Impact of crop species and crop sequencing on nematode, crown rot and common root rot inoculum loads—Northern Region

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Research Questions: *Can systems performance be improved by modifying farming systems in the northern grains region? Specifically, what impact do crop species and crop sequences have on soil- and stubble-borne pathogens?*

Key findings

1. Barley and wheat crops led to increases in *P. neglectus*, while mungbeans, wheat and chickpea led to increases in *P. thornei*.
2. The non-host summer crops (cotton, maize, mungbean and sorghum) provided the greatest reduction in crown rot inoculum while most non-host winter crops had virtually no impact.
3. There was little impact from most species on common root rot levels with wheat the worst crop option, while common root rot declined under the moderately resistant barley variety Compass⦸.

Background

While advances in agronomy and improved performance of individual crops have helped grain growers maintain their profitability, current farming systems are underperforming. Soil- and stubble-borne pathogens are believed to be a major cause of the poor performance of the farming systems across the northern grains region. The three most common pathogens responsible for yield reductions are root lesion nematodes (RLN—*Pratylenchus thornei* and *Pratylenchus neglectus*), crown rot (CR—*Fusarium* spp.) and common root rot (CRR—*Bipolaris sorokiniana*). *P. thornei* are widespread particularly on Vertosols and can feed throughout the soil profile while *P. neglectus* occur on most soils and are mainly confined to the top 10 cm. RLNs have a wide host range; the main crops used in the region host *P. thornei*, hence their populations have increased in the absence of profitable non-host (break) crops. Significant yield loss (>40%) occurs in susceptible genotypes but more tolerant genotypes can reduce their impact.

Crown rot, a stubble-borne disease of winter cereals, is endemic across the northern grains region. Yield loss can be as high as 90% in wheat and the fungus can survive in wheat stubble for up to four years. Common root rot, hosted by winter cereals, is most severe in wheat and barley. Good resistance exists in wheat cultivars but barley cultivars vary widely in susceptibility.

Using crops resistant to these diseases with greater regularity in crop rotations, is one way to mitigate yield reduction. While past research has been conducted on each of these pathogens alone, rarely have the impacts of crop rotations on the full complement of soil-borne pathogens been assessed over several years. Results from the northern farming systems research sites have been examined to see how crop species and crop sequences have altered the pathogen complex through the crop rotation.

What was done

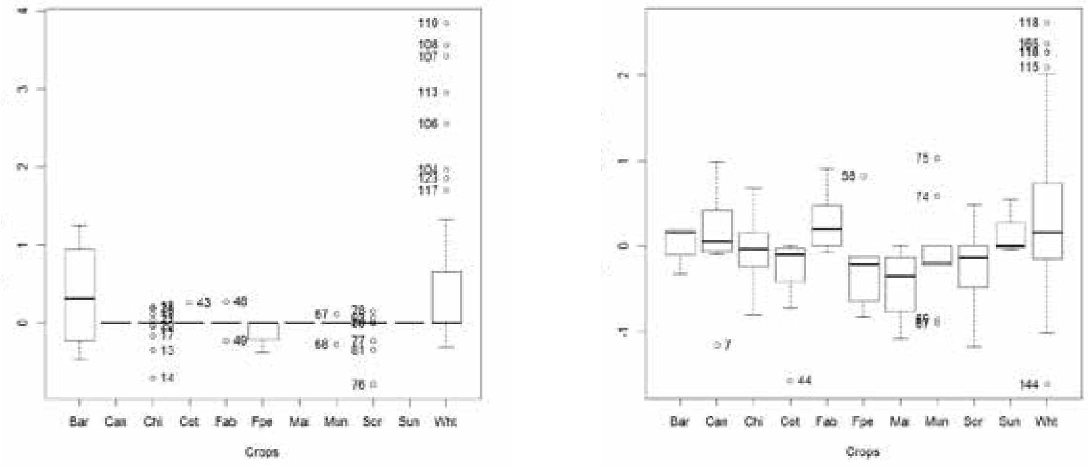
Experiments were established at seven locations; Pampas, Emerald, Billa Billa, Mungindi, Spring Ridge, Narrabri and Trangie (red and grey soils). These sites are investigating how several modifications to farming systems will impact on the performance of the cropping system as a whole over several crops in the sequence. Soil- and stubble-borne pathogens (0-30 cm) were monitored twice per year; pre-sow and post-harvest, using the PREDICTA® B DNA-based soil test. A total of 14 pathogens are being monitored across the cropping systems.

