IMPROMALT: 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. *Completed by Month 57.*
2. Design a rapid, cost-efficient and practical strategy that will result in the development of several introgression lines for the same resource level as for one line. *Completed by Month 24.*
3. Produce DH lines that combine the spring introgressions in different winter genetic backgrounds. *Completed by Month 36.*
4. Introgress winter habit genes into spring barley with minimal winter genetic background. *Completed by Month 36.*
5. Identify a candidate gene for at least one of the spring quantitative trail loci (QTL). *Completed by Month 60.*
6. Determine the effect of allelic substitutions at the introgressed loci upon the expression of other genes during the malting process. *Completed by Month 60.*

Key messages emerging from the project

1. The genetic potential for treated and untreated yield has significantly increased since 1990, but there has also been a significant decrease in specific weight.
2. Hot water extract has significantly increased for both crops, accompanied by a significant decrease in grain nitrogen content.
3. Whilst there has been a significant decrease in mildew infection in both crops and rhynchosporium infection in the winter crop, there is no evidence of any improvement in the genetic potential for brown rust resistance.
4. This information has been particularly valuable in targeting the exact segments of chromosomes effecting spring malting quality for introgression into winter barley in the BBSRC LINK sponsored work packages.
Summary of results from reporting year

All the data, up to and including harvest 2012, was analysed to generate predicted means for each genotype for 40 agronomic, yield, disease resistance, and malting quality characters, although there was insufficient data in for some characters in either the spring crop or the winter crop. For Recommended List (RL) varieties, we regressed the mean for each character against the year in which they were first placed on the RL; a significant regression indicates that the character has changed over time, reflecting breeding progress. We surveyed the period from 1990 to 2013 to confirm the improvement in treated yield reported last year, but also detected a significant improvement in untreated yield, accompanied by a significant improvement in mildew resistance in both crops. The latter could be attributed to a greater number of RL spring varieties with the mlo resistance gene, but the improvement in resistance in the winter crop must be due to the incorporation of other resistance factors as the mlo allele is not found in RL winter barley varieties. The only other improvement in disease resistance was for rhynchosporium in the winter crop. Whilst there had been an improvement in the thousand grain weight of the spring crop that might explain the yield improvement in the crop, there was no trend in the winter crop, suggesting that yield improvement in the latter must be due to other components of yield, such as increasing seed number/m².

We conducted a similar analysis for the malting quality parameters, but with an additional restriction to just those lines that had been at least given a provisional approval by the Institute of Brewing and Distilling. For both crop types, we detected a significant decrease in grain nitrogen content and a significant increase in hot water extract over time. Whilst there is a relationship between these two characters, multiple regression showed that there had still been a highly significant improvement in hot water extract over time. There was little evidence of any other strong trends over time for either crop. Significant decreases were detected for germination under 4ml and under 5ml of water for the spring crop, and for wort viscosity in the winter crop. The latter is a desirable effect but the germination effects are a slight concern, although the general levels of germination are still high.

The addition of the extra phenotypic data, coupled with the extra SNP genotypic data, has had a major impact upon the resolution of the QTL that we are introgressing into winter barley in the BBSRC-funded work packages of IMPROMALT. The confidence interval surrounding the QTLs on chromosomes 1H and 3H have at least been halved so we now have well-defined targets that can be selected using the appropriate marker combinations.

At the time of writing, we are still awaiting receipt of all the data from 2013 and 2014 trials and will conduct a re-analysis once that is all assembled into the database.

Key issues to be addressed in the next year

1. Add genotypic data from the 2014 additions to the National List to the current data set
2. Add data from 2014 Recommended List and 2011–2014 National List trials to the data sets
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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Has your project featured in any of the following in the last year?

- **Events**
  - Hot Rum Cow Magazine (October 2014)
  - Friends of The Scotsman Article (July 2014)
  - BBC Radio Scotland (April 2014)
  - Scotland on Sunday (April 2014)
  - The Times (April 2014)
  - The Scotsman (April 2014)
  - The Press and Journal (April 2014)

- **Press articles**

- **Conference presentations, papers or posters**

- **Scientific papers**

- **Other**