in wheat flour.

In pest, disease, and cultural problems, screening also is involved. Resistance or tolerance is being sought to: (a) *Pratylenchus thornei*, a nematode that attacks wheat in Mexico, and is now found in the Imperial Valley; (b) "take-all" disease, a root rot caused by Ophiobolus fungi, and Fusarium root rots; (c) aphids that attack wheat in California; and (d) drought. Should desirable genes be identified in any of these screening trials, they will be transferred to commercial cultivars and made available to plant breeders.

TABLE 1. Number of Accessions in the Riverside Collection

Triticum boeoticum	700
T. urartu	170
T. monococcum (primitive cultivar)	160
T. dicoccoides (AABB)	200
T. araraticum (AAGG)	200
Primitive AABB tetraploid cv. wheats	123
Primitive AAGG tetraploid cv. wheats	30
Primitive AABBDD hexaploid cv. wheats	150
Aegilops squarrosa	95
Aegilops speltoides	90
Other diploid *Aegilops* species	134
Polyploid *Aegilops* species	102
Miscellaneous: *Agropyron, Haynaldia, Secale, Elymus, Hordeum,* etc.	125
Total	2206

TABLE 2. Protein Content and 1000 Grain Weight of Wheats in the Riverside Collection, 1975 Harvest

Taxon	No. collections	Protein			1000 grain weight		
		Low	High	Mean	Low	High	Mean
T. Boeticum	268	17.4	26.0	21.8	6.55	16.90	12.52
T. urartu	68	18.0	23.8	21.0	8.24	15.25	10.22
T. Monococcum (cv)	28	14.9	22.9	17.1	10.72	25.16	20.11
T. dicoccoides	34	19.1	26.6	23.0	13.24	22.16	17.45
T. araraticum	39	14.7	26.7	22.9	7.90	27.82	15.23
T. durum 'Modoc'	1	12.6			53.0		
T. aestivum 'Anza'	1	11.3			38.0		
Total	439						

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