Project title:	Utilising genotyping to identify a full spectrum of genetic variants
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Project leader:	Dr Richard Harrison, NIAB
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Previous report:	NA
Key staff:	Dr Helen Bates, NIAB EMR
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Location of project:	NIAB
Industry Representative:	Harriet Duncalfe (Berry Gardens)
Date project commenced:	05 November 2019

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.

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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.