

Changes in *Fusarium* crown rot incidence in continuous wheat sequences in the low rainfall WA wheatbelt

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Abstract

Soil levels of crown rot DNA gradually increased over four years of continuous wheat in WA's low rainfall Eastern Wheatbelt. Fallow and canola breaks reduced DNA levels but these rapidly recovered even after a single wheat crop. Levels of disease expression were lower after break crops in some seasons but higher in others, even if inoculum levels were low, due to interaction between growth vigour and rainfall pattern. Nevertheless crop sequence did not affect grain yield over this period so continuous wheat remained sustainable for four years.

Key Words

Crown rot, *Fusarium*, wheat, crop sequence, break crops, Predicta-B

Introduction

Despite the well-known benefits of species diversity in crop sequences in the spatial and temporal dimensions (Kirkegaard *et al.* 2008, Angus *et al.* 2015, French *et al.* 2015, Malik *et al.* 2015) extended phases of wheat grown after wheat are common in low rainfall (<350 mm annual rainfall) agricultural areas of Western Australia, especially on heavier soils and on farms with no livestock (Lacoste *et al.* 2016). Generally, farmers grow fewer break crops and more cereals than is optimum (Robertson *et al.* 2010). This is usually attributed to break crops being riskier than cereals, and the risk aversion of most wheatbelt farmers. Factors responsible for declining wheat productivity in extended monotonic sequences include nutrient exhaustion, increasing weed populations and disease pressure, and depletion of soil water reserves (Kirkegaard *et al.* 2008). Weed populations and disease inoculum levels in particular are stochastic in nature, but can build up rapidly once they exceed a threshold level. Good management to keep weed populations and disease inoculum levels low should therefore prolong the duration for which continuous wheat sequences remain sustainable.

In this paper we describe changes in *Fusarium* crown rot infection and its effect on productivity over 4 years in a range of sequences with different intensities of wheat and different wheat cultivars with different levels of crown rot tolerance. Crown rot infects the crown and lower stems of wheat and interferes with conductive tissue in the stem; wheat therefore suffers most damage under stressful conditions during gran filling. The inoculum is carried on crowns and straw of infected crops, and has recently become increasingly prevalent in the WA wheatbelt.

Methods

Trial design and site description

Wheat was grown in 6 different 4 year sequences from 2015 to 2018 on DPIRD's Merredin Research Facility (Table 1). Sequences were repeated with three cultivars Emu Rock, which is reputed to be tolerant of crown rot (Huberli *et al.* 2017), Mace, and Magenta, giving 18 treatments, which were replicated three times. The trial was laid out as a 9 × 6 grid with replication in two dimensions. The 10 m × 15 m plots were split eight ways in 2018 for four cultivars (the original three plus AGT Scepter) sown either directly on or halfway between the previous year's rows. The trial was sown using no-till technology and all stubble of the previous year's crop was retained.

Table 1. Yearly components of six wheat-based sequences compared at Merredin, WA from 2015 to 2018.

Sequence name	2015 crop	2016 crop	2017 crop	2018 crop
WWWW	Wheat	Wheat	Wheat	Wheat
FWWW	Fallow	Wheat	Wheat	Wheat
CWWW	Canola	Wheat	Wheat	Wheat
FCWW	Fallow	Canola	Wheat	Wheat
CFWW	Canola	Fallow	Wheat	Wheat
WFCW	Wheat	Fallow	Canola	Wheat

The site was on a yellow/brown shallow loamy duplex soil (WA Soil Group 508) with a brown loam at the surface (pH_{Ca} 4.8) over a brown/white clay loam at 30 cm and pH_{Ca} at 50 cm ~ 6.0. The site had grown a crop of Mace wheat in 2014 which showed crown rot symptoms and had been grazed over the 2014/2015 summer but stubble remained on the site when the trial was established in June 2015.

Measurements

Soil levels of *F. graminearum* (crown rot) DNA were estimated each year by Predicta-B testing (Ophel-Keller *et al.* 2008). In 2015 soil samples were spiked with wheat crowns as recommended for growers using the test as a diagnostic tool, but in later years we did not spike samples with stubble. In 2016 and 2017 all soil cores were taken from within the previous year's crop rows but in 2018 separate sampling was done within and between rows.

In 2015 samples of 2014 stubble were collected prior to sowing the trial and sent to NSW DPI for plating out to confirm the presence of the crown rot fungus.

Three measures of crown rot's effect on crops were made. In 2016-2018 the density of white heads in each plot was counted on 2-3 occasions during grain filling; at maturity individual plants were sampled from each plot and the percentage of plants showing crown rot symptoms used to indicate crown rot incidence, and crown rot severity calculated using lesion size as a weighting factor. All plots were harvested with a plot harvester and weighed to estimate grain yield, and grain samples retained to determine grain quality: grain protein, hectolitre weight, and small grain screenings < 2mm.

