Cereal Chemistry

Vol. 51 September-October 1974 No. 5

A Note on Scanning Electron Microscopy of Low-and High-Protein Barley Malts[1,2]

Y. POMERANZ,[3] Barley and Malt Laboratory, USDA-ARS, Madison, Wisconsin 53705. U.S. Department of Agriculture, Manhattan, Kansas 66502

ABSTRACT

Scanning electron microscopy was used to follow modification in malting of a low- and a high-protein barley cultivar. In the low-protein cultivar, degradation of the protein matrix was extensive and some of the degraded protein was deposited in kilned malt on the starch granules. In the high-protein cultivar, much of the protein matrix was largely intact and some protein was retained in the form of a continuous thick film covering the starch granules.

The significance of protein in relation to malting and brewing characteristics of barleys has been studied extensively. In England and on the European continent barley protein was one of the first parameters used to assess quality. The consensus has been that low-protein (7 to 10%) barleys are best suited for malting and brewing. According to the recommendations of the Malting Barley Improvement Association in the United States (1), the preferred protein content should be below 12.5% (dry matter basis, N × 6.25) in midwestern 6-rowed type barleys, below 12.0% in western two-rowed type barleys, and below 9.0% in western six-rowed type barleys.

The proportion of proteins solubilized during malting decreases as total protein content increases (2). This decrease in protein solubility has been attributed to the disproportionately large increase in barley prolamines, hordeins, with increase in total protein (3–6) brought about by environmental conditions or cultural practices (i.e., heavy N fertilization). Research on chill-haze from beer in European laboratories has suggested that hordeins may be one of the haze constituents and may be responsible, in part at least, for the poor clarity and stability of beers produced from high-protein barley.

High-protein barleys generally have high amylolytic activities (7). This is

[1]Cooperative investigations between the Barley and Malt Laboratory, Agricultural Research Service, U.S. Department of Agriculture; and the Agricultural Experiment Station, University of Wisconsin, Madison.

[2]Mention of a trademark or proprietary product does not constitute a guarantee or warranty of the product by the U.S. Department of Agriculture, and does not imply its approval to the exclusion of other products that may also be suitable.

[3]Present address: Director, Grain Marketing Research Center, USDA-ARS, Manhattan, Kansas 66502.

TABLE I. DESCRIPTION OF BARLEY AND MALT SAMPLES

	Low Protein	High Protein
Kernel weight, mg.	31.5	24.3
Total extract, %	79.6	71.6
Fine-coarse grind extract, %	3.2	4.0
Barley protein (N × 6.25), %	10.7	17.8
Insoluble protein, %	7.1	13.1
Wort N/malt N, %	34.1	26.2
Diastatic power, °L.	136	212
α-Amylase, 20°	37.4	46.0

