

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

Andrew Verrell¹, Jeremy Wish², David Lawrence³, Lindsay Bell², Darren Aisthorpe³, Jon Baird¹, Jayne Gentry³, Greg Brooke¹, Andrew Erbacher³, Andrew Zull³, Kaara Klepper⁴

¹NSW Department of Primary Industries, Tamworth, NSW, 2340, andrew.verrell@dpi.nsw.gov.au

²CSIRO Agriculture, St Lucia QLD 4067

³Qld Department of Agriculture and Fisheries, Toowoomba, Qld, 4350

⁴GRDC Toowoomba Qld 4350

Abstract

Farming systems are underperforming in terms of water limited yield potential, due to challenges that include declining soil fertility, herbicide resistant weeds and increasing soil pathogens. Seven long term farming systems sites were established in 2015 across different environments from Trangie to Emerald to investigate how modifications (cropping intensity, legume frequency, cropping diversity and nutrient management strategies) to cropping systems will impact on their performance. Four major pathogens; root lesion nematodes, (*Pratylenchus thornei* and *Pratylenchus neglectus*), crown rot (*Fusarium pseudograminearum*) and common root rot (*Bipolaris sorokiniana*), were monitored, using the PREDICTA® B DNA-based soil test, across the sites and crop sequences. The effect of individual winter and summer crop species and their combined effect in a range of crop sequences, on the changes in DNA pathogen loadings, are reported.

Key Words

Farming systems, pathogen, PREDICTA® B

Introduction

While advances in agronomy and improved performance of individual crops have helped grain growers to maintain their profitability, current farming systems are underperforming; with only 30% of the crop sequences in the northern grains region (NGR) achieving 75% of their water limited yield potential (Hochman *et al.* 2014). Soil and stubble borne pathogens are believed to be a major cause of the poor performance of the farming systems across the NGR. The 3 most common pathogens responsible for yield reductions are root lesion nematodes (RLN - *P.thornei* and *P.neglectus*), crown rot (CR) and common root rot (CRR). *P. thornei* are widespread particularly on the vertosols and can feed throughout the soil profile while *P. neglectus* occur on most soils and are mainly confined to the top 10cm. RLNs have a wide host range and the main crops used in the NGR host *P. thornei*, hence their populations have increased in the absence of profitable break crops. Significant yield loss (>40%) occurs in susceptible genotypes but more tolerant genotypes can reduce their impact.

CR, a stubble borne disease of winter cereals, is endemic across the NGR. Yield loss can be as high as 90% in wheat and the fungus can survive in wheat stubble for up to four years. CRR, 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 each of these pathogens have been examined 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 pathogens through the crop rotation.

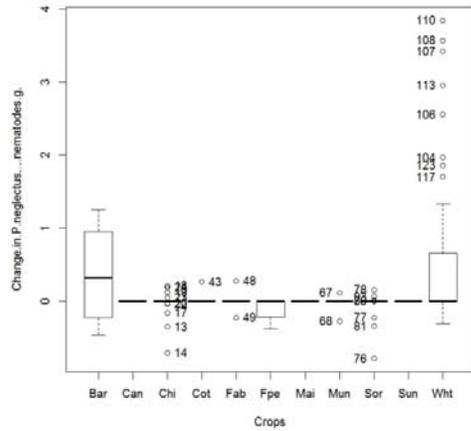
Methods

Experiments were established at seven locations; Pampas, Emerald, Billa Billa, Mungindi, Spring Ridge, Narrabri and Trangie (red & grey soils). These sites are investigating how modifications to farming systems will impact on the performance of the cropping system. The following generic systems were established at each site.

