

Project title: Utilising genotyping to identify a full spectrum of genetic variants

Project number: SF/TF 170

Project leader: Dr Richard Harrison, NIAB

Report: Annual report, October 2020

Previous report: NA

Key staff: Dr Helen Bates, NIAB EMR
Dr Matt Loose, University of Nottingham

Location of project: NIAB

Industry Representative: Harriet Duncalfe (Berry Gardens)

Date project commenced: 05 November 2019

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 2020. 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.

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.

Akinkunmi Akinyanju

PhD Student

NIAB

SignatureAkinkunmi Akinyanju..... Date

[Name]

[Position]

[Organisation]

Signature Date

Report authorised by:

RICHARD HARRISON

DIRECTOR OF NIAB, CAMBRIDGE CROP RESEARCH

Signature ...  Date3/11/20.....

[Name]

[Position]

[Organisation]

Signature Date

CONTENTS

GROWER SUMMARY	1
Headline.....	1
Background.....	1
Summary	2
Financial Benefits	2
Action Points.....	2

GROWER SUMMARY

Headline

Culture, DNA extraction and characterisation methods for studying *Fusarium oxysporum* genetics are being optimised. This project aims to reduce strawberry fruit loss by developing tools to accurately identify *Fusarium oxysporum* pathogens.

Background

Fusarium oxysporum is a species complex consisting of both non-pathogenic isolates and pathogenic sub-species known as special forms. The species is categorised into special forms by the range of their hosts. The host range of the pathogen includes over 150 different economically important horticultural and agricultural plant hosts including strawberry, lettuce and potato (Gordon, 2017). *F. oxysporum* is ranked fifth on a list of top 10 fungal pathogens based on scientific and economic importance (Geiser, 2013).

With the rise of monocultures in commercial farming, artificial selection has led to a decrease in genetic diversity in the crop population. This has had a downstream effect on the susceptibility of crops to disease known as “monoculture effect”. This effect has led to an increase the vulnerability of crops to pests and pathogens like *F. oxysporum* (Salaheen, 2019). Symptoms of Fusarium wilt vary slightly between host crops, a recurring symptom is the wilting of plant stems. *F. oxysporum* f. sp. *fragariae*, the strawberry pathogen, causes root rot, vascular wilt and crown rot in strawberry fruit. Fusarium wilt was first described in Australia in 1962 (Winks, 1965) and has since been prevalent in Europe, Asia and the Americas. In the USA, California has reported cases of Fusarium wilt in all major production sites which contributes to over 80% of fresh strawberry produced in the country. *F. oxysporum fragariae* is a threat to the \$2.22 billion dollar strawberry industry (Agriculture, 2019), in which resistant cultivars are grown however, most commonly grown cultivars are susceptible.

Currently, *F. oxysporum fragariae* is not present in the UK, but it is still a potential threat. *F. oxysporum lactucae* race 4 (lettuce pathogen) was reported during glasshouse production of lettuce in the UK in 2016. A grower in Ireland reported 10% of crops were affected but losses were more severe in subsequent crops reporting up to 100% losses (Taylor A. J., 2019). The value of lettuce grown in the UK is £167 million per year (DEFRA, 2019). If not properly managed, *F. oxysporum lactucae* could have severe impacts on crop yield and thus profits for growers.

Currently, there is no cultural mechanism completely effective against combating *F. oxysporum*. As a soil-borne pathogen, soil fumigation is used to remove it from the infected

soils after infected crops are uprooted. Asexual spores produced by the fungus can survive in soil in the absence of a host for up to six years, which makes its control very difficult (Upasani, 2016). The durability of these spores allows some to remain in the soil unaffected by fumigation meaning they can still pose an issue for crops that will be replanted in the soil.

This research project aims to develop a quick and cost-effective model pipeline using *F. oxysporum fragariae* and *lactucae* to make identification of pathogens in the laboratory and in the field more accurate and less laborious. The early and accurate diagnosis of the pathovar will allow time-sensitive countermeasures to reduce the risk of the pathogen spreading. Fusarium wilt can be a recurring issue causing significant financial losses for growers in trying to manage it in soil, which can become a problem during the propagation chain. This project aims to design a model for accurate identification of Fusarium wilt pathogens which could later be applied to other crop pathogens. Early identification will allow effective management strategies to be implemented earlier to increase crop yield.

Summary

In the first year of this project, methods for extracting DNA from different pathovars have been compared and are being refined. The optimum sampling timing was investigated using growth curve experiments. The genome of the lettuce pathogen, *F. oxysporum lactucae* (race 1), has been sequenced and is being concatenated with previous sequence data. At present, it is being analysed using computer programs. Further work will include conducting pathogenicity tests on *F. oxysporum fragariae* isolates of which have unknown pathogenicity. This test will provide information on the differences in the susceptibility of each cultivar depending on the pathovar.

Financial Benefits

In this stage of the project, there is no financial benefit.

Action Points

There are no action points for growers as the project is still at an early stage.