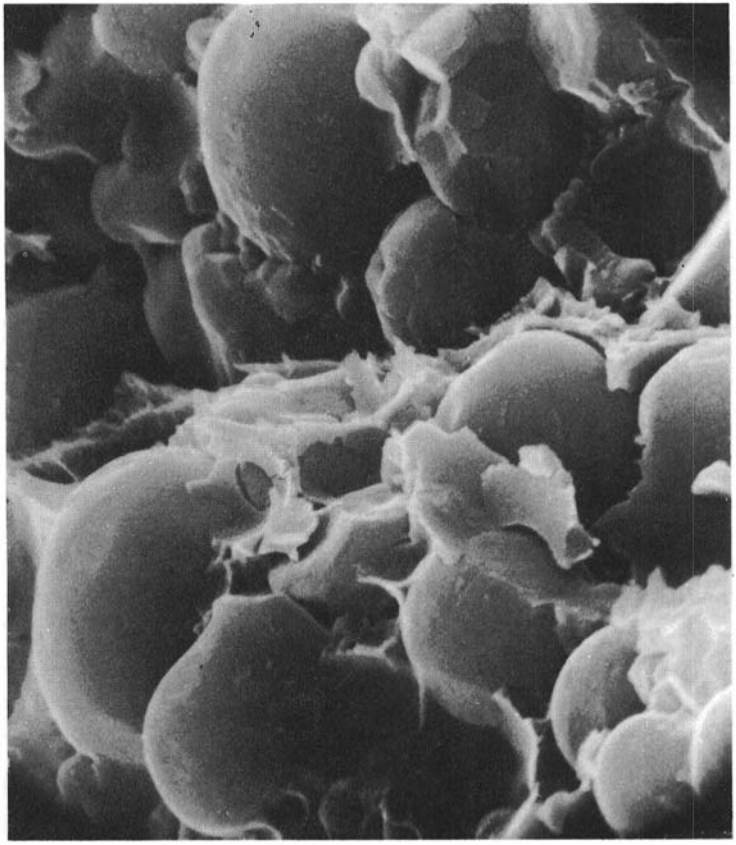

Fig. 1. Transverse section through low-protein barley (5,800×).

advantageous if the malt is used to produce beer from mashes with high levels of adjunct. However, the disadvantages of high protein may be numerous (8). High protein levels impair uniformity of steeping and malting, and reduce malting yields. Wort and beer extract yields from high-protein barleys are reduced as much as 1% per 1% increase in protein. The beers may have impaired clarities.

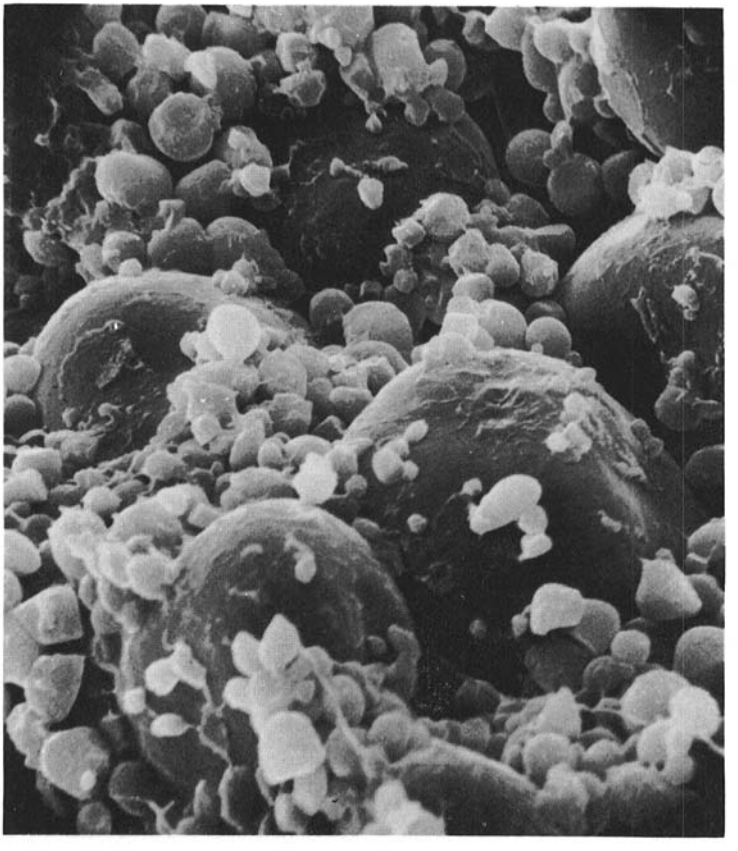

Fig. 2. Transverse section through malt from low-protein barley (2,400×).

According to Dolezalova et al. (9), the significant effects of high protein content on barley and malt quality are multifaceted. High protein affects adversely practically all malt parameters.

