Simulating the interactions of blackleg disease (Leptosphaeria maculans) and canola (Brassica napus) in APSIM next generation

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Abstract
Agricultural pests and diseases are widely acknowledged as major constraints to global food production systems, and therefore require inclusion of their effects to address crop losses. This has been a challenge in the agricultural modelling community. The few existing models that account for the biophysical impact of pests are often based on a yield reduction approach via external visual symptoms. This fails to capture the pest response to agro-ecological conditions. A process-based modelling approach is more suitable for capturing a realistic representation of pest-host interactions in the field, as it highlights the biological modelling of the pest lifecycle and how it interacts with the crop's lifecycle.

The objective of this study was to construct an integrated model encompassing pest-crop-weather-management dynamics within the APSIM Next Generation framework, using the economically important blackleg disease (*Leptosphaeria maculans*) and canola (*Brassica napus*) as a case study. The research focuses on the monocyclic phase of disease progression, and each stage of disease development interacts with the environment, crop, and potential preventive measures integrated within the APSIM framework. The case study of blackleg on canola demonstrates how crop management practices, varietal resistance, timing of disease infection relative to crop growth stage, and agrometeorological conditions collectively influence the development of blackleg inoculum on stubble and the severity of crown canker. Furthermore, this study uncovers the fundamental physiological effects of the disease on crop productivity which could enable the transition of crop-pest models previously reliant on symptoms to be more dynamic.

Keywords
Mechanistic modelling; disease assessment; oilseed rape; *Plenodomus lingam*

Introduction
Methods for quantifying yield penalties caused by pest and diseases include field surveys, scientific experiments, empirical modelling, and predictive analytics. Models simulate the dynamics of farming systems, allowing systematic analysis of management practices, genotype effects, and environmental conditions. Process-based modelling, which includes phenology, growth, disease responsiveness, and weather, offers a more realistic representation of disease-host interactions under field conditions. Crop models that describe growth and yield under various conditions are widely used in agricultural research, but they often lack integration of biotic constraints like weeds, pests, and diseases (Willocquet et al., 2022; Bondad et al., 2023a). Using blackleg disease on canola as the case study, this paper reports on the (i) development of a coupled disease-crop model within APSIM Agricultural Production Systems sIMulator; Holzworth et al., 2014) that accounts for the blackleg disease lifecycle; and (ii) evaluation the model's performance in simulating canola crop development and yield in the presence and absence of blackleg crown canker across multiple production systems.

Methods
Development of a coupled disease-crop model in APSIM
The 'Lifecycle' module that captures pest or disease dynamics requires data for various stages of disease development; we initialised these phases to represent that of blackleg disease development. Each lifecycle stage interacts with other components of APSIM, such as the canola phenology, weather and management modules, allowing simulation of dynamic interaction between the disease and the crop (Figure 1).
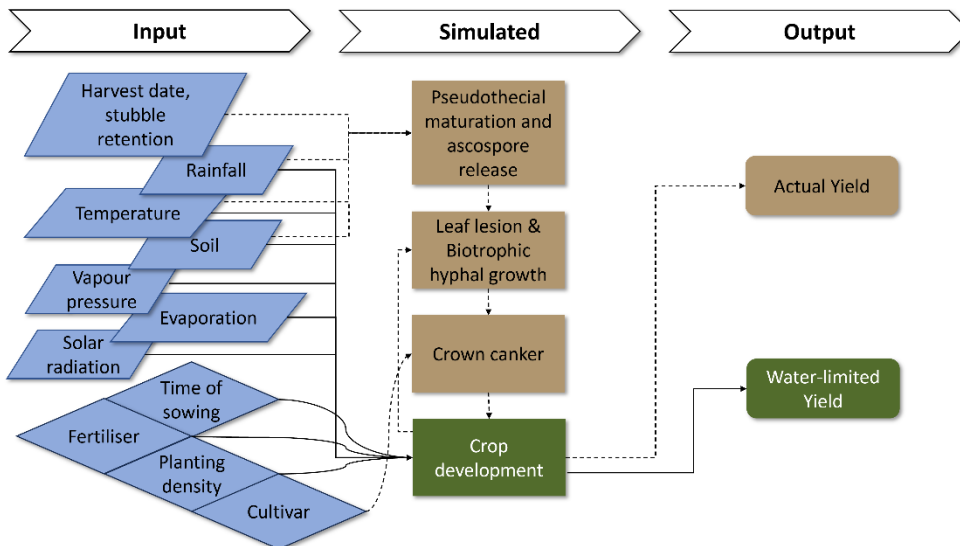
Figure 1. Schematic of new coupled disease-crop (blackleg-canola) model in APSIM Next Generation.

