Improving winter malting barley quality and developing an understanding of the interactions of introgressions with genetic background

Project number | RD-2012-3776
Start date | April 2013 | End date | March 2018

**Project aim and objectives**

Our aim is to utilise knowledge gained from a previous project to introgress specific genetic loci associated with malting quality from the spring into the winter crop to bring the overall quality level of the winter crop up to that of the spring.

Objectives:

1. Augment existing genotypic and phenotypic barley data sets by just under 20% to refine the QTL intervals for our target loci. Design a rapid, cost efficient and practical introgression strategy that will result in the development of several introgression lines for the same resource level as for one line.

2. Produce DH lines that combine the spring introgressions in different winter genetic backgrounds. Introgress winter habit genes into spring barley with minimal winter genetic background.

3. Identify a candidate gene for at least one of the spring QTL. Determine the effect of allelic substitutions at the introgressed loci upon the expression of other genes during the malting process.

**Key messages emerging from the project**

1. The genetic yield potential of spring and winter barley is continuing to increase and can be ascribed to breeding and selection of better combinations of genes.

2. The HGCA Recommended List system is effective in identifying the higher yielding lines.

3. While current spring barley varieties are much less diverse than those from the 1990s and early 2000s, there is still considerable genetic variation to make further breeding progress.

**Summary of results from the reporting year**

We have combined data from National and HGCA Recommended List fungicide-treated trials grown since 1990 to derive predicted means for more than 380 spring and more than 370 winter barley lines. Regressing these data against the year in which each line was first submitted to National List trials shows a highly significant and positive relationship. This clearly demonstrates that the genetic yield potential of both crops is increasing and can be ascribed to breeding and selection of better combinations of genes.

The results described in this summary report are interim and relate to one year. In all cases, the reports refer to projects that extend over a number of years.

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Separating the lines into three classes: those that were in National List trials but were not selected as candidates for the Recommended List, those that were selected as candidates but not placed on the Recommended List, and those that were recommended, shows that the rate of progress is greatest among the lines that were placed on the Recommended List. This clearly demonstrates that the Recommended List system is effective in identifying the higher yielding lines.

Comparison of the relationships among all lines that have been on the UK barley Recommended Lists since 1990 shows that current spring barley varieties are much less diverse than those from the 1990s and early 2000s. Nevertheless, the two most similar varieties are the winter barleys Angora and Melanie, which differ at just 42 genes from over 6,900 genetic loci (approximately 99.4% similarity). These two lines were sister selections from the same cross and could only be distinguished by different storage protein SDS-PAGE banding patterns so their extreme similarity is to be expected. The next two most similar lines are KWS Joy and Wintmalt, the latter being a parent of the former. These lines show approximately 98.2% similarity but also have contrasting aleurone colours. Montoya and Quench are the two most similar spring recommended varieties, with approximately 94.6% similarity. For comparison, Concerto and Quench, which are the parents of, for example, Chronicle, Odyssey, Overture, and Shuffle, are approximately 73% similar. This indicates that there is still considerable genetic variation that can be used to make further progress in barley breeding.

Key issues to be addressed in the next year

1. Extend the phenotypic analyses to other performance characters, especially malting quality parameters.
2. Add genotypic data from the 2014 additions to the National List to the current data set.
3. Add relevant data from 2013 Recommended List and 2011–2013 National List trials to the data sets.

Has your project featured in any of the following in the last year?

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<thead>
<tr>
<th>Events</th>
<th>Press articles</th>
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<tr>
<td>Conference presentations, papers or posters</td>
<td>Scientific papers</td>
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<td>Other</td>
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