To DP or not to DP, that is the question?

Extract from a paper presented by Dr Evans at the 29th Convention, Institute of Brewing and Distilling, Asia Pacific Section Hobart, March, 2006.

For more than a 100 years, brewers have relied on the diastatic power (DP) malt specification to predict the potential malt fermentability for brewing. However, there is a growing awareness among brewers that the DP specification may be unreliable and at times down-right misleading. As such, brewers are now looking for ways to characterise malt to ensure that it performs predictably and consistently to their fermentability expectations.

Currently brewers attempt to gauge the fermentability of their malts for brewing by measurement of diastatic power (DP), sometimes with the additional measurement of β-amylase activity and/or AAL (Apparent Attenuation Limit). These parameters usually give some guide as to potential fermentation performance but in some cases are misleading, potentially resulting in difficulties during the brewing process that may produce beer batches that do not meet the brewers desired brand specifications. As such, brewers in industry forums or in private regularly complain that malt specifications, in particular DP, do not provide sufficient guidance as to potential malt fermentability.

While DP is relatively easily and inexpensively measured, fermentability – commonly measured as AAL – is more time consuming. AAL also has biases resulting from the yeast used in its determination, accelerated conditions of fermentation, and that the commonly used Congress procedure (EBC-ASBC mashing protocol) used for wort production is not typical of modern brewing protocols. As is recognised historically by the Institute of Brewing’s infusion mash protocol, the highest fermentability is achieved by mashing in at 65°C compared to the Congress mash protocol at 45°C (Figure 1)

Such changes in the mash in temperature not only influence fermentability, but also result in changes to the fermentable sugar profile. Such changes in the sugar composition, particularly the proportion of glucose and fructose, influences yeast metabolism, the subsequent ester content and flavour of the beer.

What is malt fermentability?

Simply, malt fermentability is determined by the ability of the malt to hydrolyse its starch and that of any unmalted grain adjuncts added, into fermentable sugars, primarily maltose, glucose, and maltotriose. In addition, a modicum of available amino acids and other nutrients is required to sustain optimal yeast growth and maintenance.

It follows that an overall measure of malt starch degrading activity should be an important predictor of malt fermentability. Traditionally this overall activity has been measured by the DP malt quality parameter. DP is a measure of the starch hydrolysing enzymes that are the combined activity of β-amylase, α-amylase, limit dextrinase and α-glucosidase (Figure 2). The actions of the DP enzymes are summarised as follows:

- α-Amylase cleaves α-1,4-linkages internally (endo-acting) to primarily produce oligosaccharides, or limit dextrins.
- β-Amylase cleaves α-1,4-linkages from the ends (exo-acting) to produce maltose.
- Limit dextrinase hydrolyses internal α-1,6-linkages (endo-acting), to remove branch-points in amylopectin or α-limit dextrins.
- β-Glucosidase primarily cleaves α-1,4-linkages from the ends to produce glucose.

Of these enzymes β-amylase and limit dextrinase activity have been most often considered to be the practical limitation to starch hydrolysis.

A superior prediction of malt fermentability?

Recently it has been demonstrated that the prediction of malt fermentability can be improved from predicting ~50% of the variation with DP to ~90% by using an algorithm that combined the activities of β-amylase, limit dextrinase and α-amylase along with β-amylase thermostability and Kolbach Index (KI) (Equation 1). This algorithm is called the DP enzyme multi-linear regression model (MLR).

Equation 1: DP enzyme MLR

\[ \text{AAL} = 69.9 + 0.0174 \cdot \text{A} + 9.602 \cdot \text{B} + 0.1950 \cdot \text{C} - 0.0008 \cdot \text{D} \cdot \text{E}, \quad R^2 = 0.91. \]

Where: \( A = \) α-amylase (U/g), \( B = \) total limit dextrinase (U/g), \( C = \) KI (%), \( D = \) total β-amylase (U/g), \( E = \) β-amylase remaining (%).

The algorithm also conforms to the projected biochemical roles of these parameters in starch hydrolysis during mashing. That is, higher KI is presumably associated with improved access of the DP enzymes to starch and possibly faster access...
of water to allow starch gelatinisation. \(\alpha\) - amylase leads the primary attack on the gelatinised starch to produce substrates for \(\beta\) - amylase and limit dextrinase. Limit dextrinase cleaves the branch points in limit dextrins to produce fermentable sugars and further substrates for \(\beta\) - amylase. This is particularly important when rice is used as an adjunct because rice starch has higher levels of \(\alpha\)-1,6- linkages. \(\beta\) - amylase, the primary determinant of maltose production, is most efficient when there are higher levels of its preferred substrates. 

