Cereal Science and Malting Technology—The Future

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ABSTRACT

A detailed analysis of the endosperm of malting barley, using the friabilimeter and light and scanning electron microscopy, revealed that the patchy pattern of endosperm breakdown that can occur during malting is not readily detected by the friability tests or other methods of malt analyses. The tests performed indicated that increased knowledge of grain structure and function should not only improve the precision of currently used analytical methods but should also stimulate the development of better processing technologies. Greater analytical precision will make it possible for the maltster and brewer of the future to set more meaningful specifications from fewer analyses. One of the important consequences of this development will be that the malt specification of the future will provide a more reliable guide to the processing potential of malt in the brewhouse.

Keywords: Aleurone, Barley, Endosperm breakdown, Enzyme, Malt, Malt analyses.

Rather than reviewing previous studies, this article highlights certain important stages in the science-based technology of barley-malt production. Therefore, "looking back" is kept to a minimum except as an aid to conclusion and clarity. A number of important aspects of the science and technology of barley malt are discussed. However, it is evident that in the future other cereals such as sorghum and wheat may be malted in increased quantities (20, 24,25).

In barley-malt technology, the effectiveness of the use of a substance such as gibberellic acid (4,15,16,20) illustrates that the most efficient way of improving the performance of malting barleys is to ensure that processing procedures fit the scientific functions of the grain. This scientific approach to process control must extend from barley breeding to beer production. The failures of our recommended methods of analyses (1,6,13) to act as reliable guides to the malthouse behavior of barleys and the brewhouse performance of malts suggest that the scientific precision of these methods requires improvement. For the future, this important objective should not be avoided or ignored because of the difficulties associated with developing and using more precise analytical procedures in industry.

Now, although it is unwise to try to simplify scientific information, an attempt is made here to show that effective processing of barley and malt is controlled by the structural and functional properties of the grain, which must be understood if the industry is to continue to produce high-quality barleys, malts, and beers at economic prices.

Breeding for Barley Quality

Figure 1 shows some of the methods that are being used or considered for the production of malting barleys. Mutagen treatment has been successful in the past with regard to the production of the malting barley Golden Promise. Although this breeding method has failed to produce another barley variety of commercially acceptable quality, a recent publication indicates that a high-enzyme-producing mutant is being investigated (18). Gene transformation and tissue culture techniques (Fig. 1, Methods 2 and 4) have been proposed as the "high-tech" approach of introducing quality more quickly into barley during the breeding process. Transformed genes may offer improved disease resistance or winter hardiness or may even be capable of producing endosperm-degrading enzymes such as endo-β-1,3;1,4-glucanases that are more heat stable than the corresponding enzymes of the malted grain. Unfortunately, these techniques require further development to ensure that transformed genes complement quality and are stable (10,12). The use of restriction fragment length polymorphism as a technique (14,28) for identifying fragments of genetic material that carry useful genes for malting quality may indeed improve the precision of conventional plant breeding using parental crosses (Fig. 1, Method 1). However, irrespective of the merits of these new plant breeding methods, significant gene mutations in an advanced plant such as barley are likely to produce genetic changes, some of which may be beneficial while others may reduce expected quality. In this regard, the potential benefits of producing an anthocyanogen-free barley such as Galant were negated by the reduced capacity of the aleurone layer of this barley to produce the expected quantities of important endosperm-degrading enzymes such as endo-β-1,3;1,4-glucanase (21). Mindful of this, it is clear that all malting barleys produced by gross manipulation of genetic material should be tested rigorously before they are recommended for producing barley malt. In addition, industries such as the Scotch whisky industry may find unacceptable those barleys that contain genes transformed from microbial sources (20,29). At present, it is difficult to predict when mutagen, gene transformation, tissue culture, and double haploid techniques will be used routinely to produce new barley varieties (10,12,14,18,23,28,29). However, it is clear that the enhancement of the normal genetic qualities of conventionally bred malting barleys by applying appropriate processing techniques will, for the foreseeable future, be the most useful approach for improving the malting potentials of recommended malting barleys.

Grain Structure and Function and Malting Technology

Malting quality is a complex biological property of barley varieties. No single component of the grain should be used as an index of the overall quality. At present, three physiologically and structurally different areas of the grain have been cited as important centers of malting quality (Fig. 2). First, the embryo, as it germinates and grows into a seedling, produces the gibberellins that are transported to the aleurone layer (Fig. 3). Second, the aleurone layer is stimulated by the gibberellins from the germinated embryo to produce and secrete endosperm-degrading enzymes into the tissue of the starchy endosperm. Third, the cell walls and the small starch granule-protein matrix of the starchy endosperm are hydrated during steeping but act to limit the distribution and actions of the endosperm-degrading enzymes, most of which are released from the aleurone layer (20). Although the embryo and the aleurone layer exercise control as living tissues, the dead tissue of the starchy endosperm exercises control by

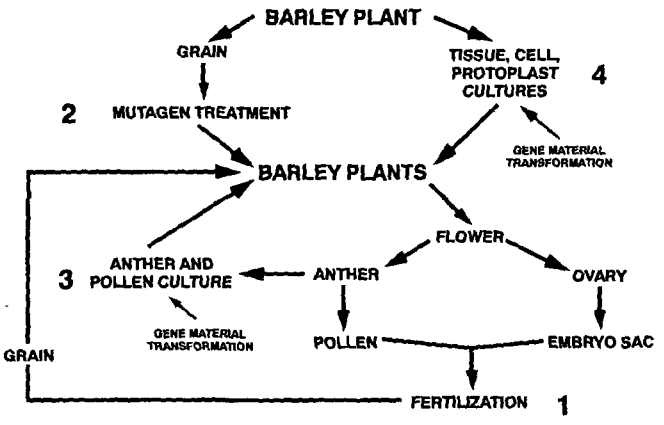

Fig. 1. Methods (1–4) of producing new barley varieties.

using its structure and the physicochemical properties of its substrates (Fig. 4) to limit the distribution and actions of endosperm-degrading enzymes.

Although these three physiologically important structures of the grain have a major influence on malting quality, variations in their functions in malting barleys are surprisingly not assessed during the determination of malting grades. Understandably, testing for these functions will be difficult; nevertheless, their physiological efficiency should be assessed, incorporated into the strategies of breeding programs, and used in the development of new malting procedures.

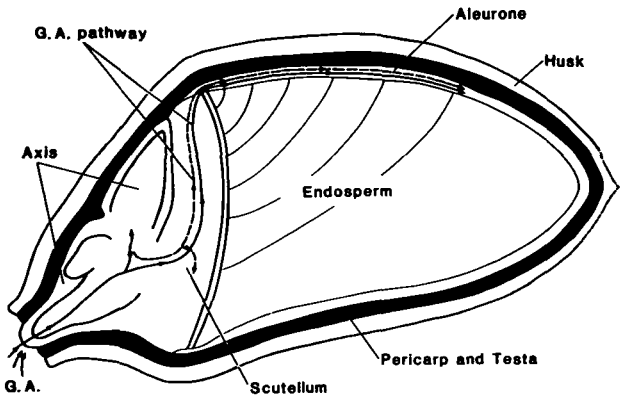

Fig. 2. Pathway of natural and exogenously applied gibberellic acid (G. A.). Note that the overall asymmetric pattern of endosperm breakdown is linked to the physiological consequences of the gibberellic acid-aleurone activity.

