

# Malting Oats: Effects on Chemical Composition of Hull-less and Hulled Genotypes

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## ABSTRACT

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Samples of hull-less oat genotypes from the Cooperative Naked Oat Test grown in Ottawa, ON, and Aberdeen, ID, were analyzed for their potential as a food malt. Malted oats had a lower concentration of petroleum ether-extractable lipid, but a much higher percentage of the lipid was in the form of free fatty acids. About 5% less starch and slightly more N was found in malted oats than in unmalted. Malted oats contained ≈8% soluble carbohydrate. During the germination phase of malting, nearly all the  $\beta$ -glucan was degraded.  $\alpha$ -Amylase activity of

malted oats approached that of malting barleys, but diastatic power was much lower. Groats of hulled cultivars grown at Madison, WI, were malted and analyzed with similar results. Because the increased levels of free fatty acids in the malted grains may lead to the development of rancid flavors, a method to curtail their increase or selections of genotypes with a minimum increase during malting may be necessary to produce a useful malted food product.

Malted barley, in addition to its major use for brewing beer and distilled spirits, has long been used in the food industry as a source of flavor, color, sweetness, enzymes, and other nutritional components (Bamforth and Barclay 1993). Bhatti (1996) investigated the properties of malted hull-less barley as a food malt. An advantage of hull-less as compared to hulled barley is that the malt can be used directly in foods without the necessity of preparing extracts or syrups.

Recent interest in breeding hull-less oats in Europe, Australia, Canada, and the United States has led to the release of a number of improved cultivars that compete more favorably with standard hulled cultivars (Valentine 1995, Barr et al 1996). Impediments to the commercialization of hull-less oats are lower yield, incomplete expression of the hull-less character, and the entrenched capacity of the oat milling industry for using hulled oats. Chemical composition and energy values of hull-less oats were tabulated by Valentine (1995). Several reports indicate that hull-less oats are a favorable feed for various ruminant and nonruminant animals (Givens and Brunnen 1987, Farrell et al 1992, Schrickel et al 1992, Cave and Burrows 1993), but the potential of hull-less oats for human food or industrial products is largely unexplored (Burrows et al 1992).

Malted hull-less oats could be used in food products such as specialty breads, cookies, confectionery, and prepared breakfast cereals (Valentine 1995). Previous studies on malting hulled oats examined the effects of gibberellic acid on enzyme activity and other characteristics relative to malted barley and other cereal grains (Palmer 1970, Pomeranz and Shands 1974).  $\alpha$ -Amylase activity of malted oats was similar to that of malted barley, but diastatic power (DP) of oats was considerably lower. Malt extract of oats was low relative to that of barley (Pomeranz and Shands 1974), possibly due to a combination of greater hull percent and higher protein concentration in oats. Phytate was reduced in oats by malting but not as much as in other grains (Larsson and Sandberg 1992). High levels of phytate in oat food products may reduce mineral absorption.

The purpose of this research was to determine the effects of malting on the composition of several hull-less oat genotypes to

evaluate the potential of malted oats for food or industrial uses. The results were compared with analyses of groats from a set of hulled cultivars that were malted in a similar fashion.

## MATERIALS AND METHODS

### Samples

Single samples of 31 hull-less oats were obtained from the 1993 Cooperative Naked Oat Test grown in Ottawa, ON. The samples included two cultivars and 29 lines (two subsequently released as named cultivars) from several plant breeding programs in the United States and Canada. Likewise, single samples of 15 genotypes were obtained from the 1995 Cooperative Naked Oat Test grown in Aberdeen, ID. Seven of these genotypes were common to both sample sets (Baton, Pennuda, MF9018-11801, MF913-148, 87Ab5932, 88Ab3073, and 90Ab1500). Samples of 10 hulled cultivars were obtained from the 1995 crop grown at Madison, WI. These were dehulled with an impact-type dehuller, and the groats were malted and analyzed.

