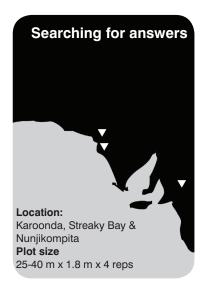
Rhizoctonia bare patch disease inoculum build-up in different cereal crops and varieties

Gupta, V.V.S.R.¹, Alan McKay², Andrew Ware³ and Nigel Wilhelm² ¹CSIRO, Waite; ²SARDI, Waite; ³SARDI, Port Lincoln



Key messages

- A significant variation in the rhizoctonia inoculum buildup exists between cereal crops wheat, barley, triticale and cereal rye and their varieties. Inoculum build-up was generally higher in the barley varieties compared to that in other crops. Results are in general agreement with observations in other experiments in the Mallee and on calcareous soils in Eyre Peninsula.
- Differences in inoculum levels carried through summer and seen at sowing in 2016 suggest that farmers may select between cereal crops and their varieties to limit inoculum building during the cereal phase. However, non-cereal break crops are the best option to reduce the pathogen inoculum in a cropping system.
- Soil physical (compaction), chemical (organic C and

nutrients) and biological (activity and composition) characteristics and seasonal (temperature and rainfall) factors can influence the growth of R. *solani* AG8 fungi and the severity of rhizoctonia disease.

Why do the trial?

In the lower rainfall southern Australian agricultural region rhizoctonia rootrot is an important soilborne disease in cereal crops. Rhizoctonia solani AG8 grows on crop residues and soil organic matter and is a good saprophyte adapted to dry conditions and lower fertility soils. An effective control of rhizoctonia disease impacts requires an integrated management program over multiple years to (i) reduce the pathogen inoculum levels and (ii) control infection and impacts on plant growth. Non-cereal crops in rotation have been shown to reduce the pathogen inoculum levels, however, reduction of inoculum build-up under cereal crops/varieties is considered to be a useful trait in the cereal phase dominated cropping systems commonly followed in the rainfed regions of Southern and Western Australia. Soil disturbance below seeding depth, N levels at seeding, soil temperature and moisture during the seedling growth stage and fungicides applied as liquid banding as part of an integrated management strategy could help reduce disease impacts.

The aim of this work is to determine the variation in the build-up of *R. solani* AG8 inoculum between cereal crops wheat, barley, triticale and cereal rye and varieties in a cropping system.

How was it done?

In 2015, a field experiment was conducted at Karoonda, SA with different varieties of wheat (Emu Rock, Harper, Mace, Scout, Yitpi), barley (Buloke, Skipper, Schooner, Fathom, Scope, Commander), cereal rye (SA Commercial, Bevy) and triticale (Fusion, Bogong) to determine the pattern of rhizoctonia inoculum build-up within the crop. After the harvest of 2015 crops, plots were maintained during the summer with chemical weed control and in 2016 Scope barley was sown @ 70kg/ha on 6 June on all plots using one pass sowing equipment with knife points. Surface soil (0-10 cm) samples collected in 2015 crop and at sowing 2016 were analysed for R. solani AG8 DNA concentrations and plant samples collected at 8 weeks were analysed for root disease incidence. Root disease incidence at 8 weeks after sowing, plant growth and grain yield were monitored. Additionally, during 2014 and 2015 crop seasons, R. solani AG8 inoculum and root growth measurements were made in field trials at Streaky Bay and Nunjikompita in Eyre Peninsula (barley and wheat experiments conducted by Andrew Ware, SARDI).

What happened?

At sowing in 2016, R. solani AG8 inoculum DNA concentrations were higher after the previous barley crop compared to other cereal crops (Figure 1c). Between the two cereal rye varieties, inoculum levels were higher after Bevy (354 + 35 pg DNA/g) compared to SA Commercial (202 \pm 38 pg DNA/g). With triticale varieties, inoculum levels were higher after Fusion compared to Bogong variety. Inoculum levels at sowing in 2016 reflect the inoculum build-up in the 2015 crop and its decline after harvest during summer (January to May 2016). With its extensive root system and high amount of crop residues, soil microbial activity after cereal rye crops is generally greater than that after cereal crops such as barley and wheat.

