Annual Project Report
April 2015 to March 2016

Project title: 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: 1 April 2013
End date: 31 March 2019

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 quantitative trait loci (QTL) intervals for our target loci. Completed by Month 57.
2. 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. Completed by Month 24.
3. Produce DH lines that combine the spring introgressions in different winter genetic backgrounds. Completed by Month 48.
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 QTL. Completed by Month 72.
6. Determine the effect of allelic substitutions at the introgressed loci upon the expression of other genes during the malting process. Completed by Month 72.

Key messages emerging from the project

1. Breeding progress is being made in spring and winter barley for yield and some quality characters.
2. There is plenty of genetic variation in RL varieties as 50% of the genetic markers are polymorphic amongst them.
3. Whilst breeding has improved untreated as well as treated yield, there is no evidence of any narrowing of the gap between fungicide treated and untreated yields.
4. Varieties that are less responsive to fungicide applications tend to carry the resistant allele at the mlo powdery mildew resistance locus.
5. Markers have enabled the rapid introgression of spring quality characters into winter lines with some lines being multiplied for evaluation in harvest 2017.

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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6. Maris Otter features in the pedigrees of all UK winter malting barley varieties but genotyping shows that more recent varieties such as SY Venture carry <70% of the alleles found in Maris Otter. Have some of Maris Otter’s attributes been lost amongst the 30% of the substituted alleles?

**Summary of results from the reporting year**

We have augmented the previous findings by adding in another 41 lines that had been added to the National Lists in 2013 and 2014 to make a total of 713. We also updated the phenotypic data to include results from harvests 2013 and 2014 so that we now have a continuous span of data from 1988 through to 2014 that has enabled us to continue to examine trends in Recommended List trials. These continue to show breeding progress for yield for a number of quality characters but there is little evidence of breeding progress for disease resistance. We also restricted the data set to sites where treated and untreated trials were in common and derived a yield response for each line at each site. This showed that, whereas breeding had improved untreated yield, it had not altered the response to fungicide treatment. In spring barley, the absence of a disease control reduced yield by an average of 11.2% but it was an 18.3% decrease in winter barley, equivalent to a loss of 1.5t/ha.

We have combined the phenotypic and genotypic data to revise our analyses of marker trait associations and find at least one genomic region affecting most of the 42 spring and 40 winter barley characters that we analysed. In total, we detected 244 significant marker trait associations for spring barley and 236 for winter with hot-spots (more than 10 significant associations) on chromosomes 2H, 3H, 5H, and 6H. We did detect significant QTL for yield response to fungicide in both crops; whilst the majority were co-located with QTL for treated and/or untreated yield, some were not, although most of these were also associated with disease resistance loci where alleles for resistance were associated with improved untreated yield, as expected.

We have combined the genotypic data with pedigree relationships to trace the persistence of alleles from the old winter malting barley variety Maris Otter through other UK winter malting barleys to current lines such as SY Venture. Some 85% of the alleles found in Maris Otter were found in older malting varieties like Halcyon and Pipkin but this had decreased to under 70% in more recent malting varieties such as Cassata and SY Venture. For comparison, the old and modern feed barleys Igri and KWS Glacier contain around 65% Maris Otter alleles, as does the modern spring barley Concerto. Clearly some of the allelic substitutions have contributed towards an increased yield but Maris Otter is claimed to have some unique flavour characteristics in brewing so some of the allelic substitutions could also have affected flavour.
Data gathered on diastatic power during the project has been used in the AHDB-funded DPGENES project to help identify bulks of extreme lines that can be used to identify genes affecting diastatic power that could be used to select for a high level of the character.

Key issues to be addressed in the next year

1. Add in new additions to the National List made in 2015 and 2016
2. Add in new phenotypic data sets
3. Publish the genotypic analysis of Maris Otter

Other issues are being addressed under the BBSRC sponsored work-packages.

Lead partner | James Hutton Institute
Scientific partners | NIAB (BBSRC sponsored work packages)
Industry partners | KWS (UK), Limagrain, MAGB, MRS, RAGT, Saaten Union, Secobra, SWRI, Syngenta
Government sponsor | BBSRC LINK, Scottish Government

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

| Events | Press articles |
| Conference presentations, papers or posters | Scientific papers |
| Other |

We have developed www.barleyhub.org as a Barley Information Portal over the past year to highlight aspects of UK barley research and the industry. IMPROMALT is featured on the site with general information available to the public and project specific information restricted to the Consortium. We have also developed https://www.facebook.com/barleyhub/ as a companion to the website and promote aspects of barley research and growing to the wider public. This has proved a useful way to highlight topics such as the persistence of Maris Otter to current winter malting barley varieties.