CHAPTER

Malts

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N. Davies
Muntons, Stowmarket, United Kingdom

INTRODUCTION

Love it or loathe it, the traditional malt specification that has been with us for many years is likely to continue in use for the foreseeable future. Notwithstanding the universal acceptance that it is in parts flawed and difficult to interpret, it is still the mainstay of evaluating the suitability of malt for brewing. Over the years many suggestions for novel methods have been researched and suggested as either descriptors of malt quality or indicators of processability. So far, novel methods have had limited acceptance even when these have been extensively peer reviewed. Even with the new methods it can still be difficult to relate the results to brewhouse performance and cause problems when integrating them into a laboratory set up to follow recommended methods which are generally robust and which use recognized equipment and techniques rather than some of the intricacies involved in some newer assays. Familiarity and tradition have bolstered the conventional malt specification and will undoubtedly ensure it remains for some time yet.

What we have to contend with is that the concept of quality is often more perceptive than well defined. In other words, the judgment of the user based on his experience is not always easily and unequivocally traceable back to a specific analytical parameter (analyte). In many instances, one brewer or distiller describes a batch of malt as superb because it runs through his plant like "rocket fuel," whereas another brewer finds the very same batch wholly unacceptable. The dilemma is how to resolve the root cause. Is it malt derived or process derived? Whatever the cause, a problem exists, but resolution may lie not with a fault in supply but rather in what has contributed to arriving at a material apparently in specification that could have been achieved in so many ways.

For consumers the link of malt analysis to product quality is not always appreciated. What malt parameters affect the enjoyment of the final product? Many factors have been found to influence drinkability and many could be attributable to malt (Davies, 2006a,b). We are aware of the influence of malt in beer either consciously or subconsciously and that affects our enjoyment of the product (Fig. 1.1). Precisely how biochemistry in malt manufacture affects some of the more curious aspects of the enjoyment of beer is largely unknown and cannot be

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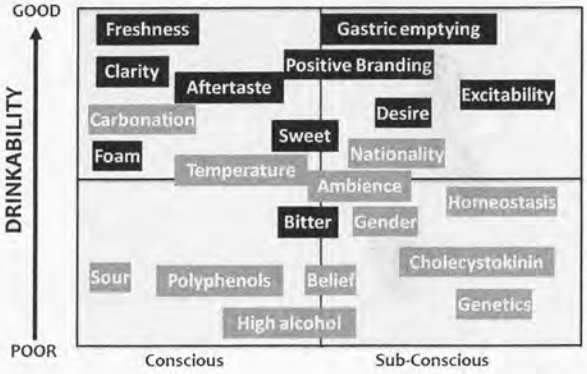

FIGURE 1.1

Factors associated with the drinkability of beer. Some factors we can consciously control and some are subconscious based on biochemistry and social or environmental factors. Arguably, the factors shaded in black are influenced by the malt component. Most of those factors can have a positive impact on the drinkability of beer.

After Davies, N.L., November 2006a. Malt - a vital part of the brewer's palette, Monograph 34: E.B.C. Symposium, "Drinkability," Edinburgh.

reflected in the traditional malt specification. For a small handful of those parameters, however, there are clear links to malt. Freshness can be achieved with a malt that is low in factors that contribute to staling. Clarity can be impacted by malt modification and beta glucan level. Foam quality is affected by malt proteins and protein breakdown. Consumer preference is likely to be more influenced by marketing among the public. If a product is described as full of malt flavor and brewed from the finest malt and hops, it may be perceived as such, whereas a product brewed in the same way but advertised with flavors associated with fruits from esters will not be judged "malty". The brewing and distilling trade has made a concerted effort to promote beer appreciation and wholesomeness of its raw materials, yet specific malt flavors or attributes still take a back seat in most sensory descriptions. In a slightly tongue in cheek attempt to describe how we enjoy beer, it has even been described mathematically. The controlling variables were beer temperature, number of people drinking, days before being back at work, venue mood, and availability of foods or snack, but with no place for the ingredients to contribute to that enjoyment (Fig. 1.2; Mindlab, 2012).

WHAT SHOULD A MALT ANALYSIS TELL YOU?

