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UNDERSTANDING THE CHALLENGES OF FUSARIUM HEAD BLIGHT FORECASTING

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ABSTRACT

Fusarium Head Blight (FHB) is one of the most important diseases of wheat and barley in U. S. During severe epidemics FHB has resulted in billions of dollars in losses and has renewed interest in developing integrated disease management strategies for this disease. Plant disease management strategies recommend the use of moderately resistant cultivars; reduction in corn residue in the field; and the use of protective fungicides, when needed. Forecasting systems can help wheat producers evaluate the risk of disease and the need for fungicide applications. In this dissertation, winter and spring wheat FHB forecasting models were developed to help growers evaluate the risk of disease epidemics in their area. Both models used weather information from seven days prior to anthesis. In additions to this weather information, the spring wheat model successfully incorporated cultivar resistance as a risk assessment factor, and the winter wheat model accounted for the presence of corn residue. Both models had accuracies above 70%. Error analysis was conducted and a decision rule was incorporated to the spring wheat model to account for drought and significantly wet periods 21 days prior to anthesis.

Challenges addressed in this research included the relationship between weather station scale level indicators and large scale FHB epidemics, methods of reducing variability introduced from cropping practices, methods for evaluating modeling approach and model selection and ranking.

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CHAPTER 1

INTRODUCTION

Wheat (*Triticum aestivum*) is produced in most states of the U.S., and every year millions of acres of wheat are planted and harvested. Two main classes of wheat are planted in the U.S.: spring and winter wheat. Typically spring and winter wheat are distributed from north to south, depending on weather and soil conditions at the time of planting (Cook and Veseth, 1991). Winter wheats and spring wheats are largely separated in their distribution by the weather conditions they will face during spring. Winter wheats are established in the fall, undergo vernalization in winter, and produce grain the following spring and summer. In contrast, the spring wheats are planted in spring, flower in early summer, and are harvested in late summer. Spring wheats are mostly planted in the northernmost states (i. e. ND, SD and MN). Note that several of these northern states do grow winter wheats in conjunction with spring wheat. There are other wheat classes such as Durum wheat that comprise a large proportion of all wheats grown. Other types of winter and spring wheats include soft red, hard red, and white (Cook and Veseth, 1991). Minimum till or no-till practices are encouraged methods to avoid soil erosion (USDA, 1999). These practices have changed the agricultural landscape, and in some cases provide a reservoir for plant pathogens.

Fusarium head blight (FHB) is among the most important residue borne diseases of wheat and barley worldwide. In the U.S. FHB has caused over $1 billion in indirect and direct losses between the years 1993-1997 (McMullen et. al., 1997; USGAO, 1999; Ngange et. al., 2004). The symptoms of head blight are easily recognized on immature heads where one or more spikelets or the entire head appears bleached (Wiese, 1998). If the rachis is infected, then the

tissue above tends to be faded. Pink to orange mycelium may also be evident on the infected area, as well as small black perithecia. Infected spikelets usually become sterile and often contain shriveled or shrunken bleached kernels that are called tombstones, because of their resemblance to pieces of light colored stone (Wiese, 1998). Head blight is caused by up to 17 species of *Fusarium*. In the U. S. the most important species is *Fusarium graminearum* (*Gibberella zeae*) (Parry et. al., 1995). Other species that cause the disease in the U.S. are *F. culmorum, F. poae, F. avenaceum* and *Microdochium nivale* (Inglis and Cook, 1981; Parry et. al., 1995). For the purposes of this dissertation we will focus on *F. graminearum*.

Fusarium head blight affects the quality of grain in two ways: direct damage to grain, and the accumulation of the mycotoxin deoxynivalenol (DON) (Bai and Shaner, 1994). Several countries in the world have set advisory levels of DON in grain. The European Union has set a limit of 0.75 ppm for cereals (and 0.5 ppm in flour) (Galtier et. al., 2000), while the USA has set an advisory level of 2 ppm in grain, and 1 ppm for processed products from wheat (USDA, 1993). The consumption of DON contaminated wheat might induce (dose dependent) muscle spasms and vomiting (Bakan, 1998; Joffe, 1986; Kuiper-Goodman, 1985; Eudes, 1998; Forsyth et al., 1977; Miller, et al. 2001; Rotter et. al., 1996; Wiese, 1998, Vesonder et al., 1976). DON ingestion leads to blood and digestive disorders (Champeil et. al., 2004). Human exposure to DON is characterized by burning sensations in the mouth and stomach, headaches, decrease in red blood cell count, bleeding, necrosis of throat and stomach, and ultimately death in the more extreme cases (Eudes et. al., 2000, Rotter et. al., 1996). In animals, exposure to more than 10 mg/kg of DON produces vomiting and irritation of the mucous membrane lining of the mouth and esophagus. Feed refusal has been observed after 2 mg DON/kg (Eudes et. al., 2000; Forsyth et al., 1977; Miller et. al., 2001, Rotter et. al., 1996). DON also has a negative effect on malting

of beer (Parry et. al., 1995), and reduced quality of dough for bread (Champeil et. al., 2004).

In summary, Fusarium Head Blight can cause direct losses of yield. For example, northeastern North Dakota average wheat yields dropped 45% (from 49 bu/harvested acre in 1992 to 26.4 bu/harvested acre in 1993) (McMullen et. al., 1997). The quality of grain can be affected, thereby affecting the price growers are paid for their harvest. As an example, during the 1993, test weight dropped to as little as 44 lb/bu (McMullen, et. al., 1997). Lastly, contamination with deoxynivalenol can greatly decrease the price paid for grain (McMullen et. al., 1997).

Biology of the pathogen

Survival in crop residue. In any given season, *F. graminearum* can survive saprophytically in the debris of wheat and barley but can also be found on many different hosts such as maize, grass and broadleaf weeds, where it survives the winter as mycelium, perithecia primordia, or as macroconidia (Atanasoff, 1920; Khonga and Sutton, 1988; Parry *et. al.*, 1995; Sutton, 1982). The fungus can survive for long periods of time and is usually found on crop debris that take longer to decompose such as the stem nodes (Pereyra et. al., 2004; Sutton, 1982). The mycelium and spores of *F. graminearum* have been recovered from corn, wheat and soybean residues after as much as three years of decomposition and weathering of the residues (Dill-Macky and Jones, 2000; Inch and Gilbert, 2003; Pereyra et. al., 2004). Macroconidia have been reported to survive up to five repeated freeze-thaw cycles, as well as up to 88 h of drought in the laboratory (Beyer et. al., 2004).

Inoculum production. Macroconidia, hyphal fragments or ascospores can serve as inoculum, although ascospores are considered as the most important of these (Parry *et. al.*, 1995). Ascospores are produced inside sexual fruiting bodies called perithecia. Perithecia are dark purple or black ovoid sexual fruiting bodies (150-350 µm in diameter). These structures arise from inconspicuous stroma. Inside the perithecia, the asci are clavate sacs measuring 8-11 µm X 60-65 µm containing eight hyaline ascospores (Wiese, 1998).

As the fungus survives the winter it begins to produce both perithecia and macroconidia in response to favorable periods of both temperature and moisture. Perithecia are known to develop between 9◦ and 30◦C, with an optimal temperature around 22◦C (Figure 1.1). Relative humidity is an important environmental factor for perithecial maturation and development (Dufault et. al., 2006). Optimal barometric pressure for the production of perithecia is below -50 bars (-5Mpa) on osmotically adjusted agar (Sung et. al., 1981). It has been reported that perithecia require precipitation amounts greater than 5 mm to develop (Inch, 2001). Light is required for perithecia production (Trail et. al., 1998). Ascospores are 3-septate, hyaline, and 17.5-26 µm in size. Ascospores require temperature between 25º-28ºC and ultraviolet light to be produced (Sutton, 1982; Caron, 1993).

Macroconidia are produced in sporodochia. The optimal temperature for macroconidia production of *F. graminearum* is 32ºC (Jenkinson and Parry, 1994; Xu, 2003). Tshanz et. al. (1976) report a favorable range of 28º-32ºC for macroconidia production, while temperatures below 16ºC or above 36ºC are inhibitory. Macroconidia are variable in size (mostly 35-62 um) and septation (3-7), are fusiform and have a distinct foot cell (Booth, 1971, Sutton, 1982).

Dispersal. Wind and rain are considered the most important factors in the dispersal of ascospores and conidia (Parry et. al., 1995; Sutton, 1982). Ascospores have to be ejected from

perithecia for further transport, and macroconidia have to be liberated from sporodochia. The specific role of rainfall and wind in inoculum release and dispersal has been contested over the years. The mechanisms for release and dispersal are different for ascospores and macroconidia. Rain has been suggested to be the most likely trigger for perithecial release of sexual ascospores, which are then nocturnally wind dispersed (Attanasoff, 1920; Parry et. al., 1995; Sutton, 1982). Fernando et. al. (2000) show that ascospore release is not directly linked to precipitation, but that ascospore release peaks 1-4 days after rain events of at least 5 mm or relative humidity exceeding 80% (Figure 1.1). A likely scenario is that ascospores are first forcibly discharged and then wind dispersed 3-5 days after rain events (Fernando et. al., 1997; Inch, 2001; Paulitz, 1996). Interestingly, these same heavy rain events seem to be inhibitory when they occur continuously throughout the day (Paulitz,1996). The mechanism for ascospore release depends heavily on perithecia dehydration (Tschantz et. al., 1976). Paulitz (1996) observed a correlation between ascospore release and increases in relative humidity in conjunction with a decrease in temperature (similar to the end of the afternoon). He also observed ascospore release before the leaves become humid with dew at the base of the canopy; temperature ranges between 11º-30ºC and humidity ranges between 60-95% were correlated with this scenario (Paulitz, 1996; Tschantz et. al., 1976). Light is not a requirement for ascospore release (Paulitz, 1996).

The mechanism for asexual macroconidia dispersal is much simpler. Macroconidia are splash-dispersed and travel shorter distances than ascospores (Gilbert and Tekauz, 2000; Parry et. al., 1995; Sutton, 1982). Sutton (1982) reports ascospore dispersal occurring at temperatures 13º-22ºC with relative humidity 95-100%. Peaks of macroconidia concentration in the air have been observed 1-2 days after rain events following a long period of drought (Fernando et. al., 2000). The macroconidia are also splash dispersed, and rain splashed spores have been found to

reach heights of 100 cm above wheat canopies (Paul et. al. 2004). Arthropods including wheat midges (*Sitodiplosis mosellana)* could transport spores to wheat heads as well (Parry et. al., 1995; Mongrain et. al., 2000).

Infection. Infection in wheat depends on the synchronism of several factors, including environmental, plant growth stage, cultivar susceptibility, and presence of the fungus (Champeil et. al., 2004; Caron, 1993; Pugh et. al., 1933). Wheat heads are vulnerable to infection shortly after head emergence and remain susceptible until maturity when the moisture level of the grain limits fungal growth. However, the most severe disease symptoms and yield losses occur when infection takes place near anthesis. Most authors consider anthesis as the key stage for infection (Champeil et. al., 2004; Caron, 1993; Pugh et. al., 1933). Infection is similar in susceptible and resistant wheat cultivars (Kang and Buchenauer, 2000).

Maximal germination of ascospores and macroconidia occurs between 0 and -0.20 MPa, and is inhibited between -6 and -8 MPa (Sung and Cook, 1981). Penetration occurs by infection hyphae on the inner surfaces of the floret (Buerstmayr et. al., 2003). Penetration is favored by low temperatures and high humidity (Rapilly et. al., 1973), requiring a large number of hyphae for infection (Schroeder, 1963). Infection by macroconidia is optimal at 100% relative humidity and 25ºC, can occur between 20º-30ºC, and decreases gradually with lower temperatures up to 15ºC (Andersen, 1948) (Figure 1.1). Periods of 4-8 days of low humidity reduce the level of infection (Andersen, 1948). Once inside the plant, the infection continues upward within the head. Symptoms start to appear as soon as three to four days after infection (Wiese, 1998; Kang and Buchenauer, 2000).

The role of DON in infection has been a challenge to understand. Some accounts point to the incidence of DON above the infection site as early as 10 days after infection (Kang and

Buchenauer, 1999). While DON is not required for initial infection on wheat heads, it acts as a virulence factor in the spread of the fungus (Bai, et. al. 2001). Virulence of DON has been identified in *Fusarium graminearum*, as well as for *F. sporotrichoides* (Bai, et. al., 2001; Desjardins, et. al. 1989). It has been proposed that wheat varieties resistant to *F. graminearum* possess a factor that disrupts deoxynivalenol (DON) synthesis (Parry et. al., 1995).

Management. FHB is best managed with an integrated approach that combines crop rotation with non-host plants, the use of disease resistance varieties, and timely application of fungicide (McMullen and Stack, 1999). While none of these components can completely eliminate the disease, their combination greatly reduces the risk of severe disease and mycotoxin contamination. Each year small grain producers must evaluate the risk of disease and choose which a management strategy that maximizes the efficiency and profitability of their operation. Developing these yearly management strategies requires a constant assessment of rotation options, variety selection and the need for fungicides applied at anthesis. A disease forecasting system that can help producers evaluate the risk of disease and the need for fungicides is an important part of this integrated management for FHB.

Forecasting systems

Forecasting systems are a tool of decision analysis that can help the user integrate all the information about the biology of the pathogen and host together with management practices that influence the risk of disease. Seven forecasting systems have been developed around the world for FHB.

These systems are diverse in their objective. FHB forecasts have been designed to

predict disease incidence, disease severity (sometimes called index), DON concentration, or a measure of risk that an event will happen. The method of prediction also varied across studies but include parametric regression types of analysis, simulation techniques and systems approaches (De Wolf et. al., 2003; Moschini and Fortugno, 1996; Vargas et. al., 2000; Hooker et. al., 2002a; Hooker et. al., 2002b; Rossi et. al., 2003; Detrixe et. al., 2003; Zhao and Yao, 1989; Zhang and Shang, 1996; Del Ponte et. al., 2005).

Table 1.1 summarizes the details of these forecasting systems. Most of the information about the FACODEM model from China (Zhang and Shang, 1996) was published only in Mandarin. All models use on-site weather information and disease observations to build the model; only Zhang's model uses off-site weather, including the temperature of the ocean. Many of these models share a similar reference point in host growth to define significant periods of weather information. For example, Brazil, Canada and Argentina use head emergence as the phenological reference point (Del Ponte et. al. 2005; Hooker et. al., 2002b; Moschini and Fortugno, 1996), while USA, Italy and Belgium use the date of anthesis (De Wolf et. al., 2003; Rossi et. al., 2003; Detrixhe et. al., 2003).

The target variable chosen depends heavily on the method of analysis to produce the forecast. Process based models, such as the Brazilian and Italian models produce an index of FHB infection (Rossi et al (2003) also produce an index for mycotoxin contamination) that is later linearly correlated to disease severity and/or disease incidence. De Wolf et. al. (2003) classify epidemics based on a threshold of 10% disease severity; Hooker et. al. (2002a) predict the concentration of deoxynivalenol in the grain; Moschini and Fortugno (1996) attempts to predict disease incidence; while Detrixhe et. al. (2003) classify epidemics based on a threshold of 10% disease incidence.

The methods of analysis are diverse among the FHB forecasting systems. Process based analyses (or mechanistic approaches) use a series of linked differential equations to follow through the different aspects of the host phenology and disease cycle such as percentage of extruded anthers and inoculum or infection factors. De Wolf et. al. (2003), Detrixhe et. al. (2003), and Moschini and Fortugno (1996) use single linear equations for their predictions. An alternative process based modeling and structural modeling (modeling in a single equation) uses a decision tree between linear equations such as the case of Hooker et. al. model (2002b).

Common to all models is the search for the critical periods of disease-favorable weather events during the growing season related to FHB epidemics. The length of these events varies from 2 to 15 days. The proof of the value of these models is how well they relate theoretical, empirical information and small scale information to large scale disease information. This is assessed by different measures of accuracy (R-squared and accuracy *sensu stricto*) that are not necessarily interchangeable or comparable. R-squared assessed models vary from 51% to 93% accuracy. Only De Wolf et. al. (2003) and Detrixhe et. al. (2003) use accuracy as such (the percentage of cases properly predicted), and are around 70% accurate when using pre-anthesis information, and 84% accurate when using additional post-anthesis information (De Wolf et. al., 2003).

In summary, there are several approaches to forecasting FHB. They vary in methods and target variables as well as in accuracy. All the models use the environmental data (mostly temperature, relative humidity and precipitation) to predict disease incidence or severity or DON concentration. It is important to learn from these models in order to identify methods, variables and ways to integrate data into a decision support system. To date none of these models consider residue management or cultivar susceptibility in the integrated management of FHB.

Table 1.1. Forecasting systems of past compared for their characteristics.

