

**REACTION OF NORTH AMERICAN OATS (*Avena sativa* L.) TO
CROWN RUST**

A Thesis

by

CAROL JEANNINE LANGE

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Approved by:

Chair of Committee,
Committee Members,
Head of Department,

Amir M.H. Ibrahim
Seth C. Murray
Charles M. Rush
David D. Baltensperger

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ABSTRACT

Crown rust, caused by the fungus *Puccinia coronata*, is a severe disease negatively impacting seed quality and yield in oat (*Avena sativa*). Host genetic resistance is the primary means for controlling this disease. The most extensive oat map contains nearly 2,500 genetic markers, many of which are restriction and amplified fragment length polymorphic (RFLP or AFLP) markers. However, the use of more abundant single nucleotide polymorphic (SNP) markers combined with diversity arrays technology (DArT) would be more advantageous for marker assisted breeding (MAB) and genome wide selection (GWS) applications due to the availability of high density genotyping technologies. The purpose of using this technology is to improve the competitiveness of oat by producing varieties with durable resistance to crown rust and desirable traits that will benefit oat growers in the U.S. Panels of winter and spring oat were evaluated for resistance to crown rust in four field environments in Texas, Louisiana, Minnesota, and North Dakota during a two-year study in 2010 and 2011. Plants representing 702 elite lines of oat were phenotyped for crown rust resistance and found to have highly diverse responses. The winter oat lines demonstrated the best crown rust resistance and are expected to yield the most QTL to be used in developing durable crown rust resistance. Heritability of crown rust resistance in this study ranged from 0.88 to 0.90 in spring and winter oats, respectively. Crown rust measurements were also found to be repeatable. Repeatability ranged from 0.56 to 0.88 at Castroville, TX in 2011 and 2010, respectively in spring oats and from 0.79 at St. Paul, MN in 2011

to 0.96 at Castroville, TX in 2010 in winter oats. Oat lines contributed by states along the *Puccinia* pathway in Texas, Louisiana, Minnesota, North Dakota, and Wisconsin on average exhibited the best crown rust resistance as compared to other areas in the country where spring and winter oat are grown. GGE biplot analysis indicated that Castroville, TX was the most representative and most ideal testing location. The above results are expected to increase knowledge of the genetic diversity of the oat germplasm, yield comprehensive genotyping and phenotyping information for North American oat breeding programs, and to promote further use of GWS and MAB for key traits regarding disease resistance in oat. Future work is to conclude the association mapping process by completing genotypic analysis.

DEDICATION

To the Lord, for blessing me with the knowledge, strength, courage and fortitude required of any hopeful student pursuing a graduate degree.

To my supportive husband, Paul Wiget, for his unfailing love, encouragement, and patience in all of my endeavors.

To my devoted parents, Charles and Kathy Lange, for imparting within me the importance and value of pursuing an education, for always telling me that I could be anything I wanted to be, and for stressing to me that college was mandatory.

To all of my siblings, Charles, Katie, Conrad, and Chris, who don't realize how much I look up to each and every one of them. I hope I can inspire and encourage them in the same manner with which they inspire me.

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NOMENCLATURE

AFLP	Amplified fragment length polymorphism
AM	Association mapping
ANOVA	Analysis of variance
BR	Baton Rouge, LA
GWS	Genome wide selection
CAS	Castroville, TX
CI	Coefficient of infection
Core	Elite lines of North American oats
DArT	Diversity arrays technology platform
DS	Disease severity
FRG	Fargo, ND
G x E	Genotype-by-environment interaction
H	Heritability
IT	Infection type
LD	Linkage disequilibrium
MAB	Marker-assisted breeding
MR	Moderately resistant
MS	Moderately susceptible
QTL	Quantitative trait loci
R	Resistance
RFLP	Restriction fragment length polymorphism
S	Susceptible
SNP	Single nucleotide polymorphism
STP	St. Paul, MN

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CHAPTER I

INTRODUCTION

Crown rust, or *Puccinia coronata*, is the most severe pathogen affecting oat in North America. Crown rust negatively impacts seed quality and yield, and can reduce overall test weights. Under the most favorable crop conditions, crown rust can successfully wipe out an entire crop. Due to successful pathogen overwintering, multiple infection cycles and increased pathogen severity, it is difficult to maintain a resistant plant population which can outlast pathogen virulence for an extended period of time (Carson, 2010). Crown rust occurs nearly everywhere that oats are grown, but is most serious in humid areas. Testing in Castroville, TX and Baton Rouge, LA is ideal due to their respective locations at the forefront of the *Puccinia* pathway (Figure 1.1). From these sites, windborne rust spores are disseminated into northern parts of the United States. This pathway is consistent for all *Puccinia* species. Castroville, TX has an additional advantage over the Baton Rouge, LA location to screen for crown rust resistance since there are more races of *Puccinia* in Texas than any other state.

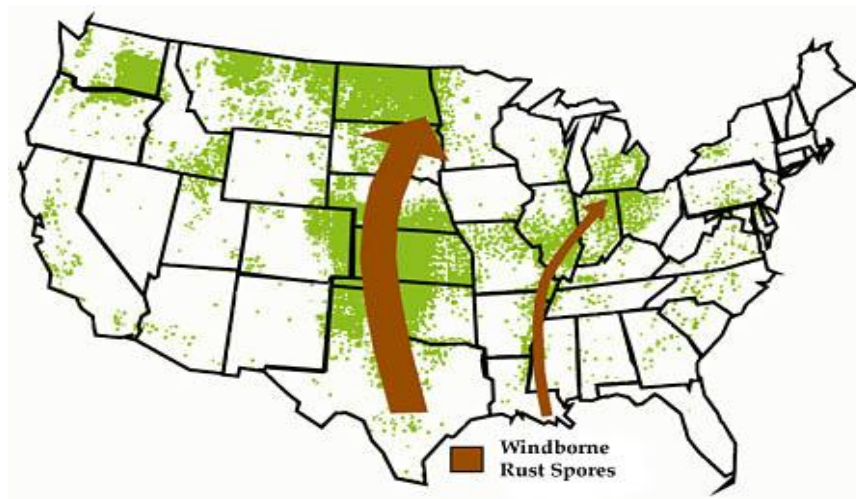


Figure 1.1. The *Puccinia* pathway. (Courtesy: Marty Carson, Cereal Disease Laboratory, St. Paul, MN)

Symptoms of oat crown rust include the appearance of orange to yellow pustules, called urediospores, on the leaves (Figure 1.2). These spores reproduce every 7-10 days until harvest. In an alternate phase, black resting spores, or teliospores, overwinter on straw or buckthorn, the alternate host, and can survive until germination in the spring (Wilson, 1955).



Figure 1.2. The symptoms of crown rust in two distinct life cycles.

Host genetic resistance is the primary means of controlling crown rust. Breeders rely on race-specific seedling genes which are expressed as some form of hypersensitive reaction phenotypically expressed as flecks of chlorosis on leaves in the absence of rust pustules. Resistance genes in cultivated hexaploid oat, *A. sativa*, were deployed, resulting in such a rapid increase in corresponding virulence in the crown rust population that virulence to most of these genes became fixed in the oat populations of North America. More recent efforts relied upon the exploitation of resistant genes in wild hexaploid oat, *A. sterilis*. The result was another corresponding increase in rust virulence which limited the lifespan of a resistant cultivar to a maximum of five years (Carson, 2010). Oat breeders and geneticists then attempted to utilize alternate sources of resistant genes in diploid species of oat, especially black oat, *A. strigosa*.

Introgressing resistance into hexaploid oats has become a challenge due to differences in ploidy levels and a lack of homology of chromosomes between black oat and common oat (Carson, 2008).

Molecular markers suitable for effective marker-assisted selection of quantitative trait loci (QTL) conferring partial (quantitative) resistance to crown rust in oat are currently lacking, but rapid developments in this area will help its use in oat improvement. The most extensive oat map to date contains 2500 genetic markers, most of which feature restriction fragment length polymorphism (RFLP) or amplified fragment length polymorphism (AFLP) technologies. RFLP are excellent markers, but are unsuitable for high throughput applications. AFLP lack consistent repeatability and are difficult to transfer. Diversity arrays technology (DArT) markers are also commonly used, but have an inadequate density for marker-assisted breeding and genome wide selection, as well as being rather expensive (Eckstein et al., 2008; Tinker et al., 2009). The solution is a proposed combination of DArT markers and single nucleotide polymorphisms (SNPs). SNPs allow high density, high throughput application, they are abundantly available and, unlike DArTs, do not rely on a specific technology platform. SNPs can also be directly related to sequence variation within candidate genes without losing stability (Chen et al., 2007).

As genetic and technological advancements are made, new methodology enables breeders to seek alternate methods of discovering and utilizing resistant genes. One such option is using an association mapping approach to link phenotypic traits to a specific gene or set of genes. Association mapping is a molecular plant breeding methodology

which statistically identifies significant QTL effects in a population with varying degrees of structure and relatedness according to linkage disequilibrium as a complement to QTL analysis. Using a large experimental population representing elite germplasm of the oat breeding programs in North America for association mapping would make information derived from this panel directly applicable to modern crop improvement. Additionally, studying a group of unrelated individuals provides variation permitting a variety of traits to be studied within the same population using the same genotypic data (Breseghello and Sorrells, 2006).

The objective of this study was to evaluate three panels of North American oats (winter, spring, and core) for resistance to crown rust in four field environments. These field trials will accompany data obtained from a similar screening experiment in greenhouse trials in the future. Together, these results will contribute to the mapping of loci controlling crown rust resistance using SNP assays and a complementary DArT platform. Ultimately, this will lead to the improved competitiveness of oats by yielding varieties with durable resistance to crown rust, as well as other desirable traits, to benefit oat growers in North America.

CHAPTER II

LITERATURE REVIEW

Common oat (*Avena sativa* L.)

Common oats are classified as an annual grass belonging to the genus *Avena* and are of the *sativa* species. Cultivated oat is a self-pollinating allohexaploid ($n=3x=21$) composed of three basic genomes, A, C and D (Rajhathy and Thomas, 1974). Domestic oat, *A. sativa*, contains 42 chromosomes, while wild tetraploids, such as *A. barbata*, have only 28 chromosomes (O'Brien, 2010).

Common oats are ranked fifth in the world's most important cereal crops, exceeded only by rice (*Oryza sativa*), wheat (*Triticum aestivum* L.), corn (*Zea mays*), and barley (*Hordeum vulgare* L.), respectively. The popularity of oats globally is increasing due to its many nutritional benefits for the human diet. Among numerated health benefits are a high content of total dietary fiber, good quality protein, and high oil content. Additionally, oats contain a higher presence of essential acids, including linoleic acid (Young and Pellett, 1994), than other cereal crops (Oliver et al., 2011).

Oats are also a rich source of the antioxidants α -tocotrienol and α -tocopherol, and avenanthramides (Young and Pellett, 1994). Tocotrienols and tocopherols are commonly associated with the prevention of heart disease (Peter et al., 1997), Alzheimer's (Zandi et al., 2004), prostate cancer (Helzlsouer et al., 2000) and glaucoma (Engin et al., 2007). Avenanthramides, phytoalexins uniquely associated with oats, are shown to modulate nitric oxide production and reduce smooth muscle proliferation in the cell wall (Nie et

al., 2006; Pearce et al., 1992). Other benefits include the lowered risks of atherosclerosis and myocardial infarctions (Liu et al., 2004; Peter et al., 1997; Ridker et al., 1989; Yue et al., 1994), and a reduction in diastolic and systolic blood pressure (el Zein et al., 2009; Gondal et al., 1996). Oat is already consumed and enjoyed in a number of whole-grain formulations, making it an effective and desirable staple food naturally providing dietary intervention of many common and serious health risks (Jackson et al., 2008).

While the many health benefits of oat increase its popularity, oat acreage in North America is dramatically decreasing each year. In the United States alone, the acreage of oat production dropped from 14 million in 1988 to 2 million in 2008. The number of research groups intent on improving oats as a crop has decreased since the 1980's from 29 to 11 (Jackson et al., 2007). At present, there are an estimated twelve publicly funded oat breeding programs in the United States and Canada (Newell et al., 2011). These breeding programs face a number of challenges that will inhibit the preservation and improvement of oats as an economically important crop for both consumers and producers (Jackson et al., 2007). These programs are focused on developing more promising oat varieties that feature disease resistance, increased yield, stress tolerance and reduced lodging (Oliver et al., 2011).

Oats are a versatile grain crop constituting the third most important cereal crop in the United States, behind corn and wheat. A useful crop for pasture and reducing soil erosion, oats are suitable to a variety of crop rotations and purposes. Oats are nutrient-rich equaling a desirable feed for horses, poultry and livestock. In addition to grain usage, oat straw is considered the best for feed or bedding (Martin and Leonard, 1949).

Currently, oat acreage in the United States is on the decline, despite high nutritional value. Considered a grass species, oats are primarily grown as a grain or forage crop (Newell et al., 2011).

There are two primary regions for oat production in the United States. In the south, including Texas and Louisiana, winter oats are planted in the fall and harvested in the spring. In the upper Midwest region, spring oats are planted between late March and mid-May and harvested in midsummer (Carson, 2010). Oats are most suitably grown in cool, temperate regions with an average of 25 inches or more of annual precipitation or irrigation. Under heat stress, blasting or the dropping of florets can occur during flowering, indicating less heat tolerance than wheat or barley. Soil pH does not typically impact oat production; however, oats cultivated in heavy soils or phosphorous lacking soils can exhibit a reduction in yield. Oats have been broadly adapted to a diverse array of environments, but are most commonly grown in the northern central regions of the United States, primarily, Minnesota, Wisconsin, Iowa, North Dakota and South Dakota (Chapman and Carter, 1976).

Oats are susceptible to several highly damaging diseases, which account for millions of dollars of losses each year. Such diseases include fungal infections, such as crown rust, stem rust (*Puccinia graminis*), loose smut (*Ustilago nuda*), *Septoria* blight, *Fusarium* blight, root rot (*Rhizoctonia solani*), powdery mildew (*Erysiphe graminis*), and halo blight (*Pseudomonas coronafaciens*). Viruses affecting the oat population include soilborne oat mosaic virus (*Bymovirus* spp.) and barley yellow dwarf virus (*Luteovirus* spp.) (Wiese, 1987). Among these, the number one pathogen threatening oat

production is crown rust, *Puccinia coronata* f. sp. *avenae*, which is found everywhere oats are cultivated. Crown rust is considered the most severe disease of oats in North America (Carson, 2009; Simons, 1985). Under the most favorable crop conditions, crown rust can devastate an entire planting, resulting in total crop failure (Carson, 2008).

Crown rust (*Puccinia coronata* f. sp. *Avenae*)

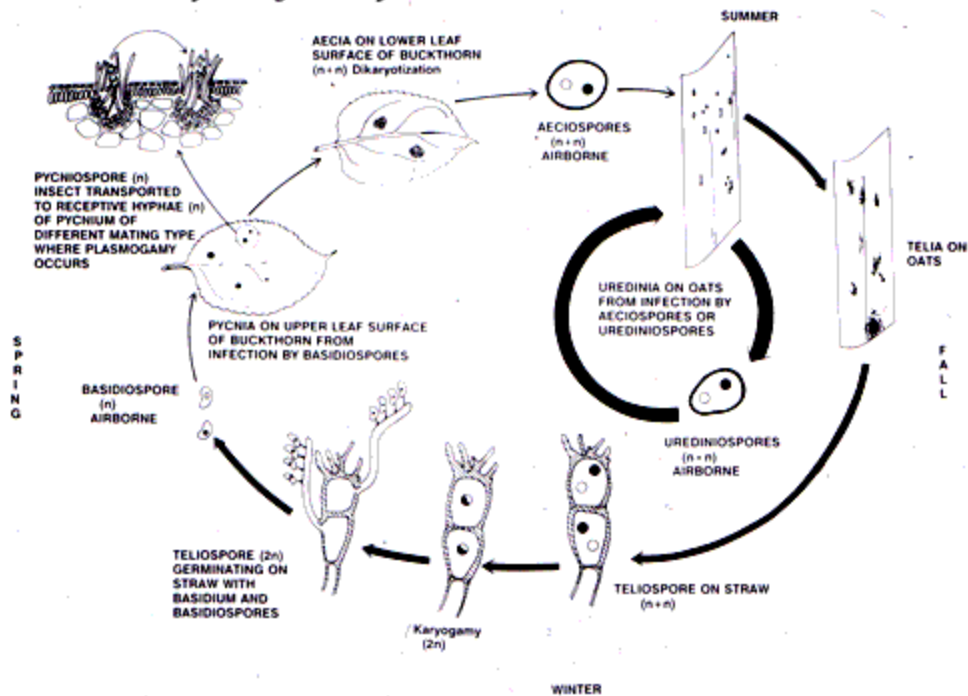
Oat crown rust is caused by a heteroecious macrocyclic fungus, *Puccinia coronata* Corda f. sp. *Avenae*, which is regarded as the most detrimental fungal disease of oat (Simons, 1985). Crown rust is widespread occurring wherever oats are grown (Carson, 2008; Leonard, 2002; Simons, 1985). While distributed globally, crown rust has the most impact under conditions of heavy dew combined with moderate to high temperatures of 20-25°C. Arid regions where cultivated and wild oats are found are usually free of crown rust infection. Conditions considered most favorable to the oat crop are also the most favorable to crown rust, often leading to complete crop failure (Carson, 2008). Under less than ideal conditions, crown rust can negatively impact yield and test weight, as well as increase lodging (Wiese, 1987).

Moderate to severe crown rust epidemics have been shown to reduce overall grain yield by as much as 10-40%. The greatest yield losses generally occur when the oat yield is expected to be the highest. Crown rust causes damage to plant leaves, specifically the flag leaf, thereby reducing photosynthesis. In oat used for grain, the presence of rust on the flag leaf inhibits the transport of photosynthesized sugars that are used in grain production. As a result, the grain that is produced tends to be shriveled

and, therefore, has a lower feed value. In oat used for forage, the damage caused to leaves can also limit plant growth and a reduction in forage value. Crown rust also impacts plants beneath the soil surface by stunting root growth and leading to poor drought tolerance (Chong, 2002; Leonard, 2002; Simons, 1985).

A crown rust infection is characterized by the formation of uredinia on the upper and lower surfaces of affected leaves, and in severe conditions, leaf sheaths. Uredinia are round to oval blister-like pustules that can be up to 5 mm long. These pustules are composed of bodies of orange-yellow spores which become exposed via rupturing on the leaf's epidermis. In a matter of weeks, the edges of the uredinia are blackened by the formation of brown-black teliospores. Black telia rings are often formed around the uredinia, but the leaf's epidermis will remain intact over the rings until the leaves expire (Chong, 2002; Simons, 1985).

Life Cycle of *Puccinia coronata*



Vickie Brewster

Figure 2.1. Life cycle of oat crown rust. (Courtesy Vickie Brewster, United States Department of Agriculture-Agricultural Research Station)

Initial infection begins on oats sown during the fall by uredinia from volunteer or wild oat plants which survived throughout the summer. This happens in moist protected habitats near streams or irrigation canals. Crown rust generally follows one of two distinct life cycles (Figure 2.1). In each cycle, the uredinia form on oats several weeks prior to the crop ripening. In the first phase of the cycle, the spores from these pustules are windborne and infect new plants, producing fresh spores every 8-10 days. Alternately, the teliospores, form on the oats, circling the blister-like pustules to overwinter on straw, post-harvest. In the spring, small spores are airborne and can infect

common buckthorn (*Rhamnus cathartica* L.), the aecial or alternate host of crown rust. The infection cycle repeats as new spores are transmitted from buckthorn to oats, where the uredinia form once more (Wiese, 1987). Common buckthorn is found in the upper Midwest of the U.S. and does not therefore serve as a host of the fungus in the southern oat regions. In these areas, wild oat (*A. fatua*) can serve as a site for overwintering (Carson, 2010). Teliospores that overwinter on the straw of buckthorn or wild oat produce basidiospores, which infect the host plants' young leaves. These infections then produce aecia, which yield aeciospores that eventually infect oat plants, repeating the cycle. Also, urediniospores and aeciospores can germinate in free water on the surfaces of leaves. The germination and infection of leaves via stomates occur at temperatures ranging from 10-25°C, but is inhibited at temperatures greater than 30°C (Chong, 2002; Simons, 1985).

Since winter oats are not durable enough in the northern parts of the U.S., crown rust does not survive the winter in the uredinial stage except in the south. Crown rust infections typically develop during the early summer in southern growing areas, such as Louisiana and Texas. Urediniospores are then disseminated to the north to infect the oats sown in the spring. This pattern follows what is referred to as the Puccinia pathway (Figure 1.1) which depicts the route of travel for most races of rust. In the upper Midwest growing regions, aeciospores from common buckthorn serve as the primary source of inocula (Chong, 2002; Chong et al., 2000; Simons, 1985). Urediniospores and aeciospores are capable of surviving a great distance during dissemination, while germination teliospores endure on the straw. When humidity is very high during the

night or rain showers occur, the teliospores can release the basidiopores which must rapidly infect other plants. Basidiospores are incapable of surviving airborne dissemination greater than several hundred meters from their original source (Chong et al., 2000; Simons, 1985).

While individual varieties of the crown rust fungus are limited to cultivated and wild oat or buckthorn, a number of other grass species may serve as hosts as well. In cultivated grass species, rye (*Secale cereal* L.) and barley can be slightly impacted by crown rust, although not by the same varieties which impact oat. Ryegrass (*Lolium* L.) and fescue (*Festuca* L.), common lawn and pasture grasses, can be severely infected by crown rust. A new form of crown rust has been discovered to infect smooth brome grass (*Bromus inermis*), an important pasture grass in the upper Midwest of the U.S. (Chong et al., 2000; Simons, 1985). Clearly, crown rust is a dangerous pathogen which impacts a variety of important plant species, is effectively disseminated, and extremely durable. Since this fungus is present virtually everywhere that cultivated oats are grown, it is in the best interest of oat breeders and growers to determine a method for controlling the spread of crown rust and protecting the oat population.

In the north-central United States, oat fields are commonly exposed to high external inoculum levels of a very diverse *P. coronata* population because the fields are often bordered by a highly dense buckthorn population. In the south, winter oats can also be exposed to high inoculum levels because the longer growing season permits more asexual reproductive cycles of the fungus than occur in the shorter growing region of the northern states (Carson, 2009).

Disease management strategies and challenges

A number of methods for controlling crown rust have been attempted, many of which are host genetic resistances which occur at the molecular level. Such methods include host genetic resistance, partial resistance, race-specific seedling genes, and multiline cultivars (Carson, 2009). Many breeders seek resistance from alternate oat sources, including diploid oat (*A. strigosa*), tetraploid oat (*A. magna*), and slender oat (*A. barbata*) and release multiline cultivars of oat derived from a method of introgression (Carson, 2010). Other breeders continue to search for additional sources of broad-spectrum and durable resistance.

Conventional methods for managing crown rust include fluctuating planting dates and eradicating the buckthorn population. In the upper Midwest where spring oat is grown, planting earlier allows the crop to mature prior to when the most severe symptoms of crown rust will develop. In colder regions, a weed management strategy targeting the common buckthorn population will delay the spread of the fungus, as well as inhibit the development of new, more virulent rust races through the use of resistant varieties maturing earlier (Wiese, 1987).

Host partial resistance is considered an alternative to the use of resistant genotypes (Luke et al., 1975; Wang et al., 1994; Wilcoxson, 1981). Resistant genotypes present qualitative resistance, but are countered by an increased selection pressure on the crown rust population. This selection pressure leads to a rapid evolution of rust races which become resistant to the host; therefore the resistant varieties are rendered ineffective and short-lived (Barbosa et al., 2006). Host partial resistance is complex as a

result of the interaction of the following components: a reduced number of lesions, increased latent period, a smaller spore production, smaller pustule size, slow disease progression, and ultimately, a smaller rate of disease development (Parlevliet, 1987).

Host genetic resistance has become the primary method of controlling crown rust. Breeders employ this method of resistance by relying heavily on race-specific seedling genes expressing as a hypersensitive reaction. Such genes were originally found in cultivated oat (*A. sativa*). Once deployed in oat cultivars, the virulence of the crown rust population increased greatly, rendering the resistant genes ineffective. At present, the virulence of crown rust to most of these deployed genes has become fixed within the North American oat population. The lifespan of resistant cultivars resides around five years maximum, presenting a new challenge for oat breeders (Carson, 2008).

Breeding for disease resistance is regarded as the most effective and economical method for managing *P. coronata*. The discovery of crown rust resistant genes has become a high priority for oat breeders. Through the use of molecular mapping, many race-specific resistance genes have been characterized, including *Pc38*, *Pc39*, *Pc48*, *Pc68*, *Pc71*, *Pc91*, *Pc92*, and *Pc94* (Wight et al., 2003). This type of resistance is easily defeated because of selection pressure on the fungus resulting from massive and lengthy cultivation practices. The durability of these genes can be extended if multiple resistance genes are pyramided (Hittalmani et al., 2000) into oat cultivars because the likelihood of the pathogen mutating simultaneously at multiple sites for virulence is much lower than a single mutation for virulence. However, gene pyramiding is difficult due to dominance and epistatic effects of deploying multiple resistance genes.

Additionally, multiple resistance genes may exhibit similar reactions to a variety of races presenting a challenge when identifying specific rust resistance genes (Chen et al., 2007).

Originally, the *Pc* genes were introgressed from cultivated and wild hexaploid oats and deployed in new cultivars (Carson, 2010). Currently, *Pc68* is the only gene providing crown rust resistance in Canadian-grown oat cultivars, but reliance on this single gene could prove to be short-lived (Chen et al., 2007). *Pc68* has demonstrated potential for introgression into the oat germplasm while maintaining positive agronomic characteristics when combined with additional strategies for improving durability. Molecular markers will be of great assistance for further use of the *Pc68* gene and the discovery of alternate resistance genes (Kulcheski et al., 2010).

Diploid and tetraploid species of oat became the primary focus of more recent efforts to utilize the *Pc* genes. Diploid black oat (*A. strigosa*) has demonstrated well-documented resistance for a significant amount of time. Introgression of this resistance into cultivated hexaploid oat is highly difficult due to differences in ploidy levels and a deficiency in chromosome homology between *A. strigosa* and *A. sativa* (Carson, 2010). Some successes of introgression include the release of a cultivar containing *Pc94* from an *A. strigosa* accession that was effective against crown rust by the University of Wisconsin-Madison and the Agriculture Agri-Foods Canada-Winnipeg oat breeding programs (Aung et al., 1996). Another success is the oat cultivar Hi-Fi, released by North Dakota State University, a tetraploid species, *A. magna* CI 8330, with the *Pc91* resistance gene (McMullen et al., 2005). Recently the United States Department of

Agriculture has systematically evaluated slender oat (*A. barbata*) for crown rust resistance. This wild tetraploid species is considered to be of poor agronomic quality, but has been a source of resistance to powdery mildew and stem rust. Some resistance was observed in accessions of the slender oat species, but has remained untapped as of yet (Carson, 2008).

While *A. barbata* as a source of broad-spectrum resistance seems possible, achieving more durable resistance than from other species remains unlikely. It is possible that a variety of new resistance genes exists in the slender oat species that could prove useful if pyramided in various combinations into deployed cultivars. Though introgression will be challenging due to varying ploidy levels between tetraploid and hexaploid oat, a backcrossing method has been successfully used with stem rust genes when irradiated and treated with colchicines while using slender oat as the female parent (Carson, 2010; Rines et al., 2006).

One proposed method for coping with crown rust is the use of multiline cultivars. The use of such cultivars would increase intra-crop diversity for disease resistance and possibly achieve more durable resistance to the highly variable *P. coronata* (Browning et al., 1979; Marshall and Weir, 1985; Wolfe, 1985). The advantages to using multilines further include a reduction in the amount of initial inoculum requirements and a lower rate of epidemic development since only part of the fungal population is virulent upon any component of a multiline (Browning et al., 1979; Garrett and Mundt, 1999; Mundt, 2002). Resistant plants serve as a barrier to spore dispersal, thereby decreasing the spread of crown rust (Carson, 2009). Another potential barrier to disease spread in

multiline is the mixture of compatible races with incompatible races infecting the plants (Garrett and Mundt, 1999; Mundt, 2002). Multilines or cultivar mixtures may potentially inhibit or slow the rise of “super races” of crown rust, but ultimately fail to provide a durable solution (Barrett, 1980; Groth, 1976).

