

# Novel ways of managing tree crop fungal diseases: Using precision diagnostic technologies to tailor disease management strategies

Thomas Heaven<sup>1</sup>, Andrew Armitage<sup>1</sup>, Matthew Goddard<sup>2</sup> and Richard Harrison<sup>1</sup>

<sup>1</sup> NIAB-EMR, New Road, East Malling, Kent, <sup>2</sup> The University of Lincoln, Lincoln, Lincolnshire

## Importance:

Apple is among the most important fruit crops globally, however apple cultivation is hampered by its susceptibility to a number of fungal pathogens. Apple scab caused by the pathogen *Venturia inaequalis* (Figure 1) and apple powdery mildew caused by *Podosphaera leucotricha* (Figure 2) can result in significant reductions in productivity. Currently growers are dependent upon heavy fungicide use. Efforts have been made to develop new scab and mildew resistant apple varieties yet durable resistance has remained elusive. A better understanding of the scab and mildew pathosystems is required. Previous research has focused upon the identification of resistance genes in the host with knowledge of the nature of virulence lagging behind. This project aims to redress this imbalance.

## Aims:

- ❖ Develop genomic resources for *P. leucotricha*, for which no reference genome is available
- ❖ Improve existing *V. inaequalis* genome assemblies
- ❖ Genetically characterize resistance breaking scab and mildew isolates, identifying candidate virulence and avirulence genes
- ❖ Assess the race structure and variation of scab and mildew in the UK, including agronomically important traits such as fungicide resistance
- ❖ To develop next generation sequencing diagnostics for apple scab and mildew

## Methods:

1) We will collect isolates from naturally occurring epidemics.

3) By sequencing and comparing the genomes of different 'races' it will be possible to identify the effector genes that distinguish resistance breaking isolates, giving them their specific host range.

2) Isolate host range will be tested, identifying isolates that are able to grow on trees known to carry resistance genes.

4) We will use knowledge about the specific set of effectors of different races in order to create next generation sequencing diagnostics that can diagnose infection of a tree to the level of race.

