

Summer crop choice in northern farming systems – impacts on root lesion nematode, charcoal rot, AMF and winter cereal crop pathogen levels

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Take home messages

- Summer crop choices are complex and should include consideration of their relative impact on pathogens and beneficial soil biota such as arbuscular mycorrhizae fungi (AMF)
- Mungbean resulted in the greatest increase in AMF populations but also elevated disease risk for charcoal rot and the root lesion nematode (*Pratylenchus thornei*) compared with sorghum, cotton, maize, sunflower and millet
- Summer crops generally reduced Fusarium crown rot risk for following winter cereal crops but variation appeared to exist in their relative effectiveness
- Maize, cotton, sorghum and mungbean appear to be potential alternate hosts for the winter cereal pathogen *Bipolaris sorokiniana* (common root rot), while sunflower does not appear to be a host
- Quantification of individual summer crop choices on pathogen levels has highlighted potential areas requiring further detailed investigation to improve management of these biotic constraints across 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, and managing pathogen inoculum loads using non-host crops to avoid or reduce risk of problematic diseases (e.g., Fusarium crown rot). This is increasingly challenging as many cropping systems face evolving diseases and weed threats. Hence, understanding how different crops impact on these aspects is critical.

With limited winter rotation crop options in the northern grains' region, summer crops offer advantages as break crops within cropping sequences. Incorporating a mix of summer and winter crops allows variation in herbicide and weed management options, often also serving as disease breaks 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 seen an increase in the frequency of other diseases (e.g., charcoal rot caused by the fungus *Macrophomina phaseolina*). Similarly, using long fallows to transition from summer to winter crop phases can induce low levels of beneficial arbuscular mycorrhizae fungi (AMF) populations associated with long-fallow disorder. In this paper, we interrogate the data collected from northern farming systems research sites over the past 6 years to

examine how different summer crop options impact on levels of both pathogen and AMF populations within farming systems.

What was done?

Seven research sites were established in 2015 to test a range of different farming systems in different environments across northern NSW, southern and central Qld. Over the life of the project, the team has sampled and analysed soil (0-30 cm) using the PreDicta® B quantitative PCR (qPCR) DNA analysis to examine how pathogens and other soil biology have varied over a range of crop sequences. A specific PreDicta® B test panel targeted at quantifying a wide range of pathogens important to the northern grains region has been used throughout the project. Here we have looked specifically at the impact of summer crops grown in these crop sequences to calculate the extent of change in DNA populations of pathogens and AMF associated with crop choices. It should be noted that populations are what have naturally developed within each system at the various sites and were not artificially inoculated.

Data from site-crop combinations where a particular pathogen or AMF was not present or below testing detection limits was excluded, as this does not provide a useful indication of the propensity of a crop choice to impact a particular pathogen or AMF population. PreDicta® B data from soil samples collected at sowing and after harvest of each summer crop were used 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 growth of different summer crops.

What did we find?

Root lesion nematodes

Root lesion nematodes (RLN, *Pratylenchus* spp.) are microscopic plant parasites which feed on crop roots. Two important species are known to infect crops in eastern Australia, namely *Pratylenchus thornei* (*Pt*) and *P. 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. *Pn* generally feeds and causes root damage in the top 15 cm of soil whilst *Pt* can feed and damage roots down the entire soil 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 prevalent at high enough densities across northern farming system sites to examine the effect of summer crop options on soil *Pt* populations.

Summer crops are known to vary in their susceptibility to *Pt* with sorghum, cotton, millet and sunflower considered moderately resistant-resistant (MR-R). Maize is considered susceptible-MR (S-MR) whilst mungbean is S-MRMS (<https://grdc.com.au/resources-and-publications/all-publications/factsheets/2019/root-lesion-nematode-northern>). The range in resistance ratings can relate to differences between varieties. Our results support these general findings. Mungbean resulted in the highest average increase in *Pt* populations, whilst sorghum favoured the lowest population increases (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
No. 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 (*Macrophomina phaseolina*)

Charcoal rot, caused by the fungus *Macrophomina phaseolina*, is primarily a disease of summer crops including sorghum, maize, cotton, mungbean 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 stress associated with dry weather occurs late in the growing season. *M. phaseolina* has a wide host range of more than 500 weed and crop species including winter cereals.

