

Identification of Some Wheat Proteins Separated by a Two-Step Acid Polyacrylamide Gel Electrophoresis and Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis Technique

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The purpose of this study was to identify some proteins revealed by the recent two-step electrophoresis technique Khelifi and Branlard (1991) used to analyze the high molecular weight (HMW) and low molecular weight (LMW) subunits of glutenins.

Several electrophoretic techniques have been developed for analyzing the diversity of the LMW subunits of glutenins. The first technique used the two-step one-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) method of Singh and Shepherd (1988) and Gupta et al (1989). The seed proteins, extracted by a Tris-HCl buffer containing SDS, were electrophoresed on an SDS-PAGE gel. The smaller extracted proteins moved more quickly into the gel and were therefore separated from the aggregated proteins, which moved more slowly and remained in the first millimeters of the resolving gel, just under the stacking gel. After reduction, these aggregated proteins were subjected to a gradient SDS-PAGE gel to separate the HMW and LMW glutenin subunits and some nonstorage proteins.

The second technique was that described by Khelifi and Branlard (1991), in which nearly all storage proteins, together with other proteins, were extracted by 2-chloroethanol. First, the gliadins, albumins, and globulins were separated from the aggregated proteins using an acid-PAGE procedure. Then the aggregated proteins, which remained in the first millimeter of the acid gel, were extracted, reduced with β -mercaptoethanol, and subjected to SDS-PAGE to separate the HMW and LMW subunits of glutenin. Several recent reports give a simplification of these two-step procedures in analyzing HMW and LMW subunits of glutenin after one-dimensional SDS-PAGE (Gupta and MacRitchie 1991, Singh et al 1991, Zhen and Mares 1992).

When the same variety was compared using both two-step electrophoresis techniques, some differences were found in the patterns of the D-zone proteins (Khelifi and Branlard 1991). The acid-PAGE-SDS-PAGE technique showed heavily stained bands of M_r 50–67 kDa that were absent in the gel of the two-step one-dimensional SDS-PAGE of Singh and Shepherd (1988) and Gupta et al (1989). These three to five unknown bands, depending on the variety, seem to have a diverse mobility from one genotype to another. Therefore, some experiments were necessary to identify these D-zone proteins.

RESULTS AND DISCUSSION

The proteins extracted by 2-chloroethanol from individual half grains of Chinese Spring nullisomic (N)-tetrasomic (T) lines NIAT1B, NIAT1D, N1BT1A, N1BT1D, and N1DT1B were subjected to the two-step acid-PAGE-SDS PAGE separation. The corresponding patterns (Fig. 1) revealed that genes that code for the D-zone proteins were located on the group 1 chromosomes. Gupta and Shepherd (1987) found nonprolamins in the D zone that were located on chromosome arms 4DL, 5BL, and 5AL. These nonprolamins seem to be absent in the D-

zone of chloroethanol extracts analyzed by the acid-PAGE-SDS-PAGE procedure. Figure 1 demonstrates that the genetic location is on the 1D chromosome for the two fastest bands and on the 1B chromosome for the other bands of Chinese Spring.

After SDS-PAGE of total reduced wheat proteins, Kasarda et al (1988) reported that the proteins with a mobility between those of the HMW and LMW subunits of glutenins were considered to be ω -gliadins. Consequently, the comparison of our D-zone proteins with the ω -gliadins seemed logical. The 2-chloroethanol extracted proteins from Chinese Spring were separated by acid-PAGE using a previously published method (Branlard et al 1990). The left and right edges of the gliadin acid gel were excised and rapidly stained with Coomassie blue to identify the mobility of the ω -gliadins. Five pieces of the unstained gel, corresponding to the five most heavily stained ω -gliadin bands of Chinese Spring identified on the edges of the stained gel, were cut. The proteins from each piece of gel were eluted with 70% ethanol overnight and then desiccated with vacuum at ambient temperature. The collected proteins were equilibrated 10 min in a Tris-SDS pH 6.8 buffer and separated by SDS-PAGE. The results are shown in Figure 2. The mobility of the most heavily stained ω -gliadins correspond to those of the D-zone proteins. The 1DS ω -gliadins corresponding to the *Gli-D1* locus, with two bands on the acid gel for Chinese Spring, show a mobility identical to those of the bands previously located on 1D in our D-zone (Fig. 2, Lanes 4 and 5). Because Chinese Spring does not possess ω -gliadins corresponding to *Gli-A1* (Metakovskiy

