

Quantitative disease traits to describe Rhizoctonia root rot severity in cereals

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Introduction

Rhizoctonia root rot, a soilborne disease that affects cereal and broadleaf crops, is caused by a long-lived necrotrophic fungus which grows through the top layer of the soil decaying and pruning the plant roots it infects, referred to as spear-tipping (Fig. 1).

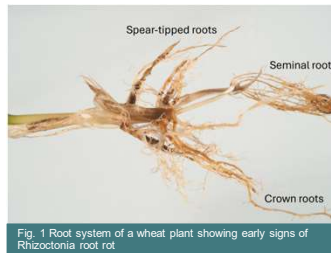


Fig. 1 Root system of a wheat plant showing early signs of Rhizoctonia root rot.

Disease severity in field trials is often assessed on plant roots using qualitative ordinal rating schemes which can differ between researchers and be used to rate the root system as a whole. The scores are often analysed as though they are metric data.

We investigated alternative quantitative root disease traits for assessing Rhizoctonia root rot severity in three field trials conducted to investigate the effects of abiotic constraints in cereals in the presence of *R. solani* AG8 and compared them with qualitative scores.

Methods

Field trials were conducted in 2020 to study the effects of nutrition, soil moisture and liming on Rhizoctonia root rot severity in cereals. 15-20 plants were randomly sampled from each plot and assessed for the presence of disease symptoms. Crown (CR) and seminal root (SR) systems were assessed separately.

Each plant was scored using the conventional ordinal qualitative scoring system described in Table 1 (CR.score, SR.score). Alternative quantitative traits recorded included counts of total and spear-tipped (<10cm) CRs to derive the proportion of spear-tipped roots (CR.spear) and the proportion of SRs with lesions to the nearest 0.1 (SR.propn). Researchers estimated the % disease severity associated with the scores (Table 1) allowing two additional traits to be derived (CR.index, SR.index) by replacing each score with the central point of the associated percentile range (Chiang et al., 2017).

Multi-trait mixed models incorporating a correlation structure to allow between-trait residual (i.e. within plant) correlations to be modelled were fitted for each trial. Quantitative traits were square-root transformed. A separate residual variance structure was modelled for each treatment level.

All analyses were implemented using the ASReml-R package (Butler et al., 2018) in the R statistical computing environment (R Core Team, 2020).

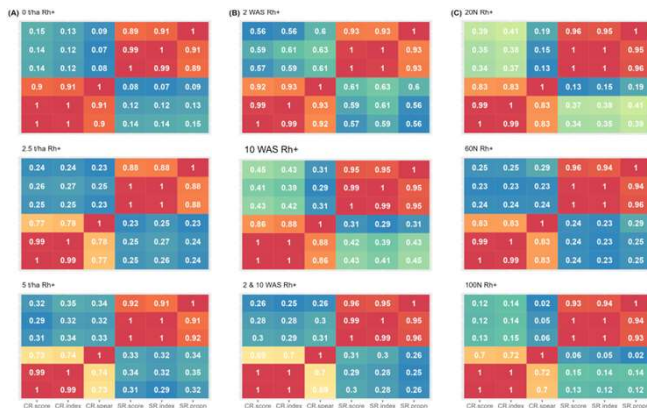


Fig. 2 Heat maps of between-trait correlations on inoculated plots for a subset of treatments from field trials investigating (A) liming (Wongan Hills), (B) soil moisture (Wongan Hills), and (C) nutrition (Muresk). WAS indicates weeks after sowing.

Table 1 Example of a bespoke rating scheme for Rhizoctonia root rot

Score	Description	% Severity
0	No disease	0%
1	Trace of disease	5%
2	Low level of brown lesions on infected roots. Most of the root system healthy.	25%
3	Medium level of brown lesions on infected roots. Similar levels of healthy and necrotic sections of roots.	50%
4	Most of the roots covered in brown lesions, little healthy root left.	75%
5	All or nearly all roots covered with brown lesions or short brown stumps.	100%

Discussion

- There is no alternative to removing plants from plots for visual assessment as infected plants can appear healthy at low levels of disease, and plants can resist infection in suppressive soils even where DNA loads are high.
- Qualitative ordinal scales simplify visual assessments for trained assessors, but at a cost. Integer labels assigned as ratings reflect membership of ordered categories with widths that may differ. As the rating schemes and category definitions can differ between researchers, results cannot be compared across trials/through time.
- Quantitative disease traits reflecting proportions of plant area expressing disease, as used in foliar disease trials, are not appropriate because there is no way to know if the entire root system has been recovered and the fungus destroys the root system through spear-tipping.
- Our approach was to focus on characteristic and countable aspects of Rhizoctonia disease symptoms. Heat maps of between trait residual correlations by treatment level (Fig. 2) show correlation with qualitative traits varied between 0.69 and 0.93 for CR.spear and 0.88 and 0.96 for SR.propn. CR.spear means differed between inoculated and uninoculated treatments (Fig. 3 shows liming trial means).
- The benefit of rating CR and SR systems separately is shown in the low correlation between CR and SR traits for most treatment levels (Fig. 2). In the liming trial, increasing rates of lime were associated with more disease symptoms on CRs and fewer disease symptoms on SRs (Fig. 3).
- The proportion of spear-tipped CRs provides a quantitative alternative to qualitative traits. It can be analysed with linear models and is easy to describe, understand and extend. Counting both spear-tipped CRs and lesioned CRs may further improve disease severity estimates.



Fig. 3 Bar plots of grain yield, proportion of spear-tipped crown roots, and proportion of seminal roots with symptoms by treatment level for the liming trial. Error bars give 0.5 +/- 0.05 LSDs.

References

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- Chiang, K. S., Liu, H. I., & Block, C. H. (2017). A discussion on disease severity index values. Part 1: warning on inherent errors and suggestions to maximise accuracy. *Annals of Applied Biology* 171, 139-154.
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