An integrative approach to understanding the pest and disease threats to agricultural biosecurity under future climates

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Abstract
Despite increasing knowledge of the predicted impacts of climate change, potential threats from pests and diseases to agriculture remain uncertain. In this study, we developed models to understand better the likely responses of pest and disease threats to the changing Australian climate. By coupling host-plant physiology, virus and vector population growth and climatic data with projected climate change scenarios, we are able to project individual species responses and shifts to historic geographic ranges. Strengthened by empirical data, these models can be incorporated into plant biosecurity management and contingency planning, forming the basis of integrated scenario-based decision support systems for emergency plant pest management. Current work focuses on developing an innovative spatial modelling environment using the bird cherry-oat aphid (Rhopalosiphum padi) which vectors barley yellow dwarf virus (BYDV). The effect of climate change on aphid feeding behaviour, flight time and synchrony with the crop, virus acquisition and transmission rates, wheat phenology changes and physiological responses are being incorporated. Experiments in the Australian Grains Free Air Carbon Dioxide Enrichment research facility have enabled field based investigations of the effects of elevated (e)CO_2 on wheat pathosystems. Wheat stripe rust (Puccinia striiformis) and crown rot (Fusarium pseudograminearum) severity, latent period, fecundity and host resistance were assessed under ambient and 550ppm CO_2. This paper presents preliminary results from eCO_2 and wheat disease studies and describes the approach used to construct a model to project the effects of climate change on the future yields of wheat infected with BYDV.

Keywords *biosecurity, climate change, CO_2, wheat, model, crop disease*

Introduction

Pest and disease outbreaks occur when changes in climatic conditions such as temperature and soil moisture, and biotic factors such as host condition and natural enemy abundance are most favourable for growth, survival and dissemination. A change in climatic conditions can cause a pest or disease to expand its normal range into a new environment, extending agricultural losses and affecting natural plant communities (Rosenzweig et al., 2001). A poleward shift in the geographical range of some pests and pathogens has been observed during the last century. For example, the northerly spread of sudden death syndrome caused by *Fusarium solani* f. sp. *glycines* is a major threat to the U.S.A. soybean production (Roy et al. 1997). Rising temperatures associated with climate change are predicted to be associated with the future poleward movement of other insects and pathogens (Coakley, 1999; Rosenzweig, 2001).

While future spatial distribution of a species can be predicted under climate change scenarios using models, there appears to be limited knowledge of how climate change will influence the biology of a pathogen or insect and the interaction with their host.

The effect of climate change on plant pathogen and insect biology may be variable (Coakley et al. 1999; Fuhrer 2003; Chakraborty et al., 2008). For example, climatic factors such as storm severity, rainfall, humidity, temperature, and CO_2, affect the life cycle of the plant, pest/pathogen, vectors and their dispersal, by changing the rate of infection or infestation (Anderson, 2004; Berry, 2002; Cannon, 1998; Chakraborty, 2000; Pimentel, 2000; Pimentel, 2001). There may also be a change in cropping patterns leading to novel plant pathogen or pest interactions (Cannon, 1998; Coakley 1999; Parker and Gilbert, 2004) through: eg.

1. the movement of a new pest/pathogen into an existing crop, which then infects a previously unaffected indigenous (native and non-native) host;
2. the introduction of a new host through changes in cropping practices, which an indigenous pest/pathogen infects; and
3. the introduction of both new host and new pest/pathogen which interact with each other.

Conversely, climate change may restrict the prevalence of a pest/pathogen or a crop, subsequently restricting the occurrence of disease or infestation.

We explore two methods of testing whether climate change will increase the risk of damage to crops by pest and diseases, through (i) field and controlled environment-based experiments examining increased atmospheric CO_2 and (ii) modelling. This paper will outline both approaches in focussing on the effects of climate change on three diseases of wheat.

The interactions of increased atmospheric CO_2 and plant pests and diseases

Studies from controlled environments and Free Air CO_2 Enrichment (FACE) experiments have shown that changes in plant anatomy, morphology and phenology under elevated CO_2 can potentially influence disease epidemiology (Chakraborty et al., 2008; Manning and von Tiedemann, 1995). Of particular concern are changes to pathogen life-cycle and host-pathogen interactions that may reduce the efficacy of current control measures or accelerate the evolution of new pathogen races.