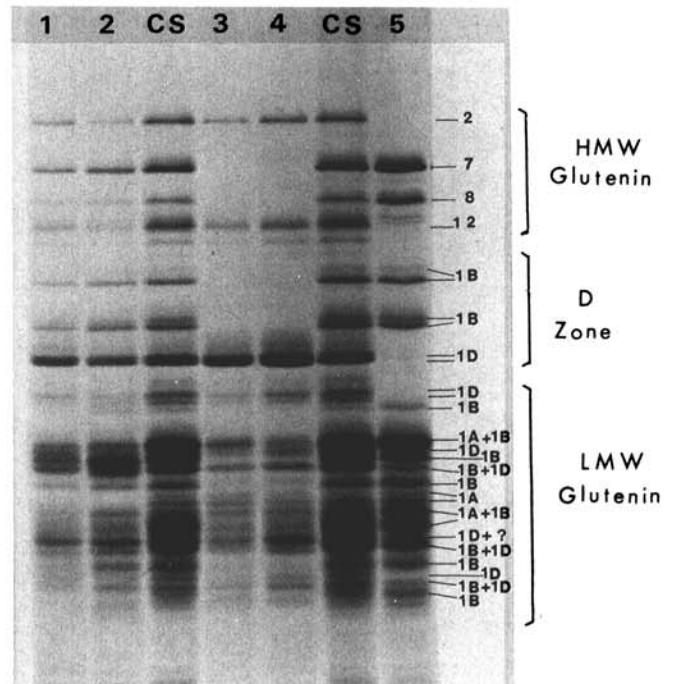


Fig. 1. Two-step acid-PAGE-SDS-PAGE patterns of the 2-chloroethanol seed proteins extracted from the Chinese Spring (CS) nullisomic (N)-tetrasomic (T) lines. Lane 1, NIAT1D; Lane 2, NIAT1B; Lane 3, N1BT1A; Lane 4, N1BT1D; Lane 5, N1DT1B. HMW = high molecular weight. LMW = low molecular weight.

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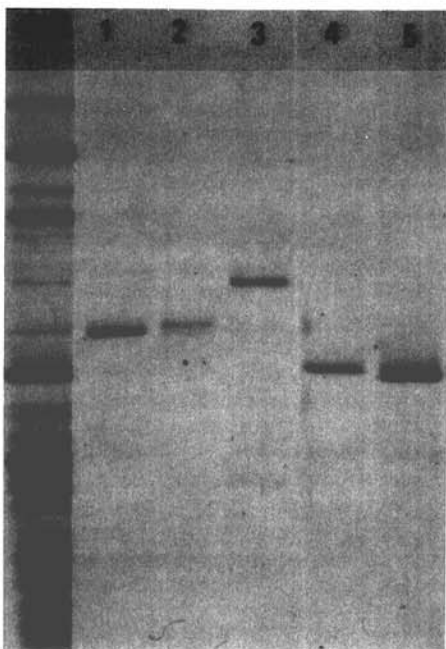


Fig. 2. Comparison of the mobility patterns of the ω -gliadins eluted from the acid gel with the mobility patterns of the D-zone proteins of Chinese Spring (CS) after two-step acid-PAGE-SDS-PAGE technique. Lanes 1-3: ω -gliadins coded by *Gli-B1* locus. Lanes 4 and 5: ω -gliadins coded by *Gli-D1* locus.

et al, 1984), the three other D-zone bands correspond to the 1BS ω -gliadins (Fig. 2, Lanes 1-3).

Using the two-step acid-PAGE-SDS-PAGE technique, we found that the D-zone proteins correspond to ω -gliadins. These ω -gliadins remained aggregated to the HMW and LMW glutenins upon initial extraction with 2-chloroethanol. Bietz et al (1975a,b) showed that glutenins do strongly associate noncovalently with gliadins. Because they were aggregated to the glutenins, some of these ω -gliadins may have functional properties different from those of the other gliadins.

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