



New Project

CP 94

HDC Studentship:

Genetic mapping and high throughput phenotyping of fruit quality traits in Fragaria x ananassa.

Project Number:	CP 94
Project Title:	Genetic mapping and high throughput phenotyping of fruit quality traits in Fragaria x ananassa HDC Studentship
Project Leader:	R J Harrison.
Contractor:	East Malling Research
Industry Representative:	Harriet Duncalfe, Maltmas Farm
Start Date:	1st October 2012
End Date:	28th February 2015
Project Cost:	£67,650

SUBJECT TO CONTRACT

Project Summary:

Marker-assisted selection (MAS) has remained an unrealised ambition of fruit breeders. However, due to recent work at EMR, we are now in a position to begin using MAS in strawberry breeding. Costs to-date have been enormous and the markers available are still limited as they aren't always linked to the phenotype of interest in all cultivars. Furthermore, MAS could still be costly, as thousands of individuals may need to be genotyped, depending upon the trait and the breeding options available.

This project aims to cut the cost of breeding by linking genotypes identified from phenotyping in the field, to both molecular-level, tissue-level and whole-plant phenotypes in the laboratory. This way, populations with desirable genotypes can be cheaply screened in the laboratory. If reliable phenotypic markers for a number of desirable traits can be determined, then the ability to quickly advance promising plants into trial would lead to significant savings.

Aims & Objectives:

(i) Project aim(s):

To map novel fruit quality and disease resistance traits in Fragaria x ananassa, and using a high-throughput phenomics approach develop inexpensive ways of linking phenotype to

genotype. We aim to answer the question: Can agronomically important phenotypes that are currently screened in the field be replicated in the laboratory and rapidly screened, in order to decrease the time and expense of traditional and marker-assisted breeding programmes?

(ii) Project objective(s):

The rigorous phenotyping (determining the characteristics) of plants in the field is a labour intensive task. Methods developed in the laboratory for fast and accurate phenotyping of model organisms (such as the weed Arabidopsis thaliana) should be adapted and applied to agronomically important crops such as strawberry in order to screen large populations for desirable and undesirable phenotypes as part of a high-throughput marker assisted selection programme. Here we propose to use strawberry as a model, however in principle these approaches can be applied to any crop species. Perennial species and fungal species are particularly appropriate as many of the ideas in this proposal stem from research work carried out on fungi.

This proposal consists of three major objectives:

Part I- linking phenotype to genotype in the field

- 1 Take an existing mapping progeny (a cross between two plants for which the segregation pattern of markers is already known) segregating for fruit quality and disease resistance, and phenotype them in the field for fruit quality traits.
- 2 Using the existing marker data from an ongoing project, identify Quantitative Trait Loci (QTL) linked to fruit quality traits.
- 3 Develop extra genetic markers, closely linked to major-effect QTL (the primary genes controlling the trait), for easy use in marker-assisted selection.

Part II- linking phenotype to genotype in the laboratory

- 4 Develop protocols in the laboratory using leaf, stem, fruit and shoot extracts to identify whether there are measurable compounds in these tissues that are correlated with the favourable fruit quality and disease resistance traits in the field.
- 5 Initiate a tissue culture collection of a set of plants from the mapping population (determined by the outcome of objectives 1. and 2.) with both favourable and unfavourable fruit traits and develop a screen to determine phenotypic markers, that are linked with the trait of interest, present in these plants at various stages of tissue culture.

Part III- testing the methods

- 6 Create a new mapping population from a different cross of unrelated progeny in the laboratory on artificial growth medium that, utilising the results from part I and II, has been pre-screened for presence of the major effect markers.
- 7 Screen this seedling population for correlated phenotypic markers determined in objectives 4 and 5.
- 8 Take progeny displaying the phenotype of interest and genotype them to validate the presence of the genetic marker.
- 9 Feed findings into the Strawberry breeding programme at East Malling Research.

Benefits to industry

If marker-assisted selection is to become a mainstream technique in perennial fruit crops, then it must yield a significant competitive advantage over traditional breeding programmes. This is likely to become a reality in the next few years in part due to the advances in DNA sequencing technologies, that so far remain underused in the applied horticultural sector. This project aims to examine, whether by applying high-throughput phenotyping methodologies, (initially developed for model organisms) to breeding programmes, along with the benefits offered by marker-assisted selection, a significant saving can be made in the early stages of variety development. Furthermore, it is likely that, if successful, this work would provide the initial data required to begin the evaluation of marker-assisted selection as a commercial service, available to other breeders and growers.

This project provides valuable training in both applied genetics and plant breeding. There is currently a lack of trained plant breeders in the UK, EMR is currently the only English institution with plant breeding expertise in strawberry. This project would train a new generation of plant breeder, who has both molecular and field skills in order to build UK expertise that can be used to aid UK growers.

No additional costs would be incurred by growers using MAS lines, indeed the cost would be anticipated to be lower due to reduced need for spray treatments etc.

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Further information

Email the HDC office (hdc@hdc.ahdb.org.uk), quoting your HDC number, alternatively contact the HDC at the address below:

HDC AHDB Stoneleigh Park Kenilworth Warwickshire CV8 2TL

Tel - 0247 669 2051

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