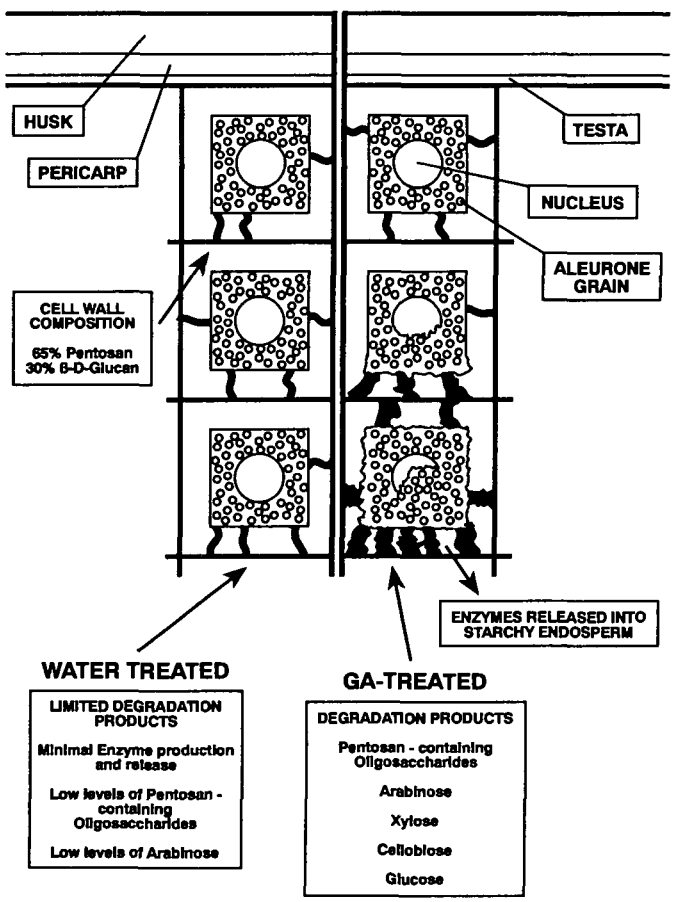

Fig. 3. Enzymatic degradation of the cell walls of aleurone cells. GA = gibberellic acid.

Germinative Potential and Embryo Quality

For the future, germinative potential will become even more critical, especially if the use of exogenously applied gibberellic acid declines. The embryo will be required to supply endogenous gibberellins of optimal quantity and quality to the aleurone layer (Fig. 2). Since initial root growth is linked to gibberellin production in the embryo and since excessive root growth causes unacceptable levels of malting loss (20), barleys that produce high concentrations of gibberellins but have limited root growth should be selected preferentially in breeding programs for this aspect of malting quality. The decline in the use of potassium bromate and the ability of abscisic acid to inhibit the development of endosperm-degrading enzymes of the aleurone layer leave the maltster with no acceptable means of controlling malting loss (20). The greater emphasis that will be placed on evenness of germination will cause maltsters to expect malting barleys to germinate at levels of 99–100%.

Dormant barleys will become even more unacceptable to the industry. Barley varieties that show long-term dormancy, irrespective of malting quality, are unlikely to be used in breeding programs. Although warm storage (30–40°C) of dried barley (11–12% moisture) can overcome dormancy, a more precise method for releasing malting barleys from dormancy is required to break short-term dormancy, which may usefully act to limit pregermination. Although the mechanism of dormancy is not understood (8,20), descriptive terms such as "water sensitivity" may have to be revised because physiologically, such barleys are sensitive to variations in oxygen levels rather than to an excess of water. Some types of dormancy may be caused by the restricting effects of the pericarp and testa or by the abilities of these layers to reduce the ingress of oxygen to the embryo (27). In the past,

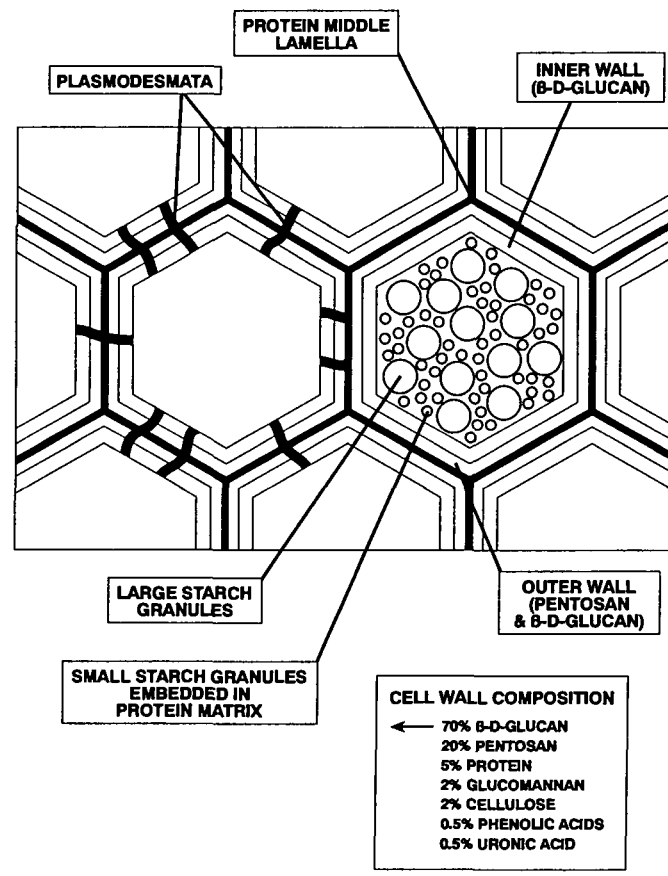

Fig. 4. Structure of cells of the starch endosperm of barley.

terms such as "covering layers" have referred to the pericarp and testa alone. Recent work by M. P. Cochrane at the Heriot-Watt University (*personal communication*) indicates that the aleurone, as a single layer of small cells, encloses the germ and may contribute to the dormancy-inducing function of the pericarp-testa. This work illustrates that our knowledge of the structure of the grain requires further development because the living cells of the aleurone may be involved not only in the synthesis of endosperm-degrading enzymes, but also in the dormancy mechanism or the oxygen ingress regulatory system of the germinating grain.

In barley breeding programs, if the embryo is selected for gibberellin potential (4,11), the aleurone layer should be selected for its capacity to respond to gibberellins (such as gibberellic acid) and to produce and secrete endosperm-degrading enzymes into the starchy endosperm (15–18,20,23,31). This is the physiological position held by the author for many years (20), and it is important for the industry to recognize that present "in-depth" research (12,18) confirms the simple concept that the aleurone layer of malting barley controls enzymatic breakdown of the starchy endosperm. Enzymes such as β-amylase and carboxypeptidase are found in the starchy endosperm of the ungerminated grain. The former is activated by proteolytic enzymes during malting. However, the mechanism of activation of the latter is not known. Major endosperm-degrading enzymes such as endo-β-1,3;1,4-glucanase, endoprotease, pentosanase, and amylase are produced in the aleurone layer (Figs. 2 and 3). In contrast, the potential of scutellar epithelial cells to produce and secrete technologically important quantities of endosperm-degrading enzymes has been proposed (17,19) but has been disputed on the grounds that morphological evidence does not support this view (see review, 20).

The recent shift in research emphasis from the scutellar epithelial cells to the aleurone layer (12) was long overdue and should lead to faster developments in malting technology. Physiologically, the aleurone layer of the grain does not respond uniformly to gibberellic acid stimulation. Recent studies (G. H. Palmer, D. H. Nimmo, and T. Shirakashi, *unpublished data*) show that the dorsal cells of the aleurone layers are more active than the ventral cells of the crease, or furrow. In addition, Figure 3 illustrates that the "inner" cells of the aleurone layer are more responsive to gibberellic acid activation in the intact grain than the "outer" cells (20). Table I also indicates that the aleurone areas associated with the embryo were more active than areas further away from the embryo (G. H. Palmer and N. M. Fischer, *unpublished data*). Taken together, these results suggest that although the aleurone layer contains similar cells, the overall response of this tissue to stimulation by gibberellins or gibberellic acid is not uniform. The results in Table I indicate that the aleurone layer of different barley varieties responded differently to the plant hormone and that differences in aleurone activities are not always reflected in the aleurone activities of the intact grain, possibly because of different degrees of physiological interactions between the embryos and their aleurone layers.

Future assessments of the malting qualities of barley varieties should include some knowledge of the potential of their aleurone layers to develop endosperm-degrading enzymes. This is extremely important in breeding programs, where a beneficial change in quality may be associated with deleterious changes that may, for example, reduce aleurone activity, as was the case with the proanthocyanogen-free barley, Galant (21). Because the embryo-induced gibberellin stimulation of the aleurone layer normally progresses from the very active embryo-attached aleurone to the less-active distally placed aleurone cells (Table I and Fig. 2), the abrasion process was developed to enable applied gibberellic acid to enter the distally placed aleurone cells at the beginning of the malting process. This technological improvement in gibberellic acid-aleurone physiology of the grains understandably accelerated enzymatic breakdown of the starchy endosperm of barleys (20).

