Tetraploid Wheats: Seed Protein Electrophoretic Patterns of the Emmer and Timopheevi Groups

Abstract. *Crude protein extracts were subjected to disk electrophoresis on polyacrylamide gel. The pattern obtained showed a fast and slow series of bands. In the fast series, the eight species of wheat of the Emmer group gave virtually identical eight-band patterns, and the four species of the Timopheevi group gave nearly identical six- or seven-band patterns. The groups consistently differed with respect to four bands. Two of these differences were attributable to the A genome.*

On the strength of cytogenetic evidence, all the tetraploid wheats share a common A genome, apparently acquired from the wild diploid *Triticum boeoticum* Boiss. Their second genome may have been derived from the same source (*1*) or from a diploid of the related genus *Aegilops* (*2*). Whether the Emmer (AABB) and Timopheevi (AAGG) groups of the tetraploids received their second genome from different donors (*3*) or the one was derived from the other (*4, 5*) is also controversial. The variation and distribution of the postulated B and G genomes in populations of the wild diploids and tetraploids could throw light on these questions. But morphological differences between the groups are tenuous, and the existence of the two differentiated genomes has been inferred largely from sterility and failure of chromosome pairing in F_1 hybrids. In this case, therefore, morphological attributes are not discriminative enough, and cytogenetic methods are too involved for classifying natural populations. However, electrophoresis of seed proteins readily distinguishes between the Emmer and Timopheevi groups and provides another way of assessing the geographic dispersion and the intrinsic variation of B and G in wild stands. Such information may help confirm the place of domestication of the cultivated tetraploids.

Wild tetraploid wheat is distributed throughout the Fertile Crescent in southern Anatolia, northern Iraq, and western Iran (*6*) where its presumed diploid progenitors come into contact. A conspicuous outpost of the distribution in the upper Jordan Valley includes the type locality for *T. dicoccoides* Körn and is occupied by the Syrio-Palestinian race of the species. Another distinct outpost in Armenia, Azerbaijan, and Georgia is occupied by the Transcaucasian race of the wild tetraploid, which includes *T. araraticum* Jakubz. (*T. dicoccoides* ssp. *armeniacum* Jakubz.) and *T. dicoccoides* var. *nudiglumis* Nabalek, the type locality of which is northern Iraq, however. The material of *T. dicoccoides* currently used for research represents the two outposts primarily, and little is known regarding the frequency of the Syrio-Palestinian and Transcaucasian races or possible intermediates in the large populations of the Fertile Crescent.

Crude protein extracts of ground seeds were made with 70 percent ethanol (*7*) from 43 accessions representing eight species of the Emmer and four of the Timopheevi groups. The Emmer species included *T. dicoccoides* and the primitive, domesticated derivative *T. dicoccum* Schübl., as well as the further derived, cultivated types, *T. turgidum* L., *T. carthlicum* Nevski, *T. durum* Desf., *T. turanicum* Jakubz., *T. polonicum* L., and *T. aethiopicum* Jakubz. The Timopheevi species included *T. araraticum, T. dicoccoides* var. *nudiglumis*, and the semicultivated derivatives *T. timopheevi* Zhuk, and *T. paleocolchicum* Men.

The extracts were fractionated by disk electrophoresis on acrylamide gels according to the method of Reisfeld, Lewis, and Williams (*8*). At *p*H 4.3, provided by β-alanine–acetic acid buffer, the proteins moved toward the cathode. Protein bands from different species were tested for homology (that is, equivalent migration velocity) by the method of Johnson, Barnhart, and Hall (*9*). Obviously, migration velocity as a criterion of band homology does not distinguish between proteins of different primary structure but equal net electric charge. Typical patterns for *T. dicoccum* and *T. timopheevi* are shown in Fig. 1, A and B, together with one (Fig. 1C) from a mixture (1 : 1 by weight) of their proteins. The mixture provides a band-by-band verification of homologies between the two species. The pattern for *T. dicoccum*, used

