

AN ABSTRACT OF THE THESIS OF

Christy A. McCarthy for the degree of Master of Science in Crop Science presented on December 1, 2016.

Title: Evaluating Field Production Issues by Investigating Grain Dormancy and Plant Segregation Patterns in Soft White Winter Wheat

Abstract approved: _____

Robert S. Zemetra

Wheat (*Triticum aestivum*) is a highly valuable crop that makes up a large portion of the world's food. However, breeding for improved varieties with desirable characteristics can be a challenge. This research examined two different issues wheat breeders deal with throughout the selection process all the way to production of Certified seed. The first study examined how 39 cultivars as well as 6 experimental crosses differ in grain dormancy expression. In order to see if dormancy has been systematically bred out of soft white winter wheat, the release date of the cultivars used in this trial ranged from 1948 to 2012. The second study investigated the source of phenotypic variation that appeared in Foundation seed fields of the recently released variety Bobtail. Bobtail was bred to be a semi-dwarf awnletted wheat that was superior in productivity and disease resistance. Plants of Bobtail were observed to segregate for awned and awnless phenotypes which also varied in plant height. Since there was variation in plant phenotypes observed in the Foundation seed field, it was important to determine what was causing the plant segregation.

The first study was conducted over the course of two years and in the first year was only planted at Corvallis, OR, while second year trials were planted at Corvallis, OR as well as Pendleton, OR. To investigate how varieties differed in dormancy expression, seed germination trials were conducted at two temperatures in the first year (4°C and 20°C), and four temperatures in the second year (4°C, 10°C, 20°C and 30°C). In the first year, the impact of temperature during seed germination as well as dry storage on the breakdown of grain dormancy expression was investigated; whereas in the second year, the effects of ripening environment and temperature during germination on dormancy expression were determined. First year results demonstrated that soft white winter wheat does not show any grain dormancy at 20°C within the first few weeks after harvest, regardless of the temperature in which the grain was stored or germinated. Results from the second year showed that grain ripening environment has an impact on seed germination rates at different temperatures. A rain event occurred two days prior to harvest at the Corvallis, OR location but not at the Pendleton, OR location. None of the varieties showed any dormancy when they were imbibed at 20°C within 48 hours after harvest. However, some varieties demonstrated high-temperature induced dormancy when they were imbibed and kept at 30°C. This temperature slowed seed germination rate and cultivars that exhibited high-temperature induced dormancy were: Brevor, Bobtail, Cayuga, Gene, Nugaines, Rely and the experimental line 11-225-6H. There was no trend linking older released varieties to higher levels of seed dormancy compared to more recently released varieties, indicating that seed dormancy has not been systematically bred out of soft white winter wheat over time.

For the second study, sixteen heads were snapped from a segregating head row that originated from a Bobtail Foundation seed field (one seed head was lost in the field). The objective of this study was to determine if the phenotypic variation was due to a contamination event or if it was a genetic variant of the variety Bobtail. There were several possibilities that could have caused the phenotypic variation such as an epistatic event, translocations, out-crossing or some type of seed contamination. To determine the source, sixteen plants from each of the fifteen heads collected from the segregating head row were grown in a greenhouse over the course of two generations. DNA samples were taken from all of the plants from the first generation. Eleven markers that showed polymorphism among a diverse panel of wheat varieties from a previous study were used in this trial and seven of the markers showed amplification and success. The results showed that there was very little variation among the individuals in this trial. The greenhouse trial that was grown to observe the plant segregation patterns revealed that the segregating lines segregated at a 3:1 awnless:awned ratio. All plants that came from an awned plant remained awned and several of the lines remained completely awnless. The marker analysis demonstrated there was no source of contamination and that plants observed segregating were a true genetic variant of the variety Bobtail. Phenotypic data showed that complete elimination of awned plants through the breeding and selection process had not occurred. Plants that came from segregating lines followed a typical Medelian segregation ratio. With this information, this variant was added to Bobtail's variety description since it was not genotypically different.

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Evaluating Field Production Issues by Investigating Grain Dormancy and Plant
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by
Christy A. McCarthy

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APPROVED:

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I understand that my thesis will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my thesis to any reader upon request.

Christy A. McCarthy, Author

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Chapter 1: General Introduction

Soft white winter wheat (*Triticum aestivum*) is a highly valuable crop in the world. In the United States it is mostly grown in Oregon, Washington, Idaho, Michigan and New York (Vocke and Ali, 2013). The majority of soft white wheat grown in the Pacific Northwest is exported to markets around the world, causing a significant impact on international trade (Robertson et al., 2004). Wheat is the most widely grown crop in the world and is nutritionally important since it provides 20% of the world's calories and protein (Reynolds et al., 2012). The grain produced by wheat growers is the raw material that will be processed into essential foods. This makes it extremely important for growers to produce high quality grain. Soft white winter wheat is often used for cakes, cookies, crackers, flat breads, batters, breakfast foods and pancakes (Fajardo, 2016). The low protein content in soft white wheat cultivars along with weak gluten strength gives the soft white wheat products a soft texture.

Plant Growth and Development

Soft white winter wheat is sown in the fall, allowing time for plant establishment prior to cold winter temperatures. The cold temperature is key to seed production since winter wheat requires a vernalization period of at least four to eight weeks in order to flower and reproduce (Hart et al., 2011). The plant goes into a dormancy period over winter and resumes growth and development in the spring when temperatures rise. During this phase, the plant produces axillary or side shoots, which form tillers. The plant's tillering phase ceases when the stems elongate in the spring and the spikes emerge. Pollination occurs not long after spike emergence and is completed by the time

the anthers emerge from the floret. The earlier tillers and the main tiller contribute to the greatest yield since they mature earlier in the season when there is more moisture present and temperature is more ideal. The kernels develop through five stages: watery, milky, soft dough, hard dough, and mature (Rogers and Quatrano, 1983). The varying climatic conditions that occur during grain fill can significantly impact the kernels on many levels. Hot temperatures along with moisture stress can cause the plant to shut down photosynthesis early. This causes the kernels to become shriveled since less carbon is being captured by the plant, resulting in a decline in the amount of sugars available to be partitioned in the developing seed. Soil moisture is essential during kernel development for higher quality grain and if moisture is limited, it can result in lower seed yields (Keim, 1974) and shriveled kernels. Mild to warm temperatures along with a moist soil environment during grain fill allow more energy and resources to be partitioned to fill the kernels during seed development.

Grain Dormancy

When producing wheat, growers should be familiar with the requirements for the cultivar they are growing. Two grower challenges include a strong seed dormancy period after sowing and a lack of seed dormancy around the time of harvest. When a variety lacks post-harvest dormancy, it can lead to pre-harvest sprouting (PHS) in areas that receive rainfall prior to harvest. The rain ultimately delays harvest and allows time for the seeds to absorb water and potentially begin sprouting while still in the spike. Pre-harvest sprout can lead to a decline in seed yield, grain quality and overall value (Simsek et al., 2013). Sprout damage is one of the most common problems experienced by growers of

soft white winter wheat, which causes a huge decline in the value of the wheat. The economic loss is due to an increase in the alpha-amylase content in the seed, and when this seed is milled into flour, it leads to less stable dough and poor quality end products. Dormancy is an important genetic mechanism that needs to be present in order to prevent PHS from occurring. The climatic conditions that occur during grain fill and ripening may also have a significant impact on the dormancy expression in wheat grain (Clarke et al., 2005).

Dormancy is the inability of viable seeds to germinate under optimal environmental conditions. Unfortunately, dormancy is rather low in soft white winter wheat varieties, making it highly susceptible to PHS if a rain event occurs close to the time of harvest. Wheat breeders often aim to have cultivars that germinate uniformly and establish quickly in order to have strong and healthy plants going into the winter months. This goal may have caused more cultivars to exhibit lower levels of dormancy, which has led to cultivars that are more susceptible to PHS (Gao and Ayele, 2014). On the other hand, if seeds exhibit strong grain dormancy, it can be challenging to sow grain the same year of seed harvest. High dormancy causes poor germination and seedling emergence prior to winter, even if the environmental conditions are favorable for germination. This leads to poor stand establishment in the fall, reduced plant survival over-winter, poor stands in the spring and ultimately reduced yields. Dormancy in wheat breaks down over time through a dry after-ripening period. Once after-ripening occurs, the seeds can be sown and they will germinate and grow (Liu et al., 2013). Since soft white winter wheat cultivars typically have a low post-harvest dormancy and higher PHS potential, a target

trait for soft white winter wheat breeders should be to increase seed dormancy. The challenge associated with breeding stronger dormancy characteristics into soft white winter wheat is the number of interacting factors such as the environmental conditions, genetic traits and plant hormones (Mares et al., 2009).

Field Production Issues

Another challenge associated with wheat production is avoiding seed contaminants or genetic variants in a variety from one generation to the next. Breeders aim to release new cultivars which perform consistently from one generation to the next without segregation, out-crossing, or contamination. Non-stable cultivars lead to variation and off-types within the variety. Soft white winter wheat is a self-pollinating crop, however, it has 0.1 to 5.6% chance of out-crossing with neighboring wheat cultivars (Martin, 1988). Throughout the breeding cycle, breeders eliminate segregating plants until the cultivar becomes genetically stable (homozygous) and reaches the breeding objectives. By the time the cultivar is released, the variety in the field should remain uniform through the Breeder seed, Foundation seed, Registered seed and Certified seed stages. However, when new variants are seen in a Foundation seed field that were not present in previous generations, it can lead to many questions on how the off-type appeared.

The variant could be part of the cultivar if phenotypic variation is genetic such as if a translocation occurred during meiosis, in which the off-types would then still be genetically identical to the developed cultivar (Stene, 1976). Another way the variant could be part of the cultivar is if epistasis is occurring. Epistasis is when the interaction of

two genes causes the expression of one of the genes to be masked. An out-crossing event with another cultivar is another possibility if the ovary of a female plant was pollinated by a different wheat cultivar. In out-crossing, the off-types would not be 100% genetically identical to the original cultivar and segregating off-types would need to be removed from the field. Another way to get off-types in a field is if seed contamination occurs through the processing of the grain. Seed contamination can occur by using unclean equipment during harvest, the cleaning process, planting, applying contaminated dry fertilizer as well as if the field is in a wheat-wheat rotation and volunteers emerge the following season (Colbach et al., 2013). In this instance, the off-types would be completely different than the desired cultivar.

Investigating Dormancy Differences (Chapter 3)

The first experiment in this research examined how germination temperature affects the expression of post-harvest grain dormancy by varying the temperatures during germination trials. The goal of this study was to detect any differences between dormancy expressions in 45 different soft white winter wheat cultivars and breeding lines at germination temperatures ranging from 4°C to 40°C. The cultivars used in this study differed based on year of release ranging from 1948 to 2012 and on head type with club and common wheat types being tested. Since 20°C is the ideal germination temperature for soft white winter wheat (Lei et al., 2013), a preliminary trial was conducted during the first year to determine how quickly the cultivars would germinate under ideal conditions. This trial would also test to determine whether any dormancy expression is observed immediately after harvest under optimum conditions. In the second year of the study, five

different germination temperatures were tested on the 45 cultivars and breeding lines grown in two separate locations, Corvallis and Pendleton, Oregon. It was hypothesized that as temperatures during germination increased, the number of seeds that germinated would decrease, demonstrating high temperature induced dormancy. It was also hypothesized that there would be more variation among cultivars for expression of dormancy as germination temperatures increased. By comparing older released cultivars to more recently released cultivars, this study should be able to determine whether breeders have selected against dormancy over time. Determining the level of dormancy in a large number of soft white winter wheat cultivars is important information for growers during cultivar selection when PHS is an issue.

Plant Segregation (Chapter 4)

The second experiment was conducted to determine the cause of variants that appeared in a Foundation seed field of the wheat cultivar Bobtail. Bobtail is an awnletted semi-dwarf soft white winter wheat cultivar that is the result of a cross between the European cultivar Einstein (awnletted) and Tubbs (awned) soft white winter wheat cultivar developed at Oregon State University (Flowers et al., 2009). In the Foundation seed field, Bobtail was planted and off-type plants started appearing that were phenotypically different than the majority of the field. There were earlier heading, semi-dwarf, awned plants that began appearing in several different Foundation seed fields. Seed heads were collected from the Foundation seed field and planted into head rows to generate the next generation of Breeder seed. In the head rows, a few of the rows showed segregation of height and head type. This indicated the variety had genetic variants or

off-types that differed from Bobtail in appearance. Fifteen heads (spikes) from awned and awnless plants were taken from a single segregating head row for further evaluation. Seed from the collected spikes were grown in the greenhouse and DNA was extracted from each plant. Molecular marker analysis was conducted to determine if off-types were genetically similar or different from Bobtail. It was hypothesized that the off-types could be the result of a possible translocation, epistatic event, seed contamination, or were the result of out-crossing. These were all potential possibilities to explain the off-types observed in the breeder seed head rows. Determining the identity of the off-type is important to diagnose whether the variation observed is characteristic of Bobtail or whether the off-type is the result of an out-cross or contamination of the Bobtail cultivar with another cultivar.

Objectives

The main objectives of the first study are to determine the degree of dormancy expression of 45 different cultivars and breeding lines of soft white winter wheat and to identify the temperature at which the most dormancy is expressed. This study will also determine the cultivars that have the highest tolerance to cold stress by the number of seeds that germinate at the lowest temperature. The objectives of the second study are to identify the source of the variants found in the Bobtail foundation seed fields and determine what caused it to appear at the Foundation seed stage. This study will also focus on determining a method to eliminate or prevent variants from appearing during seed increases of new cultivars.

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Chapter 2: Literature Review

Introduction to Seed Dormancy

Dormancy is a genetic and environmentally influenced trait that causes seeds to remain quiescent even when conditions are favorable for germination (Gao and Ayele, 2014). Dormancy is important for many crops since it prevents pre-harvest sprouting (PHS), but when dormancy is too high, it can result in problems with uniform germination. The initiation of primary dormancy typically occurs during seed maturation, while secondary dormancy is initiated in mature non-dormant seed by the influence of unfavorable environmental conditions for seed germination (Gubler et al., 2005). The maintenance of grain dormancy in mature seed depends on both the environmental conditions and the genetic characteristics of the wheat cultivar. Seed dormancy is a survival mechanism of plants for their offspring to remain quiescent and survive in more hostile environments. The dormancy period allows the seed to germinate during more favorable seasons and conditions. Since dormancy allows the seed to germinate over several different seasons, it provides the seed with a higher chance of survival. The breakdown of seed dormancy can be influenced by several factors such as after-ripening, stratification, genetic traits, temperature, and environmental conditions (Gao and Ayele, 2014).

Soft white winter wheat typically has a low level of post-harvest dormancy, which allows the seed to be harvested and re-planted within the same season. The seed goes through a short after-ripening period where the grain dormancy quickly breaks down. The low level of post-harvest dormancy in many soft white winter wheat cultivars has

resulted in a high amount of PHS if a rain event occurs near the time of harvest. Pre-harvest sprout reduces the quality of the grain since biochemical processes begin to degrade the starch granules as the seed germinates (Simsek et al., 2014). This reduces the value of the grain for both planting and baking purposes. Wheat varieties that contain a higher level of dormancy tend to be less susceptible to PHS and the quality of the grain tends to be more consistent across years (Biddulph et al., 2008). Varieties with lower levels of dormancy have a higher risk of PHS which can lead to grain quality differences from year to year.

Pre-harvest sprouting in wheat grain can reduce the value of the wheat by 20% to 50% and the harvested grain can be rejected for human consumption when more than 4% of the kernels are damaged (Simsek et al., 2014). This is because the milling and baking quality of the grain is greatly reduced resulting in poorer quality products. Grain that has high levels of PHS are typically used for animal feed but can also be used for replanting, although use of sprouted grain may result in poor plant stands. Flour yield is greatly reduced when PHS grain is milled and the functional aspects of the flour are poor for baking purposes (Yucel et al., 2011). Since grain quality can be greatly reduced due to PHS, exploring the seed mechanisms that prevent PHS and the environmental conditions that influence these mechanisms is important. Seed dormancy is the most well-known mechanism that prevents PHS, but there are several different environmental and genetic factors that can influence a seed's dormancy expression.

Environmental Impacts

The environmental conditions throughout the growth and development of wheat can have a major impact on the harvested grain. This is because the mother plant can experience several different environmental stresses such as drought, hot temperatures and/or disease, which can all affect grain quality and yield. The environmental conditions in which the grain ripens have some of the strongest influences on the grain's physical condition, which impacts its milling characteristics (Gaines et al., 1996). As the seeds ripen, the speed in which the grain matures is greatly impacted by temperature. Temperatures that are too hot can lead to grain abortion or shriveled seeds, resulting in lower quality grain. Even though the plant's genotype plays a major role in the growth and development of the plant, the environment greatly impacts the amount of time the grain has to fill and mature.

A study conducted by Gaines et al. (1996) explored the difference between several soft wheat cultivars grown in Washington and Michigan. They investigated how different growing and ripening conditions affected milling and baking qualities of soft white winter wheat. Washington had drier growing conditions than Michigan, which resulted in larger, fuller kernels that were also harder in texture. Wheat grown under these conditions in Washington had superior milling characteristics over wheat grown in Michigan under more moist conditions were softer, which led to less starch damage during the milling process. The flour milled from the softer kernels also had lower water absorption and produced bigger and less dense baked goods. The grain grown in Michigan resulted in larger cookies and better sponge cakes and the grain produced in

Washington was harder, had a higher test weight and milled better. A falling numbers test was also run on every sample and the results indicated the grain used in this experiment had no sprout damage. However, testing for average alpha-amylase activity showed that a few varieties grown in Michigan in 1987 had slightly elevated levels of alpha-amylase activity, which indicates these varieties had likely experienced some pre-harvest sprouting. This experiment demonstrated that the environmental conditions in which wheat is produced has a large impact on the quality of the grain. Even if the same variety is grown, different growing conditions can influence the grain characteristics of the variety.

Similar conclusions were made by Mikhaylenko et al. (2000), when they looked at different growing conditions for both soft and hard wheat varieties grown in Lind, WA which is semi-arid and Fairfield, WA, which has high precipitation. The flour composition and the baking qualities were found to be highly influenced by the environment in which the wheat was produced. This study illustrated the role available moisture plays in the hardness of the kernels as well as its flour composition and quality of baked products made from the grain. Kernels harvested from Lind, WA had higher protein content and water absorption levels in all tested cultivars when compared to those grown in Fairfield, WA. The grain harvested from Fairfield had softer kernels resulting in larger cookie diameter. Even though all varieties were grown at both locations, both experiments found differences in baked products when they were made from the same cultivars that were grown in different environments. Cookie diameter made from soft wheat was found to be smaller when it was made from grain grown in Lind, WA than the

cookie diameter made from the same variety grown in Fairfield, WA. However, bread volume made from hard wheat grown in Lind, WA was greater than bread volume made from wheat grown in Fairfield, WA, which is likely due to differences in grain protein levels. These experiments by Gaines et al. (1996) and Mikhaylenko et al. (2000) demonstrate the importance of growing cultivars in areas they are intended to be grown in order to produce ideal test weight, kernel hardness and end-use quality. When a cultivar is planted outside of its intended growing region, it can cause the cultivar to have unpredictable milling and baking qualities. These changes can cause millers and bakers to get lower quality products than they expected from a given cultivar.

Genetic Diversity

Wheat breeders have made substantial progress over the years in improving wheat yield and plant performance by identifying superior genotypes in different regions. Some wheat genotypes or landraces are very tolerant to drought and heat or wet and cold conditions, without sacrificing yield (Lopes et al., 2015). These traits allow the breeder to exploit the plant's desirable characteristics by making crosses with other genotypes to improve the drought and heat or wet and cold tolerance of well-known varieties. By doing this, breeders improve the number of cultivars that can perform well in certain environments.

Landrace species associated with many crops have often been used to develop improved cultivars utilizing their tolerance of many naturally occurring weather conditions in their area of origin. These landrace species can be resistant to certain pathogens which are desirable for the development and improvement of new cultivars. In

spring wheat, *Pratylenchus neglectus* and *P. thornei* are nematodes that cause substantial damage to wheat cultivars grown in the Pacific Northwest (PNW) which can result in substantial yield loss. Several wheat landrace cultivars have been found to have resistance to both *P. neglectus* and *P. thornei*, which is a highly desirable trait for growers who have an infestation of both types of nematodes in their fields. In a study by Smiley et al., 2014, two resistant landraces species and two susceptible spring wheat cultivars were tested to determine susceptibility and tolerance to nematodes in an infested field over three years. The landrace / cultivar level of susceptibility/resistance was measured by the number of nematodes present on the plant roots across the seasons and locations. The plant's tolerance to the nematodes was measured by grain yield and quality from infested and non-infested fields. One of the resistant landraces, Persia 20, was found to be moderately susceptible to the nematodes, however, the landrace also showed moderate tolerance. The other landrace cultivar AUS28451, was found to be resistant to the nematodes, however, it was very intolerant, and therefore the yield was reduced. The spring wheat cultivars Louise and Alpowa were both found to be highly susceptible to the nematodes, however, the variety Louise showed moderate tolerance to the nematodes while Alpowa was intolerant to the nematodes. The development of a spring cultivar between Louise and Persia 20 could lead to large economic benefits since it could result in a spring wheat variety that is both resistant and tolerant to the nematodes.

Even though desirable traits can be found in landrace species, many landrace traits (genes) are also linked with undesirable characteristics that make it challenging in a cropping system, such as seed shattering, so they are often crossed with current cultivars

to break the linkage between the traits. These crosses are used to attempt to isolate the desired trait from the landrace species and incorporate it into commonly grown cultivars that have been bred to perform well in a cropping system. Since it is important to preserve genetic diversity in order to make improvements in soft white winter wheat, breeders continually look for new genetic material for crossing. Landrace species tend to have more genetic diversity than many breeding lines, which makes landrace species a valuable source for genetic diversity for further cultivar improvement (Cabrera et al., 2014). Landrace species typically perform the best in the area in which they originated from, but if moved to another region, it may not show the same level of performance. Most wheat genotypes are not adapted to a large number of growing regions and therefore perform differently from one location to the next.

A plant's genotype has a big influence on how the plant interacts with its surrounding environment. Wheat is typically bred to be grown in a specific region in which the variety performs well and expresses desirable traits. There are many different soft white winter wheat cultivars that have been developed throughout the years, each with its own unique set of characteristics that help give the variety an advantage in specific areas. Its traits are unique to the cultivar such as plant height, its ability to tolerate diseases, dormancy expression, its yield or its end-use quality. The combination of traits is unique and allows the genotype to perform well in a given environment. The area in which the cultivar performs well with its specific quality attributes are important for the integrity of the cultivar along with preserving the quality of the grain for producing superior end-use products.

A plant's genotype and the environmental conditions have a huge impact on how a given cultivar performs from year to year. These interactions play a huge role on the plant's likelihood of experiencing PHS. This is because grain dormancy or PHS resistance is a genetically inherited trait which can be highly influenced by the environment (Hickey et al., 2010). There are several different classes of winter wheat that are commonly grown throughout the U.S. such as soft white winter, hard red winter, and hard white winter wheat. The genetic variation among the different classes of wheat are vast and each type has its unique set of properties which contribute to the end-use products developed from the flour they produce (Uri et al., 1994). The expression of seed dormancy can widely vary between one cultivar to the next. Wu and Carver (1999), showed sprout resistance at physiological maturity varied greatly among hard winter wheat cultivars. The hard red winter wheat cultivar, Plainsman V, had the greatest resistance to PHS compared to any other cultivar tested. Hard red winter wheat appeared to have stronger resistance to PHS than many of the hard white winter wheat cultivars. They speculated the chaff tissue had influenced the genetic differences in the cultivars' resistance to PHS. Within a wheat class, the variation of dormancy expression can vary tremendously depending on the wheat's genotype for sprout resistance as well as the environmental conditions the grain experiences through maturity.

Starch Degradation and Alpha-Amylase Activity

When wheat kernels begin to germinate in the spike, the quality of the grain drastically decreases, making it difficult for growers to sell it on the market. This is because many physiochemical properties in the grain are altered as the embryo begins to

germinate and utilize the stored reserves in the seed. As the seed begins to germinate, alpha-amylase activity is increased dramatically, causing biochemical changes in the grain that are less desirable for milling and baking. This process reduces the size of the starch molecules and decreases the water holding capacity of the resulting flour, making it less desirable for bakers. The starch in sprouted seeds are hydrolyzed and have a lower molecular weight than non-sprouted seed (Simsek et al., 2014). Starch is broken down by amylase that is produced by the germinating seed. Starch is then converted to sugar for the embryo to begin utilizing, which results in chemical changes and reduced seed quality.

Typically, starch degradation is measured by the falling number test which measures the viscosity of a gelatinized flour suspension. A falling number test is also an indirect measurement of alpha-amylase activity in grain, which helps quantify the degree of PHS grain. This test measures the time a plunger takes to fall through a slurry of heated water and wheat flour that has become a starch gelatinized suspension (McKie and McCleary, 2015). The quicker the plunger falls through the suspension, the lower the falling number is, indicating a higher level of starch damage. This is because the alpha-amylase hydrolyses the starch that is present, resulting in a less dense slurry, allowing the plunger to move through the slurry faster. In the U.S., it is undesirable to have wheat samples that have a falling number less than 300 seconds, as falling numbers below this indicates increased alpha-amylase activity, decreasing the grade of the grain due to reduced milling and baking qualities (Ross et al., 2012). Lower grades result in a large price reduction for the grower, which impacts the grower's profit. Reduction in grain

grade or having a low falling number can occur when approximately 4% of the seeds have experienced PHS (Adams, 2015). The falling number cut-off mark in Africa is 220 seconds which is lower than the U.S., but since wheat is a high value trade crop, it is an important threshold to stay above (Craven et al., 2007). Other countries have varying falling number standards, which give growers that experience PHS some flexibility in different markets. When the falling number is below the acceptable threshold where the grain is sold, it limits the grower's selling options and the value of the grain drops.

Although alpha-amylase activity has been seen to increase in grain that has experienced PHS, the degree of elevated alpha-amylase activity has been shown to be variable depending on the variety. Research conducted by Lekkala Reddy (1978) demonstrated varieties ripened and germinated under the same environmental conditions without any dormancy expression had shown significant differences in alpha-amylase activity among the germinated varieties. Two varieties with a lower level of dormancy and one variety with a higher level of dormancy had significantly higher levels of alpha-amylase activity in germinated seed than two other varieties with high dormancy levels. Even though the general trend in sprouted wheat grain is to have an increase in alpha-amylase activity compared to non-sprouted grain of the same variety, the degree in which the alpha-amylase activity is elevated is highly dependent on the cultivar (Adams, 2015). The varieties that tend to have a stronger dormancy also appear to have a lower level of alpha-amylase activity in sprouted grain, however, this is not always the case for every variety that exhibits a strong dormancy.

High levels of alpha-amylase in ripened grain can also be caused by late maturity alpha-amylase (LMA). LMA and PHS are both genetically controlled and are independent traits that cause elevated levels of alpha-amylase to be present in grain. LMA is a genetic defect that is strongly impacted by the environment and typically occurs when alpha-amylase begins being synthesized during the middle stages of seed development without any influence from moisture (Mares and Mrva, 2014). The problem of LMA is most commonly found in bread wheat and has been determined to be controlled by one or two recessive genes that act independently or in combination in response to being triggered by a cold temperature shock (Mares and Mrva, 2008). This response to a cold temperature shock must occur post-anthesis and at a specific time of seed development (25-30 days) (Mares and Mrva, 2008). In a study conducted by Farrell et al., (2013), they examined how the absence of the dwarfing gene Rht-D1b and the presence of the 1B/1R translocation affected the expression of LMA. Previously, it had been found that high levels of alpha-amylase (or a low falling number) seemed to be common in 1B/1R genotypes (Gobaa et al., 2007). This study looked at crosses that came from segregating populations for the dwarfing gene as well as the 1B/1R translocation. Their field results showed lower falling numbers for genotypes that carried the 1RS translocation and the genotypes with the 1RS translocation that lacked the Rht-D1b gene had even lower falling numbers. This study shows LMA is more likely in genotypes without the Rht-D1b gene or the presence of the 1B/1R translocation, which are two independent genetic factors.

After-Ripening and ABA Regulation

After-ripening is a process that occurs over time under dry conditions following harvest in which seed dormancy is reduced. The rate in which grain goes through the after-ripening period is highly dependent on the cultivar being grown. Wheat cultivars that are more susceptible to PHS go through the after-ripening period much quicker than varieties that exhibit a strong dormancy expression (Gerjets et al., 2010). After a seed goes through an after-ripening period, it can readily germinate after imbibition. The process of after-ripening is affected by the amount of seed moisture present and the desired moisture threshold is dependent on the species (Foley, 2008). This indicates that after-ripening will not occur in very dry seeds (Gao et al., 2012). This is because moisture allows for changes in gene expression through initiation of transcriptional and translation activities. Genes involved in cell wall modification and cell elongation are highly expressed in after-ripened seeds when compared to dormant seeds. It has also been found that many protein synthesis transcription factors are elevated in imbibed, after-ripened seeds compared to imbibed, dormant seeds (Barrero et al., 2009). The changes in after-ripened seeds which are responsible for the breakdown of dormancy can be associated with the decrease in abscisic acid (ABA) content (Liu et al., 2013).

Regulation of ABA plays a major role in embryo maturation and seed dormancy. ABA inhibits germination by repressing transcription genes that are related to chromatin assembly and cell wall modification. It also inhibits germination by activating gibberellic acid (GA) catabolic genes which help breakdown GA present in the embryo, preventing dormancy decay (Liu et al., 2013). The ABA content in a seed is controlled by the

balance between its biosynthesis and catabolism. This is regulated by two ABA biosynthetic enzymes, zeaxanthine oxidase (ZEP) and 9-cis-epoxycarotenoid dioxygenase (NCED), as well as the enzyme which catalyzes the main ABA catabolic pathway, ABA 8'OH (Nambara, et al., 2010).

In wheat, a seed's sensitivity to ABA and ABA synthesis have been shown to be involved in the onset of dormancy when the seed reaches maturity (Gerjets et al., 2009). ABA is effective at inhibiting seed germination in immature seeds in several crops such as cereals and soybeans (*Glycine max*). Typically, as ABA levels in the seed begin to decrease, the seed more readily germinates. Unlike other cereals such as barley (*Hordeum vulgare*), wheat seed dormancy is mainly due to ABA sensitivity and not ABA content (Liu et al., 2013). In a study conducted by Walker-Simmons (1987), it was found that ABA levels were consistently higher in immature embryos than in any other part of the seed until late maturation. ABA levels in the embryo continue to rise as the grain fills and maximizes when the seed reaches maximum fresh weight. As the seed begins to dry and ripen, ABA levels begin to decrease. Seeds that express higher grain dormancy have been found to have about 25% higher embryonic ABA levels than grain that express low dormancy at maximum fresh weight. Walker-Simmons (1987) also found that sprout susceptible cultivars lose sensitivity to ABA as the grain enters maturity while sprout resistant cultivars continue to show embryo sensitivity to ABA as the grain enters maturity.

Walker-Simmons (1988) isolated wheat embryos to test how ABA directly affects germination. When the embryo was removed from the seed and placed in water, it tended

to germinate readily, regardless of temperature and other factors. However, when ABA was applied directly to the embryo, dormancy was restored and the embryo became more difficult to germinate under less ideal conditions. Higher temperatures during wheat seed germination were found to enhance dormancy expression, however, ABA was 100 times more effective at repressing embryo germination than warmer temperatures. The embryo's sensitivity to ABA and the ABA level in imbibed seed greatly impacts the expression of seed dormancy. After-ripening can counteract dormancy by allowing the seeds to catabolize ABA after imbibition.

In a study by Ali-Rachedi et al. (2014), ABA levels in *Arabidopsis* were found to be different in dormant seeds when compared to after-ripened seeds. Imbibed non-dormant seeds had an increase in ABA levels within the first 6 hours of imbibition and then rapidly decreased within the first 24 hours. The ABA levels then stabilized and were found to be at a 3-fold lower value after three days than the dry seeds of the same variety. In the dormant seeds, it was noted the ABA levels decreased quickly within the first twelve hours and then continued to decrease more slowly for the next two days. The ABA levels reached half the amount as the dry seeds two days after imbibition. The ABA levels in the dormant seeds then began to increase again to reach a steady state where it was maintained for twenty days after imbibition (Ali-Rachedi et al. 2004). This demonstrated that seed dormancy is able to be maintained through the renewed accumulation of ABA after dormant seeds are imbibed (Finkelstein et al., 2008).

As ABA levels in the seed decrease, the embryo loses sensitivity to ABA, which triggers the ability of the seed to germinate. As non-dormant seeds become imbibed, the

ABA levels decrease in the seed as the seed begins to synthesize and catabolize ABA. ABA levels in the imbibed dormant seeds decrease within the first few days of imbibition, but the ABA levels then begin to increase after a few days. This demonstrates the difference in which ABA is catabolized between dormant and non-dormant seeds (Grappin et al, 2000).

Marker Selection for Pre-Harvest Sprout Resistance

Along with research being conducted which observed seed germination that determined dormancy expression or sprout resistance in soft white winter wheat, several studies have explored identifying molecular markers associated with pre-harvest sprout resistance. Fakthongphan et al. (2016) compared progeny of hard white by hard red wheat crosses testing the white seed offspring for PHS resistance. They identified markers that corresponded with PHS resistance and found marker loci associated with chromosome 3A in all the tested populations. The gene TaPHS1 has been found to regulate PHS resistance and is found on chromosome 3A of wheat. There are two common mutations that can occur in the coding region of this gene (in the coding region +646 and +666), which results in the plant being more susceptible to PHS (Liu et al., 2013). Kompetitive Allele Specific PCR (KASP) markers have been developed to help identify the two mutations and to assist in the evaluation of the plant's PHS susceptibility. These KASP markers were used to test 82 wheat cultivars and 66 cultivars were correctly identified to be associated with a strong dormancy while 16 cultivars were more susceptible to PHS. These markers can be used in marker-assisted breeding

selection to identify PHS resistance for selecting breeding lines with increased dormancy (Liu et al., 2015).

Several studies have also identified different chromosomes associated with PHS resistance in wheat. Many of these studies have resulted in the development of markers to identify these chromosome regions for use in selection for PHS resistance, however, it has been difficult to identify the exact gene or genes responsible for PHS resistance. This is because there are many different causes for PHS and the interaction of the plant's genotype and the environment play a major role in gene expression. Cabral et al. (2014), developed KASP markers from 18 single nucleotide polymorphism (SNP) flanking sequences on chromosomes 3B, 4A, 7B and 7D associated with PHS resistance. These chromosome regions were identified as QTLs for PHS resistant traits that were involved in ABA and GA metabolism. These KASP markers are designed to identify breeding lines carrying these PHS resistant traits for further evaluation.

Highly dormant wheat cultivars have been compared to non-dormant wheat cultivars and the chromosomes 3A, 3B, 3D and 4A have been reported to carry QTLs consistently associated with reduced PHS in both red and white wheat. (Nakamura et al., 2011; Kulwal et al., 2012; Mori et al., 2005; Imtiaz et al., 2008). The homeologous group 3 chromosomes has been found to be associated with the red kernel color gene as well, (Sears, 1944; Metzger and Sibbald 1970), and red wheat cultivars are known to exhibit higher levels of PHS resistance than white wheat cultivars. Singh et al., (2014) found significant QTLs with small effects on several different chromosomes (1A, 1B, 5B, 7A, 7B) that contributed to PHS resistance in a double haploid population. They also found

that PHS resistance had a higher heritability than grain yield. Even though many genes have been found to be associated with PHS, there is great debate on which chromosomes and genes are the largest contributors to PHS resistance in wheat. Many advances have been made to identify genes and chromosome locations that have a major impact on seed dormancy. Finding one standard marker or a set of markers that consistently identifies PHS resistance is challenging due to the environmental influences as well as the large number of genes that have been identified to have an impact on grain dormancy (DePauw et al., 2012).

Temperature Effects on Wheat Germination

Temperature can have a huge impact on how readily a seed germinates. Typically, the ideal temperature for germination of soft white winter wheat is around 20°C (Lei et al., 2013). Temperature can affect wheat germination in several ways. During the process of grain ripening, high and low temperatures can impact the degree of dormancy expressed by the grain during germination. It can also influence grain fill and size due to changes in photosynthetic activity. Hot temperatures during grain fill can lead to aborted or shriveled seeds (Sainin et al., 1983) due to damaged photosynthetic membranes which result in a decline of the plant's chlorophyll content (Al-Khatib and Paulsen, 1984) and photosynthate production. The temperature during germination can also impact the grain's dormancy expression if conditions are not ideal. However, the extent that temperature affects grain dormancy greatly depends on the variety being grown (Osanai et al., 2005). Variation in temperature during germination can greatly impact the rate of

water absorption, mobilization of seed reserves and movement of other substrates to the germinating embryo (Buriro et al., 2011).

The temperature in which grain ripens and matures has a huge impact on the grain's dormancy expression. Seeds that mature at warmer temperatures tend to develop and ripen rather quickly. These grains also have been reported to exhibit a lower level of dormancy than when they develop and ripen at cooler temperatures (Kigel and Galili, 1995). Even though grain ripening temperatures effect on grain dormancy can vary greatly among cultivars, general trends can typically be detected. Grain that ripens at low temperatures around 10°C tends to have the strongest dormancy expression while grain that ripens at higher temperatures have a lower level of dormancy expression. The greatest variation in grain dormancy expression can be seen in grain that develop at cooler temperatures when they are germinated at 15°C, 20°C and 26°C (Reddy et al., 1985).

In a study conducted by J.M. Nyachrio et al. (2002), ten spring wheat genotypes were evaluated for their expression of seed dormancy at varying germination temperatures. They observed that as temperatures during germination increased from 10°C to 30°C, the spring wheat cultivars expressed increased seed dormancy as a relative trend across all genotypes. A few cultivars declined in dormancy expression when the temperatures increased from 10°C to 15°C, but dormancy expression increased as temperatures increased beyond 15°C.

A similar trend was observed by L. Reddy (1978) and she noted that kernels from all the varieties in her trial that were ripened at 26.6°C had germinated readily at 15.5°C,

however, as germination temperatures increased to 20°C and 26.6°C, all varieties exhibited varying degrees of dormancy. She also observed that when the cultivars were ripened at 15.5°C, specific cultivars such as Brevor and Tom Thumb expressed slow germination at 15.5°C and failed to germinate at 20°C and 26.6°C, which was a result of high dormancy expression. This demonstrates that temperature not only affects grain dormancy expression during germination, but the ripening temperatures also impact the grain's dormancy expression. Wheat grain dormancy is influenced by several different factors, and the variety has a very large impact on grain dormancy expression. Some varieties can experience the same conditions during ripening and germination, yet they can have varying degrees of dormancy, if dormancy is expressed.

Cold Temperature Germination

Late wheat fall planting in the Pacific Northwest can be challenging for growers to achieve a sufficient plant stand in the following spring since cold soil temperatures can depress seed germination. When soil temperatures drop below a minimum temperature, seed germination can be severely slowed and the amount of time needed for plant establishment increases. Winter wheat can tolerate cold temperatures when it is in the vegetative stage, but the seeds can be very sensitive to low temperatures during germination (Li et al., 2013). Cold soil temperatures can increase the amount of time needed for seed germination and the continual decreasing temperatures can cause a dramatic loss in seedling emergence and winter survival. Cold temperatures between 0-12°C during seed germination can reduce the rate of germination which results in delayed plant emergence. Poor plant survival can lead to uneven stand establishment along with

reduced plant performance, which is ultimately reflected in yield (Zabihi-e-Mahmoodabad et al., 2011). Some wheat cultivars can be more tolerant to cold temperatures and manage to germinate and survive when planted late in the fall, when temperatures are less than favorable.

Several studies have investigated how different seed treatments affect seed germination under cooler temperature regimes. Ahmadi et al. (2007), examined the impact of available moisture for imbibition on seed germination by comparing the difference in germination rates at 11°C and 18°C between seeds that were soaked in distilled water for twelve hours and seeds that were soaked in water with polyethylene glycol (PEG) for twelve hours. Soaking the seeds in water with PEG had previously been shown to have adverse effects on seed germination since it is an osmotic solution which increases the amount of time it takes to hydrate the seed. They noted the seeds that were imbibed with distilled water had higher germination efficiency under the colder temperature regime than the seeds soaked with water and PGE. This shows soil moisture is necessary if seeds are planted in cooler soils. It also demonstrates that seeds have a better chance of germination if they have the chance to become fully imbibed. Li et al. (2014) treated wheat plants during the late grain-filling stage with exogenous ABA and found that even though the treatment decreased the overall seed weight, it favored germination and establishment of the developing seed under low temperature stress. They indicated treating winter wheat with ABA during the late grain-filling stage could be a potential approach to improve the next generation's tolerance to cold stress when seed is sown late in the fall.

The thesis research by Halitligil (1975) looked at how different temperatures and water potentials affected seed germination for the varieties Yamhill, Bezostaya and Kirac 66. Halitligil concluded that temperature had a greater impact on seed germination rate than the water potential of the seeds. At the lowest temperature of 5°C with low water potential, seed germination was greatly delayed. Temperature had the greatest effect on delaying germination, but the combination of low water potential and cold temperature had a large impact on germination rate. This is because low temperatures decrease the seed's enzyme activity and water diffusivity through the seed coat. He also noted there were significant differences between the varieties and germination times corresponding to the temperature. Kirac 66 germinated the fastest under adverse temperature conditions while Bezostaya consistently germinated the slowest. The difference in germination rates between the varieties illustrates that each variety is genetically different and has different levels of tolerance for germinating in cold temperatures. The difference in seed sensitivity to cold temperatures among many commercially available varieties has not been well studied. Mya (1987) concluded similar results to Halitligil (1975), but found more extreme differences between high and low vigor seeds. The vigor of the seeds was determined by which seeds seemed to be the strongest/healthiest allowing them to tolerate less than ideal germinating conditions. More severe environmental stresses such as low temperature reduced the germination of low vigor seeds much more than high vigor seeds. This indicates that more vigorous seeds are more tolerant of low temperatures and are more likely to germinate and survive in cold temperatures.

Pre-Harvest Sprouting Effect on Baking Quality

Pre-harvest sprout is ultimately detrimental to wheat's end-use products and affects the baking quality and integrity when flour from sprouted grain is used. This is what reduces the seed quality and value when it prematurely sprouts in the field. When wheat seed prematurely germinates before harvest, starch and proteins are degraded, making the damaged seed unacceptable for human food products. Pre-harvest sprout that results in a reduction in market grade occurs about three out of every ten years in the areas in which soft white winter wheat is grown (DePauw et al., 2012). Pre-harvest sprout reduces the quality of the wheat kernels and reduces the overall value in several different ways. When PHS occurs, the grain goes through a number of biochemical changes that causes changes in enzyme levels which greatly impact the baking qualities of the wheat. Dough made from flour milled from sprouted grain are stickier, hold less water and the time it takes to develop the dough is shortened. Flour from grain that experienced PHS also result in a dough that is less tolerant to mixing and becomes hard to handle much quicker than dough from flour from non-sprouted grain. Pre-harvest sprouting also reduces the dough stability and these undesirable characteristics increase as the percent of sprouted grain increases (Lorenz et al., 1983). Bread made from PHS grain have poor crumb grain, coarse bread texture, and the bread color is less than ideal even though the volume of the bread is unaffected (Sorrels et al., 1989).

In a study conducted by Finney et al. (1981), the impact of soft white winter wheat with PHS on the baking quality of sponge cake was examined. It had been believed that any PHS grain present would result in negative effects on quality products. However,

they found that grain containing 2.5% sprouted kernels had no negative effects on the sponge cake quality. Grain containing more than 2.5% sprout greatly reduced the volume and caused the sponge cake to become more open and coarse. They attributed the decrease in cake volume to be associated with high levels of alpha-amylase based on falling numbers for the sprouted grain being less than 140 seconds. This research demonstrated that a low level of sprout damaged grain can still be acceptable for certain products such as sponge cakes, however, there is a threshold where too much PHS becomes undesirable.

Lorenz and Valvano (1981) investigated laboratory sprouted soft white winter wheat effects on the baking quality of cakes and cookies. They had three different sprouting times of 1, 2 and 4 days before the grain was milled and baked. When the grain had been sprouted for 2 and 4 days, there were negative effects on the cakes and cookies. Cakes had a decrease in overall volume, a coarse grain, a firm texture and the cake did not hold its desired shape. The cookies had an undesired crust color that was darker than when the cookies were made from non-damaged grain. Even though the product quality decreased due to changes in the appearance of the products, the flavor was unaffected by the changes in grain quality. The length of time in which a grain sprouts impacts its overall functional quality. The longer a seed has been germinating, the more biochemical processes occur, resulting in more starch breakdown, causing products to lose their quality as germination proceeds. Even though product quality in soft white winter wheat is decreased due to PHS, Dick et al. (1974) found that durum wheat does not show the same decrease in quality from sprouted grain. They found the falling number was lower

from the sprouted durum grain which was similar to previous findings, however, they did not see any significant differences in the quality of spaghetti characteristics between four different levels of sprouted grain. Their data showed there was no impact from sprout damage on the spaghetti color, cooked weight, cooking loss, shatter scores, cooked spaghetti firmness or any challenges with its handling properties throughout the process, regardless of how long the grain experienced sprout.

Differences between baking properties of sprouted wheat can be greatly dependent on the type of wheat and its end products. Soft white winter wheat tends to have more challenges associated with sprouted grain compared to durum wheat. The increase in alpha-amylase activity in sprouted soft white winter wheat greatly impacts the crumb firmness of sponge cake. This is attributed to the increase in soluble starch, amylose and amylopectin as germination time increases and these attributes are decreased in the bread crumb as the bread is aged (Morad and Rubenthaler, 1983). The longer seed germination takes place, the more the quality of the grain is decreased. If the grain experiences one day of germination, the milled flour is not degraded, but any length of time longer than one day, the flour and end product quality begins to decline. Soft white winter wheat is the ideal wheat to be used in cookies, cakes, flat breads, and sponge cakes due to its desirable grain properties. Some PHS is tolerable for some baking purposes, but anything that has been germinating over one day and contains more than 2.5% sprout can make it difficult to produce quality products. It therefore, is less desirable for millers and bakers.

Introduction to Variety Identification and Maintenance

Varieties are typically bred to perform well in designated locations with optimal growing conditions for the given variety. In wheat breeding, selected varieties go through approximately 8 to 9 breeding cycles from start to finish before they become a stabilized cultivar ready for release. Once a breeding line has achieved the breeder's desired attributes, it will go through a series of seed increases. The variety is grown in gradually larger acres that are inspected to ensure uniformity and to remove any off-types that are present. An off-type is any plant that is not genetically identical to the variety being grown and they often differ in appearance from the cultivar. Off-types typically occur through a source of contamination. Variants can also appear in a field and these individuals appear to be different than the variety as if they are the result of contamination, however, they are genetically identical to the cultivar. The use of molecular markers for genotypic screening has allowed for the determination of whether an off-type is a contaminant or a variant. Variants will typically continue to appear in seed increases, even if they are continually rogued. This occurs especially if the trait is recessive in nature so the trait is carried in heterozygous plants from generation to generation.

The beginning of a variety's seed increase usually begins by having the variety being grown in head rows to produce breeder seed. This means seed heads from plots of the variety are collected and each seed head is planted in its own row. Typically, about 1,000 head rows will be grown for initial production of the Breeder seed generation. During the production of the Breeder seed, the wheat breeder monitors the head rows for

any rows that show a difference in phenotypes. The breeder will remove any undesirable head rows from the population that do not meet the variety's desired phenotype.

Undesirable head rows would include lines segregating for a trait or traits and/or rows that do not match the phenotype of the cultivar (susceptible to disease, too tall, too short, heading too late, heading too early, or not the correct color). The best head rows are then selected to be used as the Breeder seed stock that will be used to produce Foundation seed (Houck, 2009). The Foundation seed generation is the next step in the seed increase process that is also inspected for uniformity (genetic purity) and must pass inspection from the seed certification service, which is an independent state service. Registered seed results from the progeny of the Breeder or Foundation seed, which is also handled in the same manner to maintain the genetic purity of the variety. Certified seed can be the progeny of the Breeder seed, Foundation seed or Registered seed and is expected to meet a standard of quality and genetic purity (Oregon Seed Certification Service, 2016).

Even though there are several steps in the seed certification process that aim to maintain genetic purity, problems can still occur with reoccurring off-types and variants throughout the seed increase process. Even if the fields are continuously rogued, the variety may still have off-types appearing in the next generation of seed increase. This makes the field appear as if there is more than one phenotype that is being produced in the same field. There are several ways off-types and variants can occur during the Certified seed increase process. If seed from another wheat variety gets mixed in from a different seed source, many off-types can arise due to a seed contamination event. This does not occur very often or in high numbers because Breeder seed fields are typically

monitored and any off-types are eliminated from the seed field before the field is harvested. If variants are present, they will continually appear throughout the seed increase process due to potential out-crossing events and genetic segregation. Variants can also appear through epigenetic events which result in heritable changes in gene functions without any changes in the nucleotide sequences (House and Lukens, 2014).