In special situations, where barleys modify their endosperm very slowly, or where barleys have live aleurones but nonviable embryos, the abrasion process may find increased application in the future. Scientifically, the physiological effectiveness of the abrasion process suggests that transport of gibberellins in the aleurone is technologically slow and factors that cause high moisture losses from the aleurone layer during malting are likely to retard both the transport of gibberellins and the enzyme-producing activities of the aleurone layer; therefore, uneven enzymatic modification of the starchy endosperm will occur. For the future, malting conditions that optimize aleurone activity are likely to improve the evenness of modification and brewing qualities of malted barleys.

Recent studies (G. H. Palmer and D. H. Nimmo, *unpublished data*) show (Table II) that even in the presence of optimal levels of gibberellic acid, the enzyme-producing activity of the aleurone layer can be limited or improved by organic acids. The reasons for this observation are not yet clear. However, it may be possible that metabolic pathways involving certain organic acids may be operating suboptimally in the aleurone and could be improved by physiological or technical adjustments. If differences in the gibberellin-producing activities of the embryo (4,11) and in the enzyme-producing activities of the aleurone layer that influence malting quality are heritable, breeders should include them in their future plans for producing barleys of high malting quality.

TABLE I
Rates of α-Amylase Development in the Gibberellic Acid (GA)-Treated Aleurones and the Grains of Different Varieties of Barley (IDC[a] units per endosperm slice)

Barley Varieties	Aleurone Area[b] (24 hr)[c]			Aleurone Area[b] (42 hr)[c]			Grain[d] (96 hr)
	1	2	3	1	2	3	
Blenheim	1.8	0.5	0.0	10.0	3.5	6.5	104
Corniche	2.0	1.0	1.0	14.0	7.5	7.5	131
Grit	2.0	1.0	1.0	7.0	1.5	2.0	125
Golden Promise	2.0	0.5	0.5	8.0	8.0	10.0	98
Triumph	2.0	1.0	1.5	13.0	6.0	7.0	133
Plaisant	0.5	0.5	0.5	20.0	10.0	6.0	137

[a]IDC = iodine dextrin units (26).
[b]Slices cut from different regions of the endosperm: 1 = front (next to the scutellum), 2 = middle, 3 = distal.
[c]Incubation time at 18°C for endosperm slices in GA (0.25 μg/ml) (20).
[d]Dehusked (cold H_2SO_4), grown at 18°C in H_2O for 96 hours (20).

Enzymatic Modification of the Starchy Endosperm and Malt Quality

For over 25 years (20,22) the author has conducted a mixture of anatomical, physiological, and chemical studies of barley and malt to gain experience with and knowledge of the changes that cause enzymatic conversion of the endosperm of barley into malt or that indicate that such conversion has occurred. Important observations include: that only time-course studies give useful

TABLE II
Effects of Organic Acids on the Potential of the Aleurone Layer to Develop α-Amylase

Incubation[a] Media + GA[b]	α-Amylase Units per Aleurone
Water	23.0
1.0 m*M* Acetate	25.0
10 m*M* Acetate	14.0
10 m*M* Succinate	42.0
10 m*M* α-Ketoglutarate	44.0
10 m*M* Malonate	38.0
10 m*M* Fumarate	1.0

[a]66 hr at 25°C. Incubation medium (2 ml), containing 20 m*M* calcium chloride, pH 5.3.
[b]GA = Gibberellic acid (0.25 mg/L).

information of the patterns of enzymatic breakdown that occur in the starchy endosperm during malting; that high- and low-grade barleys contain similar levels of β-D-glucans; that during malting, β-D-glucan and the small starch granule-protein matrix are broken down faster than pentosans and the large starch granules; that enzyme levels of the malting grain do not correlate with the rate of enzymatic breakdown of the starchy endosperm; that variations in the basic structure of the starchy endosperm (illustrated in Fig. 4) are likely to limit hydration, enzyme distribution, and endosperm breakdown, causing some barleys to modify their endosperms unevenly; that malt analyses that include a milling stage can average and conceal differences in the degrees of endosperm breakdown, making it difficult to predict accurately the brewhouse performance of malt from laboratory analyses; that future improvements in the precision of malt analyses, and in the techniques of malting and brewing, are more likely to come from experimental science than from any other approach; and that improved precision of analytical methods will allow the maltster and the brewer to set fewer but more meaningful specifications that will give better guides to the malthouse behavior of barleys and to the brewhouse performance of malts.

The microscope is a very valuable analytical tool. However, one of the weaknesses of microscopic study is that the microscopist can only present a limited number of micrographs, which are really a summary of a vast amount of information and knowledge. In this context, Figure 5 illustrates that if the gross pattern of endosperm breakdown in the malting grain were asymmetric, the horizontal sections shown would give three different results of the state of enzymatic modification of one malt grain. On the other hand, if the pattern of breakdown were symmetrical, from the surface of the scutellum, similar horizontal sections would produce sections of the endosperm that would be modified equally. Since the results of sectioning the endosperm of the malting grain suggest that the pattern of enzymatic breakdown of the endosperm is asymmetric (20,27), more precise results could be obtained from the single-grain staining tests for malt modification (19,30) if malted grains were sectioned longitudinally, parallel to the furrow (crease). Improvements in the chemical specificities of these tests, as regards degrees of enzymatic hydrolysis of endosperm cell walls (7,20) and small starch granule-protein matrix materials, should

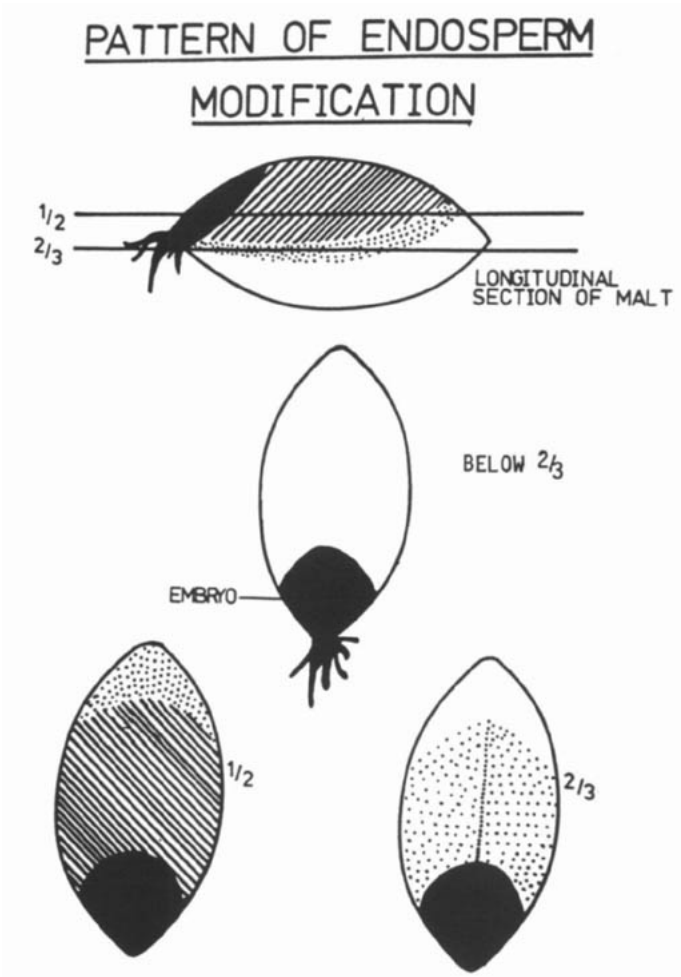

Fig. 5. Horizontal sectioning of an asymmetrically modified malt grain, showing different degrees of enzymatic breakdown of the endosperm.

