

Are root diseases limiting pulse yields?

Blake Gontar, Tara Garrard, Kelly Hill, Steve Barnett, Entesar Abood and Alan McKay; SARDI

Key findings

- Root disease is common in pulses and appears to be causing varying levels of yield loss.
- Across two years of a national survey (three years in SA), *Pythium* spp., root lesion nematode, *Phoma pinodella* and *Rhizoctonia solani* AG8 are common across a range of pulses.
- Less common but potentially more damaging *Aphanomyces* and *Phytophthora* spp. continue to be detected – these are found across Australia but only infrequently at this stage.
- *Fusarium* species are more common. Isolates vary in pathogenicity, but little is known about their role in causing root disease in Australian pulses.
- Partial control of root disease in field trials in 2020 corresponded with yield increases of up to 0.62t/ha.

Introduction

This research is investigating the causes and effects of root diseases in pulse crops.

Growers are increasingly incorporating pulses into rotations for benefits such as nitrogen fixation, grass weed control and disease break effects. More recently, high prices for food legumes such as lentil and faba bean have driven high frequency pulse cropping (e.g. wheat-lentil). However, despite an eagerness to grow more pulses, growers remain wary due to poor performance and occasional crop failure.

Poor performance of pulses is likely due to multiple factors. Many obvious above-ground issues have been resolved through resistance breeding and the development of insecticide and fungicide strategies and products. However, unexplained poor performance continues to be an issue, with soil abiotic and biotic constraints implicated.

Experience in North America and Europe indicates that soilborne diseases become important as pulse cropping frequency increases. Priority targets for international research include *Aphanomyces euteiches*, *Fusarium* spp. and *Phoma pinodella*. *Phytophthora* spp. appear more common in Australia and have a history of significance in pasture legumes and chickpea. This paper summarises the findings of surveys of pulse root diseases (three years in SA and two years nationally) and preliminary results of yield loss trials conducted in 2020.

Detecting pathogens in pulse roots

Methods

Since 2018, SARDI has encouraged growers and agronomists to submit root and lower stem samples from poor performing pulse and oilseed crops in SA. In 2019, the survey expanded nationally in collaboration with AgVic, NSW DPI, DPIRD (WA) and USQ (QLD).

In 2020, 533 samples were processed nationally, including 58 samples from the mid-north/Adelaide plains (MN), upper north (UN) and Yorke Peninsula (YP) regions of SA. Samples were scored for root health, photographed, and DNA was extracted. A suite of qPCR tests was used to quantify known pulse pathogens in the roots, and next generation sequencing (Illumina® MiSeq®) used to identify potentially important pathogens for which SARDI does not have qPCR tests. Three DNA libraries were prepared using primer pairs that target oomycetes (e.g. *Aphanomyces*, *Phytophthora* and *Pythium* spp.) and fungal species (e.g. *Fusarium* and *Sclerotinia*). The 2020 samples are currently being sequenced and the results will be reported later, however qPCR results are discussed herein.

Results

The survey is providing insight into crop symptoms which were previously unexplained e.g. poor establishment, poor vigour (as seen in Figure 1) or early/uneven senescence.



Figure 1. Poor vigour is a sign of root disease in this lentil crop grown near Curramulka, YP in 2020. The roots were assessed as part of the National Pulse Root Disease Survey; next generation sequencing identified multiple pathogens, including *Phytophthora* 'dreschleri' and *Fusarium avenaceum*.

The most common pathogens detected using qPCR were *Pythium* spp., *Pratylenchus* spp. (root lesion nematodes), *Rhizoctonia solani* AG8, and *Phoma pinodella* (Figure 2). Of the 58 MN/UN/YP samples, 55 samples contained *Pythium* clade F, with 24 >100pgDNA/g root, 50 samples contained *P. neglectus* with 0 >100 eggs/g root, 47 samples contained *P. pinodella* with 30 >100pgDNA/g roots and 27 samples contained *R. solani* AG8 with only 4 samples >100 pgDNA/g root. DNA levels in root tissue have not been correlated to yield loss, however experience over the course of the survey suggests a threshold of 100 pgDNA/g root often correlates with moderate root damage.