While the advantages of using multilines are numerous, many disadvantages were uncovered during a 2009 study. Virulence increased late in the season negatively impacting the durability of the resistance in the multilines evaluated. It was presumed that a continued cultivation of a multiline for a number of years could likely result in the production of rust super races which would effectively eradicate the multiline’s ability to reduce disease (Carson, 2009). Furthermore, the study concluded that isolates of the crown rust pathogen are able to yield a variety of unnecessary virulences without an apparent cost in fitness (Carson, 2008; Leonard, 2003). A core concept of multilines is their ability to copy occurrences in a natural ecosystem, yet the expected equilibrium between a diverse host population and the pathogen population does not demonstrate a reduction in disease levels or a lack of predomination in complex races. Iowa State University discovered that multiline cultivars are unable to compete agronomically with pure-line cultivars (Browning et al., 1979). Presumably, backcross breeding used to develop the isoline components of multilines is too conservative. By the time successful resistance has been achieved via backcrossing and a multiline has been released the agronomic performance of the recurrent parent is rendered obsolete. Additionally, the measure of crown rust control cannot compete with the high resistance of pure-lines, despite the inevitable short lifespan of the latter (Carson, 2009).

A more promising approach than multilines for oat breeding programs could be the use of race-nonspecific or partial crown rust resistance. Selection for such genes is difficult due to the low heritability, association with late maturity, and poor agronomic performance of sources of resistance. Also, it is tasking to distinguish partial resistance from race-specific seedling genes that are effective against crown rust. Even though selection for this type of resistance has been challenging, the development and use of a variety of molecular markers suitable for marker-assisted selection may remove some of the barriers to this approach (Carson, 2009).

Durable resistance is the goal, and a challenging one. The use of a wide array of resistance mechanisms in current germplasms indicates an increase in durability (Rubiales and Niks, 2000). Combining minor effects genes with race-nonspecific and race-specific seedling genes could also lead to longer lasting resistance. Molecular markers will be necessary to identify these genes (Kulcheski et al., 2010).

Association mapping

Association mapping (AM), also known as linkage-disequilibrium mapping, is a useful genetic methodology for detecting quantitative trait loci (QTL) in a diverse population in contrast to QTL linkage mapping which is generally performed on a biparental F₂ or backcross population. This is an especially useful approach in species for which mapping populations cannot be easily created. Association mapping is of particular use when attempting to exploit a wide range of genetic variation to identify QTL segregating across diverse germplasm. The ability to identify markers as closely

linked as possible to underlying QTL is reliant on how linkage disequilibrium (LD) decreases as the distance between QTL and marker increase. Linkage disequilibrium can be defined as the observed frequency of a gamete in a population minus the product of the frequencies of corresponding alleles (Bernardo, 2010). Association mapping is a method used to detect the relationships between phenotypic expression and genotypes within a population of individuals based on LD. The LD principle is based on the non-random association of alleles at adjacent loci within a population (Yu et al., 2011)(Yu et al., 2011).

The goal of genome wide association studies (GWAS) is to identify useful QTL, and hopefully genes, causal to a segregating trait of interest in the population. Association mapping can be used to identify useful allelic diversity and to generate a high resolution map detailing the diversity. Association mapping has never been conducted in oat and using this tool for detecting QTL could prove valuable to the oat breeding community (Jannink et al., 2001; Newell et al., 2011). Currently there are few bi-parental maps for oat, all of which are incomplete and fragmented (Jackson et al., 2009; Jackson et al., 2007). Expanding on these maps will significantly contribute to knowledge about the oat germplasm and could lead to important discoveries which will likely improve the performance of the oat crop.

This type of mapping is a most useful tool for screening a large population of unrelated individuals, such as a germplasm sample of an entire population. Association mapping may also be used to simultaneously analyze segregating biparental populations (Liu et al., 2011). Advantageously, association mapping is an efficient use of resources

since multiple traits can be studied simultaneously in a given population while using the same genotypic information. Additionally, more of the molecular markers are likely to be polymorphic allotting increased coverage of the studied genome than biparental maps. Multi-year and multi-location phenotypic data can also be obtained without incurring extra costs (Brescaglio and Sorrells, 2006; Rafalski, 2002).

There are several negative aspects to AM that should be considered. For example, a higher probability of making a Type I or Type II error is possible due to the presence of unaccounted subdivisions within a population structure (Pritchard et al., 2000). Covariances among individuals could arise unaccounted for in the model, generating bias in estimated allelic effects (Kennedy et al., 1992). An increase in Type II error can be attributed to lower correlation between markers and genes, an unbalanced design based on the presence of alleles at varying frequencies, or a multiple-testing problem associated with very strict genome-wide significance thresholds (Carlson et al., 2004). Ultimately, these limitations imply that association mapping will be inadequate for detecting rare variants or genes that are variable between populations while remaining fixed within subpopulations (Brescaglio and Sorrells, 2006). Nevertheless, using association mapping to evaluate quantitative traits is a promising strategy (Lu et al., 2010; Yu et al., 2011) with the potential to decode complex traits within a genome (Flint-Garcia et al., 2003).

Single nucleotide polymorphism markers

Using markers to identify genes associated with crown rust resistance will potentially remove barriers associated with achieving durable resistance (Carson, 2008). Single nucleotide polymorphism (SNP) markers are becoming increasingly popular at present because they overcome some limitations associated with other types of markers. SNPs are abundantly frequent and suitable for high throughput genotyping using automated platforms (Chen et al., 2007). These markers are highly stable and are commonly located in the gene coding region, promoting the discovery of genes associated with phenotypic traits (Yanagisawa et al., 2003). SNPs can also be found in the non-coding region. Thus, in addition to contributing directly to the phenotype, they can be associated with a phenotype via linkage disequilibrium or genetic linkage (Chen et al., 2006). Additionally, SNPs are able to be used efficiently and at a relatively low cost since a number of semi-automated scoring platforms already exist for their usage (Chen et al., 2007). SNPs have been widely employed in a variety of genetic studies for wheat (Mochida et al., 2003), barley (Close et al., 2009), sugar beet (*Beta vulgaris* L.) (Mohring et al., 2004), soybean (*Glycine max* L.) (Zhu et al., 2003), and rice (Nasu et al., 2002).

While SNPs are relatively inexpensive compared to other markers, there is a significant up-front cost associated with SNP equipment. The initial costs are offset by the abundance of benefits which can be achieved for plant breeders as SNP marker information is generated. For plant breeding purposes, SNPs feature multiplexing capabilities, such as single-base extension assay, including the facilitation of gene

pyramiding. SNPs have already been used to distinguish between plants homozygous for the rust resistance gene *Pc68* and those that are susceptible heterozygous individuals. This is useful for screening and eliminating heterozygotes early in a breeding program (Chen et al., 2006) as well as to select against plant types lacking the trait or traits of interest, especially if the trait is genetically controlled or highly complex (Bailey and Edwards, 2007).

Diversity arrays technology markers

Diversity arrays technology (DArT) markers are a relatively new technology. These markers are based on microarray hybridization which detects and compares the presence or absence of individual DNA fragments (Jaccoud et al., 2001; Wenzl et al., 2004). DArT markers, like SNPs are suitable for high throughput application and can be rapidly developed for nearly any genome. These molecular markers are capable of detecting a large number of parallel markers without requiring the development of an assay once these markers have been identified (Kilian et al., 2003). DArT markers were developed for a range of species including *Arabidopsis* (*Arabidopsis thaliana*) (Wittenberg et al., 2005) and cassava (*Manihot esculenta*) (Xia et al., 2005), but have been used in grass crops, such as wheat (Akbari et al., 2006) and rye (Bolibok-Bragoszewska et al., 2009). While these markers are being used more frequently in commonly studied plant species, crops with high polyploidy levels, such as wheat, indicate a possible decrease in map resolution (Akbari et al., 2006). The use of these markers in triticale (Badea et al., 2011) demonstrates that DArTs are an efficient tool for

evaluating genetic diversity. DArTs are expected to complement existing marker technologies and can be used for fine mapping, identifying QTL, screening genomes, and whole-genome marker-assisted selection or introgression of selected genomes (Badea et al., 2011).

DArT markers are not sufficiently usable with the aid of other markers due to a heavy reliance on the presence or absence of hybridization signals (Akbari et al., 2006). Another negative component to DArTs is that they are a dominant marker system. Therefore, it is impossible to score heterozygous individuals without resulting in a high segregation distortion (Francki et al., 2009). Additionally, DArT markers remain unsuitable for marker assisted selection with cost being the primary limiting factor preventing widespread use (Kilian et al., 2003). Another limitation of DArTs is the ownership rights of these markers, which is restricted to the company “A Diversity Arrays Technology Pty Ltd (DArT P/L) (Diversity Arrays Technology, 2009).

One advantage to this technology is that the DArT platform can provide comprehensive genome coverage without prior sequencing information (Jaccoud et al., 2001; Wenzl et al., 2004), making this an excellent tool for little-characterized genomes, such as oat. DArT markers have already been used to develop the first complete oat linkage map, shedding light on the oat genome ancestry and the crop’s domestication (Oliver et al., 2011).

Conclusions

Oats are a complex, but beneficial crop with a number of human health advantages. In order to provide oat growers and breeders with the tools to help oat succeed, more information about the oat genome is needed. Employing molecular markers, such as DArTs and SNPs, will contribute to more comprehensive QTL mapping of the oat genome. This map combined with associated phenotypic observations represents an association map study which will lead to the generation of better oat varieties. These varieties could feature many advantages, including resistance to crown rust, thereby eliminating one of the greatest challenges to global oat breeders.

CHAPTER III

METHODOLOGY

Association mapping panels

The association mapping panel consisted of three sub-panels, referred to as the ‘Winter’, ‘Spring’, and ‘Core’ panels, respectively. These panels were planted at four locations: Castroville, TX, Baton Rouge, LA, Fargo, ND and St. Paul, MN (Figure 3.1). Castroville, TX and Baton Rouge, LA serve as locations where winter oats are commonly grown, while Fargo, ND and St. Paul, MN serve as sites where spring oats are commonly grown. The panels were grown for two years at each location for a total of two repetitions, except at the Fargo, ND location, where a single rep was grown. Each of these panels was grown for a total of two years at four locations in a randomized complete block design. Spring, winter and core panels were separated in the field by a row of wheat. Seeds were planted using a Heague 1000® small grains experimental drill to plant 48 inch long head rows with 15 inch row spacing, except in Fargo, ND. At this location, seeds were planted as a hill plot nursery in 4-row plots, 2 meters (78.74 inches) long with 30 centimeter (11.81 inches) row spacing. In Castroville, TX seeds were planted on November 18, 2009 and November 17, 2010, respectively. In Baton Rouge, LA seeds were planted on December 12, 2009 and November 29, 2010, respectively. In Fargo, ND seeds were planted May 27, 2010 and May 26, 2011, respectively. In 2011, planting was delayed due to wet soil conditions; however, this delay also provided for very heavy natural crown rust infection. In St. Paul, MN seeds were planted on April

28, 2010 and May 11, 2011, respectively. Pure seed was obtained via seed increase trials for the breeder lines analyzed in this study.



Figure 3.1. The four locations where oat panels were grown.

The spring panel is composed of 360 breeder lines and six checks. Five of these checks are designated spring checks and include the following oat lines: ‘Ogle’, ‘CDC Dancer’, ‘HiFi’, ‘Leggett’, and ‘Gem’. The remaining check is a designated winter oat named ‘Horizon 270’. These checks were repeated five times each. There were a total of 414 plots in the spring evaluation panel (Table 3.1). Breeder lines were contributed by the Agricultural Research Station (ARS)-Aberdeen, ID, Cornell University,

University of Illinois, Purdue University, University of Wisconsin, ARS-Minnesota, North Dakota State University, Ottawa, University of Saskatchewan, and Winnipeg, Canada.

The winter panel consisted of 120 breeder lines, five winter checks and one spring check. The winter checks included ‘TAMO397’, ‘TAMO406’, ‘LA99016’, ‘Horizon 270’, and ‘Rodgers’. The spring check is referred to as ‘Ogle’. Each check was repeated five times. There were a total of 160 plots in the winter panel (Table 3.1). Breeder lines were contributed by Louisiana State University, Texas A&M University, and North Carolina State University.

The core panel consisted of 108 lines designated as elite material by North American oat breeders (Table 3.1). The genotypes used in this panel were included in the winter and spring panels, depending on growth habit. The core panel was not analyzed separately for the purposes of this thesis.

Table 3.1. List of genotypes, source of origin, growth habit and pedigree for all oat lines tested in this study.

NAME	SOURCE	GROWTH HABIT	PEDIGREE
001A1-24-2-4-1-3	Indiana	Spring	001A1-24-2-4-1-3
00Ab6112	Idaho	Spring	94Ab 6921/Ajay
00Ab6711	Idaho	Spring	83Ab 3250/Ab Sp9-2
00Ab6963	Idaho	Spring	82Ab 248/Ab Sp9-2
00Ab7006	Idaho	Spring	90Ab 1322/Ab Sp9-2
00Ab7085	Idaho	Spring	90Ab 1322/Ab Sp9-2
00Ab8118	Idaho	Spring	90Ab 1322/Derby
0216A1-1-55	Indiana	Spring	0216A1-1-55
0219A1-84-4-4-4-4	Indiana	Spring	0219A1-84-4-4-4-4
021A1-78-1-5	Indiana	Spring	021A1-78-1-5
0222A1-21-7-5-1-1	Indiana	Spring	0222A1-21-7-5-1-1
026A1-88-2-2	Indiana	Spring	026A1-88-2-2
027A1-87-8-1	Indiana	Spring	027A1-87-8-1
02Ab5836	Idaho	Spring	95AB1284/Powell
02Ab6078	Idaho	Spring	95Ab1284/Powell
02Ab6655	Idaho	Spring	95Ab1284/Powell
02HO-139	Idaho	Spring	Maverick/IA91324-2
02HO-209	Idaho	Spring	IA91001-2/Powell//Powell
04P07B-GT3D	Ottawa	Spring	OT2022/Leggett
0513A1-18-5	Indiana	Spring	0513A1-18-5
0514A1-16-3	Indiana	Spring	0514A1-16-3
0528A1-1	Indiana	Spring	0528A1-1
053B1-95	Indiana	Spring	053B1-95
0541A1-1	Indiana	Spring	0541A1-1
055A1-3-5-3	Indiana	Spring	055A1-3-5-3
059A1-2-2-4	Indiana	Spring	059A1-2-2-4
833-99AB118	Louisiana	Winter	PURIFICATION SLECTION OF '833
8669C2-4-6-16-33	Indiana	Spring	8669C2-4-6-16-33
95Ab12770	Idaho	Spring	86Ab1867/87Ab5597
95Ab13050	Idaho	Spring	84Ab825/86Ab5259
971A9-7-4-11	Indiana	Spring	971A9-7-4-11
97Ab7761	Idaho	Spring	IL81-2570/83Ab3250
97Ab7767	Idaho	Spring	IL81-2570/83Ab3250
9876C1-2-1-5-2-4-1	Indiana	Spring	9876C1-2-1-5-2-4-1
98Ab7265	Idaho	Spring	Corbit/88Ab3073

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
99Ab10937	Idaho	Spring	MN83207/74Ab2608
99Ab10971	Idaho	Spring	90Ab1322/Monida
99Ab10987	Idaho	Spring	90Ab1322/Monida
99Ab11098	Idaho	Spring	90Ab1322/91Ab2
99Ab11136	Idaho	Spring	90Ab1322/91Ab2
99Ab11227	Idaho	Spring	90Ab1322/SP3-2
99Ab11391	Idaho	Spring	87Ab6153/SP3-9
99Ab11787	Idaho	Spring	91Ab2/SP9-7
Aarre	Finland	Unknown	Puhti(Hannes/Ryhti) X Veli (Titus/Sisu)
Adrew	Indiana	Spring	Adrew
Ajax	Winnipeg	Spring	Victory(Milton(Sweden)/Milton(Sweden)) X Hajira(Sel from Algeria/Sel from Algeria)
Ajay	Idaho	Spring	74AB1952(unknown/unknown) X 74Ab2608(Cayuse/Otana)
Akiyutaka	Japan	Unknown	Unknown(Uknown/Unknown) X Unknown(Unknown/Unknown)
Allen	Indiana	Spring	unnamed_4878 (Purdue 5124 A6-4/Milford)/unnamed_6500 (unnamed_6496/unnamed_6499)
Anthony	Indiana	Spring	White Tartar/Victory (Milton Sweden/Milton Sweden)
ARDENTE	Norway	Spring	KANTON_X_BELINDA
Asencao	Brazil	Winter	Nora X Iowa Multiline(AsencaoE)
Assiniboia/S42	Saskatchewan	Spring	AC Assiniboia(90GC144/Robert) X S42(SunII/unnamed_18354)
Aurora	North Carolina	Winter	Red Rustproof (sel. From Red Algerian (Stanton, 1954 or introduced from Mexico Stanton, 1954/sel. From Red Algerian (Stanton, 1954 or introduced from Mexico Stanton, 1954)/Red Rustproof (sel. From Red Algerian (Stanton, 1954 or introduced from Mexico Stanton, 1954/sel. From Red Algerian (Stanton, 1954 or introduced from Mexico Stanton, 1954)
Ave117.2	Saskatchewan	Spring	INIA, Carillanca Station, Temuco, Chile
AVENY	Norway	Spring	BELINDA_X_SW 951865
Balado	United Kingdom	Spring	97-48Cn (Birnarn/92-88ACn3/1)/Kingfisher (Gerald/Chamois)
Baler_CDC	Saskatchewan	Spring	Av2401/2(Av1893/11/11/19/1 X Saladin) X SO 86044 (W79478/Calibre)
BARRA	Norway	Spring	SELMA_X_
Belinda	Sweden	Spring	Frode(SvVg75842/Dula) X Silvano(unknown/unknown)
Bia	Sweden	Spring	Unknown(Uknown/Unknown) X Unknown(Unknown/Unknown)
Biri	Norway	Spring	Grakall (Voll/Nidar II)/Lena (Sang/Unisignum)
Blaze	Illinois	Spring	IL83-7646(P72261-2-3-2/IL75-5665) X Newdak (unnamed_6609/Ogle)
Bond	North Carolina	Winter	Avena sterilis (strain from Algeria, 1918) (wild material/wild material)/Golden Rain (Probsteier/Probsteier)

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
Boudrias	Alberta	Spring	LAO-597-NZ(AC Belmont/AC Assiniboia) X LAO-597-NZ(AC Belmont/AC Assiniboia)
Bountiful	United Kingdom	Spring	Unnamed_5517(unnamed_8874/Black Winter) X Unnamed_5520(Goldfinder/Black Tartar)
Boyer_CDC	Saskatchewan	Spring	SO 82030 (Cascade/Hudson(Canada)) X OT235 (CI964P2-R4/C4963P2HHAM4)
Brooks	North Carolina	Winter	unnamed_6911 (Carolee/Fulgrain)/unnamed_14653 (Fulgrain/unnamed_14652)
Brown 1409-164	Ottawa	Spring	Brown 1409-164
Buckskin	Illinois	Spring	AC Assiniboia(90GC144/Robert) X IL92-6728(IL86-5262/unnamed_181093)
Buffalo	United Kingdom	Spring	85-47CnIII/2(84-24/Solva) X 90-153Acn2(Gerald/89-164)
Bullion	United Kingdom	Spring	08974CnI/1 (HOJ36-4/4n/07609CnV/3/5n)/ 08944Cn1 (08252CnIII/3n/08671CnI/2n)
Bw103	Saskatchewan	Spring	INTA, Barrow Station, Tres Arroyos, Argentina
Bw1103	Saskatchewan	Spring	INTA, Barrow Station, Tres Arroyos, Argentina
Bw4903	Saskatchewan	Spring	INTA, Barrow Station, Tres Arroyos, Argentina
Calibre	Saskatchewan	Spring	Gemini(bulk progeny of cross/Unknown) X Clintford(Purdue 5124A6-4/Milford)
Cantal	Ottawa	Spring	QO190.2 / QO189.5 (QO190.2 = W.B.16384 / Dorval // Fraser)
Carolee	North Carolina	Winter	Letoria (Lee/Victoria - Argentina)/unnamed_6503(Clinton/unnamed_6502)
CDC Minstrel	Saskatchewan	Spring	OT293 / CDC Dancer
CDC Orrin	Saskatchewan	Spring	OT349 / J775-1
CDC Weaver	Saskatchewan	Spring	OT369 / OT2007
Ceirch Du Boch	North Carolina	Winter	Ceirch Du Boch
Centennial	Wisconsin	Spring	N569-42-51(Holden/irradiated monosomicated monosomic alien sub. line) X Unnamed_6468(Froker/Stormont)
Chaps	Illinois	Spring	Ogle(Brave/unnamed_336) X Unnamed_5458(IL75-5667/Ogle)
Chernigovskij 27B	Ukraine	Unknown	Jaycee(WIX643-33/Putman) X Chernigovskii83(unknown/Unnamed_16170)
Cherokee	Iowa	Spring	Iowa No.D69(Richland/Green Russian) X Bond (Avena sterilis(strain from Algeria,1918)/Golden Rain)
Chinese 4	Ottawa	Spring	Chinese 4
CI 4706-2	Unknown	Unknown	Unknown X Unknown
CI1712-5	Minnesota	Spring	Siberian selection (Ottawa)
CI7035-1	Minnesota	Spring	Buck selection 1952 (Argentina)
CI8000-4	Minnesota	Spring	AR 2-31-20 (Arkansas)
Clav 6209	Unknown	Unknown	SantaFe(sel. from Argentina oat(Coffman F.A. 1977)/sel. from Argentina oat (Coffman F.A. 1977) X Benton(Sac/Sac)
CILLA	Norway	Spring	A 83180_X_STIL
CIRCLE	Norway	Spring	Sv 92158_X_Sv 923793
Classic	Indiana	Spring	Ogle (Brave/unnamed_336)/unnamed_9285 (IN09201/P8221RB1-44-6)
Clintford	Indiana	Spring	Purdue 5124 A6-4 (Clinton 59/unnamed_5254)/Milford (Victory/S172)
Clintland	Indiana	Spring	Clinton 59 (unnamed_6925/Bond)/unnamed_5257 (Clinton 59/unnamed_5258)

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
Clintonland 60	Indiana	Spring	Clintonland (Clinton 59/unnamed_5257)/unnamed_9214 (Clintonland/unnamed_9210)
Clintonland 64	Indiana	Spring	unnamed_6497 (Clintonland/unnamed_6425)/unnamed_9222 (Clintonland/unnamed_9221)
Clinton	Iowa	Spring	Iowa No.D69(Richland/Green Russian) X Bond (Avena sterilis(strain from Algeria,1918)/Golden Rain)
Clinton 59	Indiana	Spring	unnamed_6925 (Richland/Green Russian)/Bond (Avena sterilis - strain from Algeria, 1918/Golden Rain)
Coker 227	South Carolina	Winter	Unnamed_6857(Unnamed_6772/unnamed_6786) X Unnamed_6855(Suregrain/unnamed_6854)
Coker 234	South Carolina	Winter	Unnamed_6857(Unnamed_6772/unnamed_6786) X Unnamed_6855(Suregrain/unnamed_6854)
Coker 242	North Carolina	Winter	Victorgrain (Victoria - Argentinian/Fulgrain)/unnamed_12823 (Fulwood/unnamed_6315)
Coker 716	North Carolina	Winter	Coker 62-30 (unknown/unknown)/Beltsville Selection 279 (unnamed_9419/Clintonland)
Colberson	North Carolina	Winter	Colberson
Columbia	Indiana	Spring	offtype plant selection from Fulghum (Fulghum/Fulghum)/offtype plant selection from Fulghum (Fulghum/Fulghum) Red Rust Proof
Corondo	North Carolina	Winter	Corondo
Dal	Wisconsin	Spring	X660(Belar/Trispermia) X Beedee(Beacon/unnamed_4877)
Dancer_CDC	Saskatchewan	Spring	OT344(OT235/OT743) X W90279(Konrad/OT244)
Dane	Wisconsin	Spring	WI X3530-47(N569-42-51/Froker) X Ogle(Brave/Unnamed_336)
Delair	North Carolina	Winter	Fulghum (Red Rustproof/Red Rustproof)/Bond (Avena sterilis - strain from Algeria, 1918/Golden Rain)
Derby	Saskatchewan	Spring	Calibre / Cascade
DeSoto	North Carolina	Winter	Lee (Winter Turf/Aurora)/Victoria - Argentina (sel. From artificial (mass) population of lines 64q, 64r, 64t, grown in Uruguay (increased in Argentina)
Dominik (Bauer)	Germany	Spring	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
Drummond	New Zealand	Unknown	Unknown (unknown/Unknown) X Unknown(unknown/unknown)
Excel	Indiana	Spring	sle. From Wintok (Wintok/Wintok)/sle. From Wintok (Wintok/Wintok) (Hairy Culberson/Winter Fulghum)
Exeter	Winnipeg	Spring	Victory(Milton(Sweden)/Milton(Sweden)0 X Rusota(Green Russian/Green Russian)
Firth	United Kingdom	Spring	CR 3/418 (unknown/unknown)/ Flamingsvita (Marga/Selma)
FL0047-J9	Florida	Winter	Horizon 474/TX97C1168
FL0115-J2	Florida	Winter	FL97AB15-A5-B6/TX97C1130
FL0238BSB-22	Florida	Winter	TX96M1560/ND 961161
FL03001BSB-S7	Florida	Winter	LA9339E45/Bw3996
FL03053-S06-15-B-S1B	Florida	Winter	LA989IBI-51-B-II-I2/UFRGS 01B6189-6-3
FL03129-Ab7	Florida	Winter	FL92OHR28,204 /NCO348-U3//Bw 4899/3/UPF96146-5-7-2

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
FL03146BSB-S1-B-S1	Florida	Winter	TAMO 405/HZN 474
FL03167BSB-145	Florida	Winter	LA9818IBIB-I2-B-II(LA90151C11-2-1/TX96M1554)/FL0205 F1 (P973A38-3-6/202-97 (Uruguay))
FL03167BSB-147	Florida	Winter	LA9818IBIB-I2-B-II(LA90151C11-2-1/TX96M1554)/FL0205 F1 (P973A38-3-6/202-97 (Uruguay))
FL03167BSBS-3	Florida	Winter	LA9818IBIB-I2-B-II(LA90151C11-2-1/TX96M1554)/FL0205 F1 (P973A38-3-6/202-97 (Uruguay))
FL03184-FLID-B-S1	Florida	Winter	LA9824IBI-19-I2-C-14-II/UFRGS 017130-3(Naked, Porto Alegre)
FL04155-S06-31-B-S1	Florida	Winter	FL03139 F1 (TROPHY/MN00226)/FL03224 F1 (UPF94174-1/FL9605-A6-B4)
FL04178-FLID-B-S-2	Florida	Winter	FL03144 F1 (Bw 1000/SD000813) /LA9914IBI-23-12-G7
FL99084-J2	Florida	Winter	TX96D210FL/98008 F1(LA90151-BB-11-2-1/UFRGS 940556)
FL99153FBS-45-1-B-S-B-S1-B-S1	Florida	Winter	TX95C3147/FL98007 F1(SC 942283/UFRGS 940556)
FL99212-D6	Florida	Winter	UFRGS 921260/FL98091 F1 (P8674B1-2-4-2-5/TX97C1130)
Flaemingsnova	Germany	Spring	Pendek(Flamingold/Binder) X Flamingsstahl(unnamed_6736/Dippes WeiB)
Florida 167	North Carolina	Winter	Bond (Avena sterilis - strain from Algeria, 1918/Golden Rain)/Fulghum (Red Rustproof/Red Rustproof)
Florida 500	North Carolina	Winter	Florad (Floriland Irradiated/unknown)/unnamed_6485 (unnamed_6484/unnamed_6483)
Florida 501	Florida	Winter	Florad(Floriland Irradiated/Unknown) X Unnamed_6485(unnamed_6484/Unnamed_6483)
Floriland	North Carolina	Winter	Florida 167 (Bond/Fulghum)/Landhafer (Red Algerian/Red Algerian)
Ford Early Giant	Unknown	Unknown	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
Forkedeer	North Carolina	Winter	sel. From Fulghum (699-2011, CI 2499) (Flughum/Fulghum)/sel. From Fulghum (699-2011, CI 2499) (Flughum/Fulghum)
Freddy	Germany	Spring	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
FREJA	Norway	Spring	Vg 75842_X_DULA
Fulghum	Georgia	Winter	Red Rustproof(Sel from Red Algerian(Stanton 1954)or introduced from Mexico (Stranton,1954)/sel from Red Algerian (Stranton1954)or introduced from Mexico(Stranton,1954) X Red Rustproof(Sel from Red Algerian(Stanton1954)or introduced from Mexico(Stranton,1954)/Sel. from Red Algerian(Stranton1954)or introduced from Mexico (Stranton,1954)
Fulgrain	North Carolina	Winter	Big Boy (unknown/unknown)/Navarro (sel. From North American landrace/sel. From North American landrace)
Furlong	Winnipeg	Spring	W93069(Pg16)(W86226(Pg16)/Robert) X Ac Assiniboia(90GC144/Robert)
Gehl	Ottawa	Spring	06751-64-1(NO70-1/05305-63) X 06540(AC Baton/06523)
Gem	Wisconsin	Spring	WI X6051(MO 07468/unnamed_4882) X Ogle (Brave/unnamed_336)
Gere	Norway	Spring	Gere
GN04399	Norway	Spring	GN04399