Results

Initial disease levels

Before the trial was sown in 2015 13.4% of wheat crowns and 11.2% of wheat stems on the site were infected with the *Fusarium* fungus. There was an average of 6008 pg *Fusarium* DNA/g soil present in the 0-10 cm layer of soil on the site, indicating high levels of crown rot. There was only 11 and 33 pg DNA/g soil of take-all and common root rot respectively. Levels of *Rhizoctonia* and root lesion nematodes were very low.

Changes in soil DNA levels

Levels of soil DNA from 2016 onwards were not directly comparable with those measured in 2015 because soil samples for Predicta-B testing were not spiked with stubble after 2015. In 2016 there was less crown rot DNA in fallow plots from 2015 than in cropped plots, in 2017 plots that had grown wheat in 2016 had higher levels of DNA than other plots, but in 2018 all plots that had grown wheat in 2017 had similar levels of crown rot DNA while levels were very low after a two break from wheat in WFCW sequence (Figure 1A).

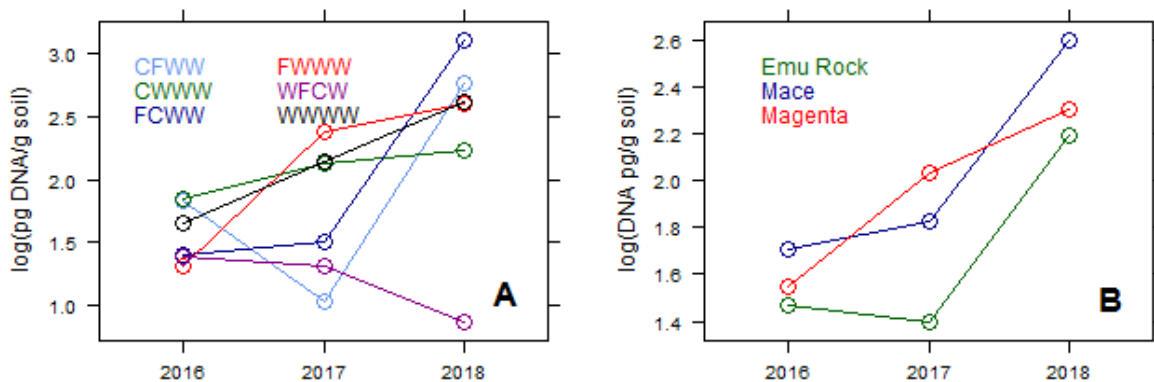


Figure 1. Changes in soil crown rot DNA levels in late summer in 6 different crop sequences (A) and for three different cultivars (B) at Merredin, WA, from 2016 to 2018.

Sequences based on Emu Rock consistently had lower crown rot DNA levels than those based on Mace or Magenta, however the difference was much greater in 2017 than 2016 or 2018 (Figure 1B).

Plant infection

Crown rot incidence and severity were significantly affected by year, sequence, and cultivar (Figure 2). There were no significant interactions between cultivar and sequence, but there were interactions between year and sequence, and year and cultivar. Wheat grown in 2017 after two breaks (CFWW and FCWW) had lower incidence and severity than wheat grown after wheat (WWWW, CWWW, FWWW) but in 2018, when incidence and severity were lower overall, this order was reversed. 2018 incidence and severity in WFCW,

also with two breaks, was also higher than in continuous wheat. Incidence and severity were lower where Emu Rock was grown than Mace or Magenta.

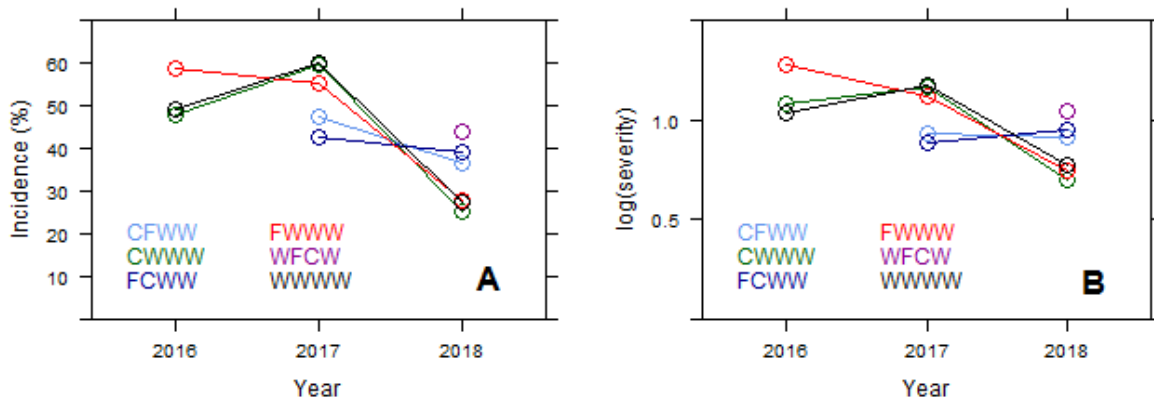


Figure 2. Changes in wheat crown rot incidence (A) and severity (B) in 6 different crop sequences at Merredin, WA, from 2016 to 2018.