As an aid to understanding those effects, changes in the aleurone layer and in the starchy endosperm of steeped, malted, and kilned barley were followed by scanning electron microscopy (10). Partial breakdown of cell walls in the center of the starchy endosperm of malted barley (11.8% protein) was accompanied by extensive dissolution of the protein matrix and "freeing" of small starch granules that were previously embedded in that matrix; the effect on the appearance of the starch granules was small. In the central endosperm of kilned barley malts, cell wall dissolution was extensive and was accompanied by mechanical breakdown of the large starch granules. This report compares the structure of the starchy endosperm in barleys and kilned malts from low- and high-protein barleys.

MATERIALS AND METHODS

Barleys and Malts

Two samples of Firlbecks, a two-rowed cultivar, grown with 0 and 120 lb.

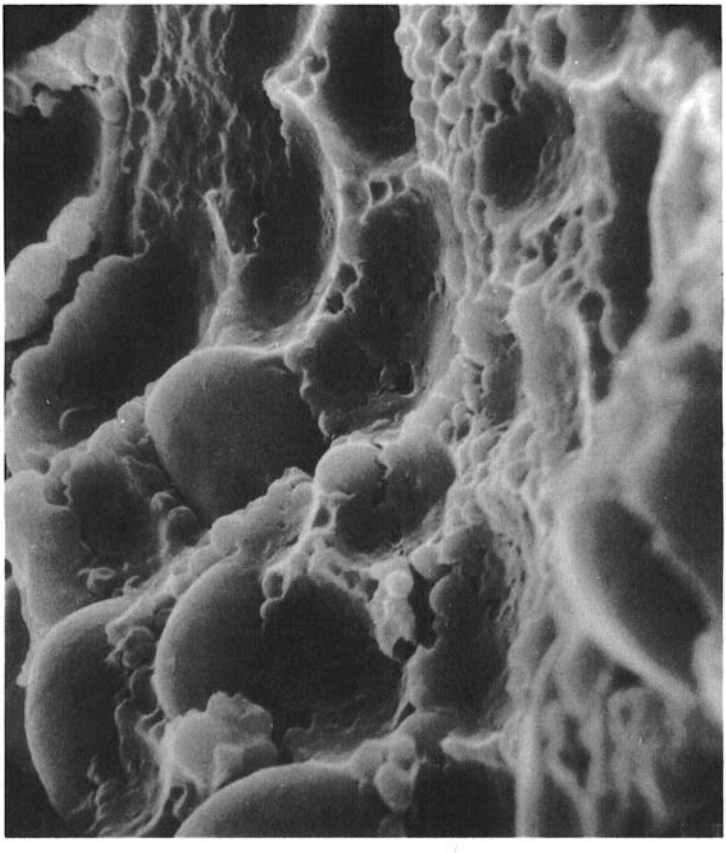

Fig. 3. Transverse section through high-protein barley (2,300×).

nitrogen per acre in 1971 in Fort Ellis, Montana, were used. The samples were steeped to 45% moisture at 16° C. and germinated under uniform conditions in malting chambers at 16° C. for 5 days (11). Final kiln temperature was 85° C. for 2 hr.

Scanning Electron Microscopy

Transversal sections were cut through the middle of the kernel. The sections were mounted on circular (9-mm. diameter) specimen holders with an adhesive, coated with graphite, and covered with a 200- to 300-Å gold layer. The specimens were examined in a Cambridge stereoscan electron microscope at 20 kv.

Analytical Determinations

The barleys and malts were analyzed for moisture, Kjeldahl-N, and malting parameters according to the methods of analysis of the American Society of Brewing Chemists (12).