Forecasting system	Type of data used	Target variable	Method used Accuracy, Notes	Variables used, time period expressed as days before (-) after (+) anthesis
Brazil (GIBSIM)	Weather, disease information	Severity and incidence. "proportion of tissue infected" Index is a combination of the 3 processes correlated to severity and incidence	Index built from decision analysis, process based Correlation to 93% in severity, 69% incidence Heading docked	Host factor: heads emerged (time); Extruded anthers (daily mean temperature, time) Inoculum factor: (daily mean RH, Position rainy day >0.3mm) Environment factor: dInfect/dSusc=(daily temp 2 day infection event) Infection event if: prec >0.3mm both days AND RH >80%; OR prec one day >0.3mm AND 80%-RH 1st day, 85% -RH 2nd day
Canada (DONCAST)	1996-2000 grain tests, weather Ontario	DON concentration	Flowchart, between 3 regression equations R squared 73% High humidity as key for disease development; docked at head emergence	Days of rain >5mm[-7,-4]; days mintemp <10ºC[-7,-4]; days daily maxtemp>32ºC [3,6]; daily rain >3mm[3,6]; daily rain >3mm[7,10]
USA	50 location-years [1982-2002] weather, disease severity	Epidemic=1/ no-epidemic=0	Logistic accuracy 70% pre; 84% post docked anthesis	7 days pre, 7pre +10dayspost; duration rain [-7,-1]; h temp 15º-30ºC [-7,-1]; TRH 15º30º 90% [0,9]
China (FACODEM)	Pacific Ocean water temperature	Disease severity	Simulation of optimal control problem, linked differential equations unknown accuracy	Ocean water temperature
Italy	Lab and field experiments: disease incidence and severity 300 head sample at milk stage; mycotoxin at harvest. Weather: T, RH, PPT, leaf wetness	Daily infection risk (DIF) based on sporulation, spore dispersal and infection; risk for mycotoxin production.	Mechanistic, systems analysis. building an Index FHB_risk vs severity (51%) TOX_risk vs DON (90%) Docked Anthesis	DIF=f(temp, rainfall, RH) Infection rate=G(temperature, wetness and the host growth stage) also sequences of rainy days; wetness duration; free water
Belgium	Weather data (station + radar), disease in 43 regions of Belgium,Recorded also: previous crop, soil preparation, crop variety, fungicide treatments	Duration of leaf wetness; disease incidence (into 2 categories: below and above 10%)	Probabilistic GIS Accuracy: 70-74% Docked anthesis	Temp, RH, wind speed, solar radiation (short and long wave), radar 1x1km rainfall. Time frame: [-8,6]. Model combines wetness duration (h), temp(0 if <12ºC; 1if>12ºC)
Argentina	Disease 1978-1990, weather 1991-1993 for validation	Disease incidence	Linear regression R-squared 86% Docked heading	2 equations [-8, 26-32], #2-day periods Rain AND RH>81% 1st day RH>78% 2nd day; daily accumulation residuals of {Tmin-9ºC}; residual Tmax-26ºC; days rain AND RH>83%

Challenges to FHB forecasting

Forecasting plant diseases present unique questions and challenges than should be thoroughly understood in order to build a successful risk assessment tool. These issues cover different aspects of FHB biology, its ability to be translated into statistical models, and the ability of these models to be implemented efficiently. In terms of the pathogen and host biology, challenges include the integration of information gathered from different experimental sources, while considering the natural spatial variation of host, pathogen, and of their interactions. Because the ultimate objective of forecasting systems is to be implemented and used by the general public, it is also important to understand the desirable properties of such as system and the possible constraints for deployment.

Biological challenges. The degree of accuracy achieved by a forecasting system is directly correlated to the amount of information available about the pathogen and the host. Considering all levels of interactions between environment, host, pathogens, time and location, there are an infinite number of combinations of disease scenarios to predict. Inherently the disease triangle represents great variation, but including the two additional dimensions of space and time, increases the level of variability exponentially. A forecasting system has to be able to represent a large section of that natural variability in order to be efficient.

In order to build a plant disease forecasting system one must be able to integrate the information about the biology of the pathogen. Ideally, the disease cycle must be separated into discrete stages such as the inoculum production, germination, and penetration. Information on disease stages should come from similar experimental conditions than allows for sequential integration. This requires that the information on each stage be compatible, for example,

experiments aimed to determine the environmental range of temperatures for perithecial development should ideally come from similarly designed experiments with complimentary environmental conditions that cover a range of temperatures previously seen under field conditions. Thus, in order to be able to integrate the stages of the disease cycle, information from them needs to be comparable and come from similar conditions.

Cultivar and isolate selection play a big role in the variability. It is practically impossible to account for all this variability. An attempt to reduce this variability can be done by ranking cultivars in terms of their susceptibility. Cropping practices affect the future risk of FHB; among these, residue management has been proven to influence the probability of disease, especially in the case of corn residue (Martin and Johnston, 1982; Seaman, 1982; Teich and Nelson, 1984). Crop rotation with non-hosts has been recommended a management strategy as well (Bai and Shaner, 1994). These cropping practices should be considered for inclusion of a forecasting system.

FHB forecasting, and particularly, assessment of the future risk of severe epidemics, requires environmental information related to the biology and interactions between host and pathogen up to the point where the forecast is relevant. In this case, relevance ends soon after wheat anthesis (Arthur, 1891; Attanasoff, 1920). Thus, required information includes, fungal survival, vegetative growth, reproduction, spread, and infection.

Current information on *Fusarium* biology is based on studies done at the scale of growth chambers and at the scale of research plots. Studies requiring microscopy, such as those on perithecial development have been carried out under controlled conditions (Andersen, 1948; Dufault et. al., 2006; Sung, and Cook, 1981; Tschantz et. al. 1975; Tschantz et al., 1976) and are very accurate at narrowing down environmental ranges. However, controlled condition experiments do not necessarily correlate to larger scale environmental information on the mean

perithecial development on a given area, because of multiple perithecia maturing at different rates and unsynchronized development, and because of differences between micro- and macroclimate measurements. On the other hand, studies on spore dispersal have mostly been done under field conditions because of the plot size requirements for these observations (Fernando et. al., 2000; Larson et. al., 2001; Sutton, 1982); these are more likely to be accurately represented at larger geographical scales, thus making it easier to relate to average large scale climate conditions used for forecasting.

Often overlooked, is the fact that different isolates used for biological experiments may differ in their response to the range of environmental conditions that occur. On the one hand, these differences allows for larger environmental variability to be correlated to the particular stage of the disease. However, if no replicated experiments are carried out with different isolates, it is possible that the target environmental range identified using one isolate is not sufficiently robust to be applied to other isolates. Additionally, asynchrony between the development stage of different individuals in the pathogen population on a field scale should be considered. This variation in development stages means that at any given time any environmental indicator will correlate (to varying degrees) to a snapshot of the range of developmental stages occurring in the field, and not to a specific individual.

This project will attempt to bridge the disconnect between information at small scales and large scales by finding and relating large scale environmental indicators of future risk of epidemics through understanding of the biology of the host and pathogen biology.

Statistical challenges. There are several issues to consider when creating a large scale forecasting system. The most pressing issue is the degree to which the collected data can be extrapolated to the rest of the spatial realm. This issue is directly related to spatial variation of cropping and environmental conditions, and to the number of observations collected from the

target area. Key questions to solve are: As we increase the dimensions of the target area, to how large an area can the data be extrapolated? Does the predicted probability of disease change gradually at regular intervals between two spatially separated estimates? These questions assume the variation among isolates and among cultivars is negligible and that the probability of disease is uniformly distributed at any particular site.

Designing a forecasting model involves defined modeling stages each of which has its potential shortfalls. Data collection and quality control are paramount. Data coming from different sources must be transformed to the same format and same units, taking into account the equipment used by cooperator. Next, indicator creation can potentially eliminate useful information from the data source but might identify isolate patterns associated to fungal development that have complimentary environmental ranges.

Given the limited number of observations is limited, the method of choice to predict the individual probabilities is critical. One must be able to accommodate the variability in each point estimates and across two dimensions. By assuming uniform probabilities, the problem can be reduced to one dimension.

The method of statistical modeling will directly affect the variance of the estimates used to determine disease risk. In business and forecasting literature there is considerable discussion on which method to use to provide forecasts. The consensus on forecasting methods is that the choice is a problem-specific matter (Cho et. at. 1991; De Veaux, 1995; Fedenczuk, 2002), due to advantages and disadvantages each modeling method can have. A relatively new way of comparing modeling methods considers the model output values as part of a partial ordered set and then ranks them. This methodology will be used in this project to rank models and modeling methods (Patil and Taillie, 2004) . This particular methodology has never before been used for this purpose in plant disease forecasting.

Implementation challenges. Model implementation poses a set of problems on its own. Delivery mechanisms have their own set of requirements and efficiency values. For weather information, it is important to note the resolution needed to forecast (spatial resolution of the final forecast). It is also important to know the possible variation in accuracy across sites due to the environmental equipment used to record the data.

Perhaps the most important issue to address on the implementation side is that the model output must be clear and simple for the target audience. Ideally, the users can understand the model and incorporate the models into their decision making process.

Modeling methods

Logistic regression; classification and regression trees, K-nearest neighbor, and neural networks were used in this project as modeling tools. These methods were compared in terms of their accuracy, sensitivity and specificity. These models were also compared through partial ordered set methodology using Hasse diagrams (Patil and Taillie, 2004). The following paragraphs will overview the methods used.

Logistic regression. Logistic regression is traditionally applied to predict binary response variables. In this case the explanatory variable was modeled as the probability of the event (epidemic, where field severity is grater or equal to 10%) hence, epidemic (=1)/ non-epidemic (=0). The probability of the event is calculated as follows.

$$P(y=1)=[\exp(a+bx)]/[1+\exp(a+bx)],$$

where a and b are parameters that solved using a maximum likelihood function (Agresti, 2002). Logistic regression has the advantage of being easy to interpret and implement by producing an equation that can be solved algebraically. Logistic regression has been used in the

past in other studies of plant diseases, such as Detrixhe et. al., 2003. De Wolf et. al. (2003) also used a logistic regression approach to assess the risk of an FHB epidemic (≥10% disease severity).

K- nearest neighbor (K-NN). The K-NN method is a non-parametric rule-based method that classifies groups of data around a kernel of value k and creates a series of orthogonal vectors to help implementation. This is the most difficult method to implement and interpret (Abbott et. al., 1998). In the K-NN rule, a sample is assigned to a class that is most frequently represented among the k nearest samples. The sample is then assigned to a group that has the minimum average distance to it (Cho et. al, 1991). The final outcome of this method is a complete assignment of all data points to a category of their peers.

Neural networks. Neural networks attempt to mimic the way the brain works, by learning patterns, and forecasting based on past experience with these patterns (DeVeaux and Ungar, 1997). Neural networks consist of a series of highly interconnected equations and are commonly considered to be "black box" approaches because it can be difficult to determine the relationship between input and output variables. In the one-layer backpropagation neural network intermediate variables (one per variable was used in this case) are linked with weather and crop management information, within variables and with the epidemic response variable, through a series of activation functions. These functions, assign optimized weights as the network learns (Bishop, 1996). The activation functions attempt to identify patterns to relate to a specific category of the binary variable. The output of this approach is a series of equations with multi-way interactions.

Classification and regression trees (CART). The CART method assigns a series of discrete rules that separate groups of data in groups based on the predictor variables. These groups are often called "leaves" and "branches", hence the term tree. In their most simple form,

a CART model assigns a discrete threshold to separate the largest number or cases into the 2 categories of the response (epidemic/non-epidemic). Further splitting of the cases results in additional separation of the groups until all the cases are separated into the desired number of categories. The optimization of a CART model involves selecting a tree that provides the maximum separation with the least number of splits (Abbott et. al., 1998).

Prioritization. The methodology, as explained by Patil and Taillie (2004), will help rank and choose between different modeling methods and models. Multi-criterion ranking uses all indicators to order the observations instead of aggregating indicators. For the objectives of this project, sensitivity and specificity will be indicators of model performance. Accuracy has elements of both indicators, and thus would be redundant in the analysis. First, the sensitivity and specificity values are calculated for each model and then a zeta matrix is created. The zeta matrix is a square array where the columns and row identifiers are th observations. The values of the zeta matrix can have values of 1 (column observation is greater or equal than the row observation), or 0 otherwise. A cover matrix is a square array similar to the zeta matrix, but only has a value of 1 if the column observation is greater than the row observation, and if there are no intermediate observations between these two observations, i.e. A covers B if A>B and there is no C such that A>C>B.

A Hasse diagram is a representation of a partial ordered set, where the elements are connected through their cover relationships. It is drawn by using the cover matrix to find which elements are connected to each other.

Objectives

In an integrated disease management context, a reliable and accurate forecasting system for FHB related decisions would justify the effective use of scientific and technological knowledge. As part of a sensible integrated management system for wheat, farmers have to consider crop residue management, cultivar selection, crop rotation, and chemical control. Each when used in combination, reduces the risk of severe disease and mycotoxin contamination. This project concerns with the development of forecasting models to asses the future risk of FHB. The models will attempt to solve some of the challenges mentioned in the previous sections. The following chapters were conceived as stand-alone papers for spring and winter wheat. The objectives of this project are to:

1. Identify patterns in weather and critical time periods that can serve as reliable predictors of disease;
2. Incorporate previous crop residue and cultivar selection into the risk prediction models; and
3. Evaluate statistical approaches for potential in modeling FHB epidemics.

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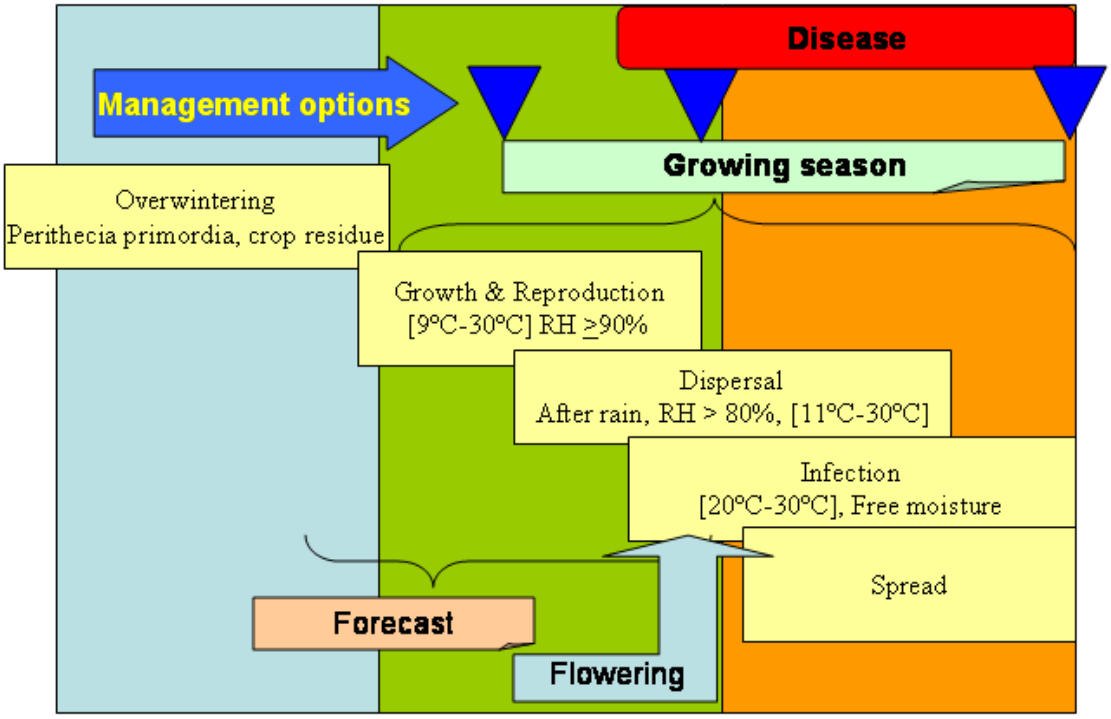
Figure 1.1. Illustration of the biological cycle of Fusarium Head Blight within a single season. Different stages of the biological cycle are presented in yellow, with the environmental ranges where these occur, while a time reference of disease is included.



CHAPTER 2

INTRODUCTION OF VARIETY RESISTANCE TO FUSARIUM HEAD BLIGHT FORECASTING IN SPRING WHEAT CULTIVARS.

Introduction

Fusarium head blight (FHB) is among the most important diseases of wheat and barley worldwide. In the U.S. FHB has caused over 1 billion dollars in losses between the years 1993-1997 (McMullen et. al., 1997; USGAO, 1999; Ngange et. al., 2004). FHB directly affects the developing grain in two ways: direct damage to grain resulting in shrunken and discolored kernels, and the accumulation of the mycotoxin deoxynivalenol (DON) (Bai and Shaner, 1994). Single year losses to FHB can be tremendous. For example, an epidemic of the disease in North Dakota during the 1993 growing season is estimated to have reduced yields by 45% and resulted in widespread contamination of grain with high levels of DON. Direct losses from this epidemic approach $12 million (McMullen et. al., 1997).

The symptoms of FHB are easily recognized on immature heads of wheat and include large tan lesions that encompass one or more spikelets or the entire head (Wiese, 1998). If the rachis is infected, then the tissue above the point of infection often becomes a pale green color. Pink to orange mycelium may be visible on the infected tissue, as well as small black perithecia. Infected spikelets may become sterile but often contain kernels that are shriveled and discolored. Head blight can be caused by up to 17 species of *Fusarium;* however, in the U. S. *F. graminearum* (*Gibberella zeae*) is considered to be the most important species (Parry et. al., 1995).

The pathogen overwinters on crop debris, and serves as the source of inoculum for each

new growing season (Khonga and Sutton, 1988). There has been considerable attention to the environmental conditions leading to inoculum production, both as ascospores, and as macroconidia. Favorable ranges of temperature for perithecia production and maturation are between 9º and 30ºC (Andersen, 1948; Dufault et. al. 2006; Lacey et. al., 1999). However, the range is not linear, but rather is an inverted parabola with an optimum close to 21ºC (Dufault et. al., 2006). Temperatures above 30ºC and below 9ºC are associated with reduced infection (Lacey et. al. 1999; Reid et. al. 1999). Moisture availability within the crop residues is also important to perithecia development. It has been reported that relative humidity greater than 90% is optimal for perithecial growth, and spore production (Andersen, 1948; Cook and Christen 1976; Dufault et. al., 2006; Fernando et. al. 1997; Rapilly et. al., 1973; Tschantz et. al. 1976). The effect of precipitation on the life cycle of FHB has been mainly investigated in relation to ascospore and macroconidia dispersal. Dispersal to heads has been reported to happen after rainfall events in the case of ascospores, and concurrent with rainfall events for splash dispersed macroconidia (Fernando et. al., 2000; Paulitz, 1996). Although infection can take place during most stages of head development, the plants are most susceptible to infection during anthesis (Andersen 1948).