In 2018 seeding on or between rows had no effect on crown rot incidence or severity. Cultivar had a highly significant effect, with Emu Rock having lower incidence and severity than Mace or Scepter which were lower than Magenta. There was also lower incidence and severity when wheat was grown in sequence after Emu Rock than Mace or Magenta but the effect was small: 28.1% compared to 32.9% and 34.1% respectively for incidence, and 7.8 compared to 9.5 and 10 respectively for severity when averaged over all four cultivars present.

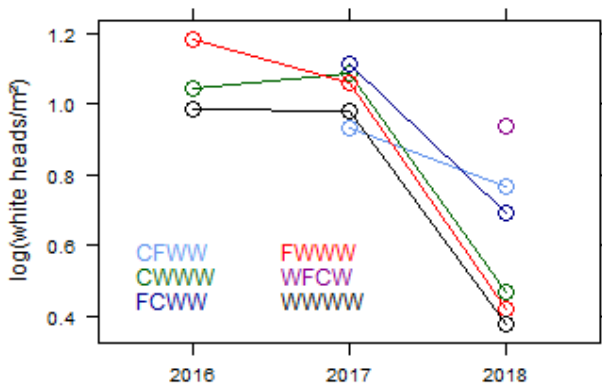


Figure 3. Changes in white head numbers severity in 6 different crop sequences at Merredin, WA, from 2016 to 2018.

White head number followed a similar pattern to crown rot incidence (Figure 3). 2018 was different from the two previous years in that overall levels were lower, and levels in sequences with two breaks were significantly higher than in other sequences. In all three years white head numbers were highest for Magenta, next highest for Mace, and much lower for Emu Rock (average over 3 years 17.7 heads/m², 9.8, and 2.2 respectively for Magenta, Mace, and Emu Rock). The response of white head number to 2018 treatments reflected that of crown rot incidence and severity: sowing on or between rows had no effect, and Emu Rock having fewer white heads than Mace or Scepter which had fewer than Magenta: 1.5, 4.8, 4.6, and 9.7/m² respectively. We attribute the higher levels of crown rot expression in 2018 in sequences including breaks, including one with significantly lower levels of crown rot DNA in the soil at the beginning of the season, than in those with a longer wheat phase to greater growth vigour in these sequences due to more plentiful soil N supply coupled with a very dry September resulting in higher levels of water deficit. This deficit was relieved by rain in early October so the highest crown rot expression levels were no higher than levels observed in 2017.

Crop performance

Despite the differences between sequences in the amount of crown rot expression there were no significant sequence effects on grain yield in any year of this trial. There were significant differences between cultivars (Figure 4) but although Emu Rock was highest yielding overall in 2016 and 2017, and Magenta the lowest yielding in most years, we cannot conclude that this is due differences between these varieties in crown rot expression because this is confounded with differences in phenology.

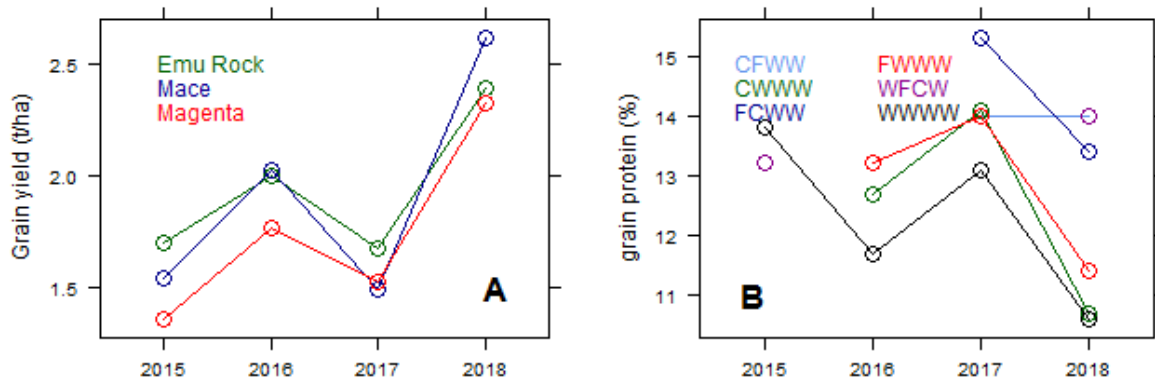


Figure 4. Grain yield of three wheat cultivars (A) and grain protein in 6 crop different sequences at Merredin, WA, from 2016 to 2018.

Although grain protein was generally high, it was related to the intensity of wheat in the sequence and season (Figure 7). Continuous wheat had lowest protein, sequences with a single break the next lowest, and sequences with two breaks the highest.

Conclusion

Non-cereal breaks in crop sequences can reduce levels of crown rot inoculum and this can lead to reduced disease expression. However break crops can also significantly improve crop vigour and this can increase disease expression even from very low levels of inoculum. Inoculum levels can also be lower when a tolerant wheat cultivar is grown but this also varies between season. Yield was not affected by levels of crown rot in this trial so continuous wheat remained sustainable over four years in this environment from the point of view of crown rot.

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