Grower Summary

CP 094

Genetic mapping and phenotyping of fruit quality and disease resistance traits in octoploid strawberry *(Fragaria × ananassa)*

Annual 2014

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Project Number:	CP 094
Project Title:	Genetic mapping and phenotyping of fruit quality and disease resistance traits in octoploid strawberry (*Fragaria* × *ananassa*)
Project Leader:	R.J. Harrison
Contractor:	East Malling Research
Industry Representative:	M. Regan, Hugh Lowe Farms
Report:	Annual Report 2014
Publication Date:	31 December 2014
Previous report/(s):	Annual Report 2013
Start Date:	01 October 2012
End Date:	01 October 2015
Project Cost:	£67,650

Headline

- Phenotypic and genotypic information can be used for quantitative trait loci (QTL) mapping approaches and enhance breeding efficiency through marker-assisted selection (MAS).

Background and expected deliverables

Strawberry is one of the most economically important fruit crops and it is essential to maintain the profitability and sustainability of this crop. Today, strawberry growers face increased production challenges, such as maintaining yield, fruit size and good fruit quality. These traits rely on good plant architecture and high levels of pest and disease resistance. In order to maintain competitiveness, the extension of cropping season and better adaptation to the particular growing environment is essential.

The objective of this project is to provide both phenotyping and genetic techniques to improve high-throughput trait identification in industry-funded breeding programmes. Currently very little is known about how different plant traits are correlated at the molecular level in strawberry, or which traits are the easiest to measure in field and glasshouse scenarios.

The primary aim of this study is to investigate correlations between different physical traits in cultivated strawberry (*Fragaria* × *ananassa*), in addition to the development of novel methods of linking phenotype to genotype. A second aim is to identify and map novel traits linked to fruit quality and disease resistance in cultivated strawberry.

Once molecular markers are identified, pre-screening process of seedlings for the presence of desired alleles can be done through MAS. This study will also illustrate the usefulness of high resolution phenotyping and genomic-assisted selection techniques for rapid, inexpensive and accurate pre-selection of superior seedlings in economically important crops such as cultivated strawberry.

Summary of the project and main conclusions

This project aims to cut the cost of breeding by developing novel phenotyping methods and identifying the most important traits to measure both linked to fruit quality and disease resistance in cultivated strawberry. A mapping population derived from the cross 'Redgauntlet' × 'Hapil' was used for phenotypic data collection over a period of 2 years (2013 and 2014), linkage map construction and saturation, as well as quantitative trai loci

(QTL) detection. The same population will be used for fruit-related trait phenotyping for the third year (2015 summer). As previously reported in the Year 1 report, over 20 different traits of 'Redgauntlet' × 'Hapil' population were recorded and correlation analysis was conducted.

This report is mainly focusing on the saturation of the existing SSR-based linkage map and preliminary QTL analysis using Year 1 (2013) phenotypic data. Twenty six novel markers were mapped to the linkage map which was used for QTL detection. Thirty-three potential QTL associated with both fruit quality and plant characteristics traits were identified. The regions of QTL detected on the linkage map suggest that there is a 'hotspot' region of the strawberry genome. The 'hotspot' region contains overlapping 9 different QTL covering major fruit quality and plant characteristics traits.

Preliminary study of the comparison of the regions between QTL associated with *Verticillium* wilt resistance obtained from the previous study and QTL detected in this study was carried out. However results are not presented in this report. Overlapping regions between *Verticillium* wilt QTL and fruit quality and plant characteristics traits were identified. Further analysis will be carried out in 2015 to investigate if disease resistance QTL are overlapped using 2 years (2013 and 2014) phenotypic data and these results will be presented in the final year report.

'Sonata' × 'SDBL123' mapping population will mainly be used to test the applicability of novel molecular markers developed in this study that can be later used in MAS.

Financial benefits

For this interim report it is not appropriate to undertake a cost/benefit analysis.

Action points for growers

There are no action points for growers at this stage of the project.