Of course, this depends who is asking. For the breeder the difference could be as simple as whether the barley is suitable for feed or malting based on broad-brush measures such as hot-water extract, disease resistance, and good agronomy. For

$$E = -(0.62T2 + 39.2W2 + 62.4P2) + (21.8T + 184.4W + 395.4P + 94.5M - 90.25V) + 50(S + F + 6.4)$$

E is a factor describing overall enjoyment.

T is the ambient temperature in degrees Celsius.

W is the number of days until you are required back at work.

P is the number of people with whom you are drinking.

M is related to your mood whilst drinking the pint.

V is related to the volume of the music being played.

S and **F** are related to the availability of snacks and food.

FIGURE 1.2

Formula to describe the enjoyment of beer. Nowhere does this equation allow for the product quality or taste. These parameters seem to be left to the brewer to control and are a given backdrop to enjoying the beverage. Although this is not a serious scientific formula, it illustrates an attitude to how alcoholic beverages are judged by the public.

From Mindlab, 2012. Formula for the Perfect Pint. www.taylor-walker.co.uk/Media/Documents/PDF/news/WPR-Mindlab-The-Perfect-Pint.pdf.

maltsters, a good variety would be one which performed well over a wide range of nitrogen (protein) contents and was easy to germinate and kiln. To a brewer often it is extract yield, color potential, clarity, and flavor. An overarching thread in all these requirements is that the best variety will reduce risk for the whole supply chain. Ideally, the breeder needs a variety that lasts up to 10 years to recoup breeding investment costs. Farmers need the certainty that a crop will grow well and be versatile in different seasonal weather conditions. Maltsters need varieties that can guarantee availability of good quality raw material free from disease and requiring the least processing utilities input. Brewers also need a secure supply of raw material and for the malt not to give rise to any negative processing or taint issues while providing good yeast nutrition and contributing to color and/or flavor. The concept of a risk premium to secure good quality malting barley at the right time is something very real in the modern malting supply chain. Risk can, of course, be managed and reduced for raw material availability, quality, and functional aspects of performance.

For many years, breeders have used their extensive knowledge of plant phenotypes to determine those best for selection from crosses which may number 30,000 individual plants. In recent years, they have been aided through marker-assisted selection or genomics. In some cases it has been possible to link genetic sequences with specific barley or malt attributes and then to select or promote the effect of those sequences in new varieties. Markers based on single-nucleotide polymorphisms (SNPs) have rapidly gained popularity among breeders (Mammadov et al., 2012). There are, however, problems with this type of selection. A major hurdle is the highly repetitive nature of the plant genome (Meyers et al., 2001). The aim is to identify genes or quantitative trait loci (QTL) that contribute to a

desired trait in the grain, with agronomy, or even in malt manufacture. Rather than generate a plethora of new QTL for scientific interest only, a recently concluded project sought to use the SNP/QTL libraries available around the world to enable breeding of specific desirable traits for malting barley into existing elite United Kingdom breeding varieties (Thomas et al., 2014; Ramsay et al., 2014). It was notable in the early stages of that research work that the major distinctions between barley varieties were associated with the vernalization gene. Unsurprisingly, we have spring and winter barley varieties as the major barley types. This is just one factor that makes selection of new varieties complex. The complex genetic interrelationships in barley make it difficult to relate process performance to such malt specification parameters as beta glucan, Kolbach index (KI), wort viscosity, fine–coarse extract difference, friability, and free-amino nitrogen (Wentz, 2000; Wentz et al., 2004). What is behind such difficulty in identifying how to breed and improve these characteristics? Many of the genetic traits are carried on different parts of the DNA sequence, on different chromosomes, and some genes exert multiple effects (pleiotropy). The result of this is that one gene or a series of linked genes may control a number of parameters on a malt specification, or that indeed some existing malt analytes are effectively redundant. Similar consequences have been found in attempting to relate diastatic power (DP) to improved fermentability (Evans et al., 2009). In that work, it was made clear that the genetic sequences controlling the three major contributing enzymes to DP (β amylase, α amylase, and limit dextrinase) are all carried on different chromosomes along with other currently unspecified Gibberellin-responsive elements. Selection to improve one of those parameters in isolation is effectively not possible and is an underlying reason why so many malting parameters are interlinked such that changing one inevitably affects a number of others. There is a further layer of uncertainty due to the thermal properties of amylolytic enzymes and the sugar profiles created (Duke and Henson, 2009b; Henson and Duke, 2014). Traits are influenced by genetics and the environment interacting which further complicates breeding selection. It is relatively straightforward to introduce a stable change in a barley variety if the trait is controlled by a heritable gene, but very uncertain and unstable when the impact of the environment on that gene is strong (Kavitha et al., 2012). So much that we think we know is due to the malting process on a current malt specification is influenced much further back in the breeding program and upstream in the mashing process.

