2023

The Effects of Residue Amounts and Variety Selection on the Development of Wheat Fungal Pathogens in South Dakota

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Recommended Citation

Tembreull, Abrielle, "The Effects of Residue Amounts and Variety Selection on the Development of Wheat Fungal Pathogens in South Dakota" (2023). *Electronic Theses and Dissertations*. 843.
https://openprairie.sdstate.edu/etd2/843

THE EFFECTS OF RESIDUE AMOUNTS AND VARIETY SELECTION ON THE DEVELOPMENT OF WHEAT FUNGAL PATHOGENS IN SOUTH DAKOTA

By:

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A thesis submitted in partial fulfillment of the requirements for the degree of

Master of Science

Major in Plant Science

SOUTH DAKOTA STATE UNIVERSITY

2023

THESIS ACCEPTANCE PAGE

Abrielle Tembreull

This thesis is approved as a creditable and independent investigation by a candidate for the master's degree and is acceptable for meeting the thesis requirements for this degree. Acceptance of this does not imply that the conclusions reached by the candidate are necessarily the conclusions of the major department.

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Acknowledgements:

Two and half years, three advisors, dozens of doctor's appointments, and so many more hurdles were jumped during the span of this experiment. Below is a list of all the people who made this project happen no matter the size of the contribution. This experiment would not have been completed without them.

Dr. Madalyn Shires

Dr. Emmanuel Byamukama

Dr. Dalitso Yabwalo

Dr. Shaukat Ali

Dr. Sharon Clay

Cody Molnar

Dr. Rebecca Lee Phillips

Dr. Maira Rodrigues Duffeck

Dr. Esneider Mahecha

Abigial Schuldt

Grace Grube

Ashley Frederickson

Jaswinder Kaur

Taite Grossman

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ABSTRACT

THE EFFECTS OF RESIDUE AMOUNTS AND VARIETY SELECTION ON THE DEVELOPMENT OF WHEAT FUNGAL PATHOGENS IN SOUTH DAKOTA

Abrielle Tembreull

2023

Roughly 50% of South Dakota cropland is under the practice of no-till, with large increases in acres of no-till in the last 20 or so years. No-till is beneficial for Great Plains states, such as South Dakota, as soil residues are withheld. Residues are shown to increase soil health through retention of moisture and increase of microorganisms, but residues can serve as a source of inoculum for fungal pathogens that can overwinter on them. As wheat is one of the most important food crops in the world, it is important to protect this vital crop from diseases. Diseases of wheat can reduce yields by a minimum of 20 percent on a global basis. Some of the most common wheat pathogens that affect plants are fungal pathogens, including leaf rusts, stripe rust, stem rusts, Stagonospora nodorum blotch, Septoria tritici blotch, and tan spot. These diseases were evaluated in seven different varieties (‘Draper’, ‘Ideal’, ‘Redfield’, ‘Thompson’, ‘Expedition’. ‘Wesley’, and ‘Oahe’) and four different residue amounts (20%, 40%, 60%, and 80% ground cover) to determine the importance of choosing a disease resistant variety and the effect of residue amounts on pathogen development and yield. The varieties were chosen due to their differences in tolerance and susceptibility to the pathogens, and the residue amounts were chosen to encompass a wide range of tillage/non-tillage systems. Results from this study indicate that there are multiple different spot pathogens present in South Dakota with the variety ‘Draper’ having significantly higher disease amounts in 2021. In 2022, the most disease amounts were seen on ‘Expedition’ which was susceptible/unrated for all leaf spot pathogens.

‘Expedition’ also had the greatest amount of stripe rust in 2021. The residue amounts were also shown to have a significant effect on disease development. The higher residue levels (60% and 80%) were often significantly higher in disease than the lower levels (20% and 40%). This study was done to establish a baseline for the types of diseases present in South Dakota wheat and to understand the effects that residues have on wheat production and disease development.

Chapter 1: Literature Review

1. History of Wheat in the U.S.

Triticum aestivum L. (wheat) is an important crop throughout the world. In the 2022-2023 marketing year, wheat was ranked as third among agricultural crops grown in the United States by the U.S Department of Agriculture (USDA-NASS, 2022). Over 1.65 billion bushels and 35.5 million acres of wheat were harvested (USDA-NASS, 2022). Wheat is the primary food grain grown in the United States, but the amount of acreage and bushels grown has been on a decline since the 1980's (USDA-NASS, 2022).

Wheat, although not native to the United States, made its way from Spain with Columbus in 1494 and new varieties from all over Europe made their way over with colonists (Ball, 1930). Although there was a large selection of varieties that moved across the Atlantic by the 1600's, the eastern coast was not the best suited for the growth of wheat, shifting the focus towards corn that was easier to grow and better adapted to the environment (Ball, 1930). The 1700's was a period of expansion into central North America, leading to an increase in wheat production and thus wheat diseases. (Ball, 1930). Multiple disease issues occurred during this time, but thanks to the French immigrants familiar with most of the diseases, producers learned methods that resulted in some control of rust, through the removal of many barbery bushes, that serve as an alternate host, as well as mildew and smut diseases that were present (Ball, 1930).

The 1800's were a period of even greater expansion in land and farming technology, allowing new areas for wheat production in the United States (Ball, 1930). These increases lead to the introduction of new varieties that would be the foundation of wheat production in the Great Plains. ‘Red Fife’ was a foundation variety for the production of hard red spring wheat in the Great Plains, while ‘Turkey’, ‘Crimean’, and ‘Kharkof’ were the foundation of hard red winter wheat in the central and southern plains (Paulsen & Shroyer, 2008). The introduction of these varieties was of great economic importance to the United States by shifting the major production of wheat to the Great Plains and led to the exportation of wheat from the United States (Paulsen & Shroyer, 2008).

‘Red Fife’ was named after the farmer who selected it, D.A. Fife, who bought the variety in Glasgow. The variety was successful and, unlike many others available, was unaffected by rust diseases; because of this, Fife was able to supply seed to neighbors who then bred it with other wheat varieties (Paulsen & Shroyer, 2008). The hard red winter wheat variety ‘Turkey’ was introduced by Mennonite settlers from Ukraine and Crimea in the late 1800’s, but the quality of the variety was not recognized for over 25 years by others because the Mennonites were a close-knit group that did not interact with others often (Paulsen & Shroyer, 2008). ‘Turkey’ and ‘Red Fife’ were the foundation stock for breeding much of today’s hard red spring and winter wheat. Both were adapted well for growth within the Great Plains and showed resistance to some of the diseases, such as rusts and mildews, that were a problem then and are still a problem more than 150 years later.

Wheat has been one of the most predominant crops in South Dakota for over a century. In the 1920’s, South Dakota was producing about 30 million bushels of wheat annually which made it the second most predominantly planted crop, only behind corn in bushels per acre produced (Hardies & Hume, 1927). The types of wheat produced were hard red spring, hard red winter and durum wheat (Hardies & Hume, 1927). In 2022, hard red winter wheat produced 41 million bushels alone in South Dakota (Gerlach, 2022), with a value of over $330 million dollars. (USDA-NASS, 2022). Wheat production in South Dakota is now third in bushels produced behind corn and soybean production (USDA-NASS, 2022).

1.2 Diseases of Importance to this Project

Rust diseases were major threats to early wheat growers in the United States and still threaten the growth of today's wheat crops. There are three major wheat rust diseases: stem rust caused by *Puccinia graminis* f. sp. *tritici*; leaf rust caused by *Puccinia triticina*; and stripe rust caused by *Puccinia striiformis* f. sp. *tritici*.

Stem rust of wheat (*Puccinia graminis* f. sp. *tritici*) was, in the past, considered the most harmful wheat rust, with yield losses of up to 50 percent (Martinez–Moreno & Solis, 2019). Stem rust can reduce a healthy crop into broken stems and black shriveled grains (Peterson, 2018). The disease is characterized by dark red-brown pustules found on the stem and leaves of the wheat (Martinez–Moreno & Solis, 2019). Stem rust is considered the most dangerous rust disease because it attacks the leaf blade, leaf sheath, stem, and the head of the wheat unlike the other rust pathogens that only affect the leaves of the plant (Eversmeyer & Kramer, 2000). The pustules burst out of the plant, causing distinct symptoms to help differentiate this rust from other rusts.

Puccinia graminis f. sp. *tritici* is a macrocyclic, heteroecious rust fungus with five distinct stages (Leonard & Szabo, 2005). The resting overwintering spores of stem rust are two-celled teliospores that remain in the straw of previous year's crops until spring. In the spring, basidium is produced, which form the basidiospores that are ejected from the basidium and carried by wind and air currents to infect alternate host in the *Barberis* genus. In the alternate host, sexual spores are created: pycniospores (male gametes) and pycnia (female gametes). Fusion of gametes leads to the production of aeciospores that infect wheat and other grass species, where production of hypha and urediniospores, that produce uredinium, occurs. Urediniospores are dispersed by wind and infect more wheat and grass species. Once the grass and wheat hosts are mature, uredinia start to produce the overwintering teliospores to continue the cycle into the next season (Leonard & Szabo, 2005). The *Barberis* alternative host species of stem rust has been mostly eradicated in the U.S. In addition, increased amounts of resistant wheat cultivars have reduced the number of stem rust races and epidemics in the United States (Kolmer et al., 2007).

Leaf rust (*Puccinia triticina)*, also referred to as brown rust, can be found in all major wheat growing regions. (Kolmer et al., 2007) and is one of the three rust diseases commonly found in North America (Kolmer, 2013). The common name is derived from the fact that the leaf rust pathogen attacks leaf blades. However, in some highly susceptible varieties, it has been found to infect the leaf sheath and glumes as well (Draz et al., 2015). Uredinia appear on the upper leaf surface and are an orange-brown color. In general, losses are most often light at less than 20 percent. However, in some notable cases, there has been complete crop loss reported when disease was severe prior to heading (USDA-CDL, 2022).

Like all wheat rust pathogens, leaf rust is a full macrocyclic and heteroecious rust that follows the same stages of development of stem rust but with different alternate hosts (Kolmer, 2013). The pycnial stage alternate hosts of leaf rust include *Thalictrum* *speciosissimum* and *Isopyrum fumaroides* which are not native to North America; the *Thalictrum* and *Isopyrum* species that are native to North America are moderately resistant to infection (Bolton, et al., 2008). Leaf rust persists in North America due to the fact that southern winter wheat fields are infected by urediniospores in the fall months. These spores infect the host and are able to survive as the wheat lies dormant during the winter (Kolmer, 2013). Once winter wheat breaks dormancy in the southern United States, urediniospore production increases as the wheat matures. These spores are dispersed by wind and eventually reach the northern states and into Canadian providences (Kolmer, 2013).

Stripe rust is a significant disease of both spring and winter wheat and has been observed to devastate wheat crops on all continents, except Antarctica. Most wheat growing areas of the world have wheat varieties with little to no resistance to the pathogen (Jamil et al., 2020). In the United States alone, stripe rust results in an estimated yearly loss of one billion dollars (Schwessinger et al., 2020). Yield losses can be up to 100 percent if the environmental conditions are correct and the infection starts early (Jamil et al., 2020). Stripe rust was first observed in the United States in 1915. Historically, it was most severe in the Pacific Northwest, but since 2000, it has become more prevalent east of the Rocky Mountains into the Great Plains (Liu et al., 2017). Stem rust was considered the most economically important rust pathogen in the United States, however as stripe rust has an expanding geographic range and an associated increase in yield and production losses, it is now considered the most damaging rust pathogen in the United States (Lyon & Broders, 2017). The disease has been reported in over 30 states and five Canadian providences as of 2016, which is a large increase from the 11 states that reported before 2000 (Lyon & Broders, 2017).

The increase in stripe rust prevalence has led to more research on the pathogen. Stripe rust infection can start as early as one-leaf stage all the way up to plant maturity, if the plants are still green (Chen, 2005). Small, orange-colored uredia form stripes as well as chlorosis and necrosis on the leaves of the infected plant (Chen, 2005). The life cycle of stripe rust is the same as stem and leaf rust, but it was only in 2010 that the alternate host was identified. In June 2009, evidence of stripe rust was observed on multiple different *Barberis* species. To prove this, scientists Jin et al. (2010) of the Cereal Disease Laboratory at the University of Minnesota inoculated several *Barberis* species with telia spores of wheat stripe rust. Aeciospores developed on the *Barberis* species and were then used to successfully reinfect wheat (Jin et al., 2010). The resulting telia on wheat was extracted and analyzed using real-time polymerase chain reactions (qPCR) to determine that wheat stripe rust was reproducing on *Barberis*, finally confirming alternate hosts for the wheat stripe rust lifecycle (Jin et al., 2010).