### Malting

Approximately 85 g of oats were steeped in 16°C water to 45% moisture (16 hr) with a 0.5-hr air rest at 12 hr. They were germinated six days at 16°C, 100% rh. Germinating oats were hand-mixed twice daily. The green malt was kilned 22 hr with increasing temperatures from 49 to 85°C. The malt was stored in a -20°C freezer. For the time course study, 10-g subsamples were removed after steeping and at two, four, and six days of germination. These samples were freeze-dried.

### Analytical Procedures

Samples were ground in a Retsch ZM-1 centrifugal mill (Brinkman, Westbury, NY) to pass a 0.5-mm sieve. All analyses were done in duplicate, except the N determinations. Lipids were extracted from 1-g samples by shaking with 10 mL of petroleum ether for 30 min. The solvent was decanted after centrifuging (2,000 × g, 10 min), and the extraction was repeated on the residue. The combined supernatants were evaporated in a rotary evaporator at 50°C under vacuum, and the petroleum ether-extractable lipid was measured gravimetrically. Free fatty acids (FFA) were solubilized from the lipid with 5 mL of isooctane and analyzed by a copper soap method (Kwon and Rhee 1986). Oleic acid was used as a standard. Starch content was measured by digestion with thermostable  $\alpha$ -amylase and amyloglucosidase followed by colorimetric determination of glucose (McCleary et al 1994) using a kit from Megazyme (Wicklow, Ireland). Malted samples were first extracted with hot 80% ethanol as indicated in the manufacturer's directions.  $\beta$ -Glucan content was measured with a Megazyme kit

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by digestion with lichenase and  $\beta$ -glucosidase, and the resulting glucose determined colorimetrically using the glucose oxidase procedure (McCleary and Codd 1991). For the time course study, the samples were not preextracted with 50% ethanol as suggested for malt analysis, as this gave unusually low values of  $\beta$ -glucan in the partially modified samples. Total N was measured by combustion with a nitrogen analyzer (Leco, model FP-428, St. Joseph, MI). Carbohydrate soluble in 80% ethanol was measured by the phenol-sulfuric acid procedure (Dubois et al 1956). For diastatic power and  $\alpha$ -amylase activity measurements, ground sample was extracted with 0.5% NaCl solution. Aliquots of the extracts were reacted with soluble starch, and reducing sugars produced were measured colorimetrically by the reduction of ferricyanide in a Technicon Autoanalyzer II (Bran and L ubbe, Elmsford, NY), with

and without first heating at 73°C for 20 min (Banasik 1971). All data are expressed on a dry weight basis except FFA concentrations, which are expressed as percentage of lipid concentration.

### Statistical Analysis

A paired *t*-test was used to compare differences between mean values for unmalted and malted oats for each parameter. Analysis of variance was performed on the seven genotypes that were available from both Ottawa and Aberdeen.

## RESULTS

In the initial experiment, the effects of malting on the lipid and FFA contents of the 31 hull-less genotypes from the Ottawa nursery were analyzed (Table I). Mean lipid concentration of unmalted samples of these genotypes was 7.3%, with a range of 5.4–9.1%.

