TOWARD A WINTER MALTING BARLEY

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INTRODUCTION

This is our seventh season of a concerted effort to develop a winter six-row malting barley. I doubt there is anything in the field today the U.S. malting and brewing industry would clamor for tomorrow. However, if we imagine a winter malting barley as a puzzle composed of interlocking genetic pieces, then I am optimistic that some pieces of the puzzle are present in our breeding program.

In envisioning a winter malting barley, we need to consider what makes a winter barley, what makes a malting barley, and what makes for profitable barley production. The first two issues we can begin to address through genetic analysis and breeding.

We have addressed winter malting barley variety development in several ways. First, we produce all our breeding lines through the doubled haploid (DH) technique. This shortens the breeding cycle and ensures that materials are homozygous. Secondly, we have been active in barley genome mapping. The idea is to locate, on maps of the seven chromosomes of barley, genes that are of economic importance. Examples of such genes are those that distinguish winter from spring varieties, that determine resistance to diseases,and that contribute to malting quality. Very often, these genes are rather elusive and we have to describe them in statistical terms - as Quantitative Trait Loci (QTL) - rather than as specific DNA sequences. In any event, if you know where the genes are, you can more effectively move them around in a conventional crossing program. To date, our DH breeding and QTL detection efforts have proceeded in an essentially parallel fashion. We are now in a position to begin integrating the two efforts.

Winter habit is determined by a number of quantitatively inherited traits, including growth habit, vernalization response, photoperiod reaction, and cold tolerance. We have used marker-based strategies to identify QTL associated with these traits in the DH progeny of a winter x spring cross (Hayes et al., 1993a; Pan et al., 1994). In the lines we have studied, the genes determining winter growth habit and those determining malting quality are not located in close proximity. Thus, there appears to be no genetic barrier to combining quality and winter growth habit.

No winter malting varieties are currently in commercial production in North America. In Europe, considerable progress has been made in winter malting barley improvement, although winter types in general have not achieved the level of quality found in spring genotypes (Schildbach, 1987) (Table 1). Malting quality specifications vary between Europe and North America, reflecting different brewing practices, and these differences are principally related to desired levels of grain protein and enzyme activities.

Malting quality is determined by a number of component traits. Foremost among these are grain protein and extract percentages, the ratio of soluble to total protein, diastatic power, α-amylase, the difference in extract percentage between finely and coarsely ground malt, and the wort ß-glucan content. A comprehensive review of the biochemical basis of malting quality in the context of barley improvement is presented by Burger.

Table 1. Performance of European winter malting barley varieties in EBC trials compared to a representative average of spring varieties. (Source: Schildbach, R. Malting barley worldwide. 1994. Brauwelt 4:292-308).

	Plaisant	Clarine	Petula	Fighter	Sprite	Astrid	Angora	Spring Ave. 13 var.
Origin/no. of rows	F/6	F/2	F/2	GB/2	GB/2	D/2	D/2	-./2
Yield, t/ha	6.4	6.3	6.1	6.2	6.1	6.1	6.4	5.4
Plump fraction, %	77	83	94	87	85	92	91	75
Protein,%	10.2	10.7	11.2	10.9	10.9	11.7	11.1	10.5
Extract	80.1	80.2	80.4	80.5	80.4	80.4	81.2	81.4

and LaBerge (1985). Briefly, malting is a carefully controlled germination processes in which complex proteolytic pathways are manipulated to develop an ideal substrate for subsequent fermentation. Kernel carbohydrates are hydrolyzed by α- and ß-amylases, and the selection criteria of a-amylase and diastatic power are thus measures of individual (α) and combined (α plus ß) enzymatic activities. Proteinase activity is expressed as the ratio of soluble to total protein (S/T). Malt extract percentage is a measure of the percentage of the malt rendered soluble. The fine-coarse difference and the wort ß-glucan percentage are additional measures of the completeness of the malting process (modification). Experimental evidence indicates that the components of malting quality are quantitatively inherited (Peterson and Foster, 1973). QTL for a number of malting quality characters have been reported in spring and winter germplasm (Hayes et al., 1993b; Hayes et al., 1996).

