



# Grower Summary

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## **CP 141**

The molecular basis of pathogenicity of *Neonectria ditissima*.

Annual 2016

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The results and conclusions in this report may be based on an investigation conducted over one year. Therefore, care must be taken with the interpretation of the results.

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## **Further information**

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AHDB Horticulture is a Division of the Agriculture and Horticulture Development Board.

**Project title:** The molecular basis of pathogenicity of *Neonectria ditissima*.

**Project number:** CP 141

**Project leader:** Richard Harrison, NIAB EMR.  
Robert Jackson, Reading University.

**Report:** Annual report, first year.

**Previous report:** NA

**Key staff:** Antonio Gomez Cortecero, NIAB EMR.

**Location of project:** NIAB EMR

**Industry Representative:** Tony Harding. Worldwide fruit. Acorn House, Unit 68-69, John Wilson Business Park, Harvey Drive, Chestfield, Whitstable, Kent, CT5 3QT.

**Date project commenced:** Oct 2015

**Date project completed** Oct 2018  
**(or expected completion date):**

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## **GROWER SUMMARY**

### **Headline**

- It is likely that rapid progress can be made in identifying the genetic basis of resistance to *N. ditissima*.

### **Background and expected deliverables**

Control of canker caused by the fungus *Neonectria ditissima* is a serious problem for apple growers in the UK and in temperate regions. The majority of modern varieties are highly susceptible to canker and in extreme cases do not survive establishment in the orchard. There are a lack of effective control methods currently available for canker. This is due to the pathogen's lifestyle, inhabiting woody tissue year-round, rather than an annual infection-reinfection cycle common to many foliar pathogens. Host resistance is a promising avenue to pursue for canker resistance, although deployment of host resistance in breeding programmes is slow, due to the long breeding cycle in apple.

Research into other host pathogen interactions shows that a dual strategy of understanding host resistance and pathogen avirulence and how the two are linked is key to the deployment of durable resistance into the field. Nevertheless, little is known about the pathogen at the molecular level. This project is focused on dissecting components of the pathogen's genome that modulate virulence in order to understand how virulence is controlled and whether there are specific differences in host resistance response to isolates of differing virulence.

This work will provide fundamental insights into the molecular basis of pathogenicity in *Neonectria ditissima*. It is hoped to identify candidate genes important in virulence in the pathogen, which could lead to novel opportunities for control by targeted disruption of the pathogen.

### **Summary of the project and main conclusions**

The results of the first year of this project are summarised as follows:

- Canker is genetically similar across the globe, this is consistent with the theory that *N. ditissima* spread from Europe to other regions of the world on imported apple plant material. This provides some hope that any resistance found is likely to be effective worldwide.
- Results to date do not support the existence of distinct pathogen races of *N. ditissima*. It may therefore be possible that any resistance found will be broad spectrum and as a consequence potentially durable.

- Different artificial tests for susceptibility to canker were performed on a range of cultivars. Future work needs to be carried out to compare the results presented in this study with trees grown outside in an orchard setting, inoculated using several different wounds (leaf scars, pruning cuts, picking wounds) to determine whether the methods developed as part of this PhD can be used for rapid selection in breeding programmes.
- The most resistant cultivar to *N. ditissima* was found to be 'Robusta 5'. This is a representative of a species that is distinct from *M. x domestica*. Little is known about natural *M. x robusta* species, since much of the material that is present in Europe was collected in Northern China.
- *N. ditissima* is not reported as a significant pathogen of apple in China, indicating that the mode of resistance in *M. x robusta* versus the cultivated apple *M. x domestica* may be of distinct evolutionary origin. This gives the opportunity to study different mechanisms of resistance. This is beneficial as some modes of resistance may be more successful than others.
- Of the commonly grown cultivars, Golden Delicious was found to be the most resistant.
- Unfortunately, crossing Golden Delicious with other cultivars displaying some resistance, didn't consistently result in resistant progeny. This suggests breeding for resistance using Golden Delicious may be difficult.

### **Financial benefits**

At this stage of the project, no financial benefits have been delivered, but if the project successfully identifies genetic resistance to apple canker, the results of the project will be used in future breeding programmes to develop varieties which offer genetic resistance to *Neonectria ditissima*, thereby overcoming the loss of trees during establishment and production of apple orchards.

### **Action points for growers**

- No action points have been developed at this stage in the project.

