Annual Project Report
April 2016 to March 2017

Project title | IMPROMALT: Improving winter malting barley quality and developing an understanding of the interactions of introgressions with genetic background
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Project number | 21130013
Start date | 1/4/13
End date | 31/3/19

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. Complete 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. Complete by Month 60.
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. Complete by Month 72.
6. Determine the effect of allelic substitutions at the introgressed loci upon the expression of other genes during the malting process. Complete by Month 72.

Key messages emerging from the project

1. There is clear evidence of separation over time in spring and winter barley varieties recommended to farmers with much less variation amongst current and more recent varieties.
2. Within spring barley, there is also clear separation between the varieties that have been derived from Triumph and other varieties, including Proctor and Golden Promise. Does this mean that some of the attributes of older UK varieties have been lost from the current elite gene-pool?
3. Deficient (absence of or rudimentary lateral florets) spike types now dominate the 2-row winter barley market and are significantly increasing in the spring market.
4. The breeding cycle is clearly in the order of 3 years within breeders own programmes. Official Testing and multiplication now takes longer than the breeding and selection of a potential new variety.
5. Lines are being grown in trials for harvest 2017 that will then be used in the initial assessment of whether the introgression of variation of selected spring segments will improve winter barley quality.

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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Summary of results from the reporting year

We were able to sow trials of introgression lines from four of the six backcross series made for the project. For each cross, we have lines that carry all three introgressed segments and these can be compared to lines that lack all three in micro-malting analyses. Using a set of selected KASP markers designed for specific iSelect 9k SNPs, we evaluated the background genotype of all the lines that have been entered into the trials together with a fifth cross that will be entered into trials for harvest 2018. These results showed that the donor allele frequency rose in the region of the introgression target but was relatively low across the rest of the genome, which reflects the genetical success of our strategy.

We were able to use our genotyping data to show that the old spring malting variety Golden Promise is more similar to Maris Otter and all other successful winter malting varieties of the past 25 years (over 50,000t purchased by MAGB member companies) than to current and other Triumph derived spring varieties. This reflects a shared ancestry of the two lines and further highlights the genetic differentiation between older and newer spring varieties.

The integration of lines added to the National List since 2014 and the associated additional phenotypic data gathered for harvest years 2014-16 has been delayed for two reasons. The first is that new genomic information has enabled the development of a 50k iSelect SNP chip that has been designed specifically for the world elite gene pool with no ascertainment bias. As this is cheaper than the 9k iSelect platform, we have delayed the genotyping of the additional lines to take advantage of the new platform that contains all the functional markers from the 9k platform and so will enable integration of the new data. In addition, we will take advantage of the cost saving to re-genotype the existing lines so we plan to have 50k (44k target SNPs) data on all the IMPROMALT lines by the end of the project. The second reason is that access to the phenotypic data has been delayed due to the implementation of a new AHDB/BSPB MTA to access the data, which is yet to be finally resolved although we think JHI and AHDB have now reached an agreed position.

Key issues to be addressed in the next year

1. Genotype the 2014-17 additions to the National List with the new iSelect 50k SNP chip
2. Re-genotype the existing IMPROMALT lines with the 50k chip
3. Integrate the relevant phenotypic data collected from harvest years 2014-16 into the dataset
4. Re-do the association analyses for at least the yield and malting quality data
5. Determine if breeding progress is still being made
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