

Examining identity, phylogeny, and pathogenicity factors in *Fusarium* species affecting pea

Sascha Jenkins^{*1}, Richard Harrison², Kerry Maguire³ and John Clarkson¹

^{*}sascha.jenkins@warwick.ac.uk; ¹University of Warwick, ²East Malling Research, ³Processors and Growers Research Organisation

Background

- Pea (*Pisum sativum L.*) is an important crop grown for human and animal consumption, with 105,000 tonnes produced in the UK in 2013 (PGRO). As peas are legumes they can fix substantial amounts of nitrogen, which makes them an ideal break crop for growers as some nitrogen is left in the soil.
- A range of *Fusarium* species have been reported to cause disease on peas resulting in symptoms of wilting and root discolouration. Research has suggested that effector genes play major roles in the pathogenicity of these fungal species. Identifying the range of *Fusarium* isolates affecting peas and understanding their pathogenicity will inform new control strategies including the breeding of resistant cultivars.

Aims

The main aims of the project are to:

- Identify the main species of *Fusarium* affecting UK peas and understand their distribution.
- Screen *Fusarium* isolates for effector genes and understand their role in pathogenicity.



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Approaches

Fusarium sequencing for identification

Sequencing of the translation elongation factor gene was carried out to identify 87 potential *Fusarium* isolates from diseased peas.

Pathogenicity testing

A ‘tube test’ developed at PGRO was used to evaluate the pathogenicity of 17 selected *Fusarium* isolates on pea seedlings (see results).

Future

Effector gene identification

Whole genome sequencing and PCR will be used to determine the presence of known and novel effectors in selected *Fusarium* isolates.

Pathogenicity testing

Further pathogenicity tests based on pea plants grown in compost will be used to determine the pathogenicity of all isolates collected.

Gene knockout systems

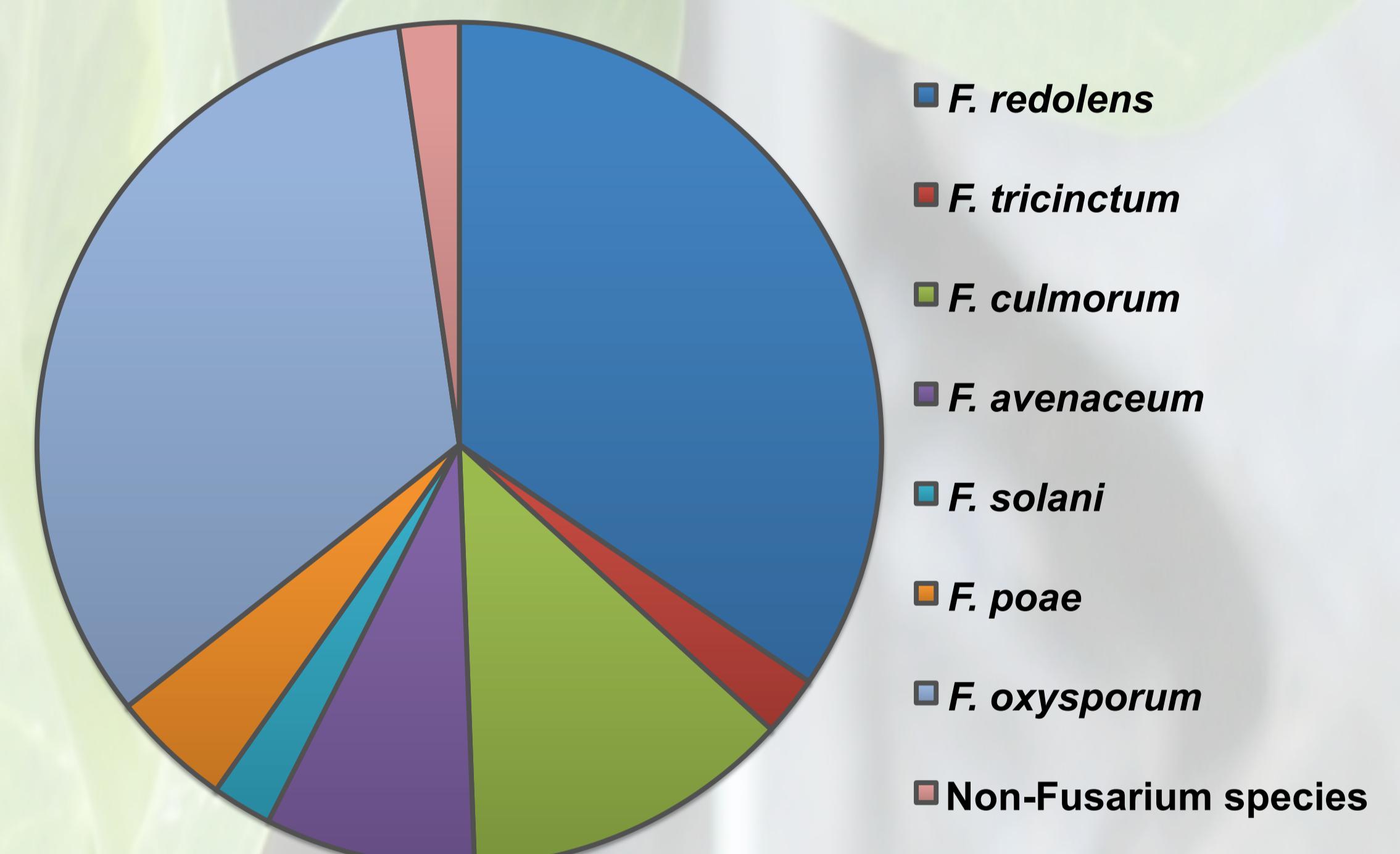
Working with East Malling Research, gene knockout systems will be developed to understand the importance of individual effector genes in *Fusarium* isolates from pea.