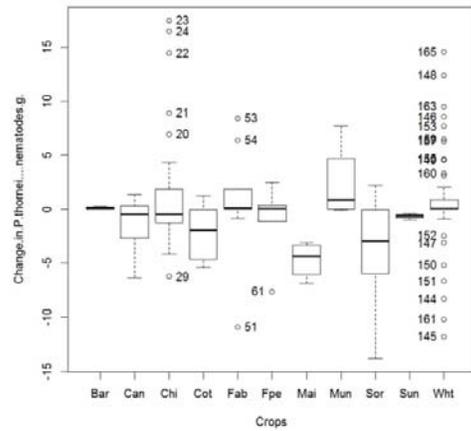
Baseline – approximation of common farming system practice in each environment: dominant crops only used; and fertilising to median crop yield potential. Higher nutrient supply – same sequences as baseline but increasing the fertiliser budget for each crop based on 90% of yield potential. Higher crop intensity – increasing the proportion of time that crops are growing by reducing the soil water threshold required to trigger a planting opportunity. Lower crop intensity systems – only growing crops when plant available soil water approaches full; higher value crops are used when possible. Higher legume frequency – every second crop is a legume and uses high biomass legumes (e.g. fababean) when possible. Higher crop diversity – a greater set of crops used with the aim of managing soil-borne pathogens and weeds. This implemented by growing 50% of crops resistant to root lesion nematodes (preferably 2 in a row) and 2 alternative crops are required before the same crop is grown

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 fourteen pathogens are being monitored across the cropping systems. Non-parametric box and whisker plots were used to examine the distribution of data. Outliers are shown as individual numbered points.

