

Final Project Summary

Project title	MAGIC map and go: deploying MAGIC populations for rapid development and dissemination of genetic markers for yield improvement in elite UK winter wheat		
Project number	21130017	Final Project Report	PR610
Start date	01/01/15	End date	28/02/19
AHDB funding	£99,544	Total cost	£803,690

What was the challenge/demand for the work?

Wheat is the UK's most important crop. Genetic gains in wheat grain yield are around 1% per year. Breeding companies would benefit from the ability to track the wheat genetic regions and genetic variants that determine yield to underpin future wheat yield genetic gains. The development of molecular tools to facilitate this would benefit breeders and, ultimately, growers, processors and consumers.

How did the project address this?

This project used a large wheat genetic mapping population, termed the 'NIAB Elite MAGIC' population. The population was generated by inter-crossing eight UK-grown wheat varieties, over three generations, to produce more than 1,100 progeny lines. In this project, these lines were grown at five UK sites over two seasons, delivering 4,996 2x6m field plots. For each plot, 18 yield, yield component and agronomic traits were measured. This generated ~90,000 trait data points that were combined with a genetic marker dataset for the population – this consisted of information for ~20,000 specific locations within the wheat genome. 376 regions of the wheat genome, which control the 18 traits, were identified. A subset (20 regions) was analysed further by:

1. Developing 58 genetic markers to predict the effect specific variants of these chromosomal locations have on the trait.
2. Predicting the gene content within these chromosomal locations and identifying subsets of these thought to most likely be involved in the relevant trait (termed 'candidate genes').
3. Identifying chemically induced mutants of candidate genes to allow studies to confirm their effect on the trait, and potentially uncover additional useful variation to help increase yield.
4. Developing pairs of wheat lines that differ only at the chromosomal location found to control the difference in trait expression – such resources allow precise characterisation of the effects of the genetic regions and provide the basis for the identification of the genes underlying each of the targeted genetic loci.

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What outputs has the project delivered?

The project has:

1. Delivered extensive datasets for 18 traits across ~5,000 field plots.
2. Extensively characterised the genetic control of these traits, identifying 376 regions of the wheat genome that influence their expression.
3. For a subset of 20 of these regions, developed genetic markers that tag the contrasting genetic variants at the target chromosomal regions.
4. Identified artificial mutations in 23 candidate genes, providing resources to identify the genes and natural variants underlying the 20 targeted chromosomal regions.
5. Developed a series of wheat stocks that contrast at each of the targeted chromosomal regions, which will help further refine and investigate the underlying genes controlling the targeted traits.

Who will benefit from this project and why?

This project will benefit:

1. The five breeding companies that co-funded the work, through the early exploitation of results and the project deliverables (e.g. genetic markers).
2. Growers, processors and consumers, through the development of new, more efficient wheat varieties.
3. The wheat R&D community, through the provision of a wide set of novel tools and resources to help identify the genes (and their natural variants) that underlie the chromosomal regions identified here as controlling yield and yield components.

If the challenge has not been specifically met, state why and how this could be overcome

N/A

Lead partner	NIAB
Scientific partners	
Industry partners	BASF, Elsoms seeds Ltd, KWS UK Ltd, Limagrain UK Ltd, RAGT Seeds Ltd.
Government sponsor	BBSRC

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