Other diseases that are a threat to wheat production today include the fungal spot pathogens which are found within residues of previous year's crops. Residue-borne pathogens present a unique danger to dryland farming states, such as South Dakota, that are more likely to practice no-till or conservation tillage. According to South Dakota State University Extension Service, from 2012 to 2017, no-till acres increase by 7% and conservation tillage acres rose by 24% (Bly, 2020). These tillage methodologies are designed to maximize soil moisture and health through leaving previous crop residues on fields. The accumulation of residues leads to an accumulation of disease as well, potentially increasing disease pressure on wheat crops. While the previously mentioned rust pathogens are not known to overwinter in South Dakota, multiple other fungal pathogens are. Residue-borne fungal diseases that are included in this study are: tan spot (*Pyrenophora tritici-repentis)*; Stagonospora nodurom blotch (*Parastagonospora nodorum)*; and Septoria tritici blotch (*Zymoseptoria tritici)*.

The most widespread fungal disease evaluated in this research is *Pyrenophora tritici-repentis*, the causal agent of tan spot of wheat, which is one of the most devastating and widespread necrotrophic wheat pathogens noted for the potential of destruction in all wheat growing areas of the world (Cotuna et al., 2015). In severe cases of tan spot, yield can be reduced 20 to 50 percent (Carigano et al., 2008). In South Dakota, tan spot alone can cause 5 to 29 percent yield losses on wheat, which is economically devastating to most producers (Abdullah et al., 2017). There are four primary factors of tan spot that determine yield loss associated with the pathogen. The first factor is the amount of inoculum present; second is the presence of the necessary period of leaf wetness after inoculation. Next is the host genotype which determines the level of resistance to the pathogen; the final factor is the growth stage of the wheat when infected (Shaber & Bockus, 1988).

The lifecycle of *P. tritici-repentis* (tan spot) is as follows: pseudothecia develop and mature on plant residues after harvest in the fall and winter. In the spring, ascospores are forced from the psuedothecia, moved via wind and/or rain splash to the lower leaves of wheat plants to begin primary infection; ascospores of this pathogen do not move far when infecting new plants as they are relatively large in size (Wegulo, 2011). Once the ascospore is moved to a new host plant, it enters the epidermis directly and grows intercellularly through the mesophyll (Ciuffetti & Tuori, 1999). Following initial infection by ascospores, the fungus begins producing conidia which serve as secondary inoculum. Conidia can also be produced on residues and serve as both primary and secondary inoculum as conidia travel farther than ascospores because of their smaller size and greater numbers (Wegulo, 2011).

Tan spot has three different host selective toxins, otherwise known as necrotrophic effectors, that determine pathogenicity. Necrosis is caused by Ptr ToxA, whereas chlorosis is caused by Ptr ToxB and ToxC (Aboukhaddour et al., 2013). Eight different races of tan spot have been isolated; these races are based upon their virulence phenotypes on a set of different lines which determine the necrotrophic effectors they produce (Liu et al., 2015). Symptoms of tan spot are typically elliptical shaped necrotic lesions with a chlorotic border (Liu et al., 2015), but symptom development is affected by both toxins produced and the race of the pathogen. Races and the associated toxins have been explored and determined as follows: Race 1- Ptr ToxA and ToxC; Race 2-Tox A; Race 3- ToxC; Race 4- no known toxins; Race 5- ToxB; Race 6- ToxB and C; Race 7- ToxA and B; and Race 8- ToxA, B, and C (Abdullah et al., 2017; Lamari et al., 2003).

The second residue-borne disease studied in this research is *Parastagonospora nodorum*, the fungal agent responsible for the development of Stagonospora nodorum blotch of wheat which is one of the most important diseases of wheat in the Northern Great Plains (Liu et al., 2015). This pathogen overwinters on wheat residues left on the field in pseudothecia and pycnidia. Ascospores from the pseudothecia are the main source of inoculum, but conidia which are rain splashed from pycnidia can start the disease cycle as well. Once plant leaves are infected, pycnidia develop within the lesions and spread conidia from the lower leaves to the upper leaves, glumes, and other plants via rain splash. Psuedothecia take longer to develop than pycnidia because two opposite mating types are required and often develop on wheat stubble to provide the primary inoculum for the following year (Mehra et al., 2019).

Stagonospora nodorum blotch causes necrotic lesions on the leaves of wheat as well as discoloration of the head (Solomon et al., 2006). The lesions are lens-shaped without an obvious chlorotic halo surrounding the necrotic tissue (Liu et al., 2015). Both the quality and the quantity of grain can be affected by the disease. Reduction in yield occurs because of the reduced photosynthetic area of the upper leaves, leading to lower thousand-kernel weight and test weight. Yield losses have been reported of up to 50 percent in the United States and Europe (Mehra et al., 2015).

The third and final fungal spot disease evaluated in this study was *Zymeoseptoria tritici,* which is an ascomycete fungal pathogen responsible for the development of Septoria tritici blotch. Septoria tritici blotch is currently the most damaging wheat disease in Europe (McDonald & Mundt, 2016) and increasingly problematic in the United States. According to the Crop Protection Network, Septoria was the cause of 2,734 thousand bushels lost during the 2021 wheat season (Friskop et al., 2021) *Zymeoseptoria tritici* has a hemibiotrophic lifecycle with two distinct phases (Kettles & Kanyuka, 2016). Inoculation of the plant occurs by wind-borne ascospores or rain-splashed conidia onto wheat leaves. The spores germinate and invade the plant through the stomata where a long asymptomatic phase of hyphal growth in the apoplastic space occurs. This phase usually lasts for 7 to 10 days, after which, the fungus switches from biotrophic growth to necrotrophic growth, causing cells to collapse and lesions with yellow flecks or blotches develop. The lesions expand and pycnidia develop around stomata in the necrotic lesions and exude conidia that are again rain-splashed, continuing the disease lifecycle. The pathogen overwinters primarily as pseudothecia but can also survive as pycnidia on crop residues (Ponomarenko et al., 2011).

All six pathogens previously mentioned are harmful to wheat crops both in the United States and other wheat growing countries of the world. The associated risks lead to a need for prediction of epidemics and, in turn, a way to prevent and control the outbreak. There are two main forms of control for wheat pathogens including fungicides and resistant varieties. Management strategies for rust diseases also include the removal of alternative hosts by herbicides and tillage. Stagonospora nodorum blotch is primarily controlled by the use of SDHIs and DMIs fungicides. In the past Qols were used, but resistance has developed due to evolution of new races of the pathogen (Figueroa et al., 2018). Septoria is effectively controlled by most commercially available fungicides; resistance is rarely detected but when detected is for QoI class of fungicides. (Figueroa et al., 2018). For the control of tan spot, fungicides can be used with little resistance risks as the pathogen is relatively new. The fungicides that have been found to work the best are QoIs, which help increase wheat yield by up to 4.4 tons per acre (Figueroa et al., 2018). Fungicides are helpful but do have two notable drawbacks: fungicides can be expensive, and by the time some of the fungal diseases are visible, it is too late to control the pathogens well. The use of a disease prediction model could help in determining if there is a need for fungicide application and determine application timings.

Predictive models for fungal pathogens are hard to develop and there are challenges such as the level of complexity needed for the model, models tend to be site and year specific, and models that do not take the effects of storage, field management, or human behavior under consideration (Prandini et al., 2009). Another issue that models must consider is that each fungal pathogen has preferred temperatures and require different periods of water. There are many different prediction models for wheat diseases, the most common of which is the FHB risk index, but they are not always easily found or accessible for producers. There are also some phone applications available, such as Plantix, Agrio, Plant Vision AI, and Plant Doctor. These applications are often advertised as free, but most require some form of advanced membership to get access to results. These applications are also often geared towards horticultural plants and not many agricultural crops. Most applications are also only used for identification and not prediction.

South Dakota producers have ease of access to several tools as South Dakota State University does provide some disease prediction tools that are readily available. The SD Mesonet Small Grains Tool can be used by producers/crop consultants to get a risk assessment for tan spot, Septoria, and leaf rust in spring and winter wheat. This tool lets producers select the growth stage, type of wheat (winter or spring), and choose a research station located closest to them. This tool is free and easy to use, but it is still limited to location within the state and common fungal pathogens. South Dakota State University also provides producers links to the FHB prediction tool in many different publications and website pages. Unlike the SD Mesonet Small Grains Tool, the FHB tool is nationwide and created by Penn State, The Ohio State University, K-State, and Scab USA. This tool allows producers to get Fusarium Head Blight risk assessments with 0-, 2-, 4-, and 6-day risk forecast. This tool helps producers to determine whether to apply fungicides or not. This tool can greatly help producers, but once again limited to only one crop and one pathogen and does not always utilize local weather conditions.

1.3 Models for Diseases of Interest

A recent study in Stagonospora nodorum blotch prediction resulted in three different models. The most accurate model was a Random Forest (RF) model which used the three variables longitude, wheat residue, and cultivar resistance that had a sensitivity rate of 0.69 (Mehra et al., 2016). This model did not take into effect the weather patterns and water availability. In Indiana, a statistical model used days without precipitation between 26 March and 4 May along with total consecutive days when the minimum temperature was equal to or less than 7 °C between 4 April and 3 May. This model explained 86 percent of the variation in Stagonospora nodorum severity among years (Coakley et al., 1988). A stripe rust model known as WINDOW showed that 87 to 89 percent of variation in disease incidence could be explained using the following variables: mean minimum temperature, mean maximum temperature, total days average temperature less than 0 °C, total days maximum temp greater than 25 °C, total precipitation, precipitation frequency, total consecutive days with precipitation, and total consecutive days without precipitation (Coakley et al., 1988). The program used for WINDOW is now obsolete due to the age of the program and the fact that it was never publicly available due to cost.

More recent research on leaf and stripe rust prediction found that the variables dew point temperature (in °C), night temperature, and relative humidity were the most significant for leaf rust and stripe rust prediction (Rodriguez-Moreno et al., 2020). This model did not investigate stem rust and did not take into account the movement of rust spores into areas in which they do not overwinter. Stripe rust is becoming an increasingly important disease in the Northern Great Plains but does not overwinter in these states. Spores must travel via air currents from the southern regions of the United States to northern states such as South Dakota. Stem rust has been well controlled by resistant varieties for many years in the United, so it is also often excluded from these models. Unfortunately, stem rust resistance can break down and mutations can occur within the disease making stem rust still a risk that should be monitored.

Another model for the prediction of tan spot and Stagonospora nodorum blotch used the variables of leaf wetness duration in hours, precipitation in millimeters, accumulated growing degree days, relative humidity, and temperature. The previous variables, when combined, created the Backpropagation neural networks (BPNN) model that had a tan spot incidence accuracy of 84% with infection and 67% without. For Stagonospora, the BPNN model had a prediction accuracy of 86% in cases without infection and 61% percent in cases with infection (De Wolf & Francl, 2000).

1.4 Purpose of Project

Currently no one model can predict all six diseases of interest to this project (stem rust, leaf rust, stripe rust, tan spot, Stagnospora nodorum blotch, Septoria tritici blotch). One of the goals of the National Predictive Modeling Tool Initiative (NPMTI), which this project is associated with, is to develop and validate predictive models for all six previously mentioned wheat diseases, and to distribute these models to the public. To develop these models, there are crucial sets of data that must be collected from the wheat growing states. Through this project, states are tasked with identifying historical wheat disease reports and incidence, collecting real-time disease data over four to five growing seasons, and submitting that information to help build comprehensive wheat disease models.

1.5 South Dakota NPMTI Objectives:

The main objectives of this research project are to collect disease information in small plot research fields to determine how weather, cultivar, and residues affect disease development. Further, collect data and monitor for disease development in commercial wheat fields across South Dakota.

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Chapter 2. Examination of the Impact of Disease on Yield in Seven Winter Wheat Varieties

1. Introduction

Wheat breeding is focused on high yields, pathogen resistance, and tolerance to abiotic stress factors (Alemu, 2019). Disease resistance is often defined as the reduction of pathogen growth on or in the plant (Kumar & Un Nabi, 2015). There are two major types of disease resistance, qualitative and quantitative. Qualitative resistance, also called race specific resistance, is resistance based on specific major genes characterized by phenotype specificity, which makes it easier for new pathogen races to overcome resistance (Kumar & Un Nabi, 2015). Quantitative disease resistance refers to an incomplete or reduced level of resistance usually controlled by multiple quantitative trait loci, making it harder for resistance to break (Gou et al., 2023). As wheat is one of the most important food crops in the world, it is important to protect this vital crop from diseases and other threats. Diseases of wheat can reduce yields by a minimum of 20 percent on a global basis, increasing the importance of disease resistance (Cowger et al., 2022). Some of the most common wheat diseases that affect plants are caused by fungal pathogens, including leaf rust, stripe rust, stem rust, Stagonospora nodorum blotch, Septoria tritici blotch, and tan spot.

As wheat is widely grown and evaluated for disease resistance, there are different categories that evaluators, like plant breeders and plant pathologists, utilize such as seedling versus adult resistance and complete versus incomplete or intermediate resistance. Seedling resistance is often qualitative and race specific, making it easier for pathogens to overcome or “break” resistance than adult resistance which is often quantitative (Rutkoski et al., 2014). Complete resistance is resistance that does not allow growth of the pathogen resulting in no signs of the disease or presence of the pathogen. Incomplete/intermediate resistance is any resistance that is not complete so there is still some growth and development of the pathogen (Ribeiro Do Vale et al., 2001). Seedling resistance is typically race specific and adult resistance is typically effective against all races (Milus et al., 2015). Incorporation of both kinds of resistances can greatly help protect against diseases at various life stages.