TABLE III
Changes in Friability (%) of Malts at Different Levels of Protein

	Percent Protein		
Barley Varieties	**9.0**	**10.0**	**12.0**
Maris Otter	90.0	88.0	88.0
Triumph	90.0	85.0	81.0

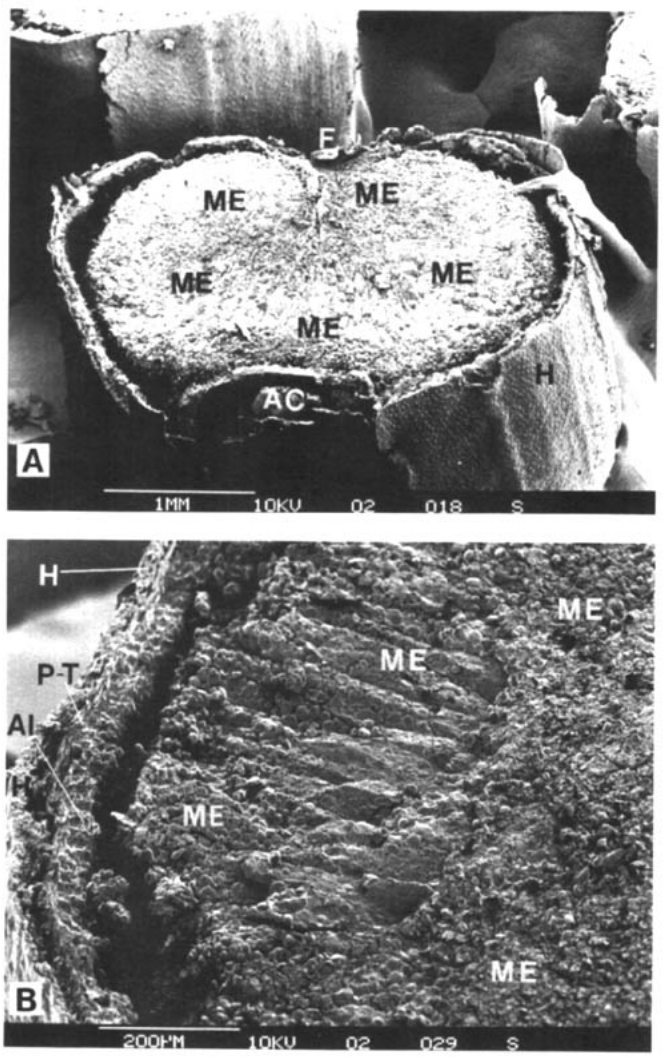

Fig. 6. Scanning electron micrographs of the endosperm of Maris Otter malt grain. **A**, transverse (vertical) cross section. Note that rapid enzymatic modification has removed endosperm cell walls (compare with Fig. 7A). **B**, Outer endosperm of the well-modified malt grain shown in **A**. Note inward progression of endosperm breakdown from the subaleurone and the absence of endosperm cell walls. ME = enzymatically modified endosperm, AC = acrospire cavity, H = husk, F = furrow (crease), P-T = pericarp-testa, Al = aleurone layer.

improve the precision of staining tests designed to assess enzymatic modification of the endosperm of malted barley.

The friabilimeter is used to assess the overall enzymatic modification of the starchy endosperm of a sample of malted barley (2,3,5). The quantity of flour released from malted barley is regarded as an index of the degree to which the endosperm had been modified enzymatically during malting. Despite the value of friability analyses (2,3,5), recent work in the author's laboratory suggests that the precision of the method is limited because partly modified malts can release undermodified flour that can be assessed wrongly as modified in the friability test. The results presented below summarize work done on the relationship between malt friability and the structural properties of the endosperms of barley and malt.

Table III shows that two malts with equal friability scores at 9% protein gave different scores as the protein content of the grains increased. Microscopic studies suggested that the less compact structure (see below) of the endosperm of the Maris Otter barleys gave higher and more consistent friability scores than the more compact starchy endosperm of Triumph barleys. These observations confirmed previous studies that indicated that, as the protein content of Triumph barleys increased, the number of small starch granules increased, causing greater compaction of the starchy endosperm (20). Although such endosperm compaction may seriously limit enzymatic breakdown of the endosperms of low-grade malting barleys, high-grade barleys that develop compaction of the starch granule-protein matrix in their endosperms at high protein content may modify more slowly than expected because of poorly understood limitations to hydration and to enzyme distribution and action in the starchy endosperm.

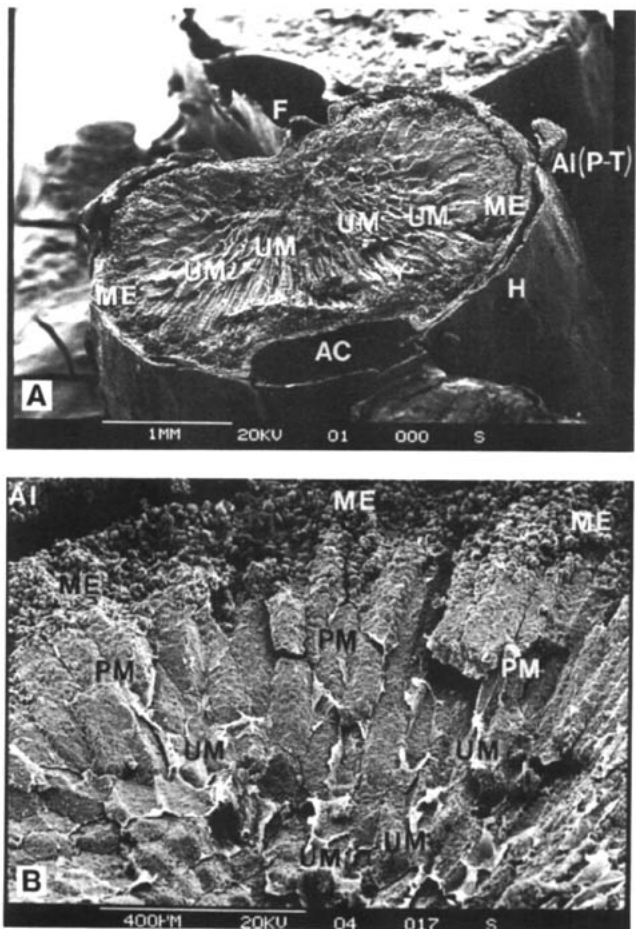

Fig. 7. Scanning electron micrographs of the endosperm of the slower malting barley variety Triumph. **A**,Transverse (vertical) cross section of the endosperm. Note the inward progression of enzymatic breakdown of the endosperm. **B**, Outer endosperm of the undermodified malt grain shown in **A**. Note the distinct inward progression of endosperm breakdown from the subaleurone and the presence of undermodified endosperm cell walls and small starch granules. AC = acrospire cavity, H = husk, ME = enzymatically modified endosperm, UM = undermodified endosperm, F = furrow (crease), AL = aleurone Layer, P-T = pericarp-testa, PM = partly modified endosperm.

Comparative microscopic studies of malts that modified readily (Fig. 6) and malts that modified more slowly (Fig. 7) suggested three important features of malt modification. First, enzymatic modification in the grain progressed from the subaleurone to the inner areas of the starchy endosperm (see Figs. 6B, 7B). However, cell wall breakdown in the starchy endosperm can occur faster than starch-protein matrix breakdown, suggesting that β-glucan levels may be an important but not a totally reliable index of overall endosperm modification (Figs. 7B and 8). In addition, malts with vastly different degrees of endosperm breakdown can have similar extents of acrospire growth (compare acrospire cavities in Figs. 6A and 7A).

From these and other microscopic studies (20) it was reasoned that the friabilimeter may cause partly modified or even unmodified pieces of endosperm to pass into the friable flour fraction and be wrongly assessed as modified. During these studies, four malts were received from a large brewing company. Two of the malts (numbers 1 and 2, Table IV) retarded wort separation even

Fig. 8. In some malted grains, small starch granule-matrix protein breakdown may not occur simultaneously with endosperm cell wall hydrolysis. Note absence of cell walls. SL = large starch granules, S_s-P = small starch granule-protein matrix.