Results

The diversity of crops grown across sites in this project provides an opportunity to compare the change in pathogen loads for various crop types across multiple seasons. *P. neglectus* levels remained unchanged for the majority of crops except barley and wheat (Figure 1a). Barley showed an increase in *P. neglectus* while wheat had a number of outliers where nematodes increased from 2-4 /g soil. All of the wheat outliers were cultivar LongReach Spitfire$^{\Phi}$ which is rated moderately susceptible to susceptible (MS-S) for *P. neglectus*. Changes in *P. thornei* levels due to individual crops were mixed (Figure 1b). *P. thornei* numbers increased under mungbeans, while both chickpea and faba beans also showed a tendency for *P. thornei* levels to increase. The summer crops, cotton, maize, sorghum and sunflowers all showed declines in *P. thornei* levels at harvest. Responses in wheat were quite varied with outliers showing increases of 2-15 nematodes/g soil, but equally levels fell by 2-13 nematodes/g soil in some cases. There was no varietal effect due to wheat cultivar as all the outliers, both increasing and decreasing in nematodes, were crops sown to LongReach Gauntlet$^{\Phi}$, which is rated moderately resistant (MR) to *P. thornei*.

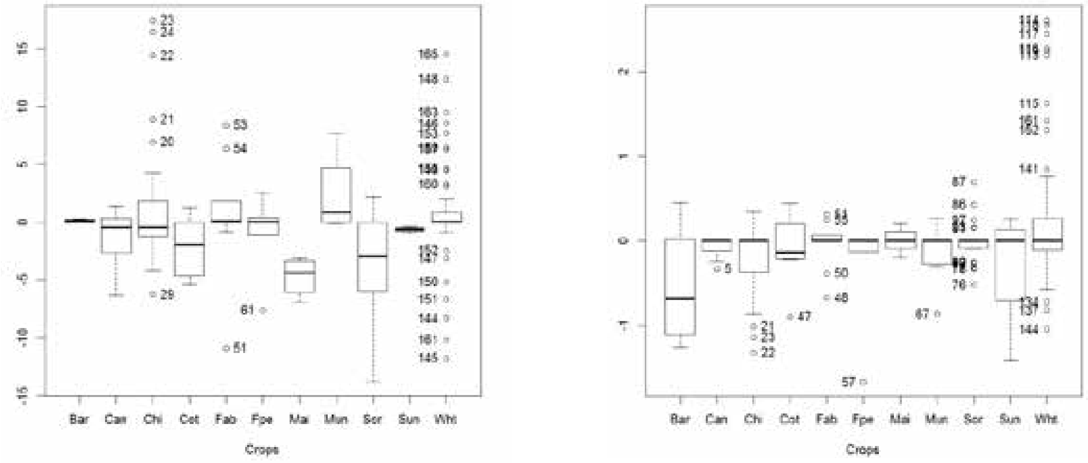
The primary host, wheat, recorded the biggest increase in CR levels along with barley (Figure 1c). The non-host winter crops; canola, chickpea and faba bean showed no reduction in CR levels while field peas showed a significant decline in the pathogen at harvest. The biggest decline was recorded in the non-host summer crops; cotton, maize, mungbean and sorghum.

Wheat, the primary host, showed no real increase in CRR, however, there were a number of outliers (Figure 1d). All bread wheat varieties sown were rated MS-S for CRR. The other crops showed no change or slight declines; the biggest decline came from the MR barley cultivar Compass$^{\Phi}$.