Rust diseases of wheat are some of the most important and widespread plant pathogens in the wheat growing areas worldwide (Kahn et al., 2013). The three major wheat rust diseases across the world include leaf, stem, and stripe rust (*Puccinia triticina, Puccinia graminis* f. sp. *tritici*, and *Puccinia striiformis* respectively). Of the three, leaf rust is the most common and, under favorable conditions, can reduce wheat yields from 15 to 50 percent worldwide (Dinh et al., 2020). In wheat, there are 79 loci catalogued for leaf rust, *Lr1-Lr79*. The leaf rust loci such as *Lr1, Lr10,* and *Lr21* are good examples of race-specific resistance genes that are effective in seedling and adult plants (Kolmer, 2013). Stem rust resistance is categorized in seedling versus adult resistance. In the United States, some of the most common stem rust resistance genes are *Sr24, Sr36,* $Sr1R^{Amigo}$, and *Sr31* (Olson et al., 2010). More than 140 quantitative trait loci for stripe rust resistance have been identified within 47 different chromosomal regions (Garnica et al., 2013). The only chromosome with no stripe rust resistance found is 5D; others such as 2B have regions that contain one or more forms of resistance (Rosewarne et al., 2013). Chromosome 2B has a region containing the race-specific seedling resistance loci *Yr27* and *Yr31* (Rosewarne et al., 2013). Some of these are the same trait loci for resistance to leaf rust such as *Lr39* and *Yr18* (Suenaga et al., 2003). Some common genes for all stage resistance used throughout the world for stripe rust resistance include *Yr1, Yr6, Yr7, Yr9, Yr10, Yr17, Yr24/26*, and *Yr27* (Feng et al., 2018).

Pyrenophora tritici-repentis (tan spot) has three different host-selective toxins (effectors), Ptr ToxA, Ptr ToxB, and Ptr ToxC. Ptr ToxA is the main effector in tan spot (See et al., 2018) and responsible for the development of necrosis while Ptr ToxB and Ptr ToxC are responsible for the development of chlorosis (Chu et al., 2008). Tan spot is then broken down into 8 different races with different combinations of the three toxins. Race 1 produces Ptr ToxA and C, Race 2 produces only Ptr ToxA, Race 3 produces only Ptr ToxC, Race 4 produces no toxins, Race 5 produces only Ptr ToxB, Race 6 produces Ptr ToxB and C, Race 7 produces Ptr ToxA and B, and Race 8 produces all three toxins (Faris et al., 2013). There are lines of wheat with qualitative resistance to better control multiple toxins, and there are quantitative lines that are resistant to specific toxins.

Like tan spot, Stagonospora nodorum blotch (*Parastagonospora nodorum*) produces many toxins, all of which are necrotrophic. These toxins are SnToxA and SnTox1-7, with SnToxA being nearly identical to PtrToxA (Altameemi et al., 2021). Breeding resistant lines is hard due to quantitative trait loci with over twenty distinct different quantitative trait loci being identified on several different chromosomes of wheat (Katoch et al., 2021). Stacking of these known quantitative trait loci can be used to created qualitative resistance in wheat lines (Altameemi et al., 2021).

Septoria tritici blotch (*Zymoseptoria tritici*) causes similar symptoms to tan spot and Stagonospora nodorum blotch and is often confused with the two. These symptoms lead scientists to believe that Septoria tritici also has toxins similar to the other two leaf spot pathogens, but few candidate compounds have been found (Anderegg et al., 2022). Resistant cultivars are one of the main ways to manage Septoria with a total of 22 resistance genes and 89 quantitative trait loci being identified for resistance as of 2020 which are used for both quantitative and qualitative resistance (Riaz et al., 2020).

With many available winter wheat varieties, it is important to know which traits are needed for the environment they are to be planted in. Where the crop is being grown, disease history, and rotation need to be considered when choosing a variety. Choosing a winter wheat variety popular in Texas to plant in South Dakota would most likely not be in the best interest of the grower because of differences in soils, pests, growing season length, and disease prevalence. If a field has a known history of disease and cannot be rotated it would be best to plant a variety with resistance. Knowing what was previously grown in a field is helpful in determining what diseases could be present in plant residues and what nutrients may be lacking, which can help determine what variety would be best (Kumar & Un Nabi, 2015). A grower needs to consider as many performance factors as possible when choosing what to grow.

1.2 Objectives

To understand the severity of disease within the different plots, records of the amount of disease on each variety throughout the experiment to determine the differences between varieties will be taken on a weekly basis throughout the growing season This will be done to investigate if the reported tolerance and susceptibility of each variety held true in a wheat on wheat no till rotation. Measurements will also be taken to determine if the difference in disease and yield increased statistically significantly with a wheat on wheat rotation during the experiment.

2. Methodology

2.1 Selection of Varieties

Seven different varieties of winter wheat were selected based on different susceptibility and tolerance of the six pathogens chosen by the National Predictive Modeling Tool Initiative for monitoring. The varieties and disease susceptibility to each of the six diseases covered in this project can be seen in Table 1. All varieties were bred in South Dakota and are heavily utilized wheat varieties across the state in the present or in the past.

2.2 Field Site Selection

Small plot trials were planted directly into previous year's winter wheat residues at South Dakota State University's Volga research station at approximately 44.300046, -96.927202. Plots were planted 8 rows across and 16 feet in length. All residue from previous years was left on the field, simulating wheat-on-wheat rotation. The plantings were done in mid-to-late September of 2020 and 2021. No fungicides were applied during the experiment to encourage disease development. Herbicides were applied in the late spring of both years to control weeds such as foxtail and amaranth species.

2.3 Disease Ratings

2021: From Feekes 10.5 to Feekes 11.3, three visual disease assessments were performed. Six tillers in 6 randomly selected locations within each plot (total of 108 ratings per plot per disease) were visually rated for Stagonospora and Septoria leaf blotches, tan spot, and leaf, stripe, and stem rusts using a standard leaf area diagram (Figure 1). Spot diseases were rated as a complex due to the inability to tell them apart and simply referred to as ‘spot’. Flag leaf, flag leaf minus one, and flag leaf minus two were rated. As the season progressed, flag leaf minus one and two senesced and could no longer be accurately rated.

2022: Disease was assessed from Feekes 9 to Feekes 11.1 for a total of four rating time points. Stand counts were extremely low, due to drought, so 6 tillers in 3 randomly selected locations within the plot were rated. Differences in amounts of disease ratings were due to the grad student not being recruited until a later date in 2021.

2.4 Plot Harvest

2021: Harvest was done the first week of July using a 1987 Wintersteiger combine. Each plot was individually bagged and manually cleaned, weighed, and measured for test weight and moisture.

2022: Harvest was done the second week of July using a Zurn small plot combine. Each plot was individually bagged and measured by the combine and manually for weight, test weight, and moisture. The bags did not have to be manually cleaned due to the improved screens on the Zurn.

2.5 Statistics

All statistics were done using Systat’s SigmaPlot Inpixion version 15.0 (Inpixon - systatsoftware.com, 2023). One-way ANOVAs were done comparing each variety at all three leaves (F, F-1, F-2) separately for both years. One-way ANOVAs were also done comparing each variety’s yield to one another, as well as comparing the two years disease severities for each variety separately. All pairwise multiple comparison procedures were done using the Holm-Sidak method with a power of preformed test alpha of 0.050. SigmaPlot was also used to create all graphs and to determine all descriptive statistics. The growth stages used for comparison were Heading (Feekes 10.5) and Milk (Feekes 11) because they were sampled in both years.

3. Results

3.1 2021 Disease Ratings

During the 2021 growing season leaf spot complex, leaf rust, and stripe rust were observed. The mean spot disease complex disease severity can be seen in Tables 2 and 3 for heading and milk stage in 2021 and it varied between varieties. There were differences between spot disease percentages in different varieties and on different leaves which can be seen in Figure 2A and 2B. Spot severity at heading was greatest in the varieties ‘Draper’ and ‘Redfield’ with p-values <0.001 on flag leaf (Table 2); with ‘Draper’ having a greater amount of spot disease than ‘Redfield’. For flag leaf minus one at heading, ‘Redfield’ and ‘Draper’ were significantly greater than ‘Ideal’ and ‘Oahe’ in amounts of spot observed (p-value <0.05). ‘Wesley’ was significantly greater than ‘Ideal’ (p-value 0.019) (Table 2). Flag leaf minus two at heading had the greatest amount of spot disease on the variety ‘Redfield’ (p-value <0.001) and there were no significant differences between the six other varieties (Table 2). To summarize ‘Draper’ had the highest amount of disease severity over all other varieties. ‘Redfield’ was greater than all but ‘Draper’, and ‘Wesley’ was only significantly higher than ‘Ideal’.

At milk stage in 2021, ‘Wesley’ had a significantly greater amount of spot disease on the flag leaf than all other varieties (p-values of <0.001 except for ‘Draper’ which had a p-value of 0.004 and ‘Redfield’ which had a p-value of 0.008 when compared to ‘Wesley’) (Table 3 and Figure 2B). Spot disease on flag minus one during milk was greatest in ‘Redfield’ with a p-value of 0.003. The second greatest amount of leaf spot disease at this timepoint was in ‘Draper’ with statistically significant (p-value 0.008). The variety ‘Wesley’ was statistically significantly higher than that of ‘Ideal with a p-value 0.019 (Table 3). In flag leaf minus two observations, ‘Redfield’ had the greatest statistically significant amount of spot disease with a p-value <0.001 over all varieties except in comparison with ‘Expedition’ which had a p-value 0.002 (Table 3).

There was a statistical difference between varieties and leaves in the amount of stripe rust at heading (p-value of <0.001), which can be seen in Figure 3A and Table 4. Stripe rust was significantly greater in the variety 'Expedition’ (p-value of <0.001) than the six other varieties (Table 4 and Figure 3A). Stripe rust on flag leaf at milk stage was significantly greater in ‘Expedition’ than all other varieties, with a p-value of <0.001 ‘Ideal’ being ranked second in severity with p-values ranging from 0.0015 to 0.038 (Table 5 and Figure 3B). There was some leaf rust on the leaves as well at milk stage, but there were no significant differences between varieties (Table 5).

3.2 2022 Disease Ratings

In 2022, only the leaf spot disease complex was observed in significant amounts, which can be seen in Table 6 and Figure 4A and 4B. A few instances of stripe rust were observed, but not enough to perform statistical analysis or for the pathogen to have any effect on the plants. The spot disease complex at heading (Feekes 10.5) was significantly greater in the variety ‘Expedition’ over varieties ‘Draper’ (p-value 0.002) and ‘Ideal’ (p-value-0.032). ‘Redfield’ and ‘Thompson’ also had significantly greater amounts of disease on flag leaf than ‘Draper’ (p-values 0.009 and 0.023 respectively) (Table 6). ‘Expedition’ was also significantly greater (p-value 0.014) than ‘Draper’ on flag leaf minus one but there were no other significant differences between varieties (Table 6 and Figure 4A). There was no difference between varieties on flag leaf minus two with a p-value of 0.116.

At milk stage (Feekes 11.2) on flag leaf, ‘Ideal’, ‘Thompson’, ‘Expedition’, and ‘Oahe’ had significantly greater amounts (p-values <0.001, 0.002, 0.008, and 0.017 respectively) of spot than ‘Draper’. ‘Thompson’ and ‘Oahe’ also had significantly greater amounts (p-values 0.017 and 0.049 respectively) of spot than ‘Ideal’ (Table 6 and Figure 4B). On flag leaf minus one the only significant difference was ‘Wesley’ and ‘Draper’ (p-value-0.040) (Table 6). Once more, there was not a significant difference between varieties on flag leaf minus two ratings with a p-value of 0.223.

A comparison of varieties to each other per growth stage per year was completed. The overall results were that there were many variables that create high amounts of significant data. ‘Draper’ continuously has more significant differences from other varieties in both years. ‘Wesley’ and ‘Ideal’ were also different from the other varieties at certain timepoints (Table 7).

3.3 Difference in Yield

There were no significant differences between varieties and years at an alpha of 0.05 (Figure 5).

4. Discussion

The objective of this study was to examine disease presence in South Dakota on seven varieties of winter wheat developed and commonly grown in the state in an effort to establish a baseline of disease severity for more advanced residue and variety trials. All varieties chosen were developed by South Dakota State University breeders and used within variety trials for height, lodging, and yield amounts within the last five years. The resistance and tolerance of each variety to the diseases surveyed can be seen in Table 1.