As long ago as 1914, a paper in the Journal of the Institute of Brewing by Harold and John Heron on the purchase of malt on the basis of analysis lamented "we feel sure that the majority of brewers fail to fully appreciate the limitations of malt analysis." Taking long leaps through countless brewing research studies over the next 60+ years, we come to the review of Hyde and Brookes (1978) in which links between Hot Water Extract, Gravity and run-off time were reasonably well correlated. They found that just four main analytes (extract, soluble nitrogen ratio, beta glucanase level, and total nitrogen) could account for 85% of the variability in the brewhouse, extract accounting for the lion's share at 70%. However, they too felt that analysis was too skewed toward commercial transactions stating "the information

they provide about brewhouse behavior is very limited and that provided about wort or beer quality virtually non-existent." Essentially, a brewer's requirements for malt can be encapsulated as follows: to produce wort as economically as possible that performs well across all brewhouse operations (O'Rourke, 2002).

A traditional malt analysis can be subdivided into five key groups: starch conversion, carbohydrate conversion, carbohydrate extract, color, and enzyme potential. Physical attributes of barley and malt affect all of these, but are not regularly considered important when assessing malt quality. This can, of course, be dangerous. Varieties that differ in grain-size distribution each year will not necessarily mill the same. Quite often, problems with malt processing in breweries can be traced back to an unchanged mill setting. In a year with grains that are wider in diameter (bold) extract yield can be dramatically diminished by generation of dust when mill gap settings are set too small. When size distribution is lower, grains may be only partly milled, giving rise to poorly digestible pieces of endosperm and undigested glucan leading to haze. Mill adjustment is such an important aspect of brewing performance yet is often the source of many hazy beers or reduced brew length. Picking up the problem at the malt specification stage by early discussion in a new season with the maltster could avoid costly volume reduction and filtration time in the brewery.

These days, a malt analysis is very much like a risk management tool. Brewers need consistency of raw materials, yet there will always be seasonal variations and barley malting performance changes throughout the year from harvest onward as the grain matures. Much of that annual change in product is seen only by the maltster who will adjust the process conditions to match the agreed specification. Seasonal changes, in which significant swings arise in the levels of protein or beta glucan or grain-size distribution, can be more of an issue that has to be considered. Grain protein content has been found to correlate with applied nitrogen and beta amylase activity (Yin et al., 2002; Qi et al., 2006). Grain size is known to affect diastatic power and hence can be seasonal (Agu et al., 2007). If the specification requires higher-limit dextrinase activity, for example in distilling or high-adjunct grists, there should be an acknowledgment that this could come at the expense of higher malting loss and reduced extract. That is because this enzyme develops appreciably only after a long germination (Sissons et al., 1993) and it has to be mashed carefully to avoid losses due to heat deactivation during mashing (Stenholm and Home, 1999). A similar trade-off has been found using dehusked barley in which filtration and amylolytic enzyme activity was worse, yet processing and predicted spirit yield improved (Agu et al., 2008). In many ways the malt analysis directs the brewer in how to avoid process difficulties by adjustment of the grist or mashing conditions.

There are many discussion papers on the relevance of laboratory mashes in relationship to brewhouse performance. Are these really an issue? The same is found in small-scale or micromalting in which process conditions that mimic true malting have to be set up quite differently to the main plant to get the best correlation. In the case of micromalt and brewing analyses, the reader is effectively using them

as a comparative benchmark. Departures from the norm are just as important as getting an analysis in range.