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
Goslin	Ottawa	Spring	OA952-3(OA797-7/02540-3-7-2) X 06196(Pc48/OA952-3)
Grane	Norway	Spring	unknown/unknown
Grenader	Norway	Spring	Hedmarkshavre/Hedmarkshavre
GUNHILD	Norway	Spring	Sv 97707_X_SANNA
H927-1-6-1-x-x-24	Unknown	Unknown	Hairy Culberson(Culberson/Culberson) X unnamed_18804(Fulghum/RedRustproof)
HA05AB10-47	Idaho	Spring	95Ab1284 / Powell
HA05AB10-51	Idaho	Spring	95Ab1284 / Powell
HA05AB16-31	Idaho	Spring	Powell / 96Ab9074
HA05AB20-1	Idaho	Spring	82Ab248/ND930122
HA05AB21-7	Idaho	Spring	90Ab1322/ND930122
HA05AB22-9	Idaho	Spring	94Ab5543/ND 930122
HA05AB29-17	Idaho	Spring	AbSP 9-2/MN 94112
HA05AB29-39	Idaho	Spring	AbSP 9-2/MN 94112
HA05AB31-15	Idaho	Spring	90Ab1322/MN 94112
HA05AB34-48	Idaho	Spring	90Ab1620/95Ab12743
HA05AB35-16	Idaho	Spring	95Ab12743/90Ab1322
HA05AB36-33	Idaho	Spring	96Ab8796/95Ab12743
HA05AB38-22	Idaho	Spring	97Ab8510/90Ab1322
HA05AB38-39	Idaho	Spring	97Ab8510/90Ab1322
HA05AB41-38	Idaho	Spring	84Ab358 / 95Ab12729
HA05AB42-20	Idaho	Spring	P909A23-1 / AbSP9-2
HA05AB53-40	Idaho	Spring	94Ab5326 / 95Ab10854
HA05AB9-32	Idaho	Spring	91Ab502 / ND930122
HA05AB9-52	Idaho	Spring	91Ab502 / ND930122
HA08-03X09-1	Idaho	Spring	98Ab6346/TAMO6-4
HA08-03X31-1	Idaho	Spring	99Ab11899/TAMO7-3
HA08-03X45-1	Idaho	Spring	Ajay/TAMO5-4
HA08-03X49-1	Idaho	Spring	CDC Dancer/Monida
Harrison	South Carolina	Winter	unknown/unknown
Hazel	Illinois	Spring	Coker 227(unnamed_6857/unnamed_6855) X unnamed_5457(Clintford/Portal)
HiFi	North Dakota	Spring	ND90141(ND894904/ND852107) X ND900118(MN78142/ND852158)
HLA05AB1-34	Idaho	Spring	95Ab12970 / 95Ab11091
Horizon 201	Florida	Winter	FL92OHR35183-Y1/TX96M1384 (=FL99201-D29-E1)
Horizon 270	Unknown	Unknown	FL95MEO29/TX93M2107
HORIZON LA976	Louisiana	Winter	FL92OHR26763/TX93M2107
Hurdal	Norway	Unknown	A90017(Unkown/Unknown) X Martin(Grakall/Tador)

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
IL00-654	Illinois	Spring	Brawn/IL95-8346
IL02-10836	Illinois	Spring	IL97-19238/SD 97852
IL02-5630	Illinois	Spring	IL95-1555/IL97-18116
IL02-8011	Illinois	Spring	Tack / IL94-3961 (IL88-14751/IL86-4189)
IL02-8658	Illinois	Spring	Tack /Spurs
IL03-2658	Illinois	Spring	IL94-784/IL94-3961
IL03-7936	Illinois	Spring	IL96-16806 /IL98-18614
IL04-2727	Illinois	Spring	Sesqui/ IL3538
IL04-3664	Illinois	Spring	Spurs/ IL96-11037
IL04-4410	Illinois	Spring	IL96-3151/ IL98-14767
IL04-7077	Illinois	Spring	Buckskin / Tack
IL05-10015	Illinois	Spring	IL00-8279/ IL00-8622
IL05-10069	Illinois	Spring	IL00-8439/ IL98-10145
IL05-11942	Illinois	Spring	P971A9-7-4/ IL00-8279
IL05-1705	Illinois	Spring	OA1021-1/ IL00-4858
IL05-1778	Illinois	Spring	OA1021-1/ IL00-8279
IL05-3337	Illinois	Spring	IL96-10351/ OA1021-1
IL05-3806	Illinois	Spring	IL98-2344/ Buckskin
IL05-3928	Illinois	Spring	IL98-2344/ IL00-8279
IL05-6223	Illinois	Spring	IL99-1515/ OA1021-1
IL05-8515	Illinois	Spring	IL00-4858/ IL2838-1
IL05-9330	Illinois	Spring	IL00-8007/ Spurs
IL05-9931	Illinois	Spring	IL00-8279/ IL00-8622
IL05-9948	Illinois	Spring	IL00-8279/ IL00-8622
IL06-1161	Illinois	Spring	P971A10-4-6/ IL00-7931
IL06-3258	Illinois	Spring	Buckskin/ Winona
IL06-3751	Illinois	Spring	IL00-205/ Buckskin
IL06-5456	Illinois	Spring	IL00-4827/ Buckskin
IL2250-15 (PI641978)	Illinois	Spring	Clintonland 64*5/IL86-5698
IL2250-18 (PI641979)	Illinois	Spring	Clintonland 64*5/IL86-5698
IL2294-1 (PI641996)	Illinois	Spring	Clintonland 64*5/IL86-6404
IL2294-2 (PI641997)	Illinois	Spring	Clintonland 64*5/IL86-6404
IL2294-3 (PI641998)	Illinois	Spring	Clintonland 64*5/IL86-6404
IL2294-8 (PI641999)	Illinois	Spring	Clintonland 64*5/IL86-6404
IL250-14 (PI641977)	Illinois	Spring	Clintonland 64*5/IL86-5698
IL250-3 (PI641976)	Illinois	Spring	Clintonland 64*5/IL86-5698

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
IL2815 (PI641965)	Illinois	Spring	IL86-5698/IL86-1156//Ogle/IL86-6404
IL2838 (PI641966)	Illinois	Spring	IL86-5698/IL86-1156//Ogle/IL86-6404
IL2858 (PI641967)	Illinois	Spring	IL86-5698/IL86-1156//Ogle/IL86-6404
IL2901 (PI641968)	Illinois	Spring	IL86-5698/IL86-1156//Ogle/IL86-6404
IL3555 (PI641970)	Illinois	Spring	IL86-5698/IL86-1156//Ogle/IL86-6404
IL75-5665	Illinois	Spring	Coker 227// Clintford / Portal
IL75-5743	Illinois	Spring	Coker 227 // CI5068 /CI 8074
IL86-1156	Illinois	Spring	Ogle*2//IL75-5743
IL86-4189	Illinois	Spring	Lang/IL75-5662//IL79-1776
IL86-5698 (PI539875)	Illinois	Spring	IL74-5234/IL75-5662//IL81-1454
IL86-5698-3	Illinois	Spring	IL86-5698(unnamed_7075/IL81-1454) X IL86-5698(unnamed_7075/IL81-1454)
IL86-6404 (PI539874)	Illinois	Spring	IL74-5234/IL75-5662//IL81-1454
IL98-10145	Illinois	Spring	IL88-854 (Newdak/IL82-1657 (Froker/Hazel)) / IL90-7147 (IL86-4467 /Pennuda)
IN09201	Indiana	Spring	IN09201
Jay	Indiana	Spring	P8640A1-31(P79103B1-7-2/Unnamed_9242) X P8640A1-31(P79103B1-7-2/Iowa H728)
Jerry	North Dakota	Spring	Valley(unnamed_2588/Porter) X ND810458 (unnamed_6644/unnamed_6645)
Kangaroo	Australia	Winter	Unnamed_15143(SV88123-104/WA84Q406) X SV86153_101(unnamed_11891/Unknown)
Kanota	Kansas	Winter	Fulghum(Red Rustproof/Red Rustproof) X Fulghum (Red Rustproof/Red Rustproof)
Kapp	Norway	Spring	Grakall (Voll/Nidar II)/Tador (Sang/Unisignum)
Kaufman	Alberta	Spring	AC Assiniboia(90GC144/Robert) X AC Medallion(90GC142.143/Dumont)
Kolbu	Norway	Spring	unknown/unknown
LA02012-S-B-139-S2-B-S2-B-S2	Louisiana	Winter	LA9513IBTB-80-I1-B/MF9424-24
LA02035-I-J1	Florida	Winter	LA978GIB-172/HZN LA976
LA0210SBSBSBSB-S1	Louisiana	Winter	9513BTB-80-I2/TX00D176
LA03012SBSBSB-12	Louisiana	Winter	LA966BIB32-1-1-B/TX01AB7097
LA03012SBSBSB-61	Louisiana	Winter	LA966BIB32-1-1-B/TX01AB7097
LA03018SBSBSB-65-S1	Louisiana	Winter	LA9819IBI-75-2-B/FL9418-A3-B4-B-I
LA03040SBSBSB-83	Louisiana	Winter	LA9339/HORIZON321
LA03046SBS7-B-S1	Louisiana	Winter	LA9339/TAMO405
LA03060SBSBSB-S1	Louisiana	Winter	TX96M1398/LA9339
LA03063SBSBSB-6	Louisiana	Winter	UFRGS 952521/LA966BIB32-1-1-B
LA03063SBSBSB-S4	Louisiana	Winter	FL92OHR26763/TX93M2107
LA03066SBS-L1	Louisiana	Winter	UFRGS 952521/LA966BIB32-1-1-B
LA04004SBSB-121	Louisiana	Winter	UFRGS995080-1/9818IBI-24-B-I1
LA04004SBSB-61-B-S1	Louisiana	Winter	LA97006GBS-30-1-C/LA90113-1-B3-AFL2-1-19-3-1
LA04014SBSB-39	Louisiana	Winter	LA97006GBS-30-1-C/LA90113-1-B3-AFL2-1-19-3-1

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
LA04018SBSB-181	Louisiana	Winter	TX96M1385/LA604//833
LA04018SBSB-86	Louisiana	Winter	HARRISON/TAMO405
LA05006GSBS-7-S1	Louisiana	Winter	HARRISON/TAMO405
LA06058SBS-32-S1	Louisiana	Winter	LA9339/TAMO 405
LA06059SBS-84-S1	Louisiana	Winter	TAMO 405/HZN LA976
LA604	Louisiana	Winter	Coker76-30/5/Coker75-27/4/Coker76-29/3/Coker76-23//Coker75-28/C18335/6/Coker84-15/4/Blizzard/3/Coker 79-21//Coker 234/C19139
LA9339	Louisiana	Winter	Coker85-13/X470
LA97006GSB-59-2-4-SBS1	Louisiana	Winter	TAMO 405/LA99016
LA99016	Louisiana	Winter	TX96M1385/SECTLA495
LA99017	Louisiana	Winter	TX96M1385/LA604
Landhafer	North Carolina	Winter	Red Algerian (native cultivated red oat of Algeria/unknown)/Red Algerian (native cultivated red oat of Algeria/unknown)
Lang	Illinois	Spring	Tyler(Clintlnd60/unnamed_4021) X Orbit (Alamo/unnamed_5461)
LAO-900-042	Ottawa	Spring	OT903 / Kaufmann // Ronald
Lee	North Carolina	Winter	Winter Turf(unknown/unknown)/Aurora (Appler/Appler)
Lena	Norway	Spring	Sang (Sv 01771/Condor)/Unisignum (Regent - Bickelmann, 1989/Phonix)
Lennon	United Kingdom	Spring	Lennon
LIPOPLUS	Norway	Spring	BELINDA_X_MATILDA
Lutz	Germany	Spring	Unnamed_11632(Flamingsstern/AJ20-61) X Fagot(unknown/unknown)
Madison	North Carolina	Winter	unnamed_8035 (Delair/Carolee)/Coker 69-20 (Coker 62-30/Beltsville Selection 279)
Maida	North Dakota	Spring	ND873126/ASSINIBOIA
Maldwyn	United Kingdom	Spring	Victory(Milton(Sweden)/Milton(Sweden)) X Radnorshire Spring(landrace/ landrace)
MAM 17-5	Wisconsin	Spring	JR2-3-3-B(N770-165-2-1/DCS 1789) X Heritage(Unnamed_11009/Marino)
Marie_AC	Winnipeg	Spring	Unnamed_4579(REG3239/OT224) X OT233(Harmon HAMXDx7)
Marion (Canada)	St. Foy, Can.	Spring	Q.O.130.4(Unnamed_7393/Unnamed_4006) X Q.O.51.27(Q.O.22.21/Q.O.21.5)
Matilda	Sweden	Spring	Unknown(Uknown/Unknown) X Unknown(Unknown/Unknown)
Maverick	Unknown	Unknown	80Ab988(74Ab1952/74Ab2603) X Monida(Cayuse/Otana)
Melys	United Kingdom	Spring	07524CnVI/6n(Maris Oberson/07022CnI/5n) X Caron(Maris Oberson/Milo)
MF9522-523	Pennsylvania	Unknown	Unknown(Uknown/Unknown) X Unknown(Unknown/Unknown)
MN 811045	Minnesota	Spring	Unknown(Uknown/Unknown) X Unknown(Unknown/Unknown)
MN06108	Minnesota	Spring	SD986600/ND981502
MN06109	Minnesota	Spring	SD986600/ND981502
MN06125	Minnesota	Spring	IL99-8803/MN01135
MN06239	Minnesota	Spring	Sask01T-602-05-06/MN01117
MN07203	Minnesota	Spring	Morton/IL95-1241

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
MN07210	Minnesota	Spring	Sesqui*2/Bettong//MN02108
MN08106	Minnesota	Spring	Sesqui/WIX7571-1//Kame
MN08123	Minnesota	Spring	Sesqui/WIX7571-1//Kame
MN08124	Minnesota	Spring	Sesqui/WIX7571-1//ND010426
MN08129	Minnesota	Spring	Kame//IL99-912/MN00206
MN08130	Minnesota	Spring	IL99-912/MN00206//Loyal
MN08131	Minnesota	Spring	Morton//IL99-912/MN00206
MN08132	Minnesota	Spring	Sask01T-602-05-06/MN00206//MN03115
MN08134	Minnesota	Spring	SA03668/MN02231
MN08137	Minnesota	Spring	SA03668/Morton
MN08139	Minnesota	Spring	Morton/SA02880
MN08141	Minnesota	Spring	SA04994/Kame
MN08146	Minnesota	Spring	MN02218/3wSQC3-10
MN08150	Minnesota	Spring	MN02231/MN03205
MN08155	Minnesota	Spring	UFRGS952521/X7464-4
MN08160	Minnesota	Spring	IL99-8803/Sesqui
MN08211	Minnesota	Spring	ACAss/S42/SA01717=SA060726
MN08212	Minnesota	Spring	OT2022/OT3006=SA061027
MN08217	Minnesota	Spring	OT2008/OT394=SA060201
MN08222	Minnesota	Spring	ACAssiniboia/S42/OT394=SO04600
MN08225	Minnesota	Spring	3wSCC2-15/MN03205
MN08230	Minnesota	Spring	W98241/CDCORRIN//ND010426
MN08234	Minnesota	Spring	Morton//IL99-912/MN00206
MN08238	Minnesota	Spring	ND010786//SA01511/Leonard
MN08242	Minnesota	Spring	SO03244//MN862055/MN00206
MN08243	Minnesota	Spring	Sesqui/WIX7571-1//SA03668
MN08251	Minnesota	Spring	SA04305/Loyal
MN08252	Minnesota	Spring	SA04913/MN02225
MN08253	Minnesota	Spring	MN02218/3wSQC3-10
MN08254	Minnesota	Spring	MN02155/3wSQC3-15
MN08260	Minnesota	Spring	MN01117/WIX7571-1
MN08262	Minnesota	Spring	ACAss/S42/OT394
MN08266	Minnesota	Spring	MN02231/MN03205
MN08268	Minnesota	Spring	MN03119/MN03205
MN08270	Minnesota	Spring	MN02231/SO04390
MN841801-1	Minnesota	Spring	MN841801(MN65B663/65B1362) X MN841801(MN65B663/65B1362)

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
Moholt	Norway	Spring	Voll (Nidar/Grenader)/Palu (Orn/Minor)
Morgan_AC	Alberta	Spring	OT526 X O*T764
Mortlock	Australia	Winter	Elan(unnamed_9330/Florida 500) X 66QO1-44(unnamed_7579/Swan)
Morton	North Dakota	Spring	ND880922(ND830775/Riel) X IAB605-X(sel.from an irradiated compsite cross pop/sel from an irradiated composite cross pop.)
Navaro	Ottawa	Spring	Navaro
ND000861	North Dakota	Spring	ND950524/HiFi
ND001397	North Dakota	Spring	BG27/BG25 NPB880304/95-40-4-4 (13/21)155
ND020290 (PO 808)	North Dakota	Spring	MN97112/ND971454 99043SSD 25/221 OBEE JUD
ND030078	North Dakota	Spring	YOUNGS/ND980479
ND040196	North Dakota	Spring	ND931314/Souris
ND040492	North Dakota	Spring	ND970216/Souris
ND050017	North Dakota	Spring	HiFi-11/ND001407 02007 14/225 BG
ND050490	North Dakota	Spring	ND981903/ND990232 02085 87/101 NRPB Pc91 lo
ND050506	North Dakota	Spring	ND981906/RONALD 02087 88/256 a Pc68 Dw
ND050578	North Dakota	Spring	ND990232/ND970216 02103 101/56 IAB a
ND051037	North Dakota	Spring	ND000306/ND980370 02160 171/64 a HiF
ND051069	North Dakota	Spring	ND000490/ND000916 02164 178/207 Ao lo Pc91HiFi
ND051236	North Dakota	Spring	ND000798/ND980370 02181 193/64 HiFi Pc91 NRPB a
ND051306	North Dakota	Spring	ND000811/ND980671 02185 199/69 Pc91 lo HiF
ND051312	North Dakota	Spring	ND000811/ND980671 02185 199/69 Pc91 lo HiF
ND051467	North Dakota	Spring	ND001336/HiFi-19 02207 220/15 BG HiFi
ND051513	North Dakota	Spring	ND001444/HiFi-51 02214 227/16 BG HiF
ND060111	North Dakota	Spring	96-503 Cn32/ND990232 03001 1/58 Pc91 lo
ND060182	North Dakota	Spring	CDC Dancer/ND011608 03016 5/228 Pc91 a
ND060223	North Dakota	Spring	HiFi-9/ND980370 03020 7/36 NRPB a
ND060235	North Dakota	Spring	HiFi-93/ND981442 03022 9/42 Pc91 lo BG Comp
ND060249	North Dakota	Spring	HiFi-117/HiFi SR1 03023 10/11 Pc91 BG
ND060342	North Dakota	Spring	Killdeer/ND000931 03033 13/135 Pc91 a
ND060418	North Dakota	Spring	ND931318/ND931314 03052 23/22 Pc91 lo
ND060432	North Dakota	Spring	ND970216/ND000750 03062 32/114 Pc91 lo? a
ND060449	North Dakota	Spring	ND980671/Souris 03065 38/30 a Pc91 lo?
ND060464	North Dakota	Spring	ND981065/ND011600 03069 40/225 Pc91 lo Hyt
ND060487	North Dakota	Spring	ND981845/HiFi-9 03077 46/7 Pc91 a
ND060507	North Dakota	Spring	ND981887/ND011288 03078 48/211 Pc45 a
ND060570	North Dakota	Spring	ND990148/ND991293 03092 55/82 Pc91 a lo?

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
ND060652	North Dakota	Spring	ND990355/ND000802 03107 64/118 Pc91 lo HiFi
ND060897	North Dakota	Spring	ND000824/ND010278 03163 122/175 HiFi Pc91 68 a
ND060925	North Dakota	Spring	ND000865/ND991056 03168 126/73 Pc91 a
ND061097	North Dakota	Spring	ND001018/Souris 03187 Tall 139/30 IAB Pc91 a Dw
ND061590	North Dakota	Spring	ND011598/ND000223 03259 224/98 Pc91 lo Hyt
ND061614	North Dakota	Spring	ND011604/ND981065 03262 227/40 Pc91 lo Hyt
ND061813	North Dakota	Spring	Tri.Crown/ND010074 03319 282/165 Pc68 a
ND061868	North Dakota	Spring	HiFi/IAN979-5-1-22 ND030288 Am Pc91
ND061975	North Dakota	Spring	Otana/M2609/Otana 03336 271/02297
ND070388	North Dakota	Spring	ND011054/ND030612 St Gr 04070
ND070813	North Dakota	Spring	ND000824/ND010848 04167 63/101 106/252
ND071063	North Dakota	Spring	ND011616/ND9508252-7-2 Drov/Jud BG 04211
ND071521	North Dakota	Spring	ND031348/ND951394 B 04271 261/37 123/33
ND071694	North Dakota	Spring	ND873126/Morton (Diego #3)
ND072258	North Dakota	Spring	ND990118/ND030288 05030 15/7
ND080724	North Dakota	Spring	Drover/MN00207 05085 32/21
ND081924	North Dakota	Spring	Triple Crown/ ND030220 Mtn 232 05383 293/123
Nes	Norway	Spring	Nes
Nice	Ottawa	Spring	Sylva // PGR8648 / Woodstock /3/ Donegal)
Noble-2	Minnesota	Spring	Noble(Tippecanoe/unnamed_10546) X Noble(Tippecanoe/unnamed_10546)
Novojatkovo	Unknown	Unknown	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
Nudist	Norway	Spring	Nudist
OA1058-4	Ottawa	Spring	AC Aylmer / 06897 (=AC Aylmer*2 / Pc96)
OA1063-8	Ottawa	Spring	05627-49(Pc68/Donegal) X Capital(Q.O.151.55/OT521)
OA1130-1	Ottawa	Spring	06914-1-1 / 06919-5-1 (= Pc48 / OAC Arrow // AC Aylmer / OAC Arrow)
OA1174-3	Ottawa	Spring	Ida / 06909-3-94
OA1176-1	Ottawa	Spring	Ida / 06909-1-19
OA1180-4	Ottawa	Spring	Ida / OA1019-6
OA1180-5	Ottawa	Spring	Ida /06909-2-26
OA1189-1	Ottawa	Spring	OA1025-1/ 07800-2-8-1-1a
OA1189-4	Ottawa	Spring	OA1025-1/ 07800-2-8-1-1a
OA1196-3	Ottawa	Spring	07800-2-8-8-1a / OA1025-1
OA1197-1	Ottawa	Spring	07800-2-8-5-1a / Sherwood
OA1202-1	Ottawa	Spring	07783-3-2-1-1a / SA99297
OA1204-2	Ottawa	Spring	MN-00222/07836-2-9-2-1a
OA1207-1	Ottawa	Spring	95Ab10854 / 07776-3-9-1-1a

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
OA1226-1	Ottawa	Spring	07836-2-9-3-1a-2 / ND960620
OA1226-4	Ottawa	Spring	07836-2-9-3-1a-2 / ND960620
OA1228-1	Ottawa	Spring	W99A747 / 07836-2-5-2-1a-4
OA1232-2	Ottawa	Spring	06973-5-10-15-2 / ND960620
OA1232-5	Ottawa	Spring	06973-5-10-15-2 / ND960620
OA1234-1	Ottawa	Spring	OT288/Triple Crown
OA1242-5	Ottawa	Spring	06909-3-94/Irish
OA1248-1	Ottawa	Spring	07836-2-9-2-1a-1/07823-2-4-3-1a-1
OA1250-1	Ottawa	Spring	Souris/07836-2-5-2-1a-2
OA1250-2	Ottawa	Spring	Souris/07836-2-5-2-1a-2
OA1251-1	Ottawa	Spring	Souris/07774-3-9-1-1a-1
OA1253-1	Ottawa	Spring	97Ab7979/07189-10-1-5
OA1256-1	Ottawa	Spring	Souris/07189-10-8-6
OA1260-1	Ottawa	Spring	OA1070-2/07834-3-1-1-1a-1
OA1262-1	Ottawa	Spring	07593-1-1-2/07989-10-1-8
OA1263-2	Ottawa	Spring	07878-3-6-5/07870-3-5-4
OA1266-1	Ottawa	Spring	07869-2-9-4/07868-2-1-1
OA1268-3	Ottawa	Spring	07868-1-71-1/07867-1-14-1
OA1272-1	Ottawa	Spring	07877-3-13-4/07878-3-7-1
Odal	Norway	Spring	Guldregn (Milton/Milton)/Foreldad Dalahavre
Ogle	Illinois	Spring	Brave(Putnam/unknown_2618) X unnamed_336(Tyler/Egdolon23)
Olam	Norway	Spring	Sv692013/POL (Bambu/Norum 206)
Osage	North Carolina	Winter	Fulton (Fulghum/Markton)/Sel.5562 (Vicotria - Argentinian/Richland)
OT3028	Saskatchewan	Spring	AC Goslin / SA96400
OT3036	Saskatchewan	Spring	OT396 / HiFi
OT3037	Saskatchewan	Spring	AC AssS42 / OT385
OT3039	Saskatchewan	Spring	OT3004 / CDC-01-499-04-227
OT3040	Saskatchewan	Spring	OT3002 / OT394
OT3045	Saskatchewan	Spring	OT3002 / OT394
OT3046	Saskatchewan	Spring	OT392 / OT557
OT3047	Saskatchewan	Spring	OT393 / OA019-1
OT3048	Saskatchewan	Spring	CDC Sol-Fi / HiFi
OT3050	Saskatchewan	Spring	OT399 / Freddy
OT380	Saskatchewan	Spring	OT366(SO 88118/J775-1) X OT356(SO 85190/SO85022)
OT399	Saskatchewan	Spring	OT368 / Gem
OT586	Saskatchewan	Spring	Unnamed_14836(Marion(Canada)/AC Assiniboia) X Unnamed_14837(Riel/Goslin)

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
OT7053	Saskatchewan	Spring	CR245-Dw // Paul / Kauf
Otana	Idaho	Spring	Clav 5345(unnamed_9199/Overland) X Zanster(unknown/unknown)
Ozark	Arkansas	Winter	Florida 167 (Bond/Fulghum)/6-81-3 (unknown/unknown)
Pacer_CDC	Saskatchewan	Spring	W84425(unnamed_6382/OT224) X OT751(unnamed_6383/unnamed_6384)
Pg11	Unknown	Unknown	SES Sel.52(Burt/Burt) X OT313(Corbit/Random)
Pg16	Unknown	Unknown	Rodney O (Rodney/unnamed_5273) X Unnamed_5321(Rodney O/unnamed_5320)
PI260616-1	Minnesota	Spring	Amarela 5282 FB 32 (Brazil)
PI266887-1	Minnesota	Spring	San Jose (Portugal)
Pinnacle_AC	Winnipeg	Spring	91RAT20(OT248/OT237) X AC Medallion(90GC142.143/Dumont)
Pioneer	North Carolina	Winter	Flughum (Red Rustproof/Red Rustproof)/Winter Turf (unknown/unknown)
PI263412-1	Minnesota	Spring	PI263412-1
POL	Norway	Spring	Bambu (unnamed_6329/unnamed_6330)/Norum 206 (unk/unk)
Porter	Indiana	Spring	P623A1-1-9-1 (CI 7684 selection/unmaed_7208)/Stout (unnamed_7447/unnamed_7471)
Prescott	Ottawa	Spring	OA1021(OA973-1/AC Aylmer) X OA1021(OA973-1/AC Aylmer)
ProFi_CDC	Saskatchewan	Spring	Gem(WI X6051/Ogle) X CDC Boyer (SO 82030/OT235)
Provena	Idaho	Spring	Pennlo(Egdolon 23/Otee) X Yung 492 (Unknown/Unknown)
Pusa Hybrid G	India	Unknown	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
Putnam 61	Indiana	Spring	Putnam (Purdue 3714A4-7-5/Clinton)/unnamed_8806 (Putnam/unnamed_8805)
Quincy Gray	North Carolina	Winter	unnamed_10592 (Victoria - Argentinian/Norton)/Red Rustproof (sel. From Red Algerian (Stanton, 1954 or introduced from Mexico Stanton, 1954)
Racoon	United Kingdom	Spring	Krypton (unknown/Solva)/91-221Cn4 (Pendragon/90-273Cn)
Ranch	France	Unknown	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
Red Algerian	North Carolina	Winter	native cultivated red oat of Algeria
Red Rustproof	California	Unknown	Sel. From Red Algerian(Stanton,1954)or introduced from Mexico(Stanton1954)(Unknown/Unknown) X Sel. From Red Algerian(Stanton,1954)or introduced from Mexico(Stranton1954)(Unknown/Unknown)
Rigodon_AC	St. Foy, Can.	Spring	Unnamed_9110(Ogle/unnamed_9109) X Q.O.174.19(A.O.9.4/Tarpan)
Ringsaker	Norway	Spring	Ringsaker
Robust	Indiana	Spring	P973A38-9-3 (P973A38/P973A38)/P973A38-9-3 (P973A38/P973A38)
Robust	Indiana	Spring	P973A38-9-3(P973A38/P973A38) X P973A38-9-3(P973A38/P973A38)
Rogers	North Carolina	Winter	Coker 80-33 (unnamed_12819/Coker 716)/NC 81-376 (Brooks/Coker 72-24)
Ronald_AC	Winnipeg	Spring	W89329(Dwarf)(W84188(tall)/Robert) X Ac Medallion(90GC142.143/Dumont)
Russell	Ottawa	Spring	Unnamed_4024(Garry/Ukraine) X Abegweit(Vanguard/Erban)
SA01223-02	Saskatchewan	Spring	Gem / CDC Boyer
SA051172	Saskatchewan	Spring	CDC Sol-Fi / HiFi
SA060605	Saskatchewan	Spring	X7535-14 / OT3002