\(\beta\) - amylase and limit dextrinase are relatively heat labile, compared to \(\alpha\) - amylase above the typical malt starch gelatinisation temperatures of 60-65°C. It has been demonstrated that there is small but important genetic variation in the thermostability of barley \(\beta\) - amylase. It has subsequently been confirmed that the Sd2H \(\beta\) - amylase type (i.e. Haruna nijo, Flagship, Buloke) confers a 2 percentage point increase in AAL compared to similar levels of \(\beta\) - amylase activity in Sd1 (i.e. Gairdner, Harrington, Barke) or Sd2L (i.e. Schooner, Clipper) \(\beta\) - amylase varieties. It should be noted that this high fermentability, is matched by varieties such as Baudin that compensates for the relative lack of \(\beta\) - amylase thermostability by having very high levels of the DP enzymes.

Commercial validation?
Two recent commercially based trials have validated the DP enzyme approach to predicting fermentability. Firstly, trials conducted with the Australian Brewing for Export Consortium (BEC) malts showed that the DP enzyme MLR predicted 90% compared to 42-54% of variation for DP alone, in limit gravity and present gravity, which are ‘in house’ brewery measures of fermentability, in the BEC pilot brewing trials. Secondly, a brewer and their supplying maltster provided a selection of 13 commercial malt blends that were observed in the brewery to have differences in their mashing and fermentability performance that could not be explained by the DP malt quality parameter (Table I). However, assessment of DP enzyme levels clearly explained the differences in mashing and fermentability performance. It is thus proposed that characterisation of malts and melting barley varieties in terms of their DP enzyme profiles will provide melting barley and malt with superior consistency and more assured brewery performance. Such a change in the commercial description of malt and malting barley will increase brewer satisfaction with maltster suppliers and provide sound malting quality targets for malting barley breeding programmes.

**Variation in the levels of DP enzymes in commercial malts**
Grain traders, maltsters and brewers, in the first instance, rely on variety (assuming acceptable grain size and protein content) as a useful indicator of malt quality and potential fermentability. Figure 3, shows that while variety provides somewhat of an indication of fermentability performance, the variation between different samples of the one variety is almost greater than between varieties. For Gairdner (Sd1), AAL varies nearly 5 percentage points, while Schooner (Sd2L) varies 4.5 percentage points. Clearly, selection of Gairdner malt batches that produce higher AAL would presumably better satisfy brewers in China and Japan that demand high fermentability for their starch adjunct brewing styles. Alternatively, Australian brewers, who use liquid adjuncts - no hydrolysis adjunct starch required, would be best satisfied by the Gairdner malt batches that produce lower AAL.

Figure 3 also indicates that Sd2H malts generally produce wort with the highest fermentability, primarily due to the greater thermostability of their \(\beta\) - amylase. Similarly, Schooner malt generally has lower fermentability than Gairdner due to its lower levels of \(\alpha\) - amylase, \(\beta\) - amylase and limit dextrinase in the samples evaluated in this trial. The variation in AAL was a result of variation between samples for the level of \(\alpha\) - amylase, \(\beta\) - amylase and limit dextrinase activity and the balance of these enzymes. Although regression analysis of the relationships between the levels of \(\alpha\) - amylase, \(\beta\) - amylase and limit dextrinase demonstrated that they were significantly correlated, these correlations only explain 17-40% (R2) of the variation. Thus it is evident that the ratios of these enzymes vary substantially in relation to each other and their interdependence, presumably explains why DP is an inferior prediction compared to the DP enzyme MLR.

**Practical implications for delivering malt that satisfies brewers**
Discussions with many brewers both in Australia and internationally have indicated that they value highly predictability and consistency of performance of their malt supplies. It is clear from the evidence presented that the measurement of the individual DP enzymes; \(\alpha\) - amylase, limit dextrinase, \(\beta\) - amylase combined with \(\beta\) - amylose thermostability and KI; provides brewers with a clearly superior prediction of malt fermentation performance.

![Figure 3: Box plots of the variation found for AAL (65°C mash protocol), DP and the activities of the DP enzymes in the 2002/2003 trials for commercial malts (Gairdner: n=18, Schooner: n=12, Sd2H: n=7). Box plots show the extent of variation (bars), with the column indicating the 25th and 75th percentiles, the mean being the horizontal red line in the column and the individual data points being the black points. The overall mean for the data set is the horizontal black line.](image-url)