**TABLE I**  
Lipid and Free Fatty Acid (FFA) Contents of Malted and Unmalted Hull-less Oats Grown in Ottawa, 1993

Genotype	Lipid (%)		FFA (% of lipid)	
	Unmalted	Malted	Unmalted	Malted
AC Lotta	6.30	5.72	5.13	12.21
Baton <sup>a</sup>	7.98	6.70	3.75	11.26
NO21-3	7.18	6.04	4.69	12.06
NO820-8	7.26	5.75	3.74	11.92
NO3-6 <sup>a</sup>	8.43	6.55	3.45	11.02
NO15-7	8.38	6.79	4.63	9.89
NO32-15	6.54	5.15	6.23	13.90
NO18-1	8.04	6.84	4.78	11.74
NO61-B	6.51	5.59	5.16	10.07
NO79-B	7.39	5.96	5.70	12.82
IL87-5622	7.19	7.02	5.00	10.20
IL87-9153	8.36	8.01	5.98	8.10
IL87-5632	6.84	6.21	5.54	9.86
Pennuda <sup>a</sup>	5.75	4.79	5.81	11.12
MF9018-5901 <sup>a</sup>	5.77	4.87	7.33	12.41
MF9018-11801 <sup>a</sup>	5.43	4.48	8.76	14.90
MF913-148	8.99	8.41	6.58	10.05
OH AN1001	7.49	5.79	4.21	11.62
OH AN1010	5.69	4.19	4.97	10.66
Paul	8.50	7.04	4.42	8.51
ND891834	6.64	5.76	9.59	14.85
ND891835	6.07	5.18	9.11	14.92
ND891838	6.43	5.83	6.00	10.30
ND891819	7.73	6.63	5.59	13.32
86Ab1616	8.24	6.88	4.20	9.11
87Ab5932 <sup>a</sup>	8.19	6.18	4.38	8.35
87Ab5939	6.97	6.04	4.52	9.95
88Ab3073 <sup>a</sup>	8.54	6.40	3.96	8.83
90Ab1416	8.24	7.58	3.53	6.27
90Ab1500 <sup>a</sup>	9.06	7.86	4.59	8.64
88AbC327	6.88	6.32	4.34	6.83
CDC Richard (barley)	1.98	1.66	3.19	5.19
Mean (oats)	7.32	6.21	5.34	10.83
<i>t</i> -Test value (oats)	12.77** <sup>b</sup>		-18.33** <sup>b</sup>	

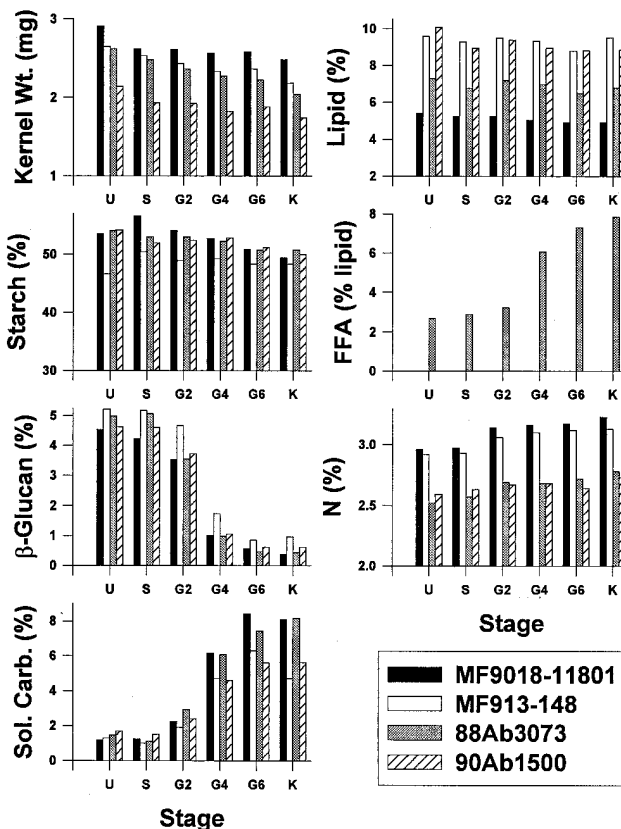
<sup>a</sup> Genotypes selected for further analysis.

<sup>b</sup> Difference between malted and unmalted significant at *P* < 0.01.

**TABLE II**  
Analysis of Selected Hull-less Oat Samples Grown in Ottawa, 1993, and Their Malts

Genotype	N (%)		Starch (%)		$\beta$ -Glucan (%)		Soluble Carbohydrate (%)
	Unmalted	Malted	Unmalted	Malted	Unmalted	Malted	Malted
Baton	2.32	2.55	61.7	56.2	4.65	0.26	8.58
NO3-6	2.33	2.52	61.2	57.3	4.55	0.19	8.12
Pennuda	2.87	3.16	60.8	56.2	4.91	0.37	7.50
MF9018-5901	2.67	3.00	60.8	57.8	4.96	0.39	6.60
MF9018-11801	2.93	3.38	60.3	54.3	5.01	0.27	8.00
87Ab5932	2.51	2.73	59.4	55.1	4.80	0.22	8.80
88Ab3073	2.62	2.99	58.7	51.8	5.10	0.16	10.24
90Ab1500	2.66	2.88	57.7	55.7	4.76	0.33	6.95
Mean	2.61	2.90	60.1	55.6	4.84	0.27	8.10
<i>t</i> -Test value	-9.02** <sup>a</sup>		8.00** <sup>a</sup>		66.68** <sup>a</sup>		

<sup>a</sup> Difference between malted and unmalted significant at *P* < 0.01.