An issue often arises when improvements in malt analysis are not matched with changes in mash profile. When more-modified malt is specified, it can improve the rate of throughput and the amount of extract and yeast nutrients. However, in many cases the mash profile remains the same as used for malts with higher protein and lower extract levels. The result is that the better malt is overmashed and foam-positive protein can be degraded, extract diminished, and overall produces a poorer product. This illustrates the importance of understanding not just raw-material quality, but the impact of that on subsequent processing.

ANALYTICAL VARIANCE

Variance of analyses between reanalysis in the same laboratory of the same sample and different samples by different laboratories is well documented and mathematically explained. This, of course, adds a degree of controversy at times to the adherence of the maltsters to the expected specification. Whether the variation from specification will actually translate into a real effect on brewing is often difficult to prove. However, it remains important for maltsters to understand the potential variance in a method and somehow to estimate the impact of drifting toward the limits of a specification. Statistically, supplying on the edge of a specification band will inevitably result in some analytical tests being outside the specification. Control of this is often agreed between maltster and brewer by setting blending limits for individual batches which are slightly wider than the blended delivery specification. When laboratories enter results on an electronic enterprise resource planning (ERP) system such as SAP it is often not possible to distinguish the significance of the amount that a particular analytical parameter (analyte) is from the desired final specification. Most systems simply allocate a percentage banding around the analyte value. Other systems are available, though mostly bespoke for each maltster, that grade the significance of each individual analyte with respect to brewing performance. This gives a greater nonconforming score to those analytes that have more significance for brewhouse performance than others. Using the bandings for laboratory variance in analysis (r95) for example, beta glucan being out of specification by one r95 band is more likely to have an impact on brewing than moisture. An effective weighting system for the importance of each parameter and the degree of variance from the specification can be determined through many different mathematical algorithms. This type of system has been around in different guises for a number of years under the general heading of quality scoring or quality number (Aalbers and Van Eerde, 1986). An example of such a systematic approach to malt analysis is shown in Fig. 1.3. Each batch of malt produced can be scored for its adherence to specification firstly for each analyte. In this case, a score of 0 is perfection and within specification. Using banding that approximates to the analytical variance of each analyte,

Beta Glucan specification: <260mg/litre Analytical range = ±20
ACTUAL VALUE: 301mg/l

RANGE			≤260	261-280	281-300	≥300
SCORE			0	50	100	200

Colour specification: 3.0-4.5°EBC Analytical range = ±0.4
ACTUAL VALUE: 4.4

RANGE		<3.0	3.0-4.5	4.5-4.9	5.0-5.4	>5.5
SCORE		100	0	50	100	200

Kolbach specification: 36-43 Analytical range = ±1.4
ACTUAL VALUE: 43.2

RANGE	33.0-34.4	34.5-35.9	36-43	43.1-44.5	44.6-45.9	≥46
SCORE	200	50	0	50	100	200

Parameter score	Batch Quality score
200	
0	250
50	

FIGURE 1.3 Example of a Quality Scoring System for Grading Malt Specifications.

If an analytical result falls outside the specification range, it is assigned a value representing the significance of that to brewing performance. The bands are set approximately matching the analytical variance of the method. Scores can increase more markedly if a parameter is particularly likely to cause a brewing problem over a certain value.

a progressively higher score is assigned to results outside the target range. For some values markedly outside the target range, a jump in quality score can be allocated to indicate this is really not an acceptable batch to blend. A combined score for all the analytes can then be calculated and compared against a grading system for how close to specification is the batch overall (Fig. 1.4). It is also then possible to compare malt production quality for a given period. If a specification is reasonably straightforward

Quality Scoring Bands

Quality Band	A	B	C	D	E	F	G	H
Quality Score	0	2-50	51-99	100-250	251-300	301-400	401-500	>500

FIGURE 1.4 Example of Quality Banding System to Evaluate Batch Performance.

Using this system, the maltster could set an overall performance target of band B. This would mean that, on average, no malt batch was more than one band outside the target specification for just one analyte. This would be a very tightly controlled specification. However, the value would most likely be set for all batches produced in a given period. If the majority of those batches were perfectly in specification and just one was out, the overall performance could still be judged satisfactory.