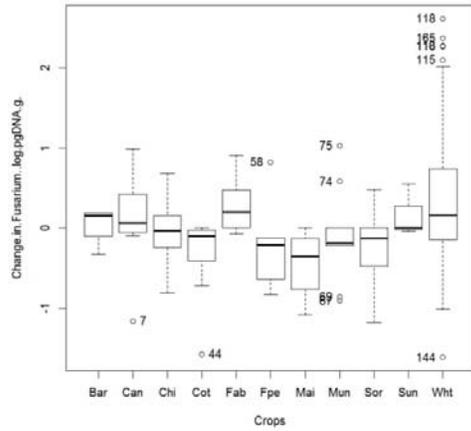
Results



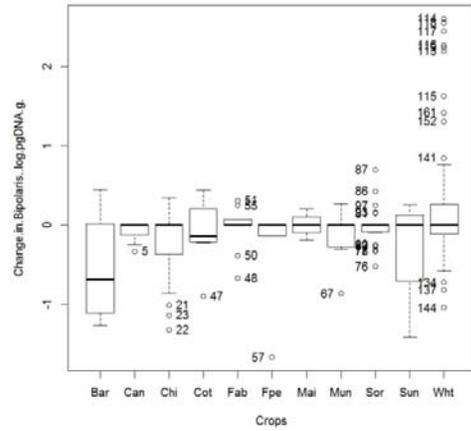
(a) *Pratylenchus neglectus*



(b) *Pratylenchus thornei*



(c) *Fusarium spp*

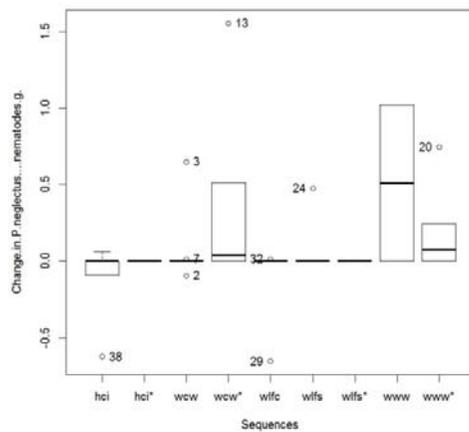


(d) *Bipolaris sorokiniana*

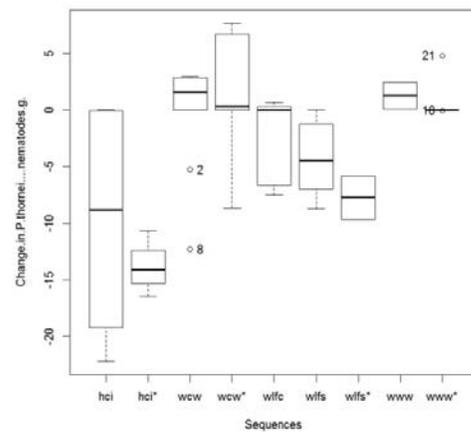
Figure 1 The change in pathogen DNA levels, transformed to log₁₀ or number of nematodes/g soil, from sowing to harvest, for a range of crops. Crops are barley (Bar), canola (Can), chickpea (Chi), cotton (Cot), faba bean (Fab), field pea (Fpe), maize (Mai), mungbean (Mun), sorghum (Sor), sunflower (Sun)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

P. neglectus levels remained unchanged for the majority of crops except barley and wheat (Fig 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 Spitfire which is rated MS-S for *P. neglectus*. Changes in *P. thornei* levels due to individual crops were mixed (Fig 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 Gauntlet, which is rated MR to *P. thornei*.

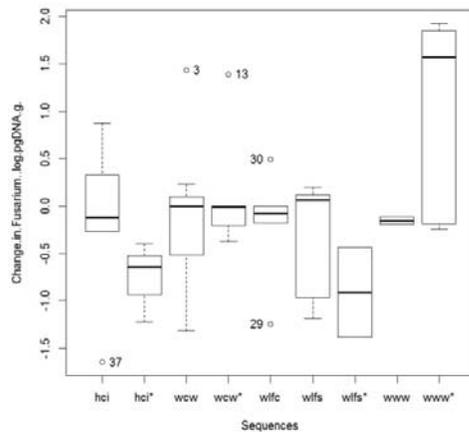
The primary CR host, wheat, recorded the biggest increase in CR levels along with barley (Fig 1c). The non-host winter crops; canola, chickpea and faba bean showed no reduction in CR levels while field peas showed a significant decline in the pathogen at harvest. The biggest decline was recorded in the non-host summer crops; cotton, maize, mungbean and sorghum. Wheat, the primary CRR host, showed no real increase in CRR, however, there were a number of outliers where CRR levels did increase (Fig 1d). All bread wheat varieties sown were rated MS-S for CRR. The other crops showed no change or slight declines, however, the biggest decline came from the MR barley cultivar Compass.



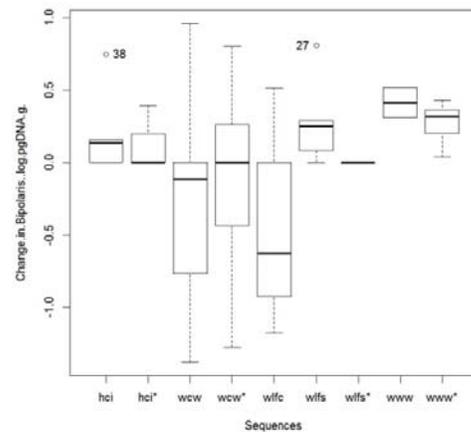
(a) *Pratylenchus neglectus*



(b) *Pratylenchus thornei*



(c) *Fusarium spp*



(d) *Bipolaris sorokiniana*

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; high crop intensity (hci), wheat/chickpea/wheat (wcw), wheat/long fallow/cotton (wlf), wheat/long fallow/sorghum (wlf), wheat/wheat/wheat (www).

The high crop intensity sequence consists of 5 crops in 3 years with a range of winter and summer crops. The majority had a mung bean crop 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). *P. thornei* was different, however, where the high crop intensity sequence led to reductions in 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 high 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 high 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).

Conclusion

In terms of individual crops, 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*, while *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 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 NGR, but this study suggests that this sequence is prone to increase *P. thornei* numbers. High crop frequency 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.

References

Hochman Z, Prestwidge D, Carberry PS (2014) Crop sequences in Australia's northern grains zone are less agronomically efficient than the sum of their parts. *Agricultural Systems* 129, pp. 124-132.