**Fig. 1.** Changes in concentrations of constituents for four oat genotypes during the course of malting. U = unmalted; S = out of steep; G2, G4, G6 = after 2, 4, or 6 days of germination; K = after kilning. Data (except N) are means of duplicate assays.

The mean value was similar to that obtained from analysis of groats from 4,000 genotypes from the World Collection (Brown and Craddock 1972). Lipid concentration in the malted samples decreased by an average of 1.1%, although in two genotypes, 87Ab5932 and 88Ab3073, lipids decreased by >2%. The regression of malted sample lipid (*M*) on unmalted sample lipid (*U*) was highly significant ( $M = -0.07 + 0.86 U$ ,  $r^2 = 0.79$ ,  $P < 0.01$ ). The decrease in lipid concentration probably results in part from lipase-catalyzed degradation of triacylglycerides to FFA and glycerol and the further oxidation of the FFA into nonlipid products. FFA concentration increased from an average of 5.3% of lipid in unmalted grains to 10.8% of lipid after malting. The regression of malted sample FFA (*M*) on unmalted sample FFA (*U*) was also significant ( $M = 5.7 + 0.95 U$ ,  $r^2 = 0.45$ ,  $P < 0.01$ ). Genotypes from the Agricultural Research Service breeding program at Aberdeen developed the least quantity of FFA in malt; malted genotypes from other breeding programs generally had higher concentrations of FFA. The lowest concentrations of FFA in malt were found in 90Ab1416 (6.3%) and 88AbC327 (6.8%), whereas MF9018-11801, ND891834, and ND891835 all developed >14% FFA. Lipid and FFA concentrations in unmalted and malted oats were considerably higher than in a sample of hull-less barley, CDC Richard, one of four cultivars studied by Bhatti (1996) (Table I).

Eight genotypes were selected for further analysis. These included the varieties Pennuda and Baton and lines from breeding

programs at Agriculture Canada (Ottawa, ON), Marshall Farm (Bellefonte, PA), and Agricultural Research Service (Aberdeen, ID). The mean differences between unmalted and malted samples for each constituent were significant at  $P < 0.01$  (Table II). Total N increased slightly in the malt, probably a result of dry matter loss from respiration. Starch decreased by an average of 4.5%, which is similar to that observed during barley malting (Briggs et al 1981).  $\beta$ -Glucan was nearly completely degraded, averaging <0.3% in the malt. This also is similar to experience with malted barley (Bhatti 1996). Soluble carbohydrate levels in the malt averaged  $\approx$ 8%, accounting for most of the loss of starch and  $\beta$ -glucan, assuming that soluble carbohydrate levels in the unmalted grain were negligible. The unmalted samples of Baton and NO3-6 were lower in N and  $\beta$ -glucan and higher in starch than the other genotypes.

The group of 15 unmalted hull-less genotypes from the 1995 Aberdeen nursery (Table III) varied considerably in lipid (5.6–10.2%) and FFA (2.1–4.8% of lipid) concentrations. Variation was somewhat less in the other parameters. Lipid concentration was >10% of the genotypes 90Ab1500 and MF913-148, but the FFA concentration (as a percentage of lipid) of 90Ab1500 was second lowest among all 15 genotypes. MF9018-11801 was low in lipid concentration and had the lowest FFA concentration of the entire group. The lipid concentration of most, but not all, genotypes decreased with malting. The average decrease of 0.5% was less than

TABLE III  
Analysis<sup>a</sup> of Unmalted and Malted Hull-less Oat Samples Grown in Aberdeen, 1995