FHB is best managed with an integrated approach that includes rotation with a non-host crop, and selection of cultivars with the best available resistance to the pathogen. When environment appears favorable for disease the risk of severe FHB, and DON can be reduced by fungicide application (Dill-Macky and Jones, 2000; McMullen 1997). The triazole fungicide, tebuconazole, is considered to be the best option for chemical control. This product is currently available for emergency use in some areas of the U.S. (Champeil et. al., 2004). The optimal timing of fungicide application is at anthesis. Anthesis can last anywhere from 3-5 days (Cook,

and Veseth, 1991). Thus, the need for current and future environmental condition information is high. A successful forecasting system can also help growers understand the biology of the pathogen and the need to use multiple disease management strategies.

In the last decade, there have been at least seven forecasting systems developed to predict epidemics of FHB. These prediction systems forecast either disease development (incidence, and /or severity) or contamination with DON, either directly or as a proxy. For example, models developed in Italy (Rossi et. al., 2003) and Brazil (Moshini and Fortugno, 1996) determine an index related to disease incidence and DON contamination, and used pre-anthesis and post-anthesis data to predict incidence and DON contamination, respectively. A model developed in Canada (Hooker et. al., 2002) attempted to forecast DON contamination by integrating the environmental variables recorded during multiple time periods during the growing season. The models described in De Wolf et. al. (2003) focused primarily on environmental conditions observed 7 days prior to flowering and predict the risk of an epidemic with greater than 10% field severity. The model with the greatest accuracy in this analysis predicted epidemics with 70% accuracy and was based on the duration of temperature between 15º-30ºC and the duration in hours of precipitation. De Wolf et. al. (2003) also presented models that use post-anthesis weather information to improve the accuracy of the predictions to 84%. All seven of the recently developed models for FHB used environmental information as an approximation following the biology of *Fusarium* (Table 1.1) and used either heading or anthesis as a reference point. All studies were based on the relationship between environmental variables, and the production of inoculum, infection and the colonization of *Fusarium* spp. on a wheat head. None of the forecasting models incorporated residue management or cultivar susceptibility.

Forecasting systems have to be designed with the end-user and the region in mind. On

one hand, forecasts have to be simple enough to let user maximize their benefit to their management decisions, but on the other hand, there are sources of variability that have to accounted for. The choice of forecasting models, has to balance complexity with ease of use and interpretation. Consideration of spatial variability, variations in cropping practices, cultivar selection, tillage schedules, and differences in virulence of spatially distributed pathogen isolates, create challenges that need to be assessed, before selecting a particular model. Scale of deployment is a very important factor to consider, since spatial variability increases exponentially with scale. Spatial and climate variability can be accounted for by repeated experiments on as many sites as possible. Ideally experimental sites must be evenly distributed on the target deployment area. All of these considerations are limited by manpower and budget.

Disease management has to be an integrated strategy. All aspects of crop management should be incorporated into an information system that attempts to mirror the state of the crop disease and to aid growers by providing timely forecasts. This would exploit the benefits of combining management strategies such as chemical treatments and cultivar resistance. The objectives of this project part from this notion. More specifically, this research attempted to identify large scale indicators of fungal development that could be used to

- Identify critical time periods for the development of epidemics
- Incorporate variety resistance in epidemic assessments
- Identify a optimal methods for the delivery of the forecasts

Models developed here were built used the model developed by De Wolf et. al. (2003) (70% accuracy) as a starting point. That model used a logistic equation to assess the risk of an epidemic (field severity greater than 10%) given environmental conditions seven days prior to

the date of flowering (De Wolf et. al., 2003).

Methods

The dataset used in this research is a combination of the 50 cases (winter wheat cases were removed) published in De Wolf et. al. (2003) together with information gathered from additional field plots and variety trials in the states of South Dakota, North Dakota, and Minnesota. Data was gathered through a collaborative effort between The Pennsylvania State University, Ohio State University, Purdue, North Dakota State and South Dakota State University, additional data contributions were accepted from the University of Minnesota. Weather stations were positioned inside the field plots where possible. The combined dataset included observations of host growth stage, hourly weather information, cultivar used, and disease severity for the years 1982-2005. Phase 1 of this project included data from 1982-2004 (N=39); and Phase 2 incorporated 2005 (N=64). The experimental design used to gather the historical observations varied by location and year, and included observations from replicated variety, and fungicide evaluations. Weather information was recorded in each experimental site with Campbell automated weather stations (Models varied, Campbell Sci, Logan Utah) equipped with sensors that monitor temperature, relative humidity, and rainfall. Research plots in each state were designed to investigate different aspects of the disease epidemiology including the impact of cultivar susceptibility, in-field inoculum sources, and planting date on the development of disease. The experimental design for the research plots was a split-split-split plot arrangement with 3 repetitions per cultivar, per planting date, per residue level. The plots were 5x20 ft separated by 40 ft borders. The date of anthesis was recorded for each of cultivar*planting date plot combination. Disease severity and incidence were evaluated by choosing 20 heads at 5

random locations (100 random heads in total) per experimental unit (e.g. Cultivar Alsen, planting date 1, no corn residue). Disease symptoms were rated 3 weeks after mid-anthesis, and then again 4 days later.

Dataset description. Weather information was split on a weekly basis, using the date of mid-anthesis (Zadoks growth stage 65) as our reference point (day zero). The weather database included measurements from 21 days before to 20 days after mid-anthesis. To be consistent with De Wolf (2003) other period durations were also explored (1, 3, 4, 5, 14, and 21 day periods).

Variable creation (Phase one and two). The hourly observations of weather were placed into consistent units and include temperature (ºC), relative humidity (%), precipitation (mm). Dew point depression was calculated when not available though a standard vapor pressure equation (Kuemmel, 1997); precipitation was zeroed at one hundredth of an inch (or 0.254 mm) for all locations to eliminate cases where dew is measured as precipitation. The weather variables were evaluated for potential errors and missing data through a combination of tabular and graphical procedures. Cases found to have missing observations or errors during time periods considered in this analysis were dropped from the data set.

The hourly observations of temperature, relative humidity and precipitation were then used to create new set of variables that summarized the weather conditions at each location. These variables included sums, means, medians, standard deviations, plus variables that were specifically designed to represent environmental conditions known to favorable to the development of inoculum and the infection process. For example, the development of perithecia by *F. graminearum* is favored by temperatures between 9º and 30ºC on a polynomial relationship (Dufault et. al., 2006). However, ascospore development does not readily occur unless temperatures are between 15º and 30ºC (Sutton, 1982). Based on this information, new variables

were created to represent the duration of temperatures ≥9ºC, ≥12ºC, ≥15ºC, 9º-30ºC, 12º-30ºC, and 15ºC-30ºC. The range from 9º-30ºC was split into 5 categories to represent the polynomial temperature response variable. Each category was assigned an increasing value starting at 9ºC with 0.2 up to 1 at the peak 20ºC; then a decreasing value was assigned from 1 at the peak down to 0.2 at 30ºC. Variables were created to represent the duration in hours of the combined temperatures — with thresholds at ≥9ºC, ≥12ºC, ≥15ºC, 9º-30ºC, 12º-30ºC, and 15º-30ºC — together with relative humidity ≥90%. Published reports of ranges of favorable environmental conditions were used for *F. graminearum* development as a template for the creation of weather intervals. To represent pieces of the life cycle of *F. graminearum,* perithecial development was focused as (Dufault et. al., 2006, Champeil et. al., 2004) a critical indicator of inoculum potential at the time of infection. These variables were represented in the data set as the frequency of a conducive weather event. For example, variables as the frequency of hours of temperature above 9ºC, 12ºC, 15ºC, 9º-30ºC, 12º-30ºC, 15º-30ºC; hours of relative humidity greater or equal to 90%; hours of precipitation above 0.254 m; or hours of dew, may have a stronger association with the biology of the fungus than the arithmetic mean of temperature, relative humidity and rainfall. All of these representations of environmental conditions were calculated for the time intervals, both before and after mid-anthesis growth stage.

Data availability limited the time periods analyzed. Phase 1 and Phase 2 only included periods within 14 days before and 13 days after anthesis [-14, +13], while Phase 3 used information on an expanded [-21, +20] days. Specific temporal windows considered in this research included (all units in days relative to crop anthesis): [-21, -1], [-21, -15], [-21, -8], [-14, -8], [-7, -1], [-8, -4], [-4, -1], [0, +3], [0, +6], [0, +13], [0, +20], [+7, +13], [+7, +20] and [+14, +20]. These intervals are an expansion to the intervals from De Wolf et. al. (2003). As a result,

each case had 57 weather variables, as a combination of the time period and the statistical moment (Appendix 1).

In order to account for cultivar resistance as a factor introducing variability into the dataset, the range for spring wheat cultivar resistance to FHB published by Ransom and Sorenson (2004) was modified. A categorical variable was created with four different levels of disease resistance: very susceptible=0; moderately susceptible=1; moderately resistant=2; and resistant=3. The number of levels on this variable depended on the amount of information gathered. The response variable was constructed according to De Wolf (2003), where field severity (sometimes called disease index) greater than or equal to 10% was coded as a binary variable with an epidemic =1, and non-epidemic =0.

Variable selection (Phase 1 and Phase 2). Best subsets method was used to select the variables related to our response variable. The best subsets method used a branch and bounds algorithm of Furnival and Wilson (1974) to find an specified number of models with the highest likelihood score (chi-square) statistic for all possible model sizes (SAS Institute, 1999). This method optimized the number of combinations of regressed models by eliminating branches of the regression tree that were equivalent and had inferior fit (Furnival and Wilson,1974). This technique was used as a guideline to select those variables with the highest correlation to the response. The models were restricted to five variables or less to avoid undo complexity.

Modeling methods (Phase 1). Logistic regression, neural networks, K-nearest neighbor (K-NN) and classification and regression trees (CART) were used to classify epidemics in this dataset (Abbott et. al., 1998; Agresti, 2002). Selected models were run with each of the four methods, and then ranked with respect to each other. Logistic regression, K-NN and CART models were analyzed using SAS Stat and SAS Enterprise Miner. Neural networks were

modeled as a single layer backpropagation network on Tiberius (Brierley, 2006).

Modeling methods (Phase 2). Phase 2 of analysis used the logistic regression approach to incorporate data from 2004 and attempt to achieve a better fit. Cultivar resistance was introduced as a factor in this phase.

Model selection (Phase 1 and Phase 2). Criteria for model selection were accuracy, sensitivity and specificity. Additionally the Wald chi-square maximum likelihood estimates, the C statistic, and the Hosmer-Lemeshow goodness of fit test were used to assess model fit in the logistic regressions. Accuracy here is defined as the number of cases correctly assigned to an epidemic/non-epidemic category, and is expressed as a percentage of the total number of observations. Sensitivity is defined as the percentage total epidemic cases correctly classified. Specificity refers to the percentage of non-epidemic cases correctly classified (i.e., number of non-epidemics correctly classified/ total number of non-epidemics x100).

For logistic regression, the Wald statistic (called Wald Chi-square in SAS (2006), is also known as Wald-likelihood ratio test score (Agresti, 2002)) tested whether the parameters were significantly different from zero using maximum likelihood estimation (Agresti, 2002). CART models were stopped when marginal yield was close to zero. K-NN and neural network models were assessed by their accuracy, sensitivity and specificity. Hasse diagrams (Patil and Taillie, 2004) were derived for model comparison and ranking by using sensitivity and specificity as indicators of an optimal model+method combination.

Model Validation (Phase 1). Cross-validation techniques were used to validate the models from Phase 1. This method split the overall dataset (N=39) into a training set (N=27) and a validation set (N=12). The split datasets had equal proportions of epidemic cases.

Model Validation (Phase 2). Two methods were used to attain the best estimates for the

parameters of the logistic regression, cross-validation, and bootstrap. Conventional cross-validation used the training (N= 45) and validation (N=19) sets to adjust the parameter estimates, while the bootstrap method (specifically the +.632 bootstrap method of Efron and Tibshirani (1997) was implemented by modifying a bootstrap macro in SAS obtained from Johnson (1996). The bootstrap method used the whole dataset and draws k samples with replacement to estimate the parameter values and found the consensus to estimate the parameter values that better generalize the whole population, as opposed to just the sample space (Efron and Tibshirani, 1997). The bootstrap method drew 2000 samples to produce the parameter estimates.

Error Analysis (Phase 3). The objective of error analysis was to identify possible improvements to the models developed by focusing on the scenarios surrounding the errors of the model. Another objective of error analysis was to correlate elements of the biology of the disease with a timeline of weather events. The dataset for error analysis (N=93) had the phase 2 dataset (N=66) plus 27 more cases from 2004 and 2005. For error analysis, the database was divided into four groups that represent different components of model accuracy: true positives, true negatives, false positives, and false negatives. True positive cases are the correctly classified epidemic cases; true negatives are correctly classified non-epidemic cases; false positives are non-epidemics classified as epidemics; and false negatives are epidemic cases classified as non-epidemics. Mean, median, first and third quantile and standard deviation were calculated for each week prior to the date of anthesis[-21, -15]; [-14, -8]; [-7, -1], as well as during and after anthesis [0, +6]; [+7, +13], and [+14, +20] for relative humidity, temperature, and precipitation. Box-plots were created for each period and group combination in order to compare weather events by period. F-tests were used to test the difference between the variances of the four aforementioned groups of data. Mean trends of relative humidity, temperature, and

precipitation with respect to time were compared in the four groups of data.

Regression tree methods were used to address the interaction between different time frames, i.e. [-21, -15], [-14, -8], and [-7, -1]. These methods used binary recursive partitioning by splitting the dataset into maximally distinct groups (Crawley, 2002). The regression models were used to create a decision rule to correct for underpredicted and overpredicted epidemics. Upon creation of the decision rule, updated values for accuracy, sensitivity and specificity were calculated for the available observations.

Results

Variable creation and selection (Phase 1): Of the 57 variables created by time period, variables from the period [-7, -1] were found to be the most informative. The best subsets approach detected three particular variables that explained the majority of the variation from our dataset: duration of temperature between 9º and 30ºC (T3), mean relative humidity (H1), and duration of precipitation (R2). Interactions were created between T3 and H1 and T3 and R2. These interactions were selected by best subsets when compared with the three variables alone. The aforementioned interactions and the single variables were selected to create statistical models for epidemic classification.

Modeling methods. Logistic regression, neural networks, classification and regression trees, and K-nearest neighbor methods were compared using three statistical models models (Table 2.1). The first model included all selected variables singly, the second and third models included one and two interaction terms, respectively. Two-way interactions variables were used to address non-linear relationships between weather components such as temperature and relative humidity; and temperature and precipitation. Models labeled 1 and 2 were variations of each

other, where model 1 did not include the interaction between temperature and rainfall (namely, T3 and R2, Table 2.1). The rationale for this variation was to test the effect of removing T3*R2 because of its counterintuitive negative signed parameter. The objective of this comparison was to determine which method would yield the arrangement of cases that would translate into better prediction accuracy.

Table 2.1. Phase 1 model results and comparison. Four modeling methods were used to compare promising models for epidemic classification in spring wheat. Accuracy is the percentage of correct cases, sensitivity is the percentage of correctly classified epidemics; specificity is the percentage of correctly classified non-epidemics.

#	Model	Modeling Method	Accuracy	Sensitivity	Specificity
1	T3 H1 R2	*Classification Tree*	84	76	89
		K-Nearest Neighbor	83	74	89
		Logistic Regression	64	65	63
		Neural Network	67	70	65
2	H1*T3	*Classification Tree*	82	94	74
		K-Nearest Neighbor	67	52	77
		Logistic Regression	72	78	68
		Neural Network	77	76	77
3	R2*T3 H1*T3	*Classification Tree*	88	90	86
		K-Nearest Neighbor	83	76	88
		Logistic Regression	82	82	82
		Neural Network	81	76	84

The most accurate model here was model 3 with 81%-88% of accuracy. Model 1 did not perform well in comparison to the other models across methods. Among the statistical methods used, CART yielded the most accurate models. Neural networks performed the worst of the methods compared. Logistic regression and K-NN were somewhere in the middle in performance. All methods but K-NN, yielded balanced sensitivity and specificity values, i.e.

disparity of more than 10% between these values.

The Hasse diagram (Figure 2.1) of the model by method comparison was derived from sensitivity and specificity values (Table 2.1). The upper level of was shared by CART models 1-3, while the second ranking was shared by K-NN models 1 and 3 and logistic regression model 3. This comparison concluded that CART performs the best overall. Model 3 was on the upper rank in all models.

As mentioned before, interpretation is a key criterion for model deployment. Interpreting results from K-NN and neural networks is difficult. Logistic regression and CART models are easier to interpret. CART analyses lack continuity. A continuous change in any of the variables does not necessarily translate into a continuous change in the response variable, thus potentially creating unnatural case classification. From Table 2.1 model 2 and 3 were chosen for further development and deployment based on their simplicity of interpretation. Logistic regression performed well, and was selected for phase 1 and phase 2 of model development.

Validation (Phase 1). The original dataset (N=39) was split into a training set (N=27) and a validation set (N=12) using the SAS procedure surveyselect and maintaining the original proportions of epidemics/non-epidemics. Phase 1 validation was carried out by simple cross-validation (Table 2.2). The best performing model is model 3, that had a training accuracy of 78% and a validation accuracy of 83%. This model also balanced high sensitivity and specificity. Model 3 was deployed during the 2004 growing season as the Fusarium Head Blight Risk Assessment Tool for all spring wheat regions (De Wolf et. al., 2004; Molineros et. al., 2004; www.wheatscab.psu.edu).

Table 2.2. Model validation for three logistic models. Original dataset N=39.

Model	Dataset	N	Accuracy	Sensitivity	Specificity
T3 H1 R2	Training	27	67	64	69
	Validation	12	58	67	50
T3*H1	Training	27	63	57	83
	Validation	12	75	71	80
T3*R2 T3*H1	Training	27	78	77	79
	Validation	12	83	83	83

Variable creation and selection (Phase 2). One additional variable was created to account for differences in cultivar selection. Variety susceptibility and mean relative humidity were selected by best subsets as the significant variables for epidemic classification. Time period selection remained the same as in phase 1.