Validation of the coupled disease-crop model in APSIM

A variety of published and unpublished datasets were used to validate the performance of the coupled model in predicting (i) the onset of pseudothecial maturation and ascospore release (Bondad et al., 2023b), (ii) the timing of leaf lesion appearance (Bondad et al., 2024), (iii) crown canker severity, (iv) water-limited yield, and (v) actual yield Kirkegaard et al. (2006); Robertson and Kirkegaard (2005); Sprague et al. (2010); Bondad et al. (2024). The performance of the coupled disease-crop model was evaluated using standard regression (R^2 and slope of observed versus predicted) and deviation statistics (RMSD, RSR, NSE, and PBIAS). Further details of model evaluation statistics are provided in Moriasi et al. (2007).

Results
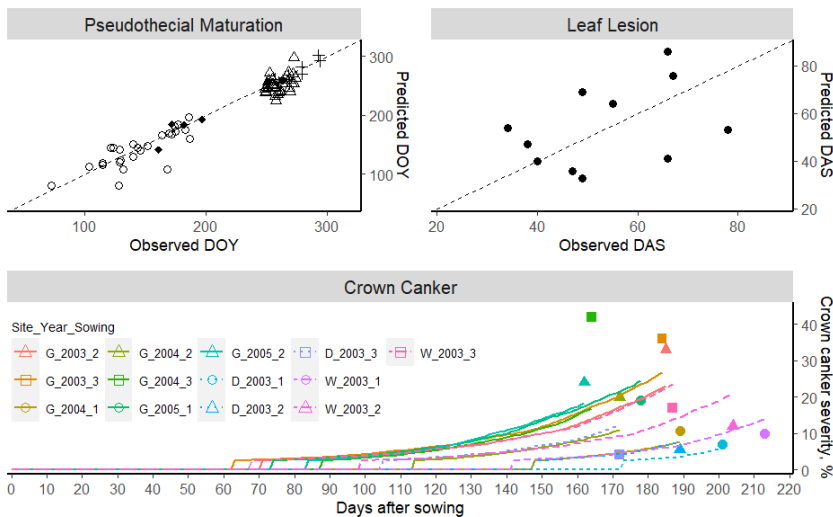*Model performance in simulating blackleg lifecycle*

Figure 2. Observed versus predicted timing of (i) onset of pseudothecial maturation and ascospore release in day of year (DOY), (ii) leaf lesion appearance days after sowing (DAS), and (iii) crown canker severity in multiple sites across Australia and other canola growing regions gloabally using the coupled disease-crop blackleg model. Dotted line represents 1:1.

Table 1. Performance of the coupled disease-crop blackleg model in predicting timing of leaf lesion appearance and crown canker severity.

Lifecycle Stage	R^2	slope	RMSD	RSR[a]	NSE[b]	PBIAS[c]
Pseudothecial maturation and ascospore release	0.94	0.96	16	0.27	0.93	2.5

Leaf lesion appearance	0.16	0.49	16	1.24	-0.55	-1.7
Crown canker severity	0.40	0.36	9.5	0.80	0.32	12.6

[a] $0.00 \leq$ RSR ≤ 0.50 (Very Good), $0.50 <$ RSR ≤ 0.60 (Good), $0.60 <$ RSR ≤ 0.70 (Satisfactory);
[b] $0.75 <$ NSE ≤ 1.00 (Very Good), $0.65 <$ NSE ≤ 0.75 (Good), $0.50 <$ NSE ≤ 0.65 (Satisfactory);
[c] (+) PBIAS = model underestimation, (-) PBIAS = model overestimation

