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**Project title**
IMPROMALT: Improving winter malting barley quality and developing an understanding of the interactions of introgressions with genetic background

**Project number**
21130013

**Start date**
1 April 2013

**End date**
31 March 2019

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**Project aim and objectives**
The aim of this work is to introgress specific genetic loci associated with malting quality from spring barley into winter barley 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.
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.
3. Produce double haploid (DH) lines that combine the spring introgressions in different winter genetic backgrounds.
4. Introgress winter habit genes into spring barley with minimal winter genetic background.
5. Identify a candidate gene for at least one of the spring QTL.
6. Determine the effect of allelic substitutions at the introgressed loci upon the expression of other genes during the malting process.

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**Key messages emerging from the project**
1. The Circle of Barley is a visualisation of the genetic relationships among barley varieties placed on the UK Recommended Lists since 1970. It shows the separation into five major groups that reflect crop type and age, with fewer differences between more modern varieties (Figure 1).
2. The Scottish barley crop is insufficient to meet the demand of the Scotch Whisky industry, with at least 200,000t needing to be supplied from outside Scotland.
3. The extra yield of winter barley more than compensates for a malting quality penalty; currently winter crop would produce more barrels per hectare.
4. Introduction of novel spring genes to improve the malting quality of the winter crop would reduce the land demand of Scotch Whisky production by approximately 20%.
5. First-year malting results indicate that the spring genes have significantly improved the malting quality of the malting winter parents across 3 different genetic backgrounds.
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### Summary of results from the reporting year

#### Figure 1 Circle of barley (UK RL varieties)

- Analysis of the micro-malting data from the first year yield trials show that introgression of the three spring genetic segments into winter barley improved the malting quality of:
  1. UK winter two-row malting barley SY Venture, an established variety
  2. UK winter two-row barley KWS Joy, a variety that was under malting tests but dropped
  3. French six-row malting barley Etincel, which is used in France and exported.
- Improvement is in Malt Extract, which will lead to an improvement in Spirit Yield for the distilling industry.
- Friability of the malt also improved significantly, indicating that the processability of winter barley malt is also likely to have been improved.
- Results for Diastatic Power (the starch digesting ability of a malt) are less clearcut but early indications that the replacement of the low beta-amylase thermostability allele found in current winter barley varieties with a medium thermostability allele found in many contemporary spring barleys has not significantly increased Diastatic Power.
- Genotypic analysis of the winter malting winter additions to the 2018 Recommended List show that Electrum is most similar to SY Venture, Craft and Talisman, whereas Coref is most similar to Archer and Cassata.
- Similarly, in spring barley, RGT Asteroid is most similar to RGT Planet and LG Diablo, and LG Tomahawk are most similar to Laureate.
- Data from trials up to harvest 2017 have been added to the project and used to detect genomic regions affecting the genetic control of a range of disease, yield and quality characters.
Key issues to be addressed in the next year

1. Harvest second-year yield trials and measure proportion of grain retained by a 2.5mm sieve on all samples and combine with grain size and weight analyses to determine if introgression of the spring genetic segments has affected these characters.
2. Select samples for micro-malting analysis by member companies of MAGB
3. Genotype 2018 NL additions, add in data up to 2018 harvest for these lines and do a final association genetics analysis to identify genetic regions affecting phenotypes measured in NL and RL trials.

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?

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<th>Events</th>
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<tr>
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