Increases in CO_2 can affect herbivore consumption rates, growth rates, fecundity and population density of insect pests (Awmack et al., 1997; Cannon, 1998; Fuhrer, 2003; Heagle et al., 2002; Jones et al., 1998; Whittaker, 1999). These effects are often associated with altered plant physiology and composition (including increased carbon:nitrogen ratio), altered concentrations of non-structural carbohydrates, starch and fibre content and other plant chemicals, but may also be associated with changes in the geographical range of native and cultivated host plant species (Cannon, 1998; Lincoln et al., 1993).

Elevated CO_2 may modify pathogen virulence and/or host susceptibility affecting the initial establishment of the pathogen on the host (Coakley et al. 1999; Matros et al. 2006; Plessl et al., 2005). In most examples, host resistance increased, possibly due to changes in host morphology, physiology and composition. However, an increase in plant canopy size (especially in combination with humidity), and an increase in host abundance can increase pathogen load (Chakraborty and Datta, 2003; Manning and von Tiedemann, 1995; Mitchell 2003; Pangga et al., 2004). Studies of BYDV infections in oats grown at eCO_2 led to an increased plant biomass compared to uninfected plants under eCO_2. Potentially this could increase the virus reservoir due to improved winter survival of infected plants (Malmstrom and Field, 1997).

Wheat Diseases and increasing atmospheric CO_2

In 2007, the Australian Grains FACE (AGFACE) facility at Horsham in Victoria (Fig. 1) was established (Mollah et al., 2009) to study changes in wheat agronomy at CO_2 concentrations projected under the IPCC emission scenario A1B. With eight 12 m diameter stainless steel rings dispersing CO_2 at a concentration of 550 ppm, the main trial was a factorial design of two CO_2 levels, two wheat varieties, two times of sowing and two levels of water supply in four replicates. Small areas of this trial have been used to study pathogen biology and host-pathogen interaction for the biotrophic

pathogen, stripe rust (*Puccinia striiformis*), the necrotrophic pathogen, crown rot (*Fusarium pseudograminearum*) and BYDV (Barley yellow dwarf virus).

eCO_2 and wheat stripe rust (*P. striiformis*)

A susceptible (H45) and a partially resistant (Janz) cultivar of wheat were planted in the AGFACE rings to determine whether wheat was more or less susceptible to stripe rust under increased atmospheric CO_2. The wheat was inoculated with spores of *P. striiformis* and the "area under disease progress" curve was recorded for infected wheat grown under ambient and eCO_2. Components of pathogen life-cycle including fecundity, incubation and latent period were also recorded over two seasons (2007 and 2008).

Figure 1. Australian Grains Free Air CO_2 Enrichment (AG FACE) experiment site, Horsham, Australia.

For the fecundity assessment, segments from 3 infected leaves of the same age group were destructively sampled from each subplot, shaken for one hour in water with 0.01% Tween 20. Urediniospore concentration was determined using a haemocytometer and expressed as pustule per unit area. Leaf segments were blotted dry, scanned and the area covered by pustules calculated and analyzed using image analysis software (Fig. 2). There was no difference in the pathogen fecundity levels between the CO_2 treatments in either season.

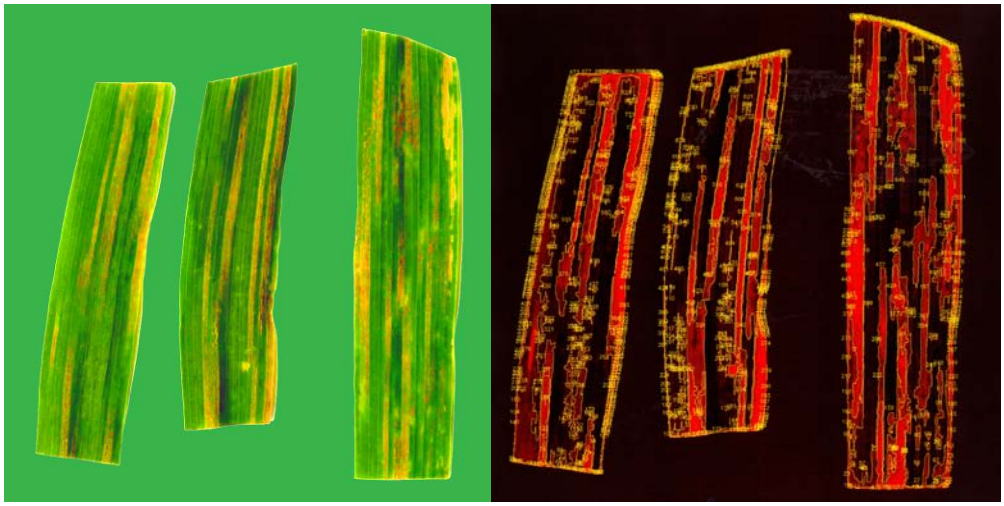

Figure 2. Wheat leaves unprocessed (left) and processed (right) using image analysis software to determine the area covered by stripe rust pustules.