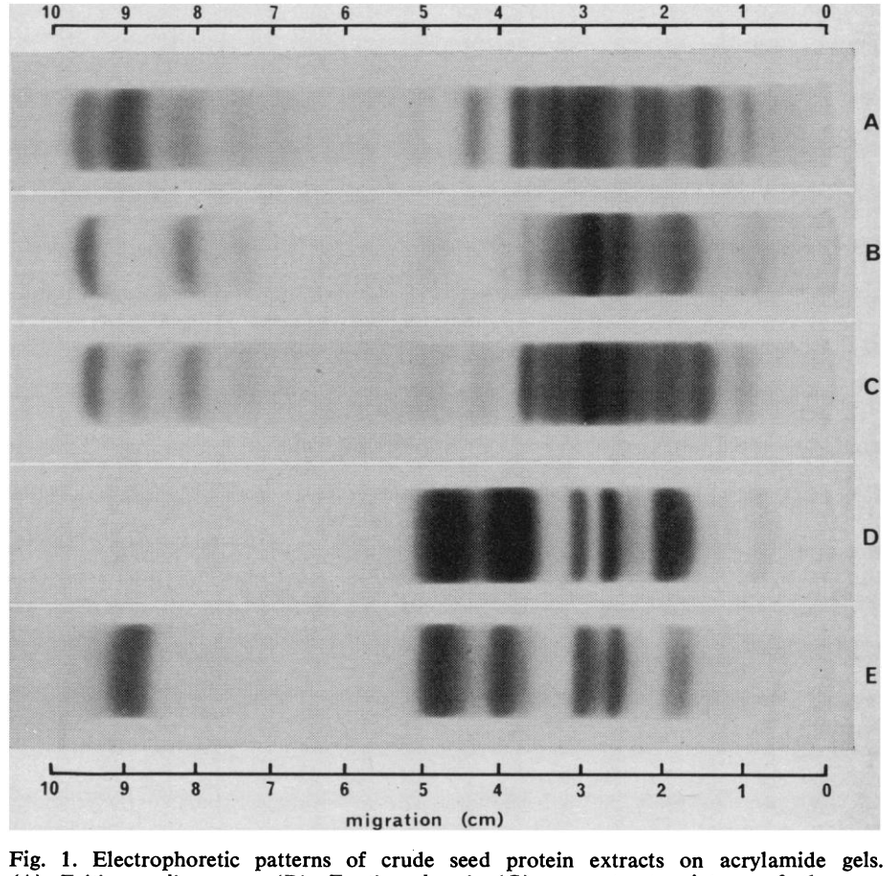

Fig. 1. Electrophoretic patterns of crude seed protein extracts on acrylamide gels. (A) *Triticum dicoccum*; (B) *T. timopheevi*; (C) an extract mixture of the two species; (D and E) *T. boeoticum*.

as a standard, was photographically enlarged to an arbitrary length of 10 cm, and the other patterns were adjusted to equivalent migration velocities by reference to their *T. dicoccum* homologs.

The tetraploid pattern invariably comprised two different series of protein fractions, a fast-moving one of broad, widely spaced bands beginning at −10.0 cm and a slow-moving one of narrow, closely spaced bands beginning at −4.0 cm. Owing partly to the degree of band separation obtained, the slower series provided inconclusive evidence on which to categorize the *Triticum* accessions, but in the fast series the tetraploids of the Emmer and Timopheevi groups were readily distinguishable.

The Syrio-Palestinian race of *T. dicoccoides* appears to be the progenitor of the Emmer group. On the basis of regular chromosome pairing in the F_1 hybrids among these tetraploids, there is general agreement that they are all of the genome constitution AABB. Their B genome is thought to have been derived from *Aegilops speltoides* Tauch.

Like *T. dicoccum* (Fig. 1), all species in the Emmer group, including the Syrio-Palestinian race of the wild tetraploid, gave a pattern with eight bands in the fast series with centers at −9.7, −9.0, −8.1, −7.4, −6.9, −6.0, −5.0, and −4.3 cm. Frequently the band at −8.1 and sometimes that at −6.9 were double. The species were essentially identical also with respect to the density of the individual bands. That at −9.0 was the densest, and those at −6.0 and −5.0 were the faintest, except in *T. carthlicum* and *T. turanicum*, where the band at −5.0 sometimes was nearly as dense as that at 9.0.