Neither 2021 nor 2022 were ideal for fungal pathogen development with low amounts of precipitation and high temperatures. From planting to harvest for the 2021 winter wheat, there was only about 260 millimeters of precipitation in total and for the 2022 winter wheat from planting to harvest there was approximately 423 millimeters of precipitation with the average amount in South Dakota per year during this time period typically around 456 millimeters (U.S. Climate, 2023). All fungal pathogens require an extended period of leaf wetness to grow and infect plants. They also have preferred temperatures for growth and development.

Leaf rust, which was rarely observed in this study, requires free water on the host and prefers temperatures ranging from 10-25 °C (Bolton et al., 2008). Stripe rust, which was seen in significant amounts on the susceptible variety 'Expedition', can grow in temperatures ranging from 2.8 to 21.7 °C but has been found to grow best at about 9.7 °C (Signh et al., 2017). Stripe rust is more similar to leaf rust with the optimal temperature for spore germination being 22 °C (Roelfs & Bushnell, 1985). The average temperature for the Volga Research Station in June of 2021 was 23 °C and the total precipitation for the month of June was 18.22 millimeters. June was the month where most surveys were done and during that time conditions were not favorable for the development of the three rust diseases. ‘Expedition’ did have significantly more stripe rust than all other varieties, but it still had less than 5 percent leaf cover on average at milk stage as seen in Figure 4A. This likely did not result in any significant decrease in overall plant health and yield being there were no significant differences between varieties and yields (Figure 5). In 2022, there was no development of any of the rust pathogens. The average temperature for the month of June was 22 °C and total precipitation was 42.69 millimeters. This should have been more favorable to rust pathogen development than 2021, but Nebraska, Kansas, Oklahoma, and Texas were abnormally dry or in drought conditions according to the U.S. Drought Monitor (Fuchs, 2023). The development of rust pathogens is also dependent on the movement of inoculum from the southern Great Plains to the Northern Great Plains.

Like the rust pathogens, the spot pathogens also have preferred temperatures and periods of wetness. Tan spot prefers temperatures of about 20 °C and needs 6 to 24 hours of free moisture to develop (Wegulo, 2011). Stagonospora nodorum blotch prefers temperatures ranging from 20 to 28 °C with extended periods of free moisture as well (Frieje & Wise, 2015). Septoria tritici prefers cooler temperatures ranging from 15 to 20 °C with frequent rain followed by 48 hours of leaf wetness or high humidity (Hollaway et al., 2022). Neither year was favorable for the development of Septoria tritici blotch.

At the time of rating, all spot disease symptoms were rated as a complex referred to as spot disease, because it is extremely hard to differentiate between the three pathogens in a field setting, but previous recordings at the Volga Research Station were of tan spot. Because tan spot had been previously recorded, we suspected it to be the most common spot disease present. With further analysis of inoculum within the residue, greater amounts of Stagonospora nodorum blotch were found than tan spot, and Septoria leaf blotch. Stagonospora often occurs in tandem with tan spot and Septoria leaf blotch and when this occurs, it can be difficult to determine which disease is present visually (Downie et al., 2021). Stagonospora nodorum blotch being present may explain some of the results that showed high amounts of spot disease. 'Draper' having the greatest amount of spot on the flag leaf at heading in 2021 was not expected as the variety has some tolerance to tan spot, but Stagonospora nodorum blotch being present along with tan spot the results would make more sense. 'Draper' has not been rated for Stagonospora nodorum blotch, so its level of tolerance or susceptibility is unknown. 'Draper' was also different from the other varieties with all three leaves rated having no significant difference in severity between them at heading. In all other varieties, there was at least a significant difference between flag leaf and flag leaf minus one at heading. 'Redfield' serves as a susceptible check in tan spot while being tolerant or unrated for the other two spot pathogens, so it was not unexpected for it to be higher at heading and milk stage if tan spot was what was present. 'Redfield' is tolerant to Stagonospora nodorum blotch, so the results further raise the question on what was affecting 'Draper'. 'Expedition' is susceptible or not rated for all diseases surveyed, except stem rust which was not seen in any variety both years, therefore it having the highest disease ratings for stripe rust at both observation points was not unexpected. 'Expedition' also had the third highest amount of spot symptoms, but as it was susceptible to both tan spot and Stagonospora nodorum blotch, the variety does not help to determine which of the two was present or most severe.

‘Draper’ being significantly lower in the amount of spot compared to other varieties in 2022 makes more sense than 2021. As previously mentioned, ‘Draper’ is tolerant to tan spot while ‘Ideal’, ‘Redfield’, ‘Thompson’, and ‘Expedition’ are susceptible (Table 1). The only variety that was not significantly higher in amounts of spot in comparison to ‘Draper’ was ‘Wesley’ which is also tolerant to tan spot (Table 1). ‘Thompson’ had the greatest amount of spot (p-value <0.001) at milk stage but is not rated for its susceptibility or tolerance for Stagonospora nodorum blotch, meaning this disease could be present as well tan spot. ‘Oahe’ was the second highest spot rating (p-value 0.0002), but unlike ‘Thompson’ is tolerant to tan spot. ‘Oahe’ has no rating for Stagonospora nodorum blotch, meaning that it could have been the pathogen causing necrotic lesions on the leaves. ‘Expedition’ was the next highest in disease ratings at milk stage in 2022, but as previously stated is susceptible to both tan spot and Stagonospora nodorum blotch. The next highest was ‘Redfield’ with a p-value 0.017 in comparison to other varieties at milk stage in 2022 which is tolerant to Stagonospora nodorum blotch and susceptible to tan spot. The results for 2022 are more in favor of tan spot than 2021. The varieties with the most disease development were all susceptible to tan spot. The one variety that raises questions in 2022 is ‘Ideal’. ‘Ideal’ is susceptible to both tan spot and Stagonospora nodorum blotch but did not have any significantly higher amounts of spot disease than all other varieties. ‘Thompson’ and ‘Oahe’ had significantly higher amounts of spot severity than ‘Ideal’ with p-values of 0.017amd 0.049 respectively. However, it is possible that Stagonospora nodorum blotch was the main disease present. ‘Thompson’ and ‘Oahe’ have not been evaluated for resistance Stagonsopora nodorum blotch and may be more susceptible than ‘Ideal’.

When comparing all varieties to each other, the were many factors that affected our ability to decipher the results. There were high amounts of significant relationships suggesting that there are too many variables to truly draw conclusions. It can be seen in Table 7 that in 2021 heading ‘Draper’ and 2021 milk ‘Wesley’ were significantly different from the other varieties. In 2022 at heading ‘Draper’ and ‘Ideal’ were different from other varieties. Interestingly, there were no significant interactions in 2022 milk stage suggesting that drought and spot disease were affecting all varieties equally. It can be hypothesized that ‘Draper’ is more resistant to tan spot, which develops early in the season, and may demonstrate some tolerance to the other spot diseases that develop later in the season, causing it to be different from other varieties.

The results were not as expected and beg the question of whether tan spot or Stagonospora nodorum blotch is the most commonly present disease in the small plots. Tan spot was what was previously believed to be the most common present, but the presence of Stagonospora nodorum blotch inoculum and ‘Draper’, a tan spot tolerant variety, having a significantly higher amount of spot pathogen development, could mean that tan spot is not the most common residue borne pathogen at the research station.

5. Conclusion

Very little amounts of diseases were observed both years in South Dakota, most likely due to unfavorable weather conditions. Spot diseases are also extremely hard to tell apart from one another so while all spot lesions were rated as a complex, they were suspected to be tan spot but some may have been Stagonospora nodorum blotch or Septoria tritici blotch. To better understand the differences between varieties and results, the study needs to continue and improve. To truly understand what is happening the identification of what spot pathogens are present through molecular methods needs to happen. A tolerance or susceptibility rating also needs to be established for both Stagonospora nodorum blotch and Septoria tritici blotch in all varieties to help narrow down what is happening in the field. This will take multiple different experiments over multiple years.

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7. Tables and Figures

Table 1: The susceptibility of the seven varieties utilized in this study to the six different pathogens of interest to this research project.

Variety	***Parastagonospora nodorum***	***Zymoseptoria tritici***	***Pyrenophora tritici-repentis***	***Puccinia triticina***	***Puccinia striiformis***	***Puccinia graminis***
Draper	No Rating	No Rating	Tolerant	Tolerant	Susceptible	Susceptible
Ideal	Susceptible	No Rating	Susceptible	Tolerant	Tolerant	Susceptible
Redfield	Tolerant	No Rating	Susceptible	Susceptible	Tolerant	Tolerant
Thompson	No Rating	No Rating	Susceptible	Tolerant	Tolerant	Tolerant
Expedition	Susceptible	No Rating	Susceptible	Susceptible	Susceptible	Tolerant
Wesley	No Rating	No Rating	Tolerant	Susceptible	Susceptible	Tolerant
Oahe	No Rating	No Rating	Tolerant	Tolerant	Tolerant	Tolerant

Table 2: The mean percentage of disease covering F, F-1, and F-2 during heading stage in 2021. Superscripts indicate significance between groups[1].

Variety	**Spot F**	**Spot F-1**	**Spot F-2**
Draper	0.416^{abcdei}	0.411^{mp}	0.429^{t}
Ideal	0.0153^{af}	0.0417^{lmo}	0.247^{r}
Redfield	0.229^{fghijk}	0.439^{ln}	1.878^{qrstuv}
Thompson	0.0174^{bg}	0.226	0.270^{s}
Expedition	0.0688^{ek}	0.263	0.921^{v}
Wesley	0.0521^{dhj}	0.382^{o}	0.489^{u}
Oahe	0.0340^{c}	0.0584^{np}	0.202^{q}

[1] P-values are as follows: a) <0.001, b) <0.001, c) <0.001, d) <0.001, e) <0.001, f) <0.001, g) <0.001, h) <0.001, i) <0.001, j) <0.001, k) 0.001, l) 0.003, m) 0.008, n) 0.013, o) 0.019, p) 0.029, q) <0.001, r) <0.001, s) <0.001, t) <0.001, u) <0.001, v) 0.002.

Table 3: The mean percentage of disease covering F and F-1 at milk stage in 2021. Superscripts indicate significance.[2]

Variety	**Spot F**	**Spot F-1**
Draper	0.538^{e}	1.101^{io}
Ideal	0.0965^{a}	0.640^{hn}
Redfield	0.581^{f}	5.894^{lmnopq}
Thompson	0.162^{c}	1.182^{jp}
Expedition	0.469^{d}	2.235^{kq}
Wesley	1.295^{abcdef}	12.654^{ghijkl}
Oahe	0.104^{b}	0.580^{gm}

[2] a) <0.001, b) <0.001, c) <0.001, d) <0.001, e) 0.004, f) 0.008, g) <0.001, h) <0.001, i) <0.001, j) <0.001, k) <0.001, l) <0.001, m) <0.001, n) <0.001, o) <0.001, p) <0.001, q) 0.006.

Table 4: Mean percentage of rust disease covering F, F-1, and F-2 at heading stage in 2021. Superscripts indicate significance.[3]

Variety	Stripe Rust F	Stripe Rust F-1	Stripe Rust F-2
Draper	0.0410^{d}	0.115	0.0489
Ideal	0.0757^{f}	0.553	0.321
Redfield	0.00486^{b}	0.0556	0.0182
Thompson	0.0361^{c}	0.174	0.213
Expedition	0.223^{abcdef}	0.164	0.171
Wesley	0.191^{e}	0.119	0.276
Oahe	0.00417^{a}	0.0660	0.0331

[3] P-values are as follows: a) <0.001, b) <0.001, c) <0.001, d) <0.001, e) 0.002, f) 0.010.

Table 5. Milk stage 2021 rust disease. Superscripts indicate significance.[4]

Variety	Leaf Rust F	Stripe Rust F	Leaf Rust F-1	Stripe Rust F-1
Draper	0.0146	0.0403^{ag}	0.000	0.117
Ideal	0.00625	1.447^{fghij}	0.0152	0.568
Redfield	0.00278	0.0667^{ci}	0.000	0.0240
Thompson	0.00486	0.189^{dj}	0.000	1.619
Expedition	0.00486	3.170^{abcdef}	0.0103	2.908
Wesley	0.00417	0.294^{e}	0.000806	0.515
Oahe	0.00486	0.0562^{bh}	0.00316	0.274

[4] a) <0.001, b) <0.001, c) <0.001, d) <0.001, e) <0.001, f) <0.001, g) 0.015, h) 0.016, i) 0.016, j) 0.038.

