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Summer crop choice in northern farming systems: pathogen and AMF impacts

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Key findings

- Summer crop choices are complex and should consider the effects they have on pathogens and beneficial soil biota, such as arbuscular mycorrhizae fungi (AMF).
- Mungbean resulted in the greatest increase in AMF populations. However, mungbean also elevated the disease risk for charcoal rot and the root lesion nematode (*Pratylenchus thornei*, (Pt), compared with sorghum, cotton, maize, sunflower and millet.
- Growing summer crops generally reduces the risk of fusarium crown rot (FCR) for the following winter cereal crops, but there is variation in this effectiveness.
- Maize, cotton, sorghum and mungbean appear to be potential alternative hosts for the winter cereal pathogen *Bipolaris sorokiniana* (common root rot), while sunflower appears not to be.
- Quantifying individual summer crop choices on pathogen levels has highlighted research areas requiring further work to improve managing these biotic constraints across the northern farming systems.

Introduction

Crop choice decisions often involve trade-offs between different aspects of farming systems. In particular, crop choice should consider:

- the need to maintain residue cover
- soil, water and nutrient availability
- managing pathogen inoculum loads using non-host crops to avoid risk from problematic diseases (e.g. fusarium crown rot).

These decisions are increasingly challenging as many cropping systems face evolving disease and weed threats. Therefore, understanding how different crops affect these obstacles is critical.

Limited water affects crop rotation options in the northern grains region and summer crops offer break crop advantages within cropping sequences. Incorporating a mix of summer and winter crops allows variation in herbicide and weed management options, often serving as a disease break within the system. For example, sorghum is known to be resistant to the root lesion nematode *Pratylenchus thornei* (Pt), allowing soil populations to decline. However, the increasing use of summer crops in many regions has caused an increased frequency of other diseases (e.g. charcoal rot caused by the fungus *Macrophomina phaseolina*).

Similarly, using long fallows to transition from the summer to winter crop phases can induce low population levels of the beneficial arbuscular mycorrhizae fungi (AMF), which is associated with long-fallow disorder.

In this experiment, we analyse the data collected from northern farming systems research sites over the past six years to examine how different summer crop options effect both pathogen and AMF populations within farming systems.

Location

Experiment sites:

- Four sites in NSW (Liverpool Plains; Narrabri; Trangie; red and grey soil)
- Four sites in Queensland (Billa Billa, Pampas, Mungindi and Emerald).

Experiment design

Eight research sites were established in 2015 to test a range of different farming systems in different environments across northern NSW, southern and central Qld.

Pathogen soil testing

- Soils were sampled and analysed (0–30 cm) at sowing and, for the life of the project, after harvest each summer.
- We used the Northern-PreDicta® B quantitative PCR (qPCR) DNA analysis to examine how pathogens and other soil biology have varied over a range of crop sequences.
- We used these measurements to calculate relative changes or multiplication factor for populations over their growing season for the various summer crop rotation options. This multiplication factor highlights the extent of increase (>1.0), maintenance (= 1.0) or decrease (<1.0) in pathogen levels following different summer crops.
- The effects of summer crops grown in these sequences has been examined to calculate the extent of the change in the DNA populations of pathogens and AMF associated with the crop choices.
- No sites were artificially inoculated, with populations developing naturally within each system.
- Data from site-crop combinations where a particular pathogen or AMF was absent or below testing detection limits was excluded, as this does not provide a useful indication of a crop choice effect on a particular pathogen or AMF population.

Results

Root lesion nematodes

Root lesion nematodes (RLN, *Pratylenchus* spp.) are microscopic plant parasites that feed on crop roots. Two important species are known to infect crops in eastern Australia: *Pt* and *Pratylenchus neglectus* (Pn). Pt is known to be the more important species in higher clay content soils in northern NSW and southern Qld while Pn is generally more prevalent in lighter soil types in south-eastern Australia. *Pratylenchus neglectus* generally feeds and causes root damage in the top 15 cm of soil while Pt can feed and damage roots down the entire profile. Root damage restricts water and nutrient uptake from the soil causing yield loss in intolerant winter cereal and chickpea varieties. Only Pt densities were high enough across northern farming system sites to examine the effect of summer crop options on their RLN populations. Low Pn numbers prevented a similar analysis with this RLN species.