Pythium and *Pratylenchus* spp. are known to have broad host ranges, *R. solani* AG8 prefers cereals but will infect a broad range of plants. *Phoma pinodella* along with *Didymella pinodes* causes blackspot of field pea, but it has a much broader host range.

There were also infrequent detections of *Aphanomyces* and *Phytophthora* genera nationally. *Aphanomyces* has been reported to cause severe and widespread yield losses in pulses in Europe and North America while *Phytophthora* spp. are important pathogens in Australia.

Phytophthora medicaginis, a known problem in northern NSW, was detected in 26 (25 chickpea, 1 faba bean) samples from northern NSW; *P. megasperma* was detected in 33 samples (multiple crop types) across Australia including one lentil sample from YP, and *P. drechsleri* (tentative identification), was detected in 14 samples, mostly lupins from WA; this species was also detected in SA, Vic and southern NSW. SARDI is currently undertaking work to confirm the identity of this species.

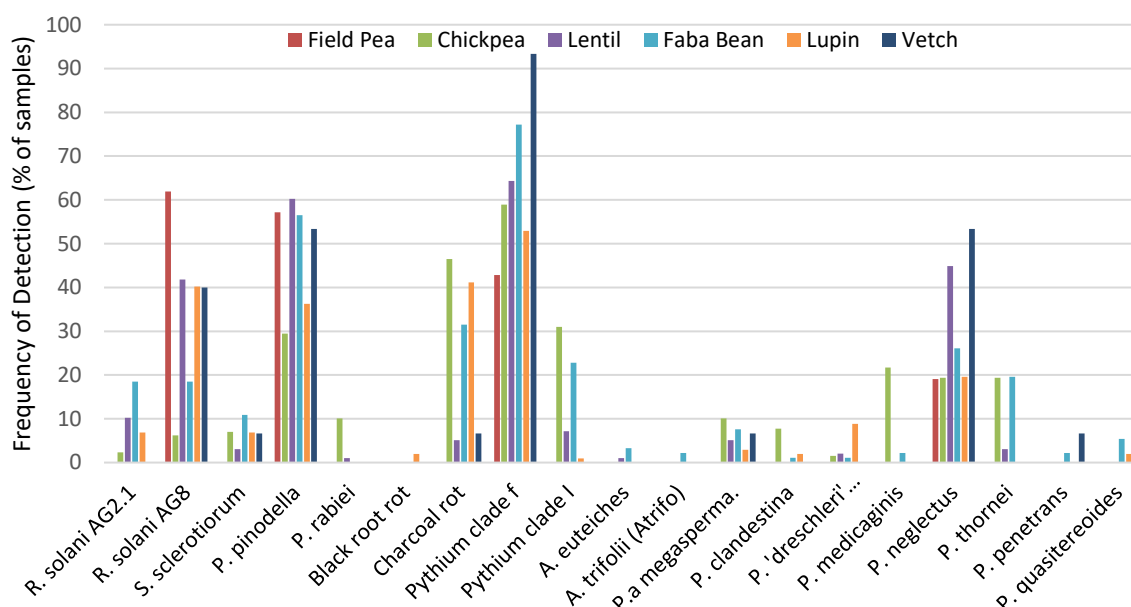


Figure 1. Frequency of detection over threshold levels of pathogens using qPCR in pulse samples received nationally in 2020.

Yield effects of pulse root diseases

In 2020, SAGIT project SUA920 was funded to investigate yield losses caused by soilborne diseases of pulses using a mixture of fungicides at 20 sites associated with the GRDC funded Southern Pulse Agronomy program, including seven sites in the Mid-North, two sites in the Upper North and two sites on the Yorke Peninsula.

Methods

At each site, two locally suited legume crops were sown with seed and soil-applied pesticides to control multiple fungal/oomycete/nematode targets. At Hart, only one crop type (lentil) was sown. Pathogen inoculum at each site was characterised through replicated soil samples. At each site, six treatments were applied, including 'untreated' and 'full treatment' (combination of three products), as well as four other individual or combination treatments. Treatments are all currently unregistered across the range of pulse crops used in these experiments. For simplicity, only the visual disease scores for the 'untreated' and 'full' treatments are presented here. Root disease was scored (0 to 5 scale) for 15 plants per plot in early spring.