Off-types can turn up throughout the seed increase process if the variety out-crosses with surrounding cultivars. This causes a change in certain individual head row's genotype leading to plant segregation in the subsequent generations. This segregation event would not be noticed in the original out-crossed parent. The out-crossing potential of wheat is rather low (around 1%) since it is a self-pollinating crop (Ekse, 1980). If the anthers are sterile but the ovary is fertile, the potential for out-crossing increases. Varieties can also show segregates when epistatic events are present in the variety, even if variants were not observed in the previous generation. Epistasis is the interaction of genes which can affect a plant's phenotype where one gene masks the expression of a second gene. There can be both dominant and recessive epistasis and the implications of epistasis can produce unexpected phenotypic variation among the progeny (Zhu et al., 2015). Another possibility that could cause segregation during the seed increase process is if a heterozygous reciprocal translocation is present in the variety. This causes the offspring of the variety to express a different phenotype than its parents depending on if the off-spring is homozygous for the translocation or homozygous for the normal chromosome (Primard et al., 1990). If this occurs, this observed trait then becomes part of

the variety and is labeled as a variant. The percentage of variants that are expected in a given field are then noted by the breeder and added to the variety's description.

The soft white winter wheat cultivar Bobtail was developed at Oregon State University and was released in 2013. The variety was bred to be a semi-dwarf awnletted wheat. It was released for its superior yield potential, disease resistance and adaptation to growing conditions in the wheat production areas of Oregon, Washington and Idaho. The parents of Bobtail are Einstein (hard red semi-dwarf awnless winter wheat with resistance to *Pseudocercospora* foot rot conferred by *Pch2*) and Tubbs (soft white semi-dwarf awned winter wheat resistant to *Pseudocercospora* foot rot conferred by the *Pch1* resistance gene) (Flowers et al., 2009). The initial cross of Einstein and Tubbs occurred in 2003 (Zemetra et al. 2012). The F₁ and F₂ generations for source population for Bobtail were grown at Hyslop Research Farm in Corvallis, OR. The seed from the F₂ generation was used to produce a recombinant inbred line population (RIL) in the greenhouse through four cycles of single seed descent. This seed was then used to produce the F₅ derived F₆ RIL which were then planted in the field in 2008 in small plots at Hyslop Research Farm.

One of the lines, line 94, demonstrated superior performance in 2009 so it was planted in plots and drill strips for advanced testing in 2010. These plots and drill strips were rogued to maintain a uniform plant stand for semi-dwarf awnletted plants. In the summer of 2011, heads were snapped from the drill strips and planted in head rows in the fall of 2011 at the Washington State University, Irrigated Agriculture Research and Extension Center, Othello Unit, in Othello, WA. These head rows were grown and any

rows that were segregating or varied phenotypically from the desired phenotype were removed. This included removing any head rows found to be segregating for the presence of awns. The remaining head rows were bulk harvested to produce Bobtail Breeder seed. The Breeder seed was then planted in fall, 2012 to produce Foundation seed (Dr. Robert Zemetra, Personal Communication). The Foundation seed was produced in four fields and a low number of awned and tall plants were observed in the fields even though undesirable phenotypes had been continuously removed throughout the variety's development. Segregating populations rarely occur in the parental material contributing to the Foundation seed source. Determining the source for the variation or the contamination is key to maintaining variety quality and purity.

Genes Responsible for Selected Traits

The interactions of genes are of great importance for the control of phenotypic traits. In wheat, the awned and awnless seed head trait is controlled by the B1 and B2 genes on chromosomes 5A and 6B (McIntosh et al., 1998). When the plant has the recessive genotype $b1b1b2b2$, it will be bearded or have a fully awned seed head. A plant with at least one dominant allele (B1 or B2) or any combinations of dominant alleles, ($B1B1B2B2$, $B1B1B2b2$, $B1B1b2b2$, $B1b1b2b2$, $b1B1b2b2$, $b1b1B2b2$, $b1b1b2B2$, $b1b1B2B2$, $B1b1B2b2$, $b1B1b2B2$, $B1B1b2B2$, $B1b1B2B2$, $b1B1B2B2$) will be awnless or awned tipped. This interaction between the B genes is an example of dominant epistasis, where the allelic composition at one gene locus can mask or overshadow the allelic composition at another gene locus. In the case of the B genes which controls the awns on wheat, having one dominant B allele present at either of the

two gene loci will mask the alleles at the other gene locus. There has been speculation of a third allele at the B2 locus that could cause the wheat head to experience a half-awned conditions. However, epistatic interactions among the B1 and B2 genes have been observed through cytogenetic analysis to cause half-awned conditions or changes in the length of the plants awns (McIntosh et al., 1998).

The wheat plants height is controlled by the Rht-B1a and Rht-D1a alleles on chromosomes 4B and 4D (McIntosh et al., 1998). There are both GA-sensitive and GA-insensitive Rht-1 genes that have an impact on the plant's height. Plants that contain the GA-sensitive Rht-1 genes originate from the wild type and have a tall plant height phenotype. The GA-insensitive Rht-1 genes occur through mutations which cause the genes to express differently than the wild type. Plants that have GA-insensitive Rht-1 genes typically express a dwarf stature. The Rht-B1 and Rht-D1 encode DELLA proteins which reduce GA-responsive growth since DELLA proteins are transcriptional regulators which repress GA signaling (Pearce et al., 2011). GA plant hormones play a major role in controlling stem elongation (Zhang et al., 2016). Decreased responsiveness to GA due to the mutant alleles, Rht-B1b and Rht-D1b, result in plants that have a semi-dwarf stature (Pearce et al., 2011). These types of mutations are often referred to as dwarfing genes. Tan et al. (2013), found the type of mutation can vary from cultivar to cultivar. Through their research, they found the Rht-A1a allele can have a nucleotide transversion resulting in an early stop codon leading to a deletion of an amino acid. Even though the Rht-A1 gene has not been directly linked to the plant's dwarfing characteristics, it is believed to have an impact on the suppressed plant height. In the Rht-B1 gene, mutations that result

in a serine deletion, amino acid substitutions, early stop codons and nucleotide transversions have been found. Stop codons and nucleotide transversions mutations have also been found in the Rht-D1 gene (Tan et al., 2013). Mutations in the Rht-B1 and Rht-D1 genes have been observed to give rise to the semi-dwarf phenotype.

Translocations

Another potential source of phenotypic variation is the presence of a chromosome translocation. A translocation is a chromosome abnormality that is caused by exchanges of parts of the chromosome between non-homologous chromosomes (Stene, 1976). This can be detected by changes in the karyotype of the plant cells during mitosis and meiosis. There are two main types of translocations that can occur in plants. Reciprocal translocations occur when two non-homologous chromosomes break and exchange fragments. This can cause a change in the size of the total chromosome length and can make a longer chromosome shorter and a shorter chromosome longer (Rachidi et al., 1999). Plants that have these types of translocations typically continue to have a normal phenotype since they still have balanced chromosomes. Translocations result in dysploidy, which is a structural change in the genome without losing or gaining any genetic information (Storme and Mason. 2014). Centric fusion, also known as a Robertsonian translocation is a second type of translocation in which the centromeres of two chromosomes fuse together to become a chromosome with a large arm and a short arm. The karyotype of an individual who has a centric fusion translocation will generally have one less chromosome than the normal diploid number of chromosomes due to the loss of the short arm of the translocated chromosome (Sawyer et al., 1994). Centric

fusions are relatively uncommon in higher plants but are the cause of many karyotype changes in animals (Jones, 1998).

The issue with the presence of translocations is they can cause problems with reproduction in plants that are heterozygous for the translocation. The changes in the chromosomes can lead to a decline in reproductive potential which leads to abortion of the developing seeds. It can also make it difficult for all the flowers to be pollinated due to the plant being semi-sterile (Talukdar, 2009). Individuals that are heterozygous for reciprocal translocations continue to have a balanced set of chromosomes and often have a normal phenotype, but the individuals have varying levels of fertility. The biggest cause of infertility comes from problems that occur during chromosome pairing and segregation during meiosis. This can lead to unbalanced gametes and offspring with unbalanced genomes. This type of translocation has the biggest impact on decreased fertility. Individuals with centric fusions are at risk for decreased fertility as well as increased risk for abortions and chromosomally unbalanced offspring (Keymolen et al., 2011). Even with reduced fertility, the majority of individuals with translocations can still produce healthy offspring.

Along with reduced fertility, Auger and Sheridan (2012) noted that translocations can reduce the amount of crossing-over that occurs near the breakpoints on the chromosomes. This isn't typically a problem for a homozygous plant with a reciprocal translocation since it can proceed in normal meiosis since the translocated chromosome has a structural homologue that it can pair with during the first division cycle of meiosis. A plant that is heterozygous for the translocation has a more complicated first division of

meiosis. This is because the translocated chromosomes cannot correctly pair with normal chromosomes in a linear fashion. During meiosis, the four chromosomes will form a quadravalent, and typically, a small region on the chromosomes will fail to pair, which is usually present at the breakage point. Due to the breakage point failing to pair with the homologous chromosome, crossing over is relatively rare in these regions. Non-homologous pairing can also cause large regions near the breakpoints to be unable to cross-over. Since there is low cross-over potential near the breakage points, traits have pseudo-linkages, where two loci that are located near the breakage point appear to be linked, even if they are present on two non-homologous chromosomes. This inability of crossing over leads to reduced chromosome recombination in these translocated regions.

As explained by Auger and Sheridan (2012), heterozygotes with translocations tend to have reduced pollen and ovule viability due to complications during meiosis. The two reciprocal chromosomes of a translocation do not have gene duplications or deletions as long as they both appear in the same cell, allowing the cell to remain viable. However, the reciprocal chromosomes for a translocation can move to two different daughter cells during meiosis in which one daughter cell will also have a normal homologue. When this occurs, the daughter cell will have a duplication of a section of a chromosome and a deficiency of a section of a chromosome. This leads to the gamete being non-functional, which results in it being aborted. For the gamete to be viable, it must either receive both of the translocated chromosomes or both of the two normal (non-translocated) chromosomes. This distribution of chromosomes occurs during anaphase 1 of the first division of meiosis. There are several different potential outcomes that can occur during

meiosis from translocated chromosomes (Auger and Sheridan, 2012) leading to a sterility rate of about 33% for plants heterozygous for a reciprocal translocation.

Out-Crossing

Wheat is a self-pollinated crop with a small out-crossing potential. Breeders generally emasculate the intended female plant and hand pollinate the female flowers with the desired male plant. This process allows for new crosses to be made in order to transfer desirable traits from both parents to the offspring. Unless the wheat heads are deliberately crossed, the out-crossing potential of wheat is low, ranging from 0.1-5.6% and is highly dependent on the cultivar (Martin, 1988) and environment. Loureiro et al. (2007), explored the out-crossing potential between two different wheat cultivars as well as between soft white wheat and durum wheat under field conditions. They used emasculated plants as females and measured the distance from the female plant to the pollen source to determine the seed set frequencies. The number of seeds set indicated the percentage of out-crossing potential at a given distance. Seed set had the highest frequency of 45% between the two different soft white wheat cultivars when the plants were directly next to each other. The soft white wheat and the durum wheat had an out-cross seed set frequency of 18% when the plants were side by side. As the distance increased to 8 m, out-crossing potential decreased to less than 1%, even though viable pollen was found 14m from the pollen source. These findings only apply to semi-arid environments as pollen dispersal can be highly environmentally dependent. These findings demonstrate how infrequently out-crossing occurs in wheat and pollen isolation can be maintained in a rather short distance.

Currently, isolation distances for wheat ranges between 3-10m, however, research by Hucl and Matus-Cadiz (2001) suggests this might not be a large enough isolation distance for cultivars that have higher out-crossing rates. In their research, they used a wheat with the blue aleurone trait to provide pollen to determine distances in which pollen could travel to pollinate four spring wheat cultivars. They determined there were two cultivars with a low out-crossing potential which did not have detectable pollen further than 3m from the pollen source. The other two cultivars had a much higher out-crossing rate and needed isolation distances around 30m since pollen was detected up to 27m from the pollen source. The out-crossing frequency of wheat as a whole is rather low, but there are large variations of out-crossing potentials between different cultivars. Another study by Hucl (2010) looked at pollen travel in Breeder seed head rows of spring wheat to detect the probability of having off-types in later generations. He looked at twelve different distances from a blue aleurone pollen source in order to estimate the frequency of out-crossing. The conclusions were similar to the previous study where cultivars with low to moderate out-crossing would need an isolation distance of at least 3.6m between cultivars. The cultivars with higher out-crossing rates needed to have an isolation distance of at least 10m or greater depending on the cultivar. Not all wheat cultivars have the same out-crossing rate and it is important to know how likely the cultivar out-crosses when determining their isolation distances.

Determining gene flow is important to help maintain genetic purity to avoid having contaminants in a field. Different cultivars have different out-crossing potentials and it is environmentally and genetically influenced. In soft white winter wheat, viable

pollen has been found to reach up to 42m from the pollen source. Hanson et al. (2005), studied the potential of out-crossing in soft white winter wheat in five locations distributed across three states, Oregon, Washington and Idaho, using a blue aleurone pollen source. The direction in which the pollen contamination occurred typically was in the direction from which the wind was blowing. Pollen contamination occurred more frequently in areas with cooler temperatures and higher humidity during the pollination period. The total amount of pollen contamination at all the sites averaged 2% and the largest amount of contamination in a given sample was 0.45%. Out of five locations, only one had pollen contamination between 30 and 42m from the pollen source, which accounted for 13% of the contamination in the field. The difference in environmental growing conditions and wheat cultivars have a huge impact on the probability for an out-cross contaminant. Since wheat has demonstrated out-crossing potential, even though it's at low frequencies, the need for isolation distances is important to maintain genetic purity. Without an adequate isolation distance for a particular cultivar, off-types can occur unexpectedly.

Other Contamination Sources and Implications

Wheat seed contamination can occur through the movement and mixing of different classes and varieties of wheat seeds. Cleaning equipment between processing different wheat classes and varieties is very important to avoid seed contamination. Seed remaining in or on a drill or a combine and then moved to another field for planting or harvest of another wheat cultivar can directly lead to seed contamination (Colbach et al., 2013). This results in unexpected off-types in the planted field or the seed stock. Wheat

seed contamination can also occur through the cleaning process of wheat grain when screens and equipment are not thoroughly cleaned. This can increase the amount of seed contaminants that are present in the seed stock. When equipment is not cleaned between the processing of one variety and another variety, growers can experience many different off-types that will need to be removed from the field prior to harvest (Harmond et al., 1968). When a field is not sprayed to remove weeds and volunteer plants from the previous crop or is in a wheat-wheat rotation, it can lead to the presence of off-types through the emergence of volunteers. Wheat seed viability in the field post-harvest can be highly variable but has been found to be able to remain viable in the soil anywhere from 16 months up to two years after harvest (Anderson and Soper, 2003). These different events can make it challenging to determine if the seed the grower received was already contaminated or if they were responsible for the off-types. The different possibilities of how an off-type appeared can make it difficult to trace the source of the contamination.

Having a mixture of wheat types and varieties growing in the same field can make it difficult for growers to receive a high grade for their grain. This is because as the number of off-types increase, the grade of the wheat begins to decrease. According to the United States Standards for Wheat (2014), the maximum number of wheat kernels present from a contrasting class (durum wheat, hard red spring wheat, hard red winter wheat, soft red winter wheat, hard white wheat, soft white wheat, unclassified wheat and mixed wheat) can only be one kernel in a 60 pound sample to receive a #1 grade. As the wheat grade decreases, the number of off-types increases by one each grade until it reaches #4 grade, in which 10 off-type kernels can be present. The majority of the time

when contaminated wheat meets the U.S. #3 grade requirements, it tends to have a very minimal impact on milling and baking quality and is still acceptable for the export market (Dr. Andrew Ross, Personal Communication). Even though a minimal level of off-types are acceptable and it does not affect the quality, when a large number of off-types are present, it can have large implications on the amount of money a grower can receive for the harvested grain. Due to this, it is important to keep off-types in a field to a minimum and to clean equipment between varieties to avoid seed contamination.

Variety Identification

It is important for breeders to ensure the variety they release remains true to its name throughout the lifetime of the variety. Maintaining the identity of the variety is essential for quality control, plant variety protection, seed certification and consumer protection (Ait Amer Meziane, 1983). When fewer varieties were on the market, it was easier to identify differences between varieties based on phenotypical and morphological differences. Currently, the number of released varieties have increased and the differences between varieties are harder to identify based on the phenotypic differences. The use of laboratory methods to determine variety identification has become valuable in identifying off-types and variants in a field to maintain genetic purity. A variant in a wheat variety is genetically similar to the variety but it may appear as an off-type. A variant can occur due to changes in a gene sequence and the variant cannot fully be eliminated since it continually occurs. Off-types are atypical plants that occur in a field that are not genetically identical to the variety and typically occur through seed

contamination, out-crossing, random mutations, residual heterozygosity and the presence of different biotypes (Giura, 2009).

Wheat variety stability is important to quantify prior to a variety's release to ensure the variety maintains its desirable attributes. Fluorescently labeled microsatellites or simple-sequence repeats (SSR) molecular markers are most widely used for variety identification in wheat cultivars because they can detect small differences among varieties (Perry and Lee, 2015). Developed SSR markers for variety identification in wheat allows for an efficient DNA profiling system (Zheng et al., 2014). Microsatellites have also been used to detect variety stability prior to release to ensure the variety remains uniform and distinct. The stability of the variety ensures there are no variations in phenotypes and agronomic performance from one generation to the next.

In research conducted by Wang et al. (2014), a total of 80 different SSR markers were used to test for homozygous and non-homozygous alleles in a wheat population at a given locus to determine the number of plants that were the same as one of the parents. By running these markers, they determined the non-homozygous alleles that were identified had different genotypes than the rest of the variety and both of the parents. In each generation, the ratio of non-homozygous alleles segregated 1:2:1. The more loci that are found to have non-homozygous alleles, the less stable the variety is due to new genotypes appearing every generation. The labeled markers allow for detection of impurities in varieties due to presences of varying genotypes due to non-homozygosity and continual segregation. SSR markers can also help identify possible contaminants or variations between plants. These markers have several useful applications as they identify

variations among plants in a population. This helps breeders to remove undesired individuals in order to maintain a stable and pure cultivar.

SSR markers have also been used to test for wheat seed purity and are desirable due to their ability to detect a high number of genotypic differences. Using SSR markers to test for seed contamination is more precise than grain gliadin analysis and protein electrophoretic tests. SSR markers are able to detect a higher percentage of off-types in a sample than previously used methods (Wang et al., 2014). Markers are a useful tool used in identification of off-types among wheat cultivars as well as for maintaining variety identification. Identifying varieties with labeled markers allows for quicker analysis and identification of off-types and variants, which helps maintain genetic purity of released cultivars.

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Chapter 3: Grain Dormancy

Abstract

Dormancy is the inability of viable seed to germinate under optimal environmental conditions. Unfortunately, the level of post-harvest dormancy is low in soft white winter wheat cultivars, making it highly susceptible to pre-harvest sprouting (PHS) if rain occurs just prior to harvest. Breeders often aim to produce cultivars that germinate rapidly and uniformly to establish strong and healthy plants going into winter. This goal may have resulted in cultivars being developed with lower levels of post-harvest dormancy which could result in cultivars that are more susceptible to PHS. Post-harvest dormancy has been reported to be reduced in wheat that experiences nutrient deficiencies, high temperatures, drought, short days and/or other stress factors during grain fill. The objective of this study was to determine the degree of post-harvest dormancy that is expressed in older commercial soft white winter wheat cultivars and compare them to recently released cultivars. This comparison was conducted to see if post-harvest dormancy has systematically been bred out of soft white winter wheat or if dormancy was always low in soft white winter wheat. This research looked at 39 cultivars released between 1940 and 2012 as well as 6 experimental lines. Varieties were planted over two years in Corvallis, OR and in Pendleton, OR the second year. Trials were planted in multiple locations to compare how different ripening environments impact seed dormancy expression. Germination trials were run at four different temperatures (4°C, 10°C, 20°C, 30°C) to determine the optimal temperature for the highest grain dormancy. The results of this research found that soft white winter wheat does not possess any post-

harvest dormancy when germinated under optimal conditions. However, certain cultivars such as Brevor, Bobtail, Cayuga, Gene, Nugaines, Rely and the experimental cross 11-225-6H, demonstrated a level of high temperature induced dormancy at 30°C, which slowed down their germination rates. There was no observed trend that linked older released varieties to a higher grain dormancy compared with more recently released varieties, indicating post-harvest dormancy was not bred out of soft white winter wheat over time. The findings of this study show the direction wheat breeding programs should be working towards to improve post-harvest dormancy in soft white winter wheat.

Introduction

Post-harvest dormancy is the inability of a viable seed to germinate under optimum environmental conditions (Bewley, 1997). Most soft white winter wheat cultivars have little post-harvest seed dormancy and the degree of dormancy varies among cultivars. Over time, post-harvest dormancy has potentially been selected against through traditional breeding methods in order to achieve a more uniform germination pattern and a rapid turnaround time from when the seed is harvested to when it is planted in the fall (Gao and Ayele, 2014). The trouble with a reduction in the wheat seed's dormancy is the increased potential for pre-harvest sprouting (PHS) if a rain event occurs prior to harvest. Many locations where soft white winter wheat is produced experience cool damp conditions prior to harvest about three out of every ten years (DePauw et al., 2012). When PHS occurs, it greatly decreases the overall grain quality and the viability of the seed. Wheat producers in areas that experience rainfall around or near harvest desire wheat varieties that have a stronger genetic dormancy period in order to reduce the

potential for PHS (Gerjets et al., 2009). Dormancy has often been seen to be reduced in wheat that experiences nutrient deficiencies, high temperatures, drought, short days and other stress factors occur during grain fill (Rodriguez et al., 2011).

In nature, dormancy is the plant's mechanism for seed survival under undesirable environmental conditions, but permits seed germination when conditions are more favorable for growth and development. Dormancy also allows seeds to initiate germination over a long period of time, which enhances the plant's survival. High levels of seed dormancy has many negative attributes in agriculture because it can delay plant emergence and can lead to plant stands that vary in maturity (Hagemann and Ciha, 1985). When a grower has a field that varies in maturity, it makes it difficult to determine the ideal time for harvest that will have the highest yields with the largest quantity of mature kernels. For these reasons, breeders have a goal to develop varieties that are able to germinate uniformly and are able to be replanted within a month after the grain is harvested.

There are many environmental factors that can affect the expression of dormancy. Temperature plays a major role in the expression of seed dormancy and impacts the degree of dormancy exhibited based on temperature during grain ripening as well as during germination of the seed. Plants that experience warm temperatures during grain ripening have a shortened grain filling period, which can lead to shriveled or aborted seeds (Saini et al., 1983). Warmer temperatures during grain maturation have been seen to produce grain with a lower expression of dormancy than when the plant experiences cooler temperatures during grain maturation (Reddy et al., 1985). During the germination

process, as temperatures rise, wheat expresses higher levels of seed dormancy, preventing the seed from sprouting (Nyachiro et al., 2002). The optimal germination temperature for wheat seed is around 20°C (Lei et al., 2013). Germination tends to occur over a longer period of time when temperatures are below 20°C, but as temperatures increase to around 30°C, the grain begins expressing high temperature induced dormancy, preventing the seed from sprouting (Nyachiro et al., 2002). The release of wheat grain dormancy can be triggered by exposure to cold temperatures, light, stratification and an after-ripening period (Tuttle et al., 2015).

Along with environmental influences, seed dormancy is also influenced by the regulation of abscisic acid (ABA). Unlike in most cereal crops where ABA content has the greatest influence on the release of grain dormancy, the sensitivity of the embryo to ABA rather than ABA content drives dormancy breakdown in wheat (Liu, et al., 2013). As the grain goes through an after-ripening period, the embryo's sensitivity to ABA tends to break down as well, allowing the seed to germinate. This is because changes in gene expression occurs from transcriptional and translation activities that take place in a dry after-ripened seed, reducing the embryo's sensitivity. Wheat that has a lower level of dormancy tends to go through the after-ripening period much quicker than varieties with higher dormancy expression (Gerjets et al., 2010). These varieties with low dormancy expression are highly susceptible to PHS since the grain can go through an after-ripening period before the grain is harvested.

When grain experiences PHS, the grain quality and integrity are decreased dramatically. This is because alpha-amylase levels are elevated for the degradation of

starch in the endosperm, thereby making the seed less desirable for human food products (Ral et al., 2016). Pre-harvest sprouted grain is difficult to bake into quality products because the dough loses its integrity and becomes sticky and difficult to handle. The dough also holds less water and is less tolerant to mixing. This makes marketing grain that has experienced PHS very difficult. Grain that has more than 2.5% sprout is typically used for animal feed since it leads to unmarketable end products (Finney et al., 1981). Bread made from PHS grain are coarse, have poor crumb structure and the loaf color is less than ideal (Sorrels et al., 1989). Not only is the grain no longer suitable for end-use products when it experiences PHS, but it also results in reduced seed viability resulting in potential reduction in field stands if the grower wanted to replant the seed in the field. Wheat seed can experience a slight degree of PHS and still be able to germinate in a field when it is planted. However, if the seed has experienced severe sprouting, the embryo can easily become desiccated when the seed dries out. A falling numbers test can be used to indirectly measure PHS damage. A falling numbers test indirectly measures the alpha-amylase activity in a given sample of flour (Adams, 2015). Grain that experiences PHS will have a lower falling number than grain that does not, due to increased alpha-amylase content in sprouted grain.

Pre-harvest sprout is difficult to control in a field situation since rainfall is unpredictable. Planting varieties that have a moderate amount of seed dormancy is the best solution to prevent PHS and loss in seed quality. Currently, little research has been conducted on determining the varying levels of seed dormancy between different soft white winter wheat varieties. The goal of this study is to investigate the degree of grain

dormancy in 45 lines of soft white winter wheat. Knowing a variety's level of dormancy under different conditions would allow growers to be more selective on the variety they grow if they consistently have low seed quality and reduced yield due to PHS. Every variety behaves differently from year to year since environmental growing conditions are never the same and germination conditions vary greatly. This study will investigate if older cultivars have a higher level of post-harvest dormancy compared to more recently released cultivars. This would indicate if dormancy has been selected against over time. However, if older varieties show the same germination trends as recently released wheat cultivars, it demonstrates soft white winter wheat has always lacked seed dormancy. Determining grain dormancy expression between different varieties would allow breeders to make crosses and select breeding lines that would have a higher dormancy expression. This would ultimately result in a new variety with reduced susceptibility to PHS. Increased PHS resistance would reduce the loss experienced by growers when a rainfall event occurs prior to harvest. By determining the degree of dormancy expression of a large number of commercially available varieties, it will help breeders in determining the aim of their breeding programs to try and avoid economic losses due to PHS.

Materials and Methods

Plant Materials

Small seed samples from thirty-eight different varieties were gathered from a thesis study conducted by Colleen Roseborough at Oregon State University in 2013. Roseborough's research examined glutenin proteins in soft white winter wheat cultivars grown in the Pacific Northwest over the past sixty-four years. One additional variety

from New York and six experimental lines were added to the experiment during the second year. Seed of the New York cultivar, Cayuga, was provided by Dr. Mark Sorrells from Cornell University and the six experimental lines that had Cayuga as one of the parents were provided by the Oregon State University wheat breeding program. The soft white winter wheat cultivars examined included: ‘Alba’, ‘Bitterroot’, ‘Bobtail’, ‘Brevor’, ‘Bruehl’, ‘Brundage’, ‘Brundage 96’, ‘Bruneau’, ‘Cara’, ‘Cayuga’, ‘Coda’, ‘Daws’, ‘Elmar’, ‘Eltan’, ‘Gaines’, ‘Gene’, ‘Goetze’, ‘Hill 81’, ‘Hyslop’, ‘Kaseberg’, ‘Ladd’, ‘Lewjain’, ‘Madsen’, ‘Malcolm’, ‘Mary’, ‘Nugaines’, ‘Omar’, ‘ORCF-101’, ‘ORCF-102’, ‘ORCF-103’, ‘ORSS-1757’, ‘Rely’, ‘Rod’, ‘Rosalyn’, ‘Skiles’, ‘Stephens’, ‘Tubbs’, ‘Tubbs-06’, ‘Xerpha’ and six experimental crosses 11-225-1C, 11-225-2C, 11-225-3C, 11-225-5C, 11-225-6H, and 11-225-7H. A table of the varieties with their year of release can be found in Appendix 1.

Field Plots Year 1

In the first year, seed from all the varieties except Cayuga and the six experimental crosses were planted in a 2:1 pattern in October, 2014 using a Hege head row planter (Salt Lake City, Utah) at OSU’s Hyslop Research farm in Corvallis, Oregon. A 2:1 planting pattern consists of two varieties that are planted in a plot with two rows missing between the different varieties and the following plot has one variety planted in the center of the plot with two rows missing plants on both sides and then the pattern repeats itself. Two replications (reps) from each variety were planted except for Alba and Bruehl, due to there only being enough seed for one replication. The plots were sprayed with Harmony and Tribenuron (DuPont, Wilmington, Delaware) at 0.07 L/ha on January

29th, 2015, 2,-4-D (Dow, Midland, Michigan) at 0.10 L/ha on February 19th, 2015, Powerflex and Huskie (Dow, Midland, Michigan; Bayer, Barmen, Germany) at 0.15 L/ha and 1.02 L/ha on March 20th, 2015, Quilt Xcel (Syngenta, Basel, Switzerland) at 1.02 L/ha on April 6th, 2015, and Prosaro (Bayer, Barmen, Germany) at 0.60 L/ha on May 5th, 2015 for weed control and disease prevention. The plots were preventively sprayed since many of the cultivars are susceptible to stripe rust (*Puccinia striiformis*) and Septoria (*Pyrenophora tritici-repentis*). The plots were fertilized with 89.67 kg/ha of nitrogen of 40-0-0-5.6 in late March, 2015. Notes on stand establishment and potential disease pressure were taken throughout the spring as the plants developed. Heading dates were taken when 50% of the spikes in the plot were above the collar of the primary leaf. The plots were continually monitored and each line's physiological maturity date was recorded when the peduncle turned from green to tan in color.

All the plots were harvested on August 4th, 2015 by hand sickling the individual heads. All of the heads from each cultivar were placed into a 25.73 cm x 17.15 cm x 36.53 cm brown paper bag (Duro, Florence, Kentucky) with a label containing the variety name and replication number. On the same day, the wheat heads were threshed using a Wintersteiger LD 350 Stationary thresher (Salt Lake City, Utah). The threshed seeds were then cleaned with a Hege small sample seed cleaner (Salt Lake City, Utah) and placed into a clear plastic container with a label containing the variety and rep. Seed moisture and test weight was taken using seed from the bulk plastic container and recorded for each plot twenty-four hours after harvest (Appendix 2). A few of the plots did not produce enough seed for measuring test weight so moisture and test weights of

these plots were not recorded. Once the seed had been cleaned, two 100 seed samples were collected using an Old Mill Company 850-2 (Knoxville, Tennessee) seed counter from every plot. Any damaged or broken seeds were eliminated during the seed counting process. One of the 100 seed counts was placed in a coin envelope labeled '4°C' along with the variety and rep number, while the second 100 seed count was placed in a coin envelope labeled '20°C' with the variety and rep number. All of the 100 seed counts were placed in two boxes based on the treatment, 4°C or 20°C.

Dry Seed Storage and Germination (Trial 1)

Every 100 seed sample was placed in a common room over night with a temperature near 25.5°C. Twenty-four hours after harvest, the 100 seed samples were placed in their designated treatment location at either 4°C with a relative humidity around 34% or 20°C with a relative humidity around 47%. These samples were kept in their treatment areas for fourteen days. They were then both placed in a room temperature chamber for seven days with a temperature of 20°C and 47% relative humidity.

In preparation for the germination test, brown germination paper was cut into circles to fit into the bottom of a 100 x 15 mm petri dish (VWR, Radnor, Pennsylvania). The petri dishes were labeled with the variety name, rep, treatment temperature and a group number. On the seventh day the seeds were removed from the room temperature chamber. Every 100 seed sample for every treatment, variety and rep were split into two groups of 50 (group 1 and group 2) for the germination trial. The germination paper was saturated with ultrapure water and placed in the bottom of a petri dish. Fifty seeds were placed on the germination paper with the embryo facing up and the crease of the seed

facing down for each experimental unit. After the seeds were placed in the petri dishes, the petri dishes were placed into a 26.82 cm x 27.31 cm (gallon) Ziploc bag and placed in a dark germination chamber. The Ziploc bag ensured the petri dishes would remain at 80% to 100% humidity. The germination chamber was set at 20°C and the seeds were kept in complete darkness while in the chamber.

The seeds were monitored every twenty-four hours for germination and to ensure the germination paper did not dry out. Once the seeds had germinated, they were counted and removed from the petri dish. The germination date and the number of seeds that had germinated were recorded each day. Germination was classified as complete with the emergence of the radicle and the coleoptile. The seeds were left in the germination chamber for a total of seven days. The seeds that began to mold throughout the trial period were removed from the petri dish and the date of removal was noted. The seeds that did not germinate or mold after seven days were removed and counted. They were then tested for viability by a tetrazolium treatment (Christina de Carvalho et al., 2013). This was done by cutting down the crease of the seed, which cut the embryo in half. The seed halves were then placed and left in the tetrazolium treatment for five minutes. The embryos that turned pink were classified as viable but dormant. The embryos that remained white were classified as non-viable and were eliminated from the total number of seeds tested from that variety.

Imbibed Seed Germination (Trial 2)

Two weeks after the field nursery was harvested, a second germination and dormancy trial was conducted based on the AOSA protocol (Association of Official Seed

Analysts, Table 6A, 2014). In preparation for the germination test, brown germination paper was cut into circles to fit into a petri dish and petri dishes were labeled with the variety, rep, treatment and a group number. Two separate 100 seeds counts were taken from the bulk plastic container for each experimental plot. The seeds were then placed in coin envelopes. The two treatments were a 4°C and 20°C germination temperature. The seeds were then further divided down into two 50 seed samples (group 1 and group 2) for each plot. The following day, fifteen days after harvest, saturated germination paper were placed in petri dishes and 50 seeds were placed on the wet germination paper. The seeds were imbibed overnight for twelve hours in a dark germination chamber at 20°C at 80-100% humidity.

After seeds were imbibed, the samples labeled 4°C were moved to a cold storage unit at 4°C and 100% relative humidity in complete darkness. These samples were left at 4°C for seven days after being imbibed and were monitored daily to ensure the germination paper remained saturated. The other samples in the 20°C treatment, remained in the germination chamber at 20°C at 80-100% humidity in complete darkness. These samples were also monitored daily to ensure that germination paper remained moist. Each day, petri dishes were checked for germination and after being counted, germinated seeds was removed and the data were recorded.

After seven days following imbibition, the petri dishes in the cold storage treatment unit were removed and brought to the germination chamber at 20°C with the remaining seeds from the 20°C treatment. All samples from the 4°C treatment were counted for the number of seeds that had germinated in the first seven days while at 4°C

prior to being placed in the 20°C chamber. The germinated seeds were recorded and removed. The petri dishes were again monitored daily for adequate moisture and seed germination. The seeds were removed and date of germination was recorded as they germinated. The seeds that molded were removed as the mold occurred. Any seed remaining in the petri dishes after seven days in the 20°C chamber were removed and counted. They were then tested for viability by a tetrazolium test. Embryos that turned pink were classified as viable but dormant, while the seeds with embryos that remained white were classified as non-viable and were eliminated from the total number of seeds tested from that variety.

Field Plots Year 2

The following October, the remaining seed from each cultivar were used for fall planting in Corvallis and Pendleton, Oregon. The variety Cayuga, provided by Dr. Mark Sorrells at Cornell University was added to the experiment as a check cultivar since it had been reported to express dormancy (Munkvold et al., 2009). Six experimental lines that came from crosses with Cayuga were also added to the experiment as additional lines. The seed from each variety and experimental lines were weighed out into 150 g samples and treated with Cruisermaxx (Syngenta, Basel, Switzerland). The seed was treated to protect against a wide spectrum of early season insects and diseases that would harm the germinating seed. At the Corvallis location, three replications of the entries were planted with 50 g of seed in each plot. They were planted in 1.52 m x 4.57 m plots with a Hege seven row seed planter (Salt Lake City, Utah). In Pendleton, OR, two replications of the

entries were planted with 75 g of seed in 1.52 m x 4.57 m plots using a Hege five row seed planter (Salt Lake City, Utah).

Plots at both locations were monitored for disease and weed pressure. Notes on stand establishment and disease pressure were taken throughout the spring as the plants developed to ensure the disease did not confound seed development or yield. All the plots in Corvallis were sprayed with Quilt Xcel (Syngenta, Basel, Switzerland) on March 30th, 2016 and again on April 26th, 2016 at a rate of 1.02 L/ha to protect the plants against stripe rust and Septoria. 89.67 kg/ha of nitrogen of 40-0-0-5.6 was applied on March 18th, 2016 and two weeks later, 33.63 kg/ha of nitrogen of 40-0-0-5.6 was applied at the Corvallis location. In Pendleton, all the plots were sprayed with Axiom DF (Bayer, Barmen, Germany) at a rate of 0.73 L/ha on October 28, 2015, and Huskie at 0.95 L/ha (Bayer, Barmen, Germany), Powerflex HL (Dow, Midland, Michigan) at 0.15 L/ha and Fitness at 0.29 L/ha (Loveland, Greenville, Mississippi) on April 1st, 2016, to protect the plants against rust and fungi. The plots in Pendleton also received 123.29 kg/ha of nitrogen, 26.90 kg/ha of P₂O₅, 14.57 kg/ha of sulfur of 32+phos solution + thiosul solution on June 26th, 2015. Heading dates in Corvallis were taken when 50% of the base of the spike in a plot were above the collar of the flag leaf. The plots were monitored for plant and seed maturity.

As the seed kernels reached the hard dough stage at the Hyslop Research Farm, five heads were snapped from each plot and placed in a 16.5 cm x 14.9 cm (sandwich size) Ziploc bag with the variety name, replication number and the date the heads were collected. The hard dough stage was distinguished when the outside seed in the third row

up from the base of the spike became hard and was difficult to dent with a fingernail. The Ziploc bags were then taken to a -80°C chamber for future testing for alpha-amylase content or germination prior to an after-ripening period. This collection stage was targeted to ensure an after-ripening period did not occur in the field setting.

All the plots in Pendleton, OR were harvested on August 2nd, 2016 and the plots in Corvallis, OR were harvested on August 15th, 2016 using a Hege combine (Salt Lake City, UT). The harvested seed was placed into a 35.56 cm x 45.75 cm cloth bag. The labels contained the variety and replication of each individual plot. All of the plots were taken and cleaned through a Hege seed cleaner (Salt Lake City, Utah) and two 6.35 cm x 10.80 cm coin envelopes were filled with approximately 3,000 seeds. One coin envelope would be used for germination trials while the other would be stored in a -80°C chamber in case additional germination trials needed to be conducted. The remaining seed was then placed back in the cloth bag with the appropriate labels. The remaining seed was used to test for moisture, protein content and test weight for every plot (Appendix 3). Once the seed had been cleaned, ten 50 seed count samples were counted out from every plot. Any damaged or broken seed were eliminated during the seed counting process. All of the 50 seed counts were placed in a 6.35 cm x 10.80 cm coin envelope labeled either 4°C , 10°C , 20°C , 30°C or 40°C along with the location, variety and rep number. Every plot had a total of 100 seeds for each of the five temperature treatments. The seeds for each treatment were labeled either group 1 or group 2 for each plot.

Based on the results from the Pendleton, OR germination tests, the 40°C temperature was dropped from the trials on the seed harvested from Corvallis, OR. The

40°C temperature severely reduced the viability of the seed, which resulted in nearly all of the seed molding. With having a very low number of seeds that germinated, there were insufficient results to run any statistical analysis on the data, and therefore, the temperature was dropped from the experiment.

Germination Tests (Year 2)

In preparation for germination tests, brown germination paper was cut into circles to fit into a petri dish and the petri dishes were appropriately labeled. The following day, within 48 hours after harvest, saturated germination paper with ultrapure water were placed into petri dishes and 50 seeds were placed on the wet germination paper. After the seeds were in the petri dish, additional water was added to ensure the seeds had adequate moisture by moistening the germination paper to the point where the paper glistened but not to the point where the seeds were partially submerged in water. The petri dishes were then placed into a 0.77 cm x 0.79 cm (gallon) Ziploc bag to ensure the germination paper would not dry out due to evaporation during the experiment. Each Ziploc bag contained four petri dishes and two different cultivars. The petri dishes with seeds were imbibed overnight in growth chambers set at either 4°C, 10°C, 20°C or 30°C in the dark at 80-100% humidity. The seeds were kept at the temperature they were imbibed at for the duration of the experiment.

After imbibition, the petri dishes were monitored daily to ensure the germination paper remained saturated and the relative humidity remained between 80-100% in the petri dish. Water was added when the germination paper was no longer glistening. Germination counts were taken each day. Germinated seeds were counted and removed

from each petri dish and the number of seeds removed were recorded. Seed was considered germinated when both the coleoptile and radical were visible. Seed that began to mold throughout the germination trial were removed and counted as non-viable. The seed germination trial ran for a total of fourteen days for each location separately.

Seeds that remained in the 30°C (for both Pendleton and Corvallis germination trials) and 40°C chamber (for the Pendleton germination trial) were moved to a 20°C chamber after nine days. This was to determine the number of seeds that remained viable but didn't germinate due to potential dormancy expression. Seeds were then continually counted until the fourteenth day of the trial or until all treatments reached 100% seed germination. There were not any seeds that did not germinate or mold by the fourteenth day, so there were no seeds to test for viability with tetrazolium from either location.

Falling Number

In 2016, summer rainfall occurred in both Pendleton, OR and in Corvallis, OR between when plants reached the hard dough stage and when the plots were harvested. The plots in Corvallis, OR received an additional rain event two days prior to harvest. Weekly rainfall data and temperature averages were recorded through the summer months at both locations (Appendix 4). With additional rain, a falling numbers test was run on each sample from both locations to determine whether alpha-amylase activity was present in seed during the second year of the study. Three hundred grams of seed from each entry and replication was tested. A 25 g sub-sample was then taken and milled in a Perten Laboratory Hammer mill (LM 3100, Perten Instruments, Inc., Springfield, IL). The mill was cleaned between each sample and an initial 15 g sample was run through

the mill before the sample used for the falling number test was milled. In between each sample run through the mill, the mill was cleaned to remove any residual flour in order to avoid contamination. The 25 g sample of flour was then placed in a 16.5 cm x 14.9 cm Ziploc bag to be used to run a falling numbers test.

The falling number test followed the protocol using the Perten Falling Number instrument with the AACC International Method 56-81.03. To run the falling numbers test, two 7 g flour samples were taken and added to two Perten Falling Numbers tubes. Next, 25 mL of deionized water (DI water) was added to each tube. A stopper was then placed over the opening of each tube, which was then placed into a Perten Shakematic (SM 1095, Perten Instruments, Inc., Springfield, IL), which mixed the flour and water together. Each tube was turned upside down to ensure all of the flour was thoroughly mixed in with the water after shaking. Falling number plungers were then used to scrape the residual slurry from the side of each tube and then the plungers were placed in each tube. The tubes with the plungers were then placed into a Perten Falling Number apparatus (FN 1700, Perten Instruments, Inc., Springfield, Illinois) boiling water bath (100°C). The flour suspension in the tubes is first exposed to boiling water in a water bath for five seconds inside the instrument and then the plungers are engaged. The flour suspension is then mixed for 60 seconds by the plungers moving up and down in the tubes. Next, the plungers move to the top of the tubes and are released. This allowed the plungers to fall freely through the slurry. The recorded falling number is then based on the time (in seconds) it takes for the plunger to reach the bottom of the tube plus 60 seconds for the time needed to mix the flour suspension.

The falling number test was run in pairs in order to achieve a good representation of the plot and to detect variability within a plot. If the falling number between the two replications was greater than 35 seconds, it indicated the coefficients of variation was too high, which could be the result of a potential error. Error could be due to differences between temperatures in the boiling water bath or large differences between the two samples. When this occurred, two additional samples were taken and run through the falling numbers test and compared. By running additional tests, it increased the precision of the results to reduce potential for error.

Single Kernel Hardness

Single Kernel Hardness data was collected using the Single Kernel Characterization System (SKCS) machine made by Perten (AACC International Method 55-31.01). Using the SKCS machine, the kernel hardness data was gathered by determining the seed's resistance to a crushing force between two metal plates. All cracked or broken seeds were removed before the seeds were placed into the machine so the hardness data is gathered on only whole, non-damaged kernels. A minimum of 200 seeds were used for each run of the machine from a given sample. Every variety and replication from both locations were run through the SKCS machine twice. This resulted in the average kernel hardness from 400 seeds from each plot. The hardness index was calculated by the average crushing force from a given variety. The SKCS machine measured the kernel hardness, diameter and moisture. The data from the SKCS was reported in hardness units (HU).

Statistical Analysis

Year 1 Germination Statistics

A full-factorial two-way analysis of variance (ANOVA) was computed the same for both germination trials in the first year. The two different trials were analyzed and computed separately. An ANOVA was run for each day of germination for the two dry storage temperatures and/or germination temperatures as the first factor and the thirty-eight varieties as the second factor. Each day was computed separately due to the continuous change in total germination percentage throughout the trial. The two temperature treatments were also computed separately and compared. The ANOVA was computed in an Excel spreadsheet (Microsoft Excel (2013), Redmond, Washington) which determined the significant differences between varieties and temperatures for each day of the trail. For the days in which the ANOVA results indicated significance between the varieties, a least significant difference test (LSD) was run on the varieties germination counts with a 0.05 significance level. The LSD test was used to determine which varieties were statistically different from each other for germination rate. The two dry storage temperatures and/or germination temperatures were kept separate for the LSD test. The LSD test was run using SAS JMP (SAS Institute Inc., Cary, North Carolina) with the fit Y by X function was run for each temperature separately for each day. The X factor was set as the varieties and the Y response was the day that was being analyzed.

Year 2 Germination Statistics

A full-factorial two-way ANOVA was run for each day of germination with the four temperatures as one factor and the forty-five different varieties the second factor

initially. The ANOVA tables were computed on an Excel spreadsheet (Microsoft Excel (2013), Redmond, Washington). Each location was run in a separate analysis and were not combined. When the ANOVA table indicated there were significant differences between temperatures and varieties, a separate ANOVA was run for each temperature and location separately. For every day the ANOVA table indicated there were significant differences between varieties, an LSD test was computed to determine the significant differences between the varieties germination rates for each day with a 0.05 significance level. The LSD test was run using SAS JMP (SAS Institute Inc., Cary, North Carolina) with the fit Y by X function was run for each temperature and location separately for each day. The X factor was set as the varieties and the Y response was the day that was being analyzed. The average for each variety was also computed, which was the average from all field replications, for a total average of 200 seeds from Pendleton and 300 seeds from Corvallis for each variety at each temperature.

Year 2 Falling Number Statistics

An ANOVA was run on the falling number data that was collected from each location separately, which investigated if there were any statistical differences between the varieties as well as between the field replications. The ANOVA tables were computed in an Excel spreadsheet (Microsoft Excel (2013) Redmond, Washington). When the results from the ANOVA table showed there were significant differences among varieties, an LSD test was performed using SAS JMP (SAS Institute Inc., Cary, North Carolina) with the fit Y by X function. The X factor was set as the varieties and the Y response was the average of the falling number results for each variety.

Year 2 Single Kernel Hardness Statistics

An ANOVA was run on the kernel hardness data that was collected from each variety and replication at each location. The analysis was done for each location separately. The ANOVA tables were computed in an Excel spreadsheet (Microsoft Excel (2013) Redmond, Washington). If the ANOVA table showed there were statistical differences between the kernel hardness of the varieties tested, an LSD test was run to determine the statistical differences between the varieties. An LSD test was performed using SAS JMP (SAS Institute Inc., Cary, North Carolina) to make all pair-wise comparisons of means on all the varieties kernel hardness data.

Results

Year 1 Trial 1

A list of summary statistics is listed in Appendix 5. The ANOVA for the first trial showed there were statistical differences between the two dry seed storage temperatures. The second day after the seeds were imbibed through the fourth day of the germination trial, there were differences in the interaction between storage temperature and the varieties as well as differences between the variety's germination rate and the temperatures the seeds were stored at for three weeks. On the third and fourth day of the germination trial, there were also differences between the field replications. On the fifth day, there were only significant differences in the interaction between the varieties and storage temperature as well as between the varieties.

Since the analysis showed there were significant differences in germination among the varieties, a least significant difference test (LSD) was run on the varieties

germination count for the second through the fifth day to determine which varieties were statistically different from each other. Tables 3.01-3.04 show the results of the LSD test with a significance level of 0.05 for the four days from the germination counts from the 20°C dry storage treatment followed by the 4°C dry storage treatment. Days one and six are not included since there was no significant differences observed for the varieties due to 0% germination (day 1) and 100% germination (day 6). Each letter indicates a significant difference from all other varieties that do not share common letters. The average for each variety is also included on the far right side, which is the average from both replications, for an average of 200 seeds from each variety at each dry storage temperature.

20°C Dry Storage Treatment LSD Test Analysis

Within forty-eight hours of the seed being placed in the 20°C germination chamber, the varieties Eltan and Lewjain had the highest number of seed that had germinated with an average of 92% and 81%, respectively (Table 3.01B). Lewjain was not found to be statistically different than the varieties Rely, Stephens, Bruneau, Rod, Coda and Omar. The lowest germinating varieties were Mary, Alba, Bruehl, and Rosalyn.

By the third day, Brevor was the lowest germinating variety with a germination of 92% (Table 3.02B). By this day, 13 varieties had completed germination, which were: Alba, Bitterroot, Bobtail, Gaines, Madsen, Rosalyn, Brundage 96, Bruneau, Cara, Skiles, Stephens, Tubbs-06 and Xerpha. On the fourth day, the variety Brevor still had the lowest germination rate, with 96% of the seeds germinated (Table 3.03B). It was not statistically different than the varieties Rod and Lewjain, in which 98% of the seeds had germinated.

There were 19 varieties that had 100% seed germination on this day. By the fifth day, there were no significant differences between varieties.