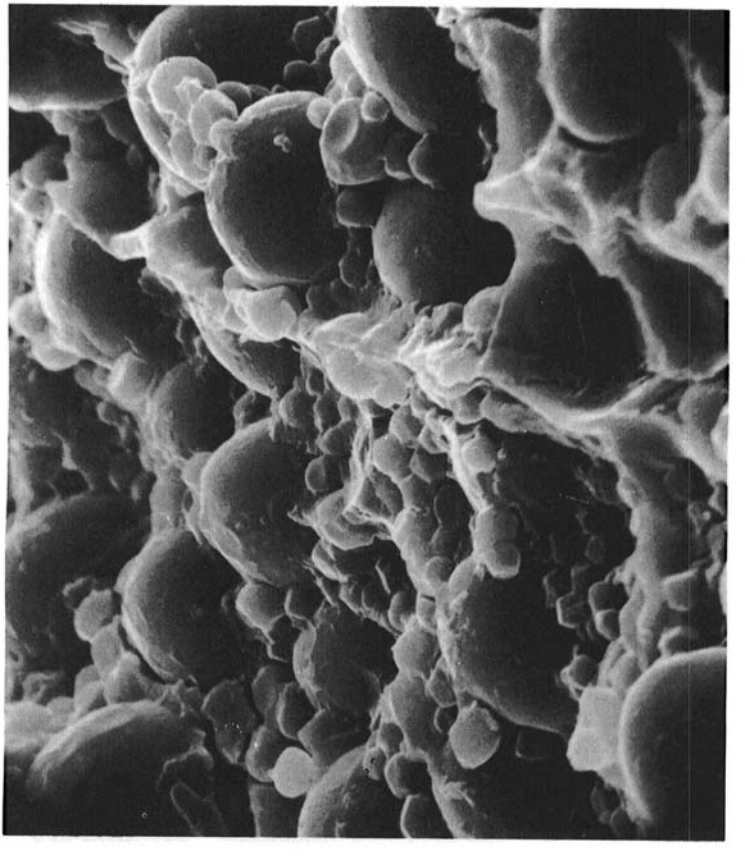

Fig. 4. Transverse section through high-protein barley (2,400×).

RESULTS AND DISCUSSION

Table I compares certain barley and malt characteristics of samples used in the study. As expected, the large increase in protein content decreased kernel weight, total extract, and the ratio of wort N and malt N; it increased fine-coarse grind extract-difference, diastatic power, and α-amylase.

Observation under the scanning electron microscope (SEM) of the central starchy endosperm of a section of the low-protein barley used in the study (Fig. 1) shows a protein matrix in which starch granules of varying sizes are embedded. Following malting and kilning, much of this protein matrix disappears, leaving free starch granules (Fig. 2). Note that the large starch granules show only limited signs of degradation but that some material (presumably heat-denatured proteins) is deposited on those granules. The thick protein matrix in the protein-rich sample of barley is shown in Figs. 3 and 4. Several typical SEM pictures of kilned malts from the protein-rich sample are shown in Figs. 5–7. Figure 5 shows some of the retained protein matrix with embedded small starch granules.