Results

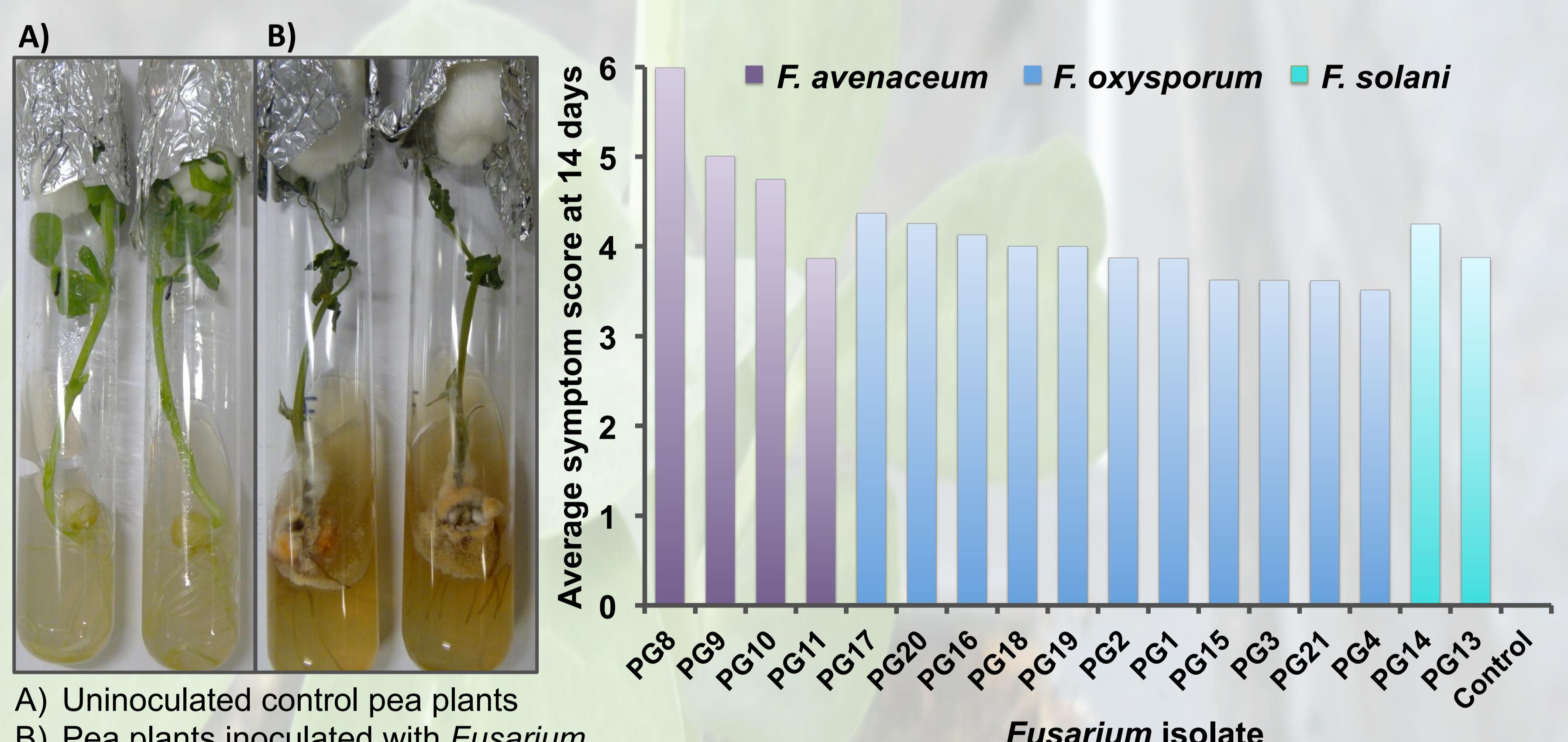
Isolate identification

- 87 isolates from PGRO were characterised by TEF gene sequencing to identify their species.
- All but two isolates were identified as *Fusarium*, with the highest percentage belonging to *F. redolens*. The second largest group were *F. oxysporum* (see pie chart).



Pathogenicity of *Fusarium* isolates

- All *Fusarium* isolates tested were pathogenic, but varied in virulence compared to an uninoculated control.
- An isolate of *F. avenaceum* (PG8) was the most pathogenic of the 17 isolates tested (see chart).



Impact

- This project will be the first to identify the range of *Fusarium* species affecting UK peas at the molecular level.
- Understanding the *Fusarium* complex in pea will help develop better control measures including breeding for resistance.
- Methods for detecting *Fusarium* effectors could aid diagnostics in the field.