4°C Dry Storage Treatment LSD Test Analysis

On the second day of seeds that were stored at 4°C being placed in the 20°C germination chamber, the varieties Lewjain, Xerpha, Eltan, Bitterroot, Rod and Tubbs were the highest germinating varieties, even though all of the varieties except Lewjain were not significantly different than other varieties (Table 3.01A). The lowest germinating variety was ORSS-1757 with 21% seed germination, which was not significantly different than 16 other varieties. By the third day, 10 varieties had reached 100% seed germination, which were Alba, Bitterroot, Daws, Gene, Bruehl, Tubbs, Brundage 96, Bruneau, Cara and Hill 81. The lowest germinating variety was Brevor, with 78% seed germination, and it was statistically lower than all of the other varieties.

On the fourth day, there were 17 varieties that reached 100% seed germination (Table 3.03A). The lowest germinating variety remained Brevor with 91% seed germination, and it remained statistically different than all of the other varieties. By the fifth day, all varieties except for Lewjain, Brevor, Skiles, Rod, Malcolm and Hyslop had reached 100% seed germination (Table 3.04A). Lewjain had the lowest number of germinated seeds with 97% germination which was statistically different from other varieties. The following day, all of the remaining seeds had germinated.

Table 3.02. Percent germination at 20°C on day three from dry seed storage at 4°C (Table 3.02A) and at 20°C (Table 3.02B) in 2014-2015. Letters denote difference in significance based on a 0.05 LSD.

Table 3.02A

4°C Day 3	Corvallis						
Variety	Mean						
Alba	100.0	A					
Bitterroot	100.0	A					
Daws	100.0	A					
Gene	100.0	A					
Bruehl	100.0	A					
Tubbs	100.0	A					
Brundage 96	100.0	A					
Bruneau	100.0	A					
Cara	100.0	A					
Hill 81	100.0	A					
Bobtail	99.5	A B					
Mary	99.5	A B					
Brundage	99.5	A B					
ORCF-101	99.5	A B					
Rely	99.5	A B					
Xerpha	99.5	A B					
Coda	99.0	A B C					
Eltan	99.0	A B C					
Goetze	99.0	A B C					
Madsen	99.0	A B C					
ORCF-102	99.0	A B C					
Rosalyn	99.0	A B C					
Kaseberg	99.0	A B C					
Gaines	98.5	A B C D					
ORCF-103	98.5	A B C D					
Tubbs-06	98.5	A B C D					
Elmar	98.0	A B C D E					
ORSS-1757	98.0	A B C D E					
Ladd	98.0	A B C D E					
Hyslop	97.5	A B C D E					
Skiles	97.5	A B C D E					
Stephens	97.0	B C D E					
Omar	96.5	C D E					
Nugaines	96.0	D E F					
Lewjain	95.5	E F G					
Rod	93.5	F G					
Malcolm	93.0	G					
Brevor	77.5						H

Table 3.02B

20°C Day 3	Corvallis						
Variety	Mean						
Alba	100.0	A					
Bitterroot	100.0	A					
Bobtail	100.0	A					
Gaines	100.0	A					
Madsen	100.0	A					
Rosalyn	100.0	A					
Brundage 96	100.0	A					
Bruneau	100.0	A					
Cara	100.0	A					
Skiles	100.0	A					
Stephens	100.0	A					
Tubbs-06	100.0	A					
Xerpha	100.0	A					
Coda	99.5	A B					
Eltan	99.5	A B					
Gene	99.5	A B					
Goetze	99.5	A B					
Hill 81	99.5	A B					
Kaseberg	99.5	A B					
ORCF-102	99.5	A B					
ORCF-103	99.5	A B					
Mary	99.5	A B					
Bruehl	99.0	A B					
Elmar	99.0	A B					
Hyslop	99.0	A B					
Omar	99.0	A B					
ORCF-101	99.0	A B					
Malcolm	99.0	A B					
Tubbs	99.0	A B					
Nugaines	99.0	A B					
Ladd	99.0	A B					
ORSS-1757	98.5	A B C					
Rely	98.5	A B C					
Brundage	98.0	A B C					
Rod	97.5	B C					
Lewjain	97.5	B C					
Daws	96.5	C					
Brevor	92.0	D					

Table 3.03. Percent germination at 20°C on day four from dry seed storage at 4°C (Table 3.03A) and at 20°C (Table 3.03B) in 2014-2015. Letters denote difference in significance based on a 0.05 LSD.

Table 3.03A

4°C Day 4	Corvallis		
Variety	Mean		
Alba	100.0	A	
Bitterroot	100.0	A	
Tubbs	100.0	A	
Kaseberg	100.0	A	
Bruehl	100.0	A	
Ladd	100.0	A	
Brundage 96	100.0	A	
Bruneau	100.0	A	
Cara	100.0	A	
Mary	100.0	A	
Daws	100.0	A	
Elmar	100.0	A	
ORCF-101	100.0	A	
Gaines	100.0	A	
Gene	100.0	A	
ORSS-1757	100.0	A	
Hill 81	100.0	A	
Bobtail	99.5	A B	
Brundage	99.5	A B	
Coda	99.5	A B	
Goetze	99.5	A B	
Madsen	99.5	A B	
ORCF-102	99.5	A B	
Malcolm	99.5	A B	
Rely	99.5	A B	
Rosalyn	99.5	A B	
Tubbs-06	99.5	A B	
Xerpha	99.5	A B	
Eltan	99.0	A B	
Hyslop	98.5	A B C	
Omar	98.5	A B C	
ORCF-103	98.5	A B C	
Nugaines	98.0	A B C	
Rod	98.0	A B C	
Skiles	97.5	B C	
Stephens	97.5	B C	
Lewjain	96.5	C	
Brevor	91.0		D

Table 3.03B

20°C Day 4	Corvallis		
Variety	Mean		
Alba	100.0	A	
Bitterroot	100.0	A	
Bobtail	100.0	A	
Ladd	100.0	A	
Madsen	100.0	A	
Mary	100.0	A	
Brundage 96	100.0	A	
Bruneau	100.0	A	
Cara	100.0	A	
ORSS-1757	100.0	A	
Rely	100.0	A	
Rosalyn	100.0	A	
Skiles	100.0	A	
Gaines	100.0	A	
Stephens	100.0	A	
Tubbs	100.0	A	
Tubbs-06	100.0	A	
Xerpha	100.0	A	
Kaseberg	100.0	A	
Coda	99.5	A B	
Daws	99.5	A B	
Eltan	99.5	A B	
Gene	99.5	A B	
Goetze	99.5	A B	
Hill 81	99.5	A B	
Nugaines	99.5	A B	
Omar	99.5	A B	
ORCF-101	99.5	A B	
ORCF-102	99.5	A B	
ORCF-103	99.5	A B	
Malcolm	99.5	A B	
Bruehl	99.0	A B C	
Elmar	99.0	A B C	
Hyslop	99.0	A B C	
Brundage	98.0	B C	
Lewjain	97.5	C D	
Rod	97.5	C D	
Brevor	96.0		D

Table 3.04. Percent germination at 20°C on day five from dry seed storage at 4°C in 2014-2015. Letters denote difference in significance based on a 0.05 LSD.

Table 3.04

4°C Day 5		Corvallis		
Variety	Mean			
Alba	100.0	A		
Bitterroot	100.0	A		
Bobtail	100.0	A		
Tubbs-06	100.0	A		
Bruehl	100.0	A		
Brundage	100.0	A		
Brundage 96	100.0	A		
Bruneau	100.0	A		
Cara	100.0	A		
Coda	100.0	A		
Daws	100.0	A		
Elmar	100.0	A		
Eltan	100.0	A		
Gaines	100.0	A		
Gene	100.0	A		
Goetze	100.0	A		
Hill 81	100.0	A		
Xerpha	100.0	A		
Kaseberg	100.0	A		
Ladd	100.0	A		
Madsen	100.0	A		
Mary	100.0	A		
Nugaines	100.0	A		
Omar	100.0	A		
ORCF-101	100.0	A		
ORCF-102	100.0	A		
ORCF-103	100.0	A		
ORSS-1757	100.0	A		
Rely	100.0	A		
Rosalyn	100.0	A		
Stephens	100.0	A		
Tubbs	100.0	A		
Hyslop	99.5	A	B	
Malcolm	99.5	A	B	
Rod	99.0		B	C
Skiles	99.0		B	C
Brevor	98.5			C
Lewjain	97.0			D

Year 1 Trial 2

The ANOVA summary statistics for the second trial are listed in Appendix 6. The ANOVA for the second trial showed there were statistical differences between the two temperatures 4°C and 20°C. The second day after the seeds were imbibed, there was a difference for the interaction between the varieties and the temperature as well as a difference between the varieties and between the temperatures. For days three and four, the only significant differences detected were differences in germination between the two different temperatures. On the fifth and sixth days, all of the seeds had germinated in the 20°C treatment while none of the seeds had been counted in the 4°C treatment. Due to a consistency in germination rates, statistics were unable to be run on these two days. As the seeds from the 4°C treatment were moved to the 20°C germination chamber, the seeds were counted prior to being placed in the new treatment. On this day, the seventh day after imbibition, there were significant differences in the interaction between the varieties and the temperatures as well as differences between varieties and temperatures. These factors stayed significant up until the twelfth day, when all seeds had completed germination. By the time the seeds in the 4°C treatment were moved to be placed in the 20°C chamber, all the seeds in the 20°C treatment had completed germination, and therefore, there was no overlapping time for seed germination between the two different temperatures. This explains the significant difference between the two temperatures. There were no significant differences between replications for any of the days throughout the trial. Since the analysis showed there were significant differences in germination among the varieties, a least significant difference test (LSD) was run on the varieties

germination count for the second, seventh, eighth, ninth, tenth and eleventh day to determine which varieties were significantly different from each other for germination rate.

Tables 3.05-3.07 show the results of the LSD test with a significance level of 0.05 for days two, seven, eight, nine, ten and eleven from the germination counts from the 20°C treatment followed by the 4°C treatment. Days three, four, five, six, and twelve are not included since the ANOVA table did not indicate significant differences. The 20°C treatment reached full germination by the fifth day and the 4°C treatment began germination counts on the seventh day, in which they were counted before they were moved into the 20°C chamber. The average for each variety is also included, which is the average from both field replications, for an average of 200 seeds from each variety at each temperature.

20°C Treatment LSD Test Analysis Year 1 Trial 2

Within forty-eight hours of the seeds being placed in the different temperature treatments, the variety Lewjain had the highest number of seeds that had germinated with an average of 77% germination. Lewjain was then followed by the varieties Bruehl, Eltan, Elmar, Hill 81 and Omar, in which Elmar, Hill 81 and Omar were not significantly different than Madsen, Coda, Rod, Bitterroot, Brundage 96, while Hill 81 and Omar were also not significantly different than the variety Gaines. The lowest germinating variety was Rosalyn with 4% germination. Other cultivars that grouped in the low germination group were ORSS-1757, Brevor, Skiles, Goetze, Tubbs, Ladd, Brundage, ORCF-101, Mary, Bobtail, Stephens and Kaseberg with a germination percentage ranging from 5-

16%. These varieties, other than Rosalyn, also were not significantly different than several other varieties.

By the third day, the variety Bruehl was the lowest germinating variety with a germination of 97%. By this day, majority of the seeds had completed germination and the ANOVA analysis showed there were no statistical differences between varieties.

4°C Treatment LSD Test Analysis Year 1 Trial 2

On the seventh day when the seeds were removed from the 4°C treatment and prior to them being placed in the 20°C temperature, Bruehl, Eltan and Bitterroot were the highest germinating varieties with an average germination ranging from 56.5-64%. The lowest germinating variety was ORSS-1757 with 1% seed germination. Other cultivars that were grouped at the low germination range were Nugaines, Mary, Rosalyn, ORCF-102, Malcolm, Ladd, ORCF-103, Kaseberg, ORCF-101, Rely, Madsen, Stephens, Skiles and Gene. After these seeds were moved to the 20°C temperature and had been at this temperature for twenty-four hours, many of the varieties had greatly increased in total germination. All of the varieties, except for Bruehl, ORCF-103 and Rod did not fall in the first significance category for highest germination percentage. The varieties Rod and ORCF-103 were the lowest significant germinating varieties with an average seed germination of 92.5% and 94% respectively.

By the ninth day, Bruehl was the slowest germinating variety with 97% seeds germination. All the other varieties, except for Mary and Bruehl, were not significantly different from each other. On the tenth day, Bruehl remained the slowest germinating variety and nothing had germinated since the previous day. All of the varieties except for

Brevor, Mary, Rosalyn and Bruehl fell into the first significance category. The first significance category for the highest germinating varieties ranged from 99.5-100% seed germination. The second significance category ranged from 99-99.5% seed germination with overlap in significance of those varieties that had 99.5% seed germination. Even though it was found to be statistically significant, the difference between 98% and 100% germination is not biologically significant. The eleventh day had similar results, where the variety Bruehl remained at 97% seed germination and it remained significantly lower than all of the other varieties. All varieties except for Brevor, Tubbs, Tubbs-06, ORCF-103, Rosalyn and Bruehl had reached 100% germination. Brevor, Tubbs, Tubbs-06, and ORCF-103 were not significantly different from the varieties that had reached 100% germination.

Table 3.06. Percent germination at 4°C on day eight (Table 3.06A) and day nine (Table 3.06B) in 2014-2015. Letters denote difference in significance based on a 0.05 LSD.

Table 3.06A

4°C Day 8	Corvallis		
Variety	Mean		
Alba	100.0	A	
Bitterroot	100.0	A	
Bobtail	100.0	A	
ORCF-102	100.0	A	
Nugaines	100.0	A	
Brundage	100.0	A	
Brundage 96	100.0	A	
Bruneau	100.0	A	
Hill 81	100.0	A	
Coda	100.0	A	
Malcolm	100.0	A	
Hyslop	100.0	A	
Madsen	100.0	A	
Gaines	100.0	A	
Gene	100.0	A	
Kaseberg	100.0	A	
ORSS-1757	100.0	A	
Elmar	99.5	A B	
Goetze	99.5	A B	
Ladd	99.5	A B	
Omar	99.5	A B	
ORCF-101	99.5	A B	
Cara	99.5	A B	
Tubbs-06	99.5	A B	
Lewjain	99.0	A B	
Eltan	99.0	A B	
Daws	99.0	A B	
Rosalyn	99.0	A B	
Skiles	99.0	A B	
Stephens	99.0	A B	
Tubbs	99.0	A B	
Xerpha	99.0	A B	
Rely	98.5	A B	
Mary	98.5	A B	
Brevor	98.0	A B	
Bruehl	97.0	B	
ORCF-103	94.0		C
Rod	92.5		C

Table 3.06B

4°C Day 9	Corvallis		
Variety	Mean		
Alba	100.0	A	
Bitterroot	100.0	A	
Bobtail	100.0	A	
ORCF-101	100.0	A	
ORCF-102	100.0	A	
Brundage	100.0	A	
Brundage 96	100.0	A	
Bruneau	100.0	A	
Cara	100.0	A	
Coda	100.0	A	
Daws	100.0	A	
ORSS-1757	100.0	A	
Rely	100.0	A	
Gaines	100.0	A	
Gene	100.0	A	
Goetze	100.0	A	
Hill 81	100.0	A	
Hyslop	100.0	A	
Kaseberg	100.0	A	
Ladd	100.0	A	
Madsen	100.0	A	
Malcolm	100.0	A	
Nugaines	100.0	A	
Omar	100.0	A	
Elmar	99.5	A B	
Eltan	99.5	A B	
ORCF-103	99.5	A B	
Lewjain	99.5	A B	
Rod	99.5	A B	
Skiles	99.5	A B	
Stephens	99.5	A B	
Tubbs	99.5	A B	
Tubbs-06	99.5	A B	
Brevor	99.0	A B	
Rosalyn	99.0	A B	
Xerpha	99.0	A B	
Mary	98.5	B	
Bruehl	97.0		C

Table 3.07. Percent germination at 4°C on day ten (Table 3.07A) and day eleven (Table 3.07B) in 2014-2015. Letters denote difference in significance based on a 0.05 LSD.

Table 3.07A

4°C Day 10	Corvallis	
Variety	Mean	
Alba	100.0	A
Bitterroot	100.0	A
Bobtail	100.0	A
Rely	100.0	A
Skiles	100.0	A
Brundage	100.0	A
Brundage 96	100.0	A
Bruneau	100.0	A
Cara	100.0	A
Coda	100.0	A
Daws	100.0	A
Elmar	100.0	A
Eltan	100.0	A
Gaines	100.0	A
Gene	100.0	A
Goetze	100.0	A
Hill 81	100.0	A
Hyslop	100.0	A
Kaseberg	100.0	A
Ladd	100.0	A
Madsen	100.0	A
Malcolm	100.0	A
Nugaines	100.0	A
Omar	100.0	A
ORCF-101	100.0	A
ORCF-102	100.0	A
ORSS-1757	100.0	A
Lewjain	99.5	A B
Rod	99.5	A B
ORCF-103	99.5	A B
Stephens	99.5	A B
Tubbs	99.5	A B
Tubbs-06	99.5	A B
Xerpha	99.5	A B
Brevor	99.0	B
Mary	99.0	B
Rosalyn	99.0	B
Bruehl	97.0	C

Table 3.07B

4°C Day 11	Corvallis	
Variety	Mean	
Alba	100.0	A
Bitterroot	100.0	A
Bobtail	100.0	A
Stephens	100.0	A
Xerpha	100.0	A
Brundage	100.0	A
Brundage 96	100.0	A
Bruneau	100.0	A
Cara	100.0	A
Coda	100.0	A
Daws	100.0	A
Elmar	100.0	A
Eltan	100.0	A
Gaines	100.0	A
Gene	100.0	A
Goetze	100.0	A
Hill 81	100.0	A
Hyslop	100.0	A
Kaseberg	100.0	A
Ladd	100.0	A
Lewjain	100.0	A
Madsen	100.0	A
Malcolm	100.0	A
Mary	100.0	A
Nugaines	100.0	A
Omar	100.0	A
ORCF-101	100.0	A
ORCF-102	100.0	A
ORSS-1757	100.0	A
Rely	100.0	A
Rod	100.0	A
Skiles	100.0	A
Brevor	99.5	A B
Tubbs	99.5	A B
Tubbs-06	99.5	A B
ORCF-103	99.5	A B
Rosalyn	99.0	B
Bruehl	97.0	C

Year 2 Germination Results

A full list of summary statistics is shown in Appendix 7. Table 3.08 and Table 3.09 below show the ANOVA tables from analyzing the seventh day of germination from seed harvested from Pendleton, OR and Corvallis, OR. Both tables show significant differences between temperatures, varieties and replications. The ANOVA tables and the germination means show a range of differences in germination rates between the two locations. Referring to Appendix 7, day three and day thirteen from Pendleton and day three, six, eight, and nine from Corvallis showed no significant differences between replications, however, there was consistently a difference between varieties, temperatures as well as the interaction between varieties and temperature across all of the days at both locations. The ANOVA table from Corvallis also shows that there were no significant differences between varieties and the interaction between varieties and temperatures on the tenth day, but there were significant differences between temperatures and field replications.

Table 3.08. ANOVA Table from the seventh day of the germination trials of the varieties (V) and temperatures (T) from seed harvested from Corvallis, OR ('S' indicates significance).

Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	539.00	22912.61				
Reps	2.00	79.59	39.80	3.50	3.02	0.03
Temp	3.00	11781.49	3927.16	345.78	2.63	0.00
Variety	44.00	1889.19	42.94	3.78	1.41	0.00
TxV	132.00	5096.35	38.61	3.40	1.26	0.00
Error	358.00	4065.98	11.36			

Table 3.09. ANOVA Table from the seventh day of the germination trials of the varieties (V) and temperatures (T) from seed harvested from Pendleton, OR ('S' indicates significance).

Day 7							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	332647.63					
Reps	1.00	2960.37	2960.37	93.48	3.87	0.00	S
Temp	3.00	265495.50	88498.50	2794.45	2.63	0.00	S
Variety	44.00	19785.13	449.66	14.20	1.41	0.00	S
TxV	132.00	33069.00	250.52	7.91	1.26	0.00	S
Error	358.00	11337.63	31.67				

Least Significant Difference Analysis from Year 2

Listed first are the LSD tests from 30°C, followed by 20°C, 10°C and 4°C treatments. The last day seed counts that were taken for each temperature are not included since this is when all of the varieties reached 100% germination, resulting in no difference between the varieties. The 30°C treatment reached full germination by the eleventh day for the seed harvested from Corvallis and by the fourteenth day for the seed harvested from Pendleton. The 20°C treatment reached full germination by the seventh day from Corvallis and by the ninth day from Pendleton. All the seeds in the 10°C treatment reached full germination by the eighth day from Corvallis and by the ninth day from Pendleton. The 4°C treatment reached full germination on the eleventh day from both locations.

30°C LSD Analysis

Tables 3.10-3.19 show the LSD results from the 30°C treatment and is referred to in this section. On the first day of the seeds being in the germination chamber at 30°C, the variety Bruehl had the highest number of seeds that germinated at both locations.

Bruehl grown in Corvallis was found to be statistically higher than all the other varieties and remained that way through the second day of germination counts. The lowest germinating varieties from Corvallis were ORSS-1757 and the breeding line 11-225-2C. Out of the highest germinating varieties from Pendleton, Bruehl was not found to be significantly different from Bitterroot and Xerpha. The lowest germinating varieties from Pendleton were Gene and Omar. There were several other varieties that were not significantly different than these varieties, however, these varieties only fell into the last significance category without any overlap in significance levels.

On the second day, the highest germinating varieties from Corvallis were the experimental crosses 11-225-1C and 11-225-3C as well as Bruehl with a germination percentage ranging from 93.5-95%. The lowest germinating varieties from Corvallis were ORSS-1757, Brevor, Kaseberg and Rosalyn which all fell in the last significance category, and Brevor, Kaseberg and Rosalyn were not found to be statistically different than a few other varieties. The highest germinating varieties from Pendleton were ORCF-103, Bitterroot, Eltan, Brundage 96, Madsen, Bruehl, Xerpha, Tubbs, Bruneau, Lewjain and Hill 81, even though some of the varieties, other than ORCF-103, Bitterroot and Eltan, were not statistically different than several other varieties. The slowest germinating varieties from Pendleton were Gene and Omar, which were statistically similar to several other varieties, however, there were no over-lapping significance levels with these two varieties.

By day three, 30 varieties harvested from Corvallis were not significantly different for being the top germinating varieties. Brevor, Alba, and the experimental cross

11-225-7H from Corvallis were the slowest germinating varieties. Alba and 11-225-7H were also not found to be significantly different from Rosalyn, 11-225-6H and ORSS-1757. Seeds from Pendleton germinated slightly slower and 10 varieties, ORCF-103, Bitterroot, Brundage 96, Madsen, Bruehl, Xerpha, Tubbs, Lewjain and Bruneau all were the highest germinating varieties. The results for the slowest germinating varieties from Pendleton were Gene, Omar and Cayuga which had no overlapping significance groups even though they fell in the same significance category with several other varieties.

On the fourth day, thirty-eight varieties harvested from Corvallis all ranked statistically similar for having a high germination rate. Brevor and Alba were ranked as the slowest germinating varieties from Corvallis while Alba was not classified to be statistically different than 11-225-7H, Rosalyn and 11-225-6H. From Pendleton, there were 12 high germinating varieties, which were the same as the previous day, with the addition of the varieties Goetze and Hill 81. Cayuga and Brevor from Pendleton had the slowest germination rate.

For the fifth day, the quicker germinating varieties from Corvallis remained the same as the previous day and the lowest germinating varieties remained the same except the variety 11-225-7H fell into the last significance category without being statistically different than ORSS-1757, Rosalyn and 11-225-6H. Results from Pendleton showed that 17 varieties were in the highest germinating significance category while 19 varieties fell into the last significance category with Cayuga having the lowest number of germinated seeds.

On the sixth day, there were 41 varieties from Corvallis that were close to reaching 100% seed germination and fell into the first significance category, while four varieties fell into the slowest germinating category. These varieties were Alba, 11-225-7H, Rosalyn and Brevor with a germination percentage ranging from 89.7-91.6%. Seeds harvested from Pendleton were very different in which the germination percentage that fell into the first significance category of 22 varieties ranged from 69.5-99%. There were 21 varieties that were in the last significance level with an average germination percentage ranging from 35.5-62.5% with Cayuga and Nugaines having the lowest germination percentage. The seventh day results from both locations were very similar to the sixth day results as the varieties from Corvallis was closer to reaching 100% germination and the varieties from Pendleton having a larger range of variation between the slowest and fastest germination rates than the seed from Corvallis.

On the eighth day, the total percentage of germination from Corvallis ranged from 93.9-100% with the advanced line 11-225-7H and Rosalyn ranking in the lowest significance level for having the lowest number of germinated seeds. A total of 32 varieties had reached 100% seed germination. The total germination percentage from Pendleton ranged from 43-99.5%. None of the varieties had completely germinated, even though Eltan was very close. Cayuga had the lowest rate of germination rate (43%).

By the ninth day of the germination trial, 41 varieties/experimental lines out of 45 fell into the first significance level with a germination percentage ranging from 98.8-100% germination. The advanced line 11-225-7H and Rosalyn were the lowest germinating varieties with 94.3% and 96.1% seed germination respectively. Eltan from

Pendleton reached 100% seed germination on this day and the first significance category had a range of 72-100% seed germination. The lowest germinating varieties without falling into multiple significance categories were Cayuga, Gene, Bobtail, Nugaines and Brevor with germination rates ranging from 50.5-53.8%.

On the tenth day, the seeds from Corvallis had 40 varieties that had reached 100% seed germination and the varieties Rosalyn, Alba and Brevor being the slowest germinating varieties with a germination percentage ranging from 97-97.7% (the ANOVA analysis showed no significance between varieties on this day). More varieties from Pendleton had reached 100% seed germination with 26 varieties showing complete germination. The lowest germinating variety was Cara, which was not significantly different from Bruehl, Gene, Brevor, ORSS-1757, ORCF-102, Rely, Kaseberg and 11-225-5C with a germination percentage ranging from 87.5-95%.

Table 3.17. Percent germination at 30°C on day eight from Corvallis (Table 3.17A) and Pendleton (Table 3.17B) in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.17A

30°C Day 8	Corvallis		
Variety	Mean		
Bruehl	100.0	A	
11-225-2C	100.0	A	
11-225-3C	100.0	A	
11-225-5C	100.0	A	
ORCF-103	100.0	A	
Goetze	100.0	A	
Rod	100.0	A	
Bitterroot	100.0	A	
Bobtail	100.0	A	
Skiles	100.0	A	
Stephens	100.0	A	
Brundage	100.0	A	
Brundage 96	100.0	A	
Tubbs	100.0	A	
Tubbs-06	100.0	A	
Cayuga	100.0	A	
Coda	100.0	A	
Daws	100.0	A	
Elmar	100.0	A	
Eltan	100.0	A	
Gaines	100.0	A	
Gene	100.0	A	
Xerpha	100.0	A	
Hill 81	100.0	A	
Hyslop	100.0	A	
Kaseberg	100.0	A	
Ladd	100.0	A	
Lewjain	100.0	A	
Madsen	100.0	A	
Omar	100.0	A	
ORCF-101	100.0	A	
ORCF-102	100.0	A	
Bruneau	99.6	A	
Malcolm	99.6	A	
11-225-1C	99.6	A	
Rely	99.6	A	
Mary	99.6	A	
Nugaines	98.9	A B	
ORSS-1757	98.8	A B	
11-225-6H	98.4	A B	
Cara	97.9	A B C	
Brevor	96.8	B C	
Alba	96.7	B C	
Rosalyn	95.6	C D	
11-225-7H	93.9		D

Table 3.17B

30°C Day 8	Pendleton								
Variety	Mean								
Eltan	99.5	A							
Brundage 96	98.0	A							
ORCF-103	97.5	A							
Bitterroot	97.5	A							
Bruneau	96.5	A B							
Madsen	93.5	A B C							
Goetze	91.5	A B C							
Tubbs	91.5	A B C							
Xerpha	91.0	A B C							
Ladd	90.4	A B C							
Lewjain	90.4	A B C							
Stephens	89.0	A B C D							
Skiles	88.5	A B C D							
11-225-1C	88.0	A B C D							
Daws	87.0	A B C D E							
Brundage	86.5	A B C D E							
Bruehl	86.0	A B C D E F							
Hill 81	86.0	A B C D E F							
Malcolm	84.5	A B C D E F G							
Coda	83.0	A B C D E F G							
11-225-3C	77.5	A B C D E F G H							
ORCF-101	76.0	A B C D E F G H							
Rod	75.0	A B C D E F G H							
Tubbs-06	74.9	A B C D E F G H							
11-225-5C	74.0	A B C D E F G H							
Kaseberg	72.5	A B C D E F G H I							
Mary	71.5	A B C D E F G H I							
Alba	70.5	A B C D E F G H I							
ORCF-102	70.5	A B C D E F G H I							
Hyslop	70.0	A B C D E F G H I							
11-225-2C	67.0	B C D E F G H I							
Elmar	65.3	C D E F G H I							
Gaines	63.5	C D E F G H I							
ORSS-1757	63.5	C D E F G H I							
Omar	59.8	D E F G H I							
Rosalyn	57.5	E F G H I							
Cara	57.0	E F G H I							
11-225-7H	56.0	F G H I							
Rely	54.5	G H I							
11-225-6H	52.3	H I							
Brevor	51.3	H I							
Bobtail	49.3	H I							
Nugaines	47.7	H I							
Gene	47.5	H I							
Cayuga	43.0	I							

Table 3.19. Percent germination at 30°C on day ten from Pendleton in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.19

30°C Day 10	Pendleton	
Variety	Mean	
11-225-1C	100.0	A
Rod	100.0	A
Xerpha	100.0	A
ORCF-101	100.0	A
Omar	100.0	A
Goetze	100.0	A
Alba	100.0	A
Bitterroot	100.0	A
Mary	100.0	A
Malcolm	100.0	A
Madsen	100.0	A
Brundage	100.0	A
Brundage 96	100.0	A
Bruneau	100.0	A
Lewjain	100.0	A
Ladd	100.0	A
Coda	100.0	A
Daws	100.0	A
Elmar	100.0	A
Eltan	100.0	A
Hyslop	100.0	A
Hill 81	100.0	A
Skiles	100.0	A
Stephens	100.0	A
Tubbs	100.0	A
Tubbs-06	100.0	A
Rosalyn	99.5	A
Cayuga	99.0	A
11-225-6H	99.0	A
ORCF-103	98.5	A
11-225-2C	98.0	A
Gaines	98.0	A
Bobtail	97.0	A B
11-225-7H	97.0	A B
Nugaines	97.0	A B
11-225-3C	95.5	A B
11-225-5C	95.0	A B C
Kaseberg	94.5	A B C
Rely	94.0	A B C
ORCF-102	93.5	A B C
ORSS-1757	92.5	A B C
Brevor	92.5	A B C
Gene	90.0	B C
Bruehl	89.5	B C
Cara	87.5	C

20°C LSD Analysis

Tables 3.20-3.22 show the LSD results from the 20°C treatment from both Corvallis and Pendleton. One day after imbibition, there were a few varieties from Corvallis that had started germinating, Bruehl being the variety with the highest mean germination of 12.7%. Pendleton, however, had a much higher number of seeds that had started germinating. Bruehl, Eltan, Brundage 96, Bruneau and Bitterroot grouped together as the varieties with the highest germination rate. These lines all significantly differed from Xerpha for germination except for Bruehl. The lowest germinating varieties from both locations did not have any seeds begin to germinate within the first twenty-four hours.

By the second day, Corvallis had a large range in seed germination. Bitterroot reached 93.7% seed germination and grouped with 18 other varieties that also had a high level of germination. The range for this group was from 78-93.7% seed germination. The lowest germinating varieties were ORSS-1757, Rosalyn, Kaseberg, ORCF-101, 11-225-2C, Skiles, 11-225-7H, Stephens, Brevor, 11-225-6H and Malcolm with a germination percentage ranging from 50.7-66.3%. Results from Pendleton had 41 varieties that grouped together in the high rate of germination, ranging from 87-98% seed germination. Brevor was the lowest germinating variety with 71% seed germination, followed by Rosalyn, 11-225-7H and Cayuga.

On the third day of seed germination, the Corvallis trial had 14 varieties reach 100% seed germination while all of the other varieties except Brevor were over 97% germination. The lowest germinating variety was Brevor, which reached 93.7% seed

germination. There were 6 varieties from Pendleton which reached 100% seed germination on the third day and all of the varieties were above 94% germination except again for Brevor, which had reached 86.5% seed germination. By the fourth day, 20 varieties had reached 100% seed germination from Corvallis and all of the other varieties had 97% germination or higher. There were no significant differences between varieties from Pendleton on the third day through the rest of the trial. By the fourth day, 20 varieties from Corvallis reached 100% seed germination. The variety Brevor was the slowest germinating variety with 97% germination.

Table 3.20. Percent germination at 20°C on day one from Corvallis (Table 3.20A) and Pendleton (Table 3.20B) in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.20A

20°C Day 1	Corvallis			
Variety	Mean			
Bruehl	12.7	A		
Bruneau	6.0	B		
Bitterroot	5.0	B	C	
Alba	2.3		C	D
Coda	2.0			D
Brundage 96	2.0			D
Eltan	1.7			D
Cayuga	1.3			D
Cara	1.0			D
Daws	1.0			D
11-225-3C	0.7			D
Elmar	0.7			D
Brundage	0.7			D
11-225-2C	0.3			D
Lewjain	0.3			D
Brevor	0.3			D
11-225-1C	0.3			D
11-225-5C	0.0			D
11-225-6H	0.0			D
Bobtail	0.0			D
11-225-7H	0.0			D
Gaines	0.0			D
Gene	0.0			D
Hill 81	0.0			D
Hyslop	0.0			D
Kaseberg	0.0			D
Ladd	0.0			D
Goetze	0.0			D
Madsen	0.0			D
Malcolm	0.0			D
Mary	0.0			D
Nugaines	0.0			D
Omar	0.0			D
ORCF-101	0.0			D
ORCF-102	0.0			D
ORCF-103	0.0			D
ORSS-1757	0.0			D
Rely	0.0			D
Rod	0.0			D
Rosalyn	0.0			D
Skiles	0.0			D
Stephens	0.0			D
Tubbs	0.0			D
Tubbs-06	0.0			D
Xerpha	0.0			D

Table 3.20B

20°C Day 1	Pendleton			
Variety	Mean			
Bruehl	32.5	A		
Eltan	30.5	A	B	
Brundage 96	28.0	A	B	
Bruneau	27.0	A	B	
Bitterroot	26.5	A	B	
Xerpha	23.1	B	C	
Rod	15.0		C	D
Daws	14.0			D E
Coda	9.5			D E F
Brundage	8.0			D E F G
Alba	6.5			D E F G
Elmar	6.0			E F G
Goetze	5.5			E F G
Lewjain	4.5			F G
11-225-5C	4.5			F G
Hill 81	4.5			F G
11-225-3C	3.5			F G
Kaseberg	2.0			F G
Brevor	2.0			F G
Tubbs-06	2.0			F G
Madsen	1.5			F G
Malcolm	1.5			F G
Ladd	1.0			F G
Cara	1.0			F G
Cayuga	1.0			F G
Tubbs	1.0			F G
11-225-1C	0.5			G
ORCF-103	0.5			G
Rely	0.5			G
11-225-6H	0.5			G
Skiles	0.5			G
Bobtail	0.5			G
Omar	0.5			G
ORCF-101	0.0			G
11-225-7H	0.0			G
11-225-2C	0.0			G
ORSS-1757	0.0			G
Gene	0.0			G
Hyslop	0.0			G
ORCF-102	0.0			G
Mary	0.0			G
Stephens	0.0			G
Nugaines	0.0			G
Gaines	0.0			G
Rosalyn	0.0			G

Table 3.21. Percent germination at 20°C on day two from Corvallis (Table 3.21A) and Pendleton (Table 3.21B) in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.21A

20°C Day 2	Corvallis														
Variety	Mean														
Bitterroot	93.7	A													
Bruneau	88.3	A	B												
Brundage 96	87.7	A	B	C											
Madsen	86.0	A	B	C											
Coda	85.3	A	B	C											
Hyslop	84.7	A	B	C											
Cayuga	84.0	A	B	C											
Daws	83.7	A	B	C											
Hill 81	83.3	A	B	C											
Goetze	83.3	A	B	C											
Rod	83.3	A	B	C											
Alba	82.0	A	B	C	D										
Lewjain	82.0	A	B	C	D										
Eltan	82.0	A	B	C	D										
Bruehl	80.3	A	B	C	D	E									
Bobtail	80.0	A	B	C	D	E	F								
11-225-3C	79.7	A	B	C	D	E	F	G							
Brundage	78.3	A	B	C	D	E	F	G	H						
Nugaines	78.0	A	B	C	D	E	F	G	H						
Gaines	77.0		B	C	D	E	F	G	H	I					
Mary	76.7		B	C	D	E	F	G	H	I	J				
Ladd	76.0		B	C	D	E	F	G	H	I	J	K			
11-225-1C	75.7		B	C	D	E	F	G	H	I	J	K			
11-225-5C	75.7		B	C	D	E	F	G	H	I	J	K			
Tubbs-06	75.7		B	C	D	E	F	G	H	I	J	K			
Xerpha	75.3		B	C	D	E	F	G	H	I	J	K			
Elmar	75.0		B	C	D	E	F	G	H	I	J	K			
Cara	74.7		B	C	D	E	F	G	H	I	J	K			
Omar	74.7		B	C	D	E	F	G	H	I	J	K			
Rely	73.0		B	C	D	E	F	G	H	I	J	K			
ORCF-102	72.7		B	C	D	E	F	G	H	I	J	K			
Tubbs	72.3		B	C	D	E	F	G	H	I	J	K			
ORCF-103	71.3			C	D	E	F	G	H	I	J	K			
Gene	71.3			C	D	E	F	G	H	I	J	K			
Malcolm	66.3				D	E	F	G	H	I	J	K	L		
11-225-6H	64.3					E	F	G	H	I	J	K	L		
Brevor	64.0						E	F	G	H	I	J	K	L	
Stephens	63.7							F	G	H	I	J	K	L	
11-225-7H	63.3								G	H	I	J	K	L	
Skiles	62.7									H	I	J	K	L	
11-225-2C	62.3										H	I	J	K	L
ORCF-101	61.3											I	J	K	L
Kaseberg	60.3												J	K	L
Rosalyn	60.0													K	L
ORSS-1757	50.7														L

Table 3.21B

20°C Day 2	Pendleton										
Variety	Mean										
Malcolm	98.0	A									
Brundage 96	98.0	A									
Rod	97.5	A									
Bruneau	97.5	A									
Daws	97.5	A									
Eltan	97.0	A									
Bitterroot	97.0	A									
Coda	97.0	A									
Alba	97.0	A									
Tubbs-06	96.5	A									
Tubbs	96.5	A									
Xerpha	96.5	A									
Hill 81	96.0	A									
Goetze	96.0	A									
Bruehl	95.5	A									
Gene	95.5	A									
Brundage	95.5	A									
ORCF-101	95.5	A									
11-225-1C	95.0	A									
Kaseberg	95.0	A									
ORCF-102	94.5	A									
Skiles	94.5	A									
Stephens	94.5	A									
Bobtail	94.5	A									
Madsen	93.0	A	B								
Elmar	93.0	A	B								
ORCF-103	93.0	A	B								
ORSS-1757	93.0	A	B								
Cara	92.0	A	B	C							
11-225-3C	91.5	A	B	C							
Hyslop	91.5	A	B	C							
Ladd	91.5	A	B	C							
Lewjain	91.5	A	B	C							
Omar	91.5	A	B	C							
Mary	90.5	A	B	C							
Gaines	90.0	A	B	C	D						
11-225-5C	89.5	A	B	C	D						
Nugaines	89.5	A	B	C	D						
11-225-2C	89.0	A	B	C	D						
Rely	87.5	A	B	C	D						
11-225-6H	87.0	A	B	C	D						
Cayuga	82.5		B	C	D	E					
11-225-7H	81.0			C	D	E					
Rosalyn	78.5				D	E					
Brevor	71.0					E					

Table 3.22. Percent germination at 20°C on day three (Table 3.22A) and day four from Corvallis (Table 3.22B) in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.22A

20°C Day 3		Corvallis		
Variety	Mean			
Bruehl	100.0	A		
11-225-2C	100.0	A		
11-225-3C	100.0	A		
11-225-5C	100.0	A		
Stephens	100.0	A		
Hill 81	100.0	A		
ORCF-102	100.0	A		
Bitterroot	100.0	A		
ORCF-101	100.0	A		
Malcolm	100.0	A		
Ladd	100.0	A		
Hyslop	100.0	A		
Brundage 96	100.0	A		
Bruneau	100.0	A		
11-225-6H	99.7	A		
11-225-1C	99.7	A		
Alba	99.7	A		
Madsen	99.7	A		
Cayuga	99.7	A		
Xerpha	99.7	A		
Brundage	99.3	A	B	
Daws	99.3	A	B	
ORCF-103	99.3	A	B	
Tubbs-06	99.3	A	B	
Eltan	99.0	A	B	C
Nugaines	99.0	A	B	C
Rely	99.0	A	B	C
Rod	99.0	A	B	C
Goetze	99.0	A	B	C
Skiles	99.0	A	B	C
Bobtail	98.7	A	B	C
11-225-7H	98.7	A	B	C
Gaines	98.7	A	B	C
Mary	98.7	A	B	C
Omar	98.7	A	B	C
Coda	98.7	A	B	C
ORSS-1757	98.7	A	B	C
Rosalyn	98.7	A	B	C
Kaseberg	98.3	A	B	C
Lewjain	98.3	A	B	C
Elmar	98.3	A	B	C
Cara	97.7		B	C
Gene	97.3			C
Tubbs	97.3			C
Brevor	93.7			D

Table 3.22B

20°C Day 4		Corvallis		
Variety	Mean			
Bruehl	100.0	A		
11-225-2C	100.0	A		
11-225-3C	100.0	A		
11-225-5C	100.0	A		
11-225-6H	100.0	A		
Daws	100.0	A		
Ladd	100.0	A		
Bitterroot	100.0	A		
ORCF-102	100.0	A		
ORCF-101	100.0	A		
Omar	100.0	A		
Brundage	100.0	A		
Brundage 96	100.0	A		
Bruneau	100.0	A		
Malcolm	100.0	A		
Hill 81	100.0	A		
Hyslop	100.0	A		
ORSS-1757	100.0	A		
Stephens	100.0	A		
Tubbs-06	100.0	A		
Coda	99.7	A	B	
Eltan	99.7	A	B	
Xerpha	99.7	A	B	
Madsen	99.7	A	B	
Mary	99.7	A	B	
Nugaines	99.7	A	B	
ORCF-103	99.7	A	B	
11-225-1C	99.7	A	B	
Alba	99.7	A	B	
Tubbs	99.7	A	B	
Cayuga	99.7	A	B	
Kaseberg	99.3	A	B	
Elmar	99.3	A	B	
Rod	99.3	A	B	
Goetze	99.3	A	B	
Gaines	99.3	A	B	
Rosalyn	99.3	A	B	
11-225-7H	99.0	A	B	
Rely	99.0	A	B	
Skiles	99.0	A	B	
Gene	99.0	A	B	
Cara	99.0	A	B	
Bobtail	98.7		B	
Lewjain	98.7		B	
Brevor	97.0			C

10°C LSD Analysis

Tables 3.23-3.25 shows the mean germination for Corvallis and Pendleton at 10°C. Three days following seed imbibition, the seeds in the 10°C treatment began to germinate. The seeds harvested from Corvallis had the highest germination rates compared to those harvested from Pendleton. From Corvallis, the varieties Bitterroot, Hyslop, Rod, 11-225-5C, Goetze, Bruehl, Eltan, Coda, Bruneau and Daws were in the first group with a germination rate ranging from 24.7-38.3% with overlapping significant groups. The varieties Rosalyn and ORSS-1757 were the lowest germinating varieties which were classified in the last group with seventeen other varieties. The varieties Bruehl and Bitterroot from Pendleton were the only varieties to germinate on the third day.

On the fourth day, the number of varieties with germination and the number of seeds germinating from Corvallis greatly increased. The varieties Bruneau and Bitterroot were the top germinating varieties with a germination rate of 91% and 90.7% and they were in a group of varieties that all had a high rate of germination. The germination of this first group ranged from 78-91%. The slower germinating varieties were ORSS-1757, Rosalyn, Rely, ORCF-102, Lewjain and ORCF-103 with a range of 54-66.7% seed germination. Some of these slower germinating varieties also fell into other significant categories. The results from Pendleton showed overall germination was lower than Corvallis with Bitterroot as the top germinating variety. The group that had the highest rate of germination from Pendleton had a germination range from 54.5-82%. The first and last significant class overlapped as the slower germinating varieties ranged from

31.5-59% seed germination. The slowest germinating variety from Pendleton was Rosalyn with 31.5% germination. The total seed germination on the fifth day was not found to be significantly different among the varieties from Corvallis or Pendleton.

By the sixth day, 41 varieties had reached 100% seed germination from Corvallis. The variety Cara had the lowest number of seeds that germinated but Cara was still over 99% germinated so while statistically different, could be considered completely germinated. There were no significant differences between varieties from Pendleton on the sixth day.

Table 3.23. Percent germination at 10°C on day three from Corvallis (Table 3.23A) and Pendleton (Table 3.23B) in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.23A

10°C Day 3	Corvallis																																
Variety	Mean																																
Bitterroot	38.3	A																															
Hyslop	36.3	A	B																														
Rod	35.3	A	B	C																													
11-225-5C	34.3	A	B	C	D																												
Goetze	32.0	A	B	C	D	E																											
Bruehl	31.3	A	B	C	D	E	F																										
Eltan	30.0	A	B	C	D	E	F																										
Coda	29.0	A	B	C	D	E	F	G																									
Bruneau	26.0	A	B	C	D	E	F	G	H																								
Daws	24.7	A	B	C	D	E	F	G	H																								
Cayuga	23.3		B	C	D	E	F	G	H	I																							
11-225-1C	23.3		B	C	D	E	F	G	H	I																							
11-225-6H	22.7		B	C	D	E	F	G	H	I																							
Brevor	22.7		B	C	D	E	F	G	H	I																							
Elmar	22.7		B	C	D	E	F	G	H	I																							
Brundage 96	22.3		B	C	D	E	F	G	H	I	J																						
11-225-3C	21.7		B	C	D	E	F	G	H	I	J																						
Tubbs	21.0			C	D	E	F	G	H	I	J																						
Nugaines	20.7				C	D	E	F	G	H	I	J	K																				
11-225-7H	20.3					D	E	F	G	H	I	J	K																				
Bobtail	19.7						D	E	F	G	H	I	J	K	L																		
Cara	19.7							D	E	F	G	H	I	J	K	L																	
Gaines	19.3								E	F	G	H	I	J	K	L																	
Mary	19.3									E	F	G	H	I	J	K	L																
Brundage	18.3										E	F	G	H	I	J	K	L															
Tubbs-06	18.3											E	F	G	H	I	J	K	L														
Alba	17.7												E	F	G	H	I	J	K	L	M												
Hill 81	17.3													E	F	G	H	I	J	K	L	M											
Madsen	17.0														F	G	H	I	J	K	L	M											
Ladd	17.0															F	G	H	I	J	K	L	M										
11-225-2C	15.0																				G	H	I	J	K	L	M						
Xerpha	15.0																						G	H	I	J	K	L	M				
Lewjain	14.3																							G	H	I	J	K	L	M			
Skiles	12.7																								H	I	J	K	L	M			
ORCF-102	12.3																									H	I	J	K	L	M		
ORCF-103	11.7																										H	I	J	K	L	M	
Rely	11.3																											H	I	J	K	L	M
Gene	11.3																											H	I	J	K	L	M
Kaseberg	11.3																											H	I	J	K	L	M
Stephens	9.7																												I	J	K	L	M
ORCF-101	7.7																													J	K	L	M
Omar	6.0																														K	L	M
Malcolm	5.3																															L	M
ORSS-1757	3.3																															M	
Rosalyn	3.0																															M	

Table 3.23B

10°C Day 3	Pendleton	
Variety	Mean	
Bruehl	3.0	A
Bitterroot	1.5	B
11-225-2C	0.0	C
11-225-3C	0.0	C
11-225-5C	0.0	C
11-225-6H	0.0	C
11-225-1C	0.0	C
Alba	0.0	C
Bobtail	0.0	C
Brevor	0.0	C
11-225-7H	0.0	C
Brundage	0.0	C
Brundage 96	0.0	C
Bruneau	0.0	C
Cara	0.0	C
Cayuga	0.0	C
Coda	0.0	C
Daws	0.0	C
Elmar	0.0	C
Eltan	0.0	C
Gaines	0.0	C
Gene	0.0	C
Goetze	0.0	C
Hill 81	0.0	C
Hyslop	0.0	C
Kaseberg	0.0	C
Ladd	0.0	C
Lewjain	0.0	C
Madsen	0.0	C
Malcolm	0.0	C
Mary	0.0	C
Nugaines	0.0	C
Omar	0.0	C
ORCF-101	0.0	C
ORCF-102	0.0	C
ORCF-103	0.0	C
ORSS-1757	0.0	C
Rely	0.0	C
Rod	0.0	C
Rosalyn	0.0	C
Skiles	0.0	C
Stephens	0.0	C
Tubbs	0.0	C
Tubbs-06	0.0	C
Xerpha	0.0	C

Table 3.25. Percent germination at 10°C on day six from Corvallis in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.25

10°C Day 6	Corvallis		
Variety	Mean		
11-225-1C	100.0	A	
11-225-2C	100.0	A	
11-225-3C	100.0	A	
11-225-5C	100.0	A	
11-225-6H	100.0	A	
11-225-7H	100.0	A	
Alba	100.0	A	
Tubbs	100.0	A	
Bobtail	100.0	A	
Brevor	100.0	A	
Bruehl	100.0	A	
Brundage	100.0	A	
Brundage 96	100.0	A	
Bruneau	100.0	A	
Tubbs-06	100.0	A	
Cayuga	100.0	A	
Coda	100.0	A	
Daws	100.0	A	
Elmar	100.0	A	
Eltan	100.0	A	
Gaines	100.0	A	
Gene	100.0	A	
Goetze	100.0	A	
Hill 81	100.0	A	
Hyslop	100.0	A	
Kaseberg	100.0	A	
Ladd	100.0	A	
Madsen	100.0	A	
Malcolm	100.0	A	
Mary	100.0	A	
Nugaines	100.0	A	
Omar	100.0	A	
ORCF-101	100.0	A	
Rosalyn	100.0	A	
ORCF-103	100.0	A	
ORSS-1757	100.0	A	
Rely	100.0	A	
Rod	100.0	A	
Xerpha	100.0	A	
Skiles	100.0	A	
Stephens	100.0	A	
Bitterroot	99.7	B	
Lewjain	99.7	B	
ORCF-102	99.7	B	
Cara	99.3		C

4°C LSD Analysis

Tables 3.26-3.29 shows the varietal germination response to the 4°C treatment for seed produced in Corvallis and Pendleton. The seeds that were placed in the 4°C treatment began germinating on the fifth day from imbibition. More seeds had germinated from the Corvallis location than from the Pendleton location. Several varieties from Corvallis were classified in the first group of varieties with a germination percentage ranging from 20.7-37.3%. Hyslop was the highest germinating variety, followed by Lewjain. The slowest germinating variety was ORSS-1757 with an average germination rate of 2.7%. The group with the lowest germination rate ranged from 2.7-19.7% seed germination. From Pendleton, the variety Bitterroot was the highest germinating variety that was significantly different than all the other varieties with an average germination percentage of 18.5%. The majority of the other varieties had not begun germinating.