However, these results need further examination because the expected difference in fecundity between the wheat varieties was not evident either. Assessments of fecundity and latent period of

P. striiformis needs a high level of precision and may be best studied in controlled environment chambers. Similarly, there was no significant effect of eCO_2 on disease progress or latent period.

These results suggest that with increasing temperature and CO_2 and decreasing water availability, the Australian wheat growing regions may be less conducive to the survival of this pathogen in future climates.

eCO_2 and crown rot (*Fusarium pseudograminearum*)

To determine if eCO_2 influenced the severity of crown rot infections in wheat, seeds from a bread wheat breeding line with partial resistance (2-49) and susceptible durum wheat (Tamaroi) were artificially inoculated with the fungal pathogen, *F. pseudograminearum.* The seeds were sown into a plot under the FACE rings and the plants were monitored for disease severity and pathogen life cycle traits. Stubble and soil samples were collected to monitor pathogen survival and fitness. Fungal biomass had significantly increased in the wheat stems grown under eCO_2 when compared to infected wheat grown at ambient CO_2 in a relative comparison of fungal DNA to wheat DNA using RT quantitative PCR (Melloy et al., 2010). This prelinimary work suggests that with increasingly drier conditions and increasing atmospheric CO_2, crown rot may become an increasing problem for the Australian wheat industry in future climates.

eCO_2, cereal yellow dwarf virus and *Rhopalosiphum padi* interactions

To determine the movement and concentration of virus particles under eCO_2, viruliferous and non-viruliferous colonies of *R. padi* have been established in glasshouse and growth rooms using the *Cereal yellow dwarf virus* (CYDV) RPV isolate as a model system. The aphids were transferred to the AGFACE rings to inoculate wheat plants (Yitpi variety) to determine whether eCO_2 changes the virus titre and rate of spread throughout the host plant. Parallel studies in closed environment chambers will complement these field studies

In conjunction with the virus studies, yellow sticky traps have been deployed in the AGFACE rings to determine if there are any changes in the vector population, seasonal abundance, aphid activity and flight times in an eCO_2 atmosphere compared to ambient CO_2. Further, understanding possible changes in the transmission and acquisition efficiency of of phloem restricted CYDV by *R. padi* to plants grown under ambient and eCO_2 is critical to predict disease occurrence and severity under future climate.

To investigate this, an electrical penetration graph (EPG), commonly used to study the feeding behaviour of aphids and other sap-sucking insect is being used. It provides, in real-time, information on aphid feeding behaviour as EPG waveforms, which can be correlated to specific feeding patterns and feeding locations (Tjallingii,1988). Measuring the time required by the aphid to reach phloem tissue and the period spent salivating in the phloem and ingesting sap, will indicate the effect of eCO_2 on virus transmission and acquisition. Data recorded from *R. padi* exposed to plants grown under eCO_2 and connected to the EPG electrode (Fig. 3) will reveal any modifications to feeding behaviour and subsequent CYDV transmission.

Figure 3. *Rhopalosiphum padi* connected to an EPG, feeding on wheat tissue.

The results generated from the AGFACE and closed environment chambers studies will be used in conjunction with other biological data to support the BYDV-*R. padi*-wheat integrated model to acurately capture the interacting effects of climate change on a crop yield. This research will assist in determining if diseases like yellow dwarf viruses, crown rot and wheat stripe rust will become an increased threat in future climates or whether they will reach thresholds beyond which their life-cycle is limited. This knowledge is important in assisting crop planting dates, varietal selection, disease surveillance protocols and control options.

Modelling the impacts of climate change on plant biosecurity

Predictions of future climatic trends indicate that the nature, extent and intensity of climatic changes will vary strongly both spatially and temporally. The response of plants, insects and pathogens to these changes is expected to be species specific and made more complex due by the degree of interaction and interdependence existing between these organisms.