(a) ***Pratylenchus neglectus*** **(RLN)**

(c) ***Fusarium*** **spp. (CR)**



(b) ***Pratylenchus thornei*** **(RLN)**

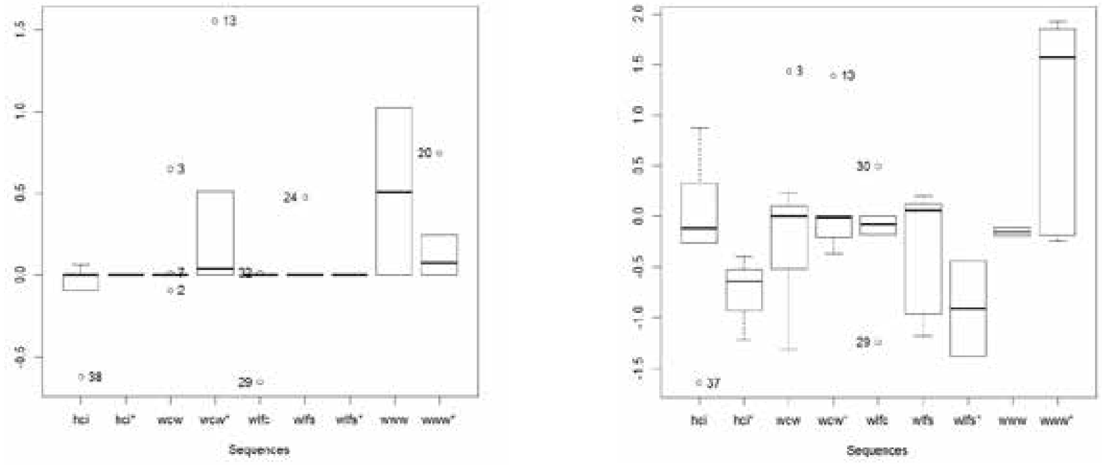
(d) ***Bipolaris sorokiniana*** **(CRR)**

Figure 1 . The change in pathogen DNA levels, transformed to log10 or number of nematodes/g soil, from sowing to harvest, for a range of crops. Crops are barley (Bar), canola (Can), chickpea (Chi), cotton (Cot), faba bean (Fab), field pea (Fpe), maize (Mai), mungbean (Mun), sorghum (Sor), sunflower (Sun) and wheat (Wht).

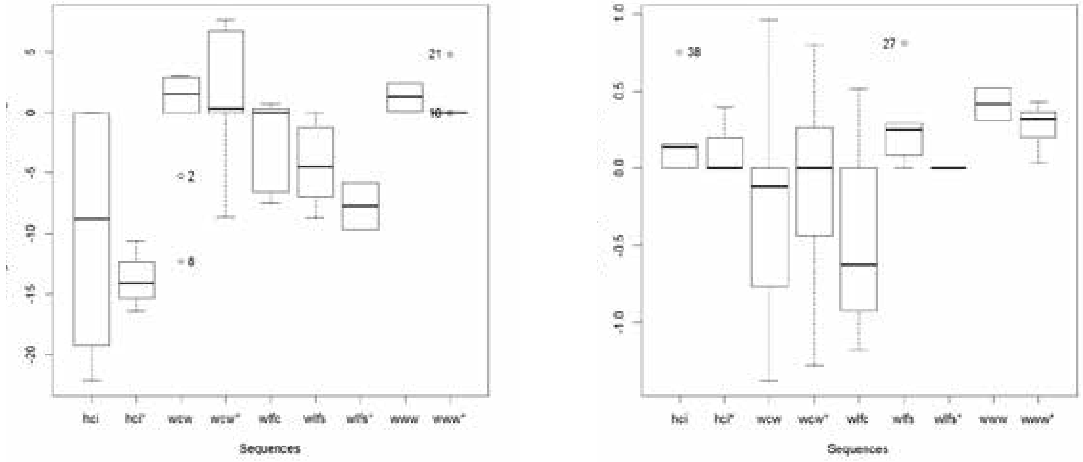
The change in pathogen loads of selected three-phase crop sequences from March 2015 to March 2018 after summer fallow or harvest of a 2017 summer crop were also investigated. The high crop intensity sequence consists of five crops in three years with a range of winter and summer crops. The majority had mungbean double cropped in 2015/16 followed by a range of sorghum and winter crops. All these sequences, except wheat/long fallow/cotton, were duplicated under high nutrition inputs (*), mainly high nitrogen (N) in cereals.