Modeling (Phase 2). In 2004 additional cases were added to the database (N=64). With the additional information, a new model was developed using logistic regression. This model included mean relative humidity (H1) for the period [-7, -1] and cultivar susceptibility (Variety). Table 2.3 contrasts the phases of model development and the models published by De Wolf et. al. (2003). The accuracy of the 2005 model was 78%, while maintaining some balance between sensitivity and specificity. The 2005 model was deployed starting the 2005 growing season as the Fusarium Head Blight Risk Assessment Tool for all spring wheat regions. The deployment and development process of these models was reported in De Wolf et. al. (2004), Molineros et. al. (2004), De Wolf et. al. (2005), and Molineros et. al. (2005).

Accuracy, sensitivity and specificity (Table 2.3) were based on the original development numbers. All pre-anthesis models were challenged with the same database (N=116) to make comparisons. Table 2.3 shows this comparison numbers inside parentheses. The model

developed for the 2005 season showed the overall values from bootstrapped validation. Models A and B from De Wolf et. al. (2003) used a post-anthesis dataset (N=61). Post-anthesis had a smaller dataset because of lacking information.

Table 2.3. Models for spring wheat. Three new equations were found to be informative for spring wheat compared to models A, B and I from De Wolf (2003). TRH9010 is the duration of temperature between 15ºC-30ºC and relative humidity ≥ 90% for [-7,2]; INT3=T15307*TRH9010, where T15307 is the duration of temperature between 15ºC-30ºC for [-7,-1]; DPPT7 is the duration of precipitation for [-7,-1] (De Wolf et. al., 2003). *p* is the threshold probability level splitting epidemic/non-epidemic cases. Values in parentheses represent the same dataset to challenge all models (N=116), the model for 2005 uses the bootstrapped accuracy. [p]Used post-anthesis dataset N=61.

Model	Equations	*p*	Accuracy	Sensitivity	Specificity
De Wolf					
A	–3.3756 + 6.8128*TRH9010	0.36	84 (75)[p]	83 (59)[p]	84 (93)[p]
B	–3.7251 + 10.5097*INT3	0.44	84 (75)[p]	83 (59)[p]	84 (93)[p]
I	–8.2175 + 8.4358*T15307 + 4.7319*DPPT7	0.50	70 (48)	56 (28)	78 (68)
Phase 1					
2004_2	-6.3906 + 0.000593*T3*H1	0.38	79 (57)	88 (90)	73 (31)
2004_3	-6.3906 -0.00048*R2*T3 + 0.000593*T3*H1	0.48	82 (68)	82 (78)	82 (60)
Phase 2					
2005	-16.9369 + 0.23839*H1 -1.5442* Variety	0.50	78	86	69

The model with the best accuracy was the model developed in Phase 2 (Table 2.3), given that it considered all the possible weather scenarios in the dataset. This model, however, had relatively low specificity (69%). Only models 2004_2, 2004_3 and 2005 had high sensitivity when compared using with the same dataset. The difference in sensitivity of 2004_2 to 2005 was 4%. Across models 2005 performed best. Figure 2.2 describes the classification of cases. The model used a threshold of 0.5 to split between epidemic (above the line) and non-epidemic cases (below the line). The figure classifies cases into four categories: true positives (TN in blue); true negatives (TN in green); false positives (FP in red); and false negatives (FN in black). True positive cases are correctly predicted epidemics; true negatives are correctly predicted non-epidemics; false negatives are epidemics predicted as being non-epidemics; and false positives are non-epidemics predicted to be epidemics. Below and above the threshold true and false cases are intermixed, this will be the topic of error analysis described below.

Figure 2.3 shows how 2005's model worked. Relative humidity is on the y axis and cultivar susceptibility is on the horizontal axis. The more resistant the cultivar is the higher the value on the x axis. The split between FP and TN with FN and FP indicates a different threshold per cultivar class. This value can be solved by using the logistic regression, replacing the desired susceptibility value (0-3), and solving for RH. The threshold is around 71% of mean relative humidity for cultivar resistance=0, and increases with resistance. The thresholds for the other categories of cultivar resistance are 77.5%, for cultivar resistance=1; 84% for cultivar resistance=2; and 90.5% for cultivar resistance=3. These thresholds can used as a guideline of the probability of epidemics in any given site.

Validation (Phase 2). Two procedures were used for Phase 2 model validation: cross-validation, and + .632 bootstrap validation. Training and validation datasets were constructed

using the previous training and validation sets. Newly added cases were selected for each data set by the surveyselect procedure in SAS at a 70/30 proportion (training vs. validation). The training set had N=45, and the validation set had N=19. The + .632 bootstrap validation method used the whole dataset (N=64). Table 2.4 compares the results from cross-validation to those of bootstrapping. The fitted bootstrapped model performs marginally better than the traditionally cross-validated model, but is more sensitive and less specific. Ultimately, the bootstrapped model was chosen for deployment in the 2005 growing season.

Table 2.4. Phase 3 model results and comparison between validation methods.

Model	Validation Method	Accuracy	Sensitivity	Specificity
Variety + H1	Training + Cross-validation	77	83	73
	+.632 Bootstrap	78	86	69

Error analysis (Phase 3). The dataset for error analysis included the original 64 cases from Phase 2, plus 29 additional cases from the 2005 growing season (N=93). Errors were classified into under-predicted and over-predicted cases. Only error cases with complete environmental information for [-21, +20] were used for error analysis (N=19). During our exploratory analysis of these errors, we found environmental patterns associated with the errors and the membership a given case had to one of four groups: true positives, true negatives, false positives (overpredicted), and false negatives (underpredicted) (Figure 2.4). Figure 2.4 shows one very important fact of FHB biology, moisture is a limiting factor for disease development. Mean relative humidity is plotted against time with respect to anthesis (F). Stars mark the mean values, while the red middle lines mark the medians. The boundaries of each box are the first and third quartiles. Mean relative humidity for true negative cases remains below 70% before anthesis, in contrast to true positives, where mean relative humidity increases up to 76%.

Overpredicted cases had a larger mean relative humidity which explains the larger risk value assigned to them. The underpredicted values could not be explained.

Temperature was not a limiting factor for epidemic development. This was associated with the seasonal temperatures in northern regions. Moisture was a limiting factor in epidemic development, implying that the fungus requires a continuing source of moisture over time. All models developed in this study used weather from only 7 days before anthesis, these did not take into account previous droughts or extremely wet conditions, i. e. the extremes of the climate distribution. Three indicators of wet and dry conditions were used to asses these wet/dry scenarios, duration of relative humidity ≥90%, duration of precipitation, and total amount of precipitation. These indicators were used in model correction.

Decision analysis correction (Phase 3). After error analysis, a decision rule was used to correct the 2005 model. Regression tree methodology found that duration of relative humidity ≥90%, duration of precipitation and the amount of precipitation for the period [-21, -15] were significant to the classification of epidemics. Three binary variables were created using the mean values of weekly precipitation duration (hours), precipitation amount (mm) and duration of relative humidity ≥ 90% (hours), these variables corresponded to dry and wet scenarios in the dataset. The wet scenario was represented by relative humidity and precipitation amount above one standard deviation from the mean. The dry scenario was represented as precipitation duration below one standard deviation from the mean. With these variables the following decision rule to modify the risk probability Pr(A) was created:

If $\text{Precipitation}_{[-21,-15]}$ (hours) < **4** then C=**.5**;

else C=**1**;

If $\text{Precipitation}_{[-21,-15]}$ (total) > **26** and $\text{RH} \geq 90\%_{[-21,-15]}$ (hours) > **45** then C=**2**;

$$Pr(C)=C*Pr(A),$$

where P(C) is the new risk probability of epidemics (severity ≥10%).

Improvements from error correction. The new rule decreased the number of false positives by 40%, and the number of false negatives 19%. This was calculated from the cases where information [-21, -15] was available (N=102, out of 111), where 37 cases were errors (FP=10; FN=27), from data up to 2005. The improvement in terms of accuracy are around 10%, but this value cannot be extrapolated to the overall dataset because there are cases for which no information for [-21, -15] was available.

Discussion

Phase 1. FHB epidemics were correlated with periods of temperature between 9º-30ºC (T3), periods of high relative humidity (H1), and of periods of precipitation (R2). Given the nature of environmental variability, the relationships between environmental information and biology are not always linear or simple to identify. Weather information was split into periods of 3-21 days. Data for 3, 4 and 5 days seemed to perform the worst at explaining epidemic classification. This is logical since short periods might miss all or a large section of biological events happening at the time concurrent with the weather period. The smallest period that was correlated to FHB epidemics in this study was of 7 days. We presume [-14, -1] and [-21, -1] day periods include too much information to correlate with the key biological processes.

Of the modeling methods chosen for this study and widely used in forecasting, K-nearest neighbor and neural networks are the most difficult to interpret and deploy because they do not provide an equation or a set of rules for implementation. This is in contrast with logistic regression and CART models. Neural networks can produce programming code (Brierley, 2006)

that makes it easy to implement, but there is no way of really knowing if the interrelationships between the variables can be related to the biology of the pathogen. CART models produce a series of rules that split the data into many groups. The greatest concern of implementing this method is that the separation of groups is discrete, thereby incorrectly leaving closely related cases, that are near the separating threshold, in different categories even if they should not be. Logistic regression has the added advantage that it is easy to implement through a simple equation, it is straight-forward to check if the variable relationships make biological sense, and is a continuous method.

Of the models developed for the 2004 growing season, model 1 dealt with epidemic classification in a linear fashion and assumed that the risk of severe disease (i.e. field severity ≥10%) held an additive relationship to relative humidity, temperature, and precipitation during the week before anthesis. Model 2 assumed a curved relationship of epidemics with relative humidity and temperature. Model 3 added another curved relationship between temperature and rainfall. The differences among these three models are accuracy and logic. The most accurate model by far was model 3 (Table 2.1 and Figure 2.1). As for logic, the signs accompanying the estimated parameters were positive for the interaction between relative humidity and temperature. The positive sign in this interaction is consistent with the biology of the pathogen. The sign of the estimator was negative for temperature by precipitation. This could mean either that the parameter works simply to balance the weights of the other estimators, or that the models are capturing (given the distribution of the data in the dataset) events in which rainfall acts as the inhibitor of ascospore release as described by Paulitz (1996). Model 3 was chosen as an experimental model to deploy at the Pennsylvania State University FHB Risk website (www.wheatscab.psu.edu) for the 2004 growing season. The deployment of these models was

reported in De Wolf et. al., (2004) and Molineros et. al. (2004).

It would be difficult for an end-user to implement model 3 on their own. Users would need to monitor temperature, relative humidity and precipitation on an hourly basis and use weekly values to assess their own probability if epidemics. It is not practical to calculate threshold values for model 3, because there are almost an infinite number of values for each variable that could be considered a threshold. What is important to note is that, in most cases, if temperature is conducive for disease and relative humidity is also conducive for disease, the probability of FHB epidemics is always going to be greater than or equal to the disease threshold. Only extremes of precipitation will overcome the effect of relative humidity on the probability of disease. In some ways, the negative sign for the interaction between precipitation and temperature duration acts as a correction factor for rare events. Unfortunately it is difficult to know how common these events are unless more observations are gathered.

Phase 2. After the 2004 growing season, new data became available. This new dataset included disease, environmental and cultural information for the 2004 growing season. Feedback from collaborators from North Dakota and South Dakota was taken into account to analyze the errors from the first year of model deployment. The accuracy of the model dropped in 2004 with the larger dataset (N_{2005}=64 vs N_{2004}=39). A new model was developed for the 2005 growing season. The new dataset contained enough information for the creation of a cultivar susceptibility variable. With cultivar susceptibility data it was possible to resolve differences in epidemic classification. The cultivar variable with four levels of susceptibility was created from the 8 category list published by Ransom and Sorenson (2004). Mean relative humidity was able to significantly explain epidemic class. The 2005 model reduced uncertainty of the negative sign of the parameter for T3*R2 and simplified the model. It makes biological sense that the limiting

environmental factor would be relative humidity, as an indicator of free moisture being available for the fungus to grow, produce perithecia, and and release ascospores. Review of the temperature ranges in the weeks prior to anthesis showed that temperature was not a limiting factor, since at least 140 of 168 hours were between 9º and 30ºC. The same criteria as before were used to compare this model to the previous models developed for FHB. Model 2005 was more accurate than the rest when the larger dataset was employed, implying a larger set of disease scenarios were encompassed by this model. Given the introduction of moderately resistant cultivars such as Alsen and Truman, it made more biological sense to include a variable that would account for the variation due to cultivar selection.

The choice of validation method used to fit the parameters of the model was based on accuracy and the reported performance benefits from using the +.632 bootstrapping method. This method produced less biased estimates than cross-validation (Efron and Tibshirani, 1997). The 2005 model was deployed starting the 2005 growing season at the same internet address. The deployment process of these models was reported in De Wolf et. al. (2005), and Molineros et. al. (2005).

Model 2005 use is much easier than model 2004. As mentioned before, there are four threshold to look for to assess the risk of severe disease. The user only has to monitor a seven day moving average of relative humidity, and choose the threshold that best represents their cropping situation. This kind of simplicity will be of great use to growers would allow them to make faster chemical treatment decisions more quickly with very little technical requirements. In 78% of the cases, the users will be able to make the correct decision.

Phase 3. Perhaps the most important lesson from creating risk assessment tools, is the error analysis. This indicated where the system could be improved, as well as identified large

scale climate patterns associated with epidemics and related them to the disease cycle. Additional environmental information on one week intervals were analyzed with respect to the date of anthesis. Figure 2.4 showed the progression by epidemic group of weekly mean relative humidity from three weeks before to three weeks after anthesis. There are four categories of data compared (Figure 2.4): epidemics are divided into correctly and incorrectly predicted, likewise are non-epidemic cases. Non-epidemics as a general case, were compared to over-predicted cases. Epidemic cases were compared to under-predicted cases.

There is a different sign in the slope of relative humidity before anthesis, between panel A and C and B and D in Figure 2.4. Most striking is that correctly predicted non-epidemics, had mean relative humidity below 70%, whereas the over-predicted cases had over 70% RH. This situation is reversed when non-epidemics were examined. The slope of relative humidity over time was different in sign, from positive for correctly predicted epidemics, to negative for under-predicted cases. The most evident result from error analysis is the importance of analyzing weather conditions long before anthesis. Weather before anthesis is an indicator of the status of the fungus. It can be inferred that if the conditions are favorable for inoculum production and release, climatic data at least three weeks before anthesis should be used. Temperature remained similar in all the cases, therefore being non-informative over the period [-21, -1]. Rainfall duration was also non-informative, when considering the time frame before pre-anthesis. Weekly precipitation amounts were also non-informative. One important thing to note is that overall, precipitation just after anthesis (i. e. [0, +6] days) did not have an effect on the probability of an epidemic. This last relationship between precipitation after anthesis has consistently been put forward to be highly associated with severe epidemics. There are no published reports of the effect of post-anthesis precipitation on disease severity. The information

on this project hints that the importance of pre-anthesis precipitation is much greater than that of post-anthesis precipitation.

Model correction. Analysis of information for [-21, -15], [-14, -8], and [-7, -1] showed that moisture conditions were very important from [-21, -15] on. The period [-14, -8] did not show a significant correlation to epidemics. This might have happened because of multiple cases from the same location, where the dates of anthesis were close to one another. It makes sense that moisture is important before and after anthesis, but this analysis showed that previous drought conditions might have a risk-lowering effect on the development of FHB. Indicators of previous drought were found by using the first quartile of the duration of precipitation variable for [-21,-15]. Extremely wet situations can also affect the risk of FHB. A wet scenario was constructed by meeting the two concurrent conditions of more than 26 mm of rainfall during [-21, -15] together with more than 45 hours (out of 168) of relative humidity ≥90%. As mentioned above, these conditions were able to explain some of the missed predictions but not all of them.

Model Implications. Model 2005 was deployed for the spring wheat region during 2005. This model served a dual purpose, 1) assessing risk of a FHB epidemic, and 2) educate farmers that cultivar choice is of crucial importance.

Future directions. It is clear from all deployed epidemic forecasting models that there are gaps in our knowledge of how to extrapolate plant disease biology across different scales, and to match environmental information to the pathogen's life cycle. What happens at the scale of the residue and single plant is difficult to extend to the whole field and even more to the regional and national scale. It is important to determine how do different scales of environmental parameters correlate to field and laboratory observations. This could be

investigated by setting field plot experiments where disease, inoculum quantity and fungal stage on crop residue would be monitored at the same time, while recording environmental conditions at the scale of crop residue, mid-plot, and national weather service weather station. These observations would yield scaling parameters to be used on a particular site. Replication in space and time would yield a notion of how much spatial variability is present.

When the goal is to forecast for large scales, further efforts should be made to identify the sources of spatial variability. One possible approach to account for this would be to first identify weather scenarios, such as low relative humidity early in the growing season, together with high rainfall during anthesis, and then dry again during milk stage. The models developed in this project can be used as a starting point to identify weather scenarios for the spring wheat growing region. There are a discrete number of possible combinations of weather patterns that account for the majority of the natural variation. With enough information it might be possible to identify the disease scenario a given year will be, thereby allowing faster disease assessments.

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Figure 2.1. Hasse diagram of the model by method comparison. The upper level is comprised by un-covered elements. Elements not linked are incomparable, i. e. #1, #9, and #5 are incomparable, where none of them is clearly superior to one another.