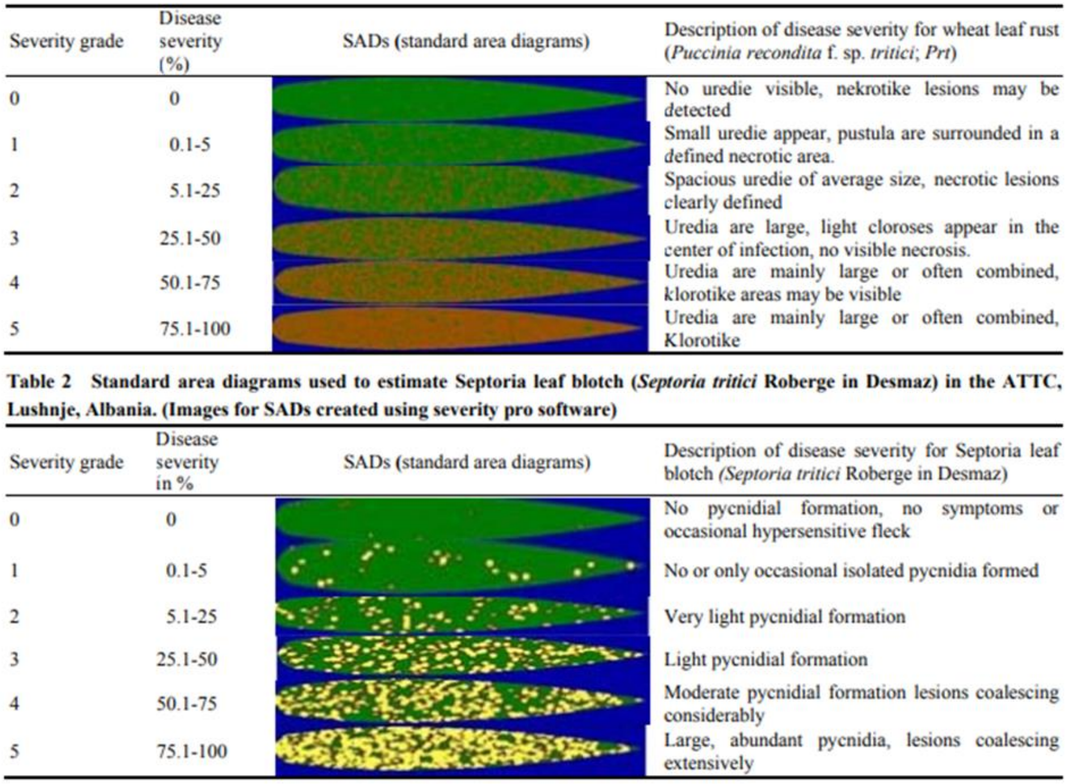
Table 6: The mean percentage of spot per leaf and variety at heading and milk in 2022. Superscripts indicate that significance occurred between groups.[5]

Variety	Draper	Ideal	Redfield	Thompson	Expedition	Wesley	Oahe
F heading	0.416^{abc}	0.0153^{d}	0.229^{c}	0.0174^{b}	0.0688^{ad}	0.0521	0.0340
F-1 heading	0.411^{e}	0.0417	0.439	0.226	0.263^{e}	0.382	0.0854
F-2 heading	0.429	0.247	1.878	0.270	0.921	0.489	0.202
F milk	3.869^{fghi}	5.149^{jk}	8.507^{i}	9.751^{fj}	8.833^{h}	7.250^{gk}	9.282
F-1 milk	23.639^{l}	29.554	31.954	35.018	35.492	39.136^{l}	36.094
F-2 milk	50.222	44.903	46.905	33.115	51.429	45.000	54.760

[5] The p-values are as follows: a) 0.002, b) 0.009, c) 0.023, d) 0.032, e) 0.014, f) <0.001, g) 0.002, h) 0.008, i) 0.017, j) 0.017, k) 0.049, l) 0.040.

Table 7: The overall mean percentage of disease at heading and milk in 2021 and 2022. Superscripts indicate significance between groups, all p-values are ≤0.005.

Variety	Heading 2021	Milk 2021	Heading 2022	Milk 2022
Draper	0.67^{abcde}	0.738 ^{out}	2.679$^{wyz!\#}$	19.229
Ideal	0.101^{afi}	0.378 ^{kptv}	3.087$^{xz@\$}$	21.927
Redfield	0.763^{fgh}	2.798 ^{pqrs}	4.657$^{!@}$	23.309
Thompson	0.171^{ch}	0.607 ^{mr}	5.938^{wx}	22.884
Expedition	0.391^{eij}	1.202 ^{nsv}	5.457^{y}	24.107
Wesley	0.297^{d}	6.526 ^{klmno}	4.021	22.5889
Oahe	0.111^{bgj}	0.293 ^{lqu}	4.53$^{\#\$}$	27.002



Severity grade	Disease severity (%)	SADs (standard area diagrams)	Description of disease severity for wheat leaf rust (*Puccinia recondita* f. sp. *tritici*; *Prt*)
0	0		No uredie visible, nekrotike lesions may be detected
1	0.1-5		Small uredie appear, pustula are surrounded in a defined necrotic area.
2	5.1-25		Spacious uredie of average size, necrotic lesions clearly defined
3	25.1-50		Uredia are large, light cloroses appear in the center of infection, no visible necrosis.
4	50.1-75		Uredia are mainly large or often combined, klorotike areas may be visible
5	75.1-100		Uredia are mainly large or often combined, Klorotike

Table 2 Standard area diagrams used to estimate Septoria leaf blotch (*Septoria tritici* Roberge in Desmaz) in the ATTC, Lushnje, Albania. (Images for SADs created using severity pro software)

Severity grade	Disease severity in %	SADs (standard area diagrams)	Description of disease severity for Septoria leaf blotch *(Septoria tritici* Roberge in Desmaz)
0	0		No pycnidial formation, no symptoms or occasional hypersensitive fleck
1	0.1-5		No or only occasional isolated pycnidia formed
2	5.1-25		Very light pycnidial formation
3	25.1-50		Light pycnidial formation
4	50.1-75		Moderate pycnidial formation lesions coalescing considerably
5	75.1-100		Large, abundant pycnidia, lesions coalescing extensively

Figure 1: Standard leaf area diagrams used to accurately estimate the percentage of leaf covered by disease. (Hakuran, et al., 2012)

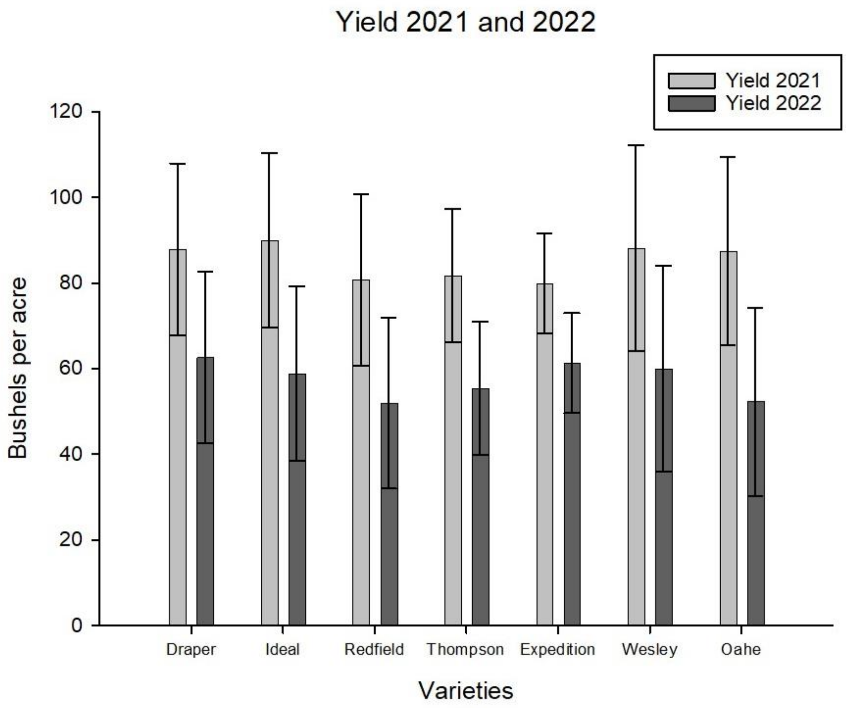


Figure 2. Yield data for both 2021 and 2022. There are no significant differences between variety or year at an alpha of 0.05.

Chapter 3: The Influence of Residue Amount on Disease Severity and Yield

1. Introduction

In recent years no-till farming has become the main cropping system for the state of South Dakota with about 50% of crops being under no-tillage (Tonneson, 2020). No-tillage is a farming practice that leaves previous residues on the soil surface and does not bury them like conventional tillage. The retention of soil residues has several benefits related to improving soil health including to help increase soil microorganisms, decrease greenhouse gas release, and improve water infiltration (Bly et al., 2019). These are all favorable to farmers and growers. Areas of South Dakota can be dry and windy, which can result in the loss of topsoil. However, there are also negative impacts with the increase in no-till cropping.

No-till and minimal tillage practices can increase the risk of disease epidemics as many pathogens can survive on residues of host plants during the winter and other periods between host crops and other rotational crops (Kerdraon et al., 2019). Previous studies have looked at the presence of disease inoculum in soybean and corn residues to determine how long they can survive as the residues decompose to help advise growers on how to rotate crops in order to avoid disease development (Melo Reis et al., 2011). Another study looked into how anthracnose leaf blight was influenced by residue in corn (Lipps, 1988). Most crop pathogens that can overwinter and survive within the residues are fungal pathogens who spend a large portion of their life cycle within the residues (Kerdraon et al., 2019). In South Dakota three fungal wheat spot pathogens, *Pyrenophora tritici-repentis,* the causal agent of tan spot; *Parastagonospora nodorum*, the causal agent of stagonospora nodorum blotch; and *Zymoseptoria tritici,* the causal agent of septoria leaf blotch can all overwinter in crop residues.

Tan spot is an economically important disease because in severe cases it can decrease yields from 20% to all 70% (Cotuna et al., 2015). Tan spot reproduces both sexually and asexually. The sexual sore are ascospores and the asexual spores are conidiophores. Ascospores survive within the residue as pseudothecia, which develop on wheat straw in the fall to survive the winter. Once spring occurs, the ascospores are released by the psuedothecia and infect the host. Once the host is infected, conidia can be produced in mature lesions, serving as another form of inoculum. Conidia can also be produced in residues and can serve as the primary inoculum because they are small, produce more, and disperse easier than ascospores (Wegulo, 2011). The ability of this pathogen to survive and reproduce in residues makes the risk of disease epidemics higher in no-till and minimal till systems.

Septoria leaf blotch is another economically important wheat spot disease that survives on residues. Septoria leaf blotch can result in yields reductions of 20% to 50% in susceptible wheat cultivars (Danon et al., 1982). The life cycle of Septoria is much the same as tan spot with infection starting with infection of the host by ascospores spread by wind and conidia on residues by rain-splash. Like tan spot, the initial form of inoculum is often ascospores but can be conidiophores that overwintered as psuedothecia or pycnidia within crop residues. Septoria reproduces and grows rapidly once infection occurs and many cycles of sexual and asexual reproduction can occur in a growing season (Ponomarenko et al., 2011). Once again, the pathogen's ability to survive and reproduce on plant residue increases the risk of epidemics in no-till and minimal till systems.

Stagonospora nodorum also known as Parastagonospora nodorum, Septoria nodorum, and Septoria nodorum blotch, is also an economically important residue borne pathogen in South Dakota. Infection can cause yields losses of 30% or greater and often can occur in combination with tan spot and Septoria leaf blotch (Downi et al., 2021). The pathogen can overwinter in crop residues in the forms of pseudothecia and pycnidia with ascospores from the psuedothecia often serving as primary inoculum; pycniospores from pycnidia can serve as primary inoculum. Infection continues to spread by rain splashed conidia on the lower portions of the plant to higher portions (Mehra et al., 2019). The increase in plant residues on the field due to no-tillage and minimum tillage once again increases the risk of an epidemic.

Many studies have been done comparing the difference in disease severity between conventional tillage, minimal tillage, and no-tillage, but the majority of them did not quantify how much of the surface of the field was covered in plant residue. (Cotuna et al., 2015) quantified minimal tillage as 30% residue left above the soil (Cotuna et al., 2015), moldboard plowing as was considered to be 8%, disking as 25%, minimal tillage as 80%, and no-tillage as 90% in by Bauder, Halsey, and Jokela in 1979 (Bauder et al., 1979). There is no one agreed upon residue amount for each type of tillage. In this experiment we explored what effects different percentages of residue cover on crops had for the wheat spot pathogens using four different residue ground cover amounts to encompass more types of minimal and no-till practices.

1.2 Objectives

The goals of this experiment were to determine if there is a significant difference in disease severity between the four levels or residue treatments, and to determine whether there is a significant effect on yield under different residue treatments.

1.3 Hypotheses

We hypothesize that as residue amounts increase so will the disease symptoms because of increased spore loads. We also hypothesize that the residue treatments will have no significant effect on yield because of the adverse effects of increased disease symptoms that will be most likely negated by the increase in moisture retention.