TABLE IV
Percent Particle Size Distribution of 50 g of Friable (Modified) Flour from Commercial Malts

	Type of Malt and Malt Number				
		Retarded Wort Separation		Normal	
Sieves[a]	Check Malt	1	2	3	4
>1 mm	39.8	36.4	31.9	33.1	37.5
710 μm	26.6	23.8	25.0	23.9	24.6
500 μm	12.8	12.2	13.2	13.2	13.1
355 μm	6.9	7.0	7.5	7.7	7.1
250 μm	5.3	5.2	5.6	6.2	5.3
180 μm	3.4	4.9	7.0	4.5	3.7
90 μm	3.7	5.4	5.9	5.6	4.5
<90 μm	1.4	4.9	3.9	5.7	4.1
Friability, %	88.0	85.0	93.0	90.0	88.0

[a]Shaken for 30 min.

though they had acceptable friability scores similar to those of two other malts (numbers 3 and 4, Table IV). In a departure from the routine test for friability, 50 g of friable flours of the five malts shown in Table IV were collected and then fractionated by shaking them through a series of Endecott sieves for 30 min (G. H. Palmer, N. Singh, and A. K. Main, *unpublished data*). The particle size distribution of the friable flours is presented in Table IV. It is clear that particle size distribution did not correlate with friability scores and that, except for particle sizes greater than 1 mm, the particle size distributions of the friable flour of all the malts were surprisingly similar, irrespective of the friability scores or the brewhouse performances of the malts from which they were collected. β-D-Glucan was determined using a Biocon kit (Megazyme, Sydney, Australia). Friable flour (2 g) was extracted by stirring in 20 ml of water at 65°C for 1 hr. The mash (extract) was centrifuged at 4,000 rpm for 10 min, and the filtered (Whatman 113v filter paper) supernatant was analyzed for β-glucan. β-Glucan levels of the sieved fractions (Table V) indicated no specific trends but showed that the malts that caused the wort separation problems (numbers 1 and 2) had the flour fractions that contained the highest levels of β-D-glucan. In addition to these observations, it was surprising to observe that particles of the friable flour of seemingly well-modified malts could have had such inconsistent and variable levels of β-D-glucans.

To determine whether the friable flours that were released from barley malted for one to five days were modified to similar degrees, Pipkin barley was steeped by submersions and air rests at 13°C: 10 hr wet, 14 hr air rest, 9 hr wet, 14 hr air rest, and 9 hr wet. The immediate out-of-steep moisture was 48%. The barley was germinated at 15.5°C. Green malt samples selected at the day 1 to day 5 stages of malting were kilned at 65°C for 18 hr and derooted. The friability scores and the distribution of particle sizes in 50-g samples of the friable flours were assessed by sieving as before (Table IV). Table VI shows that, except for the >1-mm fraction of the day 1 malt, the particle size distributions of the "modified" (friable) flour of undermodified or modified malts were again surprisingly similar. In terms of friability scores and hot-water extract values, only the day 5 malt sample was suitably modified, yet it is evident from the results in Table VI that the undermodified malts (days 1–4) released friable flours of similar particle sizes. Results in Table VII show that the fractions of the friable flours of the undermodified malts (days 1–4) contained significantly more β-D-glucans than the corresponding flour fractions of the modified (day 5) malt. The technological consequences of these observations have not yet been assessed. However, it is evident that during the friability test undermodified malts can release undermodified endosperm flour that will pass into the friable flour fraction and be wrongly assessed as enzymatically modified. In this regard, the two malt samples (numbers 1 and 2, Table IV) that impeded wort separation in a commercial brewhouse were likely to have contained undermodified endosperm areas, in spite of their high friability scores and acceptable analytical values that met the specifications set by the brewer.

Microscopic examination of the endosperm particles of the friable flour showed that many contained undermodified cell walls

TABLE V
β-D-Glucan Contents (mg/100 g) of the Friable Flour Fractions of Commercial Malts[a]

Sieves[b]	Check Malt	Type of Malt and Malt Number: Retarded Wort Separation 1	Retarded Wort Separation 2	Normal 3	Normal 4
>1 mm	14.5	96.4	67.9	23.2	19.6
710 μm	54.1	67.9	99.3	64.3	28.0
500 μm	30.2	31.2	43.5	12.8	12.7
355 μm	30.0	12.8	46.4	13.0	1.4
250 μm	49.8	75.6	69.3	42.0	43.2
180 μm	54.4	49.0	50.0	52.4	33.8
90 μm	38.9	10.9	39.1	19.6	28.0
<90 μm	40.6	13.0	41.3	34.5	25.1

[a] β-Glucan determined using a Biocon kit (Megazyme, Sydney, Australia).
[b] Sieves shaken for 30 min.

TABLE VI
Percent Particle Size Distribution (%) of 50 g of Friable (Modified) *Flour of Malt Samples*

	Days of Malting (Germination and Growth) 1	2	3	4	5
Friability, %	3.0	23.0	58.0	77.0	85.0
Extract, %	...	...	75.0	78.0	80.0
Sieves[a]					
>1 mm	42.4	38.8	36.5	36.4	38.6
710 μm	19.0	19.4	18.3	19.3	21.1
500 μm	12.4	12.8	12.3	12.4	12.1
355 μm	8.6	8.5	7.9	8.2	7.1
250 μm	6.8	6.9	7.1	6.9	5.6
180 μm	4.7	4.7	7.0	4.9	5.2
90 μm	4.1	4.9	4.4	5.2	4.2
<90 μm	2.0	3.6	6.5	6.7	6.1

[a] Sieves shaken for 30 min.

TABLE VII
β-Glucan Contents[a] (mg/100 g) of Friable Fractions of Day 1 to Day 5 Malts

Sieves	Days of Malting (Germination and Growth) 1	2	3	4	5
>1 mm	189.8	266.6	259.3	81.8	35.2
710 μm	674.0	321.5	174.2	84.2	35.2
500 μm	775.5	455.6	181.6	48.3	18.8
355 μm	565.2	519.4	136.6	77.7	21.6
250 μm	380.4	418.8	180.8	72.8	23.7
180 μm	167.7	756.6	180.8	72.8	23.7
90 μm	265.0	676.5	217.6	79.3	34.3
<90 μm	...	345.2	114.5	67.9	43.3

[a] β-Glucan determined using a Biocon kit (Megazyme, Sydney, Australia).

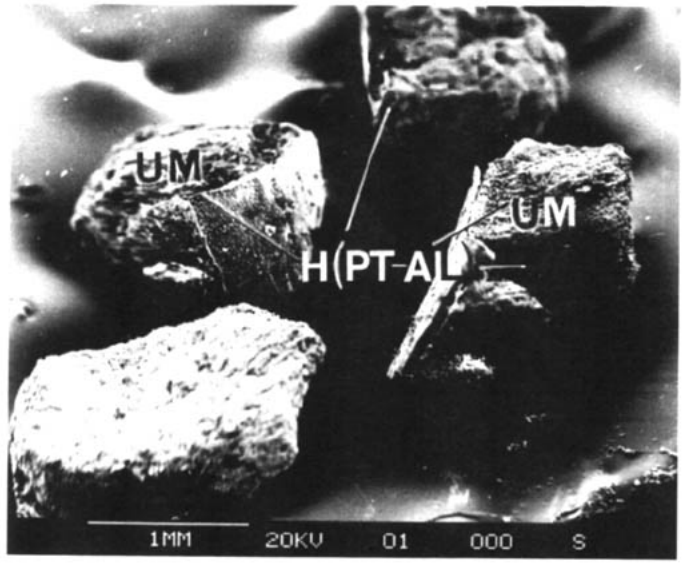

Fig. 9. Enzymatically undermodified endosperm (UM) particles from the "modified" (friable) flour of a commercial malt sample. H(PT-AL) = husk (pericarp-testa and aleurone).

and small starch granule-protein matrix materials (Figs. 9 and 10), confirming the β-D-glucan results presented in Tables V and VII. Microscopic examination (Fig. 9) showed that undermodified endosperm particles could be, but didn't have to be, associated with aleurone and husk tissue, depending on their locations in the endosperms of malted grains. Scanning electron microscopic studies of the cut surfaces of troublesome commercial malts that caused wort separation and beer filtration problems indicated (Fig. 11) that discrete areas of undermodified tissue were present in the starchy endosperm of malted barley that met brewers analytical (laboratory) specifications (22). Since it was not possible to explain how these enzymatically resistant tissue areas developed in the endosperm during malting, the barley endosperms of malts that developed these localized areas of undermodification were examined. Figure 12A depicts the endosperm structure of the barley that produced the malts shown in Figure 11. The compact tissues and the loosely packed tissues of the endosperm of the barley outlined in Figure 12A are shown at higher magnification in Figure 12B. It is not clear why such differences in the tissue structures of the starchy endosperm develop during the formation of the grain. However, observations of the malting performance of barleys that had mixtures of compact and loose endosperm tissue suggested that such barleys should be malted using submersion steeping and air rest regimes, which encourage more even hydration and better enzyme distribution and action in the endosperm during malting (20,26). Spray steeping tends to encourage the potentially uneven enzymatic digestion inherent in endosperms that have mixtures of compact and loose tissue structures (Fig. 12). Loose or mealy endosperm tissues have been described as having more free space than corresponding compact or steely tissues (20,27).