By the sixth day, Hyslop and Coda were the highest germinating varieties from Corvallis and they were grouped with 29 other varieties. The germination rate for this group ranged from 54.7-75.3% seed germination. The lowest germinating varieties were ORSS-1757, Omar, Rosalyn, Kaseberg, Rely, 11-225-7H, Malcolm and ORCF-102, and several of the varieties in the low germination group overlapped with other groups with intermediate germination. The lowest germinating category ranged from 24.3-45.3% seed germination. Bitterroot was the only variety from Pendleton that had a statistically higher germination rate than all the other varieties with 53% seed germination. The lowest germinating varieties included several varieties that had not begun germinating. The

varieties with no germination on the sixth day were Stephens, ORSS-1757, ORCF-101, Omar, Nugaines, Mary and 11-225-2C.

On the seventh day, many of the varieties from Corvallis were within 10% of reaching 100% seed germination. The varieties Hyslop and 11-225-3C were the highest germinating varieties, which were grouped with 31 other varieties with a germination percentage ranging from 88-98.3%. The lowest germinating variety was ORSS-1757, which was statistically different than all the other varieties with 60% seed germination. The two varieties Bitterroot and Brundage 96 from Pendleton had the highest germination rates with 83% and 75.5% seed germination, however, Brundage 96 was not statistically different than Eltan, Alba, Daws, and Brundage. The slowest germinating variety was Cara with 9% seed germination and it grouped with 17 other varieties also having lower germination rates.

After being in the 4°C treatment for eight days, 14 varieties from Corvallis reached 100% seed germination and were part of a group of 41 varieties that had a germination rate of 97% or higher. The varieties ORSS-1757 and Rely were the slowest germinating varieties with 93.7% and 96% seed germination. From Pendleton, only the variety Alba reached 100% seed germination by the eighth day and it was not significantly different than 17 other varieties ranging from 84-100% seed germination. The slowest germinating varieties were Cara, Mary and Omar in which Mary and Omar were not significantly different than several other varieties. The lowest germination group ranged from 48-61.5% seed germination. None of the varieties from the ninth and tenth day from both Corvallis and Pendleton were found to be significantly different.

Table 3.26. Percent germination at 4°C on day five from Corvallis (Table 3.26A) and Pendleton (Table 3.26B) in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 3.26A

4°C Day 5	Corvallis									
Variety	Mean									
Hyslop	37.3	A								
Lewjain	36.7	A B								
Bitterroot	35.3	A B C								
11-225-1C	35.0	A B C								
11-225-3C	35.0	A B C								
Brevor	34.7	A B C								
11-225-5C	34.0	A B C D								
Bruehl	33.7	A B C D								
Cara	33.7	A B C D								
Rod	33.0	A B C D E								
Nugaines	32.0	A B C D E F								
Goetze	30.0	A B C D E F G								
Eltan	28.7	A B C D E F G								
Cayuga	28.3	A B C D E F G								
Coda	27.3	A B C D E F G H								
Daws	27.0	A B C D E F G H I								
Hill 81	26.7	A B C D E F G H I								
Tubbs-06	26.7	A B C D E F G H I								
Bruneau	26.0	A B C D E F G H I								
Brundage	25.0	A B C D E F G H I								
Gaines	25.0	A B C D E F G H I								
Madsen	23.3	A B C D E F G H I J								
Alba	23.3	A B C D E F G H I J								
Xerpha	23.3	A B C D E F G H I J								
Tubbs	22.7	A B C D E F G H I J								
Mary	22.3	A B C D E F G H I J								
Bobtail	21.3	A B C D E F G H I J								
Brundage 96	20.7	A B C D E F G H I J								
11-225-6H	19.7	B C D E F G H I J K								
11-225-2C	19.0	C D E F G H I J K								
Ladd	18.3	C D E F G H I J K								
ORCF-103	17.0	D E F G H I J K								
Gene	16.7	D E F G H I J K								
Rely	15.7	E F G H I J K								
Malcolm	15.3	F G H I J K								
Elmar	15.0	F G H I J K								
ORCF-101	14.7	F G H I J K								
Stephens	14.3	G H I J K								
ORCF-102	14.0	G H I J K								
11-225-7H	14.0	G H I J K								
Skiles	12.7	G H I J K								
Kaseberg	10.3	H I J K								
Omar	9.7	I J K								
Rosalyn	6.3	J K								
ORSS-1757	2.7	K								

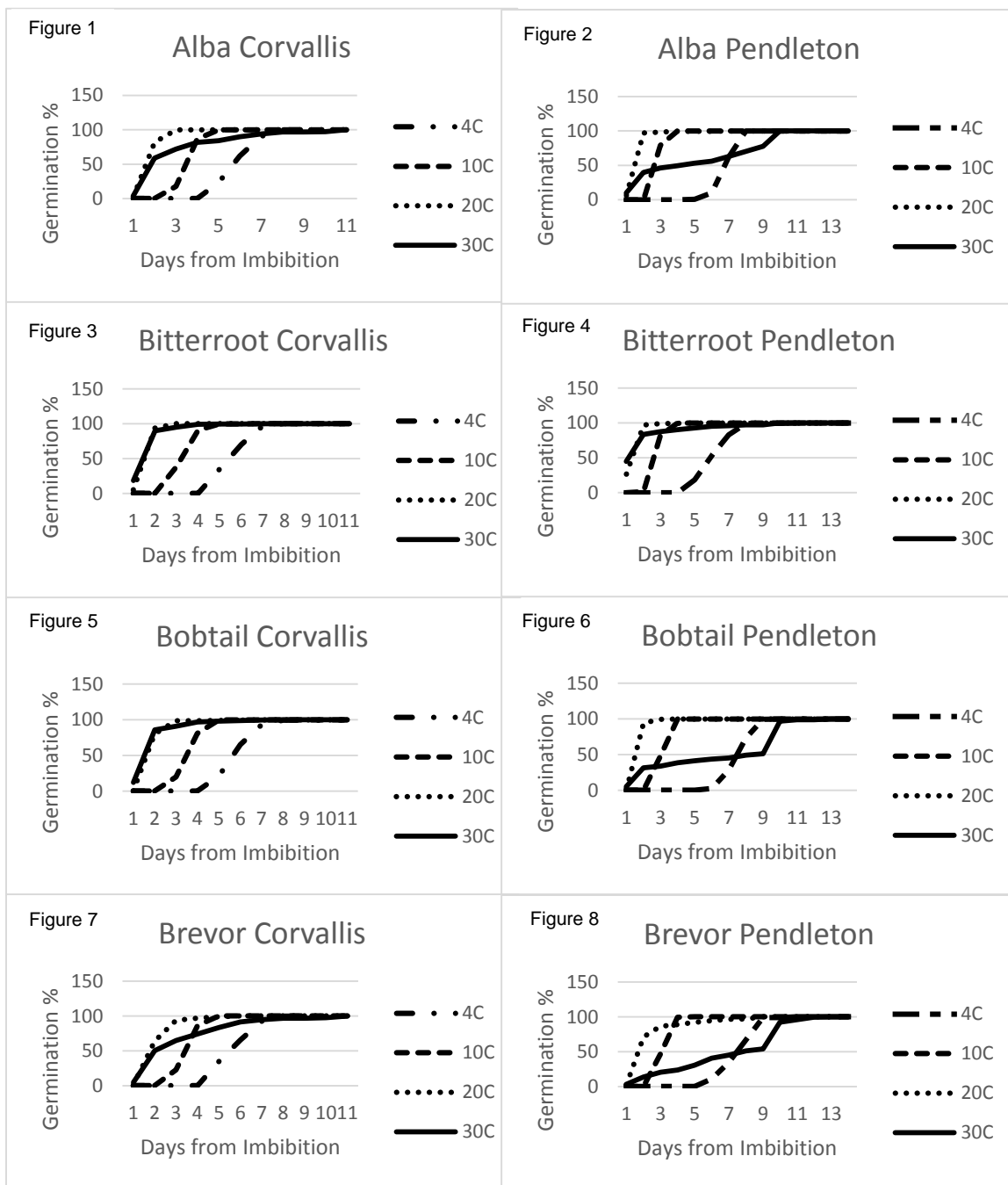
Table 3.26B

4°C Day 5	Pendleton	
Variety	Mean	
Bitterroot	18.5	A
Goetze	3.0	B
Bruneau	3.0	B
Xerpha	2.0	B C
Brundage 96	1.5	B C
Daws	1.5	B C
11-225-1C	1.0	B C
Gaines	1.0	B C
Gene	1.0	B C
Bruehl	1.0	B C
11-225-6H	1.0	B C
Madsen	0.5	C
Alba	0.5	C
Coda	0.5	C
11-225-3C	0.0	C
11-225-5C	0.0	C
Bobtail	0.0	C
Brevor	0.0	C
11-225-7H	0.0	C
Brundage	0.0	C
Cara	0.0	C
Cayuga	0.0	C
Elmar	0.0	C
Hill 81	0.0	C
Hyslop	0.0	C
Kaseberg	0.0	C
Ladd	0.0	C
Lewjain	0.0	C
11-225-2C	0.0	C
Malcolm	0.0	C
Mary	0.0	C
Nugaines	0.0	C
Omar	0.0	C
ORCF-101	0.0	C
Eltan	0.0	C
ORCF-103	0.0	C
ORSS-1757	0.0	C
Rely	0.0	C
Rod	0.0	C
ORCF-102	0.0	C
Skiles	0.0	C
Stephens	0.0	C
Tubbs	0.0	C
Tubbs-06	0.0	C
Rosalyn	0.0	C

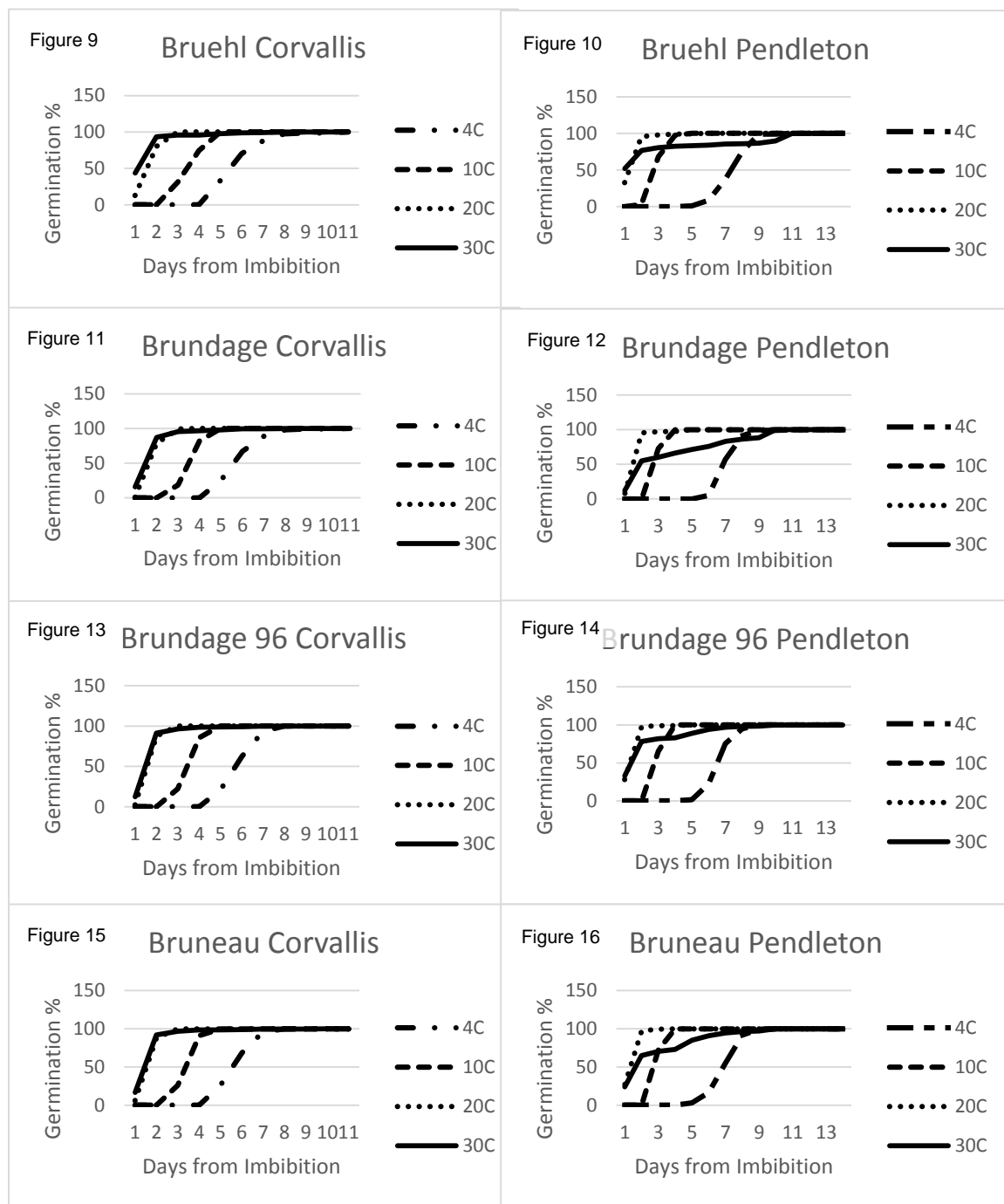
Analysis of Varietal Differences by Location

Since the statistical analysis showed there were significant differences between the varieties at each location, it showed the varieties interacted differently with the different temperature treatments. This difference is presented below (Figures 1-90) with two figures per variety illustrating each variety's response in germination percentage at each temperature. Each variety at each location has a separate graph in order to visually compare the differences between the varieties germination rate at each temperature and location. The germination patterns of the varieties tend to follow a similar trend within a location, but slight differences can be seen between germination rates at different temperatures between the two locations.

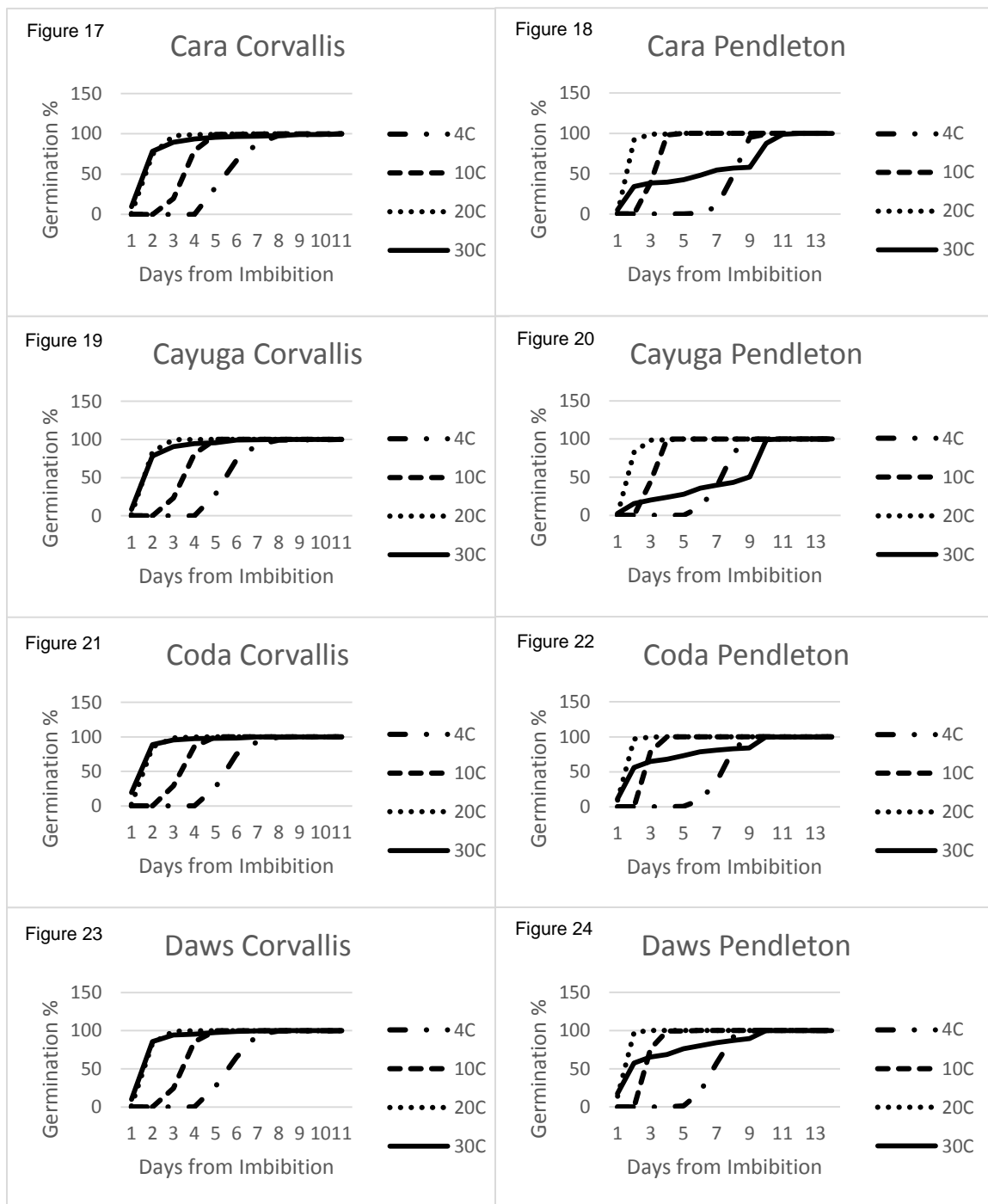
Figures 1-8. Seed germination rate under different temperature regimes across two locations.



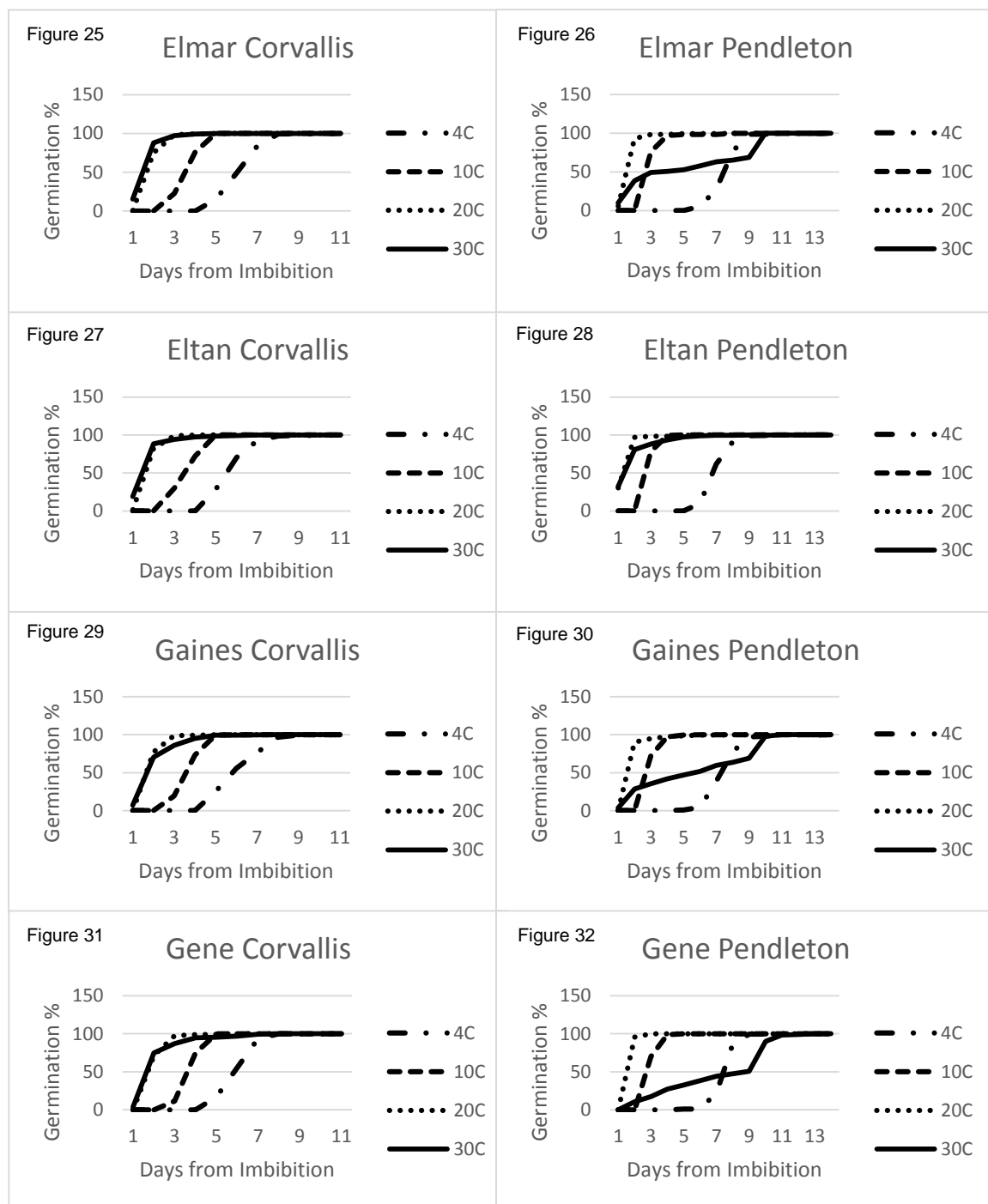
Figures 9-16. Seed germination rate under different temperature regimes across two locations.



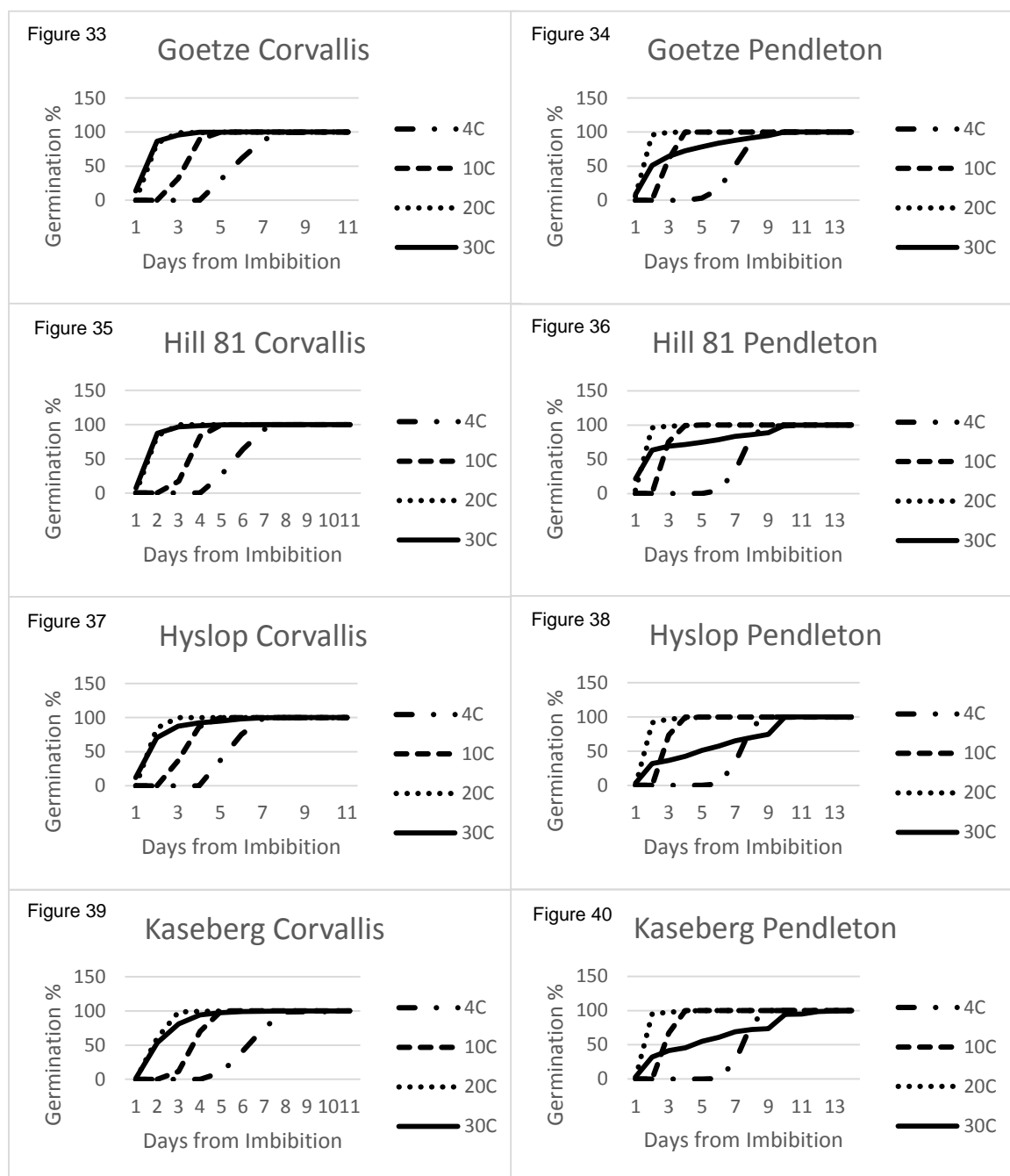
Figures 17-24. Seed germination rate under different temperature regimes across two locations.



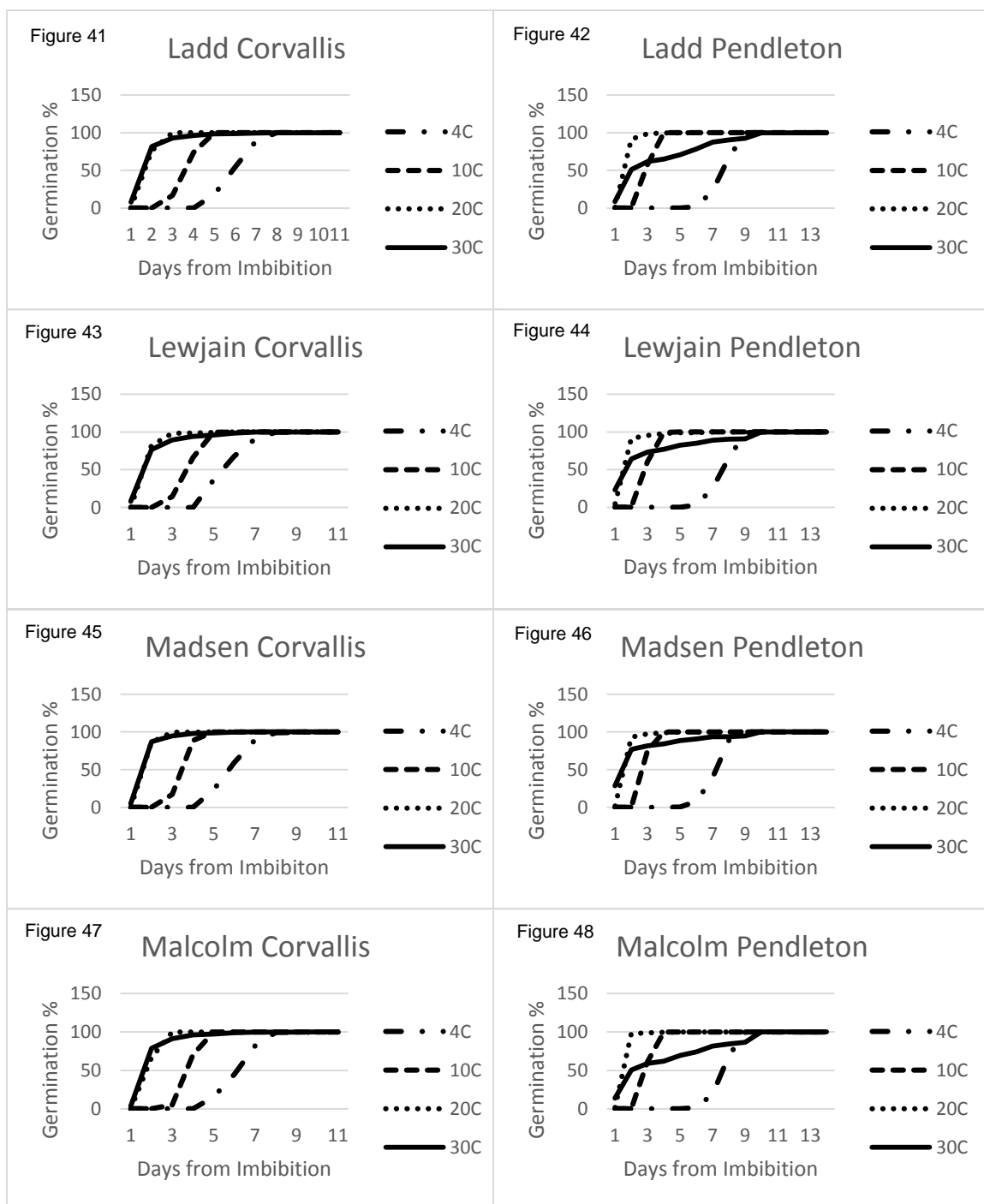
Figures 25-32. Seed germination rate under different temperature regimes across two locations.



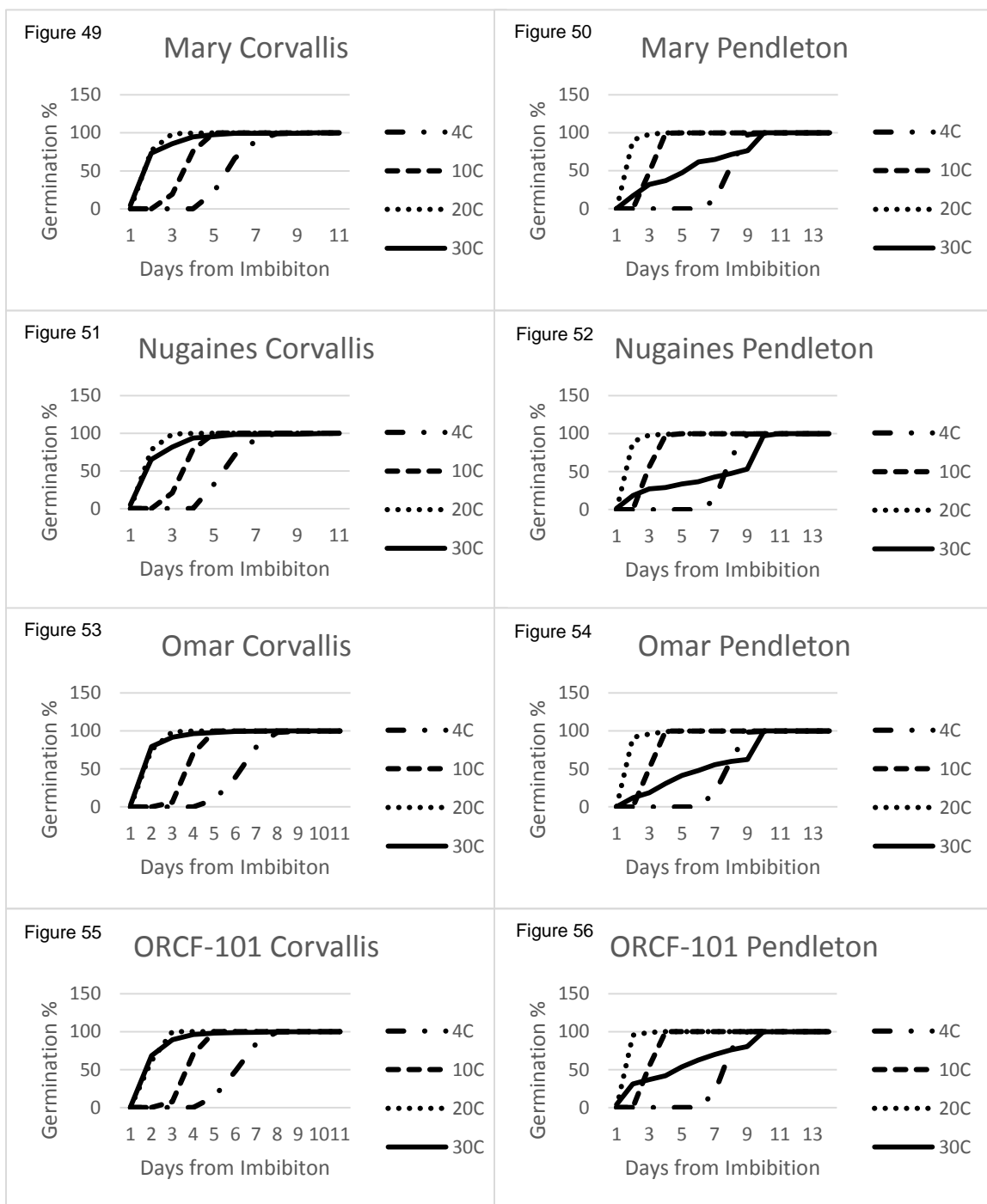
Figures 33-40. Seed germination rate under different temperature regimes across two locations.



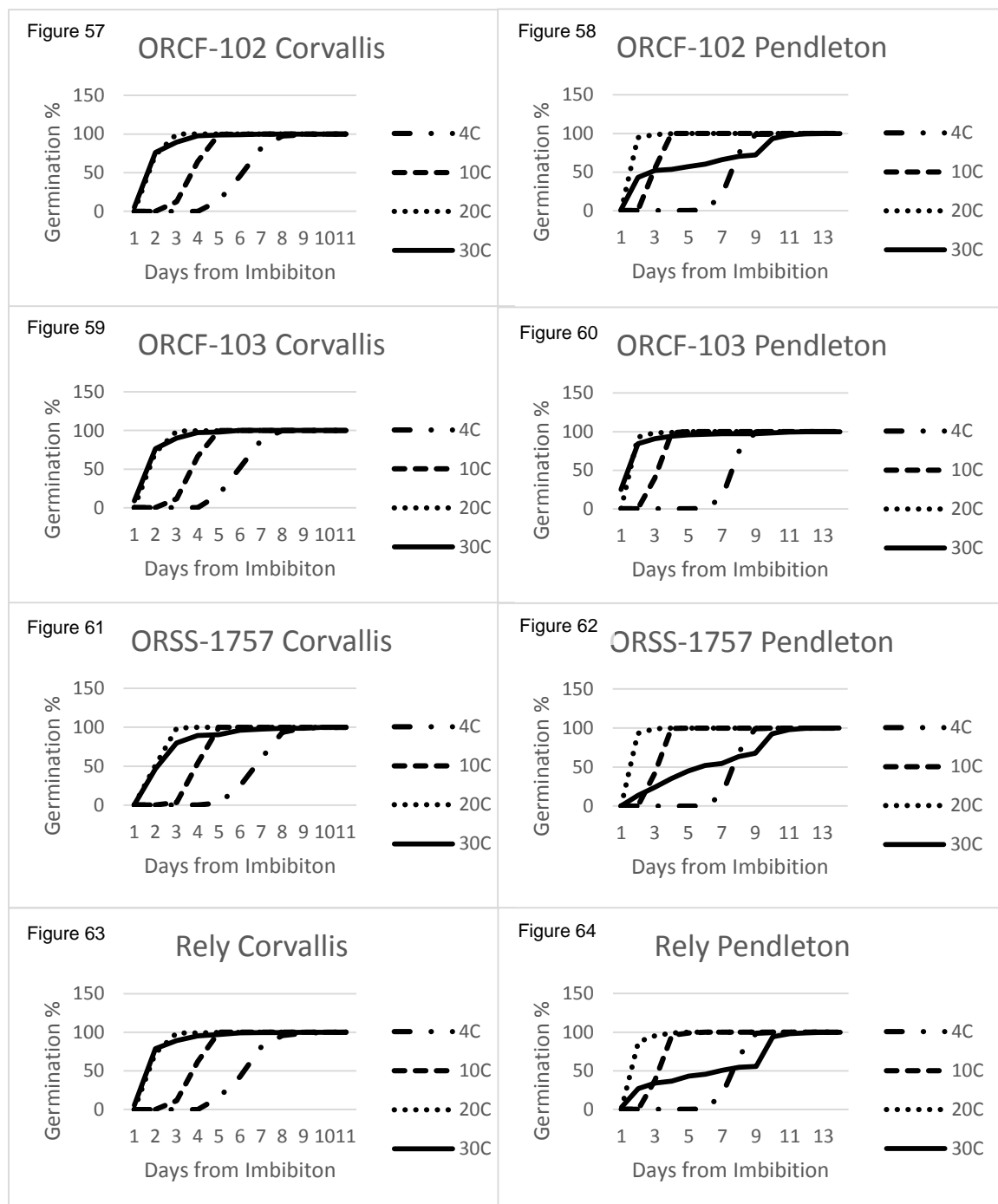
Figures 41-48. Seed germination rate under different temperature regimes across two locations.



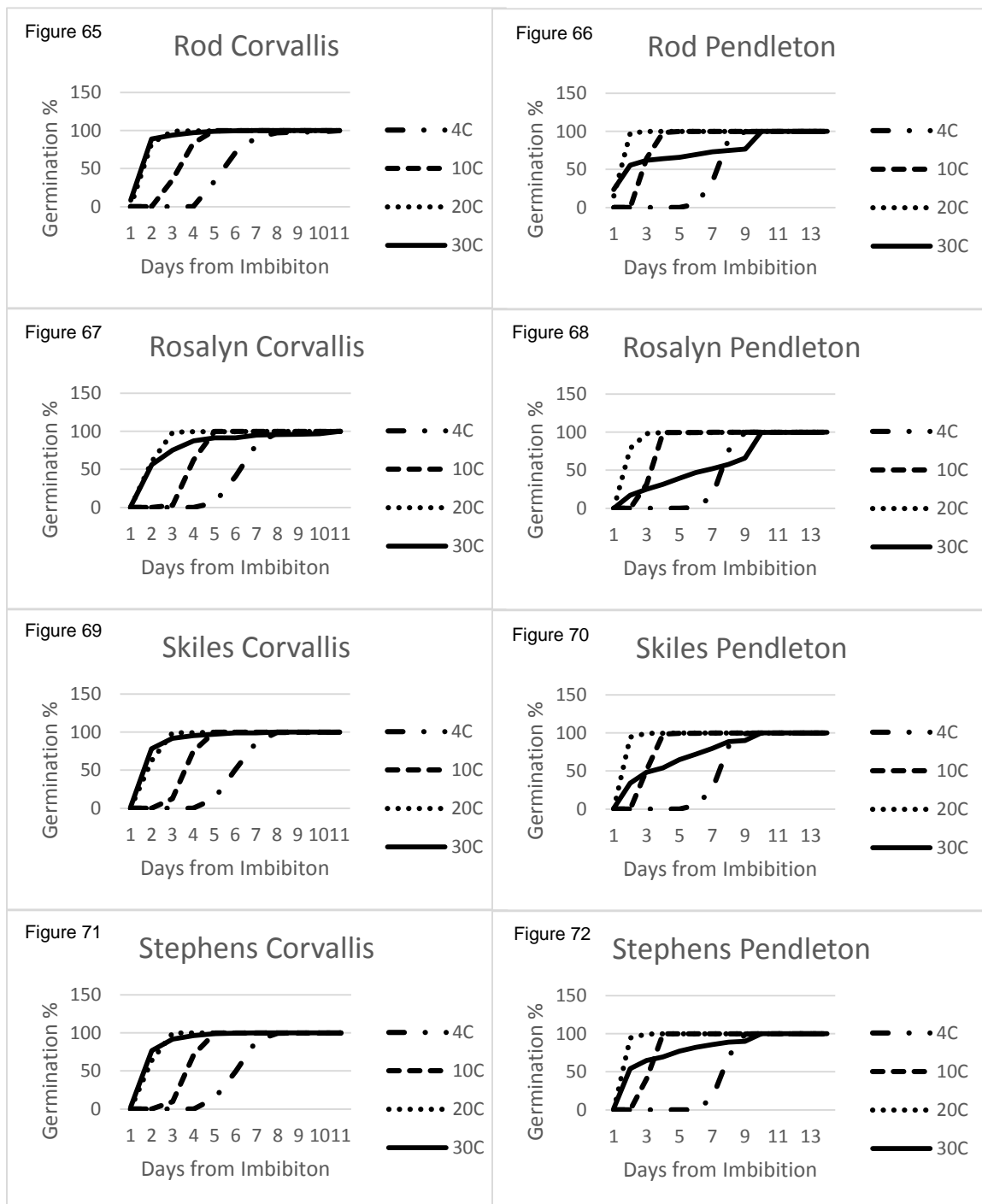
Figures 49-56. Seed germination rate under different temperature regimes across two locations.



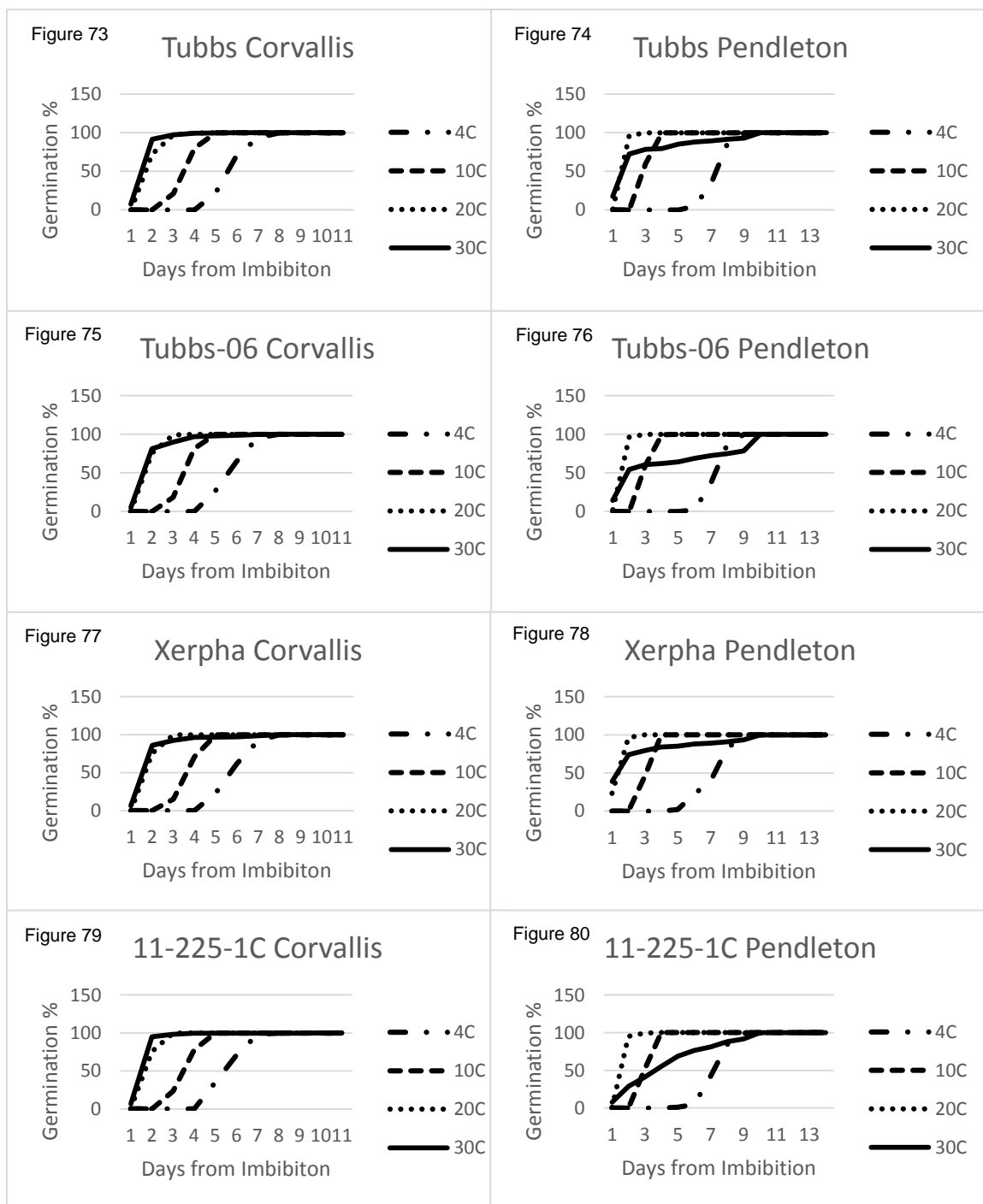
Figures 57-64. Seed germination rate under different temperature regimes across two locations.



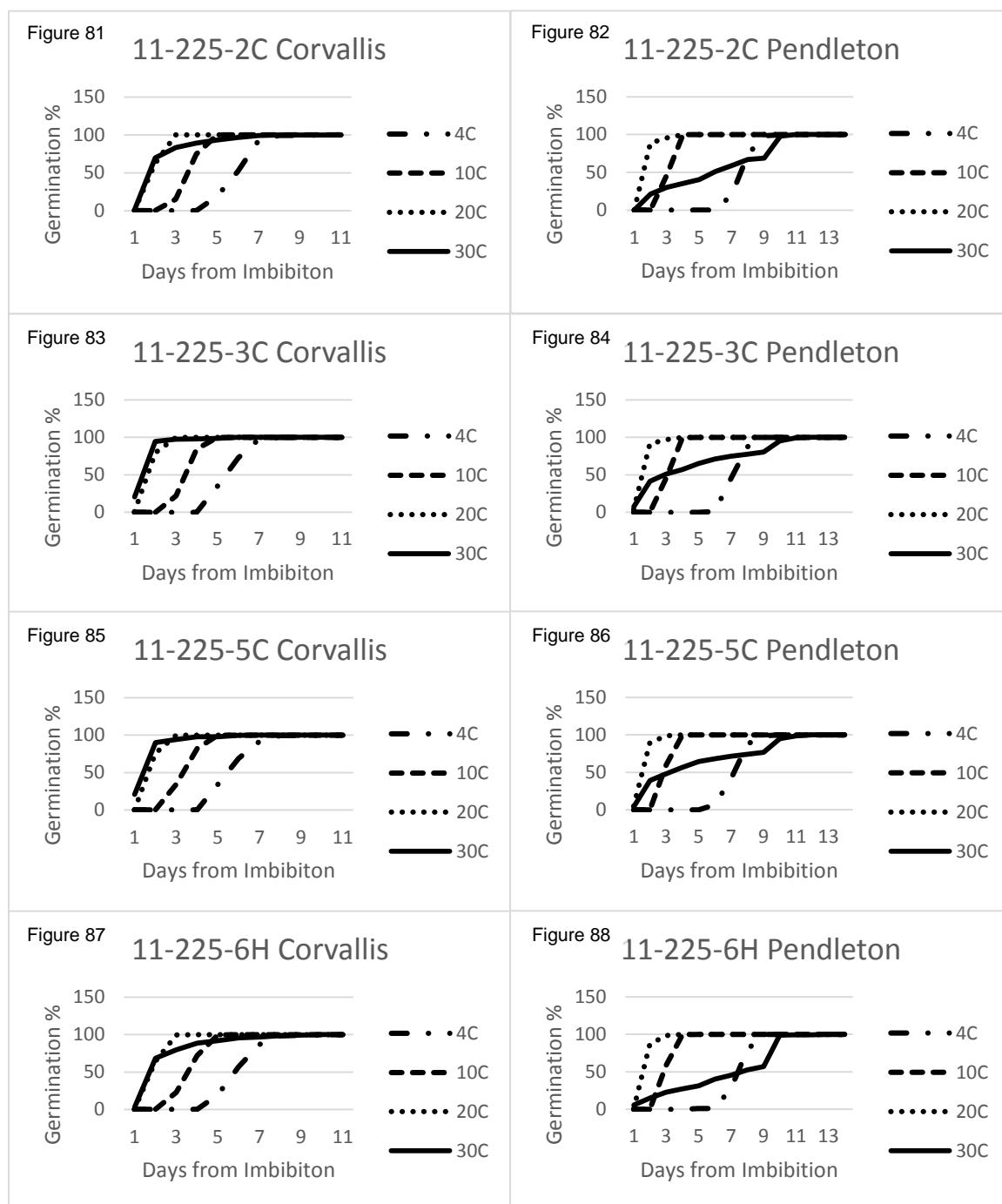
Figures 65-72. Seed germination rate under different temperature regimes across two locations.



