

Final Project Summary

Project title	The potential for association mapping from historical trait data in wheat and barley		
Project number	RD-2006-3316	Final Project Report	SR36
Start date	01 March 2007	End date	28 February 2010
AHDB Cereals & Oilseeds funding	£20,000	Total cost	£120,000

What was the challenge/demand for the work?

Plant breeding continuously produces new cultivars (varieties) of agricultural crops, which are independently evaluated in field trials prior to commercialisation. Variety evaluation has been ongoing in England and Wales since the 1930s and has been a statutory requirement in the UK since 1963. In wheat, the application and precision of molecular breeding is hampered by the comparative paucity of markers linked to economically important agronomic traits. Traditional methods of trait marker discovery are slow and expensive in terms of population production, collection of phenotype data and molecular biology.

The aim of this project was to develop generic approaches using historic plant variety phenotype data sets in association mapping studies, to test these by their application to data generated over recent decades as part of wheat variety recommendation and registration. The chosen species represent those with the most complete historic phenotype databases and the least within-variety genetic variation.

How did the project address this?

This project examined the population structure and cryptic relatedness in the available panels with reference to their confounding effects on association mapping. Different analysis methods were considered and mixed effects modelling was identified as the most reliable. Association analysis of Mendelian and quantitative traits was conducted and the results compared with the success rate expected from simulation.

Phenotypic data has been recorded on varieties in evaluation trials annually for nearly a century. Establishing the completeness of digital records and the scope for digitising additional paper records was an important step in this research. Since genetic homogeneity was expected, it was not necessary for genotyping to extend to multiple accessions from the same variety, however some replication of some varieties would serve to confirm the assumed homogeneity. There was good reason to expect population substructure within panels of wheat and barley and there evidence of kinship moving in parallel with phenotype over time.

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What outputs has the project delivered?

- Despite the current limits on panel size imposed by numbers of varieties, available data and genotyping technology, it is possible to conduct successful association studies in wheat and barley using historical phenotypes and germplasm from seed banks.
- Structure/kinship imposed by breeding activity lead to very strong confounding signals which can swamp genuine associations in many cases. These effects may be controlled by various regression techniques but the most consistently effective is mixed effects modelling. The use of a kinship matrix based on correlation is a useful way to summarise both kinship and structure in the same model.
- Using existing varieties and historic phenotypes, has proved useful and offered ready access to the ingredients necessary for association analysis.
- The barley population was more successful because the smaller, simpler diploid genome had allowed higher marker density and the diverse barley lines shared a common set of botanical descriptors which were largely independent of environment.

Who will benefit from this project and why?

The project demonstrated the strategic value to research of a contiguous and high quality dataset collected as a tactical economic imperative. It uncovered allelic variability of value to plant breeding. The project also helped the process of wheat variety breeding, selection and development, which is increasingly demanding different traits and trait combinations from new varieties and it unlocked diverse phenotype databases as raw material for association mapping. Ultimately, it delivered a new generation of varieties adapted to agriculture conducted with a stewardship focus and in a warmer and dryer climate.

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

Using varieties and historic phenotypes available for this project has proved useful and offered ready access to the ingredients necessary for association analysis. However, the short period that most varieties spend in trial (less than two years) made much of the available phenotypic data insufficient for use. This, coupled with the problem that un-registered varieties, remains the private property of breeders. Alternative sources of germplasm will be needed if association mapping is to fulfil its potential.

Lead partner	NIAB
Scientific partners	Imperial College London
Industry partners	Crop Evaluation Ltd
Government sponsor	

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