## Scab

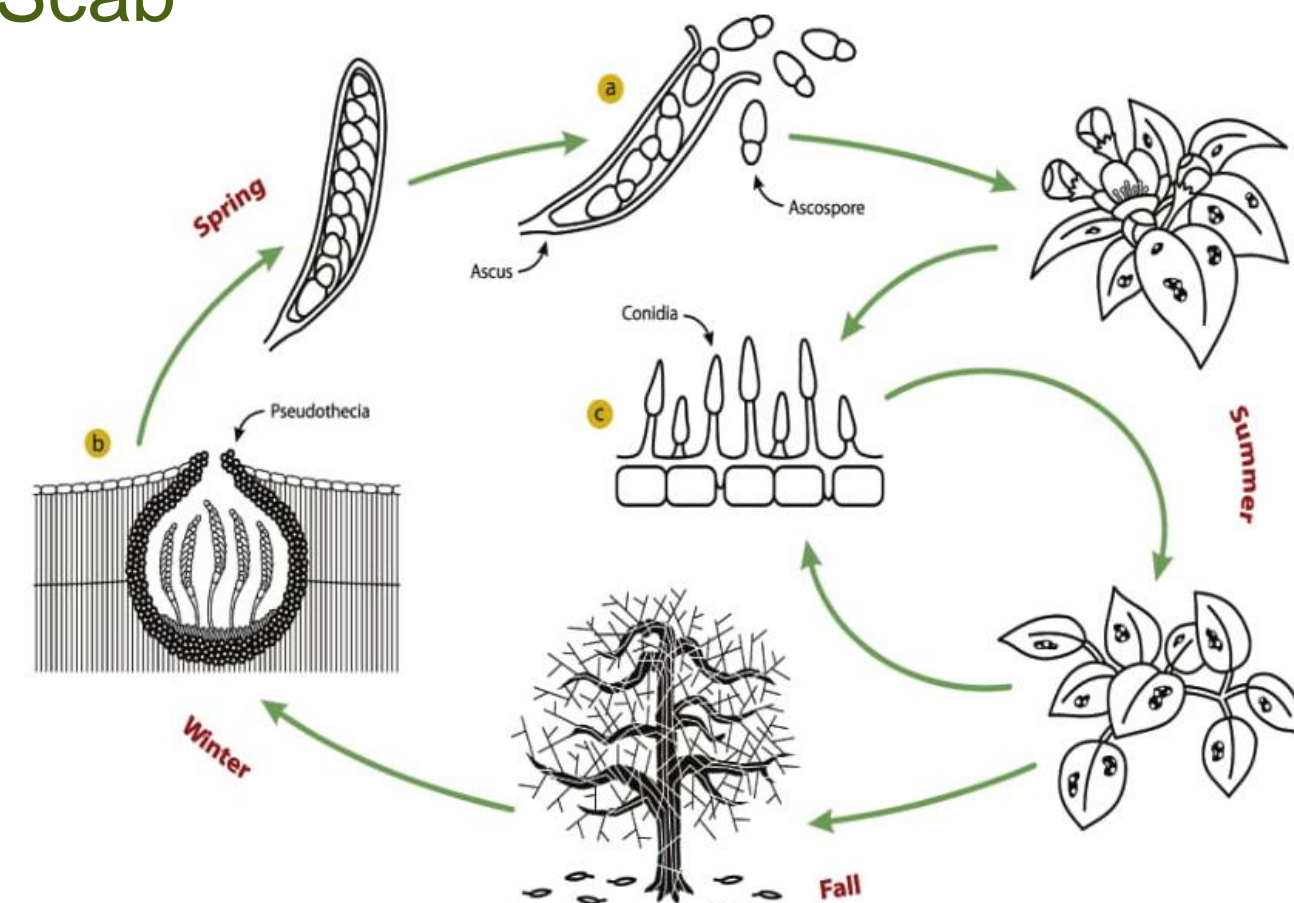
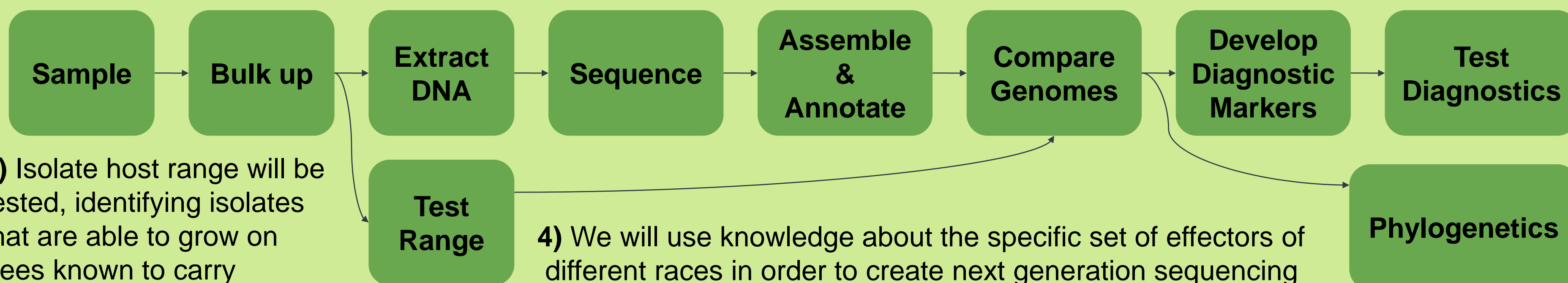