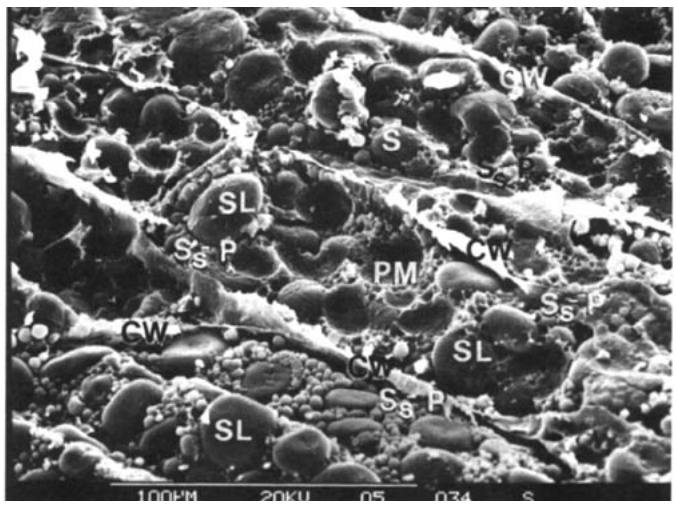

Fig. 10. Undermodified endosperm of a particle from the "modified" (friable) flour (Fig. 9). Note undermodified cell walls (CW) and small starch granule-protein matrix (S_s-P). PM = protein matrix, SL = large starch granule, S = starch.

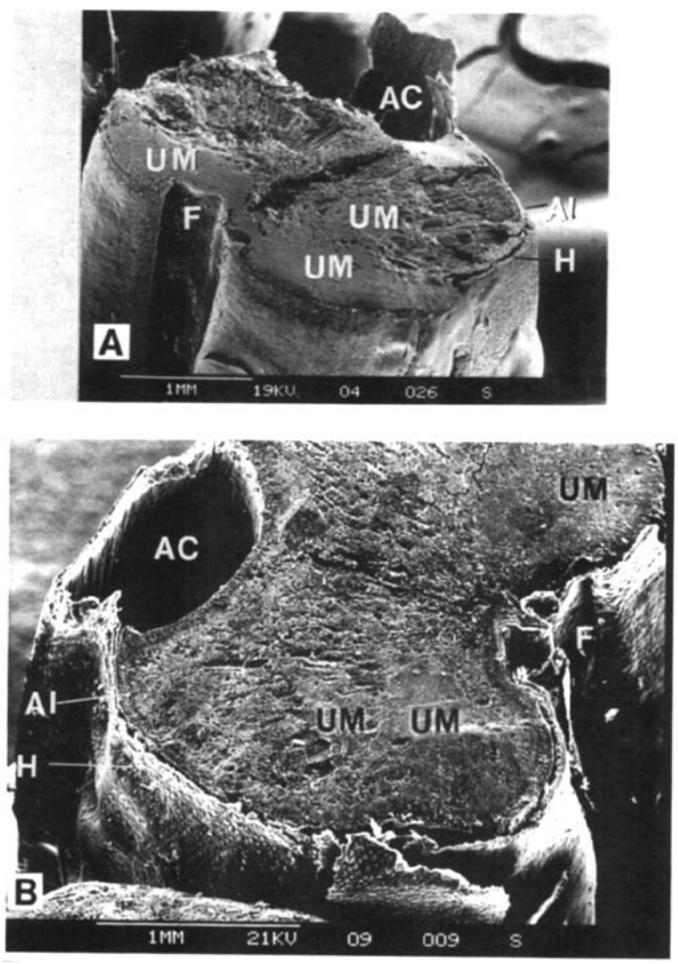

Fig. 11. Scanning electron micrographs showing undermodified basal areas of the endosperm of a malted barley grain. AC = acrospire cavity, UM = enzymatically undermodified endosperm, F = furrow (crease), Al= aleurone, H = husk.

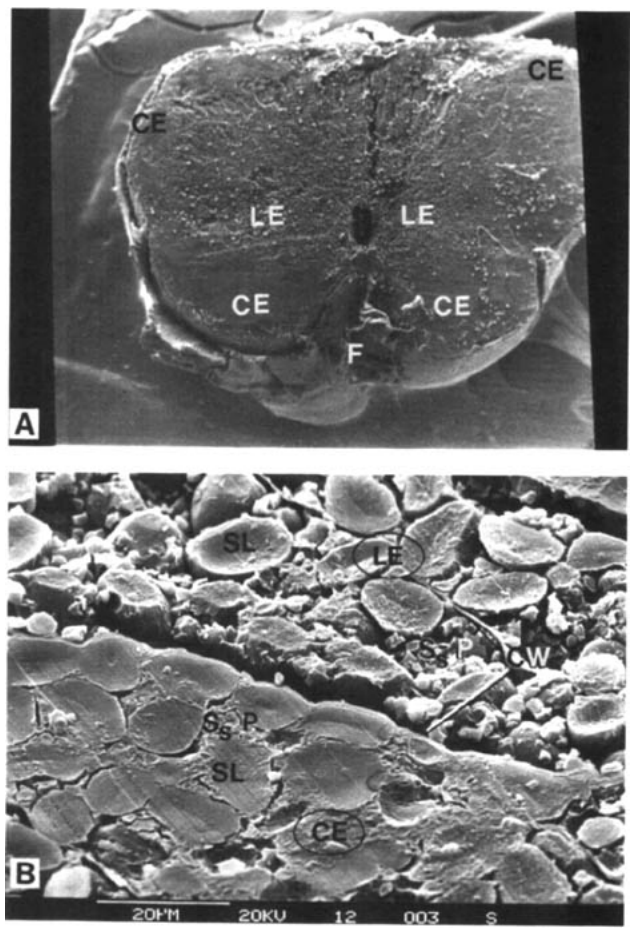

Fig. 12. A, Scanning electron micrographs of endosperm of barley from which the undermodified malts in Fig. 11 were made. Note compact endosperm (CE) tissue of outer endosperm and basal endosperm areas. **B,** transition from compact to loose endosperm tissues of barley shown in A. LE = loose endosperm tissue, F = furrow (crease), SL = large starch granules, S_s-P = small starch granule-protein matrix, CW = cell wall.

Although scanning electron microscopic analyses clearly indicated that localized undermodified tissue can be found in the endosperms of seemingly well-modified malts, and that such discrete areas are not readily detected by conventional malt analyses (22), a better means of locating these undermodified areas in malted barley was achieved using the light microscope. Similar transverse slices of malt (Figs. 13A and B) were examined using transmitted light. Undermodified areas appeared illuminated and corresponded to the compact areas previously observed in malts using the scanning electron microscope (Fig. 11). Figure 13C shows the corresponding undermodified area as dark tissue when incident light was used to examine the endosperms of unevenly modified malts. Figure 14, in which the undermodified compact tissue is illuminated, confirms that the tissue areas of the starchy endosperm that resisted enzymatic breakdown (modifications) during malting (Figs. 11 and 13) were compact tissue (compare Fig. 12A) that was present in the barley from which the malt was produced.

