



# **Grower Summary**

## **Next Generation Berries – Implementing Genome-wide Selection Approaches in Strawberry**

**CP163**

Annual report 2018

**Project title:** Next Generation Berries – Implementing Genome-wide Selection Approaches in Strawberry

**Project number:** CP163

**Project leader:** Richard Harrison, NIAB EMR  
Michael Shaw, University of Reading

**Report:** Annual Report; September 2018

**Previous report:** Annual Report, September 2017

**Key staff:** Joe Q He, NIAB EMR

**Location of project:** NIAB EMR

**Industry Representative:** Tom Rogers,  
Soloberry Ltd.,  
Rumwood Green Farm,  
Maidstone, UK,  
ME17 3ND

**Date project commenced:** 01/10/2016

## DISCLAIMER

*While the Agriculture and Horticulture Development Board seeks to ensure that the information contained within this document is accurate at the time of printing, no warranty is given in respect thereof and, to the maximum extent permitted by law the Agriculture and Horticulture Development Board accepts no liability for loss, damage or injury howsoever caused (including that caused by negligence) or suffered directly or indirectly in relation to information and opinions contained in or omitted from this document.*

*© Agriculture and Horticulture Development Board 2018. No part of this publication may be reproduced in any material form (including by photocopy or storage in any medium by electronic mean) or any copy or adaptation stored, published or distributed (by physical, electronic or other means) without prior permission in writing of the Agriculture and Horticulture Development Board, other than by reproduction in an unmodified form for the sole purpose of use as an information resource when the Agriculture and Horticulture Development Board or AHDB Horticulture is clearly acknowledged as the source, or in accordance with the provisions of the Copyright, Designs and Patents Act 1988. All rights reserved.*

*All other trademarks, logos and brand names contained in this publication are the trademarks of their respective holders. No rights are granted without the prior written permission of the relevant owners.*

*The results and conclusions in this report are based on an investigation conducted over a one-year period. The conditions under which the experiments were carried out and the results have been reported in detail and with accuracy. However, because of the biological nature of the work it must be borne in mind that different circumstances and conditions could produce different results. Therefore, care must be taken with interpretation of the results, especially if they are used as the basis for commercial product recommendations.*

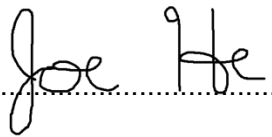
# AUTHENTICATION

We declare that this work was done under our supervision according to the procedures described herein and that the report represents a true and accurate record of the results obtained.

Joe Q He

PhD Student

NIAB EMR

Signature .....  ..... Date .....

[Name]

[Position]

[Organisation]

Signature ..... Date .....

## Report authorised by:

[Name]

[Position]

[Organisation]

Signature ..... Date .....

[Name]

[Position]

[Organisation]

Signature ..... Date .....

# GROWER SUMMARY

## Headline

Genomic Selection (GS) is likely to increase the genetic gain per unit time in strawberry breeding programmes.

## Background

Strawberry breeders aim to generate novel genotypes that express traits suitable for the industry in their target region. Over the past 200 years, significant progress has been made in traits such as flavour, berry size, yield, disease resistance and cropping season duration. Current goals in strawberry breeding include improvements in maintenance of post-harvest fruit quality, yield, texture and flavour.

Traditionally, crossing is conducted based on identification of desirable traits in parental germplasm material. Offspring from a cross are assessed throughout the growing season and scored on a weighted index of favourable traits. The highest scoring individuals are selected to progress onto further larger scale trials, where additional information, such as yield and picking speed are gathered, and to confirm the presence of the favourable traits. Additionally, the selected genotypes are assessed for suitability across a range of environmental conditions, with particular focus on the target region. Overall, making crosses to release of a novel cultivar may take between 7 and 10 years.

Genetic markers are detectable features within the genome of a plant that may differ between individuals of the same species. Markers that are physically close to genetic variants controlling economically important traits tend to be co-inherited with the desirable genetic variant when the plant produces offspring, making some markers reliable proxies for these genes. Over the past 20 years, the number of known markers has dramatically increased and the cost of identifying them has greatly decreased. It is now possible to incorporate genomic information in the breeding process to aid breeders in selection of the optimal individuals.