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
SA060830	Saskatchewan	Spring	OT399 / OT2030
SA061148	Saskatchewan	Spring	SA98741-11 / CDC ProFi
SA070089	Saskatchewan	Spring	CDC Dancer / CDC ProFi
SA070270	Saskatchewan	Spring	Ajay / OT399
SA070367	Saskatchewan	Spring	TAM2002 / CDC ProFi
SA070444	Saskatchewan	Spring	OT3007 / SA99940
SA070452	Saskatchewan	Spring	OT399 / Quoll
SA070469	Saskatchewan	Spring	OT399 / ABSP14-6
SA070513	Saskatchewan	Spring	SA01714 / 99-511Cn161
SA070576	Saskatchewan	Spring	OT559 / CDC ProFi
SA070592	Saskatchewan	Spring	Jordan / CDC Orrin
SA070631	Saskatchewan	Spring	Jordan / SA01594
SA070655	Saskatchewan	Spring	OT399 / CDC Dancer
SA070712	Saskatchewan	Spring	Leggett / CDC Orrin
SA070781	Saskatchewan	Spring	CDC Weaver / OT572
SA070845	Saskatchewan	Spring	96Ab8597 / CDC Weaver
SA070860	Saskatchewan	Spring	CDC Weaver / 98Ab6491
SA070906	Saskatchewan	Spring	CDC Sol-Fi / OT399
SA070972	Saskatchewan	Spring	94-116Cn4/1 / CDC Weaver
SA071369	Saskatchewan	Spring	SO02249 / OT3013
SA071405	Saskatchewan	Spring	CDC Weaver / Betania
SA071616	Saskatchewan	Spring	SO03224 / Betania
SA071760	Saskatchewan	Spring	CDC Weaver / Vista
Salomon	Germany	Spring	Alfred (Mg63305/Mustang(Germany)) X Unnamed_11669(Astor/Salzmunde 95560/66)
Sang	Sweden	Spring	Sv01771(unnamed_6881-Sv56687) X Condor(Minor/Express)
Santa Fe	Argentina	Winter	Sel. From Argentina oat (Coffman, F.A. 1977)/Sel. From Argentina oat (Coffman, F.A. 1977)
SECTARIAT LA495	Louisiana	Winter	Coker 84-15*2/4/'Blizzard'/3/Coker 79-21/'Coker 234'/CI9139
Sesqui	Minnesota	Spring	P8640A1-31-1(P8640A1-31/P8640A1-31) X MI 84-0-6(P72288RB1-3-4-3/unnamed_6172)
Shadow	Quebec, Can.	Spring	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
Sherwood	Ottawa	Spring	AC Aylmer / Goslin (or OA966-1 // OA952-3*2 / Pc48)
Simpson	North Carolina	Winter	Ballard (Pentagon (Stanton, 1955/Pentagon (Stanton, 1955)/S172 4Cn3/1/3/58/602Cn)
SO-1	Saskatchewan	Spring	AC Assiniboia(90GC144/Robert) X SA96121(ND870425/CDC Boyer)
Sol-Fi_CDC	Saskatchewan	Spring	N979-5-1(MO 07929/IL85-6183-1) X OT 366(SO 88118/J775-1)

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
Stout	Indiana	Spring	Unnamed_7447(Shield sib/unnamed_7216) X unnamed_7471(unnamed_7451/unnamed_7470)
Sun II-1	Sweden	Spring	Stjam(Victory/Crown) X Orn(Seger/VenLochow's Gelbhafer)
Sure Grain	North Carolina	Winter	Sure Grain
SW Betania	Sweden	Spring	Unknown(Uknown/Unknown) X Unknown(Unknown/Unknown)
SW INGEBORG	Norway	Spring	Sv 88359_X_SILVANO
SW KERSTIN	Norway	Spring	PETRA_X_BALETT
SW VAASA	Norway	Spring	Sv 841034_X_Sv 83626
Sylva	Ottawa	Spring	Shaw / Ogle
TAM O-301	Texas	Winter	AB555(Coronado/Cortez) X Unnamed_7141(unnamed_7182/unnamed_5530)
TAM O-397	Texas	Winter	re-selection from TAMO- 386(TAMO-386/TAMO -386) X reselection from TAMO-386(TAMO-386/TAMO-386)
TAMO 405	Texas	Winter	unknown (single vol. plant sel.)
TAMO 406	Texas	Winter	Mitchell/TX83Ab2923/TAMO386R
TAMO 606	Texas	Winter	Citation/84IORN#30 (=CX466-1-B4-D3-5)
Tardis	United Kingdom	Spring	87-42Cn1/2/2/1/1(87-42Cn1/2/2 X 87-42Cn1/2/2) X 95-69RCn(87-42Cn1/2/2 X 94-13)
Tift	North Carolina	Winter	Tift
Tippecanoe	Indiana	Spring	Clntland 60 (Clintland/unnamed_9214)/unnamed_4021 (clintland 60/MO 0-205)
Triactor	Saskatchewan	Spring	SW9619019 / Stork
Triple Crown	Saskatchewan	Spring	Unnamed_6891(unnamed_6893/unnamed-6892) X WW17734(unknown/unknown)
Trisparinia	North Carolina	Winter	Trisparinia
Trophy	Louisiana	Winter	LA90120C2-3-AB1/TX96M1558
Troy	South Dakota	Spring	Unnamed_8040(WI X 2221-2/unnamed_8039) X MN 78142 (Otter/unnamed_6697)
TX02U 7029	Texas	Winter	92 SAT4-4//79C1515/79C5287/80Ab2726
TX02U 7047	Texas	Winter	TAMO386ERB/TAMO386R/92SAT24-4
TX02U 7065	Texas	Winter	UFRGS Q120101-4/TAMO386ERB/92SAT24-4
TX02U 7097	Texas	Winter	TX92M1505(C5-2 1563 CR Cpx/SR Cpx/unknown)/TX83Ab2923
TX02U 7103	Texas	Winter	Mitchell/T386'S'/TAMO386ERB/TAMO386R
TX02U 7104	Texas	Winter	Mitchell/T386'S'/TAMO386ERB/TAMO386R
TX02U 7176	Texas	Winter	C5-2,1563 CRcpx/SR cpx/Unknown
TX02U 7181	Texas	Winter	C5-2,1563 CRcpx/SR cpx/Unknown
TX02U 7219	Texas	Winter	TX92M1505/TX83Ab2923
TX02U 7227	Texas	Winter	TX92M1596/TX83Ab2923
TX02U 7237	Texas	Winter	TAMO386ERB/TAMO386R/92SAT24-4
TX02U 7325	Texas	Winter	UFRGS Q120101-4/TAMO386ERB/92SAT24-4
TX02U 7443	Texas	Winter	UFRGS Q120101-4/TAMO386ERB/92SAT24-4

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
TX02U 7473	Texas	Winter	TX94Ab343/TAMO386ERB
TX02U 7479	Texas	Winter	92M1009(T386"S"/94Ab347
TX02U 7490	Texas	Winter	92M1065(TAMO386'S')/TAMO386ERB
TX02U 7518	Texas	Winter	TAMO386ERB/TX93Ab693(833'S')
TX02U 7605	Texas	Winter	TX92M1596(79Bord/Kenya SR/TAMO 386)/TX83Ab2923
TX02U 7651	Texas	Winter	Mitchell/TX83Ab2923/TAMO386R
TX02U 7682	Texas	Winter	TAMO386ERB/TX83Ab2923
TX05CS 347-1	Texas	Winter	TAMO 405/Plot Spike LA9339
TX05CS 347-2	Texas	Winter	TAMO 405/Plot Spike LA9339
TX05CS 542	Texas	Winter	Rodgers/TAMO 405
TX05CS 556	Texas	Winter	Trophy/TAMO 405
TX07CS1039	Texas	Winter	Nora//TAMO 405
TX07CS1228	Texas	Winter	Horizon 314//TAMO 405
TX07CS1268	Texas	Winter	Horizon 321//TAMO 405
TX07CS1402	Texas	Winter	TX00D276=(C81-32//76-30*4/76-29) (=CX407-1-B3-1-FL-93-103-33-37)//TAMO 405
TX07CS1564	Texas	Winter	TX00M617=(98C893) UPF85380-A-1/92M1090(TAMO 386 RESEL.)/TAMO 405
TX07CS1584	Texas	Winter	TX00M628=(98C917)TX93AB693 RESEL=H833 OFF-TYPE SEL.(97CS693DS)//TAMO 405
TX07CS1805	Texas	Winter	TAMO 406=(Mitchell/TX83Ab2923/TAMO386R)//TAMO 405
TX07CS1832	Texas	Winter	Rodgers//TAMO 405
TX07CS1948	Texas	Winter	FL9701-P30=(Horizon 314/Chapman)//TAMO 405
TX07CS1965	Texas	Winter	FL9708-P71=(Coker 92Ab719/Horizon 314)//TAMO 405
TX07CS1997	Texas	Winter	LA9535D118-4=(T91AB2965/5/C88D1547Seln:85-13/4/84-15/3/81-21//79-22*2/Omega)//TAMO 405
TX07CS2001	Texas	Winter	LA966IBI-151-1=(FL9595MEO29/TX93M2107)//TAMO 405
TX07CS2140	Texas	Winter	NC97-8972N=(Bulk Sel)//TAMO 405
TX07CS2201	Texas	Winter	SC961246=(C75-28/TAM-O-312//Coker234/CMB10/3/C76-30*4/C76-29/4/Omega)//TAMO 405
TX07CS2235	Texas	Winter	SC96R036=(C86Five(C86-13/5/C84-15*2/4/C81-21/3/C79-21//C234/6/Omega)//TAMO 405
TX07CS2350	Texas	Winter	TX00D166=(Dallas/TAMO 386 (=OX90D009-7-76-20))//TAMO 405
TX07CS2609	Texas	Winter	Dallas//TAMO 406
TX07CS2652	Texas	Winter	Harrison//TAMO 406
TX07CS2765	Texas	Winter	Horizon 321//TAMO 406
TX07CS2795	Texas	Winter	TX01B3156=(TAMO 386ERB/TX83Ab2923)//TAMO 406
Tyler	Indiana	Spring	Clintland 60 (Clintland/unnamed_9214)/unnamed_4021 (Clintland 60/MO 0-205)

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
UFRGS 8	Brazil	Winter	OA338(00072-3-5/OA123-124) X W1 X2682-1(unknown/unknown)
UFRGS 881971	Brazil	Winter	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
UFRGS 930605	Brazil	Winter	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
UFRGS077011-4	Louisiana	Winter	UFRGS 987016-1 / UFRGS 19
UFRGS077026-2	Louisiana	Winter	UFRGS 007020-2 / UFRGS 984060-1
UFRGS087023-5	Louisiana	Winter	UFRGS 995088-3 / UFRGS 960257-5
UFRGS087129-1	Louisiana	Winter	UFRGS 995078-2 / URS 21
UFRGS087157-3	Louisiana	Winter	UFRGS 995088-3 / UFRGS 006049
Ukraine reselection	Iowa	Spring	Reselection from Ukraine(CI3259)(Ukraine/Ukraine) X Reselection from Ukraine (CI3259)(Ukraine/Ukraine)
UPF95H900-10	Louisiana	Winter	UPF14/UFRGS16
UPF97H300-2-11	Louisiana	Winter	UPF90H400/UFRGS16
UPF98H2000-4	Louisiana	Winter	UPF16/UPF91AL100-1-4-3
UPFA20	Louisiana	Winter	TEIXEIRINHA
UPFA22	Louisiana	Winter	TEMPRANA
Urano	Chile	Unknown	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
URS 21	Louisiana	Winter	QION 92/162 = UFRGS 10 / CTC 84B993
URS 22	Louisiana	Winter	URS 22
VAO -58	Ottawa	Spring	AC Gwen/Gehl
VAO-44	Ottawa	Spring	2002VB-33/Gehl
Vao-48	Ottawa	Spring	VAO-1 (06751-64-1/06540)/OA516-2 (sel. of daylight insensitive dormats 119/sel. of daylight insensitive dormats 119)
VAO-51	Ottawa	Spring	2002VB-33/Gehl
Victoria	Uruguay	Unknown	Sel. From artificial(mass)pop. Of lines 64q.64r.64t grown in Uruguay(increased in Argentina)(Unknown/Unknown) X Sel. From artificial (mass) pop. Of lines 64q. 64r.64t grown in Uruguay(increased in Argentina)(Unknown/Unknown)
Vista	Wisconsin	Spring	Unnamed_6396(Ogle/MO 07468) X Centennial(N569-42-51/Unnamed_6468)
WAOAT2132	Australia	Winter	Unknown(Unknown/Unknown) X Unknown(Unknown/Unknown)
Winter Fulghum	North Carolina	Winter	sel. From Fulghum (C.I. 699) (Richland/Richland)/sel. From Fulghum (C.I. 699) (Richland/Richland)
Winter Turf	North Carolina	Winter	unknown/unknown
WNPG 01	Winnipeg	Spring	AC Ronald/00USDA05
WNPG 02	Winnipeg	Spring	AC Ronald/ND931475/AC Assiniboia
WNPG 03	Winnipeg	Spring	CR245-Dw//Paul/AC Kaufmann
WNPG 04	Winnipeg	Spring	CR245-Dw//Paul/AC Kaufmann
WNPG 05	Winnipeg	Spring	CDC Dancer//Paul/AC Kaufmann

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
WNPG 06	Winnipeg	Spring	AC Ronald/OT299
WNPG 07	Winnipeg	Spring	Assiniboia/Omskij
WNPG 08	Winnipeg	Spring	Assiniboia/Omskij
WNPG 09	Winnipeg	Spring	Omskij/Ronald
WNPG 10	Winnipeg	Spring	Omskij/Ronald
WNPG 11	Winnipeg	Spring	Baragan/Pinnacle//Ronald
WNPG 12	Winnipeg	Spring	Baragan/Pinnacle//Ronald
WNPG 13	Winnipeg	Spring	AC Mustang/Baragan//01HN3021(ND931475/ASB)
WNPG 14	Winnipeg	Spring	AC Mustang/Baragan//01HN3021(ND931475/ASB)
WNPG 15	Winnipeg	Spring	W97254/Pinnacle//Assiniboia/Omskij
WNPG 16	Winnipeg	Spring	W97254/Pinnacle//Assiniboia/Omskij
WNPG 17	Winnipeg	Spring	W97254/Pinnacle//Assiniboia/Omskij
WNPG 18	Winnipeg	Spring	01RAT26/CDC Sol-Fi
WNPG 19	Winnipeg	Spring	Leggett/01RAT23
WNPG 20	Winnipeg	Spring	Leggett/OT2022
WNPG 21	Winnipeg	Spring	Leggett/OT2022
WNPG 22	Winnipeg	Spring	OT2022/Leggett
WNPG 23	Winnipeg	Spring	OT2022/Leggett
WNPG 24	Winnipeg	Spring	OT2022/Leggett
WNPG 25	Winnipeg	Spring	OT2022/Leggett
WNPG 26	Winnipeg	Spring	OT2022/01RAT23
WNPG 27	Winnipeg	Spring	OT2022/01RAT23
WNPG 28	Winnipeg	Spring	OT2022/01RAT23
WNPG 29	Winnipeg	Spring	OT2022/01RAT23
WNPG 30	Winnipeg	Spring	AC Morgan/AC Mustang
WNPG 31	Winnipeg	Spring	AC Morgan/AC Mustang
WNPG 32	Winnipeg	Spring	AC Morgan/OT394
WNPG 33	Winnipeg	Spring	AC Morgan/OT394
WNPG 34	Winnipeg	Spring	AC Morgan//Elvy/CDC Boyer
WNPG 35	Winnipeg	Spring	AC Morgan//Elvy/CDC Boyer
WNPG 36	Winnipeg	Spring	AC Morgan//Elvy/CDC Boyer
WNPG 37	Winnipeg	Spring	OT7000(AC Belmont/AC Assiniboia)//Paul/AC Kaufmann
WNPG 38	Winnipeg	Spring	JC1624#3/HiFi#3
WNPG 39	Winnipeg	Spring	ND9508252-75/CR245-Dw
WNPG 40	Winnipeg	Spring	ND9508252-75-5//03P22A-BM1/Pc97
Woodburn	Indiana	Spring	Woodburn

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
X8787-1	Wisconsin	Spring	X7535-9 / X7395-4
X8791-1	Wisconsin	Spring	X7571-1 / X6984-3
X8826-1	Wisconsin	Spring	IL92-7186 / X6356-2
X8903-2	Wisconsin	Spring	X7728-3 / X7509-1
X8995-4	Wisconsin	Spring	OA966-1 / Vista
X9082-1	Wisconsin	Spring	X7822-3 / X7066-5
X9150-1	Wisconsin	Spring	X7994-2 / Gem
X9192-5	Wisconsin	Spring	X8191-2 / ND961161
X9195-2	Wisconsin	Spring	X8208-5 / ND961161
X9195-6	Wisconsin	Spring	X8208-5 / ND961161
X9200-4	Wisconsin	Spring	OA981-9 / X8208-6
X9221-6	Wisconsin	Spring	X8163-1 / ND961161
X9221-8	Wisconsin	Spring	X8163-1 / ND961161
X9253-1	Wisconsin	Spring	X8163-1 / X8179-1
X9258-5	Wisconsin	Spring	X8175-2 / DRUMLIN
X9270-4	Wisconsin	Spring	X8191-2 / X7571-1
X9285-1	Wisconsin	Spring	X8313-2 / X7766-1
X9287-2	Wisconsin	Spring	X8208-6 / X7464-4
X9290-2	Wisconsin	Spring	X8208-6 / DRUMLIN
X9368-1	Wisconsin	Spring	X8163-2 / X8342-6
X9375-1	Wisconsin	Spring	X8170-3 / X8179-1
X9384-2	Wisconsin	Spring	X8184-2 / X8463-3
X9386-1	Wisconsin	Spring	X8188-5 / X8163-2
X9392-1	Wisconsin	Spring	X8191-5 / X8463-3
X9395-2	Wisconsin	Spring	X8191-8 / X7994-2
X9396-1	Wisconsin	Spring	X8191-8 / X8179-1
X9396-4	Wisconsin	Spring	X8191-8 / X8179-1
X9410-1	Wisconsin	Spring	X8342-1 / X8179-1
X9410-2	Wisconsin	Spring	X8342-1 / X8179-1
X9414-1	Wisconsin	Spring	X8342-6 / X8254-5
X9421-3	Wisconsin	Spring	X8177-1 / X7535-14
X9422-1	Wisconsin	Spring	X8177-1 / X8254-5
X9435-1	Wisconsin	Spring	X8463-3 / X8179-1
X9439-1	Wisconsin	Spring	ND9508252 / X8341-3
X9449-1	Wisconsin	Spring	OA021-2 / X8341-3
X9474-2	Wisconsin	Spring	X8177-1 / X8341-3

Table 3.1 Continued

NAME	SOURCE	GROWTH HABIT	PEDIGREE
X9487-1	Wisconsin	Spring	X8402-2 / X9191-5
X9487-4	Wisconsin	Spring	X8402-2 / X9191-5
X9492-1	Wisconsin	Spring	X8416-2 / X8175-3
X9498-1	Wisconsin	Spring	X8470-6 / X8163-2
X9500-2	Wisconsin	Spring	X8470-6 / X8177-1
X9500-6	Wisconsin	Spring	X8470-6 / X8177-1
X9503-1	Wisconsin	Spring	X7994-2 / X8470-6
X9507-1	Wisconsin	Spring	X8210-2 / X8377-1
X9507-3	Wisconsin	Spring	X8210-2 / X8377-1
X9509-3	Wisconsin	Spring	X8377-1 / X8179-1
X9509-4	Wisconsin	Spring	X8377-1 / X8179-1
X9513-1	Wisconsin	Spring	X8583-1 / X8177-4
Z615-4	Unknown	Unknown	CAV2941(unknown/Unknown) X Ogle(Brave/Unnamed_336)
Zuton	United Kingdom	Spring	12799Cn4/6n (Bullion/Neon)/ Bullion (08974CnI/1/08944Cn1)

Phenotypic analysis

Traditional note-taking methods were employed to acquire disease severity and infection type ratings. This included visual screening of phenotypic disease traits of individual plants in each plot. Phenotypic data consisted of two types of ratings, disease severity and infection type (Figure 3.2). Disease severity (*DS*) refers to the percentage of the plant population exhibiting symptoms. This numerical value ranges from 0-100%. Infection type (*IT*) is a qualitative analysis of the type of symptoms being exhibited by the plant population. Infection types are limited to resistant (*R*), moderately resistant (*MR*), moderately susceptible (*MS*), or susceptible (*S*). Resistant plant types exhibit no visible signs or symptoms of crown rust. Flecks of chlorosis may be seen without pustules. Moderately resistant types are characterized by very small, non- to low sporulating pustules with surrounding chlorosis or small, low sporulating pustules with chlorosis. Moderately susceptible ratings refer to the mid-large sporulating pustules with chlorosis. Susceptible types include large, heavy sporulating pustules with very little surrounding chlorosis. Figure 3.2 depicts each infection type. Plant tissue may become brown and necrotic due to a severe disease infection. A combination of infection types were often seen within a given plot. For example, it was possible for a plot to be rated as 40 MRMS. Data was standardized across locations by converting qualitative data into quantitative measurements. Infection types were assigned a value on a scale of 0-1 (Table 3.2). To account for both types of crown rust ratings, the coefficient of infection (*CI*) was obtained. This value is calculated by multiplying *DS* ratings by *IT* numerical values as is shown: $CI = (DS \times IT)$

Table 3.2. The numerical scale assigned for each infection type (IT) rating used to generate the CI.

IT	R	RMR	MR	MRMS	MS	MSS	S
Scale	0	0.2	0.4	0.6	0.8	0.9	1

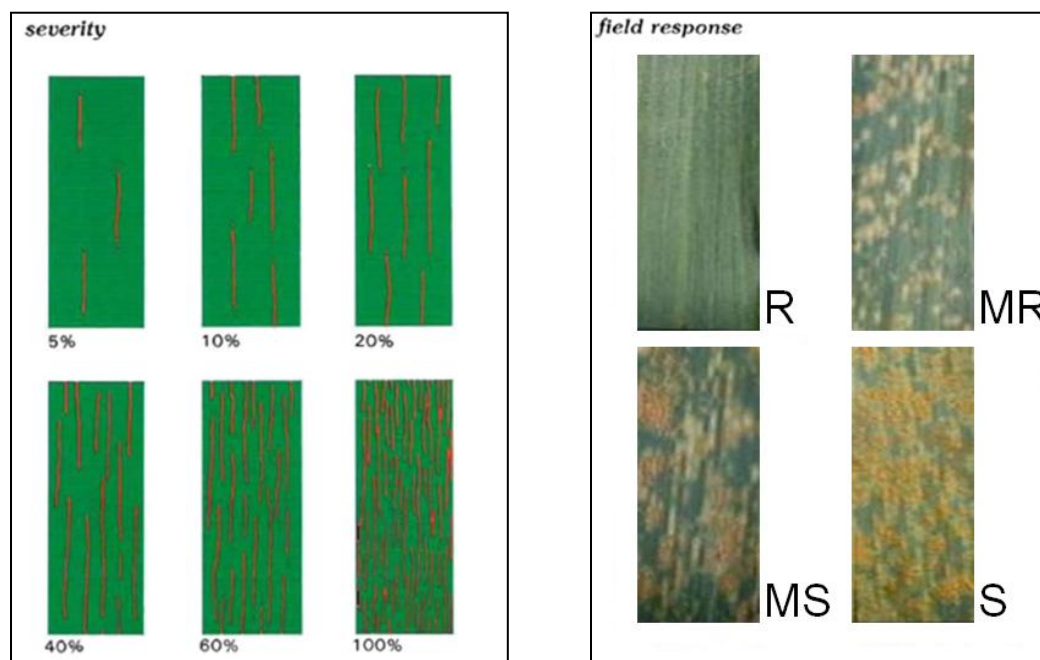


Figure 3.2. Examples of the scale used to determine disease severity (left) and infection type (percentage of oat plant tissue exhibiting disease symptoms) (right).

In addition to traditional phenotypic note-taking, representative pictures were taken of each plot and analyzed using Assess 2.0® software (Figure 3.3). Four flag leaves per plot were excised and photographed side-by-side on a basic black ring stand using a standard twelve-inch ruler to provide scale. The leaves were held in place using four cow magnets. A Canon Digital Rebel XT camera (Model Ef-F-S18-55MM) was used to take pictures from a consistent height. A neutral-colored umbrella was used to provide consistent lighting throughout the day as photographs were taken. Pre-labeled

Ziploc® bags were used to transport leaves to maintain organization and freshness while samples were queued for pictures.



Figure 3.3. Four representative flag leaves, e.g. ‘TAM O-397’. (Leaves were arranged side-by-side and held in place with four cow magnets on a basic ring stand. Photographs were taken from a consistent height. All non-leaf components are of neutral colors to avoid interference with the software’s analysis. Neutral colors refer to those which are not able to be mistaken for either leaf tissue or disease.)

The photographs were uploaded to a computer and analyzed using Assess 2.0 software, which is an application of existing image analysis algorithms to disease measurement to be used for routine disease measurement screening (Figure 3.4). The software first separates the leaf from the background images and then separates the diseased tissue from the healthy tissue within the boundary of the leaf. It is necessary for the background and the lesions to differ in some property, e.g. color or brightness. Assess relies on the Hue-Saturation-Intensity color model to distinguish between leaf material, diseased tissue, and background. The software’s effectiveness is attributed to the flexibility in using and combining various color models and color planes to extract the necessary components (Lamari, 2008). A severity rating is generated based on the

percentage of infected tissue in comparison to healthy tissue. The ratings calculated by the software were compared to the visually-acquired traditional phenotypic ratings.

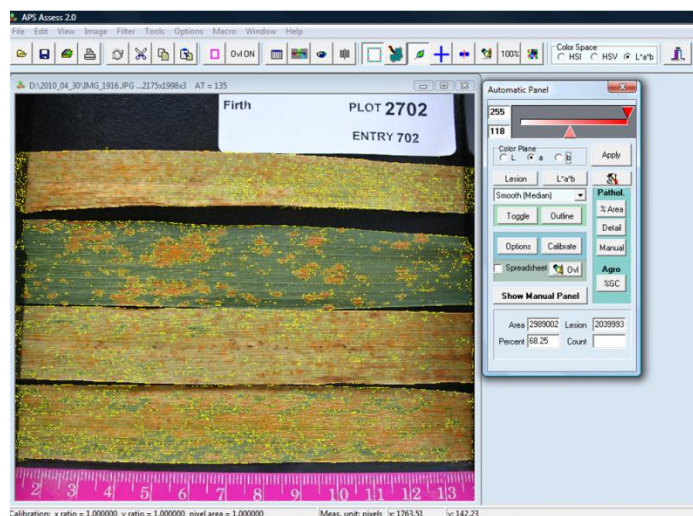


Figure 3.4. The Assess software interface used to analyze the percent of infected plant in comparison to green tissue and calculates severity.

In Castroville, TX notes were taken April 26-28, 2010 and May 13, 2011, respectively. Photographs were taken only in 2010. In 2011, due to the late presence of crown rust in the field, plants were already beginning to ripen for harvest and leaf tissue was turning brown. As the Assess software is unable to distinguish brown leaf tissue from disease, it would be ineffective to analyze photographs of each plot in this manner. In Baton Rouge, LA notes were taken in April 2010 and 2011, r. In Fargo, ND notes were taken on August 3, 2010 and July 20, 2011, respectively. In St. Paul, MN notes were taken on June 29-July 7, 2010 and July 7-July 19, 2011, respectively.