In addition to winter growth habit and malting quality, a winter barley adapted to the Pacific Northwest (PNW) needs additional attributes. It needs to equal or exceed feed barley yields and it should be resistant to barley stripe rust. Yield is the ultimate character, and can be addressed through QTL mapping procedures, although the applicability of the information may vary from cross to cross (Hayes et al., 1996). Likewise, the genetic determinants of stripe rust resistance can be located through QTL mapping procedures (Chen et al., 1994).

RESULTS AND DISCUSSION

As stated earlier, our QTL mapping efforts and our DH breeding have proceeded essentially in parallel. Our DH breeding has generated high yielding, stripe rust resistant genotypes with significantly better malt extract than the feed barley checks (Tables 2 and 3). These selections do not meet domestic quality specifications in terms of enzyme activity and viscosity. Our QTL mapping efforts have revealed the locations of malting quality genes, but often these genes are located in breeding populations that are not likely to produce variety candidates. Thus, we know that DH breeding works, but we have hit a barrier in terms of enzyme activity. We also know QTL mapping works, but much of the information is often not immediately useful. The logical step is to integrate QTL mapping with our breeding effort. Thus, we can begin putting together the puzzle pieces of the winter malting barley variety. Kold, Strider, and other advanced lines in our DH breeding nurseries are important contributors; they have good malt extracts, good yield performance, and stripe rust resistance.

Table 2. Agronomic summary of OSU winter barley selections Strider, ORW7, ORW8, ORW9 compared with check varieties; averaged over Pendleton, Pullman, Aberdeen for the years 1992-1995. Values in ( ) are # of station years.

Line	Heading date	Height	Lodging	Test weight	6/64 Plump*	Thin	Yield
	Julian	in	%	lbs/bu	%	%	lbs/A
Scio	149 (4)	36 (7)	7 (7)	49 (7)	83 (4)	3 (4)	7008 (9)
Hundred	151 (5)	35 (8)	7 (7)	48 (8)	80 (4)	4 (4)	6866 (10)
Gwen	147 (5)	38 (8)	12 (8)	49 (8)	77 (4)	4 (4)	6805 (8)
Plaisant	140 (5)	38 (8)	4 (8)	52 (8)	88 (4)	2 (4)	6220 (10)
Eight-twelve	146 (4)	34 (7)	19 (7)	49 (7)	78 (4)	4 (4)	6457 (9)
Kold	147 (5)	38 (8)	9 (8)	51 (8)	75 (4)	5 (4)	7468 (8)
Strider	145 (3)	38 (7)	9 (7)	51 (7)	89 (4)	2 (4)	7660 (9)
ORW-7	150 (3)	38 (7)	4 (7)	55 (8)	95 (4)	1 (4)	6921 (9)
ORW-8	139 (3)	39 (7)	5 (7)	55 (7)	94 (4)	1 (4)	6016 (9)
ORW-9	143 (3)	42 (7)	2 (7)	53 (7)	90 (4)	3 (4)	5714 (9)

* A 6-row malting barley should have 85% or higher plump kernels when passed over a 6/64'' sieve.

Table 3. Quality Profiles for Strider , and ORW-7, 8, and 9 with Scio and Plaisant Data from Pendleton, Pullman, Aberdeen and Corvallis locations 1991 - 1994. Lower case numbers represent number of tests.

Variety or Selection	Plump 6/64	Grain Protein	S/T*	Malt Extract	F-C	DP	α-amylase
	%	%	%	%	%	(Deg)	(20 deg)
Scio	76.2	10.1	41.4	75.6	4.1	76.2	33.9
	5	7	7	7	5	7	7
Plaisant	86.4	10.0	38.6	79.1	2.8	90.9	37.0
	12	14	14	14	11	14	14
Strider	85.1	9.6	39.8	78.9	2.1	63.8	37.7
	12	13	15	15	10	15	15
ORW-7	91.9	9.7	38.7	79.0	2.9	89.4	29.3
	12	13	14	14	9	14	14
ORW-8	90.7	10.2	40.6	79.0	2.0	92.1	41.6
	12	13	14	14	9	14	14
ORW-9	89.7	10.6	40.7	79.5	2.4	107.1	35.8
	12	13	14	14	9	14	14