2. Methodology

2.1 Field Site Preparation

2021: Seven varieties of hard red winter wheat were planted into the residue of spring wheat field at the Volga Research Station in the fall of 2020, at the approximate coordinates, 44°18'04.6"N 96°55'27.7"W. Those seven varieties were ‘Draper’, ‘Redfield’, ‘Ideal’, ‘Oahe’, ‘Expedition’, ‘Wesley’, and ‘Thompson’. 2022: The seven varieties from 2021 were planted into the residue of a soybean field at the Volga research station in the fall 2021, at the approximate coordinates, 44°18'07.3"N 96°55'38.9"W. Four replications of the seven varieties were planted each year, as four different residue ground covers were applied. The replicated blocks were separated by a border of the wheat variety ‘Expedition’, which was chosen due to its lack of resistance to tan spot and Septoria nodorum blotch and served as the positive control indicator of wheat disease (Table 1).

2.2 Residue Applications

Residue was collected in the summer after harvest (early to mid-July) in both 2021 and 2022. Wheat straw from fields that were previously infected with diseases of interest was collected and stored in bags in a non-temperature-controlled shop. In 2021, the ground cover in the 20% block removed by raking up excess stubble (due to residue being above desired 20%) while additional residue was added to the 40%, 60%, and 80% blocks. Additions of residue were done in the spring at about Feekes 6.0. In 2022, residue was added to each of the four research blocks. Additions of residue were done in the spring at about Feekes 6.0 to prevent excessive loss of residues due to wind during the fall and winter.

2.3 Disease Ratings

2021: Visual disease assessments were done from Feekes 10 to Feekes 11.3; 2022: Ratings of visual disease levels began at Feekes 9.0 and ended at Feekes 11.1 (Stages flag leaf emergence through milk stage). In both years, six tillers in six randomly selected locations in each plot were visually rated for spot diseases. Due to the inability to easily differentiate Stagonospora nodorum blotch, Septoria leaf blotch, and tan spot, all diseases were rated as a spot complex. Ratings at each time point included flag leaf, flag leaf minus one, and flag leaf minus two. As the season progressed, flag leaf minus one and minus two senesced and could no longer be accurately rated.

2.4 Residue Collection

In both years, residue was collected to determine what overwintering pathogens were present. During ratings, residue was collected by walking in a W pattern within each block. Residues were collected two to three times each season: first rating timepoint, mid-season, final rating timepoint. The residues were dried, ground, and placed in a 50 ml falcon tube until analysis. In 2021, residue samples were stored at room temperature until being sent for analysis, while in 2022, samples were stored at -20℃ until sent for analysis. Quantitative PCR (q-PCR) was performed on each sample utilizing primers specific for each of the three wheat spot pathogens by the National Agricultural Genotyping Center in Fargo, North Dakota.

2.5 Data Collection

Harvest and field data collection in 2021 and 2022 were performed utilizing the methodology outlined in Chapter two of this thesis. Briefly, plots were harvested in July and yield data was collected for each variety in each of the four residue blocks.

2.6 Statistical Analysis

All statistics were done using Systat's SigmaPlot Inpixion version 15.0 (Inpixon - systatsoftware.com, 2023). Two-way anovas were done on each variety comparing growth stages and residues to spot severity for both years separately. Data from 2021 and 2022 were not compared to one another due to differences in weather conditions. All pairwise multiple comparison procedures were done using the Holm-Sidak method with a power of preformed test alpha of 0.050. SigmaPlot was also used to create all graphs and to determine all descriptive statistics. Tables were made using Microsoft Excel and Word.

3. Results

3.1 2021 Residue Analysis

The seven varieties utilized in this study generally showed an exponential increase in spot disease from the first observation at Feekes 10.5 to the final observation at Feekes 11.3 (Figure 1). This was shown in visual observations (Table 2), as well as through qPCR testing results (Table 3). Another general trend that was observed throughout the 2021 season was that the 60% residue level had the most spot disease severity in visual observations. This was observed at Feekes 10.5 in ‘Expedition’ and ‘Wesley’; Feekes 11.2 in varieties ‘Redfield’, ‘Expedition’, and ‘Wesley’; and Feekes 11.3 in varieties ‘Thompson’, ‘Expedition’, ‘Wesley’, and ‘Oahe’ (Table 2). Figure 2 demonstrates the results of comparing all varieties at the 60% disease level for this study. The p-value was adjusted to 0.005 to account for the high amounts of variation in the large data set. It can be seen that several varieties were statistically significantly different early in the growing season. When comparing the diagnostic testing results also reflect that 60% residues had generally high titer of pathogens (Table 3). When comparing the residue levels to each other across the varieties, the most statistical differences were observed between the high levels (60% and 80%) and the low levels (20% and 40%). This statistical difference was observed at Feekes 11.2 in varieties ‘Draper’, ‘Ideal’, and ‘Redfield’ and Feekes 11.3 for ‘Draper’, ‘Ideal’, and ‘Thompson’ (Table 2).

3.2 2022 Residue Analysis

The results for this study in 2022 are similar to those in 2021, though with an overall lowered disease severity, which can be observed from visual analysis and diagnostic testing results. In general, there were significant differences in the lower residue amounts (20% and 40%) and higher residue amounts (60% and 80%) at growth stages Feekes 10.5 and Feekes 11.1 for all varieties (Table 4). Figure 4 shows the relationship between all varieties at the 60% residue level. This level was picked as it showed the most disease development. It can be seen that ‘Wesley’ is significantly different with lowered disease levels for the first three growth stages in 2022 but had the same amount of disease development as all other varieties by Feekes 11.1.

3.3 Yield Data

No conclusions or significant findings could be made with yield data in 2021 or 2022. Residue did not appear to influence yield (Figure 5). However, in 2021, it was observed that in the varieties ‘Redfield’ and ‘Oahe’ that the 40% residue treatment may have affected yield and that in the variety ‘Thompson’, yields from the 60% and 80% residues were higher when compared to 20% and 40% residues (Figure 5A). When comparing the effects of residues on plot yield in 2022, it was observed that in ‘Draper’ and ‘Thompson’, the yields of the upper-level residues were higher than those in the lower-level residues. In ‘Redfield’, the yield in the 80% was lower than the other three residue percentages. ‘Expedition’ had yields that were higher in the 80% residue block when compared to all other percentages. The yield for 20% residue was higher than all other percentages in the varieties ‘Ideal’ and ‘Wesley’ (Figure 5B).

4. Discussion

The purpose of this study was to quantify the effect of crop residue ground cover on disease development as well as yield. As many wheat growing regions look to embrace no-till or minimal tillage practices to enhance soil health, the drawbacks of the residues left on the soil in respect to disease are not well understood. It is known that many of the common wheat diseases such as tan spot, Stagonospora nodorum blotch, and Septoria leaf blotch are able to overwinter as fungal spores on wheat residues. What remains unknown and is the focus of this study is if the percentage of residue that remains each year will increase disease pressure for the following growing season. It is believed the higher residue amounts will lead to higher disease pressure as there are more fungal inoculum remaining each year to begin the infection cycle again.

The effect of residue percentage on disease development was explored in the summers of 2021 and 2022 in Volga, South Dakota. Overall, it was found that 60% residues frequently had higher disease severity when compared to the other percentages (Figures 2 and 4). This was observed in both 2021 and 2022, though more often in 2021, likely due to higher moisture observed early in the growing season that year. ‘Wesley’, ‘Expedition’, and ‘Ideal’ were significantly different from all others in the first part of the season in 2021, suggesting that these varieties were more susceptible to the combined effects of residue and disease (Figure 2). In 2022, there were less differences, but ‘Wesley’ was still significantly different from all other varieties at all growth stages except Feekes 11.1 (Figure 4). Residue levels of 80% also resulted in higher disease levels as the season progressed, which was the expected result. There was little difference between disease severity at the 20% and 40% residue amounts. Throughout the season, differences between the lower level (20% and 40%) and higher level (60% and 80%) were observed (Figures 1 and 3). More differences were observed in the earlier parts of the growing season both years, but as time progressed the differences between varieties decreased.

Disease symptoms being greater in 60% than 80% residue treatments during the 2021 growing season was unexpected as it was suspected that the highest level of residue would correlate with the highest disease levels. Bockus and Claassen (1992) performed a similar experiment in the late eighties researching tan spot severity in winter wheat under three different tillage practices: moldboard plow, chisel plow, and no-tillage. They found that no tillage under wheat-on-wheat rotation always had a statistically significant higher amount of tan spot then the other two tillage treatments (Bockus & Claassen, 1992).

An experiment done by Mehra et al. (2015) in the early 2010's looked at residue effects on the development of Stagonospora nodorum blotch. They too, looked at four different residue treatments with 0%, 30%, 60%, and 90% residue ground covers to represent different tillage treatments. The study found that the higher residue levels did increase disease severity and disease levels increased linearly throughout the growing season as well. There were very little differences in disease severity early in the growing season, but later in the growing season there were statistical differences between residue treatments (Mehra et al., 2015). The researchers found that an increased residue level of 30% resulted in greater increase in disease severity than the 60% or 90% residue levels. This was similar to our results with 40% and 60% sometimes being greater than or the same as 80%. The difference in these studies and our study was that we observed more statistical differences early in the growth season, likely influenced by the addition of residues that had extra disease inoculum. As the growing season progressed, residue amounts did not seem to influence disease progression as heavily and the various levels were not different from each other. This may have been due to the presence of multiple disease while Mehra et al. (2015) was only observing one disease.

Mehra et al. (2015) hypothesized that differences in disease incidences in residues occurred because at higher residue levels, a higher proportion of total inoculum was trapped in lower levels of the residues. There were no standing stubbles in the South Dakota trials, only enough residue to reach the desired amounts spread as evenly as possible throughout the plots for the South Dakota trials. This too could have created different layers of residue when straw was being added to the higher treatment levels.

While our study was focused on the entire wheat spot disease complex, it was originally assumed that tan spot was the predominant disease in South Dakota. While tan spot was confirmed to be present in the field trials, based on the diagnostic testing (Table 3) performed in this project for 2021, high levels of Stagonospora nodorum blotch were also found. In the beginning of the season pathogen titer was very high and those levels increased exponentially by the last data collection at Feekes 11.3, especially in the 40% and 60% residue levels. Diagnostic data collected for this pathogen in 2022 differed as pathogen levels either remained constant or dropped from Feekes 9.0 to Feekes 11.2 (Table 3), likely due to dry weather conditions. However even in 2022, this pathogen was present at high levels throughout the season in the 40% and 60% residue levels. Both years of diagnostic data suggest that Stagonospora nodorum blotch is a prevalent disease in South Dakota that overwinters in residues and appears to cause more severe levels in residues of the 40%-60% range.

The influence of tillage on the disease intensity of Septoria leaf blotch was studied by Schuh (1990) in 1987-1988. They compared conventional and conservation tillage but did not quantify residue amounts and did not look into initial spore loads. They did not find any significant difference between the tillage practices throughout the entire growing season (Schuh, 1990). Another study was performed by Bankina et al. (2015), looked at crop rotation and the severity of Septoria leaf blotch, but once again did not mention or quantify the amount of residue left on the field. They found that there was a slightly significant interaction between crop rotation and the level of disease with disease decreasing significantly when the break between wheat sowing was greater than a year (Bankina et al., 2015). Otherwise, no studies looking at the difference between Septoria leaf blotch severity and residue amounts could be found. Low levels of Septoria were found in our study leading to the conclusion that Septoria is not a major fungal pathogen in South Dakota.

In this experiment all three of the above-mentioned diseases were visually rated as a complex due to the inability to accurately tell them apart within the field. In 2021, residue samples were taken at the end of the season (Feekes 11.3) to determine what inoculum had been present throughout the growing season. Stagonospora nodorum blotch inoculum was found in all samples, tan spot inoculum was found in all but one sample from the 60% residue block and Septoria leaf blotch inoculum was found in all plots except the 80% residue block (Table 3). Residue samples were taken throughout the season to determine what inoculum was present in 2022. Stagonospora nodorum blotch and tan spot inoculum was found in all samples taken while Septoria leaf blotch inoculum was present in only four sampling instances in 2022 (Table 3).

Field location may have influenced why disease severity was so often significantly higher in the 60% residue block in 2021. In 2021, the research small plot was planted just north of an established large windbreak. The 60% residue block was the closest to this windbreak and received more hours of shade than other blocks and the topography was slightly lower in this section of the field as well. This cannot be the case for the instances of the 60% residue block being higher in disease severity than 80% in 2022. The field in 2022 was on a flat open portion of the Volga research center where there should have been no influence from windbreaks and topography. Another factor that could have affected the results in this study are that the residues added to the blocks were not uniform in the amount of disease inoculum. These residues were not tested with qPCR to determine titer before application, which could have affected the amount of inoculum that was applied to each block.

5. Conclusions

The difference between residue levels and disease severity were not as hypothesized with unexpected differences in residue amounts. To better understand the differences, this experiment needs to be repeated with some modifications. One such modification would be using qPCR to determine what pathogens are actually present on the leaves and to collect residues more often throughout the growing season. Another modification would be to have better replication of varieties within the residue treatments and to irrigate the field to encourage pathogen infection even in dry years. To truly understand what all may be influencing the amount of disease severity in correlation to residue amounts one would have to remove more variables of uncertainty. However, we were able to begin establishing a baseline in the relationship between disease severity and residue percentages under no-till conditions, which was the main goal of this study.

