



Grower Summary

FV 436

Pea Downy Mildew diversity in
the UK

Annual 2016

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Further information

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Project title: Pea Downy Mildew diversity in the UK

Project number: FV 436

Project leader: Processors and Growers Research Organisation

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Date project commenced: 1st April 2014

**Date project completed
(or expected completion date):** 31st March 2018

GROWER SUMMARY

Headline

A collection of several field-collected pea downy mildew (DM) populations from different locations across the UK has been established at PGRO but the distribution of downy mildew races could not be determined.

Background

Pea DM is a major disease of both vining and combining peas in the UK. Early infection can kill plants, while later infections can reduce yield by up to 55% in the UK. Quality standards for vining peas are high and blemish due to disease infection is not accepted by processors. Downy mildew invades pods, reducing the quality and visual appearance of the produce. Primary infection, caused by soil-borne oospores, can be suppressed by the use of the seed treatment Wakil XL (metalaxyl-M, fludioxonil and cymoxanil). Disease tolerance is present in some varieties, although DM race differentiation leads to variable levels of tolerance.

Primary infection of young seedlings can be reduced by growing peas in a rotation of one year in five. Due to the location of processing factories vining peas are grown in intensively cropped areas and, although the rotation in pea crops is maintained, the land may have supported many pea crops for a considerable period, allowing greater build-up of soil-borne inoculum. Wakil XL is used when there is a high risk of DM, either from early sowing into poor soil conditions and when weather is suitable for disease development or where disease pressure is high. Rotation and seed treatment reduce the incidence of primary infection by soil-borne oospores but secondary infection from airborne spores cannot be controlled in this way. Descriptive and recommended lists are produced annually to indicate relative tolerance of current pea varieties to DM (PGRO Vining Pea Growers Guide and PGRO Pulse Agronomy Guide) and growers use the lists to influence their choice of variety and seed treatment.

No single option to reduce the risk of the disease described above gives complete control of DM.

Varieties may be more or less susceptible than expected, in different areas of the country. This is the result of both the varied nature of the DM population and the genetic interaction between the pea variety and the pathogen. The UK DM population is made up of a number of genetically distinct races. A study carried out in the 1980s identified 11 UK races (Taylor, 1986). No studies have been undertaken since then to establish dynamics and geographic spread of these races. The project will investigate diversity and spread of DM populations

across the UK and investigate differences in pea varietal tolerances to the different DM populations.

Summary

During the 2015 growing season, 16 samples of pea DM were collected from different fields by PGRO. The samples were taken across wide region of the UK from Kent to Somerset and Yorkshire. Pea DM can only survive on a living plant (with the exception of the long-lived oospores in the soil) and it is difficult to maintain a living culture under laboratory conditions. A method was developed at PGRO to maintain a DM culture collection and 16 pea DM field samples could successfully be maintained over the whole season. The DM cultures are available at PGRO and can be cultivated to achieve freshly sporulating material for further experiments.

In order to try to determine the race structure of the DM populations, four differential pea host lines with recorded resistances and susceptibilities to UK DM races were used. The pea lines were inoculated with DM and presence or absence of DM infection recorded. This information may then be used to determine the DM race (Table 1). Infection was inconsistent within the same pea line and DM sample but differences were observed between the different DM samples (Table 2). This shows that the DM field samples most likely consist of several DM races. However, differences in susceptibility of the pea differential host lines to the different field samples were observed (see isolate 101 for example, Table 2) which indicates that the DM populations differ in different UK regions. The combined infection success rates of all field samples showed that the pea lines differ greatly in their overall tolerance levels. More than 50% of all seedlings of line JI 1272 were infected by DM whereas lines JI 15 and JI 85 only showed 12.2% and 4.4% infection rates, respectively. These data have implications for pea varietal tolerance in different UK regions.

Table 1. Susceptibility (S) or resistance (R) of four pea differential host lines (JI 411, JI 560, JI 758, JI 1272) to 11 races of downy mildew (UK pathotypes). The differential host lines can be used to determine the race of a DM culture (Taylor, 1986).

DM race	JI 411	JI 560	JI 758	JI 1272
1	S	S	S	S
2	S	S	S	R
3	S	S	R	S
4	S	R	S	S
5	S	R	R	S
6	R	S	S	S
7	R	S	S	R
8	R	S	R	S
9	R	R	S	S
10	R	R	R	S
11	R	R	R	R

Table 2. Downy mildew infection of seedlings of two pea germplasm lines (JI 15 and JI 85) and four pea differential host lines (JI 411, JI 560, JI 758, JI 1272), using six or eight seedlings per test. Number of infected plants out of total of inoculated, growing plants (in brackets).

Sample	Inoculation Date	JI 15	JI 85	JI 411	JI 560	JI 758	JI 1272
I 81	24/11/2015	2 (8)	1 (8)	0 (8)	0 (8)	0 (8)	0 (8)
I 83	02/11/2015	1 (8)	0 (8)	0 (8)	0 (8)	4 (8)	1 (8)
I 84	23/09/2015	1 (8)	0 (8)	2 (8)	6 (8)	2 (8)	8 (8)
I 85	23/09/2015	1 (8)	0 (8)	3 (8)	2 (8)	3 (3)	7 (8)
I 87	11/09/2015	2 (6)	1 (6)	2 (6)	0 (6)	3 (4)	5 (6)
I 90	11/09/2015	2 (6)	1 (6)	2 (6)	2 (6)	2 (6)	5 (6)
I 94	11/09/2015	0 (6)	1 (6)	4 (6)	6 (6)	2 (6)	6 (6)
I 94	30/09/2015	2 (8)	0 (8)	1 (7)	1 (8)	5 (8)	3 (8)
I 96	02/11/2015	0 (8)	0 (8)	4 (8)	1 (8)	0 (8)	0 (8)
I 99	30/09/2015	0 (8)	0 (8)	0 (7)	3 (8)	2 (8)	7 (8)
I 100	19/10/2015	0 (8)	0 (8)	0 (7)	2 (8)	0 (8)	3 (8)
I 101	19/10/2015	0 (8)	0 (8)	0 (7)	7 (8)	0 (8)	2 (8)
Overall % infection		12.22%	4.44%	20.93%	33.33%	27.71%	52.22%

Work at the John Innes Centre has identified a downy mildew resistance locus in the pea genome arising from JI 15 (see Table 2) and genetic markers have been developed for this locus. New crosses using pea lines that carry different sources of resistance have been developed which, in combination with DM screening, will generate further genetic information that can be used for marker-assisted breeding.

Pea leaves carrying a single DM lesion will be collected in 2016 with the assumption that the single lesion was caused by an individual DM race. These DM isolates will be used to inoculate the four differential host lines in order to determine their race. The information will be used to study race distribution in the UK. To determine geographical differences in DM populations

and to assess differences in pea variety tolerance to the different DM populations, field trials will be performed in the 2016 season. The four pea host lines and the two germplasm lines (Table 2) plus a selection of combining and vining pea lines will be grown in fields at six different locations along the East Coast of the UK and DM infection will be assessed.

Financial Benefits

No results on distribution of downy mildew populations across the UK or on pea variety tolerances to different downy mildew populations could yet be obtained and therefore, no recommendations can yet be given.

Action Points

Action points are not applicable at this stage of the project.