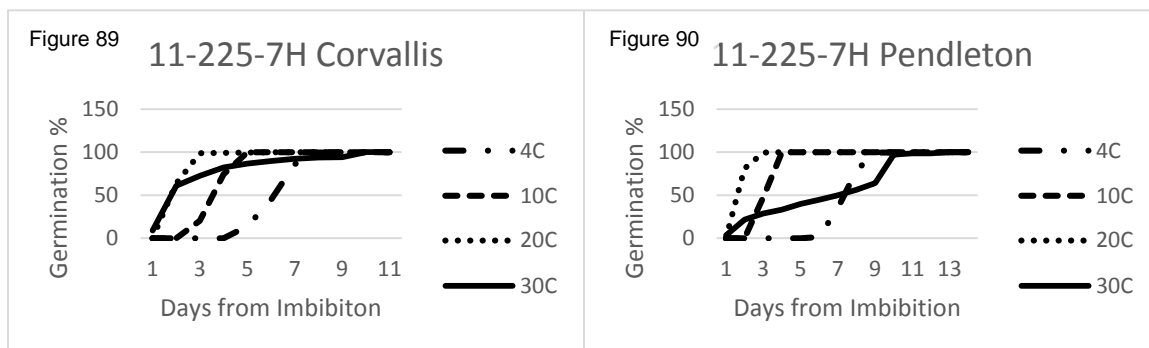
Figures 73-80. Seed germination rate under different temperature regimes across two locations.



Figures 81-88. Seed germination rate under different temperature regimes across two locations.



Figures 89-90. Seed germination rate under different temperature regimes across two locations.



Figures 1-90 all show similar trends for each temperature across the same locations. However, comparing locations, all of the temperatures show relatively the same pattern of germination rate except for the 30°C treatment. The seeds placed under the 30°C treatment from Corvallis tend to follow a similar germination rate as the seeds that were placed in the 20°C treatment. While the seeds placed in the 30°C treatment from Pendleton have a unique germination rate that is rather gradual. By looking at the 30°C treatment on the graphs above from the Pendleton location, the drastic spike in seed germination that can easily be seen in the variety Cayuga (Figure 20) or 11-225-7H (Figure 90), is the result of when the seeds were moved from the 30°C treatment to the 20°C chamber between the ninth and tenth day. The seeds in the 4°C, 10°C and 20°C treatments tend to have a spike in seed germination at a given point, but the day in which this occurs is different for each temperature. Across both locations, these temperatures have a similar pattern at each temperature for each variety. These graphs also show the wide variance in germination rates between the 45 varieties that were tested. Regardless

of the location or temperature, all of the varieties reached 100% seed germination within the fourteen days of the experiment.

Falling Number Results

A table of means for all of the falling numbers gathered from each location for each variety can be found in table 3.30. The varieties Bruehl and Brundage had falling numbers that were below 300 seconds for all three replications from Corvallis. The variety Brevor and Gene were low but still above 300 seconds. None of the varieties harvested from Pendleton had a falling number below 300 seconds.

Table 3.30. Falling number averages for each variety and location (all field replications and falling number replications were averaged for each location separately).

Variety	Pendleton	Corvallis	Variety	Pendleton	Corvallis
Alba	491	380	Malcolm	491	413
Bitterroot	463	384	Mary	461	440
Bobtail	441	404	Nugaines	474	413
Brevor	486	309	Omar	463	417
Bruehl	399	235	ORCF-101	416	391
Brundage	449	214	ORCF-102	462	384
Brundage 96	433	352	ORCF-103	455	347
Bruneau	487	412	ORSS-1757	412	418
Cara	462	424	Rely	498	456
Cayuga	450	425	Rod	464	413
Coda	518	485	Rosalyn	413	396
Daws	466	369	Skiles	464	422
Elmar	472	379	Stephens	434	412
Eltan	488	374	Tubbs	460	413
Gaines	490	435	Tubbs-06	466	405
Gene	373	303	Xerpha	471	392
Goetze	439	405	11-225-1C	405	371
Hill 81	449	401	11-225-2C	414	388
Hyslop	482	404	11-225-3C	414	383
Kaseberg	436	436	11-225-5C	415	399
Ladd	464	340	11-225-6H	415	403
Lewjain	531	440	11-225-7H	428	397
Madsen	470	423			

An analysis of variance was run on the falling number data that was collected from each location separately. Table 3.31 below shows the ANOVA table results from the falling numbers from the varieties harvested from Corvallis. The results showed there were significant differences found between the varieties. Table 3.32 shows the results of the ANOVA table from the falling number test that was taken on all the varieties harvested from Pendleton. The results show there were significant differences between replications (reps) but there were no significant differences between the varieties.

Table 3.31. ANOVA Table results from the falling numbers test from the varieties harvested from Corvallis ('S' indicates significance).

Corvallis						
Source	df	SS	MS	F	Fcritical	P-value
Total	89	748409.50				
Reps	2	2780.01	1390.01	0.29	3.10	0.75
Variety	44	327142.17	7435.05	1.56	1.51	0.04
Error	88	418487.32	4755.54			

S

Table 3.32. ANOVA Table results from the falling numbers test from the varieties harvested from Pendleton ('S' indicates significance).

Pendleton						
Source	df	SS	MS	F	Fcritical	P-value
Total	89	280010.70				
Reps	1	21329.00	21329.00	5.74	4.06	0.02
Variety	44	95304.99	2166.02	0.58	1.65	0.96
Error	44	163376.74	3713.11			

S

The results from the ANOVA table from Corvallis showed there were significant differences between varieties. To compare varieties, an LSD test was run on the data from Corvallis. No statistical comparison was done on the Pendleton site for falling number since there was no significant differences among the varieties. Table 3.33 shows the results from the LSD test.

Falling Number LSD Analysis

The varieties Brundage, Bruehl, Gene and Brevor had the lowest falling number results that were statistically significant (Table 3.33). Brundage and Bruehl were statistically the lowest and did not fall into other significant groups. Gene and Brevor fell in the next lowest significance category, however, Brevor was not found to be statistically different than the variety Ladd. Brundage and Bruehl based on their sub-300

falling number score would not be acceptable for export or for use by the baking industry in the U.S. due to the elevated levels of alpha amylase. Gene and Brevor scores would be acceptable in the US but are on the low end of acceptable falling number scores with some of the replication scores coming in under 300 seconds. The raw data from the falling number results can be found in Appendix 8.

Single Kernel Hardness Results

A complete set of data from the single kernel hardness test for all varieties from both sites is listed in Appendix 9. The data set includes the hardness average, average kernel weight, the average moisture of the kernels as well as the average diameter of the kernels. An analysis of variance was run on the kernel hardness data that was collected from each variety and replication at each location. The analysis was done for each location separately. Table 3.34 shows the ANOVA results from the data collected from the varieties that were harvested from the Corvallis location for kernel hardness. Table 3.35 shows the ANOVA results from the data collected from the varieties that were harvested from the Pendleton location for kernel hardness.

Table 3.34. The ANOVA table from the single kernel hardness data gathered from the Corvallis location ('S' indicates significance).

Corvallis						
Source	df	SS	MS	F	Fcritical	P-value
Total	89	17211.97				
Reps	2	11.45	5.72	0.05	3.10	0.95
Variety	44	8017.53	182.22	1.75	1.51	0.01
Error	88	9182.99	104.35			

S

Table 3.35. The ANOVA table from the single kernel hardness data gathered from the Pendleton location ('S' indicates significance).

Pendleton						
Source	df	SS	MS	F	Fcritical	P-value
Total	89	12863.86				
Reps	1	334.94	334.94	2.17	4.06	0.15
Variety	44	5750.58	130.70	0.85	1.65	0.71
Error	44	6778.34	154.05			

The ANOVA results show there were statistical differences between the kernel hardness from the varieties that were harvested from the Corvallis location but no differences observed among varieties grown at the Pendleton location. An LSD test was only performed on the seed harvested from Corvallis and the results can be found in Table 3.36.

Single Kernel Hardness LSD Analysis

There was a wide range of kernel hardness found among the varieties harvested from Corvallis (Table 3.36). The variety with the highest kernel hardness was the club variety Elmar, with a hardness average of 37.4 HU, while the softest variety was Kaseberg, with a kernel hardness average of 2.6 HU, which was not significantly different than ORSS-1757. The kernel hardness of the varieties from Corvallis ranged from 2.6-37.4 HU. Even though an LSD test was not performed on the varieties harvested from Pendleton, the kernel hardness ranged from 20.1-51.3 HU. The hardest kernels from Pendleton were found to be from the variety Coda, followed by Elmar and the softest kernels were from the variety ORSS-1757 and the experimental cross 11-225-1C, even though none of the varieties were found to be statically different.

Discussion

Field grain ripening conditions played a huge role in seed germination and dormancy expression. Temperature during seed germination also played a subsequent role in how quickly the grain germinated. The data from the first trial that was conducted during the first year of the study demonstrated the temperature that grain is stored at immediately after harvest can have a slight effect on germination rate. Placing dry seeds at 4°C rather than around 20°C can slightly delay seed germination within the first forty-eight hours depending on the variety. At optimal germination temperature (20°C), all the varieties germinated within a week of being imbibed, demonstrating a quick after-ripening period. For the second experiment during the first year, the seeds placed in the 20°C treatment showed how quickly the seeds germinate under ideal temperatures, which was also observed in the first experiment. It also showed that cool conditions slowed down the germination rates of the varieties. Since this second trial did not occur directly after harvest, it is possible the seed had already gone through an after-ripening period before being imbibed. From the preliminary data, it showed there is no seed dormancy expression when the seed is placed at 20°C or 4°C. This data also showed there were differences between the rates at which different varieties germinate.

Since the experimental trials were run differently between the first and second year of the study, it is difficult to compare across years due to the difference in time between when the plots were harvested and when they were placed in their respective treatments. The data does however show that some of the quickest germinating varieties such as Bitterroot and Brundage 96 were the most rapid to germinate both years at 20°C.

The best correlation between years that can be observed is between the varieties under the 4°C treatment. When comparing the seventh day from the first year when the seeds were moved to the 20°C chamber with the seventh day of the varieties in the 4°C treatment that were harvested from Pendleton, one can see that the varieties Bitterroot, Brundage 96, Eltan, Bruneau and Alba, all have the ability to germinate under cold stress. The varieties that appear to have the slowest germination rate at 4°C were Mary, Nugaines, ORSS-1757, Rosalyn, ORCF-103 and Malcolm. The varieties harvested from Corvallis the second year were not necessarily used in this comparison because the results from the first year's data and the data from Corvallis the second year were not as complimentary.

In the second year of the study, there appeared to be a large impact from the grain ripening conditions on how quickly the different varieties germinated at each temperature. The seed harvested from Corvallis germinated much quicker at 30°C, 20°C and 10°C than the seed harvested from Pendleton, while all the seed reached 100% seed germination on the same day from both locations under the 4°C treatment. Typically, one would expect to see similar trends across both locations for each treatment. However, this was not the case in this experiment.

By comparing the varietal response shown in Figures 1-90 (odd numbered figures from Corvallis; even numbered figures from Pendleton), the trends are relatively similar across each location separately, but the differences between the two locations are noteworthy. The 20°C treatment is the optimal germination temperature for soft white winter wheat according to Lei et al. (2013), and therefore, the results from this treatment illustrate which varieties tend to germinate quicker than others and which varieties tend

to take longer to germinate. For all varieties at both locations, the seeds germinated the quickest under this temperature regime. The 10°C and 4°C treatments had very similar trends at both locations where germination was delayed initially as the temperatures declined. Once the seeds began germinating at either temperature, the majority of the seeds had completed germination within a few days. Germination at 4°C had a few more varieties which had a few seeds which germinated much later than the majority of the seeds from a given variety. Regardless, all the varieties had complete seed germination within the fourteen days of the experiment. The 4°C temperature was also the only temperature in which complete seed germination occurred within the same time period at both locations. An explanation for this would be that the cold temperature eliminated any major differences among the varieties associated with the grain ripening conditions.

The largest difference between locations was observed with the 30°C treatment. As noted by Biddulph et al., 2007, higher temperatures can induce high temperature dormancy. There is higher dormancy expression illustrated from the 30°C treatment from the varieties that were grown in Pendleton, which is observed by the general slow progression of seed germination over the fourteen days of the trial. This trend is not observed from the varieties that were harvested from Corvallis. The seeds that were placed in the 30°C treatment from Corvallis tend to follow a similar germination pattern as the seeds in the 20°C treatment. A few varieties harvested from Pendleton, such as Bitterroot, show a similar germination pattern at 30°C at both locations. This would indicate that this variety has a much lower level of dormancy than other varieties such as Cayuga, which had drastic differences between germination rates at 30°C between the

two locations. As the statistical results show, the varieties that germinated the quickest at 30°C from Pendleton and had similar trends as the same variety from Corvallis, were the varieties that fell into the first significant groups, which demonstrated they had the lowest level of dormancy expression.

The two locations were originally expected to have similar results where the seeds placed in the 30°C treatment would demonstrate some level of dormancy expression with a less than ideal germination temperature. The results from this experiment partially support that expectation as the varieties as a whole from Pendleton showed a much stronger dormancy and difference in dormancy expression at 30°C than the seeds that were harvested from Corvallis. The grain ripening conditions from Pendleton were overall much warmer, while Corvallis had a milder, slightly cooler grain ripening environment. According to Nyachiro et al., 2002, this would cause the seed from Pendleton to have a lower dormancy expression than the seeds from Corvallis. However, in this experiment, the results showed that the seeds from Pendleton had a higher expression of dormancy, while not much dormancy expression was observed from the seeds harvested from Corvallis. It is possible that while warmer, the temperatures in Pendleton were not high enough to cause a decrease in dormancy. The results of this study did show that there were obvious differences in dormancy expression between the two different growing environments.

The differences in dormancy expression between the two locations could be explained by the fact that there were separate rain events that occurred prior to harvest. These rain events could have impacted the results that were found the second year. In

Corvallis, there were two major rain events that occurred before the plots were harvested and there was only one rain event that occurred in Pendleton before harvest. The second rain event, in which it rained 0.28 cm in Corvallis, had occurred two days prior to harvest and the temperatures were milder following the rain. This rain event could have primed the seeds so when they were placed in their respective treatments, many, if not all of the varieties were ready to germinate when they were imbibed. This would explain why the bulk of the varieties from Corvallis had a high germination rate within the first few days, while the same varieties from Pendleton germinated at a slower rate. This would also explain why the seeds from Corvallis didn't show dormancy expression at 30°C. When the seeds have already taken up water under more ideal temperatures, the warm temperatures of 20°C and 30°C just allowed the seeds to germinate quickly. The 30°C treatment was warm for a lot of the seeds, and since it didn't induce high temperature dormancy for the seeds from Corvallis, the seeds that were unable to germinate at 30°C ended up molding. The stronger, more vigorous seeds from Corvallis were not nearly as affected by the warmer temperature, so in turn, they readily germinated.

Since the 20°C treatment demonstrated which varieties germinated the quickest under ideal germinating temperatures, they can be correlated with which varieties showed the strongest or weakest dormancy expression at 30°C. By taking a look at the seeds harvested from Pendleton in the 20°C treatment after two days of imbibition, many of the varieties were close to reaching 100% seed germination from both locations. The varieties Brevor, Rosalyn, 11-225-7H, Cayuga, 11-225-6H, Rely, 11-225-5C and Gaines had the lowest germination percentage. After two days in the 30°C treatment, the

varieties Gene, Omar, Brevor, ORSS-1757, 11-225-6H, Cayuga, Rosalyn and Mary were found to be the slowest germinating varieties. A few of the varieties that were the lowest from the 20°C treatment were also found to be slower germinating at a warmer temperature, which is not a surprise. By the fourth day from imbibition, the slowest germinating varieties from the 20°C treatment were Brevor, Gaines, Brundage, Lewjain and Hyslop while the slowest germinating varieties from the 30°C treatment were Cayuga, Brevor, Gene, 11-225-6H, Nugaines, Omar, Rosalyn and 11-225-7H. The two varieties, Cayuga and Brevor, that had previously been reported to have dormancy expression from experiments by Munkvold et al. (2009) and Walker-Simmons (1987), both showed dormancy at 30°C from the seed harvested from Pendleton, but not from Corvallis. The variety Brevor, along with expressing dormancy at 30°C, also was found to be a slower germinating variety, even at the optimal 20°C temperature. This information questions if Brevor truly demonstrates seed dormancy or if it's simply a slow germinating variety.

The results collected from the 20°C and 30°C treatment from Corvallis can also be compared to each other, but their correlation with the results from Pendleton do not line up as well as anticipated. The slowest germinating varieties from Corvallis at 20°C after being imbibed for two days were ORSS-1757, Rosalyn, Kaseberg, ORCF-101, 11-225-2C, Skiles, 11-225-7H, Stephens and Brevor. On the same day, the slowest germinating varieties at 30°C were ORSS-1751, Brevor, Kaseberg, Rosalyn, Alba, 11-225-7H, Nugaines, ORCF-101 and 11-225-6H. From this location, there were five varieties that were observed to be slower germinating at both temperatures, which

indicate the germination rate is heavily influenced by the interaction between the genotype of the variety and the germination temperature. By the fourth day of being in their respective treatments, the slowest germinating varieties at 20°C were Brevor, Lewjain, Bobtail, Cara, Gene, Skiles, Rely and 11-225-7H while the slowest germinating varieties at 30°C were Brevor, Alba, 11-225-7H, Rosalyn, 11-225-6H, 11-225-2C, ORSS-1757 and Hyslop. The varieties in the 20°C treatment were close to having 100% seed germination, while the varieties in the 30°C treatment were not too far behind. The 30°C treatment seemed to slow down the germination rate of the varieties. Since the majority of the varieties from the 20°C treatment were close to having 100% seed germination, it is difficult to compare to the varieties from the 30°C treatment. This is because the differences between the slowest germinating varieties from the 20°C treatment was due to approximately a 1% difference in germination.

The variety Cayuga was used as a check cultivar since it had been reported to express grain dormancy in previous studies (Munkvold et al., 2009). Due to this, it would be expected that Cayuga would be a slower germinating variety due to enhanced high temperature dormancy expression when placed in the 30°C treatment. From Pendleton, Cayuga showed a slower germination rate under the 30°C treatment, however, Cayuga was not found to be one of the slower germinating varieties from Corvallis. This indicates there was an influence from the grain ripening environment at Corvallis that broke the grain's dormancy expression, which did not occur at the Pendleton location. Examination of the results from all varieties and comparisons results across locations, there is evidence of an environmental impact. The milder grain ripening environment experienced by the

varieties harvested in Corvallis could have greatly impacted the level of dormancy expressed. According to Thomason (2009), cooler temperatures just before seed maturity can lead to increased seed dormancy, however, cool and moist conditions after maturity can lead to increased PHS and the more wetting and drying cycles the seed goes through the more likely dormancy will be broken. Based on the more rapid germination observed from the varieties grown at Corvallis and the rain event that occurred close to harvest, a speculation can be made from the observed results. It is likely that the rain event that occurred in Corvallis led to a breakdown of the grain dormancy, resulting in more rapid seed germination even at 30°C. The variety Brevor also was used as a secondary check cultivar based on literature showing it had a stronger dormancy expression, however, the data shows that Brevor generally has a slower germination rate, as it is one of the slowest germinating varieties across all temperatures, including the ideal temperature of 20°C at both locations. This indicates that instead of having higher post-harvest dormancy, Brevor is just slower germinating.

The falling number results as well as the single kernel hardness data also support the conclusion that there was a large impact of the grain ripening conditions between the two locations. The data collected also support the speculation that the rain events played a major role in the differences observed during the germination trials. The seeds had already dried down in the field and therefore, they had a low water potential. This low water potential allows the seed to take up water when it rained. As a seed begins to take up water, it activates enzyme systems and phosphorylation, which act to mobilize stored reserves in the endosperm. With the activation of enzymes, GA is synthesized and in

turn, stimulates the expression of alpha and beta amylase (Mrva et al., 2005). Water uptake by seeds from Corvallis could have resulted in GA synthesis, resulting in slightly elevated levels of alpha-amylase and reduced seed dormancy expression.

Elevated levels of alpha-amylase in the different varieties can be inferred by comparing the falling number results, which indirectly measures the alpha-amylase levels of each variety between the two locations. The results from Corvallis show lower falling number results than the results from Pendleton for every variety except ORSS-1757. The varieties that had a low falling number from Corvallis also had a lower falling number from Pendleton, however, every variety from Pendleton had a falling number above 300 s, which was not the case with the varieties from Corvallis. This data shows a correlation in the varieties natural falling number range. Those varieties with a high falling number without any influence from a rain event (Pendleton) still had a higher falling number even when the seed experienced 0.28 cm of rain (Corvallis), which gives the variety a higher probability of making grade. On the flip side, those varieties that naturally have a lower falling number are less likely to make grade even when they experience a little bit of rain. The variety Bruehl appeared to be a variety that has a naturally lower falling number, and when the variety experienced a single rain event, the variety failed to make grade. This was observed when comparing the falling number of Bruehl from Pendleton and Corvallis. The falling number from Pendleton was slightly above 300 s, however, with the rain events that occurred in Corvallis, the falling number dropped below 300 s, which would make it unacceptable for market.

The seed harvested from Corvallis also had a softer kernel hardness than the seed harvested from Pendleton. The kernel hardness from Corvallis ranged from 0.6-38.8 HU, while the range of kernel hardness from Pendleton was from 15.9-56.1 HU. As stated by Maghirang and Dowell (2003), the kernel hardness is affected by the degree of adhesion between starch granules and endosperm protein matrix. The starch matrix would begin to be broken down when the seed begins to germinate. The seeds from Corvallis had a lower falling number than the seed from Pendleton, indicating the activation of starch degrading enzymes. As a general trend, the varieties with the harder kernels tended to be clubs and one of the softest varieties in this study, ORSS-1757, was bred and released as a super soft wheat.

The second year of this study showed a typical scenario of what occurs when rainfall occurs prior to harvest. There was a total of approximately 2.54 cm of rain that was received from June to harvest at the Corvallis location and 2.03 cm of rain at the Pendleton location. The rainfall at Pendleton occurred early enough during the grain ripening process in July that it did not appear to impact the varieties falling number results. Having the second rainfall event at the Corvallis location two days prior to harvest was not the ideal situation for this study, however, it provided perfect conditions to observe differences in PHS response of varieties. The amount of rain wasn't detrimental to majority of the varieties in this study, which demonstrates some varieties are more impacted by a limited amount of rainfall than others. Varieties with higher falling number values and/or higher seed dormancy when rainfall does not occur are more likely to make grade when rainfall occurs even if the seed germination patterns are

affected. With falling numbers above 300 s, the value of the grain is not downgraded, allowing the grain to be still acceptable for market. Even if the grain has a slightly lower falling number than when it is not affected by rain, as long as the falling number is above 300 s, its milling integrity and baking qualities are not compromised. Without its end-use quality being depreciated, the market value of the grain is not decreased.

If growers continually experience PHS conditions, the best variety to grow would be the variety with the highest natural falling number which germinates slower at 30°C. The benefit of having high temperature induced dormancy is that in most years, it is warm during the summer months prior to harvest. Even if a rain event occurs during this time, if the variety demonstrates dormancy at 30°C, it is less likely to completely germinate before the grain is harvested. If the variety typically has a high falling number, it provides a buffer if some rain occurs before the field is able to be harvested. The varieties Brevor and Gene have proven to be slower germinating varieties, however, they are not ideal varieties to grow in areas that receive summer rain since they naturally have a lower falling number. The three best varieties to plant in this situation would be Rely and Cayuga followed by Nugaines. All of these varieties demonstrated a higher seed dormancy at 30°C and they had rather high falling number as well. These three varieties had a falling number over 400 s at both Corvallis and Pendleton under the environmental conditions experienced in this experiment. Even though these varieties did not show dormancy expression from the seed harvested from Corvallis under the 30°C treatment, the falling number was still well above the 300 s cut off mark, which gives them a nice buffer for when they experience conditions that could lead to PHS. The variety Cayuga,

which was used as the dormancy check cultivar, also demonstrated seed dormancy in this study. The variety Rely was shown to have dormancy expression, but its degree of high temperature induced dormancy is slightly lower than Cayuga.

This study showed there were no distinct differences in year of cultivar release for dormancy response which indicates that dormancy had not been systematically bred out of soft white winter wheat in order to achieve rapid uniform germination. The varieties which showed the strongest high temperature dormancy were: Brevor, Bobtail, Cayuga, Gene, Nugaines, Rely and 11-225-6H. From these varieties, the oldest released variety was Brevor (released in 1949) and the most recently developed line was the advanced line 11-225-6H, which is still in advanced testing in the Oregon State University breeding program. If the dormancy period had been bred out of soft white winter wheat, then the oldest varieties would be expected to have had the strongest dormancy expression. However, the varieties Alba, Elmar, and Omar did not show the strongest high temperature induced dormancy expression, even though they were some of the oldest released varieties in this study. Even though some varieties showed strong high temperature induced dormancy, none of the varieties tended to show post-harvest dormancy. Since dormancy is the inability of a viable seed to germinate under optimal conditions (Gao and Ayele, 2014), from this study, none of the varieties failed to germinate under the 20°C treatment from both years and locations. This indicates that the varieties had either gone through an after-ripening period in the field prior to harvest or none of the varieties in this trial have a dormancy period to begin with, unless it is induced by high temperatures.

This study showed major differences among the 45 varieties / advanced breeding lines of soft white winter wheat for germinating at different temperatures. There are still many unknowns regarding seed dormancy expression under different dry grain ripening environments. Even though this study included practical field PHS conditions, it was unable to look at differences between dormancy expressions of the varieties with different temperature ripening conditions to see how that directly impacts dormancy. This study demonstrated that different growing environments greatly impact varietal responses to changes in the environment through seed maturity. Further studies should investigate how warmer and cooler grain ripening environments impact these variety's dormancy expression, when rainfall does not occur prior to harvest.

This experiment was conducted as efficiently as possible, however, to improve the results of this experiment, improvements could be made. The first year provided preliminary results, but major changes could have improved the results that were found. The seeds from the second experiment during the first year should have been imbibed and placed in the treatments within forty-eight hours after harvest. This is because the seeds placed at 20°C showed there was no post-harvest dormancy expressed by the seeds under these ideal conditions, but it is possible the seeds already went through an after-ripening period prior to being placed in the treatments. The first year turned out to be a learning curve and proved to be valuable for how the second year was conducted. Even during the second year, improvements on how the germinated seeds were counted could be adjusted. To do this, it would be best to remove one petri dish from the treatment at a time to count the germinated seeds. During this experiment, the seeds were counted by taking

approximately twenty-eight petri dishes out of the treatment at a time and once all of the petri dishes were counted, they were placed back in their treatment chambers. Even though they were not out of their treatments for a long period of time, it could have been long enough to impact the results. The greatest impact would have been on the seeds placed in the 4°C treatment, where it provided enough time to slightly warm the water in petri dishes prior to being placed back in the treatment. Even though this could be improved, all of the petri dishes within a treatment experienced the same conditions.

In order to gather more data that looks at seed dormancy of the 45 lines from this experiment, looking at the seed's dormancy expression as the grain dries down could indicate the period of time in which dormancy is lost. By conducting germination trials weekly from the time the grain reaches the hard dough stage to the time in which the grain reaches 12% moisture, would provide a timeline in which grain dormancy is the strongest to when the grain completely loses dormancy. It would be interesting to observe how dormancy expression changes between 20°C and 30°C treatments at each weekly stage. The current experiment showed that high temperature can induce dormancy, but the 20°C treatment demonstrated the seed's actual dormancy since dormancy would prevent a seed from germinating under ideal conditions. This proposed type of experiment would confirm or disprove that soft white winter wheat does or does not have a dormancy period by the time the grain is harvested. Results from further testing would also show if soft white winter wheat goes through an after-ripening period in the field, before it is even harvested. These results would show the period of time in which a rain event is the most detrimental and expose the grain to PHS. Knowledge of when grain

dormancy is lost or which varieties have a dormancy period would be beneficial to growers so they would know the time frame in which they should be most concerned about PHS occurring.

This current research demonstrated that soft white winter wheat can experience high temperature induced dormancy. However, if the seed has already been moistened, or if the variety experiences multiple rain events, it is likely to begin sprouting in the field. As demonstrated by the results from the second year Corvallis trial, if the seed has been exposed to rain close to the time of harvest, any high temperature induced dormancy is reduced or eliminated.

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Chapter 4: Variety Identification

Abstract

Developing cultivars that remain uniform and true to type without plant segregation and contamination can be a challenge for breeders. As new cultivars are released, they typically go through a set of seed increases from Breeder seed through Certified seed. This process monitors the performance of the new cultivar, screening for plants that do not fit the variety description. When atypical phenotypes appear during the seed increase process, these phenotypes need to be investigated to determine the cause of the variation. Awned and awnless plants that varied in plant height were found in a Foundation seed field of the soft white winter wheat cultivar, Bobtail, which is an awnletted semi-dwarf wheat. Approximately 1,000 heads were snapped from the Foundation seed field and planted into head rows. A few of the head rows were also found to be segregating for the awned and awnless phenotype, and for plant height. The objective of this study was to determine the source of the variation that was seen in the Foundation seed field as well as in the head rows. To do this, fifteen seed heads from one of the head rows that was segregating for head phenotype and height were collected, threshed and planted in the greenhouse. Each plant's DNA was extracted and all of the progeny's phenotype was observed. Seven molecular markers which had shown polymorphism amongst a diverse panel of wheat varieties were used to determine if these plants were genetically identical or dissimilar to the variety Bobtail. All of the awnless plants that came from a segregating line in the greenhouse were grown for two generations in order to observe how they segregated from one generation to the next. This

was conducted to determine whether awned plants were a genetic variant and if so, what controlled the expression of the awned trait. Results from molecular marker analysis showed there was very little variation between and within lines with the majority of the markers being identical. This proved that the awned plants were genetic variants and not contaminants. Phenotypic data revealed a 3:1 segregation pattern for the segregating lines indicating that the genetic variation was due to segregation of a single gene and not due to epistasis or a reciprocal translocation. Thus, the segregating plants are true genetic variants of Bobtail and as a result, the presence of these awned plants does not detract from the quality of the cultivar. Therefore, the cultivar is re-described to include this variant.

Introduction

The development of a soft white winter wheat variety takes approximately eight cycles of selection to achieve a unique set of attributes for a new cultivar without segregation for those traits (Knott et al., 2008). Having a genetically stable cultivar is important for the variety's release to ensure no undesirable plants are present in a plant population. Variants or off-types can be undesirable to breeders due to the possibility of having seed contamination in the seed stock. The differences between developmental maturity, resistance to lodging and diseases, and plant yield impacts the desire of growers to produce a particular cultivar. Differences between plant phenotypes in a field can lead a grower to believe a contamination occurred in his/her field, which can reduce the grower's desire to produce the cultivar due to potential problems with meeting certification standards (Storlie and Talbert, 1992). The more off-types that appear in a

given field, the larger the problem it is to remove the contaminants to have a 'clean' cultivar.

Off-types are plants that are not genetically identical to the given cultivar and can appear due to a contamination event. Seed contamination can occur in many ways such as through the harvesting and cleaning process or a possible out-crossing event (Hucl et al., 2004). Variants in a field are plants that appear to be different than the cultivar that was planted; however, it is genetically similar or identical to the particular cultivar (Abouzied, 2011) and would be considered as one of the phenotypes of the cultivar. Variants do not necessarily reduce the quality of the grain since the plants are the same as each other, even though they may appear to be different. Off-types on the other hand are undesirable because then there are two distinctly different genotypes of plants being produced in the same field. In Oregon, if off-types or other varieties are found in the same field, then the field will not eligible for certification if the amount found is greater than 0.01% for a Registered seed field and 0.03% for a Certified seed field. No other varieties or off-types are acceptable in a Foundation seed field unless it is stated otherwise in the variety description by the variety originator (Oregon Seed Certification Service, 2016).

Seed contamination is troublesome and determining the source of the contamination can be very challenging due to the large number of possibilities of how it occurred. Contamination can occur through using uncleaned equipment, during the cleaning process if two varieties become mixed, volunteers in a field, or if out-crossing from one variety to another occurs (Anderson and Soper, 2003, Boinnet, 1983). These contamination events occur rather infrequently, but the extent of the contamination can

greatly vary. Wheat has a low out-crossing potential of 0-5.6% when it is produced next to another variety, but the pollen's viability decreases with distance (Martin, 1988).

Wheat is a self-pollinated crop and the florets are often closed, further reducing the likelihood of out-crossing. Out-crossing is more likely to occur when the plant is male sterile and the ovary is pollen receptive (Loureiro et al., 2007). Male sterility may occur due to an environmental event such as a low temperature frost and a low amount of solar radiation during meiosis (Demotes-Mainard et al., 1995). The number of plants resulting from an-out-crossing that would be considered a contaminant in a field is rather low when compared to the total number of plants in the stand.

Variants in a field can lead a grower to believe there is contamination in their field since some plants may not look identical to all the other plants. When variants are found, it can be difficult to completely eliminate them in a developed variety (House and Lukens, 2014). True variants are typically listed in the variety description so the growers know what they can expect as the phenotype of the cultivar they are growing. If variants are added to the variety description, the breeder has identified the particular attributes that continuously appear. Typically, these variants are tested to see if the genetics of the variants are the same or if they differ from the rest of the variety. When the genetics of variants are confirmed to be identical, they become part of what is expected from the variety. One way a variant can occur in a cultivar is by epistasis. This is because epistasis is the interaction between two genes in which the expression of one gene can suppress or mask the expression of another gene (House and Lukens, 2014). Due to this, both dominant and recessive traits can hide in a plant's genome through many generations of

selection. The small number of variants that continuously appear in the population can be seen as a contaminant and could be removed from the field through rouging. A variant that results from epistasis can hide in plants that are heterozygotes and these plants will continue to segregate. This results in variants continuously appearing from one generation to the next, even though the all variants were removed the previous year.

Plants can also carry chromosome translocations in their genomes that will produce variants in a field as well. Translocations are chromosome abnormalities that are caused by the rearrangement of parts of the chromosome between non-homologous chromosomes (Stene, 1976). Translocations can lead to changes in chromosome sizes since chromosomes of different lengths can exchange different size fragments. These abnormalities lead to changes in the karyotype of the plants cells and can lead to phenotypic variations between plants (Storme and Mason, 2014). Due to the changes in chromosome size and possible loss of chromosomes, it can cause a reduction in plant fertility in plants heterozygous for the translocation. The loss in fertility leads to an increase in male sterility and seed abortion (Talukdar, 2009). Even with the potential for a loss in fertility, many plants with translocations still produce healthy off-spring. These progenies could be either homozygous for the translocations, homozygous for the normal chromosome configuration or heterozygous for the translocations. If the translocated chromosomes differ for the genes/alleles they carry from the normal chromosomes, then the lines homozygous for the translocation will express a different phenotype.

Developing a stable cultivar with several desirable traits is the goal of many plant breeding programs. There are many challenges associated with the development of a new

cultivar and eliminating any off-types or contaminants is essential. Once a variety is released, the breeder has to ensure to maintain the identity of the variety for quality control and seed certification (Oregon Seed Certification Service, 2016). There have been many ways that varieties are screened to ensure the variety is genetically pure. Molecular markers such as simple sequence repeats (SSRs) are commonly used for variety identification (Martin, 2011). Molecular markers are commonly used to determine the genetic identity of a cultivar since many other attributes are difficult to quantify due to the large number of commercially available wheat varieties. SSRs allow for the identification of variation among plants and they can detect if plants are genetically similar or dissimilar. Determining the source of an off-type or variant is very important for variety stability, identification, grain quality and marketability.

The main objective of this study is to determine the source of phenotypic variation observed in a Foundation seed field of the soft white winter wheat variety Bobtail. The plants began segregating for awned and awnless plants that also varied in plant height in the first production of Foundation seed. Plant segregation doesn't typically occur at the Foundation seed stage of seed increase so identifying the source and determining if the off-types are genotypically identical or genotypically different than the variety Bobtail will help narrow down the possibilities. If the plants are genotypically identical to the variety Bobtail, it will show the off-types are genetic variants of Bobtail. If they are genotypically different, then it will show the plants are the result of a contamination event. By growing out the off-types observed, it will help determine how the plants are segregating over two additional generations. This phenotypic data will help

identify if the segregating plants are the result of unexpected gene interactions such as an epistatic event or a possible translocation.

Materials and Methods

Plant Materials

Plants being evaluated in this study came from a Breeder seed increase of the cultivar Bobtail. The soft white winter wheat variety, Bobtail, was selected for its awnletted seed head trait with a semi-dwarf height as well as for its disease resistance package. Awned off-type plants that varied in plant height were noticed in the Foundation seed fields of Bobtail. Since there were phenotypic differences, 1,000 awnless seed heads were collected from the Foundation seed field. The collected wheat heads were planted into head rows in 2013 at the Washington State University Othello Field Research Station by the Washington State Crop Improvement Association. Within the 1,000 head rows, a few rows were found to be segregating for awned and awnless seed heads as well as a range of plant heights within the given head row. From one of the segregating head rows, sixteen heads that differed for awn type and height were bagged and marked indicating the height of the wheat and whether the heads were awned or awnless. One bagged head was lost prior to harvest. The remaining fifteen heads were collected when the grain was mature and they were kept bagged until they were threshed. The heads were threshed in a single head thresher (Precision Machine Co. Inc., Lincoln, Nebraska) and placed into an envelope labeled with the plant's phenotype: awned or awnless, tall or short. Sixteen seeds from each seed head were planted in rows 1.27 cm deep in 8 x 16 plug flats containing Sunshine Professional Growing Mix potting soil (Agawam, Massachusetts).

Each row was then labeled 1 through 16 and the plants were grown under greenhouse conditions in Corvallis, OR. The seeds were watered daily and the seeds germinated within the first week. When the plants reached the three leaf stage, they were sampled for DNA analysis.

DNA Extraction

Five centimeters of the youngest leaf was taken from each plant and then cut into 0.32 cm sections and placed into an Axygen 8-strip 1.1mL mini tube (Union City, CA). Each tube in the set of 8 contained a sample from a different plant. Each test tube was labeled with a number designated for each plant. For example, row one plant one was marked with 1-1 and row two plant five was labeled as 2-5. This designated number remained with the plant throughout the entire trial period. The test tubes were then placed on ice and taken to the lab for DNA extraction. DNA was extracted and isolated using the protocol of Riera-Lizarazu et al. (2000). The DNA concentration was then assessed using a NanoDrop 2000 UV-Vis Spectrophotometer (Thermo Fisher Scientific, Waltham, MA). The original DNA concentration of each plant can be found in Appendix 10. The samples were then refrigerated at 1.7°C for further analysis.

Marker Analysis

Once the DNA was extracted, eleven total markers were initially tested to determine the genetic differences between the individual plants. The initial markers tested were as follows: Xgwm 160, Xgwm 169, Xgwm 190, Xgwm 194, Xgwm 234, Xgwm 261, Xgwm 282, Xgwm 337, Xgwm 389, Xgwm 437, and Xgwm 577 (Table 4.1) (GrainGenes, USDA, Edwards, 2002). These markers were selected to be used in this

study because they had shown polymorphism amongst a diverse panel of wheat varieties in a previous study by Edwards (2002). The reverse primer for each of these markers were fluorescently labeled with either FAM (6-carboxyfluorescein) or HEX (4,7,2',4',5',7'-HEXachloro-6-carboxyfluorescein) which allowed for fluorescence-based detection of the markers (Table 4.2). The primer working stock for each marker was made up of 196 μ l of ultrapure water, 2 μ l of the forward primer and 2 μ l of the reverse primer. The mastermix for each marker consisted of 300 μ l of 10x DreamTaq buffer (Thermo Fisher Scientific, Waltham, MA), 300 μ l DNTP, 300 μ l Cresol Red (Sigma-Aldrich, Saint Louis, Missouri), 150 μ l of the desired primer, 15 μ lTaq, and 1,635 μ l of ultrapure water. Each mastermix was calculated to be sufficient for all 240 DNA samples.

Table 4.1. Allele location, size and annealing temperature for PCR amplification

Marker	Chromosomal Location	Annealing Temp (C)	No. of Alleles	Allele size range
GWM 160	4A	49.5	7	169-201
GWM 169	6A	53.2	9	106-204
GWM 190	5D	52.6	14	199-211+
GWM 194	4D	47.9	10	118-156
GWM 234	5B	52.1	12	189-242+
GWM 261	2D	52.6	11	118-209
GWM 282	7A	51	30	167-271
GWM 337	1D	52.6	15	178-220
GWM 389	3B	50.6	14	100-180
GWM 437	7D	45	13	110-161
GWM 577	7B	45.2	17	94-227

Table 4.2. Marker primers and labels for amplification detection

Marker	Forward Primer	Reverse Primer	Florescent Label
GWM 160	5' TTCAATTCAGTCTTGGCTT GG 3'	5' CTGCAGGAAAAAAGTACA CCC 3'	HEX
GWM 169	5' ACCACTGCAGAGAACACA TACG 3'	5' GTGCTCTGCTCTAAGTGTGG G 3'	FAM
GWM 190	5' GTGCTTGCTGAGCTATGAG TC 3'	5' GTGCCACGTGGTACCTTTG 3'	FAM
GWM 194	5' GATCTGCTCTACTCTCCTC C 3'	5' CGACGCAGAACTTAAACAA G 3'	FAM
GWM 234	5' GAGTCCTGATGTGAAGCT GTTG 3'	5' CTCATTGGGGTGTGTACGTG 3'	FAM
GWM 261	5' CTCCCTGTACGCCTAAGGC 3'	5' CTCGCGCTACTAGCCATTG 3'	HEX
GWM 282	5' TTGGCCGTGTAAGGCAG 3'	5' TCTCATTACACACAACACT AGC 3'	HEX
GWM 337	5' TGCTAACTGGCCTTTGCC 3'	5' CCTCTCCTCCCTCACTTAG C 3'	HEX
GWM 389	5' ATCATGTCGATCTCCTTGA CG 3'	5' TGCCATGCACATTAGCAGAT 3'	FAM
GWM 437	5' GATCAAGACTTTTGTATCT CTC 3'	5' GATGTCCAACAGTTAGCTTA 3'	FAM
GWM 577	5' ATGGCATAATTTGGTGAA ATTG 3'	5' TGTTTCAAGCCCAACTTCTA TT 3'	HEX

In a 384 well plate (Thermo Fisher Scientific, Waltham, MA), 18 μ l of mastermix was added to 240 of the wells that would later contain DNA from each individual sampled. In each well containing mastermix, 2 μ l of DNA was then added, using a new pipette tip for each sample. An adhesive PCR sealing film (Thermo Fisher Scientific,

Waltham, MA) was then placed on top of the plate to prevent evaporation and contamination during the PCR process. The prepared plate was then ready for PCR amplification.

PCR amplifications were carried out in a Bio-Rad DNA Engine Peltier Thermocycler (Berkeley, California) in a 20 μ l reaction mixture with a heated lid. The cycling parameters consisted of 2 minutes at 94°C, followed by 9 cycles of 30 seconds at 94°C, 30 seconds at 60°C with the option to increase -1°C/cycle, and 1 min at 70°C. This cycle was then followed by 30 cycles of 30 seconds at 94°C, 30 seconds at 50°C, and 1 minute at 70°C. These two cycles were then followed with 3 minutes at 70°C, and infinite time at 8°C. The PCR products from 4 consistent rows (two separate parental lines) from the 384 well plates were then run out on an agrose gel to detect successes and failures of the eleven different markers. From the eleven markers, those that showed failure of amplification were then retested by remaking the master mix and running the trays through PCR. The second run was also tested for success or failure by running them on an agrose gel. Out of the eleven markers, a total of seven markers demonstrated amplification and success after one or two separate runs through PCR. The seven successful PCR products were then prepared for fragment analysis.

The PCR products were then diluted in a 96 well plate and prepared to be sent to the Center for Genome Research and Biocomputing (CGRB) at Oregon State University for fragment analysis. For dilution, 17 μ l of ultrapure water was added to each well in a 96 well plate. Next, 1 μ l of DNA that was labeled with FAM and 2 μ l of DNA that was labeled with HEX were added to each cell. Each cell contained DNA from a different

plant and a new pipette tip was used for each DNA sample that was added. Markers that were labeled FAM were combined with markers labeled HEX when possible. These labeled markers were able to be combined due to the difference between the fluorophore colors of the two markers (FAM is fluorescently labeled blue and HEX is fluorescently labeled green). Due to the uneven numbers of FAM and HEX markers, some FAM markers were diluted without being combined. For those samples, they were diluted by adding 1 μ l DNA labeled with FAM and 19 μ l of ultrapure water. From the diluted 96 well plates, 2 μ l of the dilution was sampled and placed into a semi-skirt raised rim 96 well plate (BioExpress). The 96 well plate was then sealed with a ThermalSeal RT2RR adhesive film. The semi-skirt raised rim 96 well plates are specific and are the only plates accepted by CGRB for fragment analysis due to the restrictions of their ABI 3730 machine (Thermo Fisher Scientific, Waltham, MA).

The data received from the CGRB was processed through GeneMarker® Analysis Software (SoftGenetics LLC, State College, Pennsylvania). The settings used to examine the data received from CGRB can be found in Appendix 11. The GeneMarker® settings were then run with the imported data received from CGRB. The highest peaks that were called in the program were recorded in an Excel spreadsheet for each marker as well as whether FAM or HEX was used as the fluorescent based marker, for each individual plant/DNA sample. The stutter peaks around each major peak indicated the number of base pairs for each SSR marker. Peaks below the 100 base pair range were not called due to the settings since the peaks below 100 base pairs indicate the residual mastermix and not the SSRs. The base pair numbers were then compared across all individuals and

differences more than ± 1.5 base pairs were highlighted. Each individual was then compared across all seven markers to detect any differences and trends between markers.

Greenhouse Assessment

When the plants reached the four leaf stage in the greenhouse, they were then moved to vernalization chambers at a temperature of 8°C with a 10 hr photoperiod for seven weeks. When the plants were removed from the vernalization chamber, they were brought into the greenhouse and then transplanted into 15.24 cm x 17.78 cm pots with Sunshine Professional Growing Mix potting soil (Agawam, Massachusetts). Two plants were placed in each pot and each plant was labeled with the same labeling system used when the DNA samples were taken. The plants were then grown under greenhouse conditions which consisted of an average temperature of 21°C and a 16 hr day length. The plants were also watered every day or every other day if there was adequate moisture. The plants were then grown and heading date was recorded. Heading date were officially recorded when the first wheat head emerged and the bottom of the head was above the flag leaf collar. Once the first head emerged, notes were taken on whether the wheat head was awned or awnless. The plants remained in the greenhouse until the plants reach physiological maturity. This occurred when the peduncle at the bottom of the head turned from green to brown. At this time, the number of seed heads that each plant developed was recorded as well as the height of each individual plant. The height was measured from the top of the potting soil to the base of the spike. When the peduncle was no longer green, the individual heads were harvested and placed into an envelope with its

designated number. As the heads matured, the individual harvest date for each head was recorded.

Once all the heads were harvested, the number of seeds as well as the location of each seed on the heads were counted and recorded on a spreadsheet. At this time, the length of each individual seed head was measured and recorded. The length of the seed head was taken from the peduncle to the tip of the head, not including the length of the awns (if present). The heads were then threshed using a Hege head thresher (Salt Lake City, UT). All the seed were collected from each head and placed in a separate designated envelope. The following November, every awnless seed head from each segregating line (58 total individuals from 5 segregating lines) were then planted in the greenhouse along with one awnless individual from all non-segregating lines (5 awnless non-segregating lines) and two awned individuals from segregating lines were planted as checks (7 total check individuals). The check individuals were planted to ensure they remained true to type and continued to be homozygous for either the awned or awnless phenotype. Only the primary seed head from each plant in the segregating lines were planted since some plants produced multiple seed heads.

From each selected plant, sixteen seeds were planted 1.25 cm deep in Sunshine Professional Growing Mix potting soil (Agawam, MA) in an 8 x 16 cell tray and the lines were all labeled based on the parental plant number. The trays were placed in a greenhouse with a total of 928 planted seeds from segregating lines plus 112 seeds used for checks. The greenhouse growing conditions consisted of an average temperature of 21°C and a 16 hr day length. The plants were grown until they reached the four leaf stage

and were then placed in the vernalization chamber at 8°C with a 10 hr photoperiod for eight weeks. When the plants came out of the vernalization chamber, they were placed back in the greenhouse and transplanted into 2.54 cm tubes so that each plant would only produce one seed head. The purpose for this was to see the number of plants that continued to segregate after the initial generation in the greenhouse. The number of awned and awnless plants from each line was recorded as the heads emerged. From the collected data, a Chi-square analysis was run for both a 1 gene and 2 gene interaction.

Due to the results from the initial Chi-square analysis, additional plants were grown to strengthen the data since some plants fit both a 1 gene and 2 gene interaction analysis. An additional sixteen seeds were planted 1.27 cm deep in 8 x 16 cell trays with Sunshine Professional Growing Mix potting soil (Agawam, MA) from the same 58 awnless individuals from segregating lines. These plants were then grown under the same greenhouse conditions as before. Some of the lines did not have enough seed for planting 16 additional individuals so all the remaining seeds from these lines were planted. The plants were watered daily and when they reached the four leaf stage, they were placed in the vernalization chamber at 8°C with a 10 hr photoperiod for 8 weeks. When they were removed from the vernalization chamber, they were transplanted into 1.27 cm tubes and kept watered in the greenhouse. As the seed heads emerged, the numbers of awned and awnless seed heads were recorded for each line. A second Chi-square analysis was run combining data from the first and second planting of the 58 individuals for the seed head phenotype.