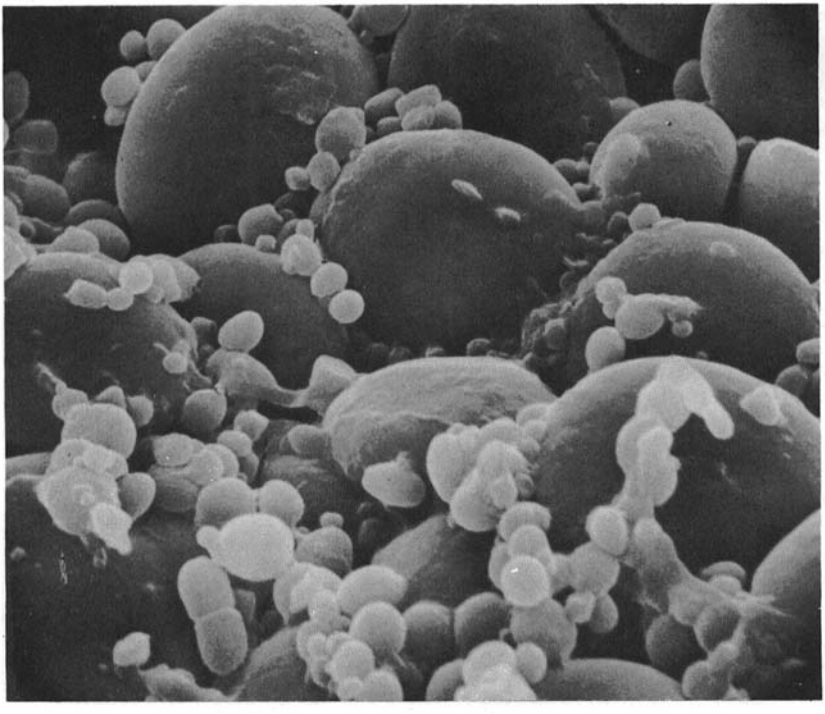

Fig. 5. Transverse section through malt from high-protein barley (2,300×).

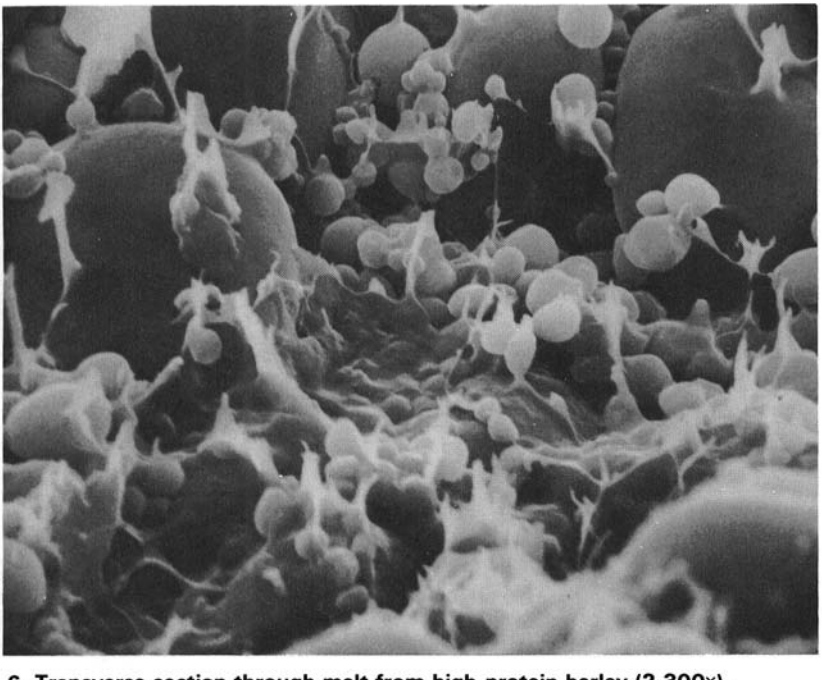

Fig. 6. Transverse section through malt from high-protein barley (2,300×).