Statistical analysis

Data was analyzed using Microsoft Excel and Statistical Analysis System Version 9.3 (SAS Institute, 2007). Individual and combined locations, genotype by environment interactions, and individual genotype means were analyzed as a randomized complete block design with PROC GLM (Table 3.3). The variable n refers to the number of environments at which the lines were evaluated. The variable r refers to the number of repetitions. The variable t refers to the number of testers, or in this circumstance, the number of genotypes which were evaluated.

Table 3.3. Summary of analysis of variance and expected mean squares.

Source of variation	DF	Expected mean square
Environment	$n-1$	$\sigma^2 + r\sigma_{GE}^2 + t\sigma_{R(E)}^2 + rt\sigma_E^2$
Rep (Environment)	$n(r-1)$	$\sigma^2 + t\sigma_{R(E)}^2$
Genotypes	$t-1$	$\sigma^2 + r\sigma_{GE}^2 + rn\sigma_G^2$
Environment * Genotypes	$(n-1)(t-1)$	$\sigma^2 + r\sigma_{GE}^2$
Error	$n(r-1)(t-1)$	σ^2

Heritability

In a breeding program, a breeder relies on the idea that phenotypic variation exists within a population. Some of this variation is due to environmental effects, while a proportion of variation can be traced back to genetics. Heritability is the proportion of phenotypic variance which is genetic in origin (Brown and Caligari, 2008).

There are two types of heritability which can be calculated using this type of data. The first, broad-sense heritability (H), refers to the amount of genetic variance (σ_G) expressed in proportion to the total phenotypic variance (σ_P), as follows:

$$H = \sigma_G / \sigma_P$$

Broad-sense heritability measures the significance of environment versus genotype in the expression of a quantitative trait (Bernardo, 2010; Brown and Caligari, 2008).

The second, narrow-sense heritability (h^2), refers to the amount of additive variance (σ_A) expressed in proportion to the total phenotypic variance (σ_P) as follows:

$$h^2 = \sigma_A / \sigma_P$$

Additive genetic variance is the variation between homozygotes in a segregating population (Brown and Caligari, 2008). Narrow-sense heritability is often considered more meaningful than broad-sense heritability because it determines the amount of progress which can be gained from selecting and recombining specific individuals in a given population. However, broad-sense heritability remains more meaningful when all types of genetic variance may be exploited. In both cases, a higher heritability value is indicative of greater breeding value (Bernardo, 2010; Brown and Caligari, 2008).

Heritability was calculated manually using the ANOVA output obtained from SAS (Table 3.4).

Table 3.4. Summary of the concept of broad-sense heritability (h^2).

Source of variation	DF	MS	Expected mean square
Environment	n-1	M1	$\sigma^2 + r\sigma_{GE}^2 + t\sigma_{R(E)}^2 + rt\sigma_E^2$
Rep (Environment)	n(r-1)	M2	$\sigma^2 + t\sigma_{R(E)}^2$
Genotypes	t-1	M3	$\sigma^2 + r\sigma_{GE}^2 + rn\sigma_G^2$
Environment * Genotypes	(n-1)(t-1)	M4	$\sigma^2 + r\sigma_{GE}^2$
Pooled error	n(r-1)(t-1)	M5	σ^2
Genotypic variance			$(\sigma^2 + r\sigma_{GE}^2 + rn\sigma_G^2) - (\sigma^2 + r\sigma_{GE}^2)$
Phenotypic variance			$\sigma_G^2 + \sigma_E^2 + \sigma_{GE}^2$
h^2			σ_G^2 / σ_P^2

Repeatability

Repeatability is the ratio of ‘between individual components’ to ‘total phenotypic variance’. A concept developed by Kempthorne and Lush in the 1900’s for use in breeding and quantitative genetics, repeatability has three primary uses. The first is to establish the upper limits of heritability for a given character. Secondly, repeatability is used to establish predictions regarding expected future performance based on previously-acquired data. Finally, this parameter may be used to determine increase in accuracy resulting from repeated measurements of the same characteristic (Kempthorne, 1957). Thus, a higher repeatability value indicates that fewer measurements would be statistically sufficient and measurements may be repeatable over space or time (Falconer, 1988; Falconer and Mackay, 1996).

Repeatability utilizes environmental variation (σ_E) rather than genetic variation (σ_G). The σ_E value is separated into temporary and permanent components during analysis, also known as temporary effects or permanent effects. These components include special environmental variance (σ_{Es}) and general environmental variance (σ_{Eg}).

The σ_{Es} value is the component of within individual variance which arises from temporary or localized circumstances. The σ_{Eg} value is the component of between individual variance which arises from permanent or non-localized circumstances (Falconer, 1988; Falconer and Mackay, 1996).

Repeatability was calculated manually using the ANOVA output obtained from SAS (Table 3.5). The variable n refers to the number of individuals, which in this circumstance refers to repetitions at each location. The variable m refers to the number of observations per individual, which in this circumstance is the number of genotypes evaluated at each location.

Table 3.5. Summary of the concept of repeatability.

Source of variation	DF	MS	Expected mean square
Between genotypes	n-1	MS _B	$\sigma^2_w + m\sigma^2_B$
Within genotypes	n(m-1)	MS _W	σ^2_w
σ^2_P			$\sigma^2_B + \sigma^2_w$
Repeatability			σ^2_B / σ_P

Components of variation used for calculating repeatability include the component due to variation between individuals (σ^2_B) and the component due to variation within individuals (σ^2_w). The σ^2_B value represents the permanent environmental variation and the total genetic variation as shown:

$$\sigma^2_B = \frac{MS_B - MS_W}{m} = \sigma_G + \sigma_{Eg}$$

Where σ_w^2 is the variation among measurements and represents the temporary environmental variance. Repeatability is derived as an intra-class correlation which expresses the proportion of variance of single measurements due to permanent, or non-localized, differences between individuals, both genetic and environmental. Thus $1 - R = \sigma_{Es} / \sigma_P$. Repeatability may be summarized as follows:

$$R = \frac{\sigma_B^2}{\sigma_B^2 + \sigma_W^2} = \frac{\sigma_G + \sigma_{Eg}}{\sigma_G + \sigma_{Eg} + \sigma_{Es}} = \frac{\sigma_G + \sigma_{Eg}}{\sigma_P}$$

Repeatability allows the estimation of σ_{Es} to be separated due to special environment as a proportion of the total variance. The advantage to calculating repeatability is that it can make up for the challenge associated with genotype-by-environment interactions, particularly the failure of a given genotype to perform the same across multiple locations. As it sets the upper limit to heritability, repeatability will always be greater than broad-sense heritability, which in turn is always greater than narrow-sense heritability ($R > h_B^2 > h_N^2$).

There are several assumptions associated with repeatability calculations. Measurements used to obtain the ‘between individual component’ are assumed to have equal variance. Also, measurements represent the same character and are not inherently rendered dissimilar by virtue of separation by time or space (Falconer, 1988; Falconer and Mackay, 1996).

Biplot analysis

A biplot analysis is conducted for further evaluation of multi-environmental trial data, with emphasis on genotype-by-environment (G x E) interaction. A biplot is a graphically displayed scatter plot which analyzes row and column factors to estimate the relationships among and across factors, including any possible underlying interactions between factors. The graphical display is used to visually represent all of these relationships simultaneously. While biplot analysis is similar to principle component analysis (PCA), biplot allows for a more comprehensive use visualizing factor interactions (Yan and Tinker, 2006). The GGEbiplot software was used for this analysis.

Mathematically, a biplot is a graphical display of matrix multiplication which is used to address several questions. First, how is the data being centered and scaled, i.e. which model is being used to generate the biplot? Second, how are the individual values being separated? This will determine whether or not the relationships may be appropriately represented. Third, what is the goodness of fit of the two-way table data? Additionally, biplots are based on the assumption that all axes are drawn to scale (Yan and Tinker, 2006).

For G x E interactions, it is necessary to establish whether or not there are relevant rank changes of a specific genotype within a given environment. For example, a winter oat line is expected to perform better in a southern environment, such as Castroville, TX, than a spring oat line. If there are not relevant rank changes, a superior genotype may be identified as a high performer in all environments. A biplot allows a

breeder to determine whether or not a single environment should be divided into multiple mega-environments to exploit or avoid any potential G x E interactions. A biplot can also assist a breeder in identifying the sources of G x E interactions. The most ideal test environments and superior genotypes can be identified through the use of biplot analysis (Yan and Tinker, 2006).

Four types of biplot views were generated for analysis of spring and winter oats. These views include representativeness of test environments, relationships among test environments, mean performance and stability of genotypes, and which-won-where.

During the two years during which the association mapping panel was grown, there was a significant amount of missing data. Missing values range from individual plots within the population to entire data sets for either year at a given location. Missing values for individual plots may be attributed to environmental conditions or human error. For the year 2010 in Baton Rouge, LA, no data was retrieved due to drought conditions which left the field too dry for plants to thrive. Additionally, crown rust relies on moisture in the air in order to spread. In Castroville, TX in 2011, crown rust spread too late in the season to collect data on the entire winter oat panel. The winter oats were already ripe by the time the spring and core panels were exhibiting symptoms of crown rust. It may be beneficial to repeat the field trials at each of the four locations for another year in order to fill in gaps within the data. This would further enhance the strength of the genotypic data when generating the association map.

CHAPTER IV

RESULTS AND DISCUSSION

Three panels of North American oats (winter, spring, and a core containing selected lines from the two growth habits) were statistically evaluated for resistance to crown rust in four field environments at Castroville, TX, Baton Rouge, LA, St. Paul, MN, and Fargo, ND for a total of two years in 2010 and 2011. Within the four environments, the winter lines consistently outperformed the spring lines in terms of crown rust resistance. The study demonstrated a high degree of repeatability and heritability for estimating coefficient of infection, while revealing the population to be highly variable. This variability, in combination with the high degree of heritability and repeatability will prove beneficial when mapping QTL for crown rust resistance.

Statistical analysis

Analysis of variance (ANOVA) was performed for crown rust coefficient of infection across locations for both years using SAS Version 9.3. Results for spring oat lines indicate significant differences across environments and within genotypes. Additionally, significant genotype-by-environment interactions were shown as well (Table 4.1).

Table 4.1. Analysis of variance of CI for spring oat lines in Castroville, TX, Baton Rouge, LA, Fargo, ND, and St. Paul, MN for 2010 and 2011.

Source of variation	DF	SS	MS	F value	P value
Environment	4	111738.05	27934.51*	269.11	<.0001
Rep (Environment)	5	4452.59	890.52*	8.58	<.0001
Genotype	360	865539.07	2404.28*	23.16	<.0001
Environment * Genotype	1431	422605.06	295.32*	2.85	<.0001
Error	1645	170756.86	103.80		
R²	0.89				
CV%	60.65				
Root MSE	10.19				
Grand Mean	16.80				

*Significant at the 0.05 probability level

Results for winter oat lines indicate significant differences across environments and within genotypes. Additionally, significant genotype-by-environment interactions were observed as well (see Table 4.2).

Table 4.2. Analysis of variance of CI for winter oat lines in Castroville, TX, Baton Rouge, LA, Fargo, ND, and St. Paul, MN for 2010 and 2011.

Source of variation	DF	SS	MS	F value	P value
Environment	3	28007.44	9335.81*	208.34	<.0001
Rep (Environment)	4	1420.63	355.16*	7.93	<.0001
Genotype	118	336852.00	2854.68*	63.71	<.0001
Environment * Genotype	352	110577.38	314.14*	7.01	<.0001
Error	446	19985.22	44.81		
R²	0.96				
CV%	38.96				
Root MSE	6.69				
Grand Mean	17.18				

*Significant at the 0.05 probability level

Significant variability exists for crown rust resistance among the North American oat germplasm as demonstrated by Tables 4.1 and 4.2. This variability is expected to contribute to the effectiveness of any oat map that will be generated as a result of this study as it is useful for identifying QTL associated with disease resistance. Raw data for analysis can be found in Tables 4.3 and 4.4.

Table 4.3. CI means of spring oat lines for individual genotypes in Castroville, TX, Baton Rouge, LA, Fargo, ND, and St. Paul, MN for 2010 and 2011.

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
1	001A1-24-2-4-1-3	24.00	8.00	11.25	1.10	0.60	8.00	13.50	9.49
2	00Ab6112	60.00	100.00	26.25	11.00	55.00	100.00	28.00	54.32
3	00Ab6711	65.00	100.00	19.50	42.30	16.00	100.00	33.50	53.76
4	00Ab6963	70.00	20.00	18.00	6.60	27.50	100.00	33.50	39.37
5	00Ab7006	80.00	100.00	33.50	6.43	0.00	100.00	27.00	49.56
6	00Ab7085	67.50	100.00	38.50	61.40	1.00	100.00	38.50	58.13
7	00Ab8118	55.00	100.00	45.00	26.40	6.00	100.00	55.00	55.34
8	0216A1-1-55	50.00	10.00	12.00	35.37	0.00	60.00	9.00	25.20
9	0219A1-84-4-4-4-4	0.00	8.00	7.50	0.00	0.00	60.00	13.50	12.71
10	021A1-78-1-5	12.00	40.00	13.50	3.30	0.00	80.00	36.00	26.40
11	0222A1-21-7-5-1-1	0.00	40.00	33.50	0.00	0.00	80.00	20.25	24.82
12	026A1-88-2-2	12.00	16.00	12.15	2.03	2.00	32.00	22.50	14.10
13	027A1-87-8-1	10.00	40.00	13.50	3.30	0.00	80.00	11.25	22.58
14	02Ab5836	82.50	100.00	30.00	48.80	70.00	100.00	48.00	68.47
15	02Ab6078	72.50	80.00	19.00	24.60	17.00	100.00	30.00	49.01
16	02Ab6655	70.00	60.00	25.00	17.60	2.00	100.00	40.00	44.94
17	02HO-139	65.00	100.00	45.00	78.17	4.00	100.00	38.50	61.52
18	02HO-209	67.50	100.00	28.50	6.60	5.00	100.00	33.50	48.73
19	04P07B-GT3D	0.00	0.00	0.50	0.17	0.00	0.00	0.40	0.15
20	0513A1-18-5	8.00	60.00	12.00	0.00	0.00	80.00	28.50	26.90
21	0514A1-16-3	10.00	20.00	11.25	0.00	0.00	60.00	9.00	15.75
22	0528A1-1	18.00	32.00	24.00	0.00	0.00	24.00	21.00	16.95
23	053B1-95	4.50	20.00	11.25	0.00	0.00	8.00	4.00	6.80

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
24	0541A1-1	2.00	20.00	6.75	0.00	0.00	8.00	13.50	7.18
25	055A1-3-5-3	15.50	4.00	3.75	0.00	0.00	32.00	1.65	8.10
26	059A1-2-2-4	25.00	10.00	7.50	0.00	0.00	32.00	13.50	12.55
27	8669C2-4-6-16-33	70.00	100.00	27.00	40.00	35.00	100.00	43.50	59.36
28	95Ab12770	70.00	100.00	35.00	61.40	19.64	100.00	33.00	59.86
29	95Ab13050	75.00	100.00	45.00	83.50	65.00	100.00	45.00	73.36
30	971A9-7-4-11	4.00	0.00	6.00	0.00	0.00	32.00	41.25	11.89
31	97Ab7761	60.00	80.00	25.00	35.60	0.00	100.00	15.00	45.09
32	97Ab7767	75.00	80.00	45.00	55.90	41.00	100.00	24.50	60.20
33	9876C1-2-1-5-2-4-1	8.00	10.00	13.50	0.00	0.00	4.00	22.50	8.29
34	98Ab7265	77.50	80.00	50.00	72.50	34.00	100.00	38.50	64.64
35	99Ab10937	67.50	100.00	19.50	67.00	4.00	100.00	38.00	56.57
36	99Ab10971	50.00	80.00	22.50	33.40	6.00	100.00	24.00	45.13
37	99Ab10987	60.00	100.00	40.00	71.30	27.00	100.00	38.50	62.40
38	99Ab11098	65.00	100.00	35.00	17.60	23.50	100.00	45.00	55.16
39	99Ab11136	70.00	60.00	23.50	41.20	10.00	100.00	17.25	45.99
40	99Ab11227	60.00	100.00	30.00	26.40	0.00	100.00	34.00	50.06
41	99Ab11391	60.00	100.00	45.00	2.20	3.00	100.00	31.75	48.85
42	99Ab11787	67.50	100.00	40.00	35.70	2.00	100.00	22.50	52.53
43	Adrew	42.50	100.00	30.00	43.30	10.00	100.00	50.00	53.69
44	Allen	45.00	100.00	28.50	4.40	30.00	100.00	55.00	51.84
45	Anthony	50.00	100.00	18.00	45.60	46.00	100.00	9.40	52.71
46	ARDENTE	45.00	100.00	50.00	32.83	5.00	100.00	43.50	53.76
47	AVENY	3.00	0.00	13.50	1.10	0.00	100.00	29.25	20.98
48	BARRA	60.00	100.00	30.00	62.10	7.20	100.00	40.00	57.04
49	Bw103	50.00	8.00	8.09	6.60	0.00	80.00	9.47	23.17
50	Bw1103	36.00	8.00	19.09	1.10	0.45	100.00	0.77	23.63
51	Bw4903	12.00	1.00	4.35	6.60	0.00	4.00	9.00	5.28
52	CDC Minstrel	0.50	40.00	11.25	0.00	0.00	8.00	18.00	11.06

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
53	CDC Orrin	45.00	60.00	21.75	26.40	0.00	100.00	18.00	38.68
54	CDC Weaver	2.00	10.00	13.50	1.10	0.36	8.00	24.00	8.42
55	Chinese 4	75.00	80.00	25.00	66.83	48.00	100.00	13.00	58.26
56	CII712-5	7.00	20.00	0.00	5.50	0.00	4.00	0.10	5.10
57	CIRCLE	70.00	100.00	50.00	55.90	16.00	100.00	60.00	64.56
58	Classic	4.00	8.00	11.25	1.10	0.00	32.00	24.00	11.48
59	Clintford	65.00	80.00	22.50	22.40	25.00	48.00	28.50	41.63
60	Clintland 60	45.00	80.00	18.00	1.10	20.00	100.00	33.00	42.44
61	Clintland 64	47.50	80.00	22.50	1.10	6.00	48.00	29.00	33.44
62	Clinton 59	65.00	100.00	40.00	44.97	12.50	100.00	55.00	59.64
63	Columbia	65.00	100.00	24.00	49.20	12.50	100.00	31.00	54.53
64	Derby	35.00	100.00	19.50	13.03	0.00	100.00	20.25	41.11
65	Firth	65.00	100.00	40.00	61.50	4.00	80.00	.	Non-est
66	FREJA	67.50	100.00	40.00	48.90	2.00	100.00	35.00	56.20
67	Gere	75.00	100.00	55.00	66.83	0.36	100.00	50.00	63.88
68	GN04399	55.00	100.00	40.00	35.60	7.00	100.00	38.50	53.73
69	Grane	45.00	80.00	50.00	50.00	1.64	100.00	45.00	53.09
70	Grenader	45.00	100.00	29.09	7.70	3.00	80.00	7.00	38.83
71	GUNHILD	70.00	100.00	40.00	56.00	0.10	100.00	20.00	55.16
72	HA05AB10-47	85.00	80.00	28.50	40.00	11.00	100.00	35.00	54.21
73	HA05AB10-51	87.50	100.00	34.00	35.60	6.00	100.00	35.00	56.87
74	HA05AB16-31	62.50	60.00	28.50	57.70	20.00	100.00	22.50	50.17
75	HA05AB20-1	70.00	100.00	43.00	45.60	7.00	100.00	31.50	56.73
76	HA05AB21-7	60.00	100.00	40.00	35.03	8.00	100.00	31.50	53.50
77	HA05AB22-9	67.50	80.00	24.00	40.00	40.00	100.00	25.00	53.79
78	HA05AB29-17	67.50	80.00	40.00	26.80	17.00	100.00	38.50	52.83
79	HA05AB29-39	57.50	100.00	15.00	8.80	2.30	100.00	43.00	46.66
80	HA05AB34-48	57.50	100.00	13.50	8.80	20.00	100.00	18.00	45.40
81	HA05AB35-16	65.00	80.00	24.75	55.83	8.00	0.00	39.00	38.94

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
82	HA05AB36-33	65.00	80.00	29.00	42.30	9.00	100.00	28.50	50.54
83	HA05AB38-22	50.00	40.00	20.25	45.60	4.00	100.00	21.50	40.19
84	HA05AB38-39	50.00	60.00	24.00	13.03	6.00	80.00	24.00	36.72
85	HA05AB41-38	40.00	100.00	30.00	26.40	25.00	100.00	42.50	51.99
86	HA05AB42-20	55.00	100.00	33.50	40.00	6.00	100.00	31.50	52.29
87	HA05AB53-40	65.00	100.00	35.00	72.50	11.50	100.00	40.00	60.57
88	HA05AB9-32	70.00	60.00	23.50	35.60	10.00	100.00	24.00	46.16
89	HA05AB9-52	47.50	100.00	28.50	13.20	16.00	100.00	30.47	47.95
90	HA08-03X09-1	36.00	8.00	28.50	11.00	34.00	100.00	26.25	34.82
91	HA08-03X31-1	60.00	100.00	40.00	26.40	0.00	100.00	38.50	52.13
92	HA08-03X49-1	50.00	80.00	31.50	44.63	8.00	100.00	22.50	48.09
93	IL00-654	40.00	60.00	28.50	17.60	9.50	32.00	33.00	31.51
94	IL02-10836	47.50	80.00	50.00	83.50	5.00	80.00	43.00	55.57
95	IL02-5630	27.50	100.00	35.00	89.17	2.30	80.00	38.50	53.21
96	IL02-8011	30.00	40.00	24.00	17.43	2.45	60.00	29.00	28.98
97	IL02-8658	6.00	8.00	29.00	2.03	6.00	8.00	22.50	11.65
98	IL03-2658	55.00	48.00	28.50	45.60	45.00	48.00	18.00	41.16
99	IL03-7936	50.00	100.00	47.00	13.20	8.00	100.00	45.00	51.89
100	IL04-2727	2.15	20.00	40.00	23.50	1.00	80.00	39.00	29.38
101	IL04-3664	38.00	60.00	23.00	77.83	55.00	100.00	27.00	54.40
102	IL04-4410	37.50	16.00	22.50	19.80	14.00	80.00	14.50	29.19
103	IL04-7077	6.45	20.00	15.75	26.80	10.00	32.00	40.00	21.57
104	IL05-10015	36.00	80.00	13.50	55.83	0.36	80.00	24.75	41.49
105	IL05-10069	35.00	80.00	22.50	19.80	0.00	100.00	29.00	40.90
106	IL05-11942	19.00	20.00	40.00	0.00	0.00	80.00	35.00	27.69
107	IL05-1778	4.50	0.00	24.75	0.00	.	8.00	27.00	Non-est
108	IL05-3337	14.00	40.00	26.00	0.00	-0.36	4.00	38.00	17.35
109	IL05-3806	40.00	32.00	38.50	4.40	2.50	80.00	38.50	33.70
110	IL05-3928	35.00	80.00	24.00	13.20	0.36	100.00	33.50	40.87

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
111	IL05-6223	31.00	8.00	4.50	33.50	0.00	4.00	22.50	14.79
112	IL05-8515	16.00	20.00	22.50	8.80	0.00	48.00	33.00	21.19
113	IL05-9330	54.00	40.00	18.00	20.00	12.00	32.00	15.75	27.39
114	IL05-9931	58.00	80.00	10.50	24.20	3.00	100.00	27.00	43.24
115	IL05-9948	32.50	20.00	28.50	35.60	4.15	100.00	24.00	34.96
116	IL06-1161	50.00	80.00	18.00	22.00	10.36	80.00	24.00	40.62
117	IL06-3258	26.00	0.00	27.00	2.03	0.00	4.00	34.00	13.29
118	IL06-3751	27.50	0.00	45.00	26.23	0.00	8.00	43.00	21.39
119	IL06-5456	56.00	100.00	13.50	61.50	10.36	100.00	43.50	54.98
120	IL2250-15-PI641978	30.00	40.00	24.00	3.30	5.30	60.00	31.50	27.73
121	IL2250-18-PI641979	30.00	40.00	28.50	37.90	1.10	32.00	33.50	29.00
122	IL2294-1-PI641996	20.45	16.00	24.00	4.40	0.30	80.00	31.50	25.24
123	IL2294-3-PI641998	22.50	8.00	30.00	4.57	7.00	100.00	37.50	29.94
124	IL250-14-PI641977	37.50	100.00	40.00	26.23	15.00	100.00	50.00	52.68
125	IL250-3-PI641976	60.00	100.00	33.50	67.00	5.00	100.00	40.00	57.93
126	IL2815-PI641965	50.00	100.00	40.00	55.90	16.00	100.00	70.00	61.70
127	IL2838-PI641966	45.00	100.00	20.25	11.00	-0.36	100.00	38.00	44.84
128	IL2858-PI641967	50.00	100.00	18.00	24.20	6.00	80.00	29.25	43.92
129	IL2901-PI641968	50.00	40.00	22.50	28.00	6.00	100.00	20.25	38.11
130	IL3555-PI641970	60.00	100.00	45.00	35.03	38.00	100.00	40.00	59.72
131	IL75-5665	55.00	60.00	45.00	28.00	19.64	80.00	43.50	47.31
132	IL75-5743	50.00	60.00	23.50	13.20	17.50	60.00	24.75	35.56
133	IL86-1156	45.00	80.00	30.00	38.90	7.00	100.00	35.00	47.99
134	IL86-5698-PI539875	56.00	60.00	35.00	17.43	12.15	80.00	29.00	41.37
135	IL86-6404-PI539874	65.00	100.00	19.50	45.60	40.00	80.00	27.00	53.87
136	IL98-10145	42.50	48.00	45.00	77.83	6.00	48.00	45.00	44.62
137	IN09201	28.00	100.00	24.00	0.17	2.00	100.00	22.50	39.52
138	Kapp	60.00	100.00	35.00	88.83	45.00	100.00	35.00	66.26
139	Lena	55.00	100.00	30.00	89.17	22.00	100.00	33.50	61.38

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
140	Lennon	60.00	60.00	28.50	35.03	65.00	100.00	.	Non-est
141	LIPOPLUS	80.00	100.00	50.00	32.83	75.00	100.00	31.50	67.05
142	Maida	0.00	1.00	13.50	2.20	0.00	16.00	27.00	8.53
143	MN06108	0.00	0.00	9.00	0.00	0.36	1.50	20.25	4.42
144	MN06125	1.00	0.00	10.50	0.00	0.00	2.00	7.50	3.00
145	MN06239	0.60	0.00	5.10	0.00	0.00	4.00	13.50	3.31
146	MN07203	0.50	4.00	9.75	0.00	0.00	32.00	1.65	6.84
147	MN07210	0.50	10.00	9.00	1.10	0.00	2.00	12.00	4.94
148	MN08106	10.00	1.00	10.50	0.00	0.00	4.00	18.00	6.21
149	MN08123	2.00	0.00	4.05	0.00	0.00	0.40	9.15	2.23
150	MN08124	0.00	0.00	0.40	0.00	0.00	0.00	6.00	0.91
151	MN08129	0.10	0.00	4.50	0.00	0.00	0.00	6.75	1.62
152	MN08130	13.50	0.00	12.00	17.43	22.50	4.00	18.00	12.49
153	MN08131	1.50	0.00	11.25	0.00	0.00	6.00	9.00	3.96
154	MN08132	0.30	0.40	7.50	4.40	0.00	16.00	18.00	6.66
155	MN08134	0.00	0.00	11.50	0.00	0.00	0.40	9.00	2.96
156	MN08137	0.00	16.00	3.75	0.00	0.00	8.00	13.50	5.89
157	MN08139	0.10	48.00	4.50	0.00	0.00	60.00	9.75	17.45
158	MN08146	7.00	4.00	7.50	0.00	0.00	4.00	20.25	6.11
159	MN08150	9.00	0.00	9.00	1.10	0.00	16.00	18.00	7.59
160	MN08155	3.50	0.00	6.45	26.23	0.00	3.00	0.60	5.68
161	MN08160	0.15	1.00	9.00	0.00	0.00	2.00	27.00	5.57
162	MN08211	2.00	0.00	0.90	0.00	0.00	0.00	0.30	0.46
163	MN08212	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
164	MN08217	15.00	8.00	13.50	3.30	0.00	4.00	11.25	7.86
165	MN08222	0.10	0.00	4.50	2.03	0.00	2.00	4.50	1.88
166	MN08225	4.00	2.00	3.60	4.40	0.00	4.00	12.00	4.29
167	MN08230	0.10	5.00	11.25	6.60	0.00	4.00	18.00	6.42
168	MN08234	25.00	10.00	11.25	5.50	0.00	80.00	18.00	21.39