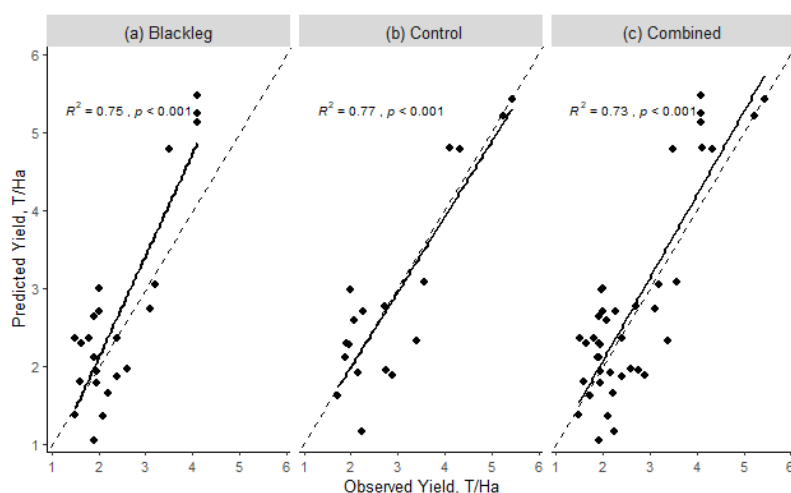*Model performance in simulating grain yield*

Figure 3. Observed versus predicted (a) actual grain yield of blackleg-infected crops, (b) water-limited grain yield of control crops, and (c) yield of blackleg-infected and control crops at Galong (2001 to 2005) and Wallendbeen (2001 to 2003), NSW. Solid line represents the regression line, dotted line represents 1:1.

The model predicted actual crop yield of diseased crops relatively well, with $R^2 = 0.75$, RMSD = 0.5 tonnes ha^{-1}, NSE = 0.84, RSR = 0.30 and PBIAS = -10% (Figure 2a). When tested against the datasets for control *B. napus* crops, the model similarly predicted water-limited crop yield with $R^2 = 0.75$, RMSD = 0.4 tonnes ha^{-1}, NSE = 0.73, RSR = 0.52 and PBIAS of 1.5% (Figure 2b). The overall performance of the model with combined diseased and control data was good ($R^2 = 0.73$, RMSD = 0.7 tonnes ha^{-1}, NSE = 0.56, RSR = 0.67 and PBIAS = -4.4%; Figure 2c)

Discussion
This paper demonstrates how a process-based disease lifecycle can be integrated within an established cropping systems framework to simulate disease-crop interactions as a function of weather and management. The dynamic simulation of disease progression in response to agroecological conditions allows more accurate representation of transitions between stages in the monocyclic phase of the disease lifecycle, including onset of ascospore release, leaf infections, and yield-limiting crown cankers. The model also demonstrates the physiological damage mechanism in plants caused by the progression of crown cankers and ensuing effects on grain yield development.

The coupled model had variable accuracy in the early lifecycle of blackleg; while prediction of pseudothecial maturation and ascospore release was closely aligned with observed measurements (Bondad et al., 2023b), simulated leaf lesion appearance was relatively poor. It is plausible that such differences reflect the quality of measured data. For instance, datasets for testing pseudothecial maturation and ascospore release were sourced from rigorous experimental studies, where disease measurement was straightforward, and the aim of the said experiments was to identify the presence of mature ascospores. Conversely, the timing of leaf lesion measurements in the datasets used to evaluate the model's predictions regarding the onset of initial leaf lesion appearance may have contributed to the model's variable accuracy. Aligning the aims of disease assessments with those of the model would likely improve model performance and contribute to the creation of disease measurement standards for model parameterisation and evaluation of the desired trait (Donatelli et al., 2017). As such, we call for further field experiments to measure the onset of leaf lesion associated with blackleg infection of canola across management and environmental scenarios.

Crown canker severity model simulated with varying success but captured trends in plant growth stage at the time of infection and thermal conditions during plant growth. Infection at the early stages of seedling growth allows greater thermal time for crown canker to progress leading to the formation of more severe cankers. Thermal conditions were also a strong driver of crown canker progression and severity. These simulation analyses offer insights into how the interaction among the onset of ascospore release, crop growth at the time of infection, sowing time and environmental conditions collectively exert a stronger influence on the development of severe crown cankers compared to the spore quantity at point scale (plant level), as documented in (Bondad et al., 2024).

Although extensive research is undertaken on the canola-blackleg pathosystem, experimental datasets that accurately capture data suitable for process-based modelling are few. This highlights the importance of collecting comprehensive data and serves to guide future disease assessments for plant pathology researchers.

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