#	Model	Method
1	1	CART
2	1	K-NN
3	1	Logistic Regression
4	1	Neural network
5	2	CART
6	2	K-NN
7	2	Logistic Regression
8	2	Neural network
9	3	CART
10	3	K-NN
11	3	Logistic Regression
12	3	Neural network

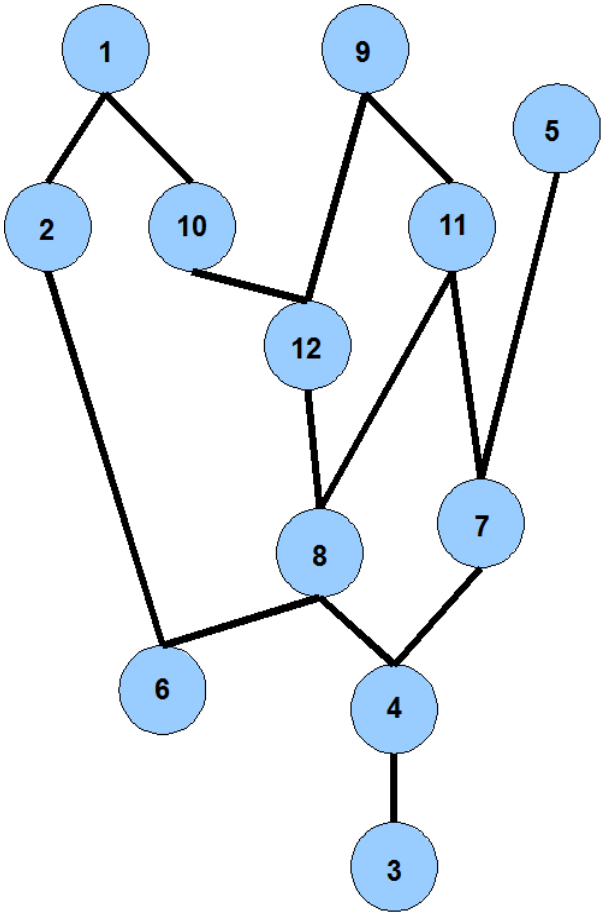


Figure 2.2. Probability of FHB epidemics vs. Relative humidity from model 2005. Dotted line show the risk threshold for epidemic classification. TP = true positives; TN= true negatives; FP= false positives; FN=false negatives.

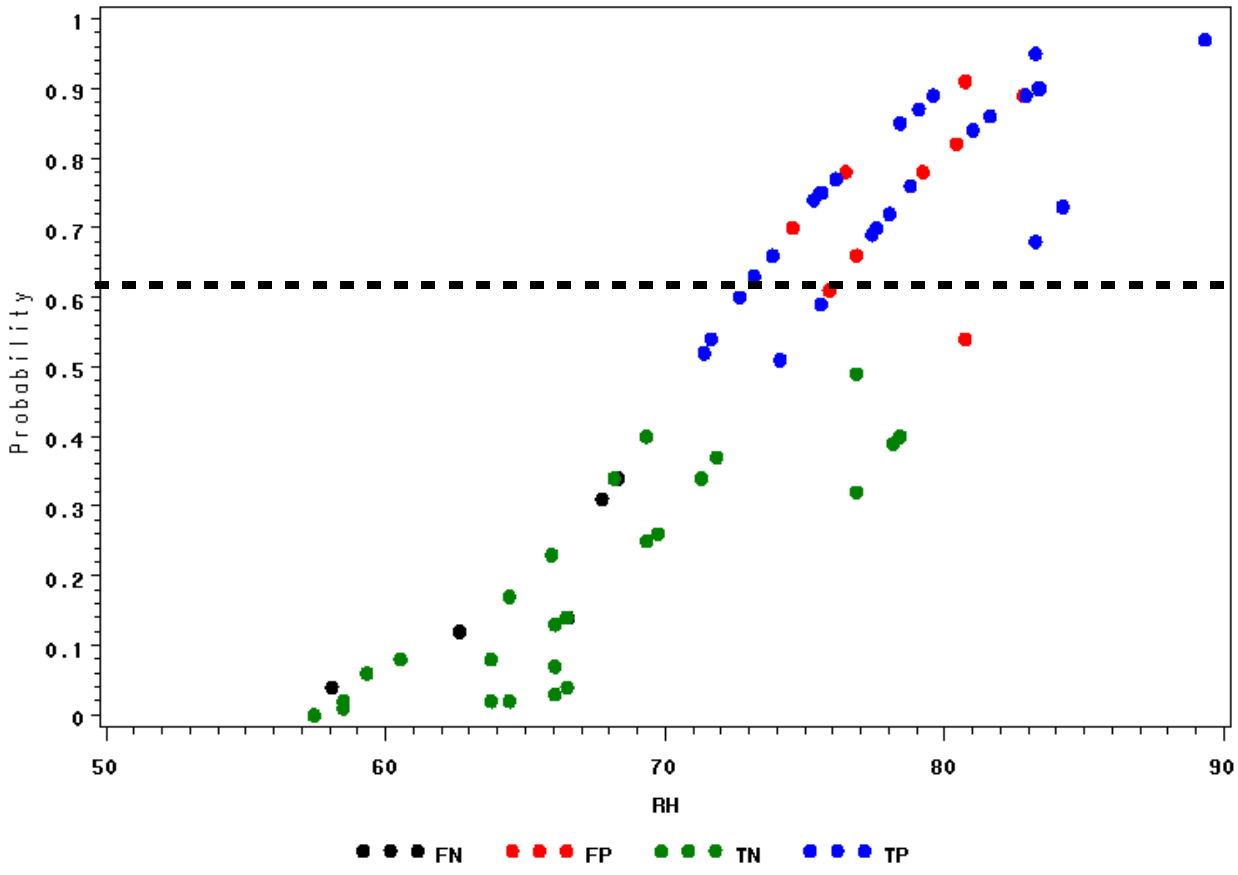


Figure 2.3. Cultivar resistance vs. Relative humidity (RH). Resistance is increasing to the right. Dashed line is the threshold of epidemic classification by cultivar resistance value. TP = true positives; TN= true negatives; FP= false positives; FN=false negatives.

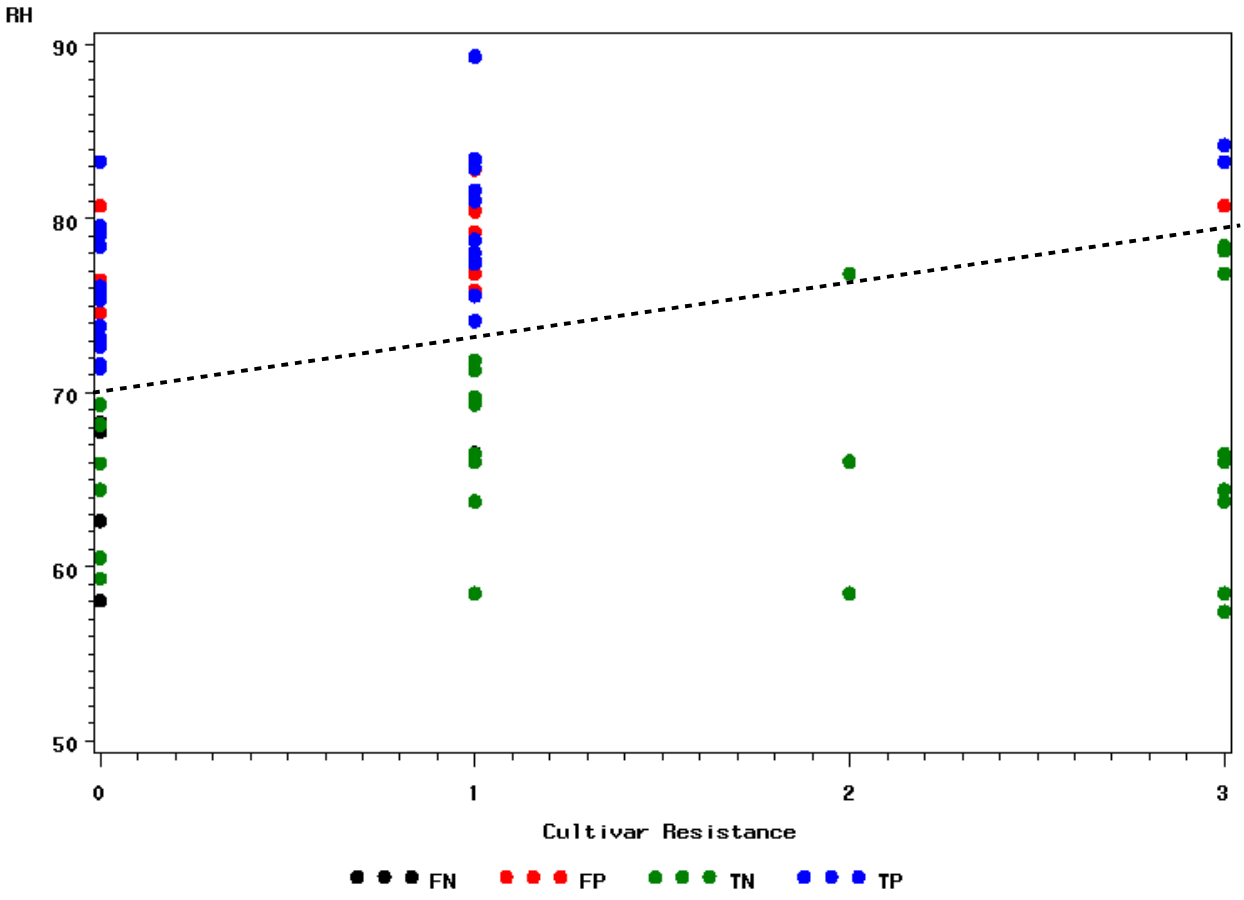
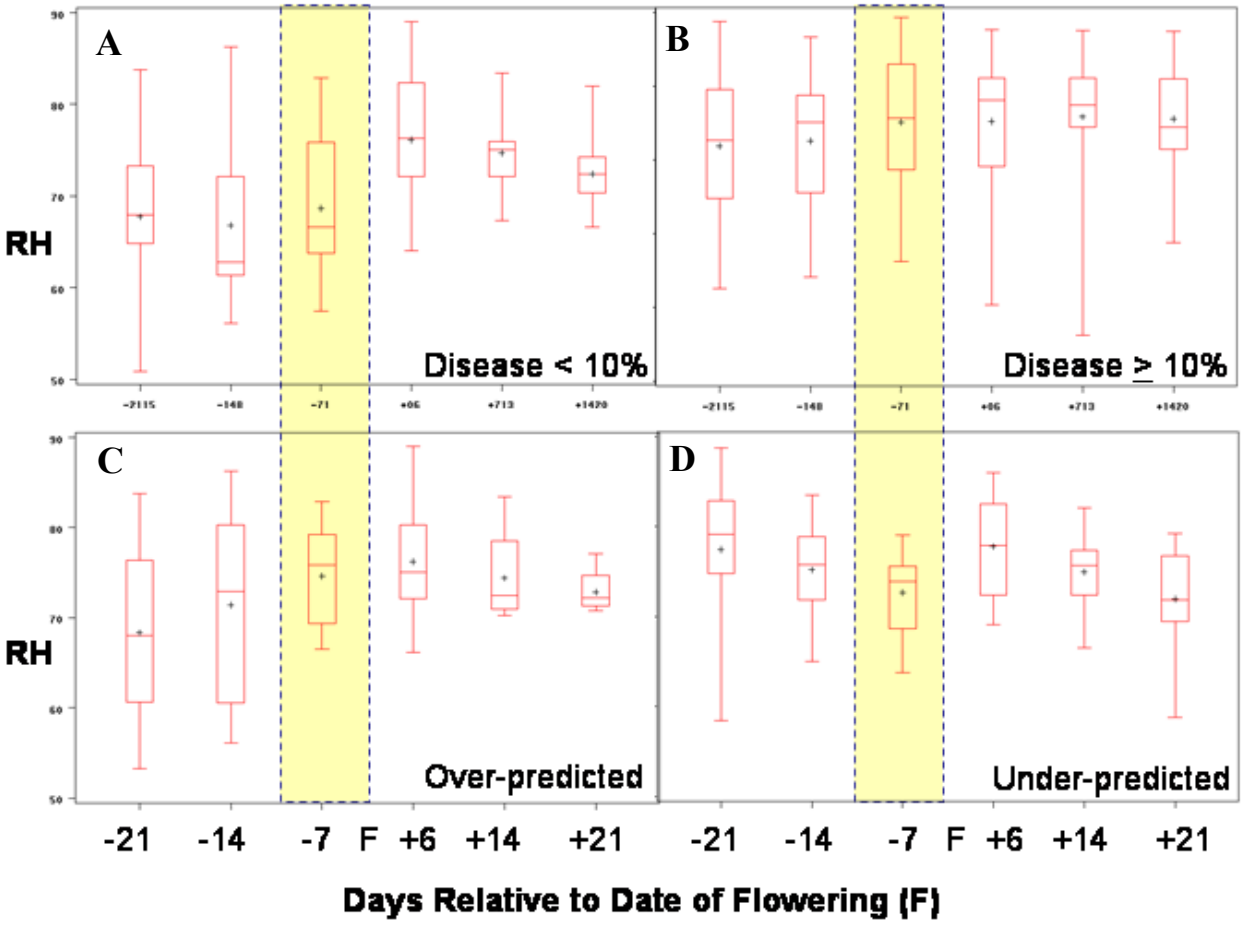


Figure 2.4 Comparison by week of relative humidity means. Boxplots bounded by first and third quartile, median line is presented in red. Mean values are presented as stars. The horizontal axis represents time with respect to anthesis (F) a week at a time. Yellow boxes are used to indicate data considered for model development. Four panels are presented as follows, clockwise from the top left: (A) True negatives , (B) true positives, © underpredicted cases, and (D) overpredicted cases.



CHAPTER 3

THE ROLE OF RESIDUE MANAGEMENT IN FHB FORECASTING

Introduction

Over the past few years, the wheat and barley industry has been hit by severe Fusarium head blight (FHB) epidemics. FHB has caused millions of dollars in losses, especially over the period 1993-1997 (McMullen et. al., 1997; USGAO, 1999; Ngange et. al., 2004). FHB affects overall yield, test weight and contaminates the grain with the mycotoxin deoxynivalenol (DON) (Bai and Shaner, 1994). Winter wheat growers in Ohio, Indiana, Michigan and Illinois have seen losses of up to $100 million in 1996 due to reduced yields, lower price and added costs (McMullen et. al., 1997).

Head blight is easily recognized by its landmark symptoms, with large tan lesions encompassing one or more spikelets or the entire head (Wiese, 1998). Tissue bleaching is common for this disease. Mycelium is pink to orange may be detected in infected spikelets. Black perithecia might be detected on infected tissue. Infected spikelets may become sterile. Kernels often become shriveled and discolored and are often called 'tombstones'. Head blight can be caused by up to 17 species of Fusarium. In the U.S., *F. graminearum* (*Gibberella zeae*) is considered to be the most common FHB causing species (Parry et. al., 1995).

The fungus overwinters on crop debris, from where new inoculum is produced and dispersed for each new growing season. Considerable efforts have been devoted to determine the environmental conditions leading to inoculum production. Perithecia production and maturation has been reported occur between 9º and 30ºC (Andersen, 1948; Dufault et. al. 2006; Lacey et. al., 1999). The relationship with temperature was described as an inverted parabola

with an optimum close to 21ºC (Dufault et. al., 2006). Environmental requirements for perithecial development and spore production include relative humidity greater than 90% in combination with the aforementioned temperature range (Andersen, 1948; Cook and Christen 1976; Dufault et. al., 2006; Fernando et. al. 1997; Rapilly et. al., 1973; Tschantz et. al. 1976). Precipitation has been reported to affect spore dispersal. Ascospore dispersal has been reported after rainfall events, while macroconidia splash with rain (Fernando et. al., 2000; Paulitz, 1996). Anthesis is the most susceptible stage of wheat. After anthesis, the probability of infection drops suddenly (Andersen 1948).

Optimal management of FHB is an integrated strategy, it is recommended to tackle all weak points of the production system. Decreasing the amount of crop debris will reduce the amount of available inoculum, minimum till and no-till practices make this a difficult task. Crop rotation with non-host crops is recommended (McMullen et. al., 1997). Planting disease resistant cultivars is recommended (McMullen et. al., 1997). There are no resistant cultivars for winter wheat on the market yet. In case environmental conditions are favorable for FHB establishment, chemical treatment is an option. Tebuconazole, a triazole fungicide, have been approved and used for preventive care of FHB with varying degrees of success (Champeil et. al. 2004). Timing of fungicide application is critical for optimal crop protection, thus increasing the need to be aware of the current and future environmental conditions. Forecasting systems to assess the timing of fungicide application help farmers decide if they need to apply protectant fungicides. Forecasting systems help farmers understand the disease, and integrate complex information for disease management.

In the case of FHB, there have been seven forecasting systems deployed across the world. Objectives for these risk assessment systems vary between forecasting incidence, severity or

contamination with DON, either directly or as a proxy. For example, the Italian model (Rossi et. al., 2003), and the Brazilian model (Moshini and Fortugno, 1996) both determines an index related to disease incidence and DON contamination by using pre-anthesis and post-anthesis data. The Canadian model (Hooker et. al., 2002a and 2002b) attempted to forecast DON contamination with environmental factors representing selected time frames throughout the growing season. The models described in De Wolf et. al. (2003) used pre-anthesis information on duration of seven day events pre-anthesis of relative humidity greater than 90%, and temperature between 15º-30ºC, as well as mean relative humidity, mean minimum temperature to predict the risk of an epidemic with greater than 10% field severity. Their best performing model used variables for the duration of temperature between 15º-30ºC and the duration in hours of precipitation, this particular model used only information before anthesis (70% accuracy). Additionally, they presented better performing models that used information from post-anthesis (84% accuracy). As varied as the target variables used across forecasting systems, have also been the time frames and variables considered for their predictions. All models used environmental information as an approximation following the biology of *Fusarium* (Table 1.1) and used either heading or anthesis as a reference point. All studies were based on the correlation of environmental conditions and *Fusarium* spp. biology. None of the forecasting models incorporated residue management as a factor affecting disease.

Disease management has to integrate all forms of crop management options. Ideally an information system will mirror the state of the crop disease, and aid growers carry out management decisions. The objectives of this project were to identify indicators of fungal development that could be used to

- Identify critical time periods for the development of epidemics

- Incorporate residue management to epidemic assessments
- Identify a usable technique for the delivery of the forecasts

This research used the risk assessment tool developed by De Wolf et. al. (2003) as a starting point to build FHB models that consider residue management. This study was split into model development, model validation, and error analysis.