Table 2. Effect of summer crop choice on *Macrophomina phaseolina* (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
No. observations	23	23	9	4	3	2

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

All six of the summer crops grown increased average *M. phaseolina* populations by between 3.9 to 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 5 to 40 times more than the other crops (Table 2).

Arbuscular mycorrhizae fungi (AMF)

AMF colonise roots of host plants and develop a hyphal network in soil which reputedly assists 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 crops (linseed, chickpea and faba beans). Although wheat and barley are considered to be low and very low AMF dependent crops respectively, they are hosts and are generally recommended as crops to grow prior to sowing more AMF dependent crop species, in order 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.

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
No. observations	41	22	10	4	3	2

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

Mungbean resulted in the highest average increase in AMF populations, whilst 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 may be a good option for restoring ground cover over summer and AMF populations which both decline following extended dry conditions.

Fusarium crown rot (*Fusarium* spp.)

Two PreDicta® B qPCR DNA assays detect genetic variants of *Fusarium pseudograminearum* with a separate third combined test detecting *F. culmorum* or *F. graminearum*. All three *Fusarium* species cause basal infection of 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 which include the retention of standing winter cereal stubble. Yield impacts however are sometimes offset by the higher levels of plant available water often available to the plant during grain fill in such systems when compared to tilled systems. The *Fusarium* spp. which cause this disease can survive 3-

4 years within winter cereal stubble depending on the rate of decomposition of these residues. 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 with shorter harvest heights of break crops such as chickpeas. Hence, changes in *Fusarium* crown rot DNA levels may 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.

Table 4. Effect of summer crop choice on *Fusarium* spp. (*Fusarium* crown rot) 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	-	-
No. observations	19	8	3	2	-	-

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

Limited observations were available to support conclusions on the relative effect of summer crops on *Fusarium* spp. associated with *Fusarium* crown rot. However, cotton and maize appeared most effective at reducing inoculum loads (Table 4). Results were more variable with sorghum and mungbean, but both generally reduced or only moderately increased *Fusarium* crown rot inoculum levels. Inoculum dynamics associated with saprophytic growth of *Fusarium* spp., potential redistribution during harvest of summer and winter break crops and the role of grass weed hosts appears worthy of further investigation to improve management of this disease across farming systems.

Common root rot (*Bipolaris sorokiniana*)

Bipolaris primarily infects the sub-crown internode of winter cereal crops causing dark brown to black discolouration of this tissue referred to as the disease 'common root rot'. Common root rot reduces the efficiency of the primary root system 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 with the increased adoption of earlier and deeper sowing of winter cereals which exacerbates 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 hosts of *B. sorokiniana*, whilst sunflowers were a non-host (Iftikhar et al. 2009). Similar research has not been conducted in Australia.

Table 5. Effect of summer crop choice on *Bipolaris sorokiniana* (common root rot) soil 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	-
No. observations	12	6	3	1	1	-

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

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 host range from Pakistan (Iftikhar et al. 2009). Mungbean, sorghum and maize appeared to generally increase populations, whilst sunflower considerably decreased levels of this pathogen (Table 5). Cotton, which was not included in the Pakistan study, also appears to generally increase *B. sorokiniana* soil populations (Table 5). These results indicate that the role of summer crops need to be considered when managing common root rot in northern farming systems. Further research is required to confirm the relative host range of this increasingly important pathogen.

What does it all mean?

Summer crop choice remains a complex balancing act but this research has highlighted some of the impacts 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 also did not appear to be as effective at reducing Fusarium crown rot risk for subsequent winter cereal crops compared with other summer crop options where data was available. The underlying reasons behind these apparent differences requires further investigation of Fusarium crown rot inoculum dynamics with a farming systems context.

These northern farming systems experiments have further highlighted the potential differential role of summer crop species as alternate hosts of the common root rot pathogen *Bipolaris sorokiniana*, supporting an overseas study. The use of qPCR within these experiments is unique in that it allows 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, in that it allows growers and their advisers to understand and manage potential changes in disease risk within their paddocks to limit impacts on profitability.

References

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. *Pak. J. Bot.* 41: 1433-1436.

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