A number of different modelling approaches have been described in the literature to investigate the potential distribution of plants as a result of changes in climatic conditions or their introduction outside of their native geographical range. Bioclimatic modelling approaches have been widely applied to study the potential distribution of invasive species (Baker et al., 2000; Kriticos & Randall 2001). Most of these programs use regression-based approaches to match current climatic parameters to species distribution in order to determine its climatic envelope. Because pest risk assessment and climate change applications demand that these models operate in an extrapolation mode, their performance in these applications is unlikely to yield robust reliable results. Other approaches (e.g. CLIMEX and NAPPFAST) use a more mechanistic approach to model the species growth and survival responses to various climatic factors, and are likely to provide more reliable projections of species geographic risk. However, despite the demonstrated usefulness of climate mapping to determine species maximum limits of establishment this approach does not typically take into consideration elements such as the timing of development of organisms, specific life stages, or the size of populations, which can be important factors to estimate the threat presented by an organism to an ecosystem or agricultural industry. Furthermore they do not capture species interactions, or dispersal mechanisms, host availability and synchrony with host

Phenological models, incorporating multiple life stages and detailed life history characteristics of both insects and plants have also been widely used. However, as with climate mapping, many phenological approaches have focused on modelling one organism at a time, assuming permanent food or host availability (Steinbauer et al 2004; Gray, 2004; Yonow et al., 2004). The structure of phenological models tend to be much more complex than that of climate mapping models and their design requires availability of species-specific data such as emergence, development and death rates. This is the case for models developed in complex programming languages such as Java used by Parry

et al. (2006) and FORTRAN or C++. The use of modular modelling software packages such as DYMEX, used by Yonow et al. (2004) or STELLA, used by Costanza and Voinov (2001) can help simplify model building and modification and make them more easily understood.

To determine if climate change would increase the risk of a pest threat to the Australian citrus industry, Aurambout et al., (2009) modelled factors influencing Asian citrus psyllid (*Diaphorina citri)* population variation in relation to increasing temperature, using an insect-host linked model developed in STELLA 9.01 in combination with a spatial modelling environment (SME: Maxwell, et al., 2002). In other work, the construction of multitrophic process-based population models (Stuart et al., 2002; Kriticos et al., 2010) has been made feasible with the development of DYMEX.

Modelling the interactions of *barley yellow dwarf virus*, its aphid vector, *R. padi* and wheat

There are few crop models with integrated pest and disease epidemiology modules that explore the interactions of environmental factors, let alone the spatial behaviour across regions (see Newman et al., 2003). Such models, however, are needed to develop robust biosecurity adaptation and mitigation strategies. In this study we focus on wheat (*Triticum aestivum*) and the bird cherry-oat aphid (*R. padi*) the vector of BYDV, an economically important cereal disease.

We are constructing a spatially explicit model that couples aphid dispersal, host-plant physiology, virus and vector population dynamics and projected climate change conditions to predict the impact on wheat yield production. Model functions are supported by empirical data of the influence of BYDV infected plants on aphid feeding behaviour, virus acquisition and transmission rates and plant physiology and growth using both growth chambers and the AGFACE resources.

Construction of a Wheat-BYDV sub-model

In this study, a model has been developed that simulates the phenology, growth and yield of the wheat crop based on a simplification of the O'Leary and Connor transpiration driven wheat model (O'Leary and Connor 1996a; 1996b; O'Leary et al. 1985). We incorporated O'Leary's equations into a preliminary model developed in the STELLA (Costanza and Voinov, 2001) modelling software, that allowed for the visualisation of interactions between variables. The model was then translated into the DYMEX (Maywald et al 2007) environment to allow the integration of this model with an aphid vector dispersal model and enable the evaluation of the impacts of BYDV on wheat at the landscape scale.

The model, running on a daily time-step comprised three modules: (1) soil water module, (2) wheat phenology and (3) wheat biomass-yield. The soil water module was a one layer simplification of the O'Leary 10 layer model and considered evaporation, transpiration and drainage. The wheat phenology model made use of a direct translation of the O'Leary equations to model the wheat phenostages; emergence, stem elongation, booting, anthesis, and maturity as a function of thermal and photothermal time. The biomass module simulated daily net biomass increment and partitioning between shoot and roots, and grain as a direct function of plant transpiration The model reads daily meterological data and CO_2 functions were taken from CropSyst (http://bsyse.wsu.edu/cropsyst/). The crop model was validated using experimental data gathered at AGFACE Horsham site in 2007.

In order to account for the effect of BYDV on wheat growth, an "infected wheat" life-cycle component was developed, with identical phenology and soil water modules to the healthy wheat model but for which biomass accumulation was modified to simulate known and hypothesised BYDV influences on wheat growth. The transition between uninfected wheat and healthy wheat components was triggered by the presence of infected ahpids, obtained from the aphid life-cycle described below.