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7. Tables and Figures

Table 1. Varieties in this study and their associated disease ratings for the three diseases in this study.

Variety	***Parastagonospora nodorum***	***Zymoseptoria tritici***	***Pyrenophora tritici-repentis***
Draper	No Rating	No Rating	Tolerant
Ideal	Susceptible	No Rating	Susceptible
Redfield	Tolerant	No Rating	Susceptible
Thompson	No Rating	No Rating	Susceptible
Expedition	Susceptible	No Rating	Susceptible
Wesley	No Rating	No Rating	Tolerant
Oahe	No Rating	No Rating	Tolerant

Table 2. Means of varieties, residues, and growth stages. Significance of residue percentage when compared to the respective growth stage is noted.[1]

Draper	**Feekes 10.5**	**Feekes 11.2**	**Feekes 11.3**
20	0.2926^{a}	4.9796	19
40	2.1528	5.3981	17.0556
60	3.5704^{a}	5.6204	17.3689
80	2.6704	8.6296	18.6944
Ideal			
20	0.2009^{a}	1.75	15
40	0.2389^{b}	2.7361	19.3611
60	0.912^{ab}	2.2611	18.6389
80	0.4157	2.4065	16.0556
Redfield			
20	0.8352^{ab}	4.887^{d}	8.6359
40	5.1667^{a}	4.6343^{e}	10.8889
60	3.7731	9.8426^{ab}	8.1389
80	4.4769^{b}	5.9556	9.9167
Thompson			
20	0.1361^{a}	3.3435	14.3944
40	0.4235^{b}	3.4306	11.1667
60	1.4343^{c}	6.5278	22.1944
80	3.5417^{abc}	6.7731	13.6944
Expedition			
20	0.6259^{ab}	5.187	18.3056
40	4.3528	7.5093	18.5556
60	8.2194^{a}	10.1296	18.7778
80	5.7407^{b}	6.5509	11.5
Wesley			
20	0.1509^{a}	2.3231^{d}	13.3333
40	0.638^{b}	3.0769^{e}	17.7222
60	8.3509^{abc}	10.4352^{edf}	22.5556
80	0.7704^{c}	4.3583^{f}	15.1667
Oahe			
20	0^{ab}	3.8815	16.5694
40	0.5019^{c}	5.7778	21.1944
60	1.988^{acd}	4.5926	21.0556
80	0.9722^{bd}	3.8657	16.6528

[1] ‘Draper’ p-values: a) 0.01000. ‘Ideal’ p-values: a) 0.0102, b) 0.01713. ‘Redfield’ p-values: a) 0.0106, b) 0.0451, c) 0.0392, d) 0.0268. ‘Thompson’ p-values: a) 0.00000, b) 0.00000 c) 0.00402. ‘Expedition’ p-values: a) 0.00001, b) 0.00617. ‘Wesley’ p-values: a) 0.00000, b) 0.00000, c) 0.00000, d) 0.00001, e) 0.00005, f) 0.00132. ‘Oahe’ p-values: a) 0.00000, b) 0.04, c) 0.00034, d) 0.029.

Table 3. Testing data that was collected from residue blocks in this study. Disease levels were higher overall in 2021. It can be observed that disease titer for Stagonospora nodorum blotch (SNB) generally stayed the same or increased throughout the season in both years whereas Tan Spot and Septoria titers generally started at high levels and decreased throughout the season.

Year	**Residue Amount**	**Growth Stage**	**SNB (Cq)**	**Tan Spot (Cq)**	**Septoria (Cq)**
2021	20	Feekes 10.5	17.32	21.03	26.94
		Feekes 11.3	13.93	25.46	29.78
	40	Feekes 10.5	13.61	20.54	23.38
		Feekes 11.3	12.95	26.38	28.83
	60	Feekes 10.5	16.01	ND	22.19
		Feekes 11.3	13.33	ND	29.86
	80	Feekes 10.5	18.19	20.7	ND
		Feekes 11.3	12.47	ND	ND
2022	20	Feekes 9.0	23.3	24.18	35.67
		Feekes 11.1	20.52	26.84	ND
	40	Feekes 9.0	21.62	23.21	ND
		Feekes 11.1	21.93	29.28	ND
	60	Feekes 9.0	21.45	25.19	38.77
		Feekes 11.1	21.78	26.15	ND
	80	Feekes 9.0	22.61	23.84	34.38
		Feekes 11.1	22.48	25.3	37.77

Table 4. Means of varieties, residues, and growth stages. Significance of residue percentage when compared to the respective growth stage is noted.[2]

Variety	Feekes 9	Feekes 10	Feekes 10.5	Feekes 11.1
‘Draper’				
20	0.0583	0.2426^{a}	2.9398	4.1824^{fg}
40	0.0704	0.2009^{b}	1.6426^{de}	11.7407
60	0.1259	0.4444^{c}	6.4833^{d}	12.8306^{f}
80	0.3093	4.7398^{abc}	6.2009^{e}	12.8009^{g}
‘Ideal’				
20	0.0333^{a}	0.0833^{cd}	1.3787^{ef}	10.888
40	0.0398^{b}	1.1417	3.3361^{gh}	11.2157
60	0.0787	1.7343^{c}	9.1407^{eg}	11.7556
80	0.2417^{ab}	2.3454^{d}	8.7^{fh}	12.1528
‘Redfield’				
20	0.0611^{a} a	0.4306^{c}	4.1296	6.6657^{g}
40	0.0194^{b} b	0.4315^{d}	3.6157^{f}	12.2296
60	0.3287	0.3926e	5.938	11.2287
80	0.6194^{ab} ab	1.8083^{cde}	8.6444^{f}	16.587^{g}
‘Thompson’				
20	0.0352^{a}	0.0778^{de}	3.7565	7.3935
40	0.0213^{b}	2.3111^{d}	5.9676	8.6648
60	0.1361^{c}	0.7639^{f}	7.188	11.5556
80	1.9685^{abc}	2.8352^{ef}	8.3593	10.5093
‘Expedition’				
20	0.0157	0.3824	2.7657^{a}	9.8528
40	0.0306	0.3074	4.8528	14.5463
60	0.3176	1.1398	4.1157	14.2796
80	0.1213	1.2907	7.8594^{a}	15.8181
‘Wesley’				
20	0.0046^{a}	0.1741^{d}	1.7343^{gh}	8.0648^{i}
40	0.1056^{b}	1.4352^{e}	6.9694	10.9898
60	1.0083^{abc}	6.1435^{def}	11.2806^{g}	16.7963^{i}
80	0.25^{c}	2.0167^{f}	11.4148^{h}	15.2176
‘Oahe’				
20	0.0639^{a}	0.0602^{c}	2.013^{f}	9.2602
40	0.0519^{b}	0.262^{d}	2.9972^{g}	9.5102
60	0.112	0.9972^{e}	5.8019	15.9306
80	0.4296^{ab}	3.8991^{cde}	8.9556^{fg}	12.162

2- ‘Draper’ p-values: a) 0.00000, b) 0.00000, c) 0.00000, d) 0.0089, e) 0.0158, f) 0.0216, g) 0.02225. ‘Ideal’ p-values: a) 0.0063, b) 0.0088, c) 0.0328, d) 0.0012, e) 0.00039, f) 0.00095, g) 0.0146, h) 0.0287. ‘Redfield’ p-values: a) 0.00054, b) 0.00016, c) 0.00013, d) 0.00013, e) 0.00008, f) 0.04591, g) 0.00597. ‘Thompson’ p-values: a) 0.00002, b) 0.00001, c) 0.00005, d) 0.0043, e) 0.00021, f) 0.00971. ‘Expedition’ p-values: a) 0.0139. ‘Wesley’ p-values: a) 0.0002, b) 0.0012, c) 0.0096, d) 0.00000, e) 0.00001, f) 0.0001, g) 0.0013, h) 0.0011, i) 0.02897. ‘Oahe’ p-values: a) 0.041, b) 0.032, c) 0.00000, d) 0.00000, e) 0.0000, f) 0.00075, g) 0.00548.

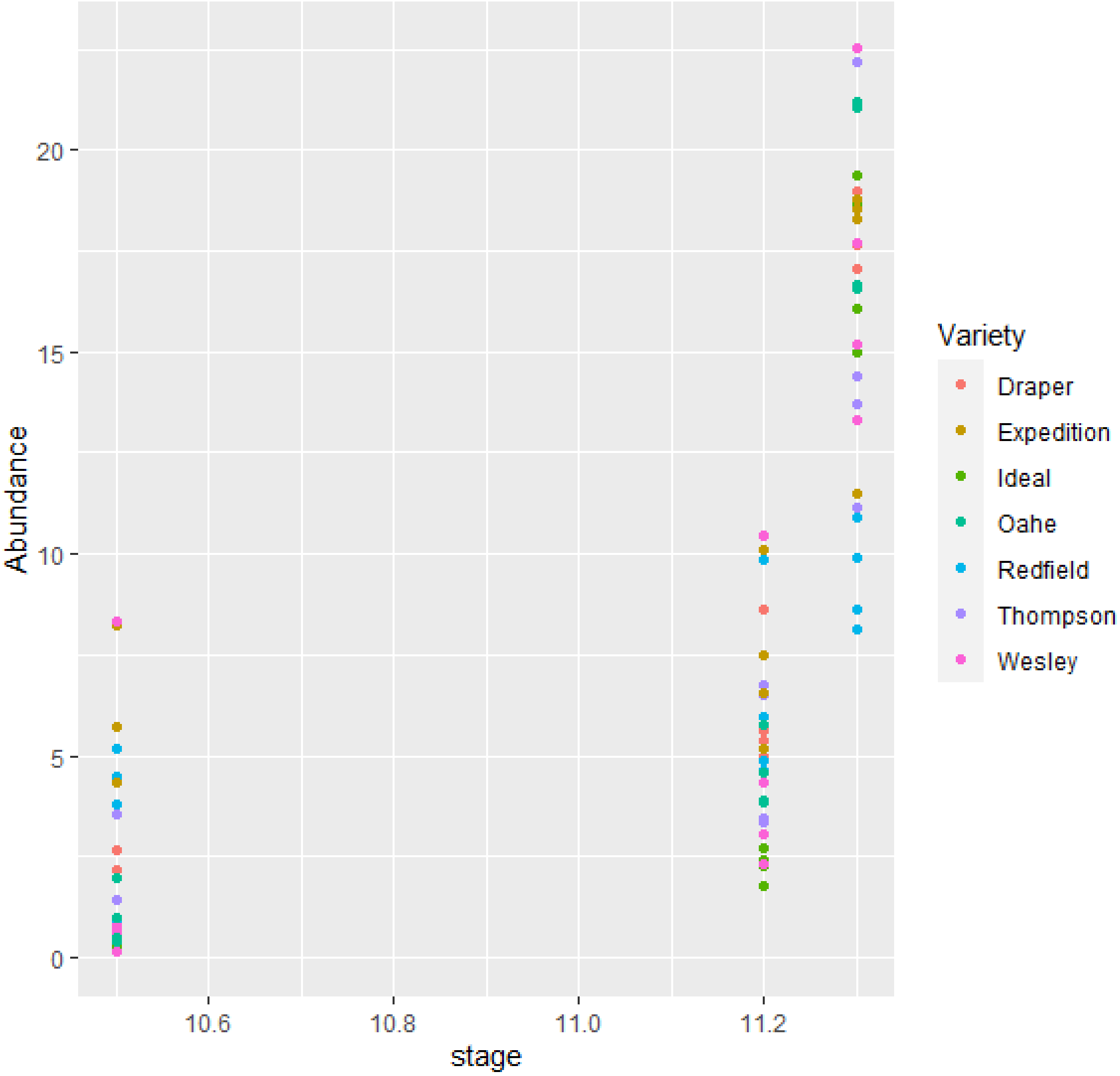

Figure 1. Comparison of disease abundance in 2021 to growth stage for each residue level of each variety. As the growing season progressed, disease abundance increased within each variety. Residue percentage did not appear to heavily influence disease abundance.