Figure 1 - The life cycle of *V. inaequalis*



## Mildew

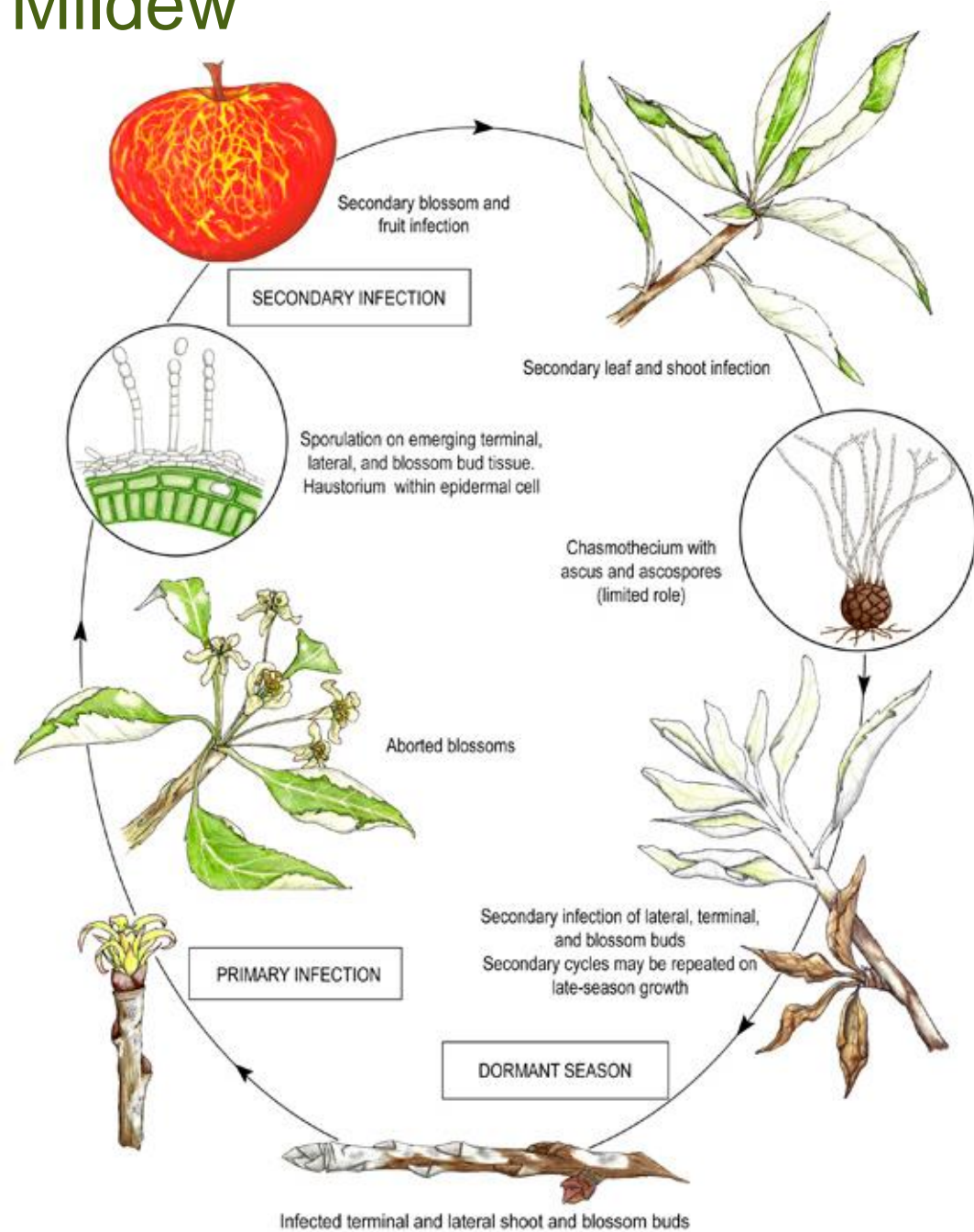


Figure 2 - The life cycle of *P. leucotricha*

## Race Structure:

Both scab and mildew pathogens are highly host specific. It is supposed that the pathogens use a compliment of effectors to suppress a host's immune system allowing infection. Scab and mildew resistance genes are proposed to follow a gene for gene model. A pathogen avirulence (Avr) gene produces an effector which is recognized specifically by the product of a host resistance gene (R). Race structures have been proposed with different races carrying different effector compliments and virulent against different resistance genes. Many host resistance genes have been identified against scab and mildew, the aim of this project is to identify virulence and avirulence genes in the pathogen populations.

## Outcomes:

- ❖ Producing a reference genome for *P. leucotricha* will accelerate future work on this pathogen, as will an improved scab genome.
- ❖ Characterization of endemic pathogen populations will inform planting and resistance breeding programs.
- ❖ Deciphering the gene for gene interactions in scab and mildew virulence and resistance will allow more targeted resistance breeding strategies to produce durable resistance.
- ❖ A precise next generation sequencing diagnostic will aid growers in disease management, providing information about which trees are susceptible to an outbreak and what fungicides will be effective.

## References

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