Genotype	Lipid (%)		FFA (% of lipid)		Starch (%)		$\beta$ -Glucan (%)		N (%)		SC (%)	$\alpha$ -AA	DP
	Unmalted	Malted	Unmalted	Malted	Unmalted	Malted	Unmalted	Malted	Unmalted	Malted	Malted	Malted	Malted
87Ab5932	7.9	4.9	4.0	10.8	56.9	46.2	4.96	0.05	2.41	3.40	7.8	38.6	40
88Ab3073	7.3	8.3	3.9	8.0	54.1	50.0	4.41	0.18	2.54	2.62	7.1	28.8	29
90Ab1500	10.2	5.1	2.6	13.6	54.2	46.9	4.75	0.10	2.69	3.05	7.7	35.1	35
93Ab-1	8.1	6.7	3.4	7.4	56.6	49.4	4.14	0.06	2.36	2.37	7.2	35.4	31
Baton	6.8	4.0	3.0	12.1	53.2	48.0	4.34	0.04	2.44	2.87	8.6	47.8	40
MF9018-117	5.9	6.4	3.5	9.3	54.0	50.2	4.31	0.06	2.59	2.68	7.1	31.3	28
MF9018-11801	5.6	8.4	2.1	8.6	53.5	45.7	4.34	0.19	3.09	3.00	6.9	41.3	28
MF9116-31	5.8	4.2	4.8	15.0	55.0	44.9	4.86	0.06	2.60	3.20	8.1	38.7	36
MF913-148	10.2	6.7	3.3	7.6	46.6	51.4	4.69	0.16	3.02	2.57	7.2	33.0	33
MF9224-336	5.7	4.4	4.1	11.5	53.8	49.7	4.49	0.04	2.94	2.79	7.9	30.8	33
NO37-3	8.2	5.7	3.6	9.6	57.5	48.5	3.42	0.11	2.64	2.65	8.6	38.3	34
NO51-1	6.5	6.1	3.4	12.9	54.7	49.5	5.02	0.10	2.62	2.60	8.6	40.8	35
NO66-1	7.3	5.9	3.0	10.9	54.9	49.9	3.67	0.10	2.67	2.85	7.1	34.9	33
NO70-1	6.8	5.5	3.1	13.0	51.7	48.5	4.32	0.04	2.74	2.77	7.7	43.8	35
Pennuda	5.8	5.4	4.0	15.4	52.7	46.2	4.53	0.03	3.14	2.90	8.0	43.1	42
Mean	7.1	5.9	3.5	11.1	53.9	48.3	4.42	0.09	2.70	2.82	7.7	37.4	34
<i>t</i> -Test value	2.66** <sup>b</sup>		-11.7** <sup>b</sup>		5.88** <sup>b</sup>		37.2** <sup>b</sup>		-1.33		1.0	1.5	4

<sup>a</sup> FFA = free fatty acids; SC = soluble carbohydrate;  $\alpha$ -AA =  $\alpha$ -amylase activity (expressed as 20 DU [dextrinizing units]); DP = diastatic power (expressed as  $^{\circ}$ ASBC [Am. Soc. Brew. Chem.]).

<sup>b</sup> Difference between malted and unmalted significant at  $P < 0.05$  (\*) or  $P < 0.01$  (\*\*).

TABLE IV  
Analysis<sup>a</sup> of Unmalted and Malted Groat Samples of Hulled Oats Grown in Madison, 1996