Genomic selection (GS) offers a range of benefits relative to conventional breeding approaches. Firstly, it allows for greater selection accuracy as the confounding environmental effects on a trait can be eliminated. Secondly, it allows for strong selection on traits that are expensive or difficult to assess or selection on traits that are apparent only under rare environmental conditions. Thirdly, as multiple traits can be assessed, GS potentially allows

selection at the juvenile stage, reducing the duration of the breeding cycle. Moreover, GS is particularly suitable for identification of traits that are controlled by many genes (polygenic traits) as its simultaneous regression of all markers on all traits reduces the likelihood of over/underestimation of effect size. GS also potentially allows control of inbreeding and elimination of certain field experiments.

## Summary

Deployment of genomic selection (GS) in strawberry breeding programmes is likely to increase genetic gain per unit time. Three areas for improvement in current GS approaches were identified to make GS more accessible for commercial breeders:

1. High-throughput Quantitative 3D Phenotyping of Strawberry Fruit. The most powerful models for GS require quantitative inputs to generate quantitative predictions of breeding value. Currently, there are a range of highly precise and quantitative techniques such as mass spectrometry, liquid chromatography and diode arrays. However, these techniques are costly to implement, have low throughput and importantly, cannot assess many of the traits of interest, such as berry morphology and colour.

An imaging platform was developed using a camera and computational algorithms to capture data in 3D and quantify seven external fruit quality traits. Analysis of 100 fruit shows good concordance with manually measured traits and greater precision. Moreover, the novel method required approximately five-fold less labour and required less than £1000 to set up.

2. Cost-effective scalable genotyping. Currently, genotyping is prohibitively expensive for most commercial strawberry breeders to routinely deploy for GS. Two methods are proposed to reduce the cost of genotyping in strawberry and are being explored in this project. Firstly, in a typical breeding programme, a large population is to be assessed, with all individuals of the same species. Multiplex processing of this population is likely to reduce time, labour and reagents required and thus reduce cost per individual genotyped. Secondly, rational selection of a subset of variants likely to be informative for GS would allow the reduction of genotyping targets with little loss of informative data, thus reducing genotyping costs. A range of rational design parameters will be implemented. Genotyping-in-Thousands and Bait Capture Genotyping will be explored as multiplexing approaches, combined with barcoding and genotype identification by sequencing with Illumina technology.

3. Statistical techniques for Genomic Selection. There are different statistical models in the literature for GS, each with different assumptions, strengths and weaknesses. Phenotypic and genotypic data was collected over 4 years as part of this project and a previous project relating to a biparental mapping population. A range of GS models will be implemented on the data to determine optimal models and a custom model may be designed based on the allo-octoploid strawberry. The models will be assessed for advantages and disadvantages and the most suitable model for GS in strawberries will be determined.

On the basis of these three approaches, GS will be deployed in a commercial strawberry breeding population. Comparisons will be made to GS implemented using the “gold standard” SNP array and selections made by breeders based on conventional selection.

To date, significant progress has been made in developing 3D image capture and cost-effective scalable genotyping. This annual report will focus on cost-effective scalable genotyping; for information relating to 3D image capture, please refer to the previous annual report and the publication “A novel 3D imaging system for strawberry phenotyping”; *Plant Methods* (He, Harrison, and Li 2017).

## **Financial Benefits**

The gold standard Affymetrix IStraw90 Axiom SNP array costs approximately £50 per sample, which is likely too high for commercial deployment for GS. Estimates of the proposed rational library design, coupled with sample multiplexing suggests reasonable power can be achieved at £5 - £10 per sample. This represents a significant saving and is likely to be commercially viable in breeding programmes.

## **Action Points**

None to date regarding cost-effective genotyping. It is hoped that a library of rationally selected variants will be developed in strawberry, which will be optimised for GS by the end of the project. Additionally, a pipeline for development will be created so different libraries can be generated according to the specific goals in breeding programmes.