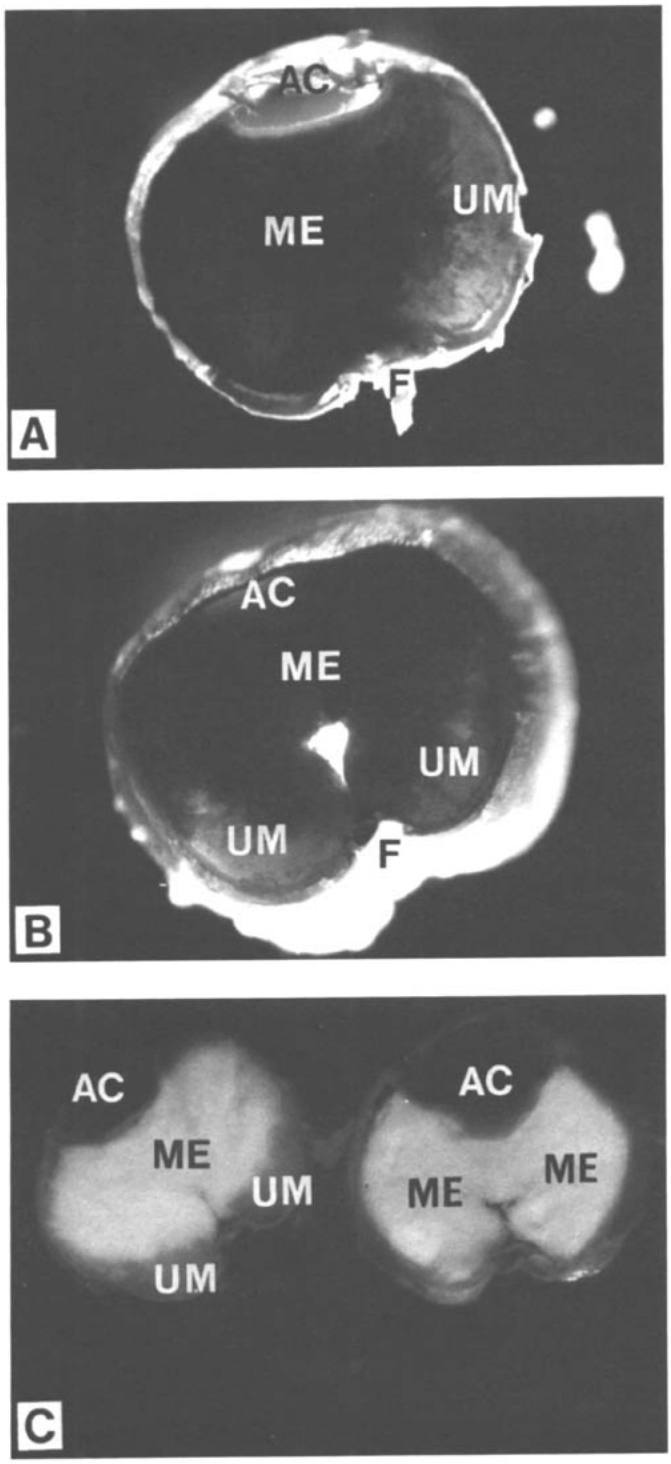

Fig. 13. Light micrographs of unevenly modified endosperms of light-illuminated cross-sections of malted barley. Note discrete areas of enzymatically undermodified tissue. AC = acrospire cavity, ME = enzymatically modified endosperm, UM = enzymatically undermodified endosperm, F = furrow (crease).

It is not clear how or why these enzymatically resistant tissue areas are formed in the endosperms of barleys during grain development. However, observations of malting barleys that developed these resistant areas of endosperm tissue indicated that grains with high protein content in drought years had a high tendency to develop this kind of small, extreme compaction of starch granule-matrix protein in their starchy endosperms (20). The structure of these compact and enzymatically resistant tissue areas of the endosperms of barley and malt require further investigation (20,22).

Thoughts on Endosperm Structure and Malt Quality

The above study has indicated that localized unevenness of enzymatic modification (breakdown) of the endosperm of malted barley that could have serious processing implications for the brewer cannot be detected reliably by present methods of malt analyses (22). The consequences of using such unevenly modified malts could include retarded wort separation; slow beer filtration; and nonbiological hazes caused by unevenly degraded endosperm cell wall, starch, and protein materials (20). Although some brewers use commercial endosperm-degrading enzymes to counteract the problems caused by uneven malt modification, it is clear that in the future barley breeders should try to produce barleys that do not develop these endosperm defects readily, even in the most unfavorable field conditions. However, if such malting barleys cannot be bred, then appropriate steeping and malting procedures must be developed to eliminate uneven endosperm breakdown (26). Indeed, the "wide quality" of a malting barley may reflect its genetic abilities to maintain its quality in a range of environments.

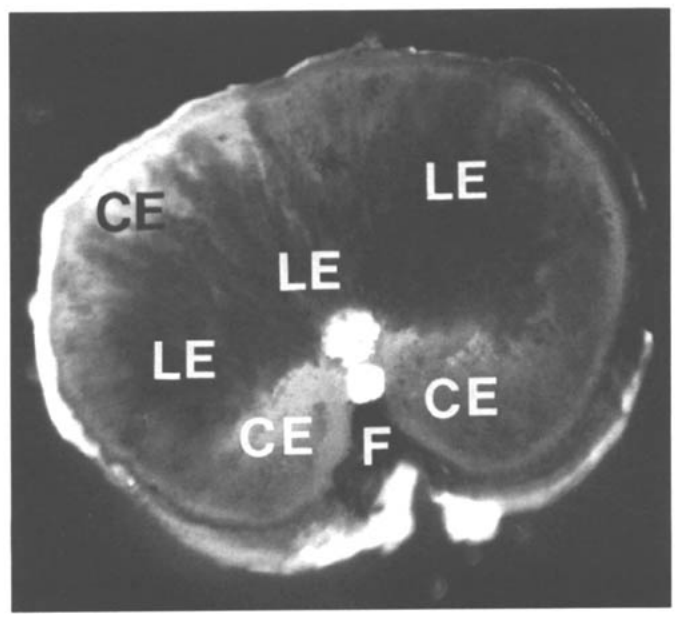

Fig. 14. Light micrograph of endosperm of the barley from which the undermodified malts in Figs. 13A and C were made. Note compact tissue of the outer endosperm and basal endosperm areas. CE = compact endosperm tissue, LE = loose endosperm tissue, F = furrow (crease).

The results from previous (20,22,26) and presented studies of the pattern of enzymatic breakdown of malting barley have led the author to conclude that efficient aleurone activity, and the overall distribution and action of endosperm-degrading enzymes in the starchy endosperm, are crucial factors in malting efficiency. Additionally, the uniformity of endosperm breakdown, which can be influenced by steeping treatment, is linked to the structure of the endosperm of the barley from which the malt is made. Regarding the mechanisms of endosperm breakdown, results from the friabilimeter studies indicate that, during malting, enzymatic disaggregation of the endosperm precedes "complete" enzymatic modification of such disaggregated but undermodified endosperm tissue (Tables VI and VII, Figs. 7 and 8). In partly modified malts, the friabilimeter can grind down undermodified disaggregated tissue, causing an overestimation of the degree of enzymatic modification of a malt sample. At present no analytical methods can distinguish these troublesome undermodified fractions when they are present in unevenly modified malts (see Figs. 8 and 13B and C).

Until the breeder can produce trouble-free barleys, increased knowledge of the science of the malting grain should be used to develop more precise methods of analysis and better malting procedures. The scientific approach here should not just be "high-tech"; it should be relevant to the needs of the industry.

Future Considerations

Efficient technology is based on relevant scientific input. In this regard, recent technological development such as modern mash filters or lauter tuns whose functions are described physically in terms of the Darcy's equation (9,32), are unlikely to show optimal efficiency until the physicochemical influences of the physiologically undermodified tissues of the endosperm of malt are included in their principles of operation. Increased knowledge of the physiological mechanisms of endosperm breakdown will help the brewer to set more meaningful specifications using fewer but more precise analyses. In this regard, the more analyses we have, the more difficult they become to interpret. Specifications should not only reflect contractual agreement; they should indicate the brewhouse processing potential of the malt. This important link between scientific principles and specification can be illustrated by the following example: For a sample of barley of known protein content and corn weight, the enzymatic modification of the derived malts should improve if the levels of hot water extract are kept constant or increased, as the values for total soluble nitrogen are reduced. In addition, a sample of malt that has a higher-than-expected color and a lower-than-expected hot water extract is likely to be unevenly modified. Although some of the traditional malt analyses will still be of value in the near future, improved precision of tests designed to assess evenness of endosperm modification and the uniformity of cell wall and small starch granule-matrix protein breakdown will enable maltsters and brewers of the future to produce high-quality malts and beers, respectively, more efficiently and more economically than hitherto. Finally, Figure 15 outlines some of the scientific properties of the malting grain that determine malt quality. The simplicity of this figure belies the considerable amount of thought and experimental work from which it was constructed (20). Figure 15 also indicates some of the research that should be conducted in the future to provide the industry with the knowledge it needs to develop the analytical and processing technologies required to maintain quality and efficiency.