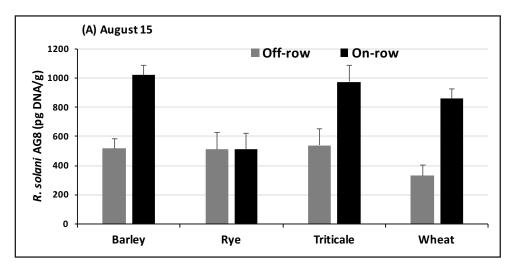
R. solani AG8 inoculum DNA concentrations in all the crop varieties and in both seasons were significantly higher (P<0.01) onrow compared to that in the soil from in between row (Figures 1 & 2) and an overall >4-fold difference between lowest and highest values. Differences in rhizoctonia inoculum levels were generally higher in 'on-row soils' compared to that in in-betweenrow soils for both wheat, barley and triticale, however for cereal rye varieties inoculum levels in the on-row and off-row samples

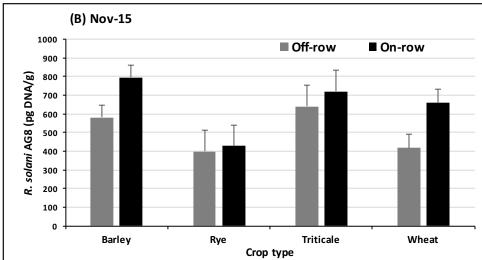
were similar (Figure 1a & 1b). Significant varietal based variation in the rhizoctonia inoculum levels was observed in soils from both sampling times (Figures 1a, 1b & 2). At Karoonda, inoculum build-up was generally higher in barley and wheat varieties such Schooner, Fathom, Scout as and Yitpi (800-1100 pg DNA/g) compared to Buloke and Emu Rock (275-440 pg DNA/g) (Figure 3). Even though inoculum levels were generally lower in the offrow, lower microbial activity in the inter-row space has the potential to contribute to the higher disease incidence, in particular in lower organic matter mallee soils.

There was a significant variation in the wheat and barley root DNA levels between varieties of both wheat and barley and root DNA concentrations. Root DNA concentrations were generally lower in the alkaline calcareous soils at Streaky Bay compared to that in the Mallee soils at Geranium and Lameroo. Although the general trends in the variation between different varieties were similar at both sampling times in 2015, there were changes in the order for amount of rhizoctonia DNA level for some varieties suggesting that root growth pattern and root architecture may play some role in the inoculum build-up. But, there was no consistent and significant relationship between root DNA and rhizoctonia DNA levels at

both locations (i.e. on-row and inbetween-row) and for both crops (R² values 0.01 to 0.3). Crop root DNA concentrations were also generally higher in on-row soils compared to that in in-betweenrow soils. There was a significant variation in the root DNA levels between varieties of both wheat and barley supporting the previous evidence that root distribution is a highly variable trait.

Differences in the mineral N levels in the soil profile at the sowing of 2016 barley crop were only seen in the cereal rye variety Bevy and not with other crops or varieties and there were no differences in soil moisture levels. There was a 25% variation in the barley plant biomass at anthesis (flowering) between highest and lowest performina previous season's variety, with highest biomass after the cereal rye (variety SA-Commercial). The effect on the grain yield was lower (9.5%) mostly due to the good in-crop rainfall, reducing the negative effects of disease on root growth. The effect of the previous season's cereal crop type and variety on the performance of 2016 barley crop is attributable to differences in mineral N levels, rhizoctonia pathogen inoculum, microbial turnover influencing nutrient (e.g. N) supply within the crop and microbial composition in roots etc.





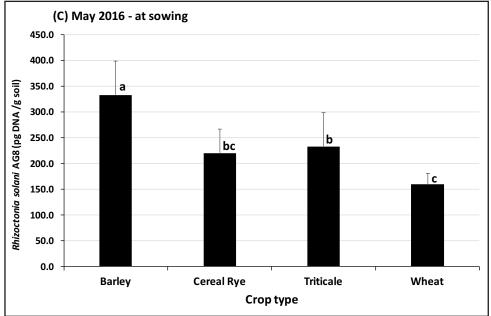


Figure 1 R. solani AG8 DNA concentrations in surface soils from on-row and off-row as influenced by cereal crop type during the (A & B) 2015 crop season and (C) at sowing in 2016 season in a field experiment at Karoonda, SA Note: A & B - Letters above bars indicate statistical significance of comparison between on-row/off-row samples; C -Letters above bars indicated statistical significance between crop types.