Methods

Dataset. The dataset used in this article combined the 50 cases (spring wheat cases were removed from this dataset) published from De Wolf et. al. (2003) together with information gathered from experimental field plots and variety trials in the states of Kansas, Kentucky, Indiana, Missouri, Michigan, Nebraska, Ohio, and Pennsylvania. Data was gathered as a collaborative effort between The Pennsylvania State University, Ohio State University, Purdue, North Dakota State University and South Dakota State University. Additional cases were submitted by contributors in Kansas, Kentucky, Missouri, Michigan and Nebraska. Weather stations were positioned inside or beside the field plots. The experimental design used to gather the historical observations varied by location and year, and included observations from replicated variety, and fungicide evaluations. Weather information was recorded in each experimental site with an automated weather station (Models varied, Campbell Sci, Logan Utah) equipped with sensors that monitor temperature, relative humidity, and rainfall. The combined dataset included observations of host growth stage, hourly weather information, cultivar used, presence of corn residue (>14% ground cover) and disease severity for the years 1982-2005. The modeling phase included data from 1982-2003 (N=60); validation$_{2004}$ incorporated data for 2004 (N=90), and validation$_{2005}$ incorporated data for 2005 (N=107). Research plots in each state were designed to

investigate different aspects of the disease epidemiology including the impact of cultivar susceptibility, in-field inoculum sources, and planting date on the development of disease. The experimental design for the research plots was a split-split-split plot arrangement with 3 repetitions per cultivar, planting date, and residue level. The plots were 5x20 ft separated by 40 ft borders. The date of anthesis was recorded for each of cultivar and planting date combination. Disease severity and incidence was evaluated by choosing 20 heads at 5 random locations (100 random heads in total) per experimental unit (e.g. Cultivar Hopewell, planting date 1, no corn residue). Disease symptoms were rated 3 weeks after mid-anthesis, and then again 4 days later. Additionally, for historical data from variety and fungicide evaluations, the experimental design varied by location and year.

Dataset description. Weather information was grouped by week, using the date of mid-anthesis (Zadoks growth stage 65) as the reference point (day zero). The weather database ranged from 21 days before anthesis to 20 days after anthesis. To be consistent with De Wolf (2003) data were grouped on 7 and 14 day sets. Other period durations explored were of 3, 4, 5, 14, and 21 days.

Variable creation. Hourly observations of weather were transformed into consistent units and include temperature (ºC), relative humidity (%), and precipitation (mm). Dew point depression was calculated when not available (Kuemmel, 1997); precipitation was zeroed at one hundredth of an inch (or 0.254 mm). Potential errors and missing data were identified through a combination of tabular and graphical procedures. Cases with missing observations or errors during were dropped from the data set.

Hourly observations of temperature, relative humidity and precipitation were used as the base for new variables to represent weather conditions at each location. These variables included

sums, means, medians, and standard deviations. Variables were designed to represent environmental conditions conducive for inoculum production and infection. For example, the development of perithecia by *F. graminearum* is favored by temperatures between 9º and 30ºC on a polynomial relationship (Dufault et. al., 2006). Ascospore development occur at temperatures between 15º and 30ºC (Sutton, 1982). This information on fungal growth was used to create new variables representing the duration of temperatures at ≥9ºC, ≥12ºC, ≥15ºC, 9º-30ºC, 12º-30ºC and 15º-30ºC. A variable was created to account for the polynomial response of perithecial growth to temperature. The range from 9º-30ºC was split into 5 categories, each category was assigned an increasing value from 0.2 to 1 peaking at 20ºC, and a decreasing value from 1 to 0.2 up to 30ºC. Variables for the duration (hours) of the combined temperature (≥9ºC, ≥12ºC, ≥15ºC, 9º-30ºC, 12º-30ºC and 15º-30ºC) and relative humidity ≥90% events were calculated. Published reports of favorable environmental conditions for *F. graminearum* development were used as a template for the creation of weather intervals. Perithecia development was considered the most important piece of information for variable design. These variables represented the frequency of conducive weather events. Among these, duration in hours of temperature above 9ºC, 12ºC, 15ºC, 9º-30ºC, 12º-30ºC, 15º-30ºC, duration of relative humidity greater or equal to 90%, duration precipitation above 0.254 mm, or duration of dew may correlate to *Fusarium* biology. All of these representations of environmental conditions were calculated for the time intervals both before and after mid-anthesis growth stage.

Data availability limited the analyzed time periods. Model development only included periods within 14 days before and 13 days after anthesis [-14, +13]; while error analysis used information on an expanded [-21, +20] days. Specific temporal windows considered in this research included (units in days relative to crop anthesis): [-21, -1], [-21, -15], [-21, -8], [-14, -8],

[-7, -1], [-8, -4], [-4, -1], [0, +3], [0, +6], [0, +13], [0, +20], [+7, +13], [+7, +20] and [+14, +20]. As a result, each case had 57 weather variables, combining the time period and the statistical moment (Appendix 1).

Presence of corn residue in the field was used as a binary variable, where corn residue=1, and no corn residue=0. The response variable was constructed according to De Wolf (2003), where field severity (sometimes called disease index) greater than or equal to 10% was coded as a binary variable with an epidemic =1, and a non-epidemic =0.

Variable selection. Best subsets method was used to select variables related to epidemic class. The best subsets method used the branch and bounds algorithm described by Furnival and Wilson (1974) to find models with the highest likelihood score (chi-square) statistic per model size (SAS Institute, 1999). This method optimized the combination of variable in a models by eliminating branches of the regression tree that were equivalent and had inferior fit (Furnival and Wilson,1974). The models were restricted to a maximum of five variables to avoid overly complex models.

Modeling methods. Logistic regression, neural networks, K-nearest neighbor (K-NN) and classification and regression trees (CART) were used to analyze this dataset. Selected models were run with each of the four methods, and then ranked with respect to each other. Logistic regression, K-NN and CART models were processed using SAS Stat and SAS Enterprise Miner (SAS, 2006). Neural networks were modeled as single layer backpropagation networks on Tiberius software (Brierley, 2006).

Model selection. Criteria for model selection were accuracy, sensitivity and specificity. Wald chi-square maximum likelihood estimates, C statistic, and the Hosmer-Lemeshow goodness of fit test were used to assess model fit in the logistic regressions. Accuracy is defined

as the number of correctly classified cases, and is expressed as a percentage of the total number of observations. Sensitivity is defined as the percentage of epidemic cases correctly classified (number of true positives/number of epidemics*100). Specificity is the percentage of non-epidemic cases correctly classified (number of true negatives/number of non-epidemics*100).

For logistic regression, the Wald statistic (called Wald Chi-square in SAS (2006) also known as Wald-likelihood ratio test score test), tested by maximum likelihood estimation if the parameters were significantly different from zero (Agresti, 2002). CART models were stopped when marginal yield was close to zero. K-NN and neural network models were assessed by their accuracy, sensitivity and specificity.

Hasse diagrams were drawn from sensitivity and specificity values for all models and methods. Hasse diagrams aid in separating observations that are superior from those that are incomparable and inferior (Patil and Taillie, 2004). This method helped in the selection of the model to deploy, as well as in method selection.

Model Validation. Cross-validation techniques were used to validate the models during model development, and then again to check the performance of the model for each year of model deployment (2004 and 2005). This method split the development dataset (N=85) into a training set (N=59) and a validation set (N=26). The dataset split for the validation phase was done with the surveyselect procedure in SAS. Training and validation sets had equal proportion of epidemic cases. More cases were added to the validation dataset in 2004 (N_{2004}=90) and in 2005 (N_{2005}=107).

Error analysis. For error analysis, the database was divided into four groups: true positives, true negatives, false positives, and false negatives. True positive cases are the correctly classified epidemic cases; true negatives are correctly classified non-epidemic cases;

false positives are non-epidemics classified as epidemics; and false negatives are epidemic cases classified as non-epidemics. Mean, median, and standard deviation, were calculated for the periods [-21, -15], [-14, -8], [-7, -1], [0, +6], [+7, +13] and [+14, +20] for relative humidity, temperature, and precipitation. Boxplots were created for each period and group combination to carry out comparisons. F-tests were used to test the difference between the variances of the four aforementioned groups. Trends with respect to time were compared in four groups: under-predicted values, over-predicted values, true epidemics and true non-epidemics.
Regression tree methods were used to address the interaction between different time frames, i. e. [-21, -15], [-14, -8] and [-7, -1]. This method used binary recursive partitioning by splitting the dataset into maximally distinct groups (Crawley, 2002).

Results

Variable creation and selection: Variables from the period [-7, -1] were found to be the most informative. The best subsets approach detected five variables in particular that explained the majority of the variation from our dataset. Duration of temperature between 9º and 30ºC (T3), mean relative humidity (H1), duration of precipitation (R2), the duration of events of concurrent temperature between 9º and 30ºC and relative humidity ≥90 (TH2), and the binary variable for corn residue (Corn). Interactions were created between Corn and T3 and H1, and between corn and T3 and R2. These interactions were preferably selected by best subsets when compared with the five variables alone. The aforementioned interactions and the single variables were selected to create statistical models for epidemic classification.

Modeling methods. Logistic regression, neural networks, classification and regression trees, and K-nearest neighbor methods were compared using three statistical models (Table 3.1).

The first model included all selected variables singly (minus TH2), the second and third models included one and two interaction terms plus TH2, respectively. Three-way interactions addressed non-linearity of the temperature and relative humidity components, as well as temperature and precipitation. Models labeled 2 and 3 were variations of each other, where model 2 did not include the interaction between corn, temperature and rainfall (namely, Corn*T3*R2, Table 2.1). The rationale for this variation was to test the effect of removing Corn*T3*R2 because of its counterintuitive negative signed parameter. The aim of this comparison was to determine which method would yield the arrangement of cases that would translate into better prediction accuracy.

Table 3.1. Model development and comparison between methods of analysis. Four modeling methods were used to compare promising models for epidemic classification in winter wheat. Accuracy is the percentage of correct cases, sensitivity is the percentage of correctly classified epidemics; specificity is the percentage of correctly classified non-epidemics.

#	Model	Modeling Method	Accuracy	Sensitivity	Specificity
1	T3 H1 R2 Corn	Classification Tree	84	76	89
		K-Nearest Neighbor	83	74	89
		Logistic Regression	74	71	76
		Neural Network	67	70	65
2	TH2 Corn*H1*T3	Classification Tree	82	94	74
		K-Nearest Neighbor	67	52	77
		Logistic Regression	69	84	61
		Neural Network	77	76	77
3	TH2 Corn*H1*T3 Corn*R2*T3	Classification Tree	88	90	86
		K-Nearest Neighbor	83	76	88
		Logistic Regression	80	81	80
		Neural Network	81	76	84

The most accurate model was model 3 with 80%-88% of accuracy. Model 1 did not perform well in comparison to the other models across methods. Among the statistical methods used, CART yielded the most accurate models (82%-84%). Neural networks performed the worst of the methods compared (67%-81%). The performances of the logistic regression (76%-85%) and K-NN (67%-83%) methods were intermediate. All methods but K-NN, yielded balanced sensitivity and specificity values, i. e. disparity of more than 10% between these values.

The Hasse diagram (Figure 3.1) compared models and methods together to create a ranking. CART models (components 1, 5 and 9) were superior. The the second level of comparison had K-NN models 1 and 3 (components 2 and 10), and logistic regression models 2 and 3 (components 7 and 11). Neural networks (components 4, 8 and 12) and performed the worst as a method.

Method selection considered accuracy and the position on the Hasse diagram. The best method overall was CART. CART separates cases into discrete categories, and has the advantage of being simple to deploy. The disadvantage of deploying CART models is that the thresholds for group separation are discrete. Discreteness can be a source of error when dealing with continuous variables such as relative humidity. CART would, for example, assign cases with relative humidities of 70% and 70.5% to different epidemic classes. CART was discarded as a method of choice. K-NN is reportedly difficult to implement, and was therefore eliminated. The simplicity of interpretation, and performance of the logistic regression made it the preferred approach for deployment. Model 3 was chosen for model development, this model had a high rate of accuracy and balanced sensitivity and specificity in all methods.

Validation. The original dataset (N=85) was split into a training set (N=59) and a

validation set (N=26) using the SAS procedure surveyselect and maintaining the original proportions of epidemics/non-epidemics. Validation was carried out by simple cross-validation (Table 3.2). Model 3 had the greatest accuracy, had a training accuracy of 81%, a validation accuracy of 77%, and kept balanced high sensitivity and specificity, as compared with model 2's 68% accuracy, and model 1's 78% accuracy. Ultimately, model 3 was deployed during the 2004 growing season as the Fusarium Head Blight Risk Assessment Tool for all winter wheat regions (De Wolf et. al., 2004; Molineros et. al., 2004; www.wheatscab.psu.edu).

Table 3.2. Model validation for three logistic models in the development phase. Original dataset N=85 was split into training and validation sets.

#	Model	Dataset	N	Accuracy	Sensitivity	Specificity
1	T3 H1 R2 Corn	Training	59	78	76	79
		Validation	26	65	60	69
2	TH2 Corn*H1*T3	Training	59	68	86	58
		Validation	26	73	80	69
3	TH2 Corn*H1*T3 Corn*R2*T3	Training	59	81	81	82
		Validation	26	77	80	75

Model 3 worked as two equations in one; when corn residue is absent from the field, only TH2 (duration of temperature 9ºC-30ºC and relative humidity ≥90%) is used, this variable was designed as an indicator of perithecial development. However, when there is corn residue in the field, H1*T3 (mean relative humidity and duration of temperature between 9º and 30ºC) and R2*T3 (precipitation duration and duration of temperature between 9º and 30ºC) are factors in the model. These two interactions are indicators of the conditions on corn residue favorable for inoculum production. Figure 3.2 shows the dispersion of cases with respect to T3 and H1. The

cases were split into true positives, true negatives, false positives, and false negatives. Most cases are above 120 hours of T3, and above 60% relative humidity. These four groups of data are sparsely distributed and overlapping.

Additional validations on model 3 were performed after the 2004 and the 2005 growing seasons. $Validation_{2004}$ contained 30 additional cases. $Validation_{2005}$ contained 17 additional cases. These additional observations increased the number of cases to 132 (Table 3.3).

Table 3.3. Model validation of model 3. The development dataset contained training and validation sets, two additional rounds of validation were done in 2004 and 2005. * means there were zero epidemic cases.

Model	Dataset	N	Accuracy	Sensitivity	Specificity
TH2 Corn*H1*T3 Corn*R2*T3	Training	59	81	81	82
	Validation	26	77	80	75
	2004	30	53	29	75
	2005	17	65	*	65
	Overall	132	74	69	77

$Validation_{2004}$ reached a 53% accuracy, while $validation_{2005}$ reached 65%. It is important to note the low level of sensitivity in 2004 (Table 3.3). Sensitivity of the model in 2005 is infinite because there were no epidemic cases in 2005. Over all cases, accuracy was 74%. In comparison to the development dataset, the model lost more sensitivity than specificity. A discussion of this reduction follows in error analysis.

Comparison to previous models for FHB. Comparisons were performed with models A, B and I from De Wolf et. al. (2003). Model A used rescaled parameters representing duration of temperature 15º-30ºC and relative ≥90% for 7 days pre-anthesis and 3 days after anthesis

(TRH9010). Model B used an interaction of rescaled duration of temperature between 15º-30ºC for 7 days pre-anthesis multiplied by the variable in model A (INT3). Model I used duration of temperature between 15º-30ºC (T15307) plus duration of precipitation (DPPT7), both were calculated for 7 days pre-anthesis. The overall dataset (N=132) was used to compare all models. The span of the comparison dataset was 1982-2005, and included 8 states. Original development numbers are presented in Table 3.3. Numbers in parentheses used the same dataset with 132 observations, models A and B use a post-anthesis dataset (N=117) with fewer cases. All models started with accuracies above 70% on their development dataset (Table 3.4), and then dropped when challenged with new information. Model 3 performed the best among these models with an overall accuracy of 74% compared to models A, B, and I, whose accuracy was below 70%. Sensitivity of model 3 dropped to 69%, while model 2 remained above 70%. Specificity was the largest in models A, B and I, model 3 was 77% specific.

Table 3.4. Models for winter wheat. A new risk assessment model was found to be informative for winter wheat, additionally model 2 is used for comparison. These models were compared to models from De Wolf et. al. (2003). TRH9010 is the duration of temperature between 15ºC-30ºC and relative humidity ≥ 90% for [-7, +2]; INT3=T15307*TRH9010, where T15307 is the duration of temperature between 15º-30ºC for [-7, -1]; DPPT7 is the duration of precipitation for [-7, -1]. *p* is the threshold probability level splitting epidemic/non-epidemic cases. Values in parentheses represent the same dataset to challenge all models (N=132), [p]Used post-anthesis dataset (N=117).

Model	Equations	*p*	Accuracy	Sensitivity	Specificity
De Wolf 2003					
A	–3.3756 + 6.8128*TRH9010	0.36	84 (62)[p]	83 (29)[p]	84 (81)[p]
B	–3.7251 + 10.5097*INT3	0.44	84 (65)[p]	83 (26)[p]	84 (87)[p]
I	–8.2175 + 8.4358*T15307 + 4.7319*DPPT7	0.50	70 (64)	56 (43)	78 (78)
Deployment					
Model 2	-6.3906 + 0.0746*TH2+ 0.000753*Corn*H1*T3	0.48	82 (68)	82 (78)	82 (60)
Model 3	-6.3906 + 0.0746*TH2+ 0.000753*Corn*H1*T3 -0.00244*Corn*T3*R2	0.38	85 (74)	87 (69)	83 (77)

Error analysis. The aim of error analysis was to find possible improvements to the models developed by focusing on the scenarios surrounding the errors of the model. Another objective of error analysis was to correlate elements of the biology of the disease with a timeline of weather events. Figure 3.2 shows the difficulty to resolve the overlap between groups of

correctly and incorrectly predicted cases. Additional information might help resolve this overlap. Therefore additional time periods of information were added to the analysis. The dataset for error analysis included weather information for periods [-21, -15], [-14, -8] and [-7, -1] for 14 cases, four overpredicted and ten underpredicted. The dataset was reduced to this size to be able to capture the weather events for 21 days pre-anthesis. Most error cases in the development database did not have information going back 21 days.

