

## Studentship Project: Annual Progress Report 10/2022 to 10/2023

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<b>Project Title:</b>	Understanding the control of continuous running and perpetual flowering in strawberry		
<b>Lead Partner:</b>	CTP		
<b>Supervisor:</b>	Dan Sargent		
<b>Start Date:</b>	20/10/2021	<b>End Date:</b>	19/09/2025

### 1. Project aims and objectives

Due to consumer demand for strawberry fruit across 12 months of the year, and the increasing cost of transportation related to imported fruit, extension of the cultivated strawberry cropping season is one of the main aims of strawberry breeding programs worldwide. Selective breeding for perpetual flowering cultivars can create new varieties that produce fruit throughout the whole growing season, and manipulation of flowering time could extend the season further still. Since the genetic mechanisms that control perpetual flowering and running are not fully understood in the cultivated strawberry, these traits cannot currently be fully exploited for marker assisted breeding or genome editing. Additionally, since there is a significant trade-off between flowering and running, further understanding the control of running can help select cultivars with continuous running phenotypes. Thus, understanding the genetic mechanisms that control everbearing and continuous running in the cultivated/wild strawberry will aid the identification of novel target genes and the development of genetic markers. Hence, the aim of this project is to dissect the control of perpetual flowering and running in strawberry by using genetic mapping and genome editing. To achieve these goals the project is divided into two main work packages:

- Work package 1 (WP1): Understanding the regulation of *TFL1* and *FT1* in *F. x ananassa*. WP1 is based on understanding the control of perpetual flowering in the cultivated strawberry.
- Work package 2 (WP2): Identifying candidate gene(s) in the pathway controlling timing of vegetative reproduction in strawberry. WP2 consists of identifying candidate genes responsible for the transition between flowering and running in the ES12xICE12 population by genetic mapping.
- Work package 3 (WP3): Functional analysis of candidate gene(s) controlling timing of vegetative reproduction in strawberry. WP3 consists of validating that the candidate gene(s) identified in WP2 have a role in running and are responsible for the continuous running trait in the population.

### 2. Key messages emerging from the project

- Understanding the regulation of key flowering genes in the cultivated strawberry will aid the use of advance breeding/ genome editing strategies for crop improvement

The results described in this summary report are interim and relate to one year. In all cases, the reports refer to projects that extend over a number of years.

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- The identification of the locus and candidate genes that control the continuous running trait in strawberry will contribute to future breeding efforts

### 3. Summary of results from the reporting year

#### WP1

- Confirmed transformed and potentially edited plants for flowering genes
- Weaned selected plants
- Designed and transformed new CRISPR constructs for the flowering genes

#### WP2

- Constructed a genetic map for the ES12xICE12 population and identified the locus responsible for the continuous running trait
- Narrowed down the region to 19 genetic markers
- Established a second ES12xICE12 population and identified 4 recombinant individuals for the continuous running trait

#### WP3

- Designed new CRISPR constructs for candidate continuous running genes
- *In vitro* seed germination and seedling growth of NOR8 and FIN56 genotypes for future transformation experiments

### 4. Key issues to be addressed in the next year

- Low transformation efficiency especially in the Malling Centenary genotype
- Difficulties with confirming genome edited plants
- Problems with plant maintenance in the glasshouses
- Problems with space availability in the Oast room
- Powdery mildew on transformed plants especially on Malling Centenary genotypes

### 5. Outputs relating to the project

*(events, press articles, conference posters or presentations, scientific papers):*

Output	Detail
Online project presentation for the Crop Science Seminars at the University of Reading (2021, 2022, 2023)	Project presentation for the Crop Science community at the University of Reading
University of Reading Crop Science symposium (2021, 2022, 2023)	Project presentation for the Crop Science symposium at the University of Reading
Presentation for the Genetic, Genomics and Breeding symposium at NIAB, East Malling (2022)	Project presentation for the GGB department symposium at NIAB East Malling
CTP events (2021, 2022, 2023)	Project presentation at the CTP events
Interview for the ITVX TV series called 'Generation Genome' (2023)	Interview about my career in science and about my project
FAR conference (2023)	Short talk at the Future Agricultural Researchers PhD Conference 2023 in Exeter

## 6. Partners (if applicable)

<b>Scientific partners</b>	Jim Dunwel, University of Reading/ Timo Hytönen, University of Helsinki
<b>Industry partners</b>	Harriet Duncalfe, Berry Gardens
<b>Government sponsor</b>	BBSRC-UKRI