Plant samples were visually assessed and DNA was extracted from the roots of those samples and tested using the Pulse Research test panel. Trials were harvested to measure yield effects. Preliminary results are presented in this paper, data analysis is progressing.

Results

Table 1 summarises the pathogens present at each site. Other pathogens, including *Fusarium* spp., for which a PREDICTA B® test has not been developed, could not be quantified but are likely to have been present and possibly played a role in disease development and response. Plant samples will be processed through NGS to detect the presence of *Fusarium* and other species.

Table 3. Initial density of pathogens detected in soil samples from 2020 field sites in the UN/YP/MN regions. Fungi results are reported as pgDNA/g soil. *Pratylenchus neglectus* are reported as nematodes/g soil.

Region	Site	R. solani AG2.1	R. solani AG8	P. pinodella	M. phaseolina	P. neglectus	Pythium clade f	Pythium clade I
MN	Eudunda	1	43	279	2	1	3	5
	Farrell Flat	248	48	9	15	1	16	2
	Hart	0	0	342	1	1	19	5
	Pinery	0	101	0	1	3	28	4
	Riverton	0	20	186	2	2	28	13
	Tarlee	2	141	104	1	1	36	4
	Turretfield	36	4	54	75	2	71	1
UN	Booleroo	21	62	2	3	0	36	0
	Warnertown	4	6	89	15	0	46	7
YP	Pt Broughton	0	0	11	89	1	13	5
	Maitland	18	0	3	1	35	21	57

These sites were selected without prior knowledge of disease risk and are representative of the pulse producing areas. Eudunda, Hart, Riverton, Tarlee all had medium-high levels of *P. pinodella*; Maitland had medium levels of *P. neglectus*; Pinery, Riverton, Tarlee, Turretfield, Booleroo and Warnertown all had medium levels of *Pythium* clade F while Maitland had a medium level of *Pythium* clade I; and Eudunda, Farrell Flat, Pinery, Tarlee and Booleroo had medium-high levels of *R. solani* AG8. Root disease developed at all sites, however severity varied (Figure 3). For example, at Farrell Flat (both lentil and faba bean), average untreated disease score was less than one – a disease level unlikely to reduce yield. At Maitland (lentil and faba bean), average untreated disease score approached three (Figure 3). At most sites, root disease scores were greater than two across a range of crop types.

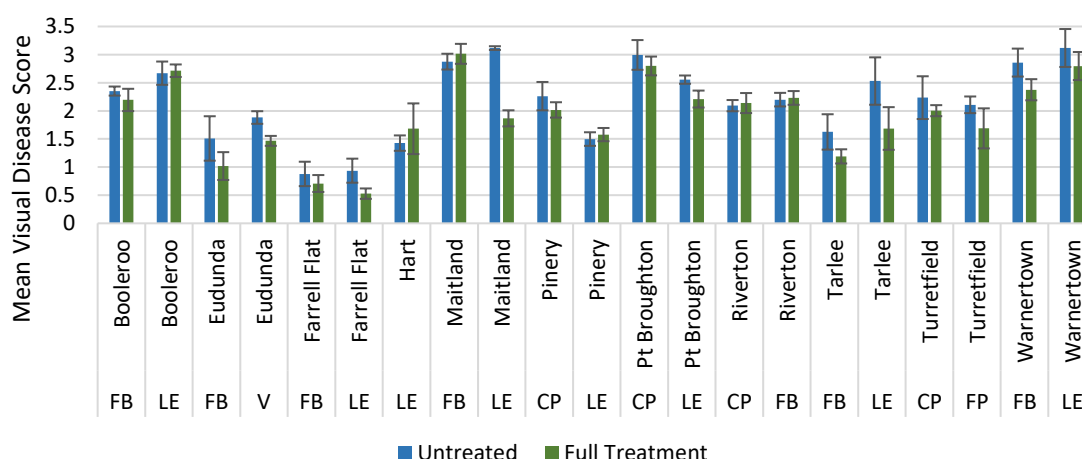


Figure 3. Root disease score of pulses either untreated or treated with a combination of pesticides selected to control fungi, oomycetes and nematodes in disease response trials located in the UN/YP/MN regions in 2020. Crop type is denoted as follows: FB = faba bean, LE = lentil, V = vetch, FP = field pea, CP = chickpea

Full treatment with a combination of pesticides appeared to reduce root disease compared with the untreated control at Maitland (lentil), Tarlee (both lentil and faba bean), Farrell Flat (lentil) and Warnertown (faba bean).