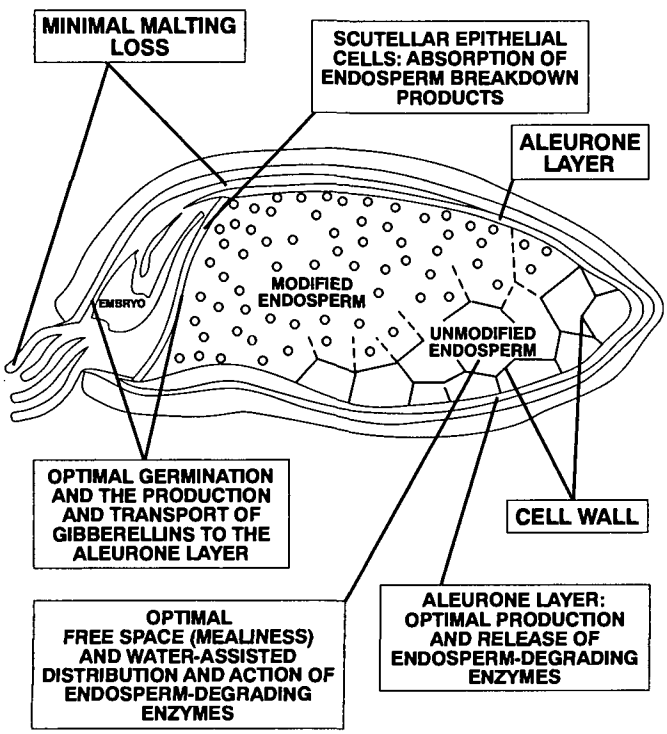

Fig. 15. Grain structure and function—tissue areas for control and optimization during malting.

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LITERATURE CITED

1. American Society of Brewing Chemists. *Methods of Analysis*, 7th ed. The Society, St. Paul, MN, 1976.
2. Baxter, E. D., and O'Farrell, D. D. Use of the friabilimeter to assess homogeneity of malt. *J. Inst. Brew.* 89:210-214, 1983.
3. Chapon, L., Erber, H. L., Kretschmer, K. F., and Kretschmer, H. L. The friabilimeter in the service of quality and efficiency in malting and brewing. *Brauwissenschaft* 33:1-11, 1980.
4. Cohen, D., and Paleg, L. G. Physiological effects of gibberellins. X. The release of gibberellinlike substances by germinating barley embryos. *Plant Physiol.* 42:1288-1296, 1967.
5. Cooper, J. N. Analysis of non-friable residues remaining from friabilimeter treatment of Scottish distilling malts. *J. Inst. Brew.* 92:255-261, 1986.
6. European Brewery Convention. *Analytica*, 4th ed. Brauerei und Getränke Rundschau, Zurich, 1987.
7. Fincher, G. B., and Stone, B. A. Cell walls and their components in cereal grain technology. In *Advances in Cereal Science and Technology*, vol. 8. Y. Pomeranz, Ed. Am. Assoc. Cereal Chem., St Paul, MN. pp. 207-295, 1986.
8. Goldbach, H., and Michael, G. Abscisic acid content of barley grains during ripening as affected by temperature and variety. *Crop Sci.* 16:797-799, 1975.
9. Hermia, J., and Rahier, G. Theoretical principles underlying the design of a new wort filter. In *Proc. J. de Clerck Chair IV*—Raw Materials and Sweet Wort Production. University Catholique de Louvain, Louvain, Belgium, 1990. (In press.)
10. Holm, P. B., Olsen, F. L., and Knudsen, S. Micro-injection, electroporation and particle bombardment as tools in the establishment of a transformation system for barley. *Eur. Brew. Conv. Symp. on Plant Biotechnology*. Monogr. 15. Helsinki, 1989, pp. 16-31.
11. Horgan, R. The evaluation of Clipper barley. *Inst. Brew. Aust. N.Z. Sect. Proc. Conv.* 11:60-70, 1970.
12. Ingversen, J. Improvement of malting barley quality. *Eur. Brew. Conv. Proc. Congr. 23rd, Lisbon, 1991*, pp. 77-84.
13. Institute of Brewing. Recommended Methods of Analysis. Institute of Brewing, London, 1986.
14. Jack, P. L. Application of DNA probes (RFLPs) in barley breeding. *Eur. Brew. Conv. Symp. on Plant Biotechnology*. Monogr. 15. Helsinki, 1989, pp. 130-136.
15. Jacobsen, J. V., Higgins, T. J. V., and Zwar, J. A. Hormonal control

of endosperm function during germination. In *The Plant Seed: Development, Preservation and Germination.* I. Rubinstein, R. L. Phillips, C. G. Green, and B. G. Gegenbach, Eds. Academic Press, London. pp. 241-262, 1979.
16. MacLeod, A. M., Duffus, J. H., and Johnston, C. S. Development of hydrolytic enzymes in germinating grain. *J. Inst. Brew.* 70:521-528, 1964.
17. McFadden, G. I., Ahluwalia, B., Clarke, A. E., and Fincher, G. B. Expression sites and developmental regulation of genes encoding (1-3,1-4)-β-glucanases in germinated barley. *Planta* 124:500-508, 1988.
18. Molina-Cano, J. L., Rubio, A., Royo, C., Ramo, T., Perez-Vendrell, A., and Palmer, G. H. Genetic changes and physiological responses of malting barley mutants. *Eur. Brew. Conv. Proc. Congr. 23rd, Lisbon, 1991*, pp. 69-76.
19. Munck, L., Gibbons, G., and Aastrup, S. Chemical and structural changes during malting. *Eur. Brew. Conv. Proc. Congr. 18th, Copenhagen, 1981*, pp. 11-30.
20. Palmer, G. H. Cereals in malting and brewing. In *Cereal Science and Technology.* G. H. Palmer, Ed. Aberdeen University Press, Aberdeen, Scotland. pp. 61-242, 1989.
21. Palmer, G. H. Enzyme development in the embryos of Galant and Triumph barleys. *J. Inst. Brew.* 94:61-63, 1988.
22. Palmer, G. H. New technology and process control. In *Proc. J. de Clerk Chair IV*: Raw Material and Sweet Wort Production. University Catholique de Louvain, Louvain, Belgium, 1990. (In press.)
23. Palmer, G. H. Physiology of barley quality. *Eur. Brew. Conv. Symp. on Plant Biotechnology.* Monograph 15. Helsinki, 1989, pp. 101-118.
24. Palmer, G. H. Sorghum: Food, beverage and brewing potentials. *Process Biochem.* 27:145-153, 1992.
25. Palmer, G. H., Etokakpan, O. U., and Igyor, M. A. Review: Sorghum as brewing material. *Mircen J. Appl. Microbiol. and Biotechnol.*. 5:265-275, 1989.
26. Palmer, G. H., Gernah, D. I., McKernan, G., Nimmo, D. H., and Laycock, G. Influence of enzyme distribution on endosperm breakdown (modification) during malting. *J. Am. Soc. Brew. Chem.* 42:17-28, 1985.
27. Palmer, G. H., Shirakashi, T., and Sanusi, L. A. Physiology of germination. *Eur. Brew. Conv. Proc. Congr. 22nd, Zurich, 1989*, pp. 63-74.
28. Sage, G. C. M. Cereal breeding and quality. In *Cereal Science and Technology.* G. H. Palmer, Ed. Aberdeen University Press, Aberdeen, Scotland. pp. 37-60, 1989.
29. Thomsen, K. K. Engineering of heat stable (1-3, 1-4)-β-glucanase for insertion into barley by transformation. *Eur. Brew. Conv. Symp. on Plant Biotechnology.* Monogr. 15. Helsinki, 1989, pp. 137-145.
30. van Eerde, P. Are you familiar with your malt? A modernised malt quality control method. *J. Inst. Brew.* 89:195-199, 1983.
31. Varner, J. E. Mode of action of plant hormones. *Int. Rev. Biochem.* 20:189-218, 1978.
32. Wilkinson, N. R. Process plant design. *Ferment* 4:388-401, 1991.

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