The Transcaucasian race of *T. dicoccoides* is apparently the progenitor of the Timopheevi group. Hybrids among these tetraploids also exhibit for the most part regular chromosome pairing, but F_1 hybrids between members of the Timopheevi and Emmer groups are highly sterile (*5*), owing to failure of pairing among chromosomes presumably of the second genome (*10*). For this reason, the Timopheevi tetraploids were originally assigned the presently controversial genome formula AAGG.

Like *T. timopheevi*, all species of the Timopheevi group, including the Transcaucasian race of *T. dicoccoides*, showed six bands in the fast series with centers at −9.7, −8.1, −7.4, −6.0, −5.5, and −5.0 cm. That at −7.4 was sometimes visibly double, and occasionally a band appeared at 4.0, or in *T. paleocolchium* at −4.3. All the species of this group also resembled *T. timopheevi* with respect to density of the successive bands.

The Emmer (AABB) and Timopheevi (AAGG) groups showed five or, infrequently, six homologous bands among the first ten band loci in the fast series. The bands at −9.0 and −6.9 were absent from all species of the Timopheevi group, and that at −4.3 was absent from all except *T. paleocolchium*. The bands at −5.5 and −4.0 were absent from all the Emmer species. These dissimilarities at four or five loci presumably are partly, but not wholly, attributable to the second genome. From many sampled accessions of the diploid wheats, the A genome showed only two bands (Fig. 1D) in the fast series, at about −5.0 and −4.0, but a recent southeastern Anatolian collection (Fig. 1E) showed an additional band at the critical locus −9.0.

Thus, the electrophoretic patterns confirm cytogenetic evidence that the Emmer and Timopheevi groups stem, respectively, from the Syrio-Palestinian (AABB) and Transcaucasian (AAGG) races of their wild progenitor, *T. dicoccoides*. Harlan and Zohary (*6*) suggested that Emmer (*T. dicoccum*) was domesticated in the upper Jordan Valley where the Syrio-Palestinian race is vigorous and abundant. However, Helbaek (*11*) reported both wild and cultivated Emmer (dating from 7000 B.C.) from archaeological excavations at Jarmo in Iraqi Kurdistan. The only accession of *T. dicoccoides* electrophoretically analyzed from that area was of the Transcaucasian race. Apparently, therefore, more information regarding the prevalence of the two races in the wild tetraploid populations of the Fertile Crescent is needed. Such information, readily obtainable by electrophoretic methods, could provide further clues to the area of first domestication of Emmer, as well as to the origin and affinities of the B and G genomes.

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Respiratory Exposure to Lead: Epidemiological and Experimental Dose-Response Relationships

Abstract. *Epidemiologic studies of blood lead levels in general and occupational groups show a logarithmic regression on estimated atmospheric exposure. Experimental results at the same and higher levels show a dose-response relationship which fits the same regression. The data imply that long-term increases in atmospheric lead will result in predictably higher blood lead levels in the exposed populations.*

Lead poisoning as an occupational hazard has been known and described for centuries. Its clinical manifestations include loss of muscle tone ("wrist drop"), intestinal colic, anemia, spontaneous abortions, and mental retardation. There is extensive literature on exposures and levels of lead in blood and urine above which toxic symptoms are likely to occur (*1, 2*). Specific biochemical lesions, such as that of blocking of delta-aminolevulinic dehydrase, are now known to affect porphyrin metabolism and the synthesis of hemoglobin (*3*). Recently reported are effects on the sodium and potassium activated adenosine triphosphatase of erythrocytes (*4, 5*).

The average daily intake of lead from food and beverages in the United States is now estimated at about 0.30 mg per day, with less than 10 percent of this being absorbed from the intestinal tract (*1*). In addition, some lead is inhaled and absorbed through the respiratory tract; the relative importance