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
169	MN08238	0.00	0.00	0.60	2.03	0.00	0.00	0.20	0.40
170	MN08242	0.00	0.00	0.60	0.17	0.00	0.40	15.00	2.31
171	MN08243	0.00	0.00	2.85	0.00	0.00	4.00	4.50	1.60
172	MN08251	1.50	4.00	1.20	4.23	0.00	8.00	4.50	3.35
173	MN08252	1.00	0.00	0.20	0.17	0.00	0.00	0.40	0.25
174	MN08253	2.15	0.00	4.50	4.40	0.00	4.00	15.75	4.40
175	MN08254	0.10	0.00	3.00	0.00	0.00	2.00	12.00	2.44
176	MN08260	0.00	0.00	2.40	0.00	0.00	0.40	0.50	0.45
177	MN08262	2.10	0.00	0.00	0.00	0.00	0.40	0.00	0.36
178	MN08266	0.20	0.00	18.00	0.17	0.00	4.00	10.50	4.70
179	MN08268	0.20	10.00	9.00	0.00	0.00	4.00	19.00	6.03
180	MN08270	0.10	0.00	6.75	0.00	0.36	0.40	13.50	3.02
181	Moholt	50.00	100.00	35.00	61.50	0.00	100.00	35.00	54.50
182	Navaro	40.00	40.00	29.00	30.80	15.00	64.00	13.50	33.19
183	ND000861	6.00	0.00	0.80	0.00	0.00	0.40	1.65	1.26
184	ND001397	40.00	60.00	35.00	53.43	59.64	100.00	36.25	54.90
185	ND020290-PO-808	8.00	20.00	19.50	1.10	0.00	32.00	15.75	13.76
186	ND030078	0.00	10.00	6.00	-0.17	0.00	8.00	18.47	6.04
187	ND040196	0.00	0.00	3.75	0.00	0.00	0.00	5.40	1.31
188	ND040492	0.00	0.00	2.25	0.00	0.00	0.00	2.85	0.73
189	ND050017	0.00	0.00	9.00	0.00	0.00	0.00	7.50	2.36
190	ND050490	0.00	5.00	4.50	3.30	0.00	4.00	7.50	3.47
191	ND050506	0.00	0.00	3.00	0.00	0.00	0.40	3.00	0.89
192	ND050578	0.00	0.00	3.00	0.00	.	0.40	8.25	Non-est
193	ND051037	0.10	0.00	2.10	0.00	0.00	0.40	6.75	1.31
194	ND051069	0.00	0.00	7.50	0.00	0.00	0.40	9.75	2.52
195	ND051236	1.00	0.00	0.60	0.00	0.00	0.00	0.55	0.31
196	ND051306	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.03
197	ND051312	0.00	0.00	0.80	0.00	0.00	0.40	0.00	0.17

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
198	ND051467	0.00	0.00	2.85	0.00	0.00	0.40	0.95	0.60
199	ND051513	0.10	0.00	0.75	0.00	0.00	0.00	1.10	0.28
200	ND060111	0.00	0.00	7.50	.	0.00	0.40	9.75	Non-est
201	ND060182	1.00	0.00	0.40	0.00	0.00	0.00	0.35	0.23
202	ND060223	0.00	0.00	3.00	0.00	0.00	0.00	6.00	1.29
203	ND060235	0.00	0.00	3.00	0.00	0.00	0.00	6.00	1.29
204	ND060249	0.00	0.00	0.30	0.00	0.00	0.00	14.85	2.16
205	ND060342	0.00	4.00	13.50	2.03	0.00	4.00	8.25	4.54
206	ND060418	0.00	0.00	4.50	0.00	0.00	0.40	15.75	2.90
207	ND060432	0.00	0.00	2.10	0.00	0.00	0.00	7.50	1.35
208	ND060449	0.00	0.00	3.00	0.00	0.00	0.40	4.50	1.13
209	ND060464	0.00	0.00	6.15	0.17	0.00	0.40	9.00	2.25
210	ND060487	0.00	0.00	0.90	0.00	0.36	0.00	0.15	0.20
211	ND060507	0.50	0.00	1.80	0.00	0.00	0.00	1.70	0.57
212	ND060570	1.00	0.00	3.75	0.00	0.00	3.00	7.50	2.18
213	ND060652	0.50	0.00	3.75	0.00	0.00	0.00	6.00	1.46
214	ND060897	0.00	0.00	1.10	0.00	0.00	0.40	4.65	0.88
215	ND060925	1.00	0.00	3.75	.	0.36	0.00	3.30	Non-est
216	ND061097	0.00	0.00	4.50	0.00	0.00	0.40	4.50	1.34
217	ND061590	0.00	0.00	3.00	0.00	0.00	0.00	6.00	1.26
218	ND061614	0.10	0.00	3.00	0.00	0.00	0.00	1.70	0.69
219	ND061813	10.00	10.00	13.50	0.00	0.00	32.00	22.50	12.55
220	ND061868	0.00	0.00	6.00	0.17	0.00	0.00	1.20	1.05
221	ND061975	0.00	0.00	3.75	0.00	0.00	0.40	8.25	1.77
222	ND070388	0.00	0.00	4.00	0.00	3.00	0.40	4.50	1.70
223	ND070813	0.00	0.00	6.00	0.00	0.00	0.40	5.25	1.66
224	ND071063	1.00	0.00	2.40	0.00	0.00	0.00	2.40	0.83
225	ND071521	4.00	1.00	11.25	0.00	0.00	8.00	11.25	5.07
226	ND071694	0.00	0.00	23.15	0.00	0.00	12.00	13.50	6.95

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
227	ND072258	0.00	40.00	26.75	4.40	0.00	100.00	28.50	28.52
228	ND080724	0.00	0.00	3.75	0.00	0.00	0.40	4.50	1.24
229	ND081924	2.00	0.00	0.60	0.00	0.00	0.40	3.75	0.96
230	Nes	70.00	100.00	50.00	78.17	1.50	100.00	55.00	64.95
231	Nice	28.00	60.00	23.50	26.23	0.00	100.00	9.75	35.35
232	Nudist	90.00	100.00	45.00	72.50	55.00	100.00	60.00	74.64
233	OA1058-4	0.00	0.00	0.00	1.10	0.00	0.00	0.10	0.17
234	OA1130-1	1.15	4.00	13.50	23.50	0.00	60.00	24.00	18.02
235	OA1174-3	0.00	8.00	6.00	0.00	0.00	12.00	15.75	5.96
236	OA1176-1	0.00	0.00	9.00	0.00	.	4.00	15.00	Non-est
237	OA1180-5	70.00	80.00	9.00	67.00	-0.06	60.00	18.00	43.42
238	OA1189-1	0.00	0.00	13.50	6.60	0.00	32.00	22.50	10.66
239	OA1189-4	3.00	0.00	3.00	0.00	0.00	0.00	4.80	1.54
240	OA1196-3	0.10	0.00	3.00	0.00	0.00	2.00	6.00	1.59
241	OA1197-1	0.00	0.00	1.80	0.00	0.00	0.40	0.30	0.36
242	OA1202-1	20.00	1.00	9.75	3.30	4.00	4.00	6.00	6.86
243	OA1204-2	16.50	4.00	7.50	0.00	5.00	8.00	1.97	6.14
244	OA1207-1	95.00	100.00	35.00	72.50	65.00	100.00	27.00	70.64
245	OA1226-1	12.00	4.00	13.50	4.57	0.00	100.00	10.50	20.65
246	OA1226-4	50.00	8.00	18.00	2.20	0.00	48.00	18.00	20.60
247	OA1228-1	0.00	0.00	2.85	0.00	0.00	100.00	2.40	15.04
248	OA1232-2	0.00	8.00	1.05	0.00	0.00	8.00	3.75	2.97
249	OA1232-5	0.00	0.00	0.90	0.00	0.00	2.00	0.45	0.48
250	OA1234-1	0.00	1.00	9.00	0.00	0.00	2.00	12.00	3.43
251	OA1242-5	0.10	0.00	14.00	0.00	0.36	32.00	15.00	8.78
252	OA1248-1	6.15	4.00	5.25	0.00	0.00	4.00	2.25	3.09
253	OA1250-1	50.00	20.00	9.00	-0.17	1.00	48.00	6.00	19.12
254	OA1250-2	45.00	8.00	8.25	0.00	2.50	100.00	6.00	24.25
255	OA1251-1	35.00	60.00	21.38	35.60	17.50	32.00	22.50	32.00

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
256	OA1253-1	27.00	40.00	21.75	0.00	0.00	4.00	24.00	16.68
257	OA1256-1	0.00	0.00	1.80	0.00	0.00	0.00	0.30	0.30
258	OA1260-1	0.00	10.00	24.00	0.00	0.00	48.00	14.50	13.79
259	OA1262-1	0.00	0.00	6.00	0.00	0.00	0.40	3.00	1.34
260	OA1263-2	27.00	0.00	1.90	0.00	.	0.40	3.00	Non-est
261	OA1266-1	0.00	0.00	7.50	0.00	0.00	2.00	0.30	1.40
262	OA1268-3	8.15	16.00	3.00	4.40	8.00	8.00	2.00	7.08
263	OA1272-1	36.00	8.00	6.00	6.60	0.00	8.00	10.50	10.73
264	Odal	70.00	100.00	40.00	40.10	12.00	80.00	35.00	53.87
265	Ollram	45.00	100.00	40.00	88.83	.	100.00	20.00	Non-est
266	OT3028	2.15	4.00	18.00	1.10	0.00	60.00	18.00	14.75
267	OT3036	30.00	80.00	17.09	34.60	4.30	48.00	24.00	34.00
268	OT3037	1.00	1.00	0.70	0.00	0.00	4.00	13.50	2.89
269	OT3039	30.00	40.00	17.09	17.43	2.00	16.00	9.50	18.86
270	OT3045	0.00	1.00	11.25	13.20	0.00	4.00	29.00	8.35
271	OT3046	0.00	20.00	33.50	0.00	0.00	80.00	33.00	23.76
272	OT3047	0.00	40.00	28.50	0.00	0.00	80.00	26.25	24.96
273	OT3048	0.00	0.00	6.75	78.00	26.00	0.40	8.25	17.06
274	OT3050	0.00	60.00	19.00	0.00	0.00	60.00	7.50	20.88
275	OT399	0.00	4.00	16.50	4.40	0.00	20.00	18.00	8.99
276	OT7053	0.00	0.00	0.20	0.00	0.00	0.40	0.45	0.15
277	Porter	60.00	60.00	35.00	40.10	8.45	80.00	24.00	43.94
278	Putnam 61	80.00	60.00	40.00	44.40	2.50	100.00	36.00	51.84
279	Ringsaker	77.50	100.00	50.00	77.83	29.00	100.00	50.00	69.19
280	Robust	3.00	16.00	13.50	0.00	0.00	32.00	16.50	11.57
281	SA01223-02	6.10	40.00	13.50	0.00	0.00	100.00	19.50	25.56
282	SA051172	0.00	8.00	7.00	0.00	0.00	0.40	4.95	2.91
283	SA061148	27.50	100.00	30.00	32.40	7.00	100.00	28.50	46.49
284	SA070089	8.10	8.00	6.00	0.00	0.00	60.00	3.00	12.13

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
285	SA070270	8.00	16.00	9.00	17.77	20.00	8.00	12.00	12.97
286	SA070367	2.00	0.00	24.75	8.63	0.00	60.00	22.50	16.84
287	SA070444	0.00	40.00	18.00	0.00	0.00	80.00	22.50	22.93
288	SA070452	2.00	40.00	50.00	2.03	0.00	100.00	33.50	32.50
289	SA070513	8.00	32.00	10.50	0.00	0.00	48.00	13.50	16.00
290	SA070576	35.00	80.00	20.00	8.63	6.00	80.00	11.25	34.41
291	SA070592	26.00	80.00	26.75	55.50	16.00	100.00	30.00	47.75
292	SA070631	0.50	20.00	18.00	0.00	0.36	4.00	13.50	8.05
293	SA070655	0.10	20.00	29.00	3.30	0.00	32.00	25.00	15.63
294	SA070712	0.00	0.00	0.60	1.10	0.00	0.00	0.00	0.19
295	SA070781	0.00	10.00	30.00	0.00	0.00	40.00	34.00	16.29
296	SA070845	0.15	10.00	23.50	-0.17	0.00	80.00	29.25	20.39
297	SA070860	8.00	10.00	35.00	0.00	0.00	8.00	24.00	12.14
298	SA070906	1.00	20.00	15.00	0.00	0.00	48.00	15.00	14.14
299	SA070972	0.10	1.00	29.00	35.37	0.00	80.00	33.50	25.52
300	SA071369	4.50	8.00	5.09	0.00	0.00	4.00	4.50	3.73
301	SA071405	1.00	20.00	15.75	4.40	0.00	48.00	21.00	15.74
302	SA071616	2.50	1.00	27.00	1.10	0.00	32.00	20.25	11.98
303	Sherwood	20.00	20.00	28.50	0.00	0.00	2.00	9.00	11.28
304	SW INGEBORG	75.00	60.00	45.00	83.50	4.00	100.00	45.00	58.93
305	SW KERSTIN	37.50	100.00	45.00	26.40	20.00	100.00	40.00	52.70
306	SW VAASA	75.00	100.00	29.00	61.50	7.64	100.00	45.00	59.73
307	Sylva	42.50	60.00	16.75	51.10	11.00	80.00	25.00	40.91
308	Tippecanoe	72.50	100.00	45.00	55.90	40.00	100.00	55.00	66.91
309	Triactor	2.15	8.00	6.00	4.23	0.36	60.00	9.00	12.82
310	Tyler	75.00	100.00	45.00	26.23	6.00	100.00	42.50	56.39
311	VAO-58	65.00	80.00	27.00	55.83	0.00	100.00	27.00	50.69
312	VAO-44	50.00	100.00	35.00	35.03	28.00	100.00	38.50	55.22
313	Vao-48	70.00	60.00	38.00	77.83	50.00	100.00	42.50	62.62

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
314	Woodburn	7.00	60.00	22.50	4.40	0.00	100.00	35.00	32.70
315	X8787-1	0.20	2.00	3.60	0.00	0.00	8.00	11.25	3.53
316	X8791-1	0.20	4.00	6.00	0.00	0.00	0.90	3.00	2.01
317	X8826-1	7.00	16.00	6.75	22.00	5.00	32.00	12.00	14.39
318	X8903-2	33.00	80.00	21.00	44.50	12.50	100.00	33.50	46.36
319	X8995-4	0.20	5.00	4.50	6.60	0.00	4.00	10.50	4.35
320	X9082-1	1.00	60.00	10.50	2.20	0.00	8.00	16.50	14.03
321	X9150-1	2.00	0.00	1.80	2.03	0.00	4.00	4.50	2.00
322	X9192-5	0.00	20.00	4.50	4.40	0.00	80.00	13.50	17.49
323	X9195-2	0.00	0.00	6.00	0.00	0.00	0.00	2.70	1.24
324	X9195-6	0.10	0.00	3.60	0.00	0.00	0.00	4.50	1.17
325	X9200-4	2.24	40.00	18.00	15.40	0.00	32.00	29.00	19.52
326	X9221-6	0.50	60.00	0.20	24.20	5.00	3.00	1.50	13.49
327	X9221-8	0.00	0.00	0.60	0.00	0.00	0.00	0.65	0.18
328	X9253-1	0.50	4.00	4.50	2.20	1.00	8.00	7.50	3.96
329	X9258-5	0.00	8.00	0.80	0.00	0.00	8.00	3.20	2.81
330	X9270-4	0.10	10.00	3.00	0.00	0.00	4.00	4.50	3.03
331	X9285-1	0.00	4.00	6.00	0.00	0.00	8.00	22.50	5.79
332	X9287-2	0.10	0.00	0.40	0.17	0.00	0.00	3.00	0.52
333	X9290-2	0.00	8.00	6.00	0.00	0.00	8.00	15.75	5.39
334	X9368-1	0.00	8.00	1.05	0.00	0.00	4.00	6.00	2.72
335	X9375-1	0.00	0.00	1.70	0.00	0.00	0.60	0.40	0.39
336	X9384-2	0.00	10.00	1.65	4.23	0.00	8.00	5.25	4.16
337	X9386-1	0.00	2.00	1.65	17.60	0.00	8.00	2.10	4.48
338	X9392-1	0.65	0.00	0.80	0.00	0.36	3.00	9.00	1.97
339	X9395-2	0.10	8.00	0.50	4.57	0.00	0.40	3.75	2.47
340	X9396-1	1.10	0.00	3.75	6.60	0.00	4.00	7.50	3.28
341	X9396-4	1.15	0.00	6.00	17.60	0.15	2.00	26.00	7.56
342	X9410-1	0.15	8.00	7.65	0.00	0.00	4.00	1.00	2.97

Table 4.3 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE	
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND		St. Paul, MN
343	X9410-2	0.00	0.00	1.70	0.00	0.00	0.00	6.00	1.10
344	X9414-1	0.10	2.00	0.20	0.00	0.00	2.00	8.25	1.79
345	X9421-3	2.00	4.00	3.00	14.30	2.00	8.00	7.50	5.83
346	X9422-1	2.00	10.00	1.70	4.40	0.00	8.00	3.00	4.16
347	X9435-1	0.20	0.00	0.00	0.00	10.00	4.00	7.50	3.10
348	X9439-1	2.50	16.00	15.00	1.10	0.36	60.00	15.00	15.71
349	X9449-1	0.00	0.00	0.40	0.00	0.00	0.00	5.25	0.76
350	X9474-2	0.00	0.00	2.10	17.43	0.36	4.00	2.25	3.73
351	X9487-1	0.20	0.00	3.00	0.00	0.00	4.00	6.00	1.89
352	X9487-4	0.20	1.00	2.85	0.00	0.00	32.00	1.65	5.39
353	X9492-1	6.00	20.00	12.00	8.80	1.00	4.00	21.00	10.40
354	X9498-1	1.00	8.00	4.20	3.30	0.36	8.00	4.50	4.19
355	X9500-2	0.00	0.00	0.35	2.37	0.00	8.00	1.50	1.75
356	X9500-6	0.00	0.00	0.90	0.00	2.00	4.00	2.25	1.31
357	X9503-1	0.10	0.00	0.58	0.00	0.36	4.00	1.50	0.91
358	X9507-1	0.50	4.00	6.50	7.70	0.00	8.00	3.75	4.35
359	X9507-3	0.50	1.00	2.50	0.00	0.00	4.00	15.00	3.26
360	X9509-3	0.65	1.00	4.50	6.60	0.00	8.00	13.50	4.89
361	X9509-4	0.00	20.00	3.75	0.00	0.00	32.00	9.00	9.25
	CV%	42.49	.	36.62	86.56	152.51	.	52.47	48.74
	Grand Mean	23.65	35.42	17.26	16.36	6.39	45.57	19.59	20.90
	Range	0 - 95.00	0 - 100.00	0 - 55.00	0 - 89.17	0 - 75.00	0 - 100.00	0 - 70.00	0 - 74.64
	LSD	19.79	.	12.55	31.29	20.23	.	20.36	8.33

Table 4.4. CI means of winter oat lines for individual genotypes in Castroville, TX, Baton Rouge, LA, Fargo, ND, and St. Paul, MN for 2010 and 2011.

ENTRY	GENOTYPE	2010			2011			AVERAGE
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Fargo, ND	St. Paul, MN	
1	833-99AB118	70.00	3.00	22.50	14.00	4.00	11.50	20.83
2	Aurora	75.00	80.00	40.00	80.00	100.00	50.00	70.83
3	Bond	75.00	100.00	35.00	55.90	100.00	29.00	65.82
4	Brooks	95.00	80.00	60.00	85.00	100.00	45.00	77.50
5	Coker 242	70.00	40.00	38.50	45.00	80.00	38.00	51.92
6	Coker 716	100.00	100.00	60.00	75.00	100.00	40.00	79.17
7	Colberson	80.00	80.00	32.25	75.00	100.00	38.50	67.63
8	Corondo	67.50	40.00	36.00	40.47	80.00	33.50	49.58
9	Delair	80.00	60.00	55.00	21.50	100.00	50.00	61.08
10	DeSoto	70.00	32.00	13.50	16.00	32.00	24.00	31.25
11	Excel	12.00	40.00	14.25	2.67	100.00	15.00	30.65
12	FL0047-J9	15.00	0.00	6.75	0.00	3.00	7.50	5.38
13	FL0115-J2	24.00	0.00	13.50	1.00	0.00	2.10	6.77
14	FL0238BSB-22	3.00	0.00	17.25	0.00	0.00	10.50	5.13
15	FL03001BSB-S7	26.00	40.00	43.00	3.00	48.00	25.50	30.92
16	FL03129-Ab7	10.00	0.00	9.00	0.00	0.00	10.50	4.92
17	FL03146BSB-S1-B-S1	10.00	0.00	7.65	0.00	0.00	5.25	3.82
18	FL03167BSB-145	1.00	0.00	1.90	0.00	.	0.80	Non-est
19	FL03167BSB-147	5.00	0.00	2.50	0.00	0.00	13.50	3.50
20	FL03167BSBS-3	12.00	0.00	13.50	0.00	2.00	15.75	7.21
21	FL03184-FLID-B-S1	42.50	0.00	7.50	0.00	0.00	6.00	9.33
22	FL04155-S06-31-B-S1	1.10	0.00	3.60	0.00	0.00	0.65	0.89
23	FL04178-FLID-B-S-2	2.00	0.00	6.00	0.00	4.00	7.50	3.25
24	FL99084-J2	6.50	0.00	5.85	0.47	0.00	12.75	4.26
25	FL99153FBS-45-1-B-S-B-S1-B-S1	0.20	0.00	12.00	0.00	0.00	9.00	3.53
26	FL99212-D6	22.00	0.00	11.00	0.00	0.00	4.50	6.25
27	Florida 167	75.00	8.00	60.00	40.00	21.00	34.00	39.67

Table 4.4 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Fargo, ND	St. Paul, MN	
28	Florida 500	68.00	60.00	60.00	0.07	80.00	45.00	52.16
29	Floriland	75.00	40.00	60.00	65.00	80.00	45.00	60.83
30	HARRISON	60.00	0.00	15.75	18.00	4.00	22.50	20.04
31	HORIZON 201	0.20	0.00	4.35	39.53	0.00	6.00	8.35
32	HORIZON LA976	0.20	0.00	4.65	0.00	0.00	2.70	1.26
33	LA02012-S-B-139-S2-B-S2-B-S2	0.20	0.00	7.50	0.00	0.00	7.50	2.53
34	LA02035-I-J1	16.00	0.00	4.65	0.00	0.00	6.75	4.57
35	LA0210SBSBSBSB-S1	80.00	60.00	55.00	12.47	100.00	50.00	59.58
36	LA03012SBSBSB-12	0.00	0.00	7.65	0.00	0.00	4.50	2.03
37	LA03012SBSBSB-61	0.00	0.00	10.50	0.00	6.00	2.10	3.10
38	LA03018SBSBSB-65-S1	24.00	0.00	13.50	0.00	0.00	9.00	7.75
39	LA03040SBSBSB-83	60.00	0.00	31.50	1.40	4.00	9.00	17.65
40	LA03046SBS7-B-S1	2.00	0.00	11.25	0.00	0.00	13.50	4.46
41	LA03060SBSBSB-S1	8.00	0.00	43.00	0.00	32.00	38.00	20.09
42	LA03063SBSBSB-6	6.10	0.00	3.00	0.00	0.00	6.00	2.52
43	LA03063SBSBSB-S4	1.00	0.00	6.15	0.00	0.30	9.00	2.74
44	LA03066SBS-L1	100.00	80.00	34.00	24.53	32.00	37.50	51.34
45	LA04004SBSB-121	5.00	0.40	18.00	0.00	4.00	38.50	10.98
46	LA04004SBSB-61-B-S1	11.00	0.00	22.50	2.50	4.00	27.00	11.17
47	LA04014SBSB-39	3.00	0.00	7.50	0.00	8.00	27.00	7.58
48	LA04018SBSB-181	0.20	0.00	13.50	3.00	0.00	5.25	3.66
49	LA04018SBSB-86	2.10	0.00	9.00	0.00	0.00	9.00	3.35
50	LA05006GSBS-7-S1	0.00	1.00	18.00	0.00	0.00	10.50	4.92
51	LA06058SBS-32-S1	20.00	0.00	6.00	0.00	0.30	4.50	5.13
52	LA06059SBS-84-S1	28.00	0.00	5.80	0.00	0.00	7.50	6.88
53	LA604	2.00	4.00	4.50	0.00	3.00	11.55	4.18
54	LA9339	20.00	4.00	31.50	4.00	8.00	15.00	13.75
55	LA97006GSB-59-2-4-SBS1	2.00	0.00	3.00	0.00	0.00	13.50	3.08
56	LA99016	0.00	0.00	7.50	0.00	0.00	3.00	1.75

Table 4.4 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Fargo, ND	St. Paul, MN	
57	LA99017	0.00	0.00	6.75	0.40	0.00	15.15	3.72
58	Lee	77.50	60.00	36.00	89.53	100.00	45.00	68.01
59	Osage	75.00	60.00	45.00	7.00	100.00	34.50	53.58
60	Ozark	90.00	60.00	50.00	60.00	48.00	27.00	55.83
61	PI260616-1	6.00	4.00	0.00	1.10	4.00	1.84	2.82
62	Quincy Gray	65.00	32.00	4.50	39.53	16.00	16.00	28.84
63	Red Algerian	55.00	20.00	27.00	14.00	80.00	35.00	38.50
64	Rogers	80.00	20.00	60.00	29.53	64.00	40.00	48.92
65	Santa Fe	70.00	100.00	60.00	55.00	100.00	43.00	71.33
66	SECTARIAT LA495	85.00	40.00	60.00	21.00	80.00	42.50	54.75
67	Simpson	92.50	80.00	55.00	65.00	100.00	21.50	69.00
68	Sure Grain	70.00	8.00	35.00	0.50	32.00	16.50	27.00
69	TAMO 405	12.00	0.00	15.75	0.00	0.00	6.00	5.63
70	TAMO 406	3.00	0.00	7.25	0.00	0.00	14.50	4.13
71	TAMO 606	70.00	24.00	12.00	2.50	4.00	19.50	22.00
72	Tift	60.00	60.00	55.00	0.00	40.00	33.50	41.42
73	Trisparinia	80.00	80.00	50.00	2.00	100.00	40.00	58.67
74	Trophy	6.00	0.00	13.50	0.00	8.00	15.00	7.08
75	TX02U 7029	1.10	4.00	6.00	0.00	3.00	3.75	2.90
76	TX02U 7047	9.50	0.00	11.25	0.00	0.00	7.35	4.68
77	TX02U 7065	18.00	0.00	5.25	0.00	0.00	9.50	5.46
78	TX02U 7097	5.00	0.00	4.35	0.00	0.00	7.50	2.81
79	TX02U 7103	0.10	0.00	18.68	0.00	0.00	4.65	3.90
80	TX02U 7104	0.00	0.00	4.50	0.00	0.00	12.00	2.75
81	TX02U 7176	1.00	0.00	6.15	0.00	0.00	1.05	1.37
82	TX02U 7181	0.00	0.00	9.00	0.00	0.00	2.00	1.83
83	TX02U 7219	0.00	0.00	1.65	0.00	0.00	1.65	0.55
84	TX02U 7227	0.20	0.00	4.80	.	0.00	1.70	Non-est
85	TX02U 7237	11.00	0.00	9.00	0.00	.	3.75	Non-est

Table 4.4 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Fargo, ND	St. Paul, MN	
86	TX02U 7325	16.00	0.00	2.25	0.00	0.00	4.50	3.79
87	TX02U 7443	20.00	0.00	4.50	0.00	0.00	3.75	4.71
88	TX02U 7473	28.00	0.00	9.75	0.00	0.00	7.50	7.54
89	TX02U 7479	0.00	0.00	0.90	0.00	0.00	3.00	0.65
90	TX02U 7490	0.00	0.00	6.75	0.00	0.00	6.75	2.25
91	TX02U 7518	2.00	1.00	3.75	0.00	0.00	6.45	2.20
92	TX02U 7605	0.20	8.00	3.00	0.00	0.00	0.70	1.98
93	TX02U 7651	0.00	0.00	9.00	0.00	0.00	2.75	1.96
94	TX02U 7682	32.00	0.00	4.50	0.00	0.00	6.00	7.08
95	TX05CS 347 1	0.50	0.00	13.50	0.00	0.00	6.00	3.33
96	TX05CS 347 2	0.00	0.00	11.25	0.00	0.00	7.50	3.13
97	TX05CS 542	50.00	0.00	7.50	0.00	0.00	9.00	11.01
98	TX05CS 556	5.00	0.00	7.65	0.00	0.00	12.75	4.23
99	TX07CS1039	12.00	4.00	6.15	0.00	0.00	5.25	4.57
100	TX07CS1228	28.00	0.00	5.25	0.00	0.00	6.75	6.67
101	TX07CS1268	20.00	0.00	18.75	1.00	4.00	10.13	8.98
102	TX07CS1402	24.00	0.00	4.50	0.00	0.00	13.50	7.00
103	TX07CS1564	20.00	0.00	9.00	0.00	0.00	7.50	6.08
104	TX07CS1584	1.10	0.00	9.00	.	0.00	25.00	Non-est
105	TX07CS1805	0.00	0.00	6.75	0.00	0.00	6.75	2.25
106	TX07CS1832	0.00	0.00	9.00	0.00	0.00	20.00	4.83
107	TX07CS1948	0.00	0.00	1.10	0.00	0.00	0.40	0.25
108	TX07CS1965	0.00	0.00	1.50	0.00	0.00	0.35	0.31
109	TX07CS1997	1.10	0.00	6.60	0.00	0.00	1.80	1.58
110	TX07CS2001	5.00	0.00	11.25	0.00	0.00	7.84	4.02
111	TX07CS2140	2.00	0.00	6.00	0.00	0.00	11.25	3.21
112	TX07CS2201	0.15	0.00	9.75	0.00	0.00	9.00	3.07
113	TX07CS2235	0.20	0.00	13.50	0.00	0.00	6.00	3.28
114	TX07CS2350	0.15	0.00	7.50	0.00	0.00	9.00	2.78

Table 4.4 Continued

ENTRY	GENOTYPE	2010			2011			AVERAGE
		Castroville, TX	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Fargo, ND	St. Paul, MN	
115	TX07CS2609	0.00	0.00	10.50	0.00	0.00	3.75	2.38
116	TX07CS2652	0.00	0.00	3.00	0.47	3.00	6.00	2.08
117	TX07CS2765	0.10	0.00	6.00	0.00	4.00	3.60	2.28
118	TX07CS2795	0.10	0.00	5.50	0.00	3.00	2.85	1.83
119	Winter Fulghum	75.00	80.00	60.00	75.00	80.00	28.50	66.42
CV%		25.41	.	41.51	61.75	.	44.87	39.05
Grand Mean		25.46	14.26	17.72	9.63	19.77	15.28	17.14
Range		0 - 100.00	0 - 100.00	0 - 60.00	0 - 89.53	0 - 100.00	0.35 - 50.00	0.25 - 79.17
LSD		12.81	.	14.93	12.58	.	13.70	5.97

Variance component heritability

Heritability is an estimate of the origin of variation, particularly the proportion of phenotypic variation to genetic variation (Brown and Caligari, 2008). A higher heritability value indicates greater breeding value and will ultimately be more useful in identifying QTL for crown rust resistance. In the spring oat panel, approximately 88% of the total phenotypic variance is estimated to be genetic in origin (Table 4.5). This is considered a high heritability value. For winter oats, approximately 90% of the phenotypic variance is estimated to be genetic in origin (Table 4.6).