Data Analysis

The SSR markers used are di-nucleotide repeats and the alleles were called in GeneMarker® based on two base pair differences in the PCR product length. Allele base pairs that varied greater than ± 1.5 base pairs in length were considered to be different alleles that were called. The base pair calls from the GeneMarker® analysis can be found in Appendix 12 for all markers and individuals tested. All data points for individuals that didn't have allele sizes that were called were treated as missing data. Even though this decreased the value of having information from all seven markers, it reduces the possibility of having a Type 1 error, which increases the accuracy of detecting genetic differences using the remaining markers.

Results

Genotypic Data

Molecular markers are very useful in detecting genotypic differences between progeny of a plant and among plants. The markers used in this analysis showed very little variation between all groups as well as within segregating groups. The main objective of this experiment was to determine if the source of the phenotypic variation that was observed in the field was due to an off-type or a genetic variant. The SSR markers that were used in this research showed very little variation in the number of base pairs across all parental lines and individuals regardless of the observed phenotype. There was only one individual that had three markers out of seven markers that varied greater than ± 1.5 than the rest of the individuals that were investigated (individual 7-16). This individual was from a segregating population originating from an awnless parent. Three other

individuals, 6-6, 13-1 and 13-16 had two out of the seven markers that varied more than ± 1.5 . These plants originated from awnless parents and they appeared in both segregating and non-segregating populations. There were a total of fifty individuals who had one out of the seven markers that varied greater than ± 1.5 than the median of the sampled population. The distribution of these individuals did not follow a consistent pattern based on the individual marker or the parental population it originated from (segregating or non-segregating). Out of a total of approximately 240 individuals, the results indicate the phenotypic variation and segregation is not a result of any type of contamination or out-crossing event. Based on the molecular marker analysis, the plants that were sampled are all genotypically similar to each other. There is only a 0.78% chance that the plants could be genetically different from each other and have the same base pair sizes that were called by all seven markers.

Phenotypic Data

The first generation of plants that were grown in the greenhouse from the original fifteen seed heads, (5 awned and 10 awnless spikes), demonstrated that none of the awned parents produced any awnless progeny. From the ten awnless spikes, five of the lines remained completely awnless, while the other five lines produced segregating populations of awned and awnless progeny. Table 4.3, shown below, shows the sixteen progeny that were produce from each original parent seed head, phenotype, their heading date is based on days after vernalization, the height of the plant and the length of the progeny's seed head. Under greenhouse conditions, the plants height and heading date was highly influenced by its location in the greenhouse, and therefore, this data was not

considered representative of the plants height and heading date if they were grown under field conditions. The seed head length was relatively consistent across the entire population.

Table 4.3. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	1-1	Awns	72.0	69.2	7.6
Awned	1-2	Awns	74.0	67.3	7.6
Semi-dwarf	1-3	Awns	84.0	51.4	6.4
	1-4	Awns	72.0	64.1	6.4
	1-5	Awns	71.0	57.2	7.0
	1-6	Awns	70.0	66.0	7.6
	1-7	Awns	69.0	52.7	5.1
	1-8	Awns	70.0	68.6	5.1
	1-9	Awns	76.0	66.7	5.7
	1-10	Awns	77.0	52.1	5.1
	1-11	Awns	68.0	64.1	7.6
	1-12	Awns	71.0	67.3	6.4
	1-13	Awns	76.0	55.9	7.6
	1-14	Awns	67.0	75.6	7.0
	1-15	Awns	77.0	71.1	8.9
	1-16	Awns	71.0	74.9	8.9
Average			72.8	64.0	6.9
	2-1	Awns	66.0	71.8	8.3
Awned	2-2	Awns	74.0	54.0	9.5
Semi-dwarf	2-3	Awns	65.0	67.3	6.4
	2-4	Awns	69.0	59.1	8.9
	2-5	Awns	67.0	62.9	8.9
	2-6	Awns	68.0	76.2	7.6
	2-7	Awns	73.0	68.6	9.5
	2-8	Awns	66.0	73.7	8.3
	2-9	Awns	71.0	73.7	8.9
	2-10	Awns	72.0	71.1	8.9
	2-11	Awns	81.0	62.9	7.0
	2-12	Awns	71.0	73.7	7.0
	2-13	Awns	66.0	71.1	8.3
	2-14	Awns	66.0	67.3	8.3
	2-15	Awns	62.0	73.7	8.3
	2-16	Awns	63.0	70.5	7.0
Average			68.8	68.6	8.2

Table 4.3 Continued. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	3-1	Awns	63.0	54.6	9.5
Awned	3-2	Awns	65.0	83.2	8.9
Semi-dwarf	3-3	Awns	66.0	69.9	8.9
	3-4	Awns	65.0	81.3	8.3
	3-5	Awns	63.0	85.7	7.0
	3-6	Awns	68.0	74.3	6.4
	3-7	Awns	75.0	76.2	7.6
	3-8	Awns	66.0	63.5	6.4
	3-9	Awns	72.0	65.4	7.6
	3-10	Awns	65.0	59.1	8.9
	3-11	Awns	69.0	67.9	7.0
	3-12	Awns	68.0	61.0	9.5
	3-13	Awns	65.0	86.4	8.9
	3-14	Awns	62.0	90.2	8.9
	3-15	Awns	62.0	71.8	8.9
	3-16	Awns	65.0	74.9	7.6
Average			66.2	72.8	8.1
	4-1	Awnless	68.0	55.9	9.5
Awnless	4-2	Awns	70.0	56.5	8.9
Semi-dwarf	4-3	Awnless	68.0	61.0	7.6
	4-4	Awnless	69.0	50.8	7.6
	4-5	Awnless	82.0	62.2	9.5
	4-6	Awns	82.0	55.2	8.3
	4-7	Awns	76.0	62.9	7.0
	4-8	Awnless	89.0	61.0	8.3
	4-9	Awnless	91.0	48.3	7.6
	4-10	Awnless	91.0	52.1	7.6
	4-11	Awnless	90.0	52.7	7.6
	4-12	Awnless	80.0	57.2	7.6
	4-13	Awns	78.0	51.4	6.4
	4-14	Awnless	71.0	49.5	7.0
	4-15	Awns	68.0	61.0	7.6
	4-16	Awnless	67.0	62.2	9.5
Average			77.5	56.2	8.0

Table 4.3 Continued. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	5-1	Awnless	63.0	71.8	9.5
Awnless	5-2	Awnless	65.0	67.3	8.9
Semi-dwarf	5-3	Awnless	67.0	63.5	7.6
	5-4	Awnless	67.0	67.3	8.3
	5-5	Awnless	71.0	71.1	8.3
	5-6	Awnless	72.0	66.0	8.3
	5-7	Awnless	93.0	58.4	7.6
	5-8	Awnless	77.0	67.3	8.3
	5-9	Awnless	74.0	70.5	8.9
	5-10	Awnless	83.0	62.2	8.3
	5-11	Awnless	78.0	59.7	7.0
	5-12	Awnless	70.0	58.4	8.3
	5-13	Awnless	73.0	57.8	7.0
	5-14	Awnless	65.0	58.4	8.3
	5-15	Awnless	66.0	61.0	8.9
	5-16	Awnless	77.0	52.1	7.0
Average			72.6	63.3	8.1
	6-1	Awnless	62.0	64.8	9.5
Awnless	6-2	Awns	63.0	59.7	7.6
Semi-dwarf	6-3	Awnless	71.0	64.1	8.3
	6-4	Awnless	74.0	63.5	8.9
	6-5	Awnless	77.0	54.0	7.6
	6-6	Awnless	78.0	59.7	8.9
	6-7	Awnless	75.0	69.2	8.3
	6-8	Awns	83.0	57.2	6.4
	6-9	Awns	83.0	55.9	6.4
	6-10	Awns	92.0	51.4	7.0
	6-11	Awnless	81.0	52.1	7.0
	6-12	Awns	80.0	50.2	6.4
	6-13	Awnless	78.0	65.4	8.3
	6-14	Awnless	67.0	67.9	8.9
	6-15	Awns	65.0	64.1	8.3
	6-16	Awnless	63.0	66.0	9.5
Average			74.5	60.3	7.9

Table 4.3 Continued. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	7-1	Awnless	61.0	84.5	8.3
Awnless	7-2	Awnless	65.0	82.6	7.0
Tall	7-3	Awnless	63.0	94.6	7.6
	7-4	Awnless	61.0	97.8	7.6
	7-5	Died			
	7-6	Awnless	76.0	78.7	7.0
	7-7	Awnless	79.0	94.0	8.9
	7-8	Awnless	70.0	92.7	9.5
	7-9	Awns	73.0	80.6	7.6
	7-10	Awns	73.0	83.8	7.6
	7-11	Awnless	70.0	94.0	8.9
	7-12	Awnless	66.0	95.9	8.9
	7-13	Awnless	67.0	96.5	8.3
	7-14	Awnless	66.0	83.8	7.6
	7-15	Awns	63.0	78.1	7.0
	7-16	Awnless	63.0	86.4	7.6
Average			67.7	88.3	8.0
	8-1	Awns	62.0	55.2	7.6
Awnless	8-2	Awnless	60.0	61.0	8.9
Tall	8-3	Awnless	66.0	78.7	7.0
	8-4	Awnless	80.0	69.9	7.0
	8-5	Awnless	80.0	80.0	6.4
	8-6	Awnless	72.0	80.0	7.0
	8-7	Awns	91.0	69.2	7.6
	8-8	Awnless	71.0	83.8	8.3
	8-9	Awns	77.0	58.4	7.6
	8-10	Awnless	74.0	73.7	8.3
	8-11	Awnless	83.0	81.3	7.0
	8-12	Awnless	69.0	80.6	7.6
	8-13	Awnless	71.0	76.8	8.9
	8-14	Awns	66.0	73.7	8.9
	8-15	Awnless	62.0	79.4	7.0
	8-16	Awnless	66.0	87.6	7.6
Average			71.9	74.3	7.7

Table 4.3 Continued. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	9-1	Awnless	61.0	99.1	8.9
Awnless	9-2	Awnless	68.0	82.0	10.2
Tall	9-3	Awnless	68.0	80.0	9.5
	9-4	Awnless	72.0	83.8	7.6
	9-5	Awnless	69.0	80.0	6.6
	9-6	Awnless	70.0	83.8	8.3
	9-7	Awnless	73.0	86.4	8.9
	9-8	Awnless	73.0	88.9	8.9
	9-9	Awnless	69.0	93.3	8.3
	9-10	Awnless	71.0	86.4	8.3
	9-11	Awnless	71.0	96.5	8.3
	9-12	Awnless	71.0	92.7	8.3
	9-13	Awnless	70.0	81.9	7.6
	9-14	Awnless	66.0	78.7	8.3
	9-15	Awnless	64.0	92.7	8.3
	9-16	Awnless	63.0	86.4	9.5
Average			68.7	87.0	8.5
	10-1	Awnless	66.0	94.0	9.5
Awnless	10-2	Awnless	66.0	85.7	8.3
Tall	10-3	Awnless	66.0	95.3	7.6
	10-4	Died			
	10-5	Awnless	67.0	97.2	8.9
	10-6	Awnless	73.0	83.2	7.6
	10-7	Awnless	75.0	78.7	7.2
	10-8	Awnless	71.0	80.6	5.7
	10-9	Awnless	68.0	78.1	8.3
	10-10	Died			
	10-11	Awnless	74.0	84.5	7.0
	10-12	Awnless	73.0	81.3	8.3
	10-13	Awnless	71.0	100.3	6.4
	10-14	Awnless	70.0	85.1	7.6
	10-15	Awnless	66.0	90.2	8.3
	10-16	Awnless	67.0	87.6	8.3
Average			69.5	87.3	7.8

Table 4.3 Continued. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	11-1	Awnless	63.0	69.9	6.4
Awnless	11-2	Awnless	63.0	74.9	7.6
Tall	11-3	Awnless	69.0	76.2	8.4
	11-4	Awns	67.0	60.3	7.0
	11-5	Awnless	80.0	58.4	7.0
	11-6	Awnless	67.0	69.9	8.3
	11-7	Awnless	74.0	95.9	8.6
	11-8	Awnless	69.0	72.4	7.6
	11-9	Awnless	76.0	76.2	7.6
	11-10	Awns	76.0	68.6	7.0
	11-11	Awnless	78.0	67.9	7.0
	11-12	Awnless	71.0	68.6	8.3
	11-13	Awnless	72.0	71.1	7.0
	11-14	Awnless	64.0	65.4	7.6
	11-15	Awns	66.0	72.4	8.9
	11-16	Awnless	67.0	71.8	8.6
Average			70.1	71.2	7.7
	12-1	Awnless	65.0	90.2	8.3
Awnless	12-2	Awnless	65.0	85.1	7.6
Tall	12-3	Awnless	69.0	90.2	8.3
	12-4	Awnless	71.0	76.2	7.0
	12-5	Awnless	69.0	81.3	8.3
	12-6	Awnless	71.0	81.3	7.6
	12-7	Awnless	71.0	76.8	8.3
	12-8	Awnless	87.0	66.7	5.6
	12-9	Awnless	76.0	68.6	5.7
	12-10	Awnless	84.0	77.5	6.6
	12-11	Awnless	70.0	87.0	9.5
	12-12	Awnless	82.0	71.1	8.3
	12-13	Awnless	74.0	74.3	7.1
	12-14	Awnless	67.0	81.3	6.4
	12-15	Awnless	65.0	81.3	7.0
	12-16	Awnless	64.0	80.0	7.0
Average			71.9	79.3	7.4

Table 4.3 Continued. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	13-1	Awnless	65.0	81.3	8.9
Awnless	13-2	Awnless	66.0	86.4	8.3
Tall	13-3	Awnless	65.0	79.4	7.0
	13-4	Awnless	71.0	88.3	6.4
	13-5	Awnless	68.0	86.4	8.3
	13-6	Awnless	73.0	99.1	8.9
	13-7	Awnless	74.0	86.4	7.6
	13-8	Awnless	68.0	81.9	7.6
	13-9	Awnless	72.0	88.9	7.6
	13-10	Awnless	72.0	90.2	8.3
	13-11	Awnless	79.0	75.6	7.0
	13-12	Awnless	70.0	81.9	5.7
	13-13	Awnless	72.0	87.0	7.6
	13-14	Awnless	76.0	65.4	5.7
	13-15	Awnless	65.0	95.3	7.6
	13-16	Awnless	65.0	94.0	8.3
Average			70.1	85.4	7.5
	14-1	Awns	69.0	71.1	9.5
Awned	14-2	Awns	66.0	62.2	8.3
Tall	14-3	Awns	71.0	76.2	7.0
	14-4	Awns	78.0	74.9	7.0
	14-5	Died			
	14-6	Awns	80.0	78.1	7.6
	14-7	Awns	78.0	78.7	7.6
	14-8	Awns	82.0	60.3	7.6
	14-9	Awns	82.0	83.2	8.3
	14-10	Awns	83.0	59.7	7.6
	14-11	Awns	72.0	81.3	8.3
	14-12	Awns	70.0	73.7	8.3
	14-13	Awns	63.0	55.9	8.3
	14-14	Awns	67.0	66.0	8.3
	14-15	Awns	67.0	73.7	8.3
	14-16	Awns	66.0	62.2	6.4
Average			72.9	70.5	7.9

Table 4.3 Continued. Progeny phenotype from the 15 parental lines with the plant's heading date based on days from vernalization and plant height.

Original Parental Type	Plot	Phenotype	Heading Date (Days)	Plant Height (cm)	Head Length (cm)
	15-1	Died			
Awned	15-2	Awns	66.0	67.3	5.1
Tall	15-3	Awns	65.0	58.4	5.1
	15-4	Died			
	15-5	Died			
	15-6	Awns	72.0	77.5	7.0
	15-7	Awns	75.0	55.9	7.6
	15-8	Awns	72.0	69.9	5.7
	15-9	Awns	68.0	47.6	5.1
	15-10	Awns	80.0	73.7	7.0
	15-11	Awns	65.0	76.2	8.3
	15-12	Awns	65.0	53.3	5.7
	15-13	Awns	65.0	55.2	6.4
	15-14	Awns	68.0	72.4	7.0
	15-15	Awns	63.0	50.2	6.4
	15-16	Awns	61.0	64.8	6.4
Average			68.1	63.3	6.4

Within the first generation that was grown in the greenhouse, there were a total of five segregating lines, as shown in Table 4.3. All the awnless seed heads from the segregating lines were planted for a second generation, with a total of thirty-two seeds planted over the course of a year from each awnless plant. A few check lines (4-2 and 8-7 were awned checks and 5-1, 9-1, 10-1, 12-1 and 13-1 were used as awnless checks) were planted to confirm they did not show segregation in the following generation. The check lines all proved to retain the same phenotype as its parental seed head.

The second generation resulted in thirty-three segregating lines, with awned and awnless progeny, and twenty-five non-segregating lines, which resulted in all awnless

progeny. The seed head phenotype (awned and awnless) of the second generation of plants grown in the greenhouse were analyzed using Chi-square analysis looking at a one gene and a two gene interaction. The one gene analysis looked at the seed head type segregation at a 3:1 ratio while the two gene analysis looked at a 15:1 segregation ratio (awnless : awned phenotype respectively). Table 4.4 below shows the t-stat and p-value from the Chi-square analysis for a one gene interaction along with the individuals who had a significant p-value based on a 0.05 significance level with 1 degree of freedom. The null hypothesis was the plants phenotype segregated 3:1 for awnless and awned seed heads. Those that were found to be significant did not follow the 3:1 segregation pattern.

Table 4.4. Chi-square analysis for a 1 gene interaction from the second generation grown from awnless plants that came from segregating lines.

Parental Lines	Total Progeny	Awnless	Awned	T-stat For 3:1 ratio	P-value	Significant
4-1	27	19	8	0.31	0.58	
4-3	26	26	0	8.67	0.00	x
4-4	26	21	5	0.46	0.50	
4-5	28	19	9	0.76	0.38	
4-8	27	19	8	0.31	0.58	
4-9	23	14	9	2.45	0.12	
4-10	25	20	5	0.33	0.57	
4-11	28	21	7	0.00	1.00	
4-12	31	31	0	10.33	0.00	x
4-14	25	25	0	8.33	0.00	x
4-16	28	20	8	0.19	0.66	
6-1	30	30	0	10.00	0.00	x
6-3	30	18	12	3.60	0.06	
6-4	30	30	0	10.00	0.00	x
6-5	24	19	5	0.22	0.22	
6-6	30	24	6	0.40	0.53	
6-7	30	30	0	10.00	0.00	x
6-11	21	21	0	7.00	0.01	x
6-13	28	20	8	0.19	0.66	
6-14	27	20	7	0.01	0.92	
6-16	29	21	8	0.10	0.75	
7-1	30	24	6	0.40	0.53	
7-2	20	20	0	6.67	0.01	x
7-3	29	29	0	9.67	0.00	x
7-4	30	30	0	10.00	0.00	x
7-6	29	29	0	9.67	0.00	x
7-7	26	26	0	8.67	0.00	x
7-8	32	23	9	0.17	0.68	
7-11	32	32	0	10.67	0.00	x
7-12	30	30	0	10.00	0.00	x

Table 4.4 Continued. Chi-square analysis for a 1 gene interaction from the second generation grown from awnless plants that came from segregating lines.

Parental Lines	Total Progeny	Awnless	Awned	T-stat For 3:1 ratio	P-value	Significant
7-13	31	23	8	0.01	0.92	
7-14	25	25	0	8.33	0.00	x
7-16	26	26	0	8.67	0.00	x
8-2	32	32	0	10.67	0.00	x
8-3	31	31	0	10.33	0.00	x
8-4	31	19	12	3.11	0.08	
8-5	23	23	0	7.67	0.01	x
8-6	32	22	10	0.67	0.41	
8-8	31	22	9	0.27	0.60	
8-10	29	29	0	9.67	0.00	x
8-11	31	24	7	0.10	0.75	
8-12	31	24	7	0.10	0.75	
8-13	31	31	0	10.33	0.00	x
8-15	32	24	8	0.00	1.00	
8-16	31	26	5	1.30	0.25	
11-1	21	15	6	0.14	0.71	
11-2	32	24	8	0.00	1.00	
11-3	32	24	8	0.00	1.00	
11-5	29	20	9	0.56	0.45	
11-6	32	32	0	10.67	0.00	x
11-7	30	21	9	0.40	0.53	
11-8	28	21	7	0.00	1.00	
11-9	28	28	0	9.33	0.00	x
11-11	30	22	8	0.04	0.84	
11-12	30	21	9	0.40	0.53	
11-13	27	27	0	9.00	0.00	x
11-14	31	25	6	0.53	0.47	
11-16	25	25	0	8.33	0.00	x

Since every individual that was found to be significantly different than the 3:1 ratio was observed to have completely awnless progeny, they were not able to be considered to follow either a 3:1 or 15:1 segregation ratio since this analysis only works for segregating populations. Every line that segregated was not found to be significantly different than the null hypothesis, and therefore, they were all found to be significantly different when they were run on a two gene analysis. This means none of the populations that were grown in this experiment showed a 15:1 ratio related to double dominant epistasis. This data supports the null hypothesis that all the segregating lines follow a 3:1 segregation ratio based on a Chi-square one gene model.

Discussion

At the beginning of this study, there were many ideas concerning the source of the awned segregates at the Foundation seed stage of the seed increase of the awnless/awnletted cultivar Bobtail. During the breeding process selection for the awnless trait, and through the final selections from drill strips to head rows, undesirable plants (awned) were rogued. Undesirable Breeder seed head rows that showed segregation for the awn/awnless trait were also removed, which should have eliminated all the awned segregates from the cultivar. Through the selection of awnless heads for Breeder seed production and the removal of any segregating Breeder seed head rows, only awnless/awnletted plants should have been left to produce the breeder seed. This should have resulted in Foundation seed fields having only the awnletted semi-dwarf wheat phenotype. The seed increase process from Breeder seed through Certified seed is set up to eliminate off-types, however, the number of segregates that appeared was more than

the breeder expected to observe, even though the numbers of awned plants were rather low in the entire population.

Due to this unexpected appearance of segregates, it was important to determine the source of the variation. Use of molecular markers makes it possible to determine if the variation is due to a genetically different off-type or if it is a genetic variant of the cultivar. As the marker results show, there is no sign of a contamination or that an out-cross occurred. This confirmation is the first step in determining how to maintain the purity, integrity and quality of the variety Bobtail. If several of the markers were different across several different lines, it would indicate that another cultivar was growing in the same field. Determining the source of a contamination would present a challenge. If some of the markers were the same across certain lines while others varied, it would indicate the potential for an out-cross having occurred recently. None of the markers for any of the lines showed the level of difference that would indicate that another variety was present in the field. The chance of having the seven markers across all of the lines with few discrepancies is very low if there were multiple genotypes present.

Having additional genotypes present in this cultivar would require a major effort of rouging in order to attempt to remove all variability. However, since the markers confirmed all the lines were genotypically similar, the variation is not from an outside source, but is part of the genetic make-up of Bobtail. With this confirmation, the awned types will still need to be removed to achieve uniformity, however, the presence of awned plants do not impact the cultivar's performance. This means, all the plants that were observed as an off-type from this population were truly a variant of Bobtail. With this

confirmation from the genetic markers used, awned and awnletted plants that can vary in height are genotypically identical to the variety Bobtail and should be added as a variant in the variety's description. With the variant added on the variety description, it provides the growers and producers with reassurance that contaminants are not present in the field and then they will know what to expect from that cultivar. When the variants are listed, it makes it easier for the growers to have their fields pass Seed Certification since the inspectors will know the range of plants that are acceptable in that variety

Since segregation was found in the Foundation seed generation despite removal of any awned types from the two previous generations, chromosomal translocation or epistasis were initially suspected to be the reason for the awned plants since the awned trait is recessive and both epistasis and chromosome translocations could mask expression of a trait. Segregation for a chromosome translocation could result in the expression of different phenotypes, but it would also result in partial sterility in the seed heads of plants heterozygous for the translocation. However, in the first generation grown in the greenhouse, there did not appear to be a sterility problem observed in the seed heads. As Talukdar (2009) and Sugiura-Ogasawara, et al., (2004) found in their studies, translocations can lead to several sterility problems and lead to the abortion of seed. Since the majority of the seed heads appeared to be completely fertile, it is unlikely a translocation had occurred, even though this does not fully rule out translocations as a possibility. Observation of the chromosomes during mitosis and meiosis of plants segregating for the awn trait would need to be done to completely eliminate the possibility that a translocation was the cause of the genetic variant.

The breeding selection method used and elimination of awned plants through this breeding selection method typically would eliminate the awned phenotype. Epistasis would have explained why the awned phenotype kept appearing in low frequencies because a single dominant allele would have overshadowed the expression of the other three recessive alleles present, causing the awned recessive phenotype to be masked and appear at a low frequency in each generation, if it appeared at all. This would have also explained how awned plants went unnoticed and were not fully eliminated from the Breeder seed stock used to plant the Foundation seed fields.

With the segregation ratio for awned and awnless phenotypes following a Mendelian segregation ratio of 3:1, this indicates it is likely that one of the two genes that impact the awned and awnless trait (B1 and B2) is fixed for two recessive alleles at one loci. Therefore, it is likely the heterozygotes carry one dominant allele and three recessive alleles and the homozygotes for awnless carry two dominant alleles for either loci, B1 or B2, and two recessive alleles at the other loci (B1B1b2b2 or b1b1B2B2). The segregation pattern observed in this experiment follows a 3:1 pattern given the number of seeds that were grown out for each parent. In a perfect world, all the plants would have perfectly fit a 3:1 or 15:1 segregation ratio, however, in this experiment, only a few lines perfectly fit a 3:1 ratio even though all the segregating lines statistically fit the 3:1 ratio. With the number of seeds that were grown out per line (a total of 32 seeds), epistasis is not completely ruled out as a cause for the awned plants. In order to completely confirm or disprove the results found in this experiment, all the seeds harvested from the first generation through the second generation would need to be grown out. Having a larger

number of offspring and plants would provide more data. Additional data would increase the probability to observe other patterns if other causal agents are causing the appearance of these variants.

To detect a 15:1 segregation ratio, a large number of plants need to be grown out in order to ensure awned plants would be present in the lines. When the first sixteen seeds were grown out in the second generation, a few of the lines had segregation ratios that were rather close to fitting a 15:1 ratio, where they had 14 awnless plants and 2 awned plants. However, by doubling the numbers of offspring contributing to the data by growing out sixteen additional seeds from the same lines, it greatly changed the populations that appeared to be segregating for a two gene interaction. The additional plants in the second planting confirmed the lines were actually segregating following a one gene segregation ratio. Increasing the numbers made a huge impact on the results. Since there were still several lines that remained completely awnless, it would be beneficial to grow out any remaining seeds from those parents to see if there is even one or two awned plants that just happened to not be planted in the first two grow outs. To further confirm or disprove the findings of this research, growing out all the lines that appeared to remain completely awnless to see if awned plants appeared in future generations would help confirm if epistasis is involved in any way or if the entire population truly follows a typical Mendelian segregation for a one gene model.

A possible explanation for changes in plant height and seed head morphology after several selection cycles would be if transposable elements are somehow involved. Transposable elements are also known as “jumping genes” where small sequences of

DNA are moved from one location in the genome to another location (McClintock, 1980). McClintock (1980) mentioned that this movement of DNA sequences can play a major role in gene expression and it typically occurs when a “shock” event occurs to the plant, which causes the genome to be forced to rearrange itself for survival. In her study with *Zea mays*, she observed new traits appearing in mutant seedling lines that produced a completely unexpected phenotype that varied widely between progenies. McClintock saw that modified patterns of gene expression were occurring, which seemed to be the result of an event that occurred in an ancestor cell that gave rise to a change in the phenotype. If movement of a transposable element occurred in Bobtail, it could potentially give rise to head rows that were segregating for height as well as seed head morphology. Since the few head rows that were eliminated from the breeder seed were widely sporadic and none of them were uniform for one trait, either height or spike phenotype, it brings up the possibility that transposable elements are one possibility. This could explain why the height from the segregating lines greatly varied and was inconsistent with whether it came from a semi-dwarf or tall parent. The height trait however, would be difficult to identify as the result of one particular event since these plants were grown under greenhouse conditions and not out in the field. A greenhouse environment provides many factors that can impact a plant’s height, such as the location of light sources and variability in temperature from one location to the next in the greenhouse. The genome of Bobtail would need to be sequenced in order to see if sequences of DNA were moved from one location to another.

Developing awnless varieties always provides a challenge to breeders to assure the population has reached homozygosity. Since the awnless trait is controlled by a dominant allele, heterozygotes can pose a problem in achieving homozygosity without occurrence of awned plants. To help screen to eliminate all awned and heterozygote plants from a breeding population, a breeder can take an extra year to ensure there are no segregating populations remaining. The breeder can harvest the head rows individually and plant each head row in its own 1.52 m x 4.57 m plot. This is the seed that would typically be the source for Foundation seed, but instead of bulking the desired head rows, the plots can be used as an extra step to achieve uniformity before being used to plant Foundation seed fields. When the plants are growing in plots, if any individual plot shows any presence of an awned plant or plants, the breeder can eliminate that entire plot so it can't be advanced forward. Any plots that remain 100% awnless and matches the phenotype and desirable characteristics of the breeding objectives can be bulked. This bulked seed will then serve as the Breeder seed that is used to produce the Foundation seed. By adding an extra selection cycle, it will help avoid any heterozygotes from making it through the head rows and appearing in the Foundation seed fields. Using this method will eliminate any plants that would normally segregate following Mendelian genetics for a one gene trait.

This segregating population provides the opportunity for the breeder to select for a new awned variety that will contain the same agronomic traits as Bobtail. Awned cultivars are more popular among growers since the presence of the awns can decrease the amount of damage and loss caused by wildlife since wildlife does not prefer

consuming awned wheat (Harper and Blair, 2015). The additions of awns in a new variety can also have the possibility of increasing the test weight of this line (Rebetzke et al., 2016; Grundbacher, 1963). Bobtail is well known for having a lower than desired test weight, especially if there is late season moisture stress. By selecting for characteristics that are naturally occurring in a population and are difficult to eliminate, selecting the plants for a new population instead of eliminating them can be beneficial. The breeding process for wheat can be rather challenging when traits unexpectedly appear or change. The breeders must identify the source of the problem and find ways to prevent the problem from occurring again in the future. Having the breeders involved when problems occur helps maintain the genetic integrity of released cultivars.

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Chapter 5: Low Temperature Germination of Soft White Winter Wheat Cultivars

Introduction

Winter wheat depends on idealized temperatures in the fall to begin germination and for plant establishment prior to the cool temperatures that occur throughout the winter months. The ideal temperature for seed germination of soft white winter wheat is around 20°C (Gao and Ayele, 2014), which is the typical soil temperature in the Willamette Valley in Oregon from September to October. Planting later in the season can result in cooler soil temperatures that are less than ideal for seed germination (Buriro et al., 2011). Due to earlier than expected rain events or late harvest of a crop such as sugar beets (*Beta vulgaris*), wheat producers sometimes have no choice but to plant later than desired. Having cooler soil temperatures can decrease seed germination rates which can result in lower seedling establishment, ultimately impacting grain yield (Li et al., 2013). This is one of the major drawbacks of late fall planting of winter wheat. With slower germination rates, the seedlings are smaller as they go into the winter months, reducing the hardiness and survivability of these smaller plants (Zabihi-e-Mahmoodabad et al., 2011). Even though wheat typically produces more tillers when there is open space around them, the total number of tillers is inadequate to compensate for the number of plants that were lost, therefore, grain yield is greatly reduced. If growers had information on which varieties germinated rapidly at low temperatures as well as which varieties have a slow germination rate at low temperatures, they could select varieties that had a greater potential of establishment when a late fall planting occurs. The objective of this study was to identify which varieties germinate more quickly under cool temperatures as well

as which varieties germinate more slowly to identify which varieties are the best and worst to plant in late fall.

Methods

In this study, we investigated how quickly 39 commercial varieties as well as 6 experimental lines of soft white winter wheat germinated at 4°C. This temperature is less than the optimum germination temperature of 20°C, but it is sufficiently low enough to demonstrate differences between varieties in their ability to germinate under cooler, more stressful conditions. This data relates to how quickly the varieties would germinate in cooler soils. The trial was conducted over two years and seed was harvested in August from the Hyslop Research Farm in Corvallis, OR for both years and from CBARC (Columbia Basin Agricultural Research Station) near Pendleton, OR the second year. There were two replications of each variety planted the first year and during the second year in Pendleton, OR and three replications in Corvallis, OR the second year. A total of 100 seeds were used from each plot in this germination trial. For each year, two 50 seed counts were placed on wet germination paper in a 100 x 15 mm petri dish (VWR, Radnor, Pennsylvania) for each field plot. This equaled a total of 700 seeds from each variety over the course of two years. Once seeds were placed in petri dishes, they were enclosed in 26.82 cm x 27.31 cm Ziploc bags to keep the seeds at 80-100% relative humidity (each Ziploc bag contained four petri dishes and two varieties). They were then placed in a cold storage unit in complete darkness at 4°C through the duration of the trial. The petri dishes were continually monitored to ensure the germination paper remained moist. During the first year, seed germination for each entry was counted after being in a

cold storage unit at 4°C after seven days, and seed germination counts were taken daily starting at seed imbibition during the second year. As seeds germinated, they were continually removed from the petri dish. Seeds were monitored until all varieties reached 100% seed germination.

Statistical Analysis

A full-factorial, two-way analysis of variance (ANOVA) was computed in the same manner for both years of the germination trials. Each year and location was computed separately as there were different numbers of varieties and/or replications tested across years and locations as well as the two experiments were conducted differently. An ANOVA was run for each day of germination to determine if there were significant differences among varieties for their germination rates (Appendix 13 and Appendix 14). The ANOVA was computed in an Excel spreadsheet (Microsoft Excel (2013), Redmond, Washington) which determined if there were significant differences between varieties for each day of the trial. For the days in which the ANOVA results indicated significance between the varieties, a least significant difference test (LSD) was run on the varieties germination counts. The LSD test was used to determine which varieties were statistically different from each other for germination rate. The LSD test was run using SAS JMP (SAS Institute Inc., Cary, North Carolina) with the fit Y by X function, which was run for each year and day separately. The X factor was set as the varieties and the Y response was the day that was being analyzed. The LSD test results from the first year can be found in Table 5.1 and the LSD results from the second year can be found in Tables 5.2-5.9.

Results and Discussion

There were significant differences observed among the cultivars for rate of germination at low temperature (Table 5.1). During the first year, the varieties Bruehl, Eltan and Bitterroot had the highest germination rate after a week in the 4°C treatment with a germination percentage ranging from 56.5-64%, followed by Bruneau with 45.5% germination, Coda with 42% germination and Brundage 96 with 41.5% germination. The slowest germinating varieties were ORSS-1757, Nugaines, Mary and Rosalyn.

During the second year, there was a difference among the varieties for rate of germination at 4°C between locations (Table 5.2-5.5). The variety that germinated the most rapidly from the Pendleton, OR site was Bitterroot, which also had the highest number of seeds that had germinated starting on the fifth day after imbibition, up until the eighth day, when the variety Alba had reached 100% seed germination. On the eighth day, Bitterroot was 99% germinated, followed by Brundage 96 that was 95% germinated and Bruneau which was 92% germinated. There were fifteen varieties that had reached complete seed germination on the ninth day. These varieties were as follows: Alba, Brundage 96, Madsen, Tubbs-06, Goetze, 11-225-3C, Tubbs, Hyslop, Kaseberg, Coda, the advanced breeding line 11-225-6H, ORCF-101 Rosalyn, Malcolm, and Ladd. There were 12 varieties that had reached 99.5% seed germination on this day as well. The variety that germinated the slowest from Pendleton, OR was Cara, in which by the seventh day, only 9% of the seeds had germinated. Mary, Nugaines, ORSS-1757, ORCF-103, Stephens and Rosalyn also had lower numbers of seeds that had germinated by the seventh day. However, by the ninth day, when several varieties completed germination, Cara was 95% germinated, followed by Gaines that was 97% germinated, and Mary with 97.5% seed germination. By the tenth day at 4°C, all the seeds from every variety had germinated.

The seed harvested from Corvallis, OR began germinating five days after imbibition, in which the variety Hyslop had the highest number of seeds that had germinated. By the seventh day of this trial, the varieties Hyslop, 11-225-1C, 11-225-3C, Bitterroot and Bruneau had the most amount of seed that had germinated. On the eighth

day, fourteen varieties were completely germinated. These varieties were; Hyslop, 11-225-1C, 11-225-3C, Bitterroot, Xerpha, Nugaines, Tubbs-06, Hill 81, Gene, Ladd, Tubbs, ORCF-103, Brundage 96 and Bruneau. Even though Hyslop germinated the quickest within the first week, other varieties were able to reach full seed germination on the same day. By the eighth day, the majority of the other varieties were just a few seeds away from 100% germination. From seeds harvested at Corvallis, OR, the slowest germinating variety was ORSS-1757, in which by the seventh day, 60% of the seeds had germinated. By the eighth day, ORSS-1757 was 93.7% germinated. On the ninth day, however, Rod had the most seeds that had not germinated, with 98% seed germinated, followed by Rely and Bruehl, which had 98.7% seed germination, and ORSS-1757, Rosalyn, Kaseberg, ORCF-102, Cara, and 11-225-6H which all 99% germinated. By the eleventh day of being in the germination chamber at 4°C, all the seeds from all of the varieties had germinated.

Table 5.2. Percent germination at 4°C on day five from Corvallis (Table 5.2A) and Pendleton (Table 5.2B) in 2015-2016. Letters denote difference in significance based on a 0.05 LSD.

Table 5.2A

4°C Day 5	Corvallis																		
Variety	Mean																		
Hyslop	37.3	A																	
Lewjain	36.7	A	B																
Bitterroot	35.3	A	B	C															
11-225-1C	35.0	A	B	C															
11-225-3C	35.0	A	B	C															
Brevor	34.7	A	B	C															
11-225-5C	34.0	A	B	C	D														
Bruehl	33.7	A	B	C	D														
Cara	33.7	A	B	C	D														
Rod	33.0	A	B	C	D	E													
Nugaines	32.0	A	B	C	D	E	F												
Goetze	30.0	A	B	C	D	E	F	G											
Eltan	28.7	A	B	C	D	E	F	G											
Cayuga	28.3	A	B	C	D	E	F	G											
Coda	27.3	A	B	C	D	E	F	G	H										
Daws	27.0	A	B	C	D	E	F	G	H	I									
Hill 81	26.7	A	B	C	D	E	F	G	H	I									
Tubbs-06	26.7	A	B	C	D	E	F	G	H	I									
Bruneau	26.0	A	B	C	D	E	F	G	H	I									
Brundage	25.0	A	B	C	D	E	F	G	H	I									
Gaines	25.0	A	B	C	D	E	F	G	H	I									
Madsen	23.3	A	B	C	D	E	F	G	H	I	J								
Alba	23.3	A	B	C	D	E	F	G	H	I	J								
Xerpha	23.3	A	B	C	D	E	F	G	H	I	J								
Tubbs	22.7	A	B	C	D	E	F	G	H	I	J								
Mary	22.3	A	B	C	D	E	F	G	H	I	J								
Bobtail	21.3	A	B	C	D	E	F	G	H	I	J								
Brundage 96	20.7	A	B	C	D	E	F	G	H	I	J								
11-225-6H	19.7		B	C	D	E	F	G	H	I	J	K							
11-225-2C	19.0			C	D	E	F	G	H	I	J	K							
Ladd	18.3				C	D	E	F	G	H	I	J	K						
ORCF-103	17.0					D	E	F	G	H	I	J	K						
Gene	16.7						D	E	F	G	H	I	J	K					
Rely	15.7							E	F	G	H	I	J	K					
Malcolm	15.3								F	G	H	I	J	K					
Elmar	15.0									F	G	H	I	J	K				
ORCF-101	14.7										F	G	H	I	J	K			
Stephens	14.3											G	H	I	J	K			
ORCF-102	14.0												G	H	I	J	K		
11-225-7H	14.0													G	H	I	J	K	
Skiles	12.7														G	H	I	J	K
Kaseberg	10.3															H	I	J	K
Omar	9.7																I	J	K
Rosalyn	6.3																	J	K
ORSS-1757	2.7																		K

Table 5.2B

4°C Day 5	Pendleton			
Variety	Mean			
Bitterroot	18.5	A		
Goetze	3.0		B	
Bruneau	3.0		B	
Xerpha	2.0		B	C
Brundage 96	1.5		B	C
Daws	1.5		B	C
11-225-1C	1.0		B	C
Gaines	1.0		B	C
Gene	1.0		B	C
Bruehl	1.0		B	C
11-225-6H	1.0		B	C
Madsen	0.5			C
Alba	0.5			C
Coda	0.5			C
11-225-3C	0.0			C
11-225-5C	0.0			C
Bobtail	0.0			C
Brevor	0.0			C
11-225-7H	0.0			C
Brundage	0.0			C
Cara	0.0			C
Cayuga	0.0			C
Elmar	0.0			C
Hill 81	0.0			C
Hyslop	0.0			C
Kaseberg	0.0			C
Ladd	0.0			C
Lewjain	0.0			C
11-225-2C	0.0			C
Malcolm	0.0			C
Mary	0.0			C
Nugaines	0.0			C
Omar	0.0			C
ORCF-101	0.0			C
Eltan	0.0			C
ORCF-103	0.0			C
ORSS-1757	0.0			C
Rely	0.0			C
Rod	0.0			C
ORCF-102	0.0			C
Skiles	0.0			C
Stephens	0.0			C
Tubbs	0.0			C
Tubbs-06	0.0			C
Rosalyn	0.0			C

There were differences in seed germination rates between varieties depending on the location in which they were harvested from. This shows that there are environment factors during seed development and ripening that can impact the ability of seed to germinate at a low temperature. In this study, all varieties reached full germination within fourteen days. The three varieties that were the quickest germinating varieties over years and locations were Bitterroot, Brundage 96 and Bruneau. The varieties that were the slowest germinating in cold temperatures were ORSS-1757 and Rely. There were also discrepancies between the locations in which Kaseberg, 11-225-6H and Rosalyn had reached full germination earlier when they were harvested from Pendleton, OR, however, they were some of the slower germinating varieties harvested from Corvallis, OR. Even though this was observed, the difference between reaching full germination and being a slower germinating variety in this instance was only about 1.5%. Hill 81 also had a discrepancy between locations in which it was one of the slower germinating varieties from Pendleton, OR and was one of the top germinating varieties from Corvallis, OR. However, this difference between germination rankings is based on about a 1% difference between the total percentages of germinated seeds from Pendleton, OR.

The findings from this research is beneficial to growers when they end up planting late in the fall. This research demonstrates which varieties are able to germinate quicker under less than ideal temperatures. Those varieties that have a quicker start have a greater chance of developing a stronger stand establishment prior to the winter months since the seeds appear to be more vigorous. Some varieties consistently had a quick germination pattern, and these varieties would be the best to plant when planting into

cool soil temperatures. Even though this data demonstrates germination rate, it does not test for seedling vigor at this temperature. Germination was considered complete with the emergence of the radicle and coleoptile. Future experiments should include measuring seedling growth following germination to see which varieties demonstrate quicker coleoptile growth. Information on seedling vigor would be useful since it would show a wider range of seedling hardiness under these conditions. Seed germination rates in this study demonstrated which varieties would have the quickest seedling emergence the quickest, however, cool temperatures would also slow down growth rate, which was not measured in this experiment. There is a wide range of seed germination rates among varieties at 4°C, however, since all seeds had germinated in this experiment within the fourteen experimental days, the results showed that there weren't any of the varieties tested that were unable to germinate due to the temperature being too cold. Soft white winter wheat prefers temperatures around 20°C for germination, however, they are still able to germinate under less ideal temperatures. Seed germination was greatly slowed under cooler temperatures, which would relate to a slower seedling emergence rate when soil temperatures are cool. The data collected in this research found on average, seed that is germinated at 4°C is delayed by approximately five days when compared to when seed is germinated at 20°C. By selecting the quickest low temperature germinating varieties, such as Bitterroot, when planting late in the fall, it increases the probability of establishing a stronger, healthier plant stand prior to winter than if a slower germinating variety was planted.

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Chapter 6: Conclusions

Introduction

Soft white winter wheat is a valuable economic crop which is mainly produced in Oregon, Washington, Idaho, Michigan, and New York (Vocke and Ali, 2013). Wheat is the most widely grown crop in the world and it is nutritionally important as it provides 20% of the calories and protein of the world's diet (Reynolds et al., 2012). A large proportion of soft white winter wheat is exported from the Pacific Northwest (PNW) to markets around the world, resulting in it having a large impact on the United States' balance of trade (Robertson et al., 2004). Wheat is the raw material that makes up essential foods around the world. For growers, it is important to produce high quality grain in order to receive a higher market value for the grain, as damaged grain results in lower market value and poor quality end products. Soft white winter wheat is used for cakes and cookies as well as many other products (Fajardo, 2016). Soft white winter wheat typically has a lower protein content and a weaker gluten strength than other types of wheat, which allows the products made from soft white winter wheat to have a softer texture. When wheat is harvested that contains a mixture of different types of wheat or the grain has begun to sprout, the quality of the end products made from the wheat are often reduced. Grain that is contaminated or has experienced pre-harvest sprouting (PHS), receive a lower market grade, and therefore the growers reduce their profit when this occurs.

Objectives

The objective of the first study was to determine the degree of post-harvest dormancy that is expressed in older commercial soft white winter wheat cultivars and compare them to recently released cultivars to examine if post-harvest dormancy has been slowly bred out of soft white winter wheat or if it was always low. It was important to compare how different ripening environments impact seed dormancy expression to focus on how different temperatures during grain maturation and seed germination impact dormancy expression. The results of this research will help direct the direction wheat breeding programs should be working to improve post-harvest dormancy in soft white winter wheat. The objectives of the second study which looked into varietal identification was to determine the cause of variants that appeared in Foundation seed fields of the recently released wheat cultivar Bobtail. The second objective of this study was also to determine a method which could be used to eliminate or prevent variants from appearing during seed increases of new cultivars.

Results and Discussion from the Post-Harvest Dormancy Study

By examining 45 different cultivars and breeding lines that ranged in release dates from the 1940's to 2012, this experiment was able to see if there were any patterns in dormancy expression based on release dates. It also looked at which varieties appeared to have the highest dormancy expression at what temperature. Germination was quickest at 20°C, followed by 10°C and 4°C. The highest level of dormancy expression occurred in the 30°C treatment from the seed harvested from Pendleton. The seed in the 30°C treatment from Corvallis did not show the same level of dormancy expression and

followed a similar trend as the germination rate at 20°C. The varieties that expressed the highest level of dormancy were Brevor, Bobtail, Cayuga, Gene, Nugaines, Rely and 11-225-6H in the 30°C treatment. When the wheat seeds were placed under optimal germination conditions, they did not appear to express any dormancy directly after harvest. The lack of post-harvest dormancy being observed in this study could have been due to an after- ripening event occurring prior to harvest. If this was not the case, then soft white winter wheat does not possess any post-harvest dormancy. However, high temperatures did appear to induce dormancy expression in several soft white winter wheat cultivars, which was also observed in spring wheat by Nyachiro et al. (2002).

All of the temperatures had similar germination trends across locations except for the 30°C treatment. This is likely due to the seeds from Corvallis experiencing a rain event two days prior to harvest. None of the varieties that were harvested from the Corvallis location showed any high temperature dormancy expression. These result demonstrated that when wheat seed goes through cycles of wetting and drying, high temperature post-harvest dormancy is broken in wheat, which may lead to increased susceptibility to PHS (Thomason, 2009). From the data, there were no trends observed that linked earlier released cultivars to having a higher level of post-harvest dormancy than newer cultivars.

Falling number data was also collected on all the varieties from Corvallis and Pendleton. The data showed variation among the cultivars and between the sites supporting the assumption that rainfall impacted the germination results. The falling numbers from all of the cultivars harvested in Corvallis were lower than those from

Pendleton, indicating elevated levels of α -amylase. To reduce the impact of PHS, one approach would be to breed and select lines with some level of high temperature post-harvest dormancy and a higher than average falling number. The key for identifying these lines is to use seed from sites that have not undergone a late season rain event prior to harvest.

Results and Discussion from the Variety Identification Study

By growing out the seeds from different heads from a segregating head row of Bobtail Breeder seed and taking DNA samples from each individual grown the first generation, it was determined that the presence of plant segregation observed in the Bobtail Foundation seed field was due to a genetic variant of Bobtail. The DNA markers used in this study did not show the presence of any contaminant, off-type or progeny from out-crossing which resulted in plant segregation. All of the markers used showed similar results among the plants tested showing all of the plants were genetically identical. This initial analysis was important to determine how to maintain the purity, integrity and quality of the variety Bobtail. From the phenotypic data collected from growing out two generations in the greenhouse from all segregating lines, the Chi-square analysis showed the segregation ratio of awless to awned plants followed a typical Mendelian segregation pattern of 3:1. This shows that an epistatic interaction is not the cause of varying phenotypes. The lack of sterility observed from the seed heads gathered throughout the two generations also show that a chromosomal translocation is not highly likely to be causing the phenotypic variation either.