Genotype	Lipid (%)		FFA (% of lipid)		Starch (%)		$\beta$ -Glucan (%)		N (%)		SC (%)	$\alpha$ -AA	DP
	Unmalted	Malted	Unmalted	Malted	Unmalted	Malted	Unmalted	Malted	Unmalted	Malted	Malted	Malted	Malted
Bay	6.3	8.2	2.4	15.9	52.9	40.4	6.01	0.15	2.96	2.92	8.3	46.1	39
Dane	6.7	9.5	1.9	10.4	58.8	44.6	4.67	0.30	2.56	2.60	6.9	35.6	31
Gem	4.4	6.0	2.9	11.7	55.7	50.7	6.12	0.22	2.83	2.20	7.4	38.5	40
Hazel	9.6	5.3	1.5	14.9	55.2	38.9	5.33	0.26	2.54	3.14	7.7	50.4	43
Horicon	7.6	7.1	2.1	6.9	57.1	52.8	4.74	0.20	2.58	2.64	6.2	31.7	29
Jim	6.8	7.4	1.7	13.5	55.6	47.7	4.43	0.17	2.48	2.60	6.6	36.2	33
Ogle	6.4	6.8	1.9	12.5	58.3	54.0	5.10	0.18	2.49	2.57	5.5	35.6	29
Porter	8.5	5.6	2.3	14.9	53.0	46.1	5.13	0.15	2.76	3.09	6.8	36.9	32
Prairie	6.3	6.0	2.0	13.7	59.4	48.6	5.04	0.16	2.22	2.55	7.3	49.3	35
Troy	6.1	4.2	2.3	13.8	54.6	48.8	5.31	0.22	2.97	3.34	5.6	42.9	36
Mean	6.9	6.6	2.1	12.8	56.1	47.3	5.19	0.21	2.64	2.77	6.8	40.3	35
<i>t</i> -Test value	0.36		-12.7** <sup>b</sup>		6.40** <sup>b</sup>		28.6** <sup>b</sup>		-1.21				

<sup>a</sup> FFA = free fatty acids; SC = soluble carbohydrate;  $\alpha$ -AA =  $\alpha$ -amylase activity (expressed as 20 DU [dextrinizing units]); DP = diastatic power (expressed as  $^{\circ}$ ASBC [Am. Soc. Brew. Chem.]).

<sup>b</sup> Difference between malted and unmalted significant at  $P < 0.01$ .

that observed in the Ottawa data set. The FFA increased by an average of 8.0%. The lowest FFA concentrations in malted samples occurred in 93Ab-1, MF913-148, and 88Ab3073. The mean starch concentration decreased  $\approx$ 5% in malted, as compared to unmalted samples, whereas the mean N concentration increased slightly.  $\beta$ -Glucan was nearly eliminated with malting. The malted samples averaged 7.7% soluble carbohydrate (6.9–8.6%).  $\alpha$ -Amylase activities ranged from 29 to 48 (mean = 37) dextrinizing units (DU); the higher values approach those achieved in malting barleys. However, diastatic power was very low as compared to malting barley, averaging only 34° ASBC. Unlike the Ottawa data set, regressions of malted on unmalted samples were not significant for any constituent.

An analysis of variance on the seven genotypes available from both Ottawa and Aberdeen revealed significant genotypic differences only for unmalted lipid and N concentrations (data not shown). This suggests that the other parameters may be subject to environmental influences, although an experiment with replicated samples from several environments would be needed to establish the relative effects of genotype, environment, and their interaction.

Four of the Aberdeen-grown samples were selected for a time course analysis of changes during malting (Fig. 1). (Only one genotype, 88Ab3073, was available for the FFA analysis.) MF9018-11801 was selected for high protein and low lipid. MF913-148 and 90Ab1500 are high lipid, and 88Ab3073 has about average constituent values. Kernel weight decreased in all genotypes due to respiratory losses. The time course study showed a threefold increase in FFA mostly during the germination phase.  $\beta$ -Glucans were rapidly degraded between days 2 and 4 of germination. Trends for increasing N and decreasing lipid were steady throughout the malting process. Starch concentration declined during germination in all genotypes, accompanied by increased soluble carbohydrate.

The average lipid concentrations of unmalted and malted groats from the Madison group of hulled cultivars were slightly higher than those of the hull-less genotypes (Table IV). Lipid concentrations increased in some cultivars and decreased in others with malting; the mean difference between unmalted and malted was not significant. The unmalted sample of Gem had the lowest lipid of any sample. FFA concentrations of the unmalted groats averaged lower than those in the hull-less genotypes, but a greater increase with malting led to higher concentrations than in the malted hull-less genotypes. The cultivar Horicon was unusual, with only 6.9% FFA in the malt. Starch and  $\beta$ -glucan concentrations were higher in the unmalted groats than in the Aberdeen set of hull-less genotypes, but these concentrations in the malted samples were similar between the two sample sets. N concentration ranged from 2.2 to 3.0% and increased with malting in most cultivars.  $\alpha$ -Amylase activity averaged 40 DU. The cultivar Hazel was notable with 50 DU, an acceptable value for malting barley. DP was low and similar to that of the hull-less genotypes.