Table 4.5. Variance-component heritability for spring oat lines across all locations for 2010 and 2011.

Source of variation	DF	MS	σ^2
Environment	4	27934.51	
Rep (Environment)	5	890.52	
Genotypes	360	2404.28	2404.28
Environment * Genotypes	1431	295.32	
Error	1645	103.80	
Phenotypic variance			30634.11
$h^2 = 0.88$			

Table 4.6. Variance-component heritability for winter oat lines across all locations for 2010 and 2011.

Source of variation	DF	MS	σ^2
Environment	3	9335.81	
Rep (Environment)	4	355.16	
Genotypes	118	2854.68	2854.68
Environment * Genotypes	352	314.14	
Error	446	44.81	
Phenotypic variance			12504.63
$h^2 = 0.90$			

Repeatability

Repeatability is a theoretical estimate of the upper limits of heritability indicating that selection for crown rust resistance is predictable within certain environments (Hakizimana et al., 2000). Higher repeatability values indicate that fewer measurements can be taken and that these measurements are capable of repetition over space or time (Falconer, 1988; Falconer and Mackay, 1996). Repeatability will be useful for the future work of this study because this value can help eliminate any testing environments in which oat lines do not perform consistently. Also this value indicates the quality of the information generated by data collection for 2010 and 2011. The higher the value, the more useful the data is in the ability to identify QTL for crown rust resistance.

For spring oat lines, repeatability was highest for Castroville, TX in 2010 with a value of 0.88. Repeatability was the lowest for Castroville, TX in 2011 with a value of 0.56. The repeatability values across the two years for Castroville, TX could be indicative of the large number of rust races found in this part of the country. Additionally, due to limited rainfall during 2011, crown rust infections took longer to establish in the crop, since crown rust relies on moisture for effective spread. St. Paul, MN revealed a repeatability value of 0.82 in 2010 and 0.61 in 2011. In Baton Rouge, LA in 2011, repeatability was estimated to be 0.64 (Table 4.7). Repeatability could not be calculated for the spring oat lines in Fargo, ND because only one rep was grown at this location.

Table 4.7. Repeatability for spring oat lines in Baton Rouge, LA, Castroville, TX, and St. Paul, MN for 2010 and 2011.

Source of variation	DF	2010		2011		
		Castroville, TX	St. Paul, MN	Baton Rouge, LA	Castroville, TX	St. Paul, MN
Between genotypes	1	715.05	187.88	358.08	119.54	165.08
Within genotypes	360	101.01	39.96	200.61	95.01	105.66
σ_p^2		816.06	227.84	558.69	214.55	270.73
Repeatability		0.88	0.82	0.64	0.56	0.61

For winter oat lines, repeatability was the highest for Castroville, TX in 2010 with a rating of 0.96. The lowest repeatability is for St. Paul, MN in 2011 at 0.79. In 2010, the repeatability for St. Paul, MN was calculated as 0.84. Baton Rouge, LA in 2011 had the second highest repeatability value at 0.92 (Table 4.8). Repeatability could not be calculated for the winter oat lines in Fargo, ND because only one rep was grown at this location.

Table 4.8. Repeatability for winter oat lines in Baton Rouge, LA, Castroville, TX, and St. Paul, MN for 2010 and 2011.

Source of variation	DF	2010		2011	
		Castroville, TX	St. Paul, MN	Baton Rouge, LA	St. Paul, MN
Between genotypes	1	984.23	294.60	422.55	173.27
Within genotypes	118	41.86	54.07	35.36	47.02
σ_p^2		1026.09	348.67	457.91	220.29
Repeatability		0.96	0.84	0.92	0.79

Crown rust measurements were highly heritable and repeatable. Heritability is necessary in order to guarantee that any resistance genes identified via association mapping will be carried on through future plant generations. Without high heritability, it would be difficult to ensure resistance for oat growers and breeders. Repeatability is also important in order to guarantee that resistance will be found in other locations within the genotypes featuring such resistance.

Field observations vs. Assess ratings

Three panels of oats (spring, winter and a core representation of each type of growth habit) were grown at four locations for two years. The four locations consist of Baton Rouge, LA, Castroville, TX, Fargo, ND, and St. Paul, MN. The spring oat panel consists of 360 breeder lines. The winter panel consists of 120 breeder lines. The core panel consisted of 108 lines of elite material designated by North American oat breeders. The spring and winter oat panels were evaluated for crown rust infection using traditional phenotypic note-taking methods. These methods included rating each plot based on crown rust severity and infection type. Severity refers to the percentage of the plot exhibiting crown rust symptoms. Infection type refers to the level of disease each plot is exhibiting. Infection types include resistant, moderately resistant, moderately susceptible, susceptible, or any combination thereof.

In addition to traditional phenotypic notes, pictures of each plot were obtained in Castroville for 2010. The photographs were of four representative flag leaves for each plot. These photographs were analyzed using Assess software (The American

Phytopathological Society), which generated an estimation for disease severity. The disease severity ratings obtained by the software were compared graphically to the traditional disease severity notes.

The software was only used for crown rust observations made in 2010 for Castroville, TX. A high correlation between the field observations and the Assess software ratings was found (Figure 4.1). In general, the software was aligned with the ratings obtained manually in the field. This correlation indicates the stability of the software for disease evaluation. However, due to certain limitations, the software may not be capable of entirely replacing human screening and traditional note-taking methods, but remains a valuable diagnostic tool nonetheless.

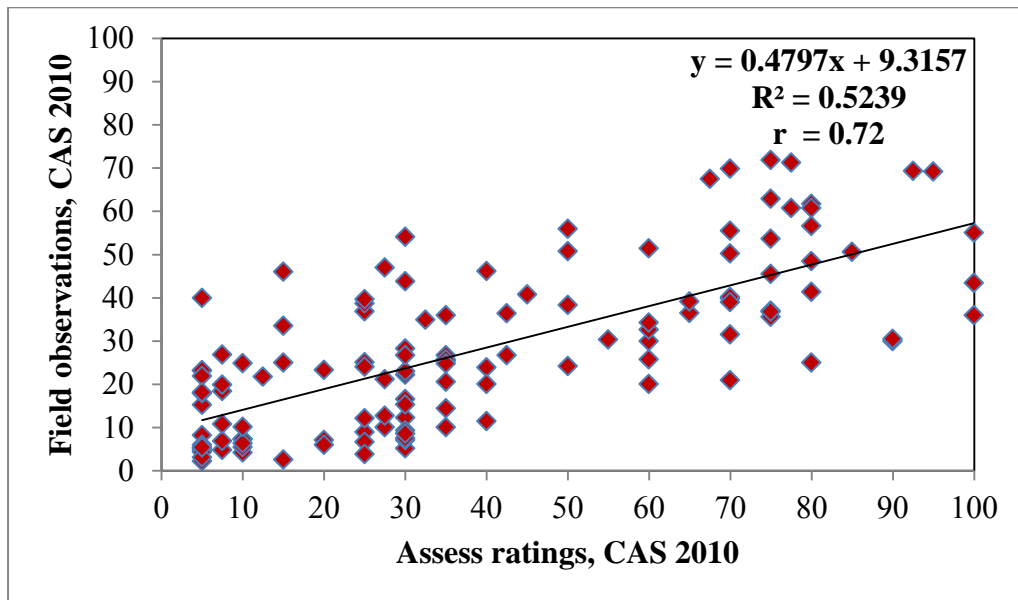


Figure 4.1. Correlation between Assess software and manual disease ratings.

Spring vs. winter comparisons

To compare the spring lines to the winter lines, the average coefficient of infection (CI) for all lines was calculated. This CI value was calculated by multiplying the numerical infection type ratings by the disease severity ratings to generate a quantitative measurement of disease. Severity ratings were based on a scale of 0-100%. Infection was classified as resistant, moderately resistant, moderately susceptible, susceptible, or any combination thereof. These infection types were assigned a numerical value on a scale of 0-1 for conversion and calculation of CI. The lower the CI value is, the more tolerant the line is to crown rust. On average, the winter lines performed better than the spring lines regarding rust susceptibility (Figure 4.2).

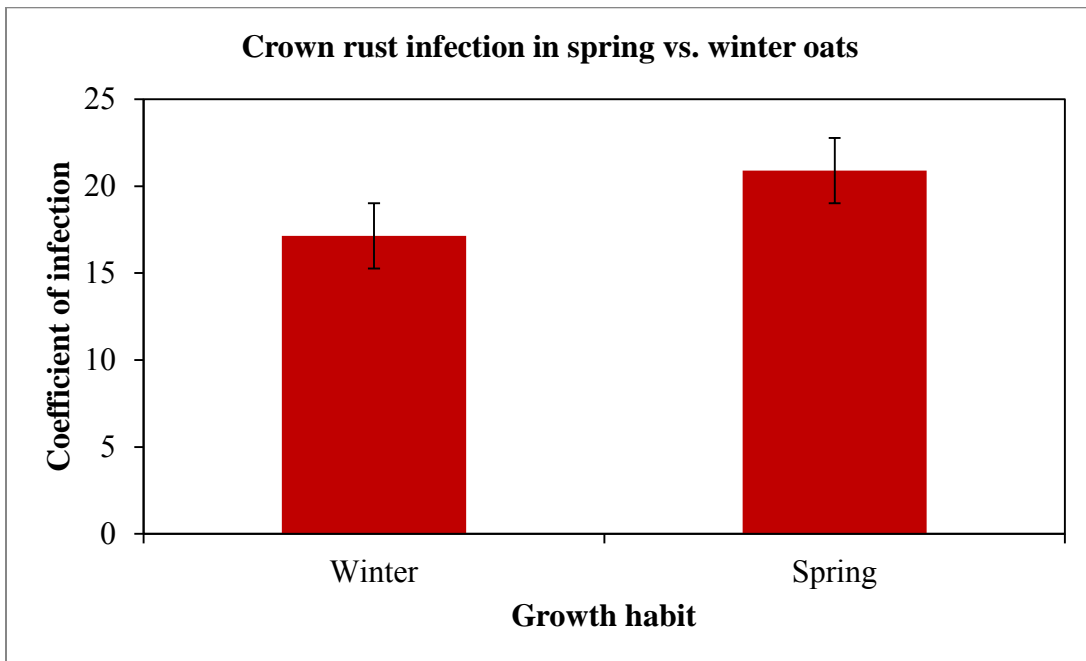


Figure 4.2. The average CI for all winter lines in comparison to the average coefficient of infection of all the spring lines.

The average CI was also evaluated according to the source of origin. Lines originating in Manitoba, Canada, Minnesota, North Dakota, Ottawa, Canada and Wisconsin performed the best in terms of crown rust resistance. The lines which performed the worst were those originating in Germany, Idaho, Missouri, Norway, Sweden and the United Kingdom. There was a large amount of variability across lines according to the source of origin (Figure 4.3).

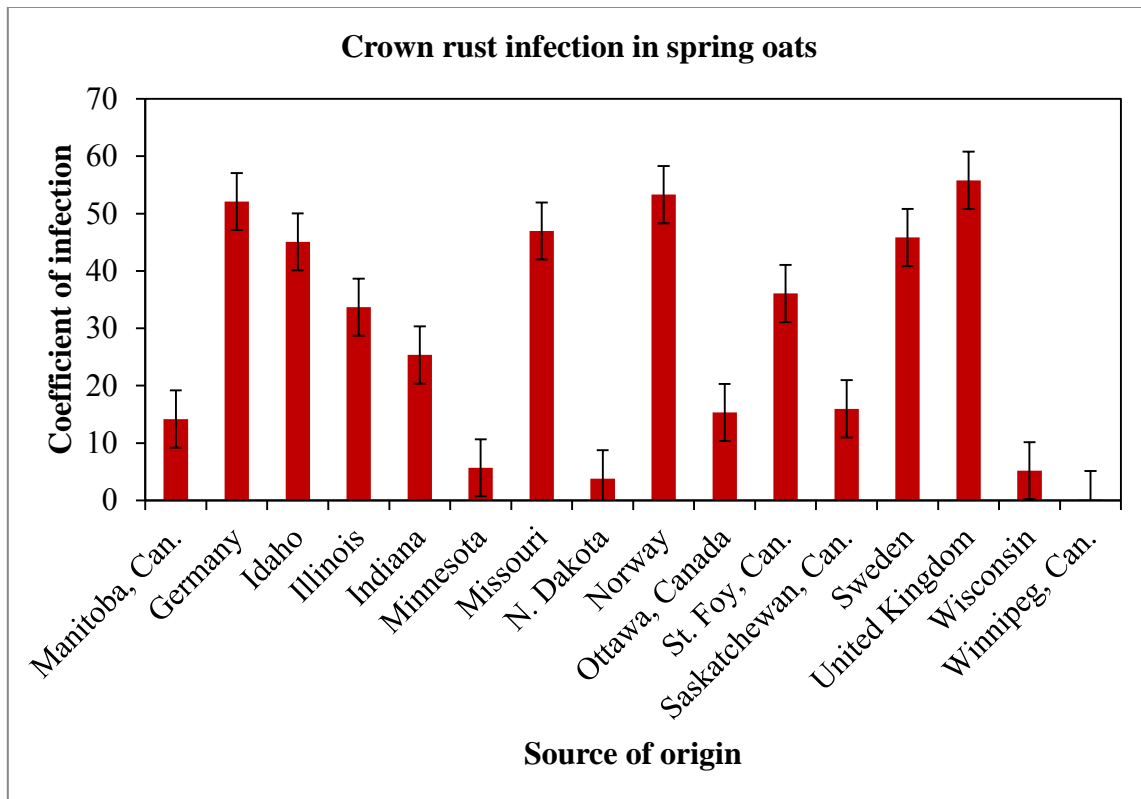


Figure 4.3. The average CI for all spring lines originating from a given location.

For winter oats, the lines originating in Brazil, Florida, Louisiana, and Texas performed the best in terms of crown rust resistance. The lines which were the most susceptible to crown rust were those originating in Argentina, Australia, Georgia and Virginia. Again, a large amount of variability across lines can be visualized when separated according to source of origin (Figure 4.4).

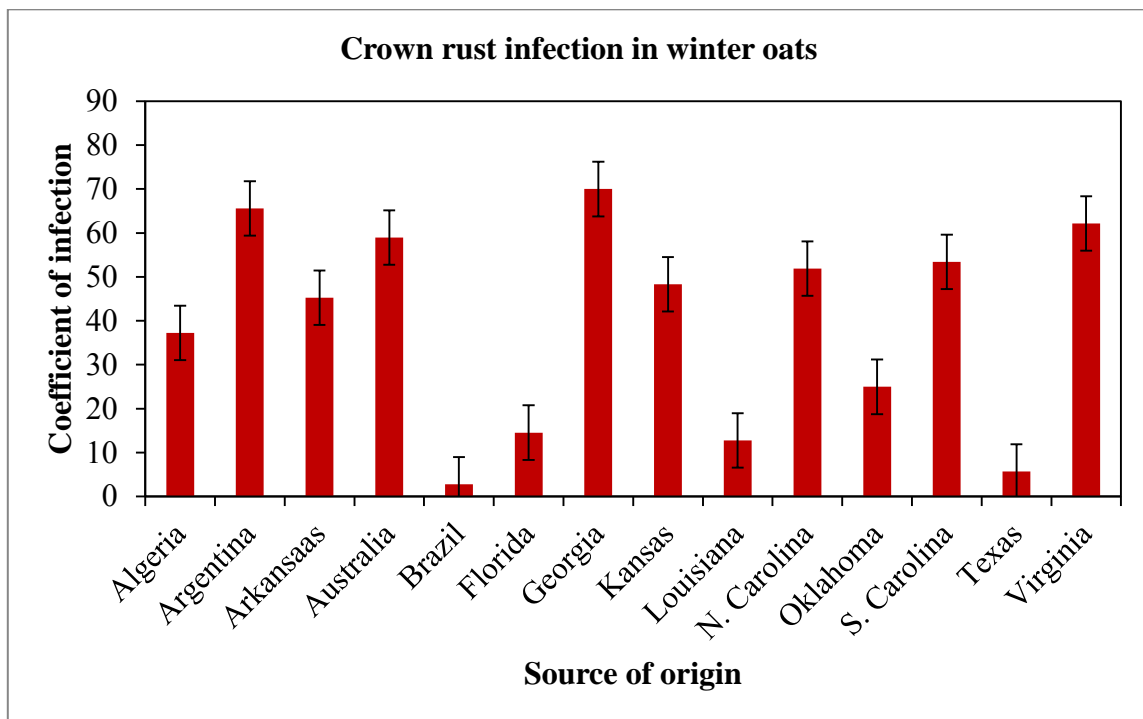


Figure 4.4. The average CI for all winter lines originating from a given location.

On average, the winter lines performed better than the spring lines in terms of crown rust resistance. Most of the winter lines grown in North America have been developed and released in Texas and Louisiana. These two states are located at the

forefront of the *Puccinia* pathway, where crown rust infections are consistently at their highest. It is necessary for breeders in these areas to place emphasis on resistance to crown rust. In areas where spring oats are more commonly grown, breeders may not feel the need to select for resistance to this pathogen since it is less of a problem for them. Other plant traits, such as yield or resistance to other diseases may outrank crown rust resistance making developed varieties more susceptible.

Of the winter oat lines, the Texas lines featured the highest and most consistent resistance to crown rust. It is necessary for the best-performing varieties to be crown rust resistant if grown in the Texas area, where there is likely a higher exposure to many races of rust than in other locations. Within the United States, the North Carolina and South Carolina oat lines performed the worst. This is understandable since crown rust is not a serious problem for the east coast area.

Within the spring oat lines, the best performing lines were found in Minnesota, North Dakota, and Wisconsin. These three states lie along the rust corridor, so breeders there focused on crown rust resistance, perhaps more so than breeders in places such as Idaho.

States in the rust corridor feature the best crown rust resistance. This type of resistance is expected as these genotypes are exposed to the most severe crown rust infections, and therefore, feature better natural resistance to the pathogen.

GGE Biplot analysis

GGE Biplot has proven a valuable statistical tool with many different uses, including such things as multi-environment testing, locations discriminating value and stability, and genotype-by-environment interaction. This tool allows for data to be analyzed graphically in an effective and convenient manner. Mathematically, a biplot is a graphical display of a two-way table that breaks a product matrix into its respective column and row vectors (Yan and Tinker, 2006). The numbers found on each of the biplot views refers to entry number of respective spring and winter genotypes, and can be found in Tables 4.5 and 4.6.

Figures 4.5 and 4.6 are used to determine discriminativeness versus representativeness of environments where crown rust testing was done. The lines connecting the test environments are referred to as environment vectors. A longer environmental vector is indicative of a more discriminative environment as determined by more variability measured in standard deviation units. An important component of this biplot view is the average-environment axis (AEA). The average environment is

represented by a small circle and is the average coordinate of all test environments. The AEA is the line which passes through the origin and the average environment. A test environment which has a smaller angle with the AEA is considered the most representative. A test environment which combines discriminativeness and representativeness is a good location for selecting genotypes that will be adapted over a large geographic area (Yan and Tinker, 2006). An environment which is discriminating, but not representative can be useful for selecting specifically adapted genotypes for a specific mega-environment, as well as for eliminating unstable genotypes (Yan and Tinker, 2006).

In Figure 4.5, 2011 Castroville, TX was ranked as the most discriminative environment for spring oat lines. The 2010 Castroville, TX environment was the most representative environment for spring oat lines as determined by proximity to the AEA. Castroville, TX was regarded as the most ideal testing environment because more races of rust are found in Texas than any other state in the United States.

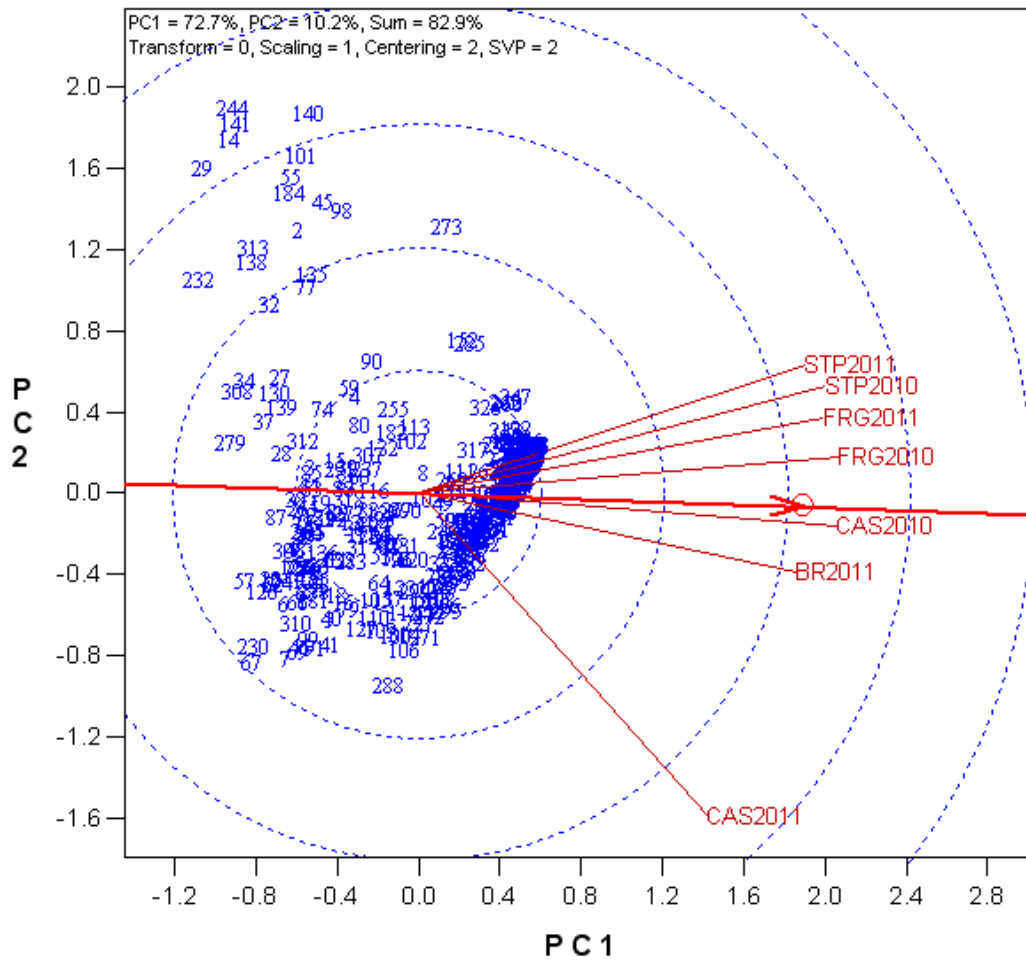


Figure 4.5. The discrimination and representativeness view of the GGE biplot to show the discriminating ability and representativeness of the test environments for spring oat lines.

In Figure 4.6, St. Paul, MN and Baton Rouge, LA for 2010 and 2011, respectively, were ranked as the most discriminative environments for winter oat lines. However, the differences in length for each environmental vector were minimal. The 2010 Castroville, TX and 2011 Fargo, ND environments were ranked as the most representative environments for winter oat lines.

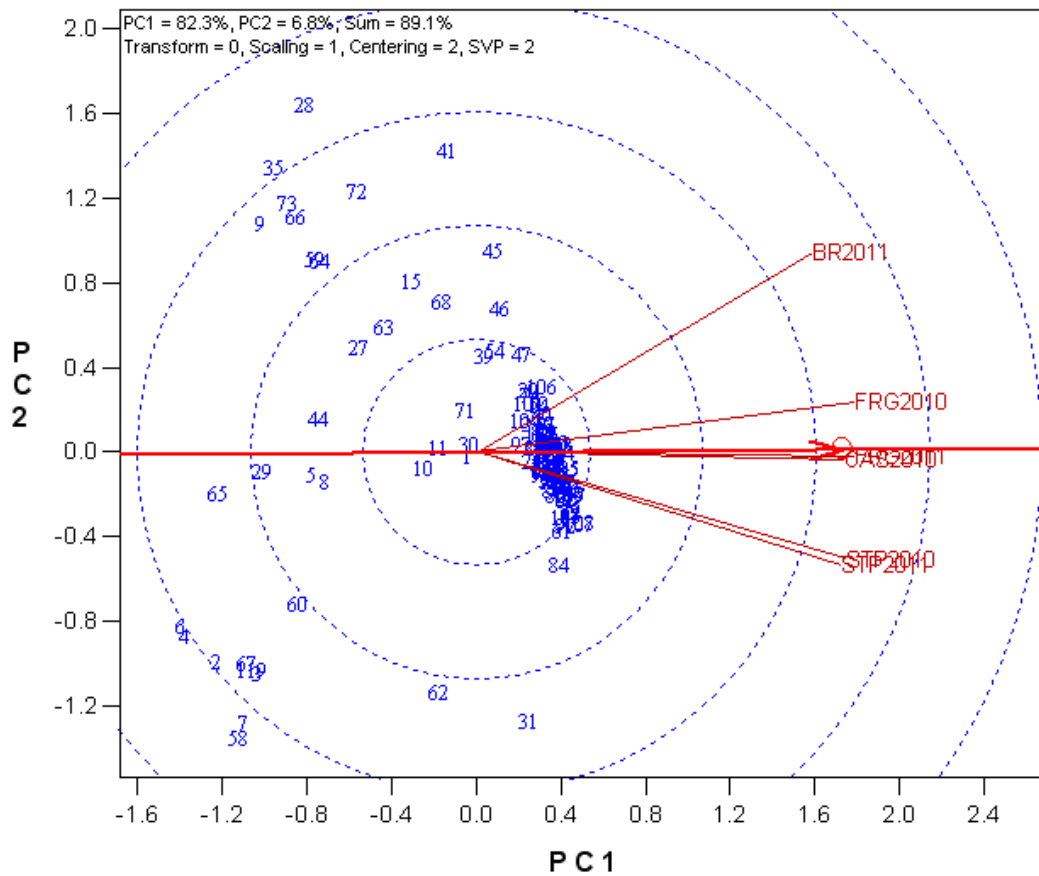


Figure 4.6. The discrimination and representativeness view of the GGE biplot to show the discriminating ability and representativeness of the test environments for winter oat lines.