All weather information was summarized into weeks before anthesis (i.e [-21, -15]; [-14, -8]; and [-7, -1]) as in table 3.5, and then separated them into our four categories of prediction. Table 3.4 shows that the mean of overpredicted relative humidities are consistently larger than those for non-epidemic cases (71%-79% vs. 79%-82%), but they are within the standard deviation of the development dataset's non-epidemics. In the case of underpredicted epidemic cases, mean relative humidity was similar to epidemic cases up to one week before anthesis, and then it dropped to 74%. For underpredicted epidemics, mean temperature was considerably higher than that of correctly predicted epidemics. This difference is within one standard deviation. Precipitation variables did not show any measurable pattern of error. It is important to note, that the models were developed using exclusively data from the period [-7, -1] days pre-anthesis.

Table 3.5. Error analysis of unpredicted and overpredicted cases by environmental time period. Means of relative humidity, temperature and duration of precipitation were calculated, standard deviations are presented in parentheses.

		Time Period		
		-21, -15	**-14, -8**	**-7, -1**
Relative Humidity (%)	**Correct Non Epidemic (N=117)**	71.17 (7.41)	74.89 (6.73)	78.65 (8.17)
	Overpredicted (N=3)	79.8 (8.4)	78.46 (6.18)	82.15 (7.9)
	Correct Epidemic (N=51)	73.33 (7.22)	74.82 (5.67)	79.64 (6.19)
	Under predicted (N=15)	74.56 (8.77)	76.57 (6.74)	74.27 (6.36)
Temperature (ºC)	**Correct Non Epidemic (N=117)**	13.57 (2.19)	17.03 (3.52)	17.61 (2.81)
	Overpredicted (N=3)	13.44 (2.71)	17.68 (2.87)	18.39 (2.12)
	Correct Epidemic (N=51)	14.04 (2.18)	14.81 (4.04)	16.67 (2.64)
	Under predicted (N=15)	15.39 (1.96)	16.33 (1.58)	18.38 (2.57)
Precipitation (Hrs)	**Correct Non Epidemic (N=117)**	10.99 (6.6)	10.14 (7.85)	11.88 (7.54)
	Overpredicted (N=3)	14.75 (4.42)	8.5 (4.93)	8.5 (9.98)
	Correct Epidemic (N=51)	16.61 (9.24)	10.5 (6.04)	10.52 (6.54)
	Under predicted (N=15)	12.5 (4.53)	6.25 (8.17)	8.54 (6.52)

A graphical illustration of the means of relative humidity is presented in Figures 3.3 and 3.4. These figures compared boxplots of weekly means of relative humidity between the over predicted cases and the non-epidemic cases (with and without corn); and under predicted cases against epidemic cases (with and without corn). There were no overpredicted cases with corn residue. Using this figure, and taking into account the source of the development data, it is appears that most of the over predicted cases had high relative humidity (75% and above, Figure 3.3). For the epidemic cases during the period before anthesis (Figure 3.4), relative humidity was lower than expected from the development dataset. This reliance in only one period of weather may be due to be autocorrelation between successive periods of weather and epidemics.

One way to illustrate this interaction is to view a classification tree model as in Figure 3.5 This tree model attempts to separate groups of high disease by using environmental information from three weeks pre-anthesis [-21, -15], [-14, -8], and [-7, -1]. Figure 3.5 presents the variable being split with the following nomenclature: variable name followed by pre-anthesis period. For example, $TH2_{21}$ is variable TH2 for period [-21,-15], $T3_{14}$ is T3 for [-14,-8] and $TH2_{7}$ is TH2 for [-7,-1]. The value accompanying the variable is the threshold where the variable was split. The first split occurs at the threshold of 30 hours of favorable temperature and humidity at [-21,-15] ($TH2_{21}$). At the right branch, the split for $TH2_{7}$ greater than 80 hours (out of 168) leads to severe disease (a mean of 43.9% severity). On the left, the split of temperature $T3_{14}$ for [-14,-8] at 146 hours also leads to severe epidemics in one out of four leaves (30.4%). This figure illustrates the complex intermixing of favorable environment at different time periods. Note that the most severe epidemics occur at the right of the first split, with mean values between 5.3-43.9 (5 of 7 are above 9.5), while those in the left have mean values between 1.5-30.4 (1 in 4 is above 9.5).

Discussion

Our objective has been to incorporate the presence of crop residue, such as corn, to the predictive assessment of FHB risk. It has been reported that presence of crop residue increases the risk of severe FHB epidemics (Atanasoff, 1920; Khonga and Sutton, 1988; Parry et. al., 1995; Sutton, 1982) . Winter wheat, in our case, is particularly suitable for this kind of analysis because of the widespread rotation of winter wheat and corn, and because of data availability.

Model Development. Membership to the FHB epidemic group is correlated with periods of temperature between 9º-30ºC (T3 and TH2), periods of high relative humidity (H1 and TH2), and periods of precipitation (R2). When considering the special case of the presence of corn residue, FHB epidemics are related to periods of temperature between 9º-30ºC (T3), periods of high relative humidity (H1), and periods of precipitation (R2). Weather information was split into periods of 3-21 days. Information for 3, 4 and 5 days performed the worst in explaining epidemic classification. This is because shorter periods are more likely to contain too little information of a biological process and might miss a specific window of time when these are occurring. The smallest period that worked in this study was 7 days. We presume 14 and 21 day periods include too much information to be able to correlate to the whole *F. graminearum* life cycle. From the perspective of fungal biology, it makes sense that the week prior to infection potential is correlated with favorable environmental conditions for growth and development of fungal inoculum. In this case the correlation goes one step further. By involving corn residue in the field, we are introducing a more focused indicator of the conditions in the soil residue that will maximize inoculum potential at anthesis.

Modeling methods varied in accuracy, sensitivity and specificity (67-88, 52-94, and 65-89, respectively). Although there is no perfect method or perfect model, CART and logistic

regression methods provided very high accuracies on balanced models (sensitivity and specificity at similar levels). K-nearest neighbor is the most difficult method to implement and interpret, aside from its poor performance with the models. Neural networks are promising for risk assessment, especially since some programs like Tiberius (Brierley, 2006) allow for a quick interface for implementation, and since they can learn and dynamically adjust the model to accommodate new incoming information. Unfortunately, neural networks at their best also require increasing computing power, maintenance and storage and would be very expensive to deploy. CART is a very accurate method, is simple to implement, but poses a big hurdle when dealing with continuous processes. CART treats continuous processes as discrete, thereby separating two similar adjacent values when they are virtually equal. The discreteness problem is found especially close to the decision thresholds to divide groups. The statistical method that targets this problem is called multivariate adaptive regression splines (MARS, Friedman 1991). This method builds flexible regression models by fitting separate splines (or basis functions) to distinct intervals of the predictor variables. MARS is reportedly difficult method to implement, but its advantages might be worth deploying it. Logistic regression produces a simple equation for deployment, and offers the ability to be able to make comparisons when one or more variables are held constant. Logistic regression has the advantage of being able to examine the sign of the parameters associated to environmental parameters as a consistency check.

Three models were selected for comparison and successive deployment. Model 1 deals with epidemic classification in a linear fashion, assumes that the risk of severe disease (i. e. field severity $\geq$10%) has an additive relationship with relative humidity, temperature, and precipitation during the week before anthesis. Corn residue in model 1 is treated as a second intercept. Model 2 assumes a curved relationship of epidemics with relative humidity and

temperature for cases with corn residue, and assumes a linear relationship of epidemic classification with duration of both temperature and relative humidity as a single event. Model 3 adds another curved relationship between temperature and rainfall to model 2.

The choice between these three models was based on two basic criteria, accuracy and logic. The most accurate model is model 3 (Table 3.1). The selected model has to make biological sense. The signs accompanying the estimated parameters are positive for the interaction between relative humidity and temperature, this is consistent with the biology of the pathogen. However, the sign of the estimator is negative for temperature by precipitation. This could mean either that the parameter is functioning to balance the weights of the other estimator, or that the models are capturing events in which rainfall acts as inhibitor of ascospore release as described by Paulitz (1996). Because this is a descriptive model, and not a mechanistic model, there is no way of matching one to one the biological processes in play (such as ascospore inhibition by heavy rainfall). Model 3 was chosen as an experimental model to deploy at the Pennsylvania State University FHB Risk website (www.wheatscab.psu.edu) for the 2004 growing season. The deployment of these models was reported in De Wolf et. al., (2004) and Molineros et. al. (2004).

Model 3 used indicators that related large-scale weather to disease epidemics. In the general case, epidemic classification is handled by conducive environment seven days pre-anthesis. It is not possible to determine if this indicator (TH2) relates to one specific portion of the fungus biology. The observations taken for this models were taken at a field plot level of scale, where there is variability between plant and fungal growth stages. Thus the environmental information used here will reflect a snapshot of the development stage of the pathogen at the field plot scale, and this reflects a particular inoculum potential. Inoculum potential here

represents the proportion of the fungi that are growing, producing perithecia, maturing perithecia, and releasing ascospores and macroconidia, as well, as a proportion of spores germinating on plant tissue, and penetrating wheat heads in that particular week. Variation in inoculum potential could be taken into account with additional replication of field experiments at different times and locations.

Validation. It is important to validate models with previously unused observations to have an idea of the performance the model will have once deployed. Therefore a validation dataset has to be representative of the conditions the model will face. Out in the real world, the model will be challenged with a higher level of variability. The ability of a model to perform in multiple validations is an indicator of how well it is likely to perform once it is implemented.

Model validation of the three models using logistic regression was an additional criterion used in model selection. Training (N=59) and validation sets (N=26) were created and used for each model. Model 3 had the highest training and validation accuracy (Table 3.2).

Model validation of model 3 was a three step process. The first validation was performed at model development, and then after the 2004 and 2005 growing seasons. Model 3 accuracy dropped dramatically in 2004 to 53% (Table 3.3), and then again in 2005 it dropped to 65%. However this is not the overall model accuracy, but the performance of the model in those years alone. It is possible that the years 2004 and 2005 were extremes of the same climate distribution. Where 2004 was an extremely wet year (mean duration of precipitation for [-7, -1] 9.8 $\pm$ 7.5), and 2005 was dry (mean duration of precipitation for [-7, -1] 3.1 $\pm$ 2.2). The development period 1982-2003 had a larger range of conditions (mean duration of precipitation for [-7, -1] 8.9 $\pm$ 7.5). On the overall dataset, 1982-2005, model 3's accuracy remained above 70%.

Comparisons to previously published models from De Wolf et. al. (2003) were done.

The models selected were model A, B, and I. Model I is the only one using information from pre-anthesis. Model A and B incorporated three additional days after anthesis. All models I, 2 and 3 used the same dataset, while models A and B had fewer cases due to missing information (Table 3.3). Model accuracy in parentheses, compared with the development dataset values, dropped for all models. Model 3 remained above 70% in accuracy and maintains balanced sensitivity and specificity, as opposed to models A, B, and I that are unbalanced. The drop in sensitivity and specificity over all models is the reason to perform error analysis.

Error analysis. For error analysis additional time periods were examined. This is based on the notion that past information could have an effect on the study period [-7, -1]. Prior information could potentially be related to the state of inoculum potential at the time of flowering. Figure 3.5 illustrates the interrelationships between time period and the development of severe epidemics. Temperature and relative humidity were selected over the 3 weeks pre-anthesis as indicators of epidemics. This may indicate that there is serial dependency between time periods. This dependency was not resolved. A mechanistic approach or a method that matches previous climate scenarios to epidemics might perform better at separating seemingly similar cases that belong to different epidemic categories.

From the dataset to date it can inferred that winter wheat FHB epidemic assessment is a complex process to analyze, especially when complete information is lacking. Ideally, information for months before anthesis should be examined for indicators of fungal processes and their interaction with the plant and the environment.

In conclusion, a model that incorporated crop residue in FHB risk assessment was successfully developed and validated. Since its deployment, the model was validated three times through cross-validation. Accuracy fell with successive validations, indicating the need to

recalibrate or modify the present model using prior weather information. Re-parametrization will only be possible with more years of information on several weeks prior to anthesis. Nonetheless, the model does performed well on the majority of years (1982-2003), and achieves 74% accuracy on all cases.

Future directions. It is possible that a re-parametrization will correct the aforementioned problems. A different model development/validation technique pair, such as bootstrapping may increase the overall accuracy by refitting the same model to a larger dataset. However, the inclusion of information from the periods [-21, -15] and [-14, -8] would be useful and might provide a better indicator of the real state of inoculum potential at time of infection.

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Figure 3.1. Hasse diagram of the model by method comparison. The upper level is comprised by un-covered elements. Elements not linked are incomparable, i. e. #1, #9, and #5 are incomparable, where none of them is clearly superior to one another.

#	Model	Method
1	1	CART
2	1	K-NN
3	1	Logistic Regression
4	1	Neural network
5	2	CART
6	2	K-NN
7	2	Logistic Regression
8	2	Neural network
9	3	CART
10	3	K-NN
11	3	Logistic Regression
12	3	Neural network

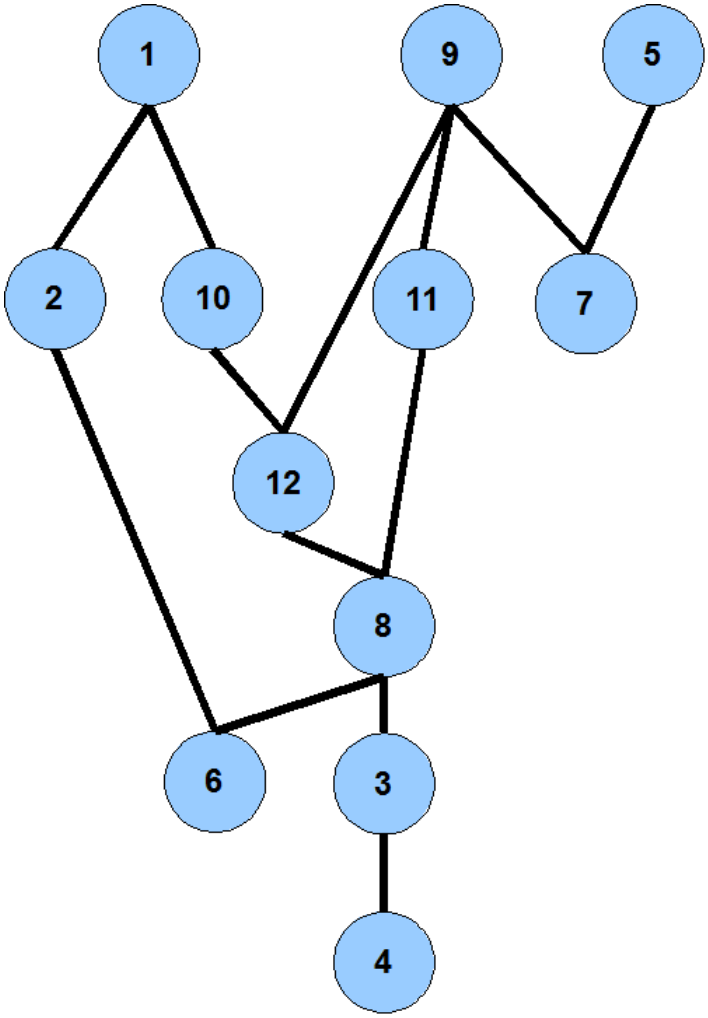


Figure 3.2. Plot of model 3. This model contains interactions between temperature (T3) and relative humidity (H1) and temperature and precipitation. The observations are separated into true positives, true negatives, false positives and false negatives. The maximum number of hours for T3 is 168 hours, while H1 is bounded at 100% relative humidity.

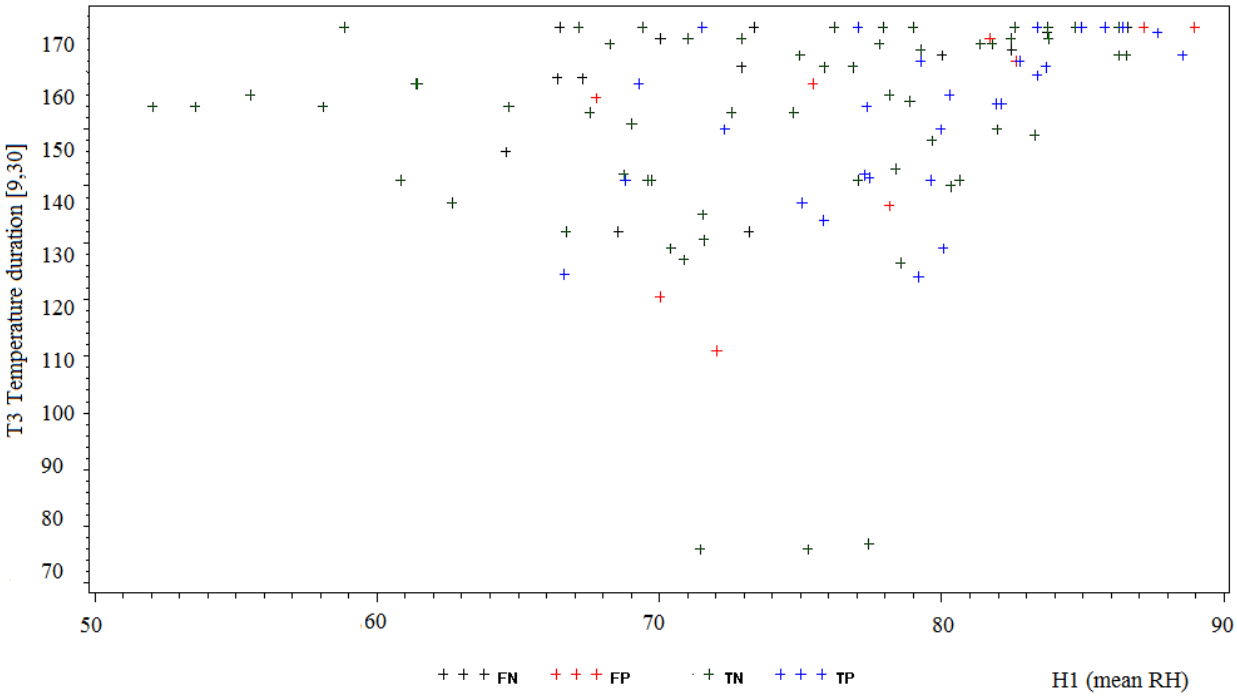


Figure 3.3 Overpredicted values boxplots by presence/ absence of corn residue. Top left, overpredicted cases where corn is absent; bottom left, non-epidemic cases without corn; bottom right, non-epidemic cases with corn residue. Vertical axis is mean relative humidity (%), the horizontal axis is divided into time periods [-21, -15], [-14, -8] and [-7, -1].