* For malt analysis, samples of barley grain are malted in a small-scale pilot malting unit. A number of chemical analyses are conducted on the products of this malt. While the specific target quality profile will vary depending on the type of barley (6-row or 2-row) and the intended use (domestic vs. export/microbrewery) the following definitions and ranges of trait expression are adequate generalizations. The total grain protein should be less than 13.5%. S/T is a measure of the soluble to total protein ratio and should be around 40%. Malt extract should be greater than 78%. F-C is the difference in extract between fine and coarse-ground malt and should be around 2%. DP is diastatic power, which is a measure of total enzymatic activity. Domestic brewers would like to see this value greater than 130, but microbrewers and the export market want it less than 100. α-amylase values should be greater than 40% for all markets. In general, there is a negative correlation between grain protein and malt extract and a positive relationship between grain protein and enzymatic activity. Thus, malt quality is a balance of extract, total protein, and activity of certain enzymes.

Table 4. Malting quality data for winter barley varieties and selections grown six years in irrigated winter barley trials at Aberdeen, Idaho, 1988-89 to 1993-94.

Entry	Plump	Malt extract	F-C	Grain protein	S/T	DP	Alpha amylase
	(%)	(%)	(%)	(%)	(%)	(Deg)	(20 deg Units)
88Ab536+	89	77.5	2.2	13.7	37.8	152	39.5
Wintermalt	79	74.5	4.1	13.4	31.9	114	30.0

Table 5. Summary of agronomic data for 88Ab536 and selected winter barley varieties grown under irrigation at Aberdeen, Idaho, 1989-90, 1991-92 and 1992-93.

Entry	Yield	Test weight	Height	Heading Date	Lodging
	(bu/A)	(lbs/bu)	(in)	(Julian)	%
No. Years	3	3	3	3	2
88Ab536	154.7	51.8	35	141	5
Eight-Twelve	200.0	51.8	32	146	4
Schuyler	183.5	50.9	34	152	10
Scio	195.8	50.9	31	148	4

The other contributor is 88Ab536-B. This genotype, developed by Dr. Darrell Wesenberg (USDA-ARS, Aberdeen, Idaho) has the best malting quality profile ever seen in a U. S. winter 6-row barley (Table 4). However, it pays a significant yield penalty in comparison to feed barleys (Table 5). Although it is cold tolerant, its growth habit is completely inappropriate for regions with fluctuating winter temperatures. It will try to flower at the first warm spell. can begin putting together the puzzle pieces of the winter malting barley variety. Kold, Strider, and other advanced lines in our DH breed ing nurseries are important contributors; they have good malt extracts, good yield performance, and stripe rust resistance.

What we propose to do in the coming years is focus on putting these puzzle pieces together. DH production plays a central role, as we will make large DH populations for crosses of OSU lines with 88Ab536-B. Phenotyping plays an important role. Our strategy will be to check actual performance, whenever possible. For example, we can determine photoperiod response (heading date) in field or greenhouse plantings at Corvallis. Winter survival can be determined in controlled freeze tests in cooperation with Hungarian colleagues who are expert in such things, and stripe rust reaction can be determined in cooperation with PNW pathologists and in our cooperative program with ICARDA/CIMMYT. At the same time, molecular markers can be used to identify those lines that have the maximum overall genome composition, and maximum genome composition in target areas, tracing to 88Ab536-B. The lines coming out of these selection programs can be rapidly advanced to multiple location testing in Oregon, Idaho, and Washington for yield and quality confirmation. At any point, retroactive mapping can be used to locate determinants of key traits, to determine if negative genetic associations are limiting selection response, or to ensure that specific loci are pyramided into single genotypes.

Is the investment in winter malting barley worth it? Intuitively, it seems that winter barley has a place in certain regions of the PNW and that a malt premium would make production even more attractive. However, economic constraints need to be identified and rigorously defined. Our strategy is to develop lines that equal or exceed current feed types in yield, test weight, and kernel sizing and that have superior quality. While our efforts may be modest compared to those in Europe that have produced the quality profiles shown in Table 1, our program has contributed to generating basic knowledge regarding gene location and expression and should provide varieties adapted to the Pacific Northwest.

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