Figures 4.7 and 4.8 demonstrate the relationships among test environments for spring and winter oats, respectively. Essentially this view is the same as the previous view without the AEA. The lines connecting the test environments are referred to as environment vectors. The cosine of the angle between two environments estimates correlation between these environments. The distance between two environments measures dissimilarity in discriminating genotypes.

Figure 4.7 shows two distinct environment groups. The first contains all the environments except 2011 Castroville, TX, which comprises the second distinct group.

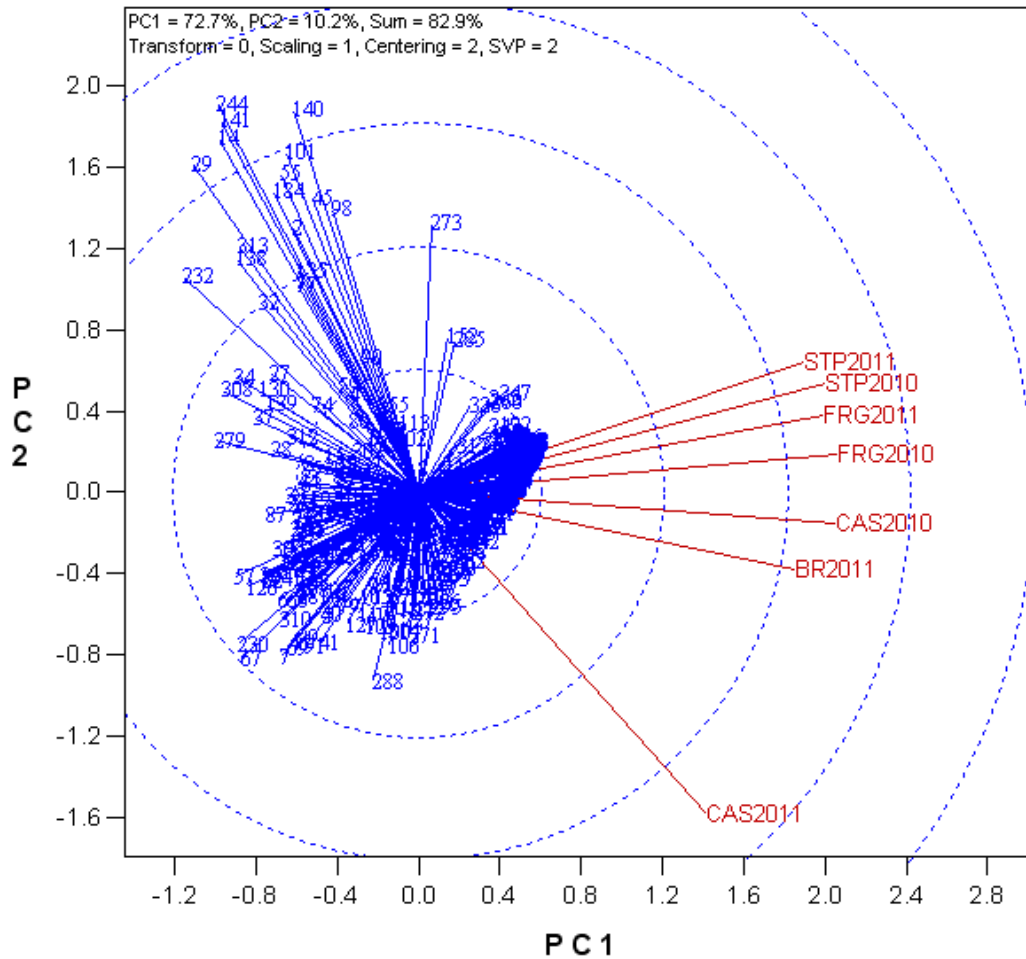


Figure 4.7. The environment-vector view of the GGE biplot to show similarities among test environments in discriminating the spring genotypes.

Figure 4.8 shows three environmental groupings, but is less distinct than shown for spring oat lines. The first group consists of 2011 Baton Rouge, LA. The second

group encompasses Fargo, ND for 2010 and 2011, and 2010 Castroville, TX. The final group consists of St. Paul, MN for both 2010 and 2011.

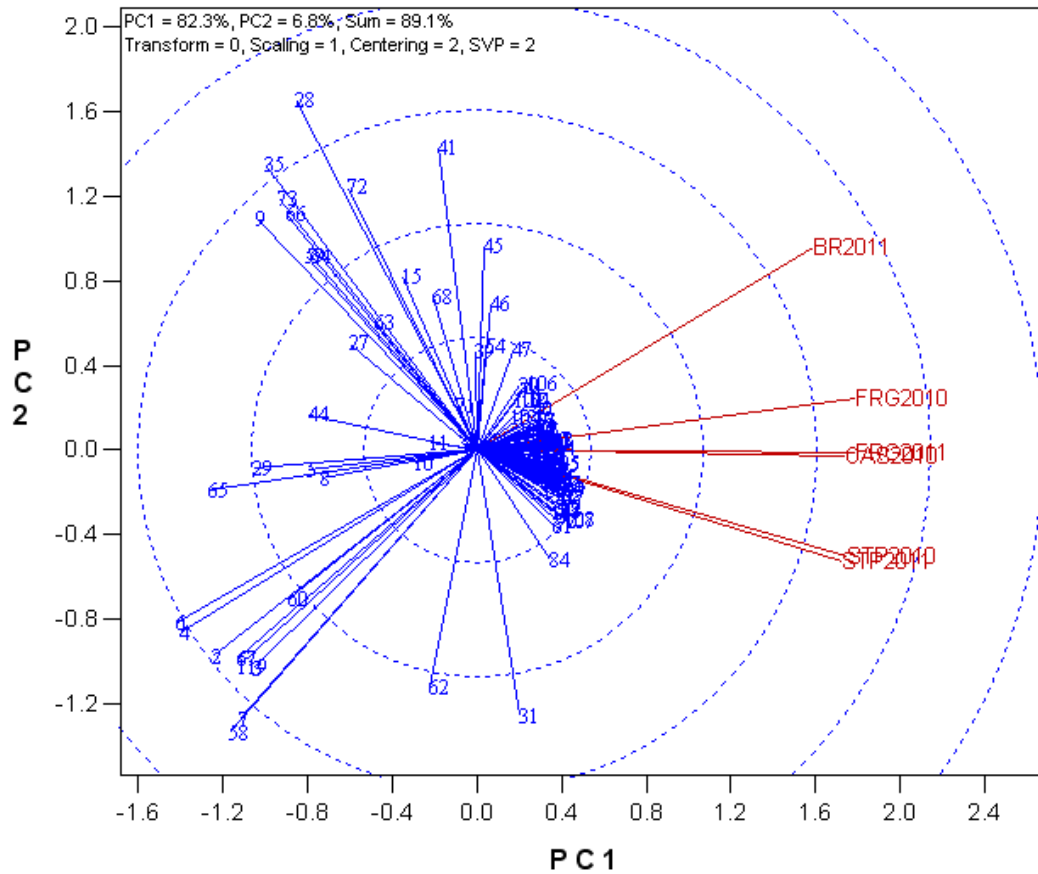


Figure 4.8. The environment-vector view of the GGE biplot to show similarities among test environments in discriminating the winter genotypes.

Figures 4.9 and 4.10 depict the mean performance and stability of spring genotypes. The genotypes were evaluated on both performance and stability across environments. The red arrow points to better crown rust tolerance across environments; while the blue arrows indicate variability or decreased stability in either direction. The genotypes located to the right of the blue vertical line consistently had higher crown rust resistance across all locations. In Figure 4.9, 'Nudist' was the farthest on the negative side and was the most susceptible to crown rust, followed by '95Ab13050'. The genotypes '95Ab13050', 'OA1207-1', 'LIPOPLUS', '02Ab5836', 'Lennon', 'IL04-3664', 'OT3048', and 'SA070452' were among the most instable lines.

In Figure 4.10, 'Coker 716' was the farthest on the negative side and was the most susceptible to crown rust, followed by 'Brooks'. The genotypes 'Florida500', 'LA0210SBSBSBSB-S1', 'Tift', 'LA03060SBSBSB-S1', 'Horizon 201', 'Quincy Gray', and 'Lee' are among the most instable lines.

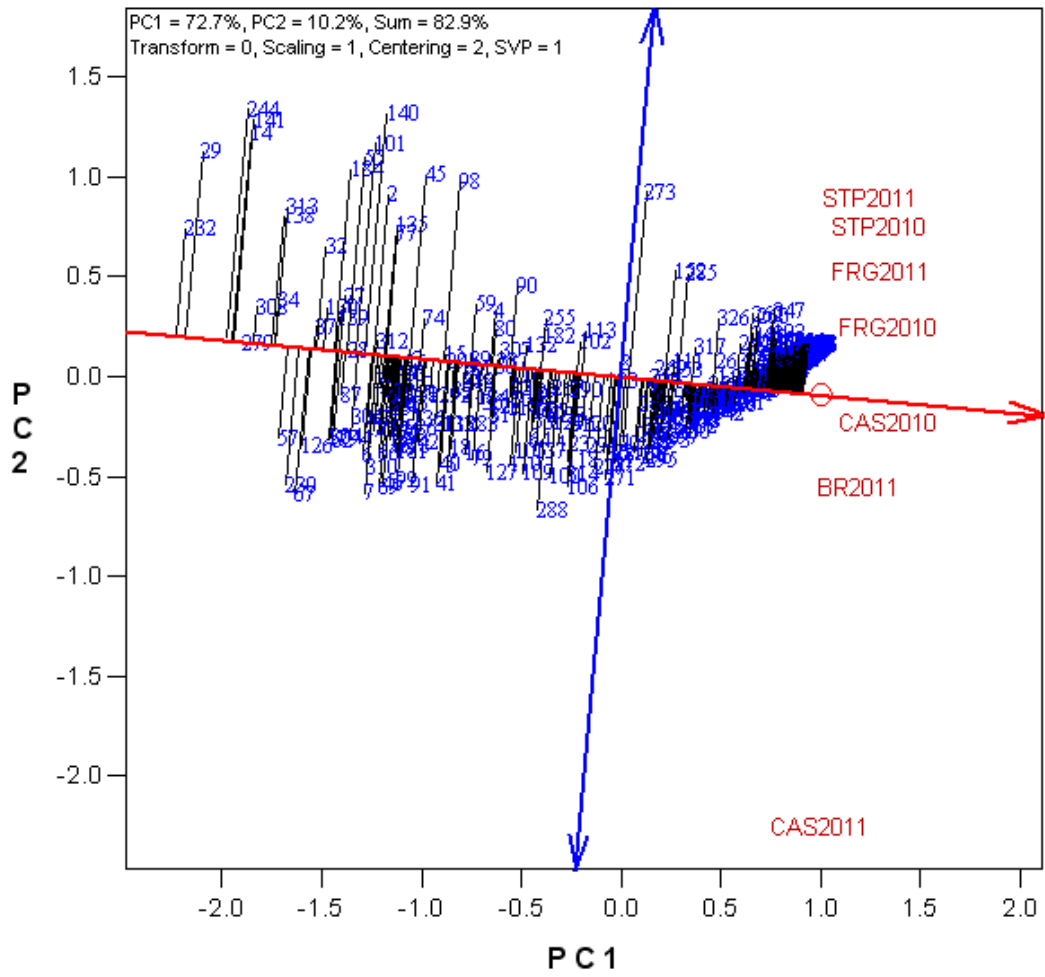


Figure 4.9. The average-environment coordination view to show the mean performance and stability of the spring genotypes.

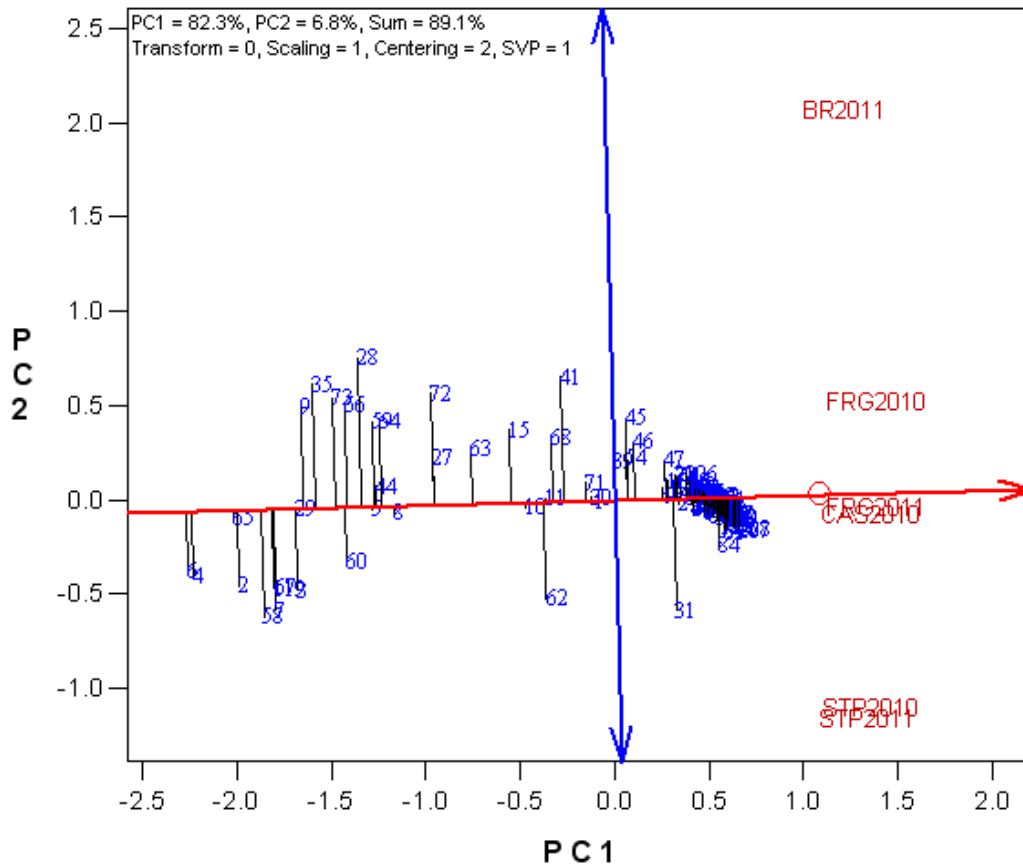


Figure 4.10. The average-environment coordination view to show the mean performance and stability of the winter genotypes.

One of the most attractive elements of biplot analysis is the which-won-where pattern of a G x E dataset. The polygon is drawn on genotypes that are the farthest away from the biplot origin in order to encompass all other genotypes within the polygon's parameters. Genotypes located on the vertices of the polygon performed either the best or the worst in multiple environments (Yan and Tinker, 2006). Figures 4.11 and 4.12 demonstrate which genotypes performed the best at each environment for spring and winter genotypes, respectively.

In Figure 4.11, ‘Gere’ did not perform well in any of the test environments. Other vertices indicating best or worst performance include ‘Lennon’, ‘OT3048’, and ‘SA070452’. ‘SA070452’ performed the best in Castroville, TX for 2011.

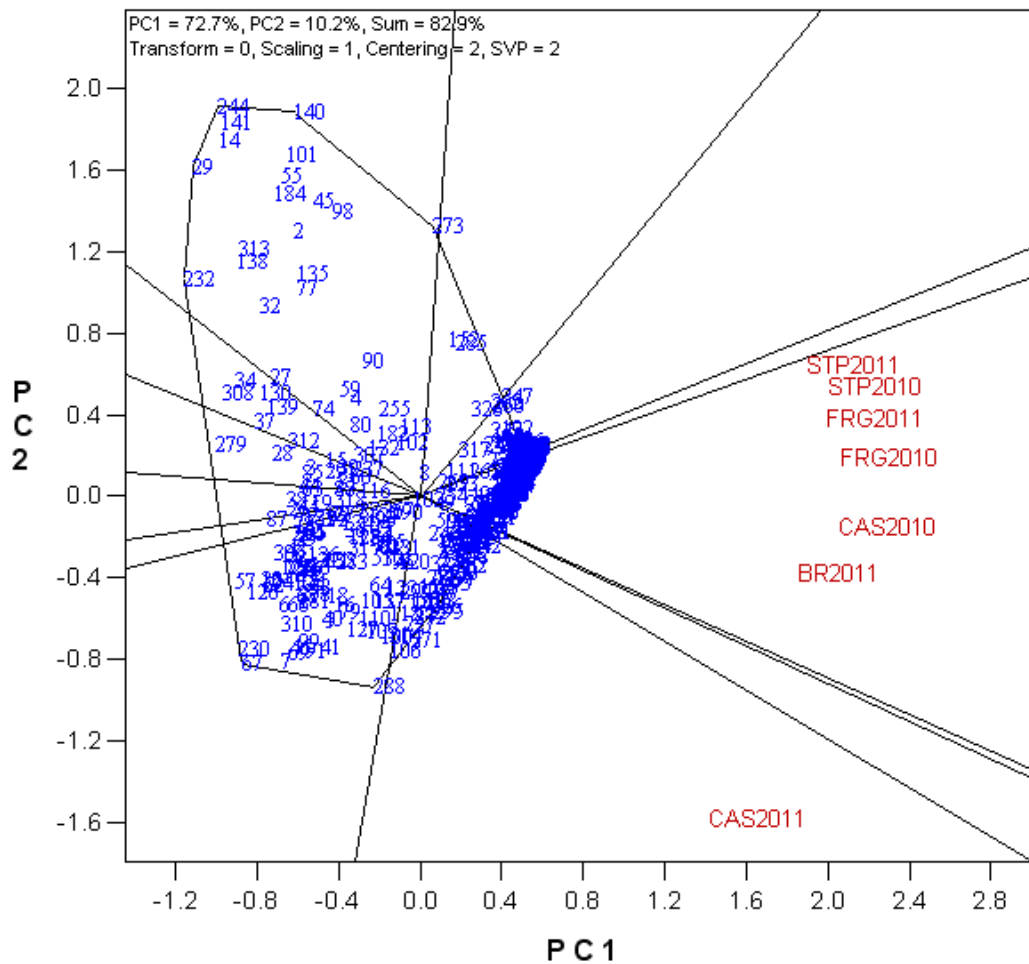


Figure 4.11. The which-won-where view of the GGE biplot shows which spring genotypes performed best in which environments.

Table 4.9. Correlations among locations for spring oats in 2010 and 2011 determined using CI means.

	2010		2011			
	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Castroville, TX	Fargo, ND	St. Paul, MN
Castroville, TX 2010	0.86	0.75	0.76	0.58	0.79	0.69
Fargo, ND 2010		0.77	0.73	0.51	0.83	0.74
St. Paul, MN 2010			0.67	0.45	0.78	0.84
Baton Rouge, LA 2011				0.55	0.64	0.62
Castroville, TX 2011					0.47	0.43
Fargo, ND 2011						0.73

Table 4.10. Correlations among locations for winter oats in 2010 and 2011 determined using CI means.

Environment	2010		2011		
	Fargo, ND	St. Paul, MN	Baton Rouge, LA	Fargo, ND	St. Paul, MN
Castroville, TX 2010	0.82	0.82	0.73	0.80	0.78
Fargo, ND 2010		0.80	0.78	0.91	0.78
St. Paul, MN 2010			0.66	0.84	0.85
Baton Rouge, LA 2011				0.75	0.66
Fargo, ND 2011					0.84

Future work

Greenhouse studies

A greenhouse study should be carried out to conduct single race screenings. The locations for greenhouses will be College Station, TX, Aberdeen, ID and St. Paul, MN. In these studies, seedlings of each genotype used in the field analysis should be grown and inoculated with pure strains of crown rust. Phenotypic notes should be taken using quantitative measurements paralleling those of the field trials. Additionally, photographs may also be taken and analyzed using Assess software. These studies will contribute to more robust phenotypes for association mapping.

Genotypic work

To complete the goals laid out in this study, it will be necessary to continue on with the genotypic analysis. This component of the research includes the generation of a comprehensive association map of the oat germplasm. Mapping of crown rust resistance will facilitate marker-assisted breeding via digital genotyping and genome-wide selection.

Conclusions

Highlights of this thesis include 1) significant differences across environments, within genotypes, and genotype-by-environment interactions; 2) high heritability and repeatability values for crown rust observations in spring and winter oat lines; 3) the use of Assess software as a helpful diagnostic tool; 4) performance of spring versus winter oat lines; 5) identification of an ideal location to screen for crown rust resistance in oats.

For both spring and winter oat lines, significant differences across environments and within genotypes were identified. Also, significant genotype-by-environment interactions were found using the output generated by SAS. This variability will contribute to the generation of a more effective oat map and the identification of significant QTL for crown rust resistance.

High heritability values will also be useful in identifying QTL for crown rust resistance. The heritability of crown rust resistance was 0.88 and 0.90 for spring and winter oat lines, respectively. These values indicate that approximately 88% and 90%, respectively, of the phenotypic variance associated with crown rust is genetic in origin.

High repeatability values indicate the predictability of crown rust disease performance of a given oat line within certain environments. The repeatability values for spring oat lines were calculated as 0.88 for Castroville, TX and 0.82 for St. Paul, MN in 2010, 0.64 for Baton Rouge, LA, 0.56 for Castroville, TX, and 0.61 for St. Paul, MN in 2011. For winter oats, the repeatability values were calculated as 0.96 for Castroville, TX and 0.84 for St. Paul, MN for 2010, 0.92 for Baton Rouge, LA and 0.79 for St. Paul, MN for 2011. Discrepancies between these values at the same location across years can be attributed to variety among *Puccinia* races or environmental effects, including amount of rainfall. Additionally, the component of human error cannot be ignored.

Assess software, Version 2.0 (The American Phytopathological Society) was used to corroborate disease severity ratings obtained via traditional note-taking methods. The software calculates the percentage of plant tissue exhibiting disease symptoms in comparison to the total plant tissue area by analyzing an image of four flag leaves

obtained from each plot. The software ratings were plotted against the disease severity ratings (percentage of infected plant tissue for a given plot) obtained manually in the field. A high correlation between these two types of ratings was found, indicating the helpfulness of this software as a diagnostic tool. Despite this high correlation, it is unlikely that such a software program will replace human beings as the sole means of collecting disease data. While a less objective disease rater, Assess has a number of limitations which contribute to a possible larger margin of error than human error. For example, the software cannot rate diseases whose symptoms are not visible as red-orange-brown in color. Also, the software can only be used to identify disease on plant tissue that is normally green in color. Due to such specific parameters, human beings will always be more flexible in their ability to identify and rate disease.

The spring oat lines were compared to the winter oat lines regarding crown rust infection. The CI values were calculated for each oat line by multiplying the severity ratings against the infection type numerical values. When the CI values for spring oats were compared to those of winter oats, the winter oat lines were shown to be more tolerant to crown rust than the spring oat lines. More of the winter oats are derived from locations along the *Puccinia* pathway, where crown rust resistance is an ideal and highly selected for trait. Spring oats are more commonly grown in areas where crown rust is less of a problem than for the winter oats, which means that other traits are given preference by breeders when developing a new oat variety.

Of the spring oat lines, those which featured higher tolerance to crown rust originated from Manitoba, Canada, Minnesota, North Dakota and Wisconsin. These

locations are found along the *Puccinia* pathway, which means they are generally exposed to the pathogen. The spring oat lines which were found to be the most susceptible to crown rust originated from Germany, Idaho, Missouri, Norway, Sweden, and the United Kingdom.

Of the winter oat lines, higher tolerance was found in lines originating in Brazil, Florida, Louisiana, and Texas. Louisiana and Texas lines are at the forefront of the *Puccinia* pathway, and lines in Texas are exposed to more races of *Puccinia* than any other state. Resistance to crown rust is necessary for lines developed in these two locations. As for Brazil and Florida, the humidity and moisture levels of these locations would contribute to an outbreak of crown rust, which may indicate why lines derived in these places have a higher tolerance to crown rust as well. The worst performing winter oat lines came from Argentina, Australia, Georgia, North Carolina, South Carolina and Virginia. Lines in states such as North and South Carolina are not exposed to severe crown rust infections, making this trait less important than perhaps other diseases.

Ultimately, through the use of GGE Biplot analysis, Castroville, TX was identified as the most representative and most ideal testing location of those locations used in this study. More races of *Puccinia* are found in this location which sits at the forefront of the *Puccinia* pathway. Castroville, TX features ideal humidity and temperatures for crown rust infection allowing for the best disease screening practices.

The phenotypic data obtained through this study is highly useful, however incomplete. The value of this data will increase greatly when paired with greenhouse studies and genotypic analysis. Together these components can be used to generate the

most comprehensive oat map to date. This study will bring North American oat breeders one step closer to improving the oat germplasm through the development of new and improved oat varieties. Better oat varieties will contribute to the competitiveness of oats as a sustainable food and feed crop in North American agriculture.

CHAPTER V

SUMMARY

Crown rust is the most severe pathogen impacting North American oats. Limited resistance to this pathogen creates a problem for oat growers who will likely suffer yield loss due to devastating infestations of *P. coronata*. In order to increase acreage of the oat crop with more durable resistance to crown rust, a more comprehensive oat map is needed.

To aid in the development of this oat map 702 lines of North American oat were grown and evaluated for susceptibility to crown rust at four locations for a total of two years. These lines represent spring and winter oat varieties, as well as 108 of the most commonly grown lines in Canada and the United States. The four locations, Castroville, TX, Baton Rouge, LA, Fargo, ND, and St. Paul, MN, were used to represent regions where winter and spring oats are commonly grown, respectively.

The results of this study indicate significant variation among the oat genotypes evaluated. This variability increases the likelihood that the molecular markers used in association mapping will identify useful QTL, thus producing a stronger map of the oat germplasm than currently exists. A stronger oat map will assist oat breeders in developing new varieties of oats with better tolerance to crown rust, contributing to the competitiveness of oats in North American agriculture.

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APPENDIX

A-1 PROC GLM code for individual location analysis in SAS; Spring

```
options nodate;
data spring;
input genotype $ source $ rep environment $ CI;
cards;
_001A1_24_2_4_1_3 INDIANA 1 BR2011 0
...
X9509_4 WISCONSIN 2 STP2011 6
;
title 'Individual Locations Spring';
proc sort data=spring; by environment rep;
proc glm;
class rep genotype;
model CI= rep genotype;
by environment;
lsmeans genotype / stderr;
means genotype / lsd lines;
run;
```

A-2 PROC GLM code for individual location analysis in SAS; Winter

```
options nodate;
data winter;
input genotype $ source $ rep environment $ CI;
cards;
_833_99AB118 UNK_LOUISIANA 1 BR2011 16
...
Winter_Fulghum VIRGINIA 2 STP2011 30
;
title 'Individual Locations Winter';
proc sort data=winter; by environment rep;
proc glm;
class rep genotype;
model CI= rep genotype;
by environment;
lsmeans genotype / stderr;
means genotype / lsd lines;
run;
```

A-3 PROC GLM code for combined analysis in SAS; Spring

```
options nodate;
data spring;
input genotype $ source $ rep environment $ CI;
cards;
_001A1_24_2_4_1_3 INDIANA 1 BR2011 0
...
X9509_4 WISCONSIN 2 STP2011 6
;
title 'Combined analysis spring';
proc glm;
class environment rep entry;
model CI= environment rep(environment) entry
environment*entry;
means entry /lsd lines;
lsmeans entry;
run;
```

A-4 PROC GLM code for combined analysis in SAS; Winter

```
options nodate;
data winter;
input genotype $ source $ rep environment $ CI;
cards;
_833_99AB118 UNK_LOUISIANA 1 BR2011 16
...
Winter_Fulghum VIRGINIA 2 STP2011 30
;
title 'Combined analysis winter';
proc glm;
class environment rep entry;
model CI= environment rep(environment) entry
environment*entry;
means entry /lsd lines;
lsmeans entry;
run;
```

A-5 PROC CORR code for Pearson Correlation in SAS; Spring

```
options nodate;
data spring;
input ENTRY      CAS2010    FRG2010    STP2010    BR2011
      FRG2011    STP2011    AVG;
cards;
1      24.00 8.00  11.25 1.10  0.60  8.00  13.50 9.49
...
361    0.00 20.00 3.75 0.00  0.00  32.00 9.00  9.25
;
proc corr; var CAS2010    FRG2010    STP2010    BR2011
            CAS2011    FRG2011    STP2011    AVG;
run;
```

A-6 PROC CORR code for Pearson Correlation in SAS; Winter

```
options nodate;
data winter;
input ENTRY      CAS2010    FRG2010    STP2010    BR2011
      FRG2011    STP2011    AVG;
cards;
1      70    3    22.5 14    4    11.5 20.8333333
...
119    75    80    60    75    80    28.5 66.4166667
;
proc corr; var CAS2010    FRG2010    STP2010    BR2011
            CAS2011    FRG2011    STP2011    AVG;
run;
```