Complete disease control was not achieved at any site, despite the inclusion of a combination of products applied at robust rates. For example, the difference at Tarlee (lentil) was approximately one unit of a 0-5 scale. This indicates that current (unregistered) products are not particularly effective on pulse root diseases under the range of field conditions experienced at sites in 2020.

Despite only partial disease control, yield effects were observed at two lentil and two faba bean sites (Table 2). However, the yield responses to various treatments did not follow the same trend across sites; the untreated control often was not the worst yielding treatment. For example, at Tarlee (lentil) the oomycete control alone increased yield by 0.42 t/ha over the untreated, but the further addition of fungicides appeared to reduce yields – this suggests *Pythium* was likely a constraint in lentil at this site, but also indicates phytotoxic effects of the other chemistry. At Maitland, all fungicide/oomycete treatments increased yield.

The variation in responses suggests the relationship between plant, pathogen and fungicide control options is not simple. However, these results demonstrate that, where a target pathogen is present, even partial control can have yield benefits, indicating that soilborne disease are likely a production constraint. Yield responses of up to 0.62 t/ha were observed at other sites around SA in 2020, generally at sites in the higher rainfall zones such as Bool Lagoon in the south-east of SA.

Table 4. Average yields and standard error (SE) of treatments applied to pulse seed and soil at soilborne disease response sites in MN/UN/YP in 2020. All treatments are currently unregistered and have been coded: O = treatment selected to control oomycetes (Pythium & Phytophthora), F1 = selected to control Rhizoctonia, Phoma etc., N = selected to control nematodes.

Crop	Site	Treatment				SE	p-value
		Nil	O	O + F1	O + F1 + N		
Lentil	Booleroo	1.94	1.75	1.65	1.92	0.28	0.146
	Farrell Flat	1.99	2.06	1.78	2.02	0.11	0.144
	Maitland	2.86	2.99	2.99	3.07	0.10	0.007
	Tarlee	3.11	3.53	2.82	3.15	0.21	<0.001
	Pinery	2.72	2.83	2.71	2.73	0.05	0.062
	Warnertown	2.19	2.27	2.17	2.18	0.07	0.577
	Hart	1.94	1.94	1.91	1.97	0.09	0.511
Faba bean	Booleroo	2.59	2.21	2.32	2.16	0.32	0.931
	Eudunda	3.97	3.89	3.74	3.62	0.09	0.058
	Farrell Flat	4.86	4.94	4.83	5.01	0.10	0.288
	Maitland	4.52	4.47	4.56	4.68	0.11	0.199
	Riverton	4.37	4.48	4.08	4.51	0.14	0.015
	Tarlee	3.59	3.72	3.79	3.58	0.09	<0.001
	Warnertown	2.25	2.30	2.26	2.33	0.05	0.478

Conclusion

Surveys undertaken by this project show root disease is common in Australian pulse crops, including those in the MN/UN/YP. Pathogens are generally present in complex. Some pathogens are very common across grain legume regions and crop types i.e. *P. pinodella*, *P. neglectus*, *Pythium* spp., *Fusarium* spp. and *Rhizoctonia solani* AG8. We suspect these have some effects on yield across many crops in many regions, although they are unlikely to pose a threat of complete loss.

Several pathogens were detected including *Aphanomyces euteiches* and *Phytophthora* spp. that caused substantial yield loss in isolated crops. These pathogens are favoured by wet conditions and could cause large losses in above average rainfall seasons.

Yield losses up to 0.62 t/ha yield in faba beans at Bool Lagoon, associated with partial control of moderate-high root disease, is an indication that soilborne diseases can be a significant constraint to pulse yields. Smaller responses such as at Yeelanna indicate that there is likely some small gains even where pathogen loads and environmental conditions are not highly-conducive to disease.

Acknowledgements

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