Summer crops are known to vary in their susceptibility to Pt:

- Sorghum, cotton, millet and sunflower are considered moderately resistant–resistant (MR–R).
- maize is considered susceptible–MR (S–MR) while mungbean is S–moderately resistant/moderately susceptible (MRMS). See Strategies to help reduce losses caused by root lesion nematodes, *GRDC root lesion nematode fact sheet* (https://grdc.com.au/__data/assets/pdf_file/0031/385627/GRDC_FS_RootLeNematodesNorth_1902_13.pdf).
- The range in resistance ratings can relate to differences between varieties with the results from this experiment supporting these findings.

Mungbean crops resulted in the highest average increase in Pt populations, while sorghum had the lowest (Table 1).

Table 1 Effect of summer crop choice on *Pratylenchus thornei* soil populations.

	Sorghum	Mungbean	Cotton	Maize	Sunflower	Millet
Multiplication factor*	1.4	8.3	3.2	2.0	3.4	5.0
Range	0.2–6.6	4.0–21.3	0.8–13.7	1.4–2.8	3.2–3.7	4.0–6.0
Number of observations	31	20	10	5	3	2

*Multiplication factor highlights the extent of increase (>1.0), maintenance (= 1.0) or decrease (<1.0).

Charcoal rot

Charcoal rot is primarily a summer crop disease including sorghum, maize, cotton, mungbean (Figure 1) and sunflower in northern NSW and Qld. Infection causes light brown lesions on crowns and roots and results in increased lodging and/or premature plant death when stressed by dry weather late in the growing season. *Macrophomina phaseolina* has a wide host range of more than 500 weed and crop species including winter cereals.

All six of the summer crops grown increased charcoal rot populations by between 3.9–150.0 times, demonstrating the known wide host range of this fungal pathogen (Table 2). However, considerable differences were evident between the various summer crop options with mungbean elevating populations approximately 5–40 times more than the other crops (Table 2).

Table 2 Effect of summer crop choice on charcoal rot soil populations.

	Sorghum	Mungbean	Cotton	Maize	Sunflower	Millet
Multiplication factor*	9.5	150.0	20.8	7.2	28.9	3.9
Range	1–27	5–1191	1–117	4–11	6–50	2–6
Number of observations	23	23	9	4	3	2

*Multiplication factor highlights the extent of increase (>1.0), maintenance (= 1.0) or decrease (<1.0).

Figure 1 Charcoal rot in mungbean, Gordon Cumming.

Arbuscular mycorrhizae fungi

Arbuscular mycorrhizae fungi are beneficial fungi that colonise the roots of host plants and develop a hyphal network in soil that helps the plant to access phosphorus and zinc. Low levels of AMF have been associated with long-fallow disorder in dependent summer (cotton, sunflower, mungbean and maize) and winter (linseed, chickpea and faba beans) crops. Although wheat and barley are considered to be low and very low AMF-dependent crops respectively, they are hosts and it is generally recommended that these are grown before sowing AMF-dependent crops to elevate AMF populations.

There are two PreDicta B qPCR DNA assays for AMF with combined results from both assays presented. It is important to remember that in contrast to all the other pathogen assays outlined, AMF is a beneficial fungus, so higher multiplication factors are good within a farming system context.

Mungbean had in the highest average increase in AMF populations, whilet sorghum was the lowest (Table 3). Interestingly, even though millet was grown as a short cover crop twice within these farming systems, it resulted in around a 7-fold increase in AMF populations. Hence, millet could be a good option for restoring ground cover over summer and AMF populations, both of which decline following extended dry conditions.

Table 3 Effect of summer crop choice on arbuscular mycorrhizae fungi (AMF) soil populations.

	Sorghum	Mungbean	Cotton	Maize	Sunflower	Millet
Multiplication factor*	3.5	26.8	10.7	5.7	12.0	7.2
Range	0.4–12.4	2.2–61.5	1.8–32.0	3.4–8.0	6.3–17.6	6.5–7.9
Number of observations	41	22	10	4	3	2

*Multiplication factor highlights the extent of increase (>1.0), maintenance (= 1.0) or decrease (<1.0).

Fusarium crown rot

Two PreDicta B qPCR DNA assays detect variants of *Fusarium pseudograminearum* with a separate third combined test detecting *F. culmorum* or *F. graminearum*. All three Fusarium species cause basal infection in winter cereal stems resulting in fusarium crown rot and the expression of whiteheads when heat and/or moisture stress occurs during grain filling. Fusarium crown rot has increased in northern farming systems with the adoption of conservation cropping practices, including retaining standing winter cereal stubble. Yield effects can be offset by higher amounts of plant available water levels being available during grain fill, compared with conventional tillage systems. The *Fusarium* spp., which causes this disease, can survive 3–4 years within winter cereal stubble, depending on the rate of residue decomposition.

