COMPARISON OF ω-GLIADIN COMPONENTS BY N-TERMINAL AMINO ACID SEQUENCING

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ω-Gliadin proteins from bread wheat (Triticum aestivum variety Justin), Triticum monococcum, and Aegilops squarrosa were compared by n-terminal amino acid sequencing. Components extracted from seeds were purified by gel-filtration and ion-exchange chromatography. Each of two gliadins from Justin (one controlled by a gene on chromosome 1D and the other by a gene on chromosome 1B) gave mainly a single band upon gel electrophoresis in aluminum lactate buffer (pH 3.2); the component from T. monococcum also gave mainly a single band upon electrophoresis. These three components were sequenced through 25-28 residues from the N-terminus of each of the proteins. The fraction prepared from Ae. squarrosa gave two closely-spaced bands upon electrophoresis. Only enough of this fraction was obtained for a single experiment that was carried through 14 cycles. All of these ω-gliadins differed from one another in sequence although some homology was evident among them. Homology could be improved by a judicious realignment of sequences based on the assumption that insertions into or deletions from the base sequence of an ancestral structural gene have occurred during the course of evolution of the structural genes coding for these proteins. The component from T. monococcum gave a double sequence with the minor sequence being the same as the major sequence except for being displaced by one residue as a consequence of the absence of the N-terminal amino acid. This apparently pure component was actually a mixture of two components that differed from one another by a single N-terminal amino acid. Evidence for a repeating sequence of five amino acids was found in two of the components.
Realignment of sequences to emphasize Homology

$\omega$-GLI (J-ID)

$\omega$-GLI (T.M.)

A = ALA,  R = ARG,  Q = GLN,  L = LEU,  N = ASN,  P = PRO,  S = SER,  D = ASP,
E = GLU,  Y = TYR,  F = PHE,  K = LYS,  G = GLY,  H = HIS,  T = THR