*Construction of the virus vector (*Rhopalosiphum padi*) lifecycle sub-model*

The model is initiated by populations of aphids building up in irrigated pastures, often some distance from wheat fields illustrated by a simplified model diagram, Figure 4. These populations begin as apterous (wingless) aphids when temperatures are cool enough to sustain a population (temperatures above 30 °C cause high mortality of *R. padi*). When densities are high enough alate (winged) nymphs form. When these alates become adults they may migrate if conditions are favourable (particularly local temperature, wind speed, physiological age and relative humidity). A spatial model that incorporates the effects of wind speed and direction is used to simulate the aphid movement across the landscape each day.

Alate exules (migrants) arrive from irrigated grassland into wheat fields at the start of the season. Once a population establishes in the wheat field the lifecycle begins, with the production of apterous nymphs. These become adults, and as the population density increases the proportion of nymphs that are alate increases. Mortality affects the population largely by the impact of high temperatures. When alate nymphs become adults they mainly 'flit' between plants or, if conditions are optimal, eg. wind speed, aphid physiological age, temperature and relative humidity, the aphid may migrate longer distances, using the same spatial modelling as the alate exule migration for the irrigated pasture to initiate the wheat population (as above).

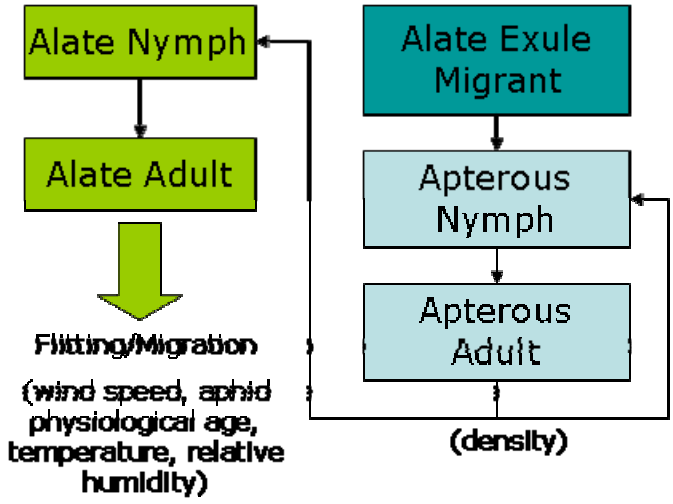

Figure 4. Simplified conceptual diagram of the within-field aphid model.

The integrated wheat-aphid-virus model

The integrated wheat-aphid-virus model is being constructed in DYMEX (Maywald et al., 2007). The DYMEX model was modified to better support dispersal modelling and the incorporation of spatial and spatio-temporal variables and processes.

This model operates at a regional extent, focusing on wheat growing areas of Western Australia, South Australia and Victoria initially. The model scale is a 5km grid, with the area of wheat and irrigated grassland contained within each grid cell assigned as a value to the grid cell. An estimated area of roadside grassland will also be assigned to each cell, as this can harbour aphids, acting as a 'green bridge' for migrants from the irrigated pasture at the start of the season.

The integrated model consisted of two main components: an aphid life-cycle and a wheat life-cycle, which run as a set of parallel lifecycles, one per model gridcell. The life-cycles only interact through dispersal, and life processes (growth, development and reproduction and user-defined processes) are all driven by either global variables (e.g., [CO_2], or spatially- or spatio-temporally-explicit variables. For example, the aphids can respond to the availability of environmental variables that allow them to

persist in favourable habitats such as irrigated perennial ryegrass pastures over summer. As temperatures fall, they respond to cues to start producing alate nymphs. The resulting alate adults then fly on prevailing winds when they are suitable for dispersal.

A set of planting rules was used to cue the initialisation of the wheat lifecycle. If the aphids arrive in a cell and wheat plants are present, then the wheat is colonised, and if the aphids are infected with the virus, they can transmit the virus to the wheat plants. The impact of the virus on wheat yield then depends upon the phenostage at which it is infected, and the time course of growing conditions, and the [CO_2] value. The subsequent results of the modelled impact of BYDV on wheat yield under future climates will be published separate to this paper.

Due to the number and diversity of plants, insects and pathogens it is difficult to empirically evaluate the true extent of each species' response in a generic construct. Each pathogen or insect's response is not only inexplicably tied to its host but it is also modulated by evolutionary processes where adaptation to changes in the host and changes its environment will occur. Nonetheless the continued improvement of computer models, based on theoretically, or empirically established rules will improve our understanding of these processes and assist in measuring general trends for future plant biosecurity planning. Most importantly there is a critical need to continue to monitor biological changes to crops and their pest and pathogen species in order to develop these models.

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