## DISCUSSION

For malted hull-less oats to become commercially viable, several criteria should be met: 1) the oats must be adaptable to existing malting technology with minimal adaptation of facilities or procedures; 2) the malted product must possess useful characteristics that either are not available or are more costly from other sources; 3) malt characteristics should be predictable from the properties of the unmalted grain; 4) the malted oats must be stable and free of undesirable characteristics. Some of these criteria have been partially addressed in this study.

Steeping time was reduced relative to hulled barley, because the absence of hulls facilitates rapid imbibition. This was also shown for hull-less barley (Bhatty 1996). Germination time, however, was extended to six days to achieve a well-modified malt (by visual observation of acrospire growth). This compares to four-

five-day germination times for hulled barley malting. Slower germination rate may result from lower enzyme activity in oat (Pomeranz and Shands 1974). Malting conditions have not yet been optimized. Handling characteristics may be less robust for oat than for hulled barley, due to a softer endosperm and absence of the protective hull. Our laboratory scale study did not address this point.

Malted oats were high in protein and lipid, had moderate amounts of starch, and were low in  $\beta$ -glucan. Because  $\beta$ -glucan contributes to high viscosity, low levels are considered desirable for poultry feed (Cave et al 1990) and brewing (Burger and LaBerge 1985). For human food, high  $\beta$ -glucan is desired to lower cholesterol levels, reducing the risk of heart disease (Anderson et al 1990). The physical characteristics contributed by  $\beta$ -glucan are important for product applications in the food industry (Autio et al 1987). The low  $\beta$ -glucan concentration of malted oats may be desirable or undesirable, depending on the application. Increased levels of soluble carbohydrates (reducing sugars) should contribute sweetness. Previous research showed that germination increased the proportion of lysine in protein of maize (Tsai et al 1975) and barley (Bhatty 1996), and may also do so for oats. Lysine is the first limiting amino acid in cereals for human nutrition.

There were only modest changes in N, starch, and lipid upon malting. Concentrations of these constituents could be predicted from concentrations in the unmalted oats for the Ottawa data set, but not for Aberdeen or Madison samples. The potentially wide variation in N and lipid among genotypes enables selection of appropriate genotypes for specific applications.

The increase in FFA observed during the germination phase is not desirable, as this can lead to hydrolytic or oxidative rancidity (Haydanek and McGorin 1986). Galliard (1983) stated "oats may be considered unfit for processing into food products if the FFA level exceeds 5% of the hexane-extractable lipid". The wide range in FFA values indicate a possibility to identify genotypes with a lower development of malt FFA than was seen in this group of genotypes. The next steps will be to search oat germplasm for genotypes with the least development of FFA and to devise malting conditions that minimize their development. Because the hull-less character is conditioned by a single dominant gene together with a small number of modifying genes (Simons et al 1978), one strategy might be to seek hulled genotypes that exhibit minimal FFA development, and breed the hull-less characteristic into them by backcrossing. Although only one hulled genotype had low FFA concentration in malt, the gene pool is much larger for hulled genotypes. While lipase is known to hydrolyze triacylglycerides to FFA and glycerol, the relationship between lipase activity levels and development of high concentrations of FFA is undetermined. This work is in progress. Oats are known to be relatively high in lipase activity (O'Connor et al 1992), and activity was shown to increase with germination (Urquhart et al 1984).

Further research is needed to determine whether the malt has acceptable flavor characteristics and is stable. Welch (1977) found an increase in FFA in sound grain stored at 10.5% moisture for almost one year. He demonstrated that the level of hydrolytic rancidity in hull-less oats exceeded that in hulled oats only if the grain was severely bruised.

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