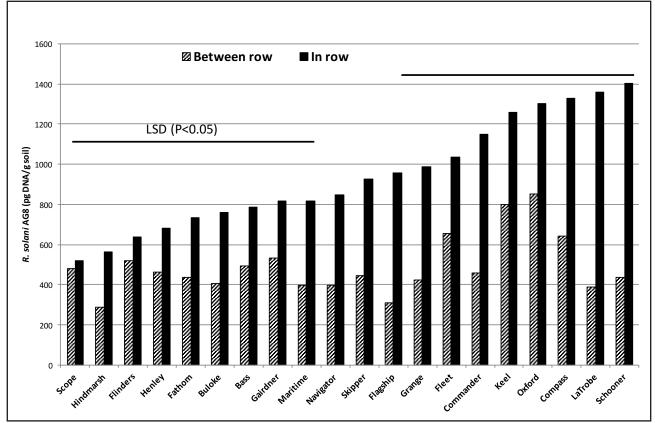


Figure 2 R. solani AG8 DNA concentrations in soils from barley variety experiment at Streaky Bay during August 2014

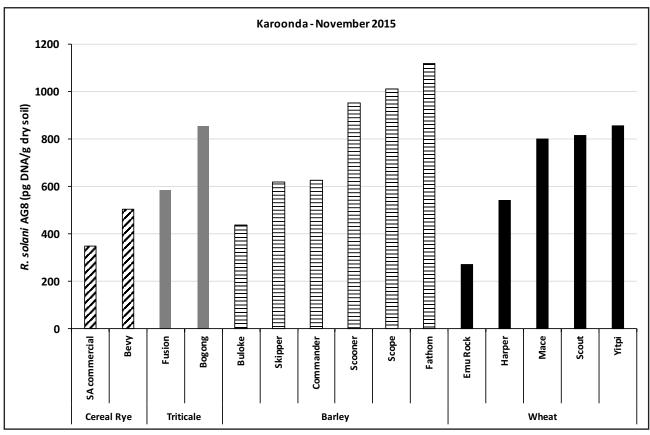


Figure 3 R. solani AG8 DNA concentrations in surface soils as influenced by cereal crop varieties at the end of 2015 crop season in a field experiment at Karoonda, SA

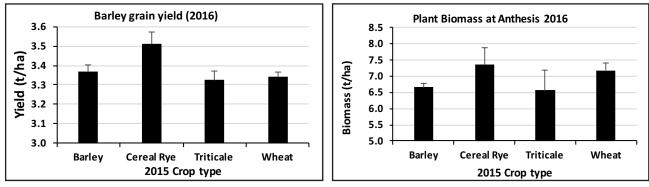


Figure 4 Plant biomass at anthesis and grain yield of barley following previous season's crop type in a field experiment at Karoonda, SA

What does this mean?

A significant variation in the rhizoctonia inoculum build-up exists between cereal crops wheat, barley, cereal rye and triticale and between varieties of each crop. Previous research has shown that non-cereal break reduce pathogen crops can inoculum levels significantly but farmers may also be able to utilize the variation between cereal crops and their varieties to manage rhizoctonia disease impacts in an integrated management strategy over multiple seasons.

A research strategy targeting the identification of mechanisms that enable cereal cultivars to limit build-up of *R. solani* AG8 is required to determine if the benefits justify breeders selecting this trait. This can be complemented with improved understanding of why rhizoctonia pathogen infect these crops but not build up inoculum during the season.

Acknowledgements

GRDC for funding, project codes DAS00125, MSF00003. Farmers at Karoonda (Loller family), Streaky Bay and Nunjikompita for allowing us to conduct the rhizoctonia trials on their farm during 2014, 2015 and 2016 seasons. Willie Shoobridge, Bill Davoren, Stasia Kroker, Paul Adkins, Marcus Hicks, Leigh Davis, Brenton Spriggs and Sue Budarick for field and laboratory work.

GRDC Factsheet - https:// grdc.com.au/Resources/ Factsheets/2016/02/Rhizoctonia