The crop sequences saw virtually no change in *P. neglectus* numbers except for continuous wheat which led to an increase in nematodes over three years (Fig 2a). The *Higher crop intensity* sequence led to reductions in *P. thornei* nematodes. The wheat/long fallow/sorghum sequence also saw a decline in *P. thornei* numbers, and in both sequences the addition of high N inputs resulted in a greater decline in *P. thornei.* The wheat/chickpea/wheat and continuous wheat sequences led to modest increases in *P. thornei* numbers (Fig 2b).

The high N *Higher crop intensity* and wheat/long fallow/sorghum systems had large declines in CR inoculum, however, the addition of high N into a continuous wheat system led to a large increase in CR inoculum (2c). The popular wheat/chickpea/wheat system had no effect on CR inoculum loads (Fig 2c). The wheat/long fallow/cotton sequence had the biggest impact on reducing CRR inoculum (Fig 2d). The *Higher crop intensity* and wheat/long fallow/sorghum systems led to modest increases while the continuous wheat system gave the biggest increase in CRR inoculum (Fig. 2d).


(a) ***Pratylenchus neglectus*** **(RLN)**

(c) ***Fusarium*** **spp. (CR)**


(b) ***Pratylenchus thornei*** **(RLN)**

(d) ***Bipolaris sorokiniana*** **(CRR)**

Figure 2 . The change in pathogen DNA levels, transformed to log10, or number of nematodes/g soil, from pre-sow in March 2015 to post fallow or harvest in March 2018 for a range of cropping and high nutrition (*) sequences. Sequences are; *Higher crop intensity* (hci), wheat/chickpea/wheat (wcw), wheat/long fallow/cotton (wlfc), wheat/long fallow/sorghum (wlfs), wheat/wheat/wheat (www).

Implications for growers

In terms of individual crop response to RLN, both barley and wheat led to increases in *P. neglectus*, while mungbeans, wheat and to a lesser extent chickpea led to increases in *P. thornei*. *P. thornei* numbers declined following cotton, maize and sorghum crops. The non-CR host crops (cotton, maize, mungbean and sorghum) provided the best way to reduce CR inoculum while the non-host winter crops (canola, chickpea and faba bean) had virtually no impact on CR inoculum. There was little impact from most species on CRR levels with the primary host, wheat, the worst crop option while CRR declined under the MR barley variety Compass⚓.

The sequencing of crops can provide the biggest changes in pathogen loads. In regards to *P. neglectus,* the monoculture wheat system increased numbers, yet the remaining rotations had virtually no impact on population numbers.

Wheat/chickpea/wheat sequences are common in the northern grains region, but this study suggests that this sequence is prone to increase *P. thornei* numbers. *Higher crop intensity* systems using resistant host crops such as sorghum and maize under high nutrition reduced *P. thornei* numbers dramatically, but these systems are environment specific and are only economically viable in the higher rainfall regions.

In addition to increasing *P. thornei* numbers, the common sequence wheat/chickpea/wheat, with a single non-host pulse crop had no impact on CR levels, while the high crop intensity and long fallow summer crop systems had the biggest reductions in CR inoculum. This was probably due to these systems providing more time or an improved environment for stubble breakdown. High N input continuous wheat systems led to the largest increase in CR inoculum and highlights why this rotation is actively discouraged, especially in environments where stubble breakdown is slow.

CRR inoculum increased under continuous wheat, its primary host, but also under sorghum which warrants further investigation regarding its host status for this fungus. This observation is of concern, with the inclusion of summer crops such as sorghum providing a disease break for other pathogens such as CR and *P. thornei.*

Resistant or non-host crops may reduce inoculum loads, but several consecutive resistant crops coupled with fallows offer the best rotation option to reduce very high pathogen loads. Once reduced, applying rules to limit the consecutive use of host crops may reduce the rate of population growth and keep pathogens under threshold levels.

Acknowledgements

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PREDICTA® B sampling conducted on the row post-harvest at Emerald.