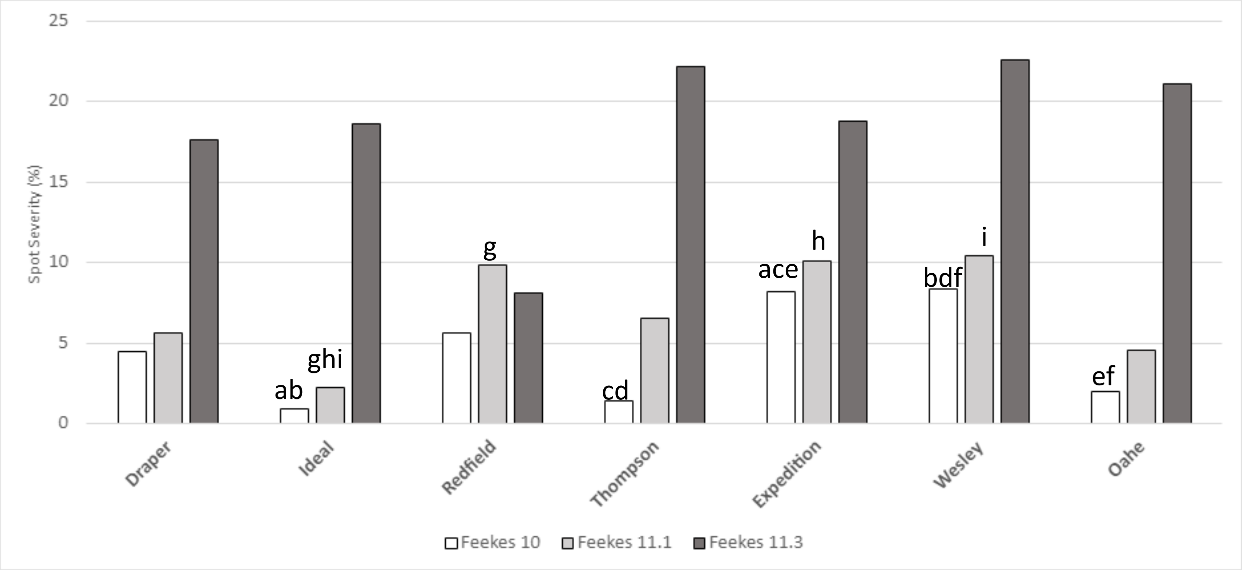

Figure 2. The results from comparison of all varieties at the 60% residue level showed more significance early in the season and no significance later in the season. ‘Wesley’, ‘Expedition’, and ‘Ideal’ were significantly different from all others in the first part of the season, suggesting that these varieties were more susceptible to the combined effects of residue and disease.

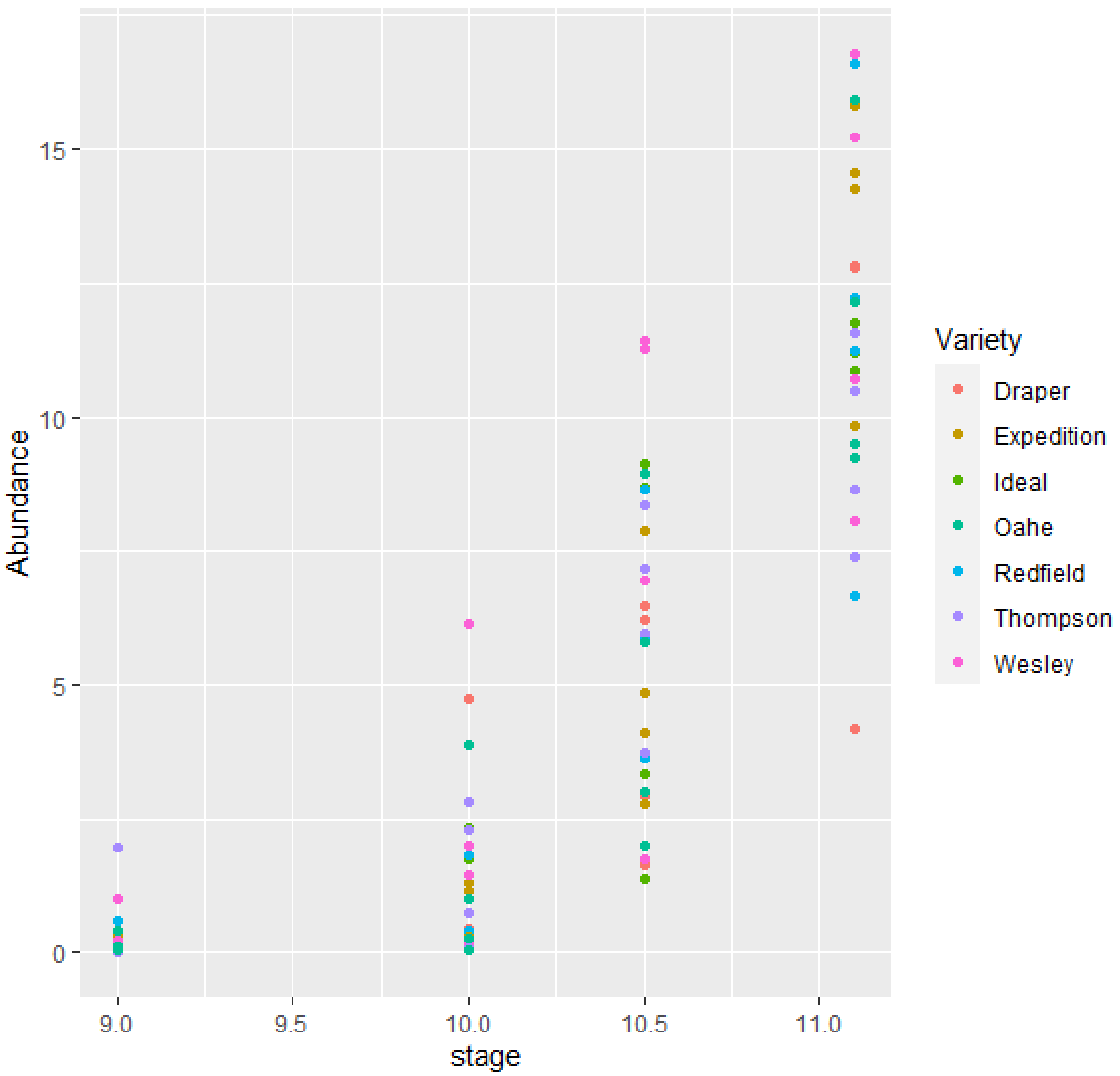

Figure 3. Comparison of disease abundance in 2022 to growth stage for each residue level of each variety. As the growing season progressed, disease abundance increased within each variety. Residue percentage did not appear to heavily influence disease abundance.

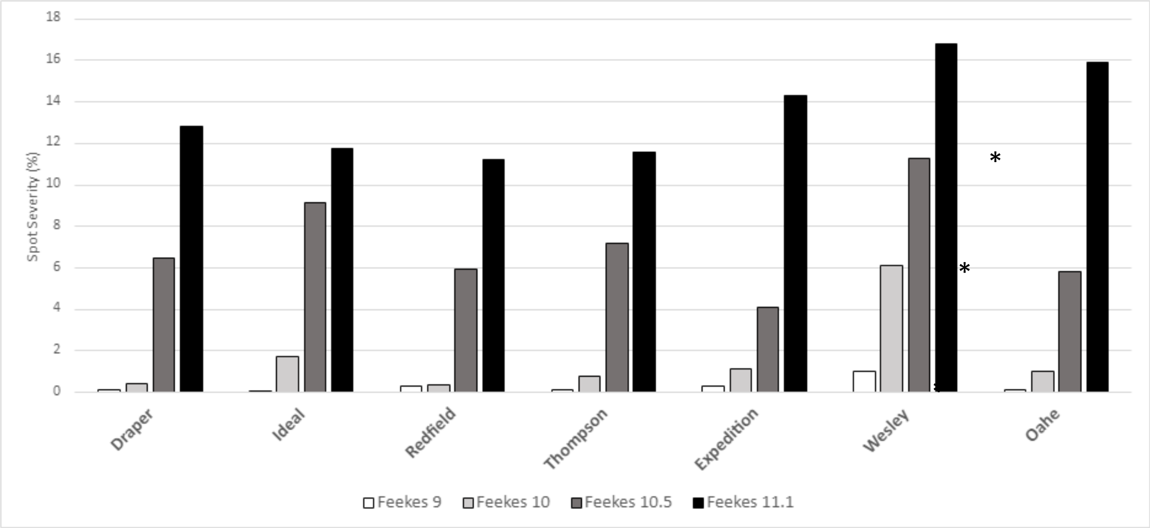

Figure 4. Comparison of all varieties at the 60% residue timepoint, which was selected as it had the most significant relationships. Wesley (*) was significantly different from all other varieties at all growth stages except Feekes 11.1.

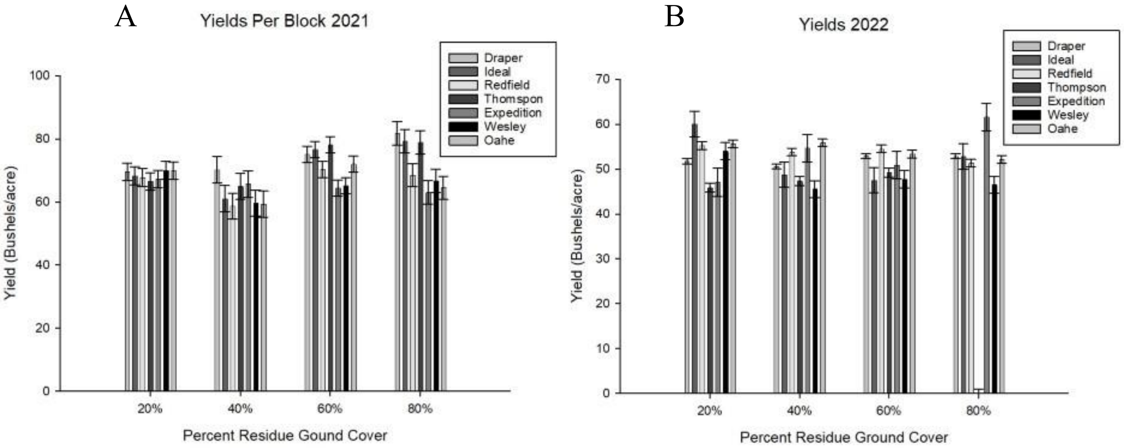

Figure 5. Demonstration of yield for each variety per residue percentage. A) 2021 yield, B) 2022 yield.

Chapter 4 Overall Conclusions

This project was initially designed by the National Predictive Modeling Tool Initiative (NPMTI) to develop a new predictive model for wheat fungal pathogens throughout the United States using both historical and newly collected data. For the project, researchers were tasked with investigation of many variables including but not limited to: residue amounts (amount of ground covered by previous years wheat straws), weather variables (temperature, precipitation, relative humidity, etc.), overwintering spore loads, residue spore loads, and airborne spore loads. South Dakota lacked any large historical disease data sets that could be used, so this project focused on establishing the baselines of types and amounts of diseases in the state. The six diseases of interest for which data was collected in this project were leaf rust (*Puccinia triticina*), stem rust (*Puccinia graminis*), stripe rust (*Puccinia striiformis*), tan spot (*Pyrenophora tritici-repentis*), Stagonospora nodorum blotch (*Parastagonospora nodorum*), and Septoria leaf blotch (*Pyrenophora tritici-repentis*).

The varieties that were selected for this study were seven varieties that were either bred in or commonly grown in South Dakota. All varieties have been evaluated for their response to four to six of the diseases covered in this study (Chapter 2, Table 1). The findings of this study are as follows. In both years of the study, rust disease levels were very low with few instances of any rust disease in 2022. Spot disease levels were high in both years, though more in 2021 due to early season moisture. It was also found that Stagnospora nordorum blotch was prominent in South Dakota, which was an unexpected finding. This finding explained why many of the tan spot tolerant varieties still developed spot diseases in both years of this study.

The residue levels chosen for this experiment were 20%, 40%, 60%, and 80% ground cover. Previous experiments considered these treatments to be approximately 0%, 30%, and 90% ground cover (Dill-Macky & Jones, 2000; Otilia Cotuna et al., 2015). The use of 20%, 40%, 60%, and 80% ground cover was done to encompass more variability in residue amounts due to the wide variety of soil conservation and tillage practices employed in South Dakota. The results of our study were that the upper-level residue amounts of 60% and 80% appeared to increase disease severity. This was an expected based on previous literature. The 60% residue level appeared to increase disease severity the most, but that finding was no consistent across all varieties in both years.

2. Future Directions

To better understand what is occurring with disease levels and occurrence, more experiments will need to be done. To better understand the ecology of the pathogens within the residue, molecular testing should be done to accurately identify pathogens and then experiments should be done looking at each pathogen separately in various residue amounts. Then in more controlled experiments, such as a greenhouse, to establish a baseline, different pathogen combinations should be introduced to each residue amount and determine the effects of the disease combinations. The information from a controlled environment would set a baseline for expectations of field experiments. In future continuation of the South Dakota NPMTI trials, other varieties should be evaluated for their response to these diseases. Additionally, factors such as the addition of irrigation to encourage disease development, should be utilized to standardize field studies.

3. Literature Cited

Cotuna, O., Paraschivu, M., Paraschivu, A., Sărăţeanu, V. 2015. The influence of tillage, crop rotation and residue management on tan spot (*Drechslera tritici repentis. Died. Shoemaker*) in winter wheat. *Research Journal of Agricultural Science*, 47(2): 13-21.

Dill-Macky, R., & Jones, R.K. 2000. The Effect of Previous Crop Residues and Tillage on Fusarium Head Blight of Wheat. *Plant Disease*, 84(1):71-76.

4. Figures

Figure 1: Scan of different flag leaves from Feekes 11 in 2021.