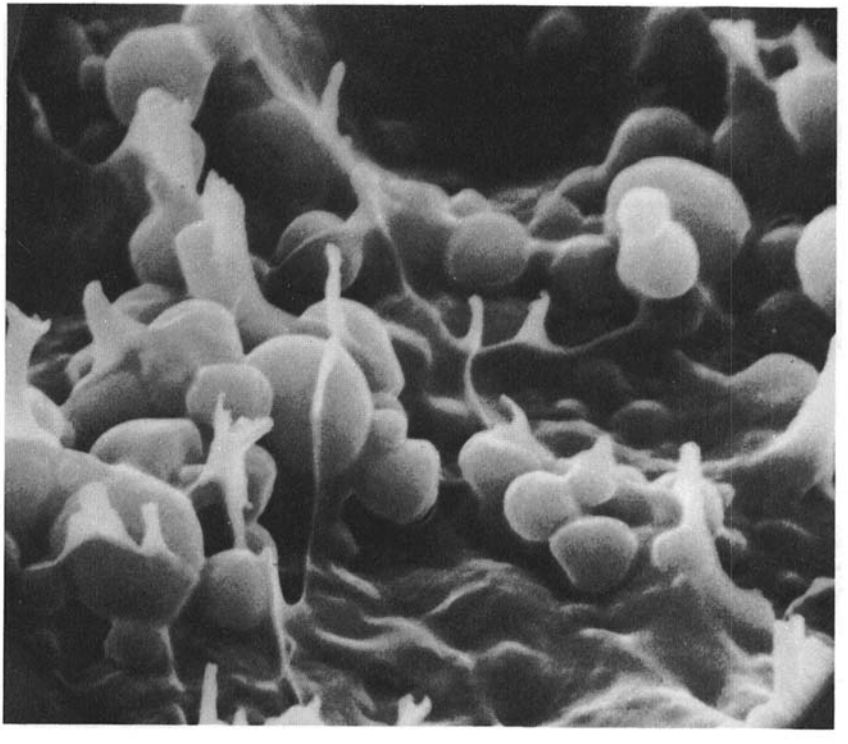

Fig. 7. Transverse section through malt from high-protein barley (5,500×).

Figures 5, 6, and 7 show little denatured protein is deposited on the surface of the starch granules (unlike in Fig. 2) and the surface of the large starch granules in malt from high-protein barley is relatively clean. On the other hand, some of the thick protein matrix is largely intact or retained in the form of a continuous thick film covering the starch granules (Figs. 6 and 7).

The data in Table I show that the malt from the high-protein barley contains almost twice the amount of insoluble protein contained in the low-protein barley (13.1 and 7.1%, respectively). Scanning electron microscopy shows that not only are there large quantitative differences in the concentrations and amounts of degraded proteins, but also that there are qualitative differences in the forms of degradation products. Those quantitative and qualitative differences might be responsible for difficulties in malting of high-protein barleys, reduction of wort extract, and persistence of undegraded proteins which enhance chill-haze formation in beer.

Literature Cited

1. MALTING BARLEY IMPROVEMENT ASSOCIATION. Malting barley-protein content.

Protein requirements for malting. The Association: Milwaukee, Wisconsin (1972).
2. STANDRIDGE, N. N., GOPLIN, E. D., and POMERANZ, Y. Evaluation of two-row and six-row malting barley. Brew. Dig. 45(12): 58 (1970).
3. BISHOP, L. R. Statistical studies of the analytical data accumulated in the course of barley investigations. I. The prediction of extract. J. Inst. Brew. 36: 421 (1930).
4. BISHOP, L. R. The proteins of barley during development and storage in the mature grain. The composition and quantitative estimation of barley proteins. III. J. Inst. Brew. 36: 336 (1930).
5. ANDERSON, J. A., and AYRE, C. A. Varietal differences in barleys and malts. I. Nitrogen distribution among protein fractions of barley. Can. J. Res. C16: 377 (1938).
6. ANDERSON, J. A., SALLANS, H. R., and MEREDITH, W. O. S. Varietal differences in barley and malts. XII. Summary of correlations between 18 major barley, malt, and malting properties. Can. J. Res. C16: 278 (1941).
7. REISENAUER, H. M., and DICKSON, A. D. Effects of nitrogen and sulfur fertilizer on yield and malting quality of barley. Agron. J. 53: 192 (1961).
8. DICKSON, A. C. Why maltsters and brewers require certain protein levels. Proc. Red River Valley Day: Grand Forks, N. Dak. (1964).
9. DOLEZALOVA, A., VRTELOVA, H., and TRKAU, M. Influence of protein content on barley quality. Kvasny Prum. 19(1): 3 (1973). [Abstr. in Brauwissenschaft 26(6): 199 (1973).]
10. POMERANZ, Y. Scanning electron microscopy of the endosperm of malted barley. Cereal Chem. 49: 5 (1972).
11. POMERANZ, Y., STANDRIDGE, N. N., and SHANDS, H. L. Functional and biochemical changes in maturing barley. I. Changes in malting and brewing characteristics. Crop Sci. 11: 85 (1971).
12. AMERICAN SOCIETY OF BREWING CHEMISTS. Methods of analysis. The Society: St. Paul, Minn. (1958).

[Received November 2, 1973. Accepted January 18, 1974]