Recent research from PhD student Toni Petronaitis has also highlighted that inoculum levels can increase during fallow and non-host crop periods, with saprophytic vertical growth of the pathogen inside standing stubble under wet conditions. Inoculum within standing winter cereal stubble can then potentially be redistributed across a paddock in following seasons with the shorter harvest heights of break crops such as chickpeas. Hence, changes in fusarium crown rot DNA levels might not represent actual hosting of the pathogen; rather they potentially include inoculum dynamics associated with saprophytic growth and/or redistribution of winter cereal stubble inoculum during harvest. DNA data for all three tests were combined for this interpretation to provide an overall level of *Fusarium* spp. DNA.

Limited observations were available to support conclusions on the relative effect of summer crops on *Fusarium* spp. which were:

- cotton and maize appeared most effective at reducing inoculum loads (Table 4)
- sorghum and mungbean results were more variable, but both generally reduced or only moderately increased fusarium crown rot inoculum levels.

Table 4 Effect of summer crop choice on *Fusarium* spp. soil populations.

	Sorghum	Mungbean	Cotton	Maize	Sunflower	Millet
Multiplication factor*	1.7	2.9	0.4	0.5	–	–
Range	0.03–10.3	0.4–9.7	0.1–1.0	0.2–0.8	–	–
Number of observations	19	8	3	2	–	–

*Multiplication factor highlights the extent of increase (>1.0), maintenance (= 1.0) or decrease (<1.0).

Inoculum dynamics associated with the potential redistribution of *Fusarium* spp. saprophytic growth while harvesting summer and winter break crops, and the role of grass weed hosts, appears worthy of further investigation to improve disease management across farming systems.

Common root rot

Common root rot (CRR) primarily infects the sub-crown internode of winter cereal crops causing dark brown to black discolouration of this tissue. Common root rot reduces primary root system's efficiency in susceptible wheat and barley varieties resulting in reduced tillering and general ill-thrift in infected crops.

This disease has increased in prevalence across the northern region over the last decade as increased adoption of earlier and deeper sowing of winter cereals has exacerbated infection.

There is little information on the effect of summer crop options on *B. sorokiniana* levels within Australian farming systems. One international study from Pakistan determined that millet, sorghum, mungbean and maize were *B. sorokiniana* hosts, while sunflowers were a non-host (Iftikhar et al. 2009). Similar research has not been conducted in Australia.

Although limited observations were available to support conclusions on the relative effect of summer crops on *B. sorokiniana* populations, the data appears to support the only previous study of the host range.

- Mungbean, sorghum and maize appear generally to increase populations.
- Sunflower decreased pathogen levels considerably (Table 5).
- Cotton, which was not included in the Pakistan study, also appears to increase *B. sorokiniana* soil populations (Table 5).

These results indicate that the role of summer crops needs to be considered when managing CRR in northern farming systems, with further research required to confirm the host range of this increasingly important pathogen.

Table 5 Effect of summer crop choice on *B. sorokiniana* populations.

	Sorghum	Mungbean	Cotton	Maize	Sunflower	Millet
Multiplication factor*	3.9	2.6	6.8	7.4	0.04	–
Range	0.5–9.6	0.3–9.3	0.3–12.0	na	na	–
Number of observations	12	6	3	1	1	–

*Multiplication factor highlights the extent of increase (>1.0), maintenance (= 1.0) or decrease (<1.0).

Conclusions

Summer crop choice remains a complex balancing act, but this research has highlighted some of the effects on pathogen and AMF populations. For example, mungbean had the largest increase in beneficial AMF levels, but had the negatives of elevating charcoal rot and Pt risk, compared with the other summer crop options examined.

Mungbean did not appear to be as effective at reducing fusarium crown rot risk for subsequent winter cereal crops compared with other summer crop options. The underlying reasons behind these apparent differences requires further investigation of FCR inoculum dynamics within a farming systems context.

These northern farming systems experiments have further highlighted the different roles of summer crops as alternative hosts of the CRR pathogen *Bipolaris sorokiniana*, supporting an overseas study.

Using PreDicta® B qPCR analysis in these experiments is unique in allowing the relative changes in pathogen or AMF levels associated with various summer and/or winter crop choices to be quantified. This is more valuable than simple presence/absence data, allowing growers and their advisers to understand and manage potential changes in disease risk within their paddocks, which can impact profitability.

Reference

Iftikar S, Asad S, Munir A, Sultan A and Ahmad I. (2009). Hosts of *Bipolaris sorokiniana*, the major pathogen of spot blotch of wheat in Pakistan. *Pakistan Journal of Botany*. 41: 1433–1436.

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