

# Grower Summary

CP 113

Capability in vegetable crop pathology (Fellowship)

**Annual Report 2015** 

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Before using all pesticides check the approval status and conditions of use.

Read the label before use: use pesticides safely.

#### **Further information**

If you would like a copy of the full report, please email the AHDB Horticulture office (hort.info.@ahdb.org.uk), quoting your AHDB Horticulture number, alternatively contact AHDB Horticulture at the address below.

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#### **GROWER SUMMARY**

#### Headline

The pathogenicity of a set of *Fusarium oxysporum* isolates from onion was determined. A strong correlation between the presence of an effector gene and the ability of isolates to cause disease on seedlings or bulbs was observed. This gene (and others) may therefore form the basis of a future diagnostic test for *Fusarium oxysporum* f.sp. *cepae* (FOC) infecting onion.

### **Background**

#### Onion diseases

Onion is a crucially important crop both in the UK and worldwide. Losses due to fungal pathogens can be devastating and annual losses due to Fusarium basal rot alone are estimated at £10-11 million. The pathogen causes symptoms at every stage of crop development and can occur in stores even when seemingly symptomless bulbs are harvested. Therefore, understanding the pathogen and developing diagnostic tools would be hugely beneficial for future control and monitoring of FOC.

#### **Carrot diseases**

Two major virus complexes can affect carrot / parsnip; parsnip yellow fleck virus (PYFV) / anthriscus yellows virus (AYV) and carrot redleaf virus (CRLV) / carrot mottle virus (CMoV) / carrot redleaf associated RNA (CLRaRNA). The incidence of these viruses on wild hosts was previously being investigated by Dez Barbara as they potentially provide a means of survival of viruses between crops and hence may be important sources of inoculum or pathogen vectors for crop plants. The data from these studies however had not been collated and summarised.

Cavity spot disease of carrots (caused predominantly by *Pythium violae*) is the most damaging disease for UK carrot growers. Infection leads to small, sunken, elliptical lesions and eventually the skin ruptures to form an open cavity (Hiltunen and White 2002). Currently, the only control option is the use of metalaxyl as a drench applied 6 weeks after drilling but losses due to the disease can still be high. In order to understand the dynamics of the pathogen and improve management, a specific and quantifiable diagnostic is required.

#### Summary

#### **Onion diseases**

A set of 33 F. oxysporum isolates from UK onions were characterised through pathogenicity testing on onion seedlings and bulbs. These assays clearly distinguished pathogenic and non-pathogenic isolates, which are common soil inhabitants. DNA was extracted from all isolates and a set of genes analysed / sequenced. A partial correlation between the sequence of housekeeping genes ('standard' genes that are always expressed and present in all isolates) and pathogenicity on onion bulbs and seedlings was observed. However, there was a very strong correlation between the presence / absence of an effector gene (SIX7) and pathogenicity. Furthermore, the sequence of this gene is unique to FOC allowing it to be distinguished from other forms of F. oxysporum pathogenic on different crops and hence has the potential as the basis for a future diagnostic test. Such a test would allow field / stored onions and sets to be assessed for levels of FOC and potential risk of disease. Other effector genes in FOC are also being investigated in a related BBSRC HAPI project. Plants with symptoms of onion white rot and downy mildew were sampled and the pathogens isolated. DNA was extracted and molecular characterisation is in progress. Isolates associated with Botrytis neck rot (B. allii and B. aclada) are also being characterised. These new fungal isolates are now in long-term storage and will provide a resource for future resistance screening or other work.

#### **Carrot diseases**

Wild umbellifer hosts were tested for the presence of carrot / parsnip virus RNA and positive samples were sequenced. The analysis of CRLV sequences showed that the vast majority of genotypes from carrot were quite different from those from the wild hosts. However, some samples from carrots did have the same genotype as those from wild hosts suggesting that transmission to carrots from one of many potential wild hosts could potentially pose a future problem. Overall, wild hosts do not represent a significant source of CRLV inoculum for carrots and hence control approaches should focus on the crop. In contrast, many of the PYFV genotypes found in carrot were also found in cow parsley and hogweed suggesting that wild umbellifers present a source of inoculum. Control measures for PYFV should take into account wild hosts but further work is needed to investigate the changes in virus frequency in the most important wild umbellifers over time. Finally, AYV genotypes were found in all wild hosts but not carrot. This supports previous findings that carrot is not a host for AYV and it may not be a limiting factor as a 'helper' virus enabling PYFV infection in carrots.

A quantitative test (quantitative PCR) has been developed in order to assess levels of *P. violae* DNA in the soil throughout the growing season.

# **Financial Benefits**

None to report at this time.

# **Action Points**

None to report at this time.