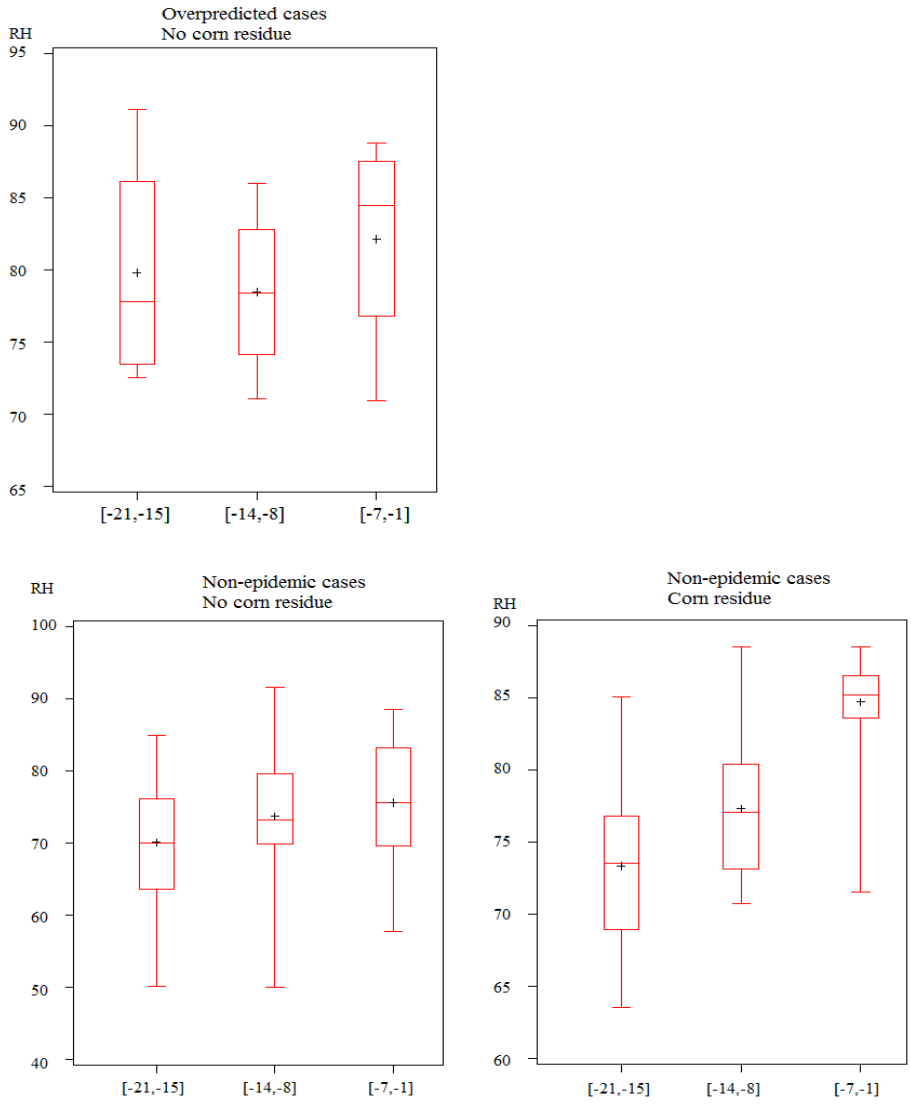


Figure 3.4. Underpredicted values boxplots by presence/ absence of corn residue. Top left, overpredicted cases where corn is absent; top right, underpredicted cases where corn residue is present; bottom left, non-epidemic cases without corn; bottom right, non-epidemic cases with corn residue. Vertical axis is mean relative humidity (%), the horizontal axis is divided into time periods [-21, -15], [-14, -8] and [-7, -1].

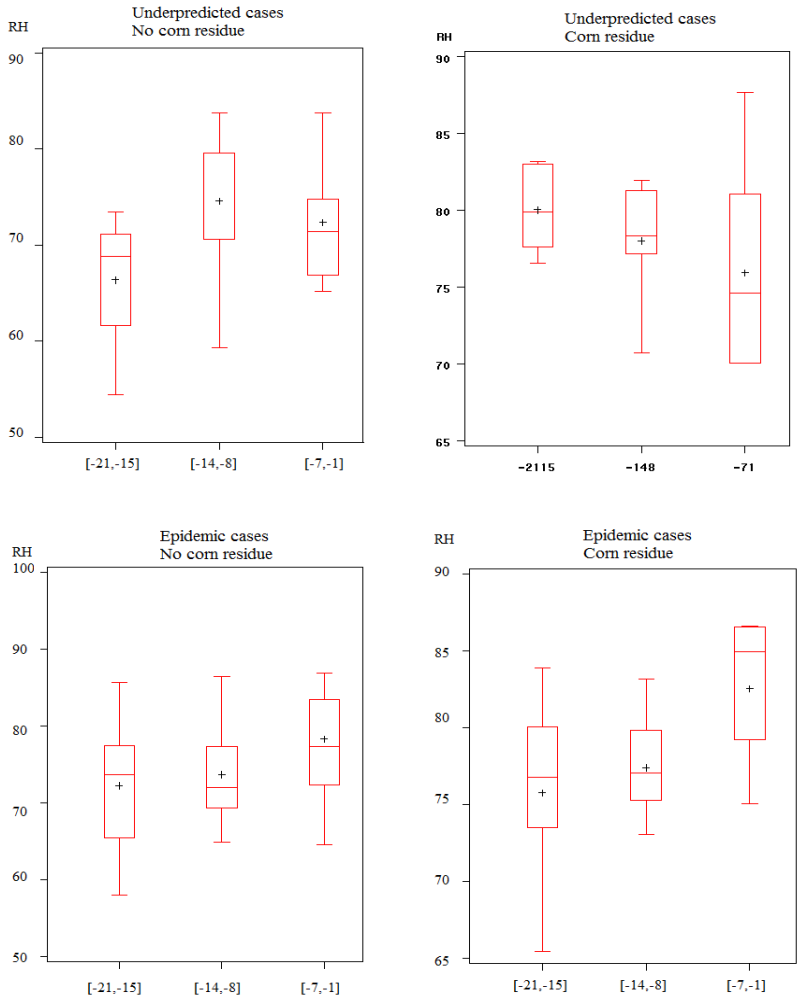
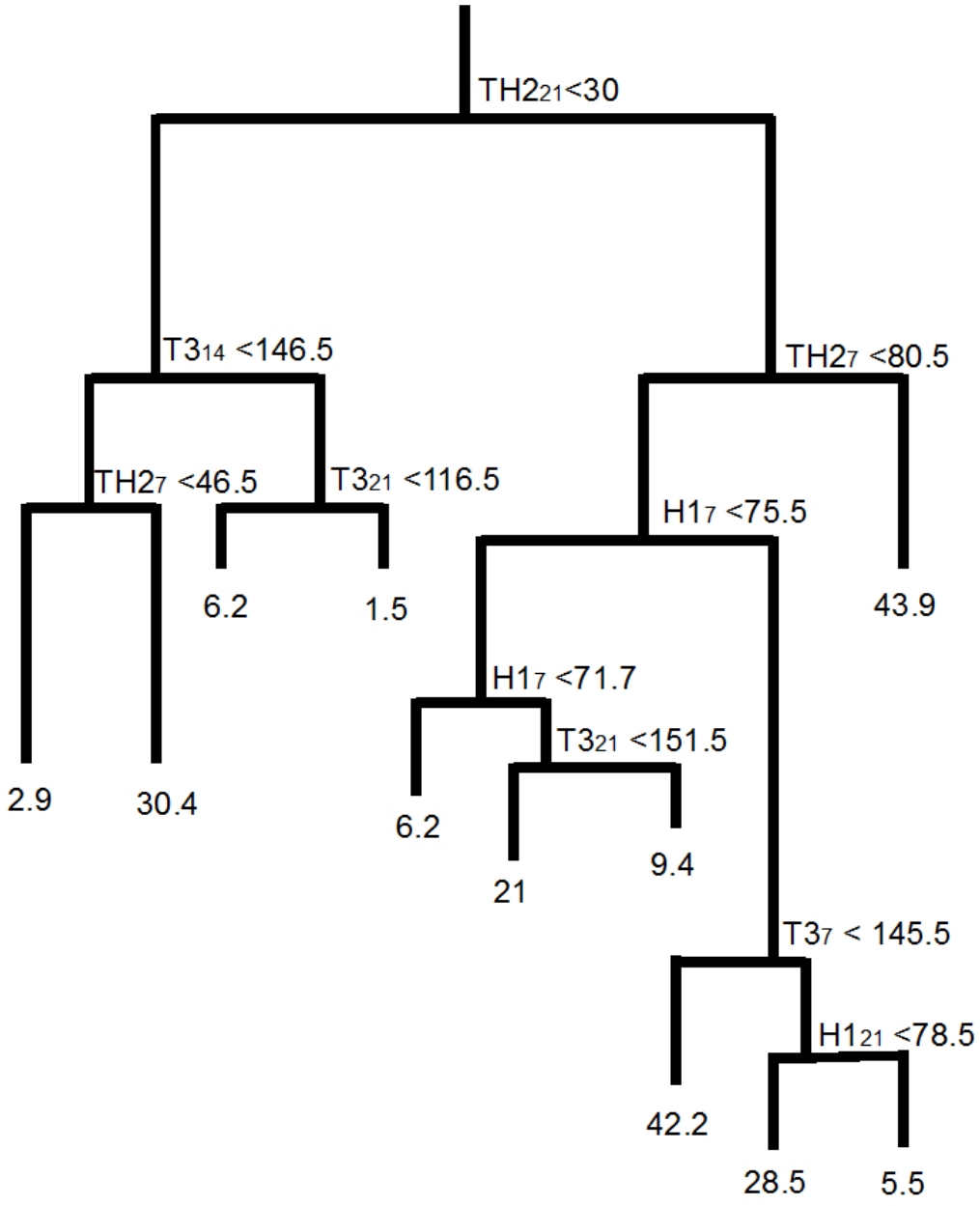


Figure 3.5 . Tree model for historical weather associations. Variables on top of the split is named as variable name plus the period referred, e.g $TH2_{21}$ is TH2 for [-21, -15], and $T3_{14}$ is T3 for [-14, -8]. The numbers at the bottom of the split are the mean field severity (%) of the cases in that division.



CHAPTER 4

CONCLUSION

The overall objectives of this dissertation were to create suitable models for deployment to forecast Fusarium head blight (FHB) risk in spring and winter wheat. Given the current status of the development of moderately resistant cultivars, spring wheat was the perfect candidate to test new models. Winter wheat, on the other hand, lacks commercially available moderately resistant cultivars. But this was not the only rationale to divide these two types of wheat. Spring and winter wheats are grown in sufficiently different weather scenarios to require a separate models. In areas where winter wheat is grown, there is also the practice of rotating wheat with corn. This practice is increasing in frequency in spring wheat areas due to the increased demand for ethanol or biodiesel production from corn.

From our results and error analyses, one model was selected for each type of wheat. The spring wheat model incorporated cultivar susceptibility as a categorical variable. The winter wheat model incorporated the presence of corn residue on the field as a dummy variable. Following validation, it can be concluded that the spring wheat model performed better in its dataset, than the winter wheat model in its dataset.

A consensus of both models indicated the need to use information up to three weeks before anthesis to better describe the development of inoculum, and thus account for more model variation. Important lessons were learned on ways to account for the variability inherent in the system. Recommendations were given to advance the study of the relationship between environmental variables at the scale of the weather station, and the pathogen's development. Important indicators at the weather station level were identified and used for model development.

These indicators could be used as a starting point for new improvements on FHB forecasting.

The choice of modeling methods could be expanded to include multivariate regression splines, in order to take the discreteness out of CART. Hasse diagrams provided useful information and should continue to be used as model and method performance ranking mechanisms.

APPENDIX 1

Variables created for model development. Variables were created for all the time periods in the table.

Variable	Units	Description
Response		
Y	None	FHB severity ≥10%=1; FHB severity <10%=0
y5	None	FHB severity ≥5%=1; FHB severity <5%=0
y7	None	FHB severity ≥7%=1; FHB severity <7%=0
Severity	%	FHB field severity
Cultivars		
Variety	None	Categories of susceptibility
Corn residue		
Corn	None	Presence=1; Absence=0
Corn.5	None	High=1; Medium=0.5; Absence=0
Corn-1	None	Presence=1; Absence=-1
Relative Humidity		
RH90	Hours	Duration of RH ≥90%
H1	%	Mean RH

Table continued

Variable	Units	Description
Temperature		
mTemp	ºC	Mean Temperature
T9	Hours	Duration of Temperature ≥ 9ºC
T12	Hours	Duration of Temperature ≥ 12ºC
T15	Hours	Duration of Temperature ≥ 15ºC
T3	Hours	Duration of Temperature ≥ 9ºC but ≤30ºC
T1230	Hours	Duration of Temperature ≥ 9ºC but ≤30ºC
T1530	Hours	Duration of Temperature ≥ 9ºC but ≤30ºC
ptemp	none	Polynomial temperature categorization
Precipitation		
Sum Precipitation	mm	Total precipitation
R1	Hours	Duration of measurable rain events >0 mm
R2	Hours	Duration of measurable rain events >0.01 mm
R3	Hours	Duration of measurable rain events >0.025 mm
Dew point		
MDewPoint Temperature	ºC	Mean Dew point temperature
Dew 90	Hours	Duration of Dew Point when DP=0.9 * Temperature
Dew 98	Hours	Duration of Dew Point when DP=0.98 * Temperature
Dew 100	Hours	Duration of Dew Point when DP= Temperature
Temperature RH		
TRH 9 90	Hours	Duration of Temperature ≥ 9ºC AND RH ≥ 90%
TRH 12 90	Hours	Duration of Temperature ≥ 12ºC AND RH ≥ 90%

Table continued

Variable	Units	Description
TRH 15 90	Hours	Duration of Temperature ≥ 15ºC AND RH ≥ 90%
TH2	Hours	Duration of Temperature ≥ 9ºC AND ≤ 30ºC AND RH ≥ 90%
TRH 1230 90	Hours	Duration of Temperature ≥ 9ºC AND ≤ 30ºC AND RH ≥ 90%
TRH 1530 90	Hours	Duration of Temperature ≥ 9ºC AND ≤ 30ºC ANDRH ≥ 90%
ptempRH90	Hours	Duration of polynomial temperature curve AND RH ≥ 90%
Temperature Dewpoint		
TDP 9 90	Hours	Duration of Temperature ≥ 9ºC AND DP ≥0.9*Temperature
TDP 12 90	Hours	Duration of Temperature ≥ 12ºC AND DP ≥0.9*Temperature
TDP 15 90	Hours	Duration of Temperature ≥ 15ºC AND DP ≥0.9*Temperature
TDP 930 90	Hours	Duration of Temperature ≥ 9ºC AND ≤ 30ºC AND DP ≥0.9*Temperature
TDP 1230 90	Hours	Duration of Temperature ≥ 9ºC AND ≤ 30ºC AND DP ≥0.9*Temperature
TDP 1530 90	Hours	Duration of Temperature ≥ 9ºC AND ≤ 30ºC AND DP ≥0.9*Temperature

Time periods for model development								
[-21,-1]	[-14, -1]	[-7, -1]	[-8, -5]	[-6, -4]	[-6, -4]	[-5,-1]	[-7,+2]	[0, +6]
[-21,-8]	[-14,-8]		[-4, -1]		[-3, -1]			[0, +3]
[-21,-15]								

Glossary

Field severity=Disease index. Disease severity over the whole field, taken as a random sample of wheat heads, and considering the percentage of each head infected.

Epidemic. An epidemic is generally a widespread disease that affects many individuals in a population.

Serial dependency. Here, dependency of one time period by other time period, i. e. [-14,-8] depends of [-21, -15].

Autocorrelation. Correlation of the error terms from different observations of the same variable. Also called serial correlation.

Activation function. Function that describes the output behavior of a neuron in neural networks. Meaning the function relating input variables, intermediate variables (neurons), and output.

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EDUCATION

PhD. Plant Pathology, minor Statistics. The Pennsylvania State University, May 2007.
Dissertation: Understanding the challenges of Fusarium Head Blight forecasting.
Advisors: Erick De Wolf, PhD; Scott A. Isard, PhD.

MS. Agricultural and Environmental Economics. The Pennsylvania State University, May 2003.
Thesis: Land allocation inefficiency in four South American countries: The problem of Deforestation.
Advisor: James Shortle, PhD.

B.S. Biology. Pontificia Universidad Católica del Ecuador, November 1998.
Thesis: Territorial Behavior, Vocalizations and Life History of *Colostethus* sp. (aff *marchesianus*) in Ecuadorian Amazon.
Advisor: Luis Coloma, PhD.

TEACHING EXPERIENCE

PPATH 597A . Scientific computing. Schedule number 615241. The Pennsylvania State University. Instructors: Molineros, J., and De Wolf, E. Fall 2005.

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