The 3:1 segregation ratio indicates it is likely one of the two genes that controls the awned and awnless trait (B1 and B2) is fixed for two recessive alleles at one loci. Due to this, the heterozygotes carry one dominant allele and three recessive alleles and the homozygotes for awnless carry two dominant alleles for either loci, B1 or B2, and two recessive alleles at the other loci (b2b2 or b1b1B2B2). With the continuation of plant segregation observed in this study, determining a way to ensure all heterozygotes are eliminated through the breeding process is important. To help screen for heterozygotes, a breeder can take an extra year to ensure there are no segregating populations remaining. The breeder can harvest the head rows individually and plant each head row in a 1.52 m x 4.57 m plot. This seed would typically be the breeder seed, but by adding this extra year, the breeder can bulk all of the non-segregating plots together to use as the breeder seed, and eliminate any segregating plots to eliminate all heterozygotes.

Future Research

These studies both play a vital role in soft white winter wheat seed quality. Any aspect that can negatively impact varietal identification or seed quality will ultimately impact the marketability of the seed. Maintaining genetic purity and quality are both important aspects with the production of soft white winter wheat. These studies indicate ways to identify superior cultivars and how to identify when variants or off-types are seen in a field. Even though these studies conducted provided viable information, further actions can be taken to explore the data further. From the first study, future studies that look at seed dormancy weekly from when the grain reaches the hard dough stage to the time it reaches 12% moisture would help confirm or disprove that soft white winter wheat

does not have a dormancy period under optimal conditions. By taking seed samples every week and placing the seed at 20°C and 30°C for seed germination, it could show if dormancy expression changes as the grain ripens. By investigating these aspects further, it would provide more in-depth information that would complement the findings of this research.

From the second study, growing out larger plant populations from all of the awned lines should be explored to ensure these lines do not segregate 15:1, which would indicate that epistatic interactions could be occurring. The findings from this would show if the heterozygotes were truly missed through the breeding selection cycle or if the genes were interacting in a way that would 'hide' the awned phenotype in the heterozygotes. If epistatic interactions were occurring, it would occur in low frequencies that this study would not have detected because too few progeny were grown out to observe this 15:1 segregation pattern. By having this segregating population, it provides the breeder the opportunity to select for a new awned variety that will contain the same desirable agronomic traits as the variety Bobtail. Awned cultivars are more popular among growers as they are less desirable to wildlife and prevent economic losses due to foraging animals. These two studies examined a small proportion of everything that can be explored with what impacts seed dormancy and maintaining genetic purity. Further studies can complement the findings from this research to provide growers with more information with the soft white winter wheat varieties they produce.

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Appendix

Appendix 1: Wheat Varieties and Their Year of Release

Table 7.01. Wheat varieties used in the dormancy study with their year of release.

Variety	Year of Release	Variety	Year of Release
Alba	1948	Malcolm	1987
Bitterroot	2008	Mary	2011
Bobtail	2012	Nugaines	1965
Brevor	1949	Omar	1955
Bruehl	2000	ORCF-101	2003
Brundage	1997	ORCF-102	2004
Brundage 96	2001	ORCF-103	2008
Bruneau	2009	ORSS-1757	2005
Cara	2007	Rely	1991
Cayuga	1996	Rod	1991
Coda	1998	Rosalyn	2012
Daws	1976	Skiles	2008
Elmar	1949	Stephens	1977
Eltan	1990	Tubbs	2002
Gaines	1961	Tubbs-06	2006
Gene	1991	Xerpha	2007
Goetze	2007	11-225-1C	N/A
Hill 81	1982	11-225-2C	N/A
Hyslop	1971	11-225-3C	N/A
Kaseberg	2012	11-225-5C	N/A
Ladd	2012	11-225-6H	N/A
Lewjain	1982	11-225-7H	N/A
Madsen	1988		

Appendix 2: Test Weights from Plots Grown in Year 1

Table 7.02. All of the varieties and replications harvested in year 1 with the seed moisture content and test weight of each replication. An 'X' indicates the plots that did not produce enough seed for the analysis.

Variety	Replication	Seed Moisture	Test Weight
Alba	R1	11	57.6
Bitterroot	R1	11.2	60.4
Bobtail	R1	11.1	59.1
Brevor	R1	11.0	57.9
Bruehl	R1	x	x
Brundage	R1	11.2	51.2
Brundage 96	R1	10.7	57.5
Bruneau	R1	10.9	59.7
Cara	R1	10.7	58.0
Coda	R1	11.0	57.0
Daws	R1	x	x
Elmar	R1	11.2	59.5
Eltan	R1	11.0	59.6
Gaines	R1	11.2	61.3
Gene	R1	10.9	59.6
Goetze	R1	10.8	59.3
Hill 81	R1	10.8	59.0
Hyslop	R1	10.8	58.6
Kaseberg	R1	10.8	60.4
Ladd	R1	10.4	59.5
Lewjain	R1	11.3	42.3
Madsen	R1	10.8	58.7
Malcolm	R1	10.6	60.6
Mary	R1	11.0	60.1
Nugaines	R1	11.2	60.6
Omar	R1	11.0	60.5
ORCF-101	R1	10.9	60.7
ORCF-102	R1	10.9	61.1
ORCF-103	R1	11.1	59.6
ORSS-1757	R1	11.1	59.2
Rely	R1	11.1	58.1
Rod	R1	10.8	42.2
Rosalyn	R1	10.9	59.1
Skiles	R1	10.8	60.7
Stephens	R1	10.7	57.9

Table 7.02 Continued. All of the varieties and replications harvested in year 1 with the seed moisture content and test weight of each replication. An 'X' indicates the plots that did not produce enough seed for the analysis.

Variety	Replication	Seed Moisture	Test Weight
Tubbs	R1	10.8	59.8
Tubbs-06	R1	10.9	60.0
Xerpha	R1	10.6	59.6
Alba	R2	x	x
Bitterroot	R2	11.1	60.7
Bobtail	R2	11.1	59.5
Brevor	R2	10.9	60.6
Bruehl	R2	x	x
Brundage	R2	11.2	62
Brundage 96	R2	10.8	59.4
Bruneau	R2	10.7	61.0
Cara	R2	10.6	59.0
Coda	R2	10.7	51.0
Daws	R2	10.9	50.1
Elmar	R2	11.0	60.1
Eltan	R2	11.0	59.6
Gaines	R2	11.3	59.1
Gene	R2	11.0	59.7
Goetze	R2	11.1	59.8
Hill 81	R2	11.0	60.0
Hyslop	R2	10.6	58.8
Kaseberg	R2	10.9	60.8
Ladd	R2	10.2	60.6
Lewjain	R2	11.2	59.0
Madsen	R2	10.8	57.6
Malcolm	R2	10.9	58.8
Mary	R2	11.0	59.9
Nugaines	R2	x	x
Omar	R2	x	x
ORCF-101	R2	10.9	60.4
ORCF-102	R2	10.9	60.4
ORCF-103	R2	11.0	59.4
ORSS-1757	R2	10.9	59.9
Rely	R2	11.0	58.5
Rod	R2	x	x
Rosalyn	R2	11.1	60.2

Table 7.02 Continued. All of the varieties and replications harvested in year 1 with the seed moisture content and test weight of each replication. An 'X' indicates the plots that did not produce enough seed for the analysis.

Variety	Replication	Seed Moisture	Test Weight
Skiles	R2	10.9	60.3
Stephens	R2	x	x
Tubbs	R2	10.5	58.7
Tubbs-06	R2	10.7	60.4
Xerpha	R2	10.7	58.4

Appendix 3: Test Weights from Plots Grown in Year 2

Table 7.03. All of the varieties and replications harvested in year 2 with the seed moisture content and test weight from each location.

Location	Variety	Replication	Protein %	Moisture	Test Weight
Corvallis	Alba	R1	8.3	10.4	53.9
Corvallis	Bitterroot	R1	8.0	10.3	56.7
Corvallis	Bobtail	R1	8.5	10.2	55.7
Corvallis	Brevor	R1	8.9	10.2	59.2
Corvallis	Bruehl	R1	8.1	10.0	56.5
Corvallis	Brundage	R1	8.4	10.1	59.3
Corvallis	Brundage 96	R1	8.1	10.3	58.4
Corvallis	Bruneau	R1	8.3	10.2	58.6
Corvallis	Cara	R1	8.3	10.1	57.1
Corvallis	Cayuga	R1	10.0	10.3	59.6
Corvallis	Coda	R1	8.9	10.0	59.1
Corvallis	Daws	R1	8.3	10.1	59.0
Corvallis	Elmar	R1	8.4	10.2	58.3
Corvallis	Eltan	R1	7.3	10.4	56.8
Corvallis	Gaines	R1	7.7	10.3	58.6
Corvallis	Gene	R1	7.8	10.2	55.2
Corvallis	Goetze	R1	8.4	10.4	57.5
Corvallis	Hill 81	R1	8.9	10.2	58.8
Corvallis	Hyslop	R1	8.8	9.9	55.6
Corvallis	Kaseberg	R1	8.3	10.3	58.4
Corvallis	Ladd	R1	9.3	10.2	58.3
Corvallis	Lewjain	R1	8.5	10.3	59.0
Corvallis	Madsen	R1	9.1	10.2	56.8
Corvallis	Malcolm	R1	8.5	10.1	56.9
Corvallis	Mary	R1	7.8	10.2	58.0
Corvallis	Nugaines	R1	8.2	10.2	59.9
Corvallis	Omar	R1	8.9	10.1	58.4
Corvallis	ORCF-101	R1	8.6	10.0	55.8
Corvallis	ORCF-102	R1	8.4	10.3	57.2
Corvallis	ORCF-103	R1	8.3	10.1	56.7
Corvallis	ORSS-1757	R1	8.0	10.3	58.5
Corvallis	Rely	R1	8.4	10.1	57.9
Corvallis	Rod	R1	7.9	10.1	53.6
Corvallis	Rosalyn	R1	8.2	10.4	55.0
Corvallis	Skiles	R1	9.6	10.1	57.4

Table 7.03 Continued. All of the varieties and replications harvested in year 2 with the seed moisture content and test weight from each location.

Location	Variety	Replication	Protein %	Moisture	Test Weight
Corvallis	Stephens	R1	8.6	10.2	56.9
Corvallis	Tubbs-06	R1	8.4	10.2	57.0
Corvallis	Xerpha	R1	8.2	10.2	58.5
Corvallis	11-225-1C	R1	9.0	10.4	58.0
Corvallis	11-225-2C	R1	9.0	10.1	54.8
Corvallis	11-225-3C	R1	9.2	10.5	57.7
Corvallis	11-225-5C	R1	9.9	10.3	56.5
Corvallis	11-225-6H	R1	9.2	10.3	55.2
Corvallis	11-225-7H	R1	8.9	10.3	58.0
Corvallis	Alba	R2	9.9	10.5	56.9
Corvallis	Bitterroot	R2	7.5	10.5	58.7
Corvallis	Bobtail	R2	8.0	10.4	56.9
Corvallis	Brevor	R2	8.4	10.4	61.0
Corvallis	Bruehl	R2	8.3	10.0	56.4
Corvallis	Brundage	R2	8.3	10.3	60.7
Corvallis	Brundage 96	R2	8.2	10.3	58.6
Corvallis	Bruneau	R2	8.4	10.2	59.5
Corvallis	Cara	R2	7.8	10.3	59.1
Corvallis	Cayuga	R2	9.4	10.6	61.3
Corvallis	Coda	R2	8.6	10.1	60.1
Corvallis	Daws	R2	8.1	10.4	60.0
Corvallis	Elmar	R2	9.0	10.3	59.1
Corvallis	Eltan	R2	8.7	10.4	59.0
Corvallis	Gaines	R2	8.0	10.3	60.6
Corvallis	Gene	R2	8.7	10.3	57.7
Corvallis	Goetze	R2	9.9	10.3	59.4
Corvallis	Hill 81	R2	8.1	10.4	58.6
Corvallis	Hyslop	R2	7.7	10.2	58.4
Corvallis	Kaseberg	R2	7.3	10.3	57.8
Corvallis	Ladd	R2	8.6	10.4	58.8
Corvallis	Lewjain	R2	8.4	10.4	60.2
Corvallis	Madsen	R2	8.6	10.4	59.7
Corvallis	Malcolm	R2	8.6	10.3	60.2
Corvallis	Mary	R2	7.6	10.1	58.9
Corvallis	Nugaines	R2	8.1	10.3	61.0
Corvallis	Omar	R2	9.5	10.3	58.5
Corvallis	ORCF-101	R2	8.7	10.3	58.9
Corvallis	ORCF-102	R2	8.1	10.4	58.3

Table 7.03 Continued. All of the varieties and replications harvested in year 2 with the seed moisture content and test weight from each location.

Location	Variety	Replication	Protein %	Moisture	Test Weight
Corvallis	ORCF-103	R2	8.0	10.3	58.5
Corvallis	ORSS-1757	R2	8.2	10.3	59.9
Corvallis	Rely	R2	7.8	10.2	58.7
Corvallis	Rod	R2	7.7	10.2	58.2
Corvallis	Rosalyn	R2	7.2	10.3	57.7
Corvallis	Skiles	R2	9.0	10.1	58.9
Corvallis	Stephens	R2	8.5	10.4	59.6
Corvallis	Tubbs	R2	8.1	10.3	59.1
Corvallis	Tubbs-06	R2	8.4	10.3	59.4
Corvallis	Xerpha	R2	8.3	10.1	60.0
Corvallis	11-225-1C	R2	8.8	10.6	57.5
Corvallis	11-225-2C	R2	7.9	10.3	57.2
Corvallis	11-225-3C	R2	9.1	10.4	59.5
Corvallis	11-225-5C	R2	9.1	10.4	58.2
Corvallis	11-225-6H	R2	8.8	10.5	58.8
Corvallis	11-225-7H	R2	8.7	10.3	57.6
Corvallis	Alba	R3	7.5	10.8	55.7
Corvallis	Bitterroot	R3	7.8	10.5	58.3
Corvallis	Bobtail	R3	7.1	10.8	55.8
Corvallis	Brevor	R3	7.7	10.3	60.1
Corvallis	Bruehl	R3	8.6	10.6	59.8
Corvallis	Brundage	R3	8.4	10.6	57.4
Corvallis	Brundage 96	R3	8.7	10.9	57.1
Corvallis	Bruneau	R3	7.8	10.9	55.9
Corvallis	Cara	R3	7.3	10.6	56.0
Corvallis	Cayuga	R3	9.4	10.7	60.0
Corvallis	Coda	R3	8.2	10.4	57.5
Corvallis	Daws	R3	7.9	10.8	57.0
Corvallis	Elmar	R3	8.6	10.4	58.7
Corvallis	Eltan	R3	8.2	10.6	56.9
Corvallis	Gaines	R3	8.0	10.4	60.2
Corvallis	Gene	R3	8.6	10.4	53.3
Corvallis	Goetze	R3	9.1	10.5	58.5
Corvallis	Hill 81	R3	8.2	10.9	58.6
Corvallis	Hyslop	R3	8.2	10.0	57.3
Corvallis	Kaseberg	R3	7.5	10.5	57.1
Corvallis	Ladd	R3	8.8	10.7	56.9
Corvallis	Lewjain	R3	8.0	10.8	57.4

Table 7.03 Continued. All of the varieties and replications harvested in year 2 with the seed moisture content and test weight from each location.

Location	Variety	Replication	Protein %	Moisture	Test Weight
Corvallis	Madsen	R3	8.1	10.5	58.0
Corvallis	Malcolm	R3	8.0	10.4	57.2
Corvallis	Mary	R3	7.6	10.3	56.7
Corvallis	Nugaines	R3	8.3	10.4	59.9
Corvallis	Omar	R3	8.7	10.2	59.0
Corvallis	ORCF-101	R3	8.1	11.0	56.0
Corvallis	ORCF-102	R3	8.1	10.7	59.1
Corvallis	ORCF-103	R3	8.1	10.5	56.1
Corvallis	ORSS-1757	R3	8.2	10.4	57.7
Corvallis	Rely	R3	6.9	10.5	55.8
Corvallis	Rod	R3	8.0	10.9	55.2
Corvallis	Rosalyn	R3	7.0	10.7	54.2
Corvallis	Skiles	R3	8.6	10.4	57.1
Corvallis	Stephens	R3	8.8	10.4	56.3
Corvallis	Tubbs	R3	7.9	10.6	57.2
Corvallis	Tubbs	R3	8.8	10.3	56.8
Corvallis	Tubbs-06	R3	7.8	10.5	58.5
Corvallis	Xerpha	R3	8.1	10.4	58.4
Corvallis	11-225-1C	R3	8.5	10.6	56.0
Corvallis	11-225-2C	R3	8.4	10.5	54.5
Corvallis	11-225-3C	R3	9.1	10.5	57.1
Corvallis	11-225-5C	R3	9.1	10.5	57.7
Corvallis	11-225-6H	R3	8.6	10.5	57.6
Corvallis	11-225-7H	R3	8.5	10.6	57.3
Pendleton	Alba	R1	15.4	9.1	57.9
Pendleton	Bitterroot	R1	13.5	9.1	57.8
Pendleton	Bobtail	R1	13.9	8.6	52.1
Pendleton	Brevor	R1	13.0	9.1	59.5
Pendleton	Bruehl	R1	12.7	8.5	53.4
Pendleton	Brundage	R1	12.6	9.0	57.7
Pendleton	Brundage 96	R1	12.5	8.9	55.9
Pendleton	Bruneau	R1	11.7	8.8	57.3
Pendleton	Cara	R1	14.5	8.6	53.3
Pendleton	Cayuga	R1	15.2	9.2	57.5
Pendleton	Coda	R1	13.2	8.6	56.9
Pendleton	Daws	R1	14.5	8.8	53.2
Pendleton	Elmar	R1	12.7	9.2	57.8
Pendleton	Eltan	R1	12.3	12.3	58.9

Table 7.03 Continued. All of the varieties and replications harvested in year 2 with the seed moisture content and test weight from each location.

Location	Variety	Replication	Protein %	Moisture	Test Weight
Pendleton	Gaines	R1	12.6	12.6	56.9
Pendleton	Gene	R1	12.6	12.6	53.1
Pendleton	Goetze	R1	11.7	11.7	55.3
Pendleton	Hill 81	R1	13.1	13.1	57.4
Pendleton	Hyslop	R1	14.1	14.1	53.0
Pendleton	Kaseberg	R1	11.7	11.7	54.7
Pendleton	Ladd	R1	11.8	11.8	58.0
Pendleton	Lewjain	R1	13.9	13.9	57.6
Pendleton	Madsen	R1	13.8	13.8	55.8
Pendleton	Malcolm	R1	11.2	11.3	56.8
Pendleton	Mary	R1	12.7	12.7	57.5
Pendleton	Nugaines	R1	11.2	11.2	58.5
Pendleton	Omar	R1	12.0	12.0	59.2
Pendleton	ORCF-101	R1	13.7	13.7	55.9
Pendleton	ORCF-102	R1	14.0	14.0	57.5
Pendleton	ORCF-103	R1	11.9	11.9	58.1
Pendleton	ORSS-1757	R1	11.0	11.0	56.9
Pendleton	Rely	R1	12.6	12.6	54.3
Pendleton	Rod	R1	11.8	11.8	55.7
Pendleton	Rosalyn	R1	10.2	10.2	57.1
Pendleton	Skiles	R1	11.3	11.3	58.2
Pendleton	Stephens	R1	12.1	12.1	54.0
Pendleton	Tubbs	R1	11.5	11.5	54.6
Pendleton	Tubbs-06	R1	11.7	11.7	55.8
Pendleton	Xerpha	R1	12.9	12.9	57.2
Pendleton	11-225-1C	R1	11.8	9.1	56.9
Pendleton	11-225-2C	R1	11.5	9.4	57.0
Pendleton	11-225-3C	R1	13.7	8.6	56.5
Pendleton	11-225-5C	R1	14.3	8.7	55.9
Pendleton	11-225-6H	R1	10.8	8.6	56.5
Pendleton	11-225-7H	R1	12.5	9.0	56.1
Pendleton	Alba	R2	13.1	8.9	59.0
Pendleton	Bitterroot	R2	10.7	8.9	60.7
Pendleton	Bobtail	R2	10.5	8.3	57.9
Pendleton	Brevor	R2	11.6	9.5	61.1
Pendleton	Bruehl	R2	11.4	8.6	57.4
Pendleton	Brundage	R2	11.1	8.2	58.3
Pendleton	Brundage 96	R2	10.8	8.8	58.5

Table 7.03 Continued. All of the varieties and replications harvested in year 2 with the seed moisture content and test weight from each location.

Location	Variety	Replication	Protein %	Moisture	Test Weight
Pendleton	Bruneau	R2	10.4	8.1	59.8
Pendleton	Cara	R2	10.8	9.0	57.5
Pendleton	Cayuga	R2	11.8	9.4	65.1
Pendleton	Coda	R2	9.8	8.7	60.6
Pendleton	Daws	R2	10.3	9.3	59.7
Pendleton	Elmar	R2	12.4	8.9	58.9
Pendleton	Eltan	R2	10.1	10.1	60.2
Pendleton	Gaines	R2	11.1	11.1	59.3
Pendleton	Gene	R2	10.1	10.1	57.8
Pendleton	Goetze	R2	9.1	9.1	58.5
Pendleton	Hill 81	R2	11.9	11.9	59.4
Pendleton	Hyslop	R2	10.5	10.5	57.2
Pendleton	Kaseberg	R2	10.6	10.6	56.0
Pendleton	Ladd	R2	11.3	11.3	57.5
Pendleton	Lewjain	R2	11.2	11.2	58.7
Pendleton	Madsen	R2	9.3	9.3	59.6
Pendleton	Malcolm	R2	11.6	11.6	57.9
Pendleton	Mary	R2	10.8	10.8	59.6
Pendleton	Nugaines	R2	11.4	11.4	58.7
Pendleton	Omar	R2	12.2	12.2	60.1
Pendleton	ORCF-101	R2	11.9	11.9	58.5
Pendleton	ORCF-102	R2	10.8	10.8	60.7
Pendleton	ORCF-103	R2	10.8	10.8	59.2
Pendleton	ORSS-1757	R2	8.8	8.8	58.7
Pendleton	Rely	R2	10.9	10.9	56.7
Pendleton	Rod	R2	10.2	10.2	57.9
Pendleton	Rosalyn	R2	8.8	8.8	59.1
Pendleton	Skiles	R2	10.2	10.2	60.0
Pendleton	Stephens	R2	10.0	10.0	58.1
Pendleton	Tubbs	R2	10.5	10.5	57.5
Pendleton	Tubbs-06	R2	11.0	11.0	58.0
Pendleton	Xerpha	R2	8.4	8.4	60.0
Pendleton	11-225-1C	R2	10.8	9.1	58.8
Pendleton	11-225-2C	R2	10.0	9.3	57.7
Pendleton	11-225-3C	R2	10.4	8.6	59.7
Pendleton	11-225-5C	R2	10.4	8.4	60.6
Pendleton	11-225-6H	R2	10.7	8.4	57.7
Pendleton	11-225-7H	R2	10.6	8.5	58.4

Appendix 4: Weather Data from Corvallis and Pendleton from Year 2

Table 7.04 Weather Data from Pendleton, OR.

Date (2016)	Max Temp (°C)	Min Temp (°C)	Rainfall (cm)	Total Rainfall (cm)	Monthly Rainfall Total (cm)
June 1-4th	30.3	12.6	0.01	0.03	June 2.36
June 5-11	29.9	13.1	0.13	0.94	
June 12-18	21.9	7.3	0.19	1.35	July 2.03
June 19-25	26.0	10.0	0.01	0.05	
June 26-July 2	33.5	13.8	0.00	0.00	August 0.18
July 3-9	26.6	13.7	0.26	1.85	
July 10-16	27.2	12.3	0.03	0.18	
July 17-23	29.4	13.5	0.00	0.00	
July 24-30	36.0	15.9	0.00	0.00	
July 31-Aug 6	30.7	13.0	0.00	0.00	
Aug 7-13	29.8	12.1	0.03	0.18	
Aug 14-20	34.6	15.0	0.00	0.00	
Aug 21-27	30.7	12.9	0.00	0.00	
Aug 28-31	29.7	13.2	0.00	0.00	

Table 7.05 Weather Data from Corvallis, OR.

Date (2016)	Max Temp (°C)	Min Temp (°C)	Rainfall (cm)	Total Rainfall (cm)	Monthly Rainfall Total (cm)
June 1-4th	27.08	12.36	0.03	0.13	June 0.91
June 5-11	27.78	11.03	0.00	0.00	
June 12-18	20.56	7.06	0.11	0.76	July 2.24
June 19-25	23.25	8.73	0.00	0.03	
June 26-Jul 2	28.81	10.40	0.00	0.00	August 0.28
July 3-9	26.03	10.79	0.15	1.04	
July 10-16	24.76	11.03	0.17	1.19	
July 17-23	24.84	12.30	0.00	0.00	
July 24-30	31.83	12.38	0.00	0.00	
July 31-Aug 6	28.65	8.97	0.00	0.00	
Aug 7-13	27.06	10.24	0.04	0.28	
Aug 14-20	34.05	11.67	0.00	0.00	
Aug 21-27	30.71	10.08	0.00	0.00	
Aug 28-31	24.72	11.67	0.00	0.00	

Appendix 5: ANOVA Results from Year 1 Trial 1

Table 7.06. ANOVA table for each day from seed imbibition from year 1 trial 1 for seed germination from dry seed storage at 4°C and 20°C with the seed germinating at 20°C ('S' indicates significance).

Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	41131.55				
Rep	1.00	40.03	40.03	0.76	3.97	0.38
Temp	1.00	6925.50	6925.50	132.30	3.97	0.00
Variety	37.00	24701.05	667.60	12.75	1.57	0.00
TxV	37.00	5539.00	149.70	2.86	1.57	0.00
Error	75.00	3925.97	52.35			
Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	1403.68				
Rep	1.00	8.06	8.06	4.86	3.97	0.03
Temp	1.00	43.16	43.16	26.02	3.97	0.00
Variety	37.00	947.43	25.61	15.43	1.57	0.00
TxV	37.00	280.59	7.58	4.57	1.57	0.00
Error	75.00	124.44	1.66			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	327.20				
Rep	1.00	3.48	3.48	4.74	3.97	0.03
Temp	1.00	3.48	3.48	4.74	3.97	0.03
Variety	37.00	204.45	5.53	7.53	1.57	0.00
TxV	37.00	60.77	1.64	2.24	1.57	0.00
Error	75.00	55.02	0.73			
Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	61.55				
Rep	1.00	0.42	0.42	1.46	3.97	0.23
Temp	1.00	0.00	0.00	0.00	3.97	1.00
Variety	37.00	20.05	0.54	1.88	1.57	0.01
TxV	37.00	19.50	0.53	1.83	1.57	0.01
Error	75.00	21.58	0.29			

Table 7.07. ANOVA table for each day from seed imbibition from year 1 trial 1 for seed germination from dry seed storage at 20°C with the seed germinating at 20°C looking at significance between varieties ('S' indicates significance).

Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	16531.53				
Rep	1.00	8.89	8.89	0.20	4.11	0.66
Variety	37.00	14885.53	402.31	9.09	1.73	0.00
Error	37.00	1637.11	44.25			
Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	199.53				
Rep	1.00	0.47	0.47	0.38	4.11	0.54
Variety	37.00	152.53	4.12	3.28	1.73	0.00
Error	37.00	46.53	1.26			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	82.95				
Rep	1.00	0.00	0.00	0.00	4.11	1.00
Variety	37.00	55.95	1.51	2.07	1.73	0.01
Error	37.00	27.00	0.73			
Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	26.78				
Rep	1.00	0.33	0.33	0.86	4.11	0.36
Variety	37.00	12.28	0.33	0.87	1.73	0.67
Error	37.00	14.17	0.38			

Table 7.08. ANOVA table for each day from seed imbibition from year 1 trial 1 for seed germination from dry seed storage at 4°C with the seed germinating at 20°C looking at significance between varieties ('S' indicates significance).

Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	17674.53				
Rep	1.00	35.58	35.58	0.58	4.11	0.45
Variety	37.00	15354.53	414.99	6.72	1.73	0.00
Error	37.00	2284.42	61.74			

Table 7.08 Continued. ANOVA table for each day from seed imbibition from year 1 trial 1 for seed germination from dry seed storage at 4°C with the seed germinating at 20°C looking at significance between varieties ('S' indicates significance).

Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	1152.99				
Rep	1.00	9.59	9.59	5.73	4.11	0.02
Variety	37.00	1081.49	29.23	17.47	1.73	0.00
Error	37.00	61.91	1.67			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	237.41				
Rep	1.00	5.80	5.80	5.55	4.11	0.02
Variety	37.00	192.91	5.21	4.99	1.73	0.00
Error	37.00	38.70	1.05			
Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	30.04				
Rep	1.00	0.33	0.33	2.35	4.11	0.13
Variety	37.00	24.54	0.66	4.75	1.73	0.00
Error	37.00	5.17	0.14			

Appendix 6: ANOVA Results from Year 1 Trial 2

Table 7.09. ANOVA tables for each day from seed imbibition for year 1 trial 2 for seed germination at 4°C and 20°C with no difference between seed storage temperatures ('S' indicates significance).

Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	42262.10				
Rep	1.00	59.38	59.38	2.64	3.97	0.11
Temp	1.00	24176.90	24176.90	1076.68	3.97	0.00
Variety	37.00	8170.85	220.83	9.83	1.57	0.00
TxV	37.00	8170.85	220.83	9.83	1.57	0.00
Error	75.00	1684.13	22.46			
Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	375510.08				
Rep	1.00	0.95	0.95	1.87	3.97	0.18
Temp	1.00	375413.92	375413.92	739923.70	3.97	0.00
Variety	37.00	28.58	0.77	1.52	1.57	0.06
TxV	37.00	28.58	0.77	1.52	1.57	0.06
Error	75.00	38.05	0.51			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	379900.99				
Rep	1.00	0.01	0.01	1.00	3.97	0.32
Temp	1.00	379900.01	379900.01	57744801.07	3.97	0.00
Variety	37.00	0.24	0.01	1.00	1.57	0.49
TxV	37.00	0.24	0.01	1.00	1.57	0.49
Error	75.00	0.49	0.01			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	152.00	268365.47				
Rep	1.00	3.18	3.18	0.28	3.97	0.60
Temp	1.00	246088.53	246088.53	21566.14	3.97	0.00
Variety	37.00	10708.97	289.43	25.36	1.57	0.00
TxV	37.00	10708.97	289.43	25.36	1.57	0.00
Error	75.00	855.82	11.41			

Table 7.09 Continued. ANOVA tables for each day from seed imbibition for year 1 trial 2 for seed germination at 4°C and 20°C with no difference between seed storage temperatures ('S' indicates significance).

Day 8							
Source	df	SS	MS	F	Fcritical	P-value	
Total	152.00	281.34					
Rep	1.00	1.68	1.68	1.82	3.97	0.18	
Temp	1.00	28.66	28.66	31.01	3.97	0.00	S
Variety	37.00	90.84	2.46	2.66	1.57	0.00	S
TxV	37.00	90.84	2.46	2.66	1.57	0.00	S
Error	75.00	69.32	0.92				
Day 9							
Source	df	SS	MS	F	Fcritical	P-value	
Total	152.00	40.21					
Rep	1.00	0.03	0.03	0.18	3.97	0.67	
Temp	1.00	3.79	3.79	25.90	3.97	0.00	S
Variety	37.00	12.71	0.34	2.35	1.57	0.00	S
TxV	37.00	12.71	0.34	2.35	1.57	0.00	S
Error	75.00	10.97	0.15				
Day 10							
Source	df	SS	MS	F	Fcritical	P-value	
Total	152.00	32.63					
Rep	1.00	0.01	0.01	0.07	3.97	0.80	
Temp	1.00	2.38	2.38	23.77	3.97	0.00	S
Variety	37.00	11.38	0.31	3.08	1.57	0.00	S
TxV	37.00	11.38	0.31	3.08	1.57	0.00	S
Error	75.00	7.49	0.10				
Day 11							
Source	df	SS	MS	F	Fcritical	P-value	
Total	152.00	27.05					
Rep	1.00	0.03	0.03	0.33	3.97	0.57	
Temp	1.00	0.95	0.95	11.89	3.97	0.00	S
Variety	37.00	10.05	0.27	3.41	1.57	0.00	S
TxV	37.00	10.05	0.27	3.41	1.57	0.00	S
Error	75.00	5.97	0.08				

Table 7.10. ANOVA tables from year 1 trial 2 20°C germination trials at for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	18085.20				
Rep	1.00	118.75	118.75	2.70	4.11	0.11
Variety	37.00	16341.70	441.67	10.06	1.73	0.00
Error	37.00	1624.75	43.91			
Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	96.16				
Rep	1.00	1.89	1.89	1.89	4.11	0.18
Variety	37.00	57.16	1.54	1.54	1.73	0.10
Error	37.00	37.11	1.00			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	0.99				
Rep	1.00	0.01	0.01	1.00	4.11	0.32
Variety	37.00	0.49	0.01	1.00	1.73	0.50
Error	37.00	0.49	0.01			

Table 7.11. ANOVA tables from year 1 trial 2 4°C germination trials at for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 7						
Source	df	SS	MS	F	Fcritical	P-Value
Total	1.00	22276.95				
Rep	1.00	6.37	6.37	0.28	4.11	0.60
Variety	37.00	21417.95	578.86	25.12	1.73	0.00
Error	37.00	852.63	23.04			
Day 8						
Source	df	SS	MS	F	Fcritical	P-Value
Total	1.00	252.68				
Rep	1.00	3.37	3.37	1.84	4.11	0.18
Variety	37.00	181.68	4.91	2.69	1.73	0.00
Error	37.00	67.63	1.83			

Table 7.11 Continued. ANOVA tables from year 1 trial 2 4°C germination trials at for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 9						
Source	df	SS	MS	F	Fcritical	P-Value
Total	1.00	36.42				
Rep	1.00	0.05	0.05	0.18	4.11	0.68
Variety	37.00	25.42	0.69	2.32	1.73	0.01
Error	37.00	10.95	0.30			
Day 10						
Source	df	SS	MS	F	Fcritical	P-Value
Total	1.00	30.25				
Rep	1.00	0.01	0.01	0.07	4.11	0.80
Variety	37.00	22.75	0.61	3.04	1.73	0.00
Error	37.00	7.49	0.20			
Day 11						
Source	df	SS	MS	F	Fcritical	P-Value
Total	1.00	26.11				
Rep	1.00	0.05	0.05	0.33	4.11	0.57
Variety	37.00	20.11	0.54	3.38	1.73	0.00
Error	37.00	5.95	0.16			

Appendix 7: ANOVA Results from Year 2

Table 7.12. ANOVA tables from the Corvallis germination trials for each day throughout the trial looking at significance between temperatures and varieties ('S' indicates significance).

Day 1							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	20554.02					
Rep	2.00	330.47	165.23	15.92	3.02	0.00	S
Temp	3.00	7872.04	2624.01	252.87	2.63	0.00	S
Variety	44.00	3024.10	68.73	6.62	1.41	0.00	S
TxV	132.00	5612.43	42.52	4.10	1.26	0.00	S
Error	358.00	3714.99	10.38				
Day 2							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	840573.69					
Rep	2.00	410.63	205.31	5.61	3.02	0.00	S
Temp	3.00	795758.13	265252.71	7249.01	2.63	0.00	S
Variety	44.00	12964.80	294.65	8.05	1.41	0.00	S
TxV	132.00	18340.36	138.94	3.80	1.26	0.00	S
Error	358.00	13099.78	36.59				
Day 3							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	1025875.97					
Rep	2.00	4.27	2.14	0.07	3.02	0.93	
Temp	3.00	997570.09	332523.36	11486.97	2.63	0.00	S
Variety	44.00	10936.08	248.55	8.59	1.41	0.00	S
TxV	132.00	7002.19	53.05	1.83	1.26	0.00	S
Error	358.00	10363.34	28.95				
Day 4							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	888586.40					
Rep	2.00	959.39	479.69	20.86	3.02	0.00	S
Temp	3.00	866511.00	288837.00	12560.31	2.63	0.00	S
Variety	44.00	3663.12	83.25	3.62	1.41	0.00	S
TxV	132.00	9220.31	69.85	3.04	1.26	0.00	S
Error	358.00	8232.57	23.00				

Table 7.12 Continued. ANOVA tables from the Corvallis germination trials for each day throughout the trial looking at significance between temperatures and varieties ('S' indicates significance).

Day 5							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	603216.58					
Rep	2.00	624.51	312.25	10.23	3.02	0.00	S
Temp	3.00	579384.48	193128.16	6327.55	2.63	0.00	S
Variety	44.00	3373.88	76.68	2.51	1.41	0.00	S
TxV	132.00	8906.92	67.48	2.21	1.26	0.00	S
Error	358.00	10926.80	30.52				
Day 6							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	197573.02					
Rep	2.00	136.30	68.15	1.48	3.02	0.23	
Temp	3.00	161635.83	53878.61	1173.41	2.63	0.00	S
Variety	44.00	5303.94	120.54	2.63	1.41	0.00	S
TxV	132.00	14058.97	106.51	2.32	1.26	0.00	S
Error	358.00	16437.98	45.92				
Day 7							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	22912.61					
Rep	2.00	79.59	39.80	3.50	3.02	0.03	S
Temp	3.00	11781.49	3927.16	345.78	2.63	0.00	S
Variety	44.00	1889.19	42.94	3.78	1.41	0.00	S
TxV	132.00	5096.35	38.61	3.40	1.26	0.00	S
Error	358.00	4065.98	11.36				
Day 8							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	987.23					
Rep	2.00	7.28	3.64	2.93	3.02	0.05	
Temp	3.00	86.71	28.90	23.23	2.63	0.00	S
Variety	44.00	121.09	2.75	2.21	1.41	0.00	S
TxV	132.00	326.68	2.47	1.99	1.26	0.00	S
Error	358.00	445.47	1.24				

Table 7.12 Continued. ANOVA tables from the Corvallis germination trials for each day throughout the trial looking at significance between temperatures and varieties ('S' indicates significance).

Day 9							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	507.13					
Rep	2.00	3.66	1.83	2.58	3.02	0.08	
Temp	3.00	28.91	9.64	13.56	2.63	0.00	S
Variety	44.00	57.23	1.30	1.83	1.41	0.00	S
TxV	132.00	162.88	1.23	1.74	1.26	0.00	S
Error	358.00	254.45	0.71				
Day 10							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	251.94					
Rep	2.00	3.70	1.85	4.31	3.02	0.01	S
Temp	3.00	10.15	3.38	7.89	2.63	0.00	S
Variety	44.00	22.15	0.50	1.17	1.41	0.22	
TxV	132.00	62.44	0.47	1.10	1.26	0.24	
Error	358.00	153.50	0.43				

Table 7.13. ANOVA tables from the Pendleton germination trials for each day throughout the trial looking at significance between temperatures and varieties ('S' indicates significance).

Day 1							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	34811.51					
Rep	1.00	155.06	155.06	18.08	3.87	0.00	S
Temp	3.00	8785.06	2928.35	341.49	2.63	0.00	S
Variety	44.00	10246.82	232.88	27.16	1.41	0.00	S
TxV	132.00	12554.61	95.11	11.09	1.26	0.00	S
Error	358.00	3069.95	8.58				
Day 2							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	578050.14					
Rep	1.00	807.34	807.34	49.39	3.87	0.00	S
Temp	3.00	524409.20	174803.07	10692.90	2.63	0.00	S
Variety	44.00	15138.44	344.06	21.05	1.41	0.00	S
TxV	132.00	31842.73	241.23	14.76	1.26	0.00	S
Error	358.00	5852.43	16.35				

Table 7.13 Continued. ANOVA tables from the Pendleton germination trials for each day throughout the trial looking at significance between temperatures and varieties ('S' indicates significance).

Day 3							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	511595.79					
Rep	1.00	36.10	36.10	0.93	3.87	0.34	
Temp	3.00	439510.35	146503.45	3764.19	2.63	0.00	S
Variety	44.00	20859.67	474.08	12.18	1.41	0.00	S
TxV	132.00	37256.20	282.24	7.25	1.26	0.00	S
Error	358.00	13933.48	38.92				
Day 4							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	643246.45					
Rep	1.00	938.68	938.68	60.51	3.87	0.00	S
Temp	3.00	598784.55	199594.85	12865.80	2.63	0.00	S
Variety	44.00	9910.35	225.24	14.52	1.41	0.00	S
TxV	132.00	28059.00	212.57	13.70	1.26	0.00	S
Error	358.00	5553.87	15.51				
Day 5							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	634384.18					
Rep	1.00	1467.03	1467.03	73.85	3.87	0.00	S
Temp	3.00	589848.46	196616.15	9897.80	2.63	0.00	S
Variety	44.00	10056.35	228.55	11.51	1.41	0.00	S
TxV	132.00	25900.80	196.22	9.88	1.26	0.00	S
Error	358.00	7111.54	19.86				
Day 6							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	574712.80					
Rep	1.00	1908.31	1908.31	76.25	3.87	0.00	S
Temp	3.00	525514.70	175171.57	6999.31	2.63	0.00	S
Variety	44.00	13341.15	303.21	12.12	1.41	0.00	S
TxV	132.00	24988.98	189.31	7.56	1.26	0.00	S
Error	358.00	8959.66	25.03				

Table 7.13 Continued. ANOVA tables from the Pendleton germination trials for each day throughout the trial looking at significance between temperatures and varieties ('S' indicates significance).

Day 7							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	332647.63					
Rep	1.00	2960.37	2960.37	93.48	3.87	0.00	S
Temp	3.00	265495.50	88498.50	2794.45	2.63	0.00	S
Variety	44.00	19785.13	449.66	14.20	1.41	0.00	S
TxV	132.00	33069.00	250.52	7.91	1.26	0.00	S
Error	358.00	11337.63	31.67				
Day 8							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	94929.60					
Rep	1.00	1572.08	1572.08	47.24	3.87	0.00	S
Temp	3.00	47025.52	15675.17	471.02	2.63	0.00	S
Variety	44.00	11984.76	272.38	8.18	1.41	0.00	S
TxV	132.00	22433.30	169.95	5.11	1.26	0.00	S
Error	358.00	11913.93	33.28				
Day 9							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	62812.87					
Rep	1.00	1728.16	1728.16	73.37	3.87	0.00	S
Temp	3.00	32083.88	10694.63	454.03	2.63	0.00	S
Variety	44.00	5309.08	120.66	5.12	1.41	0.00	S
TxV	132.00	15259.12	115.60	4.91	1.26	0.00	S
Error	358.00	8432.62	23.55				
Day 10							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	1923.32					
Rep	1.00	37.97	37.97	21.23	3.87	0.00	S
Temp	3.00	262.14	87.38	48.85	2.63	0.00	S
Variety	44.00	268.40	6.10	3.41	1.41	0.00	S
TxV	132.00	714.46	5.41	3.03	1.26	0.00	S
Error	358.00	640.35	1.79				

Table 7.13 Continued. ANOVA tables from the Pendleton germination trials for each day throughout the trial looking at significance between temperatures and varieties ('S' indicates significance).

Day 11							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	211.38					
Rep	1.00	2.02	2.02	8.05	3.87	0.00	S
Temp	3.00	18.46	6.15	24.58	2.63	0.00	S
Variety	44.00	25.33	0.58	2.30	1.41	0.00	S
TxV	132.00	75.98	0.58	2.30	1.26	0.00	S
Error	358.00	89.60	0.25				
Day 12							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	30.22					
Rep	1.00	0.34	0.34	9.12	3.87	0.00	S
Temp	3.00	2.41	0.80	21.84	2.63	0.00	S
Variety	44.00	3.57	0.08	2.21	1.41	0.00	S
TxV	132.00	10.72	0.08	2.21	1.26	0.00	S
Error	358.00	13.17	0.04				
Day 13							
Source	df	SS	MS	F	Fcritical	P-value	
Total	539.00	1.99					
Rep	1.00	0.01	0.01	4.02	3.87	0.05	
Temp	3.00	0.03	0.01	4.02	2.63	0.01	S
Variety	44.00	0.24	0.01	1.97	1.41	0.00	S
TxV	132.00	0.72	0.01	1.97	1.26	0.00	S
Error	358.00	0.99	0.00				

Table 7.14. ANOVA tables from the 30°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 1							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	11764.95					
Rep	2.00	984.03	492.01	15.60	3.10	0.00	S
Variety	44.00	8004.83	181.93	5.77	1.51	0.00	S
Error	88.00	2776.09	31.55				

Table 7.14 Continued. ANOVA tables from the 30°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	24070.53				
Rep	2.00	305.12	152.56	3.55	3.10	0.03
Variety	44.00	19987.45	454.26	10.58	1.51	0.00
Error	88.00	3777.96	42.93			
Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	10301.85				
Rep	2.00	11.62	5.81	0.20	3.10	0.82
Variety	44.00	7713.57	175.31	5.99	1.51	0.00
Error	88.00	2576.66	29.28			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	5431.81				
Rep	2.00	241.72	120.86	6.21	3.10	0.00
Variety	44.00	3478.52	79.06	4.06	1.51	0.00
Error	88.00	1711.57	19.45			
Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	3149.60				
Rep	2.00	61.23	30.61	2.37	3.10	0.10
Variety	44.00	1952.29	44.37	3.44	1.51	0.00
Error	88.00	1136.08	12.91			
Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	1984.22				
Rep	2.00	28.18	14.09	1.17	3.10	0.31
Variety	44.00	899.28	20.44	1.70	1.51	0.02
Error	88.00	1056.76	12.01			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	878.03				
Rep	2.00	15.58	15.58	1.50	4.06	0.23
Variety	44.00	404.45	202.22	19.43	3.21	0.00
Error	88.00	458.00	10.41			

Table 7.14 Continued. ANOVA tables from the 30°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 8						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	449.88				
Rep	2.00	7.16	3.58	1.44	3.10	0.24
Variety	44.00	224.47	5.10	2.06	1.51	0.00
Error	88.00	218.26	2.48			
Day 9						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	380.89				
Rep	2.00	3.94	1.97	0.93	3.10	0.40
Variety	44.00	191.44	4.35	2.06	1.51	0.00
Error	88.00	185.50	2.11			
Day 10						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	170.49				
Rep	2.00	3.08	1.54	1.27	3.10	0.29
Variety	44.00	60.62	1.38	1.14	1.51	0.30
Error	88.00	106.79	1.21			

Table 7.15. ANOVA tables from the 20°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 1						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	917.04				
Rep	2.00	39.13	19.56	6.99	3.10	0.00
Variety	44.00	631.70	14.36	5.13	1.51	0.00
Error	88.00	246.21	2.80			
Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	20745.04				
Rep	2.00	892.99	446.50	4.60	3.10	0.01
Variety	44.00	11317.70	257.22	2.65	1.51	0.00
Error	88.00	8534.34	96.98			

Table 7.15 Continued. ANOVA tables from the 20°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	294.55				
Rep	2.00	8.46	4.23	3.05	3.10	0.05
Variety	44.00	163.88	3.72	2.68	1.51	0.00
Error	88.00	122.21	1.39			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	84.59				
Rep	2.00	3.79	1.90	4.29	3.10	0.02
Variety	44.00	41.93	0.95	2.16	1.51	0.00
Error	88.00	38.87	0.44			
Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	29.73				
Rep	2.00	0.84	0.42	2.01	3.10	0.14
Variety	44.00	10.40	0.24	1.13	1.51	0.32
Error	88.00	18.49	0.21			
Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	2.93				
Rep	2.00	0.04	0.02	1.00	3.10	0.37
Variety	44.00	0.93	0.02	0.95	1.51	0.56
Error	88.00	1.96	0.02			

Table 7.16. ANOVA tables from the 10°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	17,709.48				
Rep	2.00	6.95	3.47	0.04	3.10	0.96
Variety	44.00	10,060.81	228.65	2.63	1.51	0.00
Error	88.00	7,641.72	86.84			

Table 7.16 Continued. ANOVA tables from the 10°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	16,558.99				
Rep	2.00	2,161.13	1,080.56	18.89	3.10	0.00
Variety	44.00	9,362.99	212.80	3.72	1.51	0.00
Error	88.00	5,034.87	57.21			
Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	10.40				
Rep	2.00	0.40	0.20	2.81	3.10	0.07
Variety	44.00	3.73	0.08	1.19	1.51	0.24
Error	88.00	6.27	0.07			
Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	4.81				
Rep	2.00	0.10	0.05	1.78	3.10	0.17
Variety	44.00	2.15	0.05	1.68	1.51	0.02
Error	88.00	2.56	0.03			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	0.99				
Rep	2.00	0.01	0.01	1.00	3.10	0.37
Variety	44.00	0.33	0.01	1.00	1.51	0.49
Error	88.00	0.65	0.01			

Table 7.17. ANOVA tables from the 4°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	14029.93				
Rep	2.00	1665.66	832.83	35.75	3.10	0.00
Variety	44.00	10314.37	234.42	10.06	1.51	0.00
Error	88.00	2049.90	23.29			

Table 7.17 Continued. ANOVA tables from the 4°C Corvallis germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	23001.00				
Rep	2.00	562.59	281.30	6.22	3.10	0.00
Variety	44.00	18460.55	419.56	9.28	1.51	0.00
Error	88.00	3977.86	45.20			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	7001.41				
Rep	2.00	336.90	168.45	177.03	3.10	0.00
Variety	44.00	6580.77	149.56	157.18	1.51	0.00
Error	88.00	83.73	0.95			
Day 8						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	301.95				
Rep	2.00	7.57	3.79	4.69	3.10	0.01
Variety	44.00	223.30	5.08	6.28	1.51	0.00
Error	88.00	71.07	0.81			
Day 9						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	54.36				
Rep	2.00	3.51	1.76	6.97	3.10	0.00
Variety	44.00	28.67	0.65	2.59	1.51	0.00
Error	88.00	22.18	0.25			
Day 10						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	50.78				
Rep	2.00	4.46	2.23	8.78	3.10	0.00
Variety	44.00	23.97	0.54	2.15	1.51	0.00
Error	88.00	22.35	0.25			

Table 7.18. ANOVA tables from the 30°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 1							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	17268.36					
Rep	1.00	158.53	158.53	3.17	4.06	0.08	
Variety	44.00	14909.94	338.86	6.78	1.65	0.00	S
Error	44.00	2199.88	50.00				
Day 2							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	49417.46					
Rep	1.00	1858.42	1858.42	24.86	4.06	0.00	S
Variety	44.00	44269.16	1006.12	13.46	1.65	0.00	S
Error	44.00	3289.89	74.77				
Day 3							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	46690.09					
Rep	1.00	2063.77	2063.77	31.23	4.06	0.00	S
Variety	44.00	41718.99	948.16	14.35	1.65	0.00	S
Error	44.00	2907.33	66.08				
Day 4							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	43844.01					
Rep	1.00	3279.63	3279.63	49.19	4.06	0.00	S
Variety	44.00	37630.48	855.24	12.83	1.65	0.00	S
Error	44.00	2933.90	66.68				
Day 5							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	43506.29					
Rep	1.00	5486.61	5486.61	83.51	4.06	0.00	S
Variety	44.00	35128.74	798.38	12.15	1.65	0.00	S
Error	44.00	2890.93	65.70				
Day 6							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	40620.27					
Rep	1.00	6705.16	6705.16	89.00	4.06	0.00	S
Variety	44.00	30600.32	695.46	9.23	1.65	0.00	S
Error	44.00	3314.79	75.34				

Table 7.18 Continued. ANOVA tables from the 30°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 7							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	37877.72					
Rep	1.00	7242.28	7242.28	99.82	4.06	0.00	S
Variety	44.00	27443.22	623.71	8.60	1.65	0.00	S
Error	44.00	3192.22	72.55				
Day 8							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	33958.52					
Rep	1.00	7116.38	7116.38	100.21	4.06	0.00	S
Variety	44.00	23717.50	539.03	7.59	1.65	0.00	S
Error	44.00	3124.63	71.01				
Day 9							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	30583.86					
Rep	1.00	6652.23	6652.23	85.09	4.06	0.00	S
Variety	44.00	20491.58	465.72	5.96	1.65	0.00	S
Error	44.00	3440.05	78.18				
Day 10							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	1625.18					
Rep	1.00	136.68	136.68	11.48	4.06	0.00	S
Variety	44.00	964.86	21.93	1.84	1.65	0.02	S
Error	44.00	523.64	11.90				
Day 11							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	192.92					
Rep	1.00	8.06	8.06	4.25	4.06	0.05	S
Variety	44.00	101.31	2.30	1.21	1.65	0.26	
Error	44.00	83.55	1.90				
Day 12							
Source	df	SS	MS	F	Fcritical	P-value	
Total	1.00	27.81					
Rep	1.00	1.34	1.34	4.85	4.06	0.03	S
Variety	44.00	14.30	0.32	1.17	1.65	0.30	
Error	44.00	12.17	0.28				

Table 7.18 Continued. ANOVA tables from the 30°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 13						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	1.96				
Rep	1.00	0.04	0.04	2.05	4.06	0.16
Variety	44.00	0.96	0.02	1.00	1.65	0.50
Error	44.00	0.96	0.02			

Table 7.19. ANOVA tables from the 20°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 1						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	8758.09				
Rep	1.00	151.63	151.63	9.33	4.06	0.00
Variety	44.00	7891.50	179.35	11.04	1.65	0.00
Error	44.00	714.97	16.25			
Day 2						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	4201.38				
Rep	1.00	185.31	185.31	6.15	4.06	0.02
Variety	44.00	2690.40	61.15	2.03	1.65	0.01
Error	44.00	1325.66	30.13			
Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	780.47				
Rep	1.00	31.24	31.24	4.37	4.06	0.04
Variety	44.00	434.99	9.89	1.38	1.65	0.14
Error	44.00	314.24	7.14			
Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	486.51				
Rep	1.00	15.23	15.23	3.10	4.06	0.09
Variety	44.00	254.99	5.80	1.18	1.65	0.29
Error	44.00	216.29	4.92			

Table 7.19 Continued. ANOVA tables from the 20°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	262.93				
Rep	1.00	5.89	5.89	2.03	4.06	0.16
Variety	44.00	129.41	2.94	1.01	1.65	0.48
Error	44.00	127.63	2.90			
Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	125.82				
Rep	1.00	3.22	3.22	2.31	4.06	0.14
Variety	44.00	61.30	1.39	1.00	1.65	0.50
Error	44.00	61.30	1.39			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	50.89				
Rep	1.00	1.11	1.11	1.96	4.06	0.17
Variety	44.00	24.89	0.57	1.00	1.65	0.50
Error	44.00	24.89	0.57			
Day 8						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	35.60				
Rep	1.00	0.40	0.40	1.00	4.06	0.32
Variety	44.00	17.60	0.40	1.00	1.65	0.50
Error	44.00	17.60	0.40			

Table 7.20. ANOVA tables from the 10°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 3						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	24614.89				
Rep	1.00	1521.11	1521.11	9.38	4.06	0.00 S
Variety	44.00	15961.89	362.77	2.24	1.65	0.00 S
Error	44.00	7131.89	162.09			

Table 7.20 Continued. ANOVA tables from the 10°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 4						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	131.39				
Rep	1.00	0.01	0.01	0.01	4.06	0.92
Variety	44.00	83.89	1.91	1.77	1.65	0.03
Error	44.00	47.49	1.08			
Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	16.10				
Rep	1.00	0.10	0.10	0.52	4.06	0.47
Variety	44.00	7.60	0.17	0.90	1.65	0.63
Error	44.00	8.40	0.19			
Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	10.72				
Rep	1.00	0.01	0.01	0.09	4.06	0.77
Variety	44.00	5.22	0.12	0.95	1.65	0.57
Error	44.00	5.49	0.12			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	8.90				
Rep	1.00	0.10	0.10	1.00	4.06	0.32
Variety	44.00	4.40	0.10	1.00	1.65	0.50
Error	44.00	4.40	0.10			

Table 7.21. ANOVA tables from the 4°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	750.40				
Rep	1.00	0.04	0.04	0.03	4.06	0.86
Variety	44.00	691.40	15.71	11.73	1.65	0.00
Error	44.00	58.96	1.34			

Table 7.21 Continued. ANOVA tables from the 4°C Pendleton germination trials for each day throughout the trial looking at significance between varieties ('S' indicates significance).

Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	8441.29				
Rep	1.00	12.84	12.84	0.74	4.06	0.39
Variety	44.00	7663.29	174.17	10.02	1.65	0.00
Error	44.00	765.16	17.39			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	29214.62				
Rep	1.00	499.38	499.38	6.59	4.06	0.01
Variety	44.00	25381.62	576.86	7.61	1.65	0.00
Error	44.00	3333.62	75.76			
Day 8						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	13909.96				
Rep	1.00	32.40	32.40	0.45	4.06	0.51
Variety	44.00	10682.96	242.79	3.34	1.65	0.00
Error	44.00	3194.60	72.60			
Day 9						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	145.12				
Rep	1.00	2.50	2.50	0.88	4.06	0.35
Variety	44.00	18.00	0.41	0.14	1.65	1.00
Error	44.00	124.62	2.83			
Day 10						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	36.00				
Rep	1.00	0.40	0.40	0.49	4.06	0.49
Variety	44.00	0.00	0.00	0.00	1.65	1.00
Error	44.00	35.60	0.81			

Appendix 8: Falling Number Data from Corvallis and Pendleton

Table 7.22. Raw Falling Number data gathered from Corvallis. Each field replication was replicated twice for the falling number test.

Variety	Replication	Location	FN 1	FN 2	Average
Alba	R1	Corvallis	333	316	324.5
Bitterroot	R1	Corvallis	381	375	378.0
Bobtail	R1	Corvallis	389	394	391.5
Brevor	R1	Corvallis	293	283	288.0
Bruehl	R1	Corvallis	227	230	228.5
Brundage	R1	Corvallis	216	208	212.0
Brundage 96	R1	Corvallis	331	328	329.5
Bruneau	R1	Corvallis	378	394	386.0
Cara	R1	Corvallis	433	426	429.5
Cayuga	R1	Corvallis	417	423	420.0
Coda	R1	Corvallis	492	470	481.0
Daws	R1	Corvallis	388	391	389.5
Elmar	R1	Corvallis	364	377	370.5
Eltan	R1	Corvallis	355	369	362.0
Gaines	R1	Corvallis	447	418	432.5
Gene	R1	Corvallis	303	308	305.5
Goetze	R1	Corvallis	382	386	384.0
Hill 81	R1	Corvallis	383	401	392.0
Hyslop	R1	Corvallis	414	385	399.5
Kaseberg	R1	Corvallis	423	412	417.5
Ladd	R1	Corvallis	335	348	341.5
Lewjain	R1	Corvallis	417	413	415.0
Madsen	R1	Corvallis	446	429	437.5
Malcolm	R1	Corvallis	419	407	413.0
Mary	R1	Corvallis	433	444	438.5
Nugaines	R1	Corvallis	402	388	395.0
Omar	R1	Corvallis	415	416	415.5
ORCF-101	R1	Corvallis	411	414	412.5
ORCF-102	R1	Corvallis	370	377	373.5
ORCF-103	R1	Corvallis	333	343	338.0
ORSS-1757	R1	Corvallis	415	416	415.5
Rely	R1	Corvallis	452	468	460.0
Rod	R1	Corvallis	440	436	438.0
Rosalyn	R1	Corvallis	413	423	418.0
Skiles	R1	Corvallis	426	433	429.5
Stephens	R1	Corvallis	414	400	407.0

Table 7.22 Continued. Raw Falling Number data gathered from Corvallis. Each field replication was replicated twice for the falling number test.

Variety	Replication	Location	FN 1	FN 2	Average
Tubbs	R1	Corvallis	427	444	435.5
Tubbs-06	R1	Corvallis	411	410	410.5
Xerpha	R1	Corvallis	404	428	416.0
11-225-1C	R1	Corvallis	356	333	344.5
11-225-2C	R1	Corvallis	391	384	387.5
11-225-3C	R1	Corvallis	357	368	362.5
11-225-5C	R1	Corvallis	397	406	401.5
11-225-6H	R1	Corvallis	428	409	418.5
11-225-7H	R1	Corvallis	389	399	394.0
Alba	R2	Corvallis	378	407	392.5
Bitterroot	R2	Corvallis	402	391	396.5
Bobtail	R2	Corvallis	401	397	399.0
Brevor	R2	Corvallis	321	321	321.0
Bruehl	R2	Corvallis	282	288	285.0
Brundage	R2	Corvallis	187	190	188.5
Brundage 96	R2	Corvallis	328	326	327.0
Bruneau	R2	Corvallis	414	398	406.0
Cara	R2	Corvallis	428	431	429.5
Cayuga	R2	Corvallis	419	419	419.0
Coda	R2	Corvallis	484	480	482.0
Daws	R2	Corvallis	373	369	371.0
Elmar	R2	Corvallis	393	396	394.5
Eltan	R2	Corvallis	386	369	377.5
Gaines	R2	Corvallis	425	432	428.5
Gene	R2	Corvallis	257	262	259.5
Goetze	R2	Corvallis	403	407	405.0
Hill 81	R2	Corvallis	400	402	401.0
Hyslop	R2	Corvallis	414	401	407.5
Kaseberg	R2	Corvallis	461	444	452.5
Ladd	R2	Corvallis	346	345	345.5
Lewjain	R2	Corvallis	452	475	463.5
Madsen	R2	Corvallis	419	397	408.0
Malcolm	R2	Corvallis	416	420	418.0
Mary	R2	Corvallis	436	406	421.0
Nugaines	R2	Corvallis	405	415	410.0
Omar	R2	Corvallis	420	432	426.0
ORCF-101	R2	Corvallis	364	363	363.5

Table 7.22 Continued. Raw Falling Number data gathered from Corvallis. Each field replication was replicated twice for the falling number test.

Variety	Replication	Location	FN 1	FN 2	Average
ORCF-102	R2	Corvallis	386	371	378.5
ORCF-103	R2	Corvallis	351	353	352.0
ORSS-1757	R2	Corvallis	406	398	402.0
Rely	R2	Corvallis	446	478	462.0
Rod	R2	Corvallis	394	408	401.0
Rosalyn	R2	Corvallis	378	355	366.5
Skiles	R2	Corvallis	404	436	420.0
Stephens	R2	Corvallis	390	388	389.0
Tubbs	R2	Corvallis	390	371	380.5
Tubbs-06	R2	Corvallis	411	404	407.5
Xerpha	R2	Corvallis	368	386	377.0
11-225-1C	R2	Corvallis	386	371	378.5
11-225-2C	R2	Corvallis	394	378	386.0
11-225-3C	R2	Corvallis	376	369	372.5
11-225-5C	R2	Corvallis	389	407	398.0
11-225-6H	R2	Corvallis	397	400	398.5
11-225-7H	R2	Corvallis	408	410	409.0
Alba	R3	Corvallis	421	426	423.5
Bitterroot	R3	Corvallis	387	370	378.5
Bobtail	R3	Corvallis	410	431	420.5
Brevor	R3	Corvallis	324	312	318.0
Bruehl	R3	Corvallis	198	186	192.0
Brundage	R3	Corvallis	241	241	241.0
Brundage 96	R3	Corvallis	395	406	400.5
Bruneau	R3	Corvallis	437	451	444.0
Cara	R3	Corvallis	405	422	413.5
Cayuga	R3	Corvallis	435	439	437.0
Coda	R3	Corvallis	499	484	491.5
Daws	R3	Corvallis	338	353	345.5
Elmar	R3	Corvallis	368	376	372.0
Eltan	R3	Corvallis	372	392	382.0
Gaines	R3	Corvallis	447	441	444.0
Gene	R3	Corvallis	348	342	345.0
Goetze	R3	Corvallis	428	422	425.0
Hill 81	R3	Corvallis	415	403	409.0
Hyslop	R3	Corvallis	392	417	404.5
Kaseberg	R3	Corvallis	431	443	437.0

Table 7.22 Continued. Raw Falling Number data gathered from Corvallis. Each field replication was replicated twice for the falling number test.

Variety	Replication	Location	FN 1	FN 2	Average
Ladd	R3	Corvallis	334	330	332.0
Lewjain	R3	Corvallis	442	439	440.5
Madsen	R3	Corvallis	439	410	424.5
Malcolm	R3	Corvallis	406	408	407.0
Mary	R3	Corvallis	460	462	461.0
Nugaines	R3	Corvallis	438	427	432.5
Omar	R3	Corvallis	424	394	409.0
ORCF-101	R3	Corvallis	401	393	397.0
ORCF-102	R3	Corvallis	388	409	398.5
ORCF-103	R3	Corvallis	358	341	349.5
ORSS-1757	R3	Corvallis	438	432	435.0
Rely	R3	Corvallis	450	442	446.0
Rod	R3	Corvallis	386	413	399.5
Rosalyn	R3	Corvallis	397	409	403.0
Skiles	R3	Corvallis	419	413	416.0
Stephens	R3	Corvallis	454	426	440.0
Tubbs	R3	Corvallis	419	425	422.0
Tubbs-06	R3	Corvallis	392	404	398.0
Xerpha	R3	Corvallis	387	376	381.5
11-225-1C	R3	Corvallis	407	375	391.0
11-225-2C	R3	Corvallis	386	396	391.0
11-225-3C	R3	Corvallis	413	413	413.0
11-225-5C	R3	Corvallis	388	409	398.5
11-225-6H	R3	Corvallis	390	394	392.0
11-225-7H	R3	Corvallis	390	387	388.5

Table 7.23. Raw Falling Number data gathered from Pendleton. Each field replication was replicated twice for the falling number test.

Variety	Replication	Location	FN 1	FN 2	Average
Alba	R1	Pendleton	498	485	491.5
Bitterroot	R1	Pendleton	485	484	484.5
Bobtail	R1	Pendleton	460	431	445.5
Brevor	R1	Pendleton	488	477	482.5
Bruehl	R1	Pendleton	427	450	438.5
Brundage	R1	Pendleton	451	470	460.5
Brundage 96	R1	Pendleton	415	436	425.5
Bruneau	R1	Pendleton	511	484	497.5
Cara	R1	Pendleton	488	505	496.5
Cayuga	R1	Pendleton	471	467	469
Coda	R1	Pendleton	527	526	526.5
Daws	R1	Pendleton	490	530	510
Elmar	R1	Pendleton	470	469	469.5
Eltan	R1	Pendleton	520	500	510
Gaines	R1	Pendleton	507	490	498.5
Gene	R1	Pendleton	430	409	419.5
Goetze	R1	Pendleton	463	447	455
Hill 81	R1	Pendleton	448	444	446
Hyslop	R1	Pendleton	513	522	517.5
Kaseberg	R1	Pendleton	447	435	441
Ladd	R1	Pendleton	478	454	466
Lewjain	R1	Pendleton	553	566	559.5
Madsen	R1	Pendleton	481	500	490.5
Malcolm	R1	Pendleton	498	482	490
Mary	R1	Pendleton	487	495	491
Nugaines	R1	Pendleton	475	490	482.5
Omar	R1	Pendleton	475	471	473
ORCF-101	R1	Pendleton	433	440	436.5
ORCF-102	R1	Pendleton	485	464	474.5
ORCF-103	R1	Pendleton	471	444	457.5
ORSS-1757	R1	Pendleton	436	426	431
Rely	R1	Pendleton	518	500	509
Rod	R1	Pendleton	468	493	480.5
Rosalyn	R1	Pendleton	443	424	433.5
Skiles	R1	Pendleton	475	489	482
Stephens	R1	Pendleton	440	452	446

Table 7.23 Continued. Raw Falling Number data gathered from Pendleton. Each field replication was replicated twice for the falling number test.

Variety	Replication	Location	FN 1	FN 2	Average
Tubbs	R1	Pendleton	482	466	474
Tubbs-06	R1	Pendleton	450	464	457
Xerpha	R1	Pendleton	528	510	519
11-225-1C	R1	Pendleton	408	405	406.5
11-225-2C	R1	Pendleton	423	429	426
11-225-3C	R1	Pendleton	458	429	443.5
11-225-5C	R1	Pendleton	439	434	436.5
11-225-6H	R1	Pendleton	443	415	429
11-225-7H	R1	Pendleton	447	436	441.5
Alba	R2	Pendleton	481	500	490.5
Bitterroot	R2	Pendleton	445	438	441.5
Bobtail	R2	Pendleton	437	435	436
Brevor	R2	Pendleton	501	479	490
Bruehl	R2	Pendleton	359	361	360
Brundage	R2	Pendleton	444	430	437
Brundage 96	R2	Pendleton	437	442	439.5
Bruneau	R2	Pendleton	490	463	476.5
Cara	R2	Pendleton	438	415	426.5
Cayuga	R2	Pendleton	446	415	430.5
Coda	R2	Pendleton	508	512	510
Daws	R2	Pendleton	408	437	422.5
Elmar	R2	Pendleton	481	468	474.5
Eltan	R2	Pendleton	474	457	465.5
Gaines	R2	Pendleton	487	477	482
Gene	R2	Pendleton	325	329	327
Goetze	R2	Pendleton	423	424	423.5
Hill 81	R2	Pendleton	451	454	452.5
Hyslop	R2	Pendleton	452	441	446.5
Kaseberg	R2	Pendleton	444	419	431.5
Ladd	R2	Pendleton	460	464	462
Lewjain	R2	Pendleton	515	489	502
Madsen	R2	Pendleton	454	445	449.5
Malcolm	R2	Pendleton	504	478	491
Mary	R2	Pendleton	444	417	430.5
Nugaines	R2	Pendleton	477	452	464.5
Omar	R2	Pendleton	453	452	452.5
ORCF-101	R2	Pendleton	392	398	395

Table 7.23 Continued. Raw Falling Number data gathered from Pendleton. Each field replication was replicated twice for the falling number test.

Variety	Replication	Location	FN 1	FN 2	Average
ORCF-102	R2	Pendleton	449	448	448.5
ORCF-103	R2	Pendleton	450	453	451.5
ORSS-1757	R2	Pendleton	392	395	393.5
Rely	R2	Pendleton	490	482	486
Rod	R2	Pendleton	440	455	447.5
Rosalyn	R2	Pendleton	391	392	391.5
Skiles	R2	Pendleton	447	443	445
Stephens	R2	Pendleton	435	409	422
Tubbs	R2	Pendleton	446	444	445
Tubbs-06	R2	Pendleton	467	482	474.5
Xerpha	R2	Pendleton	415	431	423
11-225-1C	R2	Pendleton	414	391	402.5
11-225-2C	R2	Pendleton	399	403	401
11-225-3C	R2	Pendleton	382	387	384.5
11-225-5C	R2	Pendleton	387	398	392.5
11-225-6H	R2	Pendleton	400	403	401.5
11-225-7H	R2	Pendleton	411	419	415

Appendix 9: Data Collected from Single Kernel Characterization System

Table 7.24. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Corvallis	R1	11-225-1C	9.26	14.55	48.17	14.14	10.87	0.32	3.12	0.42
Corvallis	R1	11-225-1C	9.23	15.57	48.35	13.18	10.85	0.34	3.14	0.39
Corvallis	R1	11-225-2C	25.99	17.01	38.23	13.31	10.54	0.56	2.84	0.42
Corvallis	R1	11-225-2C	26.01	17.63	37.26	13.01	10.56	0.55	2.82	0.38
Corvallis	R1	11-225-3C	16.86	14.32	45.59	13.69	10.90	0.33	3.07	0.39
Corvallis	R1	11-225-3C	17.67	16.51	42.84	14.32	10.90	0.39	3.00	0.44
Corvallis	R1	11-225-5C	18.98	19.38	40.23	15.19	10.70	0.53	2.91	0.47
Corvallis	R1	11-225-5C	18.82	18.53	38.52	14.15	10.73	0.49	2.85	0.43
Corvallis	R1	11-225-6H	16.35	15.91	39.73	13.05	10.87	0.38	2.89	0.40
Corvallis	R1	11-225-6H	13.90	17.88	41.43	13.06	10.84	0.47	2.94	0.41
Corvallis	R1	11-225-7H	9.00	17.89	46.58	13.56	10.79	0.37	3.05	0.41
Corvallis	R1	11-225-7H	11.75	18.76	48.07	13.19	10.77	0.44	3.09	0.40
Corvallis	R1	Alba	17.85	16.41	40.40	9.75	10.85	0.36	3.04	0.37
Corvallis	R1	Alba	17.84	16.80	40.96	9.10	10.92	0.32	3.01	0.31
Corvallis	R1	Bitterroot	17.08	14.92	35.08	11.17	10.43	0.69	2.83	0.42
Corvallis	R1	Bitterroot	18.58	17.72	35.85	11.94	10.47	0.61	2.85	0.40
Corvallis	R1	Bobtail	7.88	15.29	45.95	11.02	10.75	0.39	3.08	0.32
Corvallis	R1	Bobtail	5.33	13.99	46.33	9.87	10.77	0.34	3.09	0.31
Corvallis	R1	Brevor	14.15	14.64	41.08	9.36	10.30	0.54	3.01	0.32
Corvallis	R1	Brevor	15.78	14.88	39.78	9.97	10.31	0.47	2.96	0.36
Corvallis	R1	Bruehl	23.82	14.85	43.94	11.18	10.55	0.41	2.87	0.41
Corvallis	R1	Bruehl	24.06	14.20	43.06	10.52	10.60	0.40	2.86	0.39
Corvallis	R1	Brundage	21.83	18.13	44.00	12.58	10.72	0.45	2.98	0.39
Corvallis	R1	Brundage	20.53	20.00	45.00	12.01	10.76	0.44	2.99	0.35
Corvallis	R1	Brundage 96	13.75	16.58	42.60	10.27	10.83	0.47	2.98	0.37
Corvallis	R1	Brundage 96	15.27	15.74	43.98	11.06	10.84	0.36	3.00	0.34
Corvallis	R1	Bruneau	17.24	17.56	42.94	11.87	10.51	0.57	2.95	0.37
Corvallis	R1	Bruneau	17.81	17.49	41.49	12.82	10.46	0.52	2.91	0.38
Corvallis	R1	Cara	25.06	16.08	36.83	10.06	10.32	0.64	2.73	0.36
Corvallis	R1	Cara	26.14	15.58	34.53	10.62	10.25	0.72	2.68	0.37
Corvallis	R1	Cayuga	19.94	14.20	40.19	10.36	10.86	0.44	2.93	0.34
Corvallis	R1	Cayuga	20.41	12.63	40.38	10.25	10.95	0.28	2.94	0.33
Corvallis	R1	Coda	33.51	14.77	36.81	7.77	10.40	0.44	2.90	0.32
Corvallis	R1	Coda	31.35	15.62	36.24	8.47	10.38	0.46	2.85	0.32
Corvallis	R1	Daws	19.54	16.55	46.04	11.91	10.41	0.41	3.07	0.37
Corvallis	R1	Daws	19.65	16.03	45.23	12.49	10.41	0.51	3.07	0.39
Corvallis	R1	Elmar	34.92	14.20	34.47	7.81	10.81	0.37	2.75	0.34
Corvallis	R1	Elmar	35.74	16.65	34.41	7.47	10.76	0.41	2.74	0.31

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Corvallis	R1	Eltan	16.87	16.22	39.22	10.58	10.78	0.45	2.84	0.40
Corvallis	R1	Eltan	15.36	15.24	39.99	9.56	10.87	0.30	2.91	0.38
Corvallis	R1	Gaines	15.23	13.77	38.77	11.41	10.71	0.46	2.89	0.37
Corvallis	R1	Gaines	14.75	15.77	35.61	11.81	10.72	0.43	2.80	0.40
Corvallis	R1	Gene	15.61	17.52	40.99	13.08	10.88	0.49	2.85	0.38
Corvallis	R1	Gene	12.10	15.14	41.48	12.00	10.92	0.38	2.85	0.38
Corvallis	R1	Goetze	23.00	14.50	45.89	11.91	10.70	0.48	3.22	0.37
Corvallis	R1	Goetze	24.25	13.80	46.43	13.08	10.67	0.47	3.21	0.42
Corvallis	R1	Hill 81	27.78	15.89	40.15	11.68	10.50	0.45	2.85	0.36
Corvallis	R1	Hill 81	26.14	15.19	40.60	11.29	10.52	0.42	2.87	0.37
Corvallis	R1	Hyslop	31.39	15.60	37.36	11.60	10.10	0.72	2.81	0.39
Corvallis	R1	Hyslop	32.91	16.17	37.98	11.63	10.11	0.68	2.85	0.39
Corvallis	R1	Kaseberg	6.45	15.39	38.77	10.42	10.73	0.44	2.88	0.37
Corvallis	R1	Kaseberg	5.77	15.81	40.77	10.60	10.75	0.44	2.96	0.38
Corvallis	R1	Ladd	20.34	13.88	48.96	11.57	10.79	0.34	3.15	0.35
Corvallis	R1	Ladd	22.01	14.18	47.13	11.31	10.81	0.36	3.12	0.35
Corvallis	R1	Lewjain	24.08	14.62	38.53	12.07	10.71	0.61	2.85	0.44
Corvallis	R1	Lewjain	23.31	15.41	38.85	12.14	10.68	0.63	2.85	0.40
Corvallis	R1	Madsen	30.49	15.64	37.90	10.85	10.53	0.51	2.89	0.36
Corvallis	R1	Madsen	28.76	14.87	37.55	10.88	10.56	0.53	2.88	0.37
Corvallis	R1	Malcolm	31.20	16.53	37.35	12.74	10.51	0.62	2.83	0.40
Corvallis	R1	Malcolm	32.05	17.28	38.47	11.71	10.55	0.62	2.87	0.39
Corvallis	R1	Mary	18.84	15.42	41.71	11.70	10.57	0.48	2.96	0.36
Corvallis	R1	Mary	20.53	16.61	42.75	11.92	10.51	0.53	2.99	0.38
Corvallis	R1	Nugaines	19.58	16.40	42.28	11.21	10.53	0.43	3.04	0.37
Corvallis	R1	Nugaines	18.75	17.45	41.04	11.05	10.50	0.50	3.00	0.37
Corvallis	R1	Omar	30.24	16.76	35.81	8.79	10.50	0.44	2.78	0.32
Corvallis	R1	Omar	30.93	17.35	34.91	9.54	10.45	0.60	2.74	0.36
Corvallis	R1	ORCF-101	22.51	16.17	38.49	11.91	10.53	0.49	2.92	0.41
Corvallis	R1	ORCF-101	24.87	18.32	37.98	12.27	10.49	0.53	2.88	0.42
Corvallis	R1	ORCF-102	28.48	16.09	45.71	13.12	10.78	0.39	3.04	0.40
Corvallis	R1	ORCF-102	29.33	15.39	43.97	12.55	10.79	0.39	2.97	0.39
Corvallis	R1	ORCF-103	17.38	15.62	41.99	11.77	10.59	0.47	2.91	0.41
Corvallis	R1	ORCF-103	17.62	17.26	41.53	11.82	10.56	0.50	2.92	0.41
Corvallis	R1	ORSS-1757	4.52	15.83	48.06	11.32	10.80	0.33	3.10	0.32
Corvallis	R1	ORSS-1757	4.70	15.14	46.59	10.81	10.78	0.44	3.07	0.33
Corvallis	R1	Rely	33.08	18.66	38.22	10.79	10.48	0.52	2.81	0.38
Corvallis	R1	Rely	30.20	15.69	39.33	10.35	10.59	0.42	2.88	0.35
Corvallis	R1	Rod	18.53	21.38	37.35	11.60	10.75	0.50	2.76	0.37
Corvallis	R1	Rod	18.90	22.38	35.90	11.54	10.70	0.55	2.73	0.36

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Corvallis	R1	Rosalyn	25.38	18.46	38.22	12.23	11.08	0.43	2.83	0.38
Corvallis	R1	Rosalyn	25.54	20.70	37.79	13.38	11.03	0.48	2.81	0.43
Corvallis	R1	Skiles	18.96	16.88	43.41	12.80	10.66	0.46	2.92	0.42
Corvallis	R1	Skiles	17.12	17.17	44.92	12.01	10.73	0.39	2.96	0.40
Corvallis	R1	Stephens	20.80	16.27	48.01	13.70	10.70	0.39	3.13	0.42
Corvallis	R1	Stephens	21.02	17.78	45.88	14.72	10.60	0.48	3.02	0.44
Corvallis	R1	Tubbs	35.78	17.01	40.60	12.94	10.69	0.54	2.97	0.45
Corvallis	R1	Tubbs	35.69	17.89	39.19	11.74	10.69	0.43	2.92	0.41
Corvallis	R1	Tubbs-06	35.30	19.16	40.00	14.85	10.64	0.63	2.91	0.45
Corvallis	R1	Tubbs-06	35.38	18.02	40.73	14.22	10.71	0.47	2.92	0.45
Corvallis	R1	Xerpha	31.75	20.73	39.70	10.55	10.82	0.42	2.89	0.38
Corvallis	R1	Xerpha	32.11	19.54	41.14	11.07	10.88	0.30	2.92	0.38
Corvallis	R2	11-225-1C	11.30	15.68	38.29	13.76	10.96	0.42	2.85	0.44
Corvallis	R2	11-225-1C	9.82	15.58	42.60	14.57	10.99	0.41	2.99	0.47
Corvallis	R2	11-225-2C	25.39	16.08	38.75	12.08	10.88	0.31	2.89	0.38
Corvallis	R2	11-225-2C	24.97	14.88	39.29	11.66	10.85	0.40	2.87	0.36
Corvallis	R2	11-225-3C	14.01	16.54	46.40	13.89	10.69	0.48	3.09	0.46
Corvallis	R2	11-225-3C	15.23	15.36	47.13	13.34	10.76	0.32	3.09	0.43
Corvallis	R2	11-225-5C	18.39	19.15	39.89	13.96	10.89	0.50	2.89	0.42
Corvallis	R2	11-225-5C	18.51	17.10	37.81	12.43	10.90	0.46	2.83	0.42
Corvallis	R2	11-225-6H	13.34	17.47	45.40	14.06	10.84	0.44	3.02	0.45
Corvallis	R2	11-225-6H	11.84	17.68	41.99	13.52	10.90	0.34	2.94	0.42
Corvallis	R2	11-225-7H	12.39	19.43	40.42	13.27	10.68	0.46	2.87	0.38
Corvallis	R2	11-225-7H	13.67	19.23	40.18	12.87	10.69	0.35	2.91	0.40
Corvallis	R2	Alba	26.35	17.82	40.62	11.38	10.67	0.50	2.99	0.37
Corvallis	R2	Alba	24.84	15.15	41.88	11.76	10.64	0.54	3.03	0.36
Corvallis	R2	Bitterroot	19.32	15.10	37.76	10.79	10.79	0.47	2.89	0.38
Corvallis	R2	Bitterroot	18.84	17.28	38.25	10.94	10.83	0.46	2.91	0.39
Corvallis	R2	Bobtail	9.08	14.77	42.58	11.24	10.95	0.39	2.96	0.37
Corvallis	R2	Bobtail	7.04	16.79	43.18	12.11	10.94	0.39	2.96	0.36
Corvallis	R2	Brevor	21.01	15.32	40.97	11.14	10.66	0.36	2.96	0.36
Corvallis	R2	Brevor	20.94	14.26	41.18	9.45	10.67	0.34	2.99	0.33
Corvallis	R2	Bruehl	26.78	16.89	37.01	11.37	10.44	0.61	2.65	0.38
Corvallis	R2	Bruehl	24.33	17.06	37.47	10.72	10.47	0.57	2.67	0.36
Corvallis	R2	Brundage	18.95	17.51	48.22	12.51	10.85	0.32	3.10	0.37
Corvallis	R2	Brundage	19.22	17.12	45.45	13.81	10.85	0.37	3.00	0.38
Corvallis	R2	Brundage 96	13.69	19.08	39.24	11.16	10.91	0.36	2.86	0.37
Corvallis	R2	Brundage 96	14.56	17.78	39.12	12.70	10.83	0.57	2.84	0.38
Corvallis	R2	Bruneau	16.36	16.62	40.66	12.72	10.45	0.51	2.88	0.39
Corvallis	R2	Bruneau	18.83	17.54	39.87	11.95	10.54	0.42	2.89	0.38

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Corvallis	R2	Cara	22.64	14.20	36.75	10.77	10.47	0.44	2.75	0.38
Corvallis	R2	Cara	21.54	14.72	38.72	10.89	10.48	0.59	2.79	0.36
Corvallis	R2	Cayuga	20.33	15.15	41.50	10.44	11.09	0.29	2.97	0.36
Corvallis	R2	Cayuga	20.41	13.06	43.22	10.55	11.07	0.32	3.02	0.33
Corvallis	R2	Coda	31.76	15.12	36.53	8.26	10.33	0.53	2.85	0.33
Corvallis	R2	Coda	32.85	16.38	37.95	8.69	10.30	0.58	2.92	0.34
Corvallis	R2	Daws	18.47	15.94	47.56	11.62	10.76	0.35	3.14	0.37
Corvallis	R2	Daws	20.44	16.54	46.99	12.13	10.79	0.29	3.10	0.36
Corvallis	R2	Elmar	39.62	17.09	34.07	8.27	10.70	0.38	2.73	0.32
Corvallis	R2	Elmar	38.23	16.59	33.16	9.23	10.64	0.52	2.68	0.36
Corvallis	R2	Eltan	24.14	14.45	36.63	11.07	10.54	0.57	2.79	0.39
Corvallis	R2	Eltan	23.22	14.54	40.24	11.45	10.64	0.43	2.85	0.40
Corvallis	R2	Gaines	16.41	15.85	37.76	11.68	10.75	0.41	2.86	0.39
Corvallis	R2	Gaines	15.64	15.07	39.57	11.06	10.75	0.31	2.89	0.34
Corvallis	R2	Gene	13.79	15.42	43.25	11.42	11.04	0.27	2.93	0.39
Corvallis	R2	Gene	11.77	14.51	45.11	12.16	10.99	0.35	2.97	0.40
Corvallis	R2	Goetze	27.61	14.93	46.29	13.24	10.46	0.44	3.14	0.42
Corvallis	R2	Goetze	30.66	17.56	43.28	13.54	10.44	0.55	3.08	0.42
Corvallis	R2	Hill 81	24.89	17.21	37.79	10.45	10.77	0.37	2.81	0.34
Corvallis	R2	Hill 81	27.00	17.84	35.22	11.39	10.68	0.51	2.73	0.40
Corvallis	R2	Hyslop	28.38	15.46	42.10	10.67	10.41	0.60	2.98	0.38
Corvallis	R2	Hyslop	26.97	15.84	42.61	10.88	10.48	0.53	2.99	0.36
Corvallis	R2	Kaseberg	1.82	16.43	35.22	9.98	10.58	0.52	2.82	0.36
Corvallis	R2	Kaseberg	0.28	16.01	38.26	10.40	10.64	0.53	2.90	0.37
Corvallis	R2	Ladd	19.16	13.83	47.82	12.27	10.95	0.29	3.10	0.39
Corvallis	R2	Ladd	18.95	14.10	49.09	11.52	10.97	0.32	3.18	0.37
Corvallis	R2	Lewjain	26.05	15.54	37.94	11.77	11.02	0.34	2.82	0.42
Corvallis	R2	Lewjain	22.40	16.34	38.67	12.01	11.03	0.38	2.82	0.40
Corvallis	R2	Madsen	27.00	14.14	42.81	10.09	10.69	0.42	3.02	0.33
Corvallis	R2	Madsen	27.68	13.22	42.31	10.27	10.62	0.41	2.98	0.34
Corvallis	R2	Malcolm	26.46	14.87	47.21	12.70	10.65	0.52	3.13	0.41
Corvallis	R2	Malcolm	28.22	15.29	46.70	13.47	10.61	0.50	3.08	0.41
Corvallis	R2	Mary	19.88	16.39	41.28	11.78	10.31	0.61	2.93	0.35
Corvallis	R2	Mary	16.38	16.32	44.21	11.68	10.42	0.47	3.00	0.37
Corvallis	R2	Nugaines	16.82	15.48	39.78	10.67	10.68	0.37	2.94	0.37
Corvallis	R2	Nugaines	19.26	18.71	41.62	9.95	10.77	0.35	2.97	0.31
Corvallis	R2	Omar	34.51	18.34	35.77	10.59	10.58	0.52	2.77	0.37
Corvallis	R2	Omar	33.59	17.59	34.94	10.90	10.50	0.65	2.72	0.36
Corvallis	R2	ORCF-101	18.96	14.69	44.86	11.96	10.66	0.41	3.07	0.40
Corvallis	R2	ORCF-101	20.18	15.59	43.46	11.32	10.65	0.38	3.06	0.38

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Corvallis	R2	ORCF-102	26.47	18.15	42.93	12.39	10.73	0.49	2.96	0.38
Corvallis	R2	ORCF-102	25.64	16.48	41.23	13.07	10.65	0.58	2.92	0.40
Corvallis	R2	ORCF-103	18.34	15.13	41.91	11.28	10.64	0.46	2.89	0.38
Corvallis	R2	ORCF-103	19.08	18.44	42.93	12.83	10.58	0.48	2.88	0.41
Corvallis	R2	ORSS-1757	4.75	15.10	48.85	10.22	10.68	0.26	3.10	0.33
Corvallis	R2	ORSS-1757	5.24	15.25	48.30	10.03	10.69	0.36	3.09	0.33
Corvallis	R2	Rely	31.96	16.77	35.70	9.29	10.85	0.42	2.76	0.33
Corvallis	R2	Rely	30.86	17.12	33.55	9.16	10.76	0.48	2.68	0.33
Corvallis	R2	Rod	13.43	18.31	44.20	11.97	10.62	0.46	2.95	0.39
Corvallis	R2	Rod	18.25	18.81	43.94	12.49	10.57	0.53	2.96	0.40
Corvallis	R2	Rosalyn	14.81	17.51	44.28	12.09	10.94	0.49	3.03	0.39
Corvallis	R2	Rosalyn	14.95	17.23	46.10	12.36	11.02	0.35	3.04	0.37
Corvallis	R2	Skiles	13.90	19.15	42.49	12.33	10.60	0.46	2.87	0.38
Corvallis	R2	Skiles	17.19	18.48	42.94	12.12	10.62	0.40	2.91	0.38
Corvallis	R2	Stephens	23.30	18.14	52.33	14.84	10.63	0.37	3.20	0.44
Corvallis	R2	Stephens	22.89	18.44	50.04	13.38	10.68	0.35	3.18	0.42
Corvallis	R2	Tubbs	33.76	15.24	45.88	12.18	10.81	0.37	3.09	0.40
Corvallis	R2	Tubbs	33.39	15.03	45.00	11.52	10.84	0.35	3.07	0.36
Corvallis	R2	Tubbs-06	30.95	17.18	50.30	13.54	10.82	0.29	3.19	0.39
Corvallis	R2	Tubbs-06	31.05	16.21	48.09	15.08	10.72	0.49	3.13	0.46
Corvallis	R2	Xerpha	36.15	16.84	42.12	11.45	10.66	0.44	2.97	0.37
Corvallis	R2	Xerpha	34.77	19.26	41.72	12.16	10.67	0.50	2.93	0.39
Corvallis	R3	11-225-1C	7.63	14.90	39.30	11.18	11.25	0.39	2.89	0.36
Corvallis	R3	11-225-1C	8.55	15.70	39.63	11.14	11.21	0.44	2.92	0.35
Corvallis	R3	11-225-2C	25.68	17.57	37.56	9.89	11.08	0.41	2.84	0.33
Corvallis	R3	11-225-2C	24.01	14.39	36.78	11.00	11.06	0.43	2.81	0.36
Corvallis	R3	11-225-3C	16.93	18.04	37.23	12.51	10.99	0.45	2.85	0.40
Corvallis	R3	11-225-3C	14.95	17.78	35.66	11.69	10.99	0.50	2.78	0.40
Corvallis	R3	11-225-5C	15.75	16.96	36.68	12.21	11.04	0.45	2.83	0.41
Corvallis	R3	11-225-5C	16.52	17.45	38.87	12.08	11.10	0.41	2.84	0.37
Corvallis	R3	11-225-6H	12.67	18.47	43.18	12.94	11.16	0.36	2.98	0.40
Corvallis	R3	11-225-6H	12.34	17.22	43.98	14.16	11.14	0.39	2.96	0.43
Corvallis	R3	11-225-7H	10.95	20.01	38.84	11.76	11.08	0.37	2.82	0.38
Corvallis	R3	11-225-7H	9.98	17.99	40.52	12.68	11.06	0.41	2.89	0.41
Corvallis	R3	Alba	31.32	17.36	36.67	9.73	11.06	0.46	2.88	0.35
Corvallis	R3	Alba	32.69	17.29	36.52	10.13	11.06	0.38	2.87	0.34
Corvallis	R3	Bitterroot	16.98	15.42	39.58	9.80	10.94	0.46	2.92	0.33
Corvallis	R3	Bitterroot	16.24	16.72	38.93	10.23	10.91	0.51	2.93	0.36
Corvallis	R3	Bobtial	8.39	16.04	43.04	11.29	11.14	0.31	2.92	0.34
Corvallis	R3	Bobtial	10.45	15.31	40.13	11.97	11.07	0.39	2.86	0.36

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Corvallis	R3	Brevor	17.52	15.57	42.17	10.10	11.02	0.27	3.00	0.34
Corvallis	R3	Brevor	17.56	16.03	43.19	9.56	10.98	0.30	3.04	0.33
Corvallis	R3	Bruehl	23.56	16.16	42.49	10.75	11.16	0.41	2.82	0.39
Corvallis	R3	Bruehl	21.53	15.59	42.23	10.27	11.19	0.34	2.80	0.37
Corvallis	R3	Brundage	18.04	17.93	39.66	11.90	11.20	0.32	2.84	0.37
Corvallis	R3	Brundage	20.68	16.52	40.04	12.35	11.21	0.41	2.85	0.38
Corvallis	R3	Brundage 96	15.89	18.16	34.92	11.07	11.38	0.51	2.74	0.37
Corvallis	R3	Brundage 96	15.34	19.26	36.16	10.86	11.42	0.34	2.74	0.35
Corvallis	R3	Bruneau	13.13	18.45	33.67	10.29	11.28	0.44	2.69	0.36
Corvallis	R3	Bruneau	12.62	19.54	34.58	9.81	11.27	0.44	2.71	0.37
Corvallis	R3	Cara	20.10	13.54	35.27	9.32	10.92	0.51	2.70	0.34
Corvallis	R3	Cara	21.21	15.12	33.84	9.49	10.85	0.52	2.66	0.32
Corvallis	R3	Cayuga	19.87	16.20	40.44	11.39	11.23	0.37	2.94	0.38
Corvallis	R3	Cayuga	20.03	17.00	39.92	9.71	11.26	0.34	2.90	0.35
Corvallis	R3	Coda	34.46	15.71	32.62	8.53	10.71	0.45	2.71	0.31
Corvallis	R3	Coda	33.98	15.75	34.25	9.05	10.73	0.38	2.77	0.34
Corvallis	R3	Daws	20.93	17.01	41.13	10.51	11.20	0.40	2.93	0.35
Corvallis	R3	Daws	23.20	17.73	40.70	12.13	11.19	0.40	2.93	0.39
Corvallis	R3	Elmar	37.98	16.76	33.59	9.20	11.08	0.34	2.72	0.33
Corvallis	R3	Elmar	37.94	15.08	34.55	7.59	11.09	0.33	2.79	0.31
Corvallis	R3	Eltan	21.29	14.99	38.42	11.20	11.02	0.46	2.80	0.40
Corvallis	R3	Eltan	25.17	14.14	39.62	11.59	11.00	0.41	2.85	0.40
Corvallis	R3	Gaines	12.94	16.17	36.97	11.28	10.92	0.39	2.83	0.36
Corvallis	R3	Gaines	17.20	15.12	37.92	10.36	10.97	0.33	2.87	0.33
Corvallis	R3	Gene	16.21	17.53	36.96	11.60	11.08	0.39	2.73	0.36
Corvallis	R3	Gene	16.71	16.13	36.15	10.61	11.07	0.44	2.70	0.35
Corvallis	R3	Goetze	27.96	15.74	44.24	12.76	10.78	0.34	3.11	0.40
Corvallis	R3	Goetze	26.95	16.53	43.63	13.70	10.74	0.32	3.08	0.44
Corvallis	R3	Hill 81	24.94	15.81	35.66	10.51	10.77	0.43	2.77	0.39
Corvallis	R3	Hill 81	24.11	16.17	36.38	9.95	10.78	0.45	2.77	0.37
Corvallis	R3	Hyslop	28.39	14.98	41.73	9.84	10.39	0.49	2.95	0.35
Corvallis	R3	Hyslop	28.56	14.78	41.79	9.82	10.42	0.43	2.96	0.33
Corvallis	R3	Kaseberg	0.54	15.20	37.07	10.29	11.18	0.34	2.84	0.35
Corvallis	R3	Kaseberg	0.71	15.34	38.26	9.63	11.17	0.28	2.89	0.36
Corvallis	R3	Ladd	19.53	13.37	47.04	10.54	11.27	0.25	3.10	0.34
Corvallis	R3	Ladd	19.94	15.29	49.52	10.52	11.22	0.28	3.15	0.35
Corvallis	R3	Lewjain	23.71	15.45	32.70	10.27	11.39	0.32	2.65	0.34
Corvallis	R3	Lewjain	24.54	17.13	32.85	10.31	11.36	0.44	2.65	0.36
Corvallis	R3	Madsen	27.37	13.14	37.31	10.01	10.73	0.43	2.86	0.34
Corvallis	R3	Madsen	26.90	16.58	36.81	9.59	10.67	0.52	2.82	0.33

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Corvallis	R3	Malcolm	26.27	18.75	41.19	10.83	11.18	0.33	2.95	0.36
Corvallis	R3	Malcolm	27.89	16.54	41.33	11.75	11.15	0.30	2.98	0.38
Corvallis	R3	Mary	19.97	17.05	39.28	11.04	10.66	0.54	2.84	0.34
Corvallis	R3	Mary	19.43	17.29	40.06	10.55	10.69	0.42	2.90	0.35
Corvallis	R3	Nugaines	20.11	16.34	35.88	11.37	10.85	0.39	2.81	0.38
Corvallis	R3	Nugaines	23.22	16.88	37.74	11.16	10.88	0.33	2.87	0.38
Corvallis	R3	Omar	27.57	14.88	37.06	8.21	10.63	0.42	2.82	0.31
Corvallis	R3	Omar	29.75	17.94	36.97	8.15	10.61	0.39	2.83	0.32
Corvallis	R3	ORCF-101	19.29	13.79	39.97	11.32	11.45	0.34	2.94	0.38
Corvallis	R3	ORCF-101	20.45	15.95	39.87	11.25	11.50	0.27	2.99	0.42
Corvallis	R3	ORCF-102	26.58	15.90	44.68	10.27	11.06	0.28	3.00	0.31
Corvallis	R3	ORCF-102	27.27	17.44	43.26	11.90	10.99	0.38	2.97	0.37
Corvallis	R3	ORCF-103	18.79	17.56	39.56	10.70	11.06	0.36	2.83	0.37
Corvallis	R3	ORCF-103	17.74	16.70	38.71	10.28	11.04	0.39	2.81	0.38
Corvallis	R3	ORSS-1757	3.91	15.87	44.03	10.99	11.00	0.37	2.98	0.34
Corvallis	R3	ORSS-1757	5.72	17.33	43.31	10.87	10.99	0.42	2.96	0.34
Corvallis	R3	Rely	28.02	15.95	33.45	8.36	11.07	0.43	2.67	0.33
Corvallis	R3	Rely	29.24	18.01	33.62	8.74	11.10	0.42	2.68	0.33
Corvallis	R3	Rod	19.48	20.90	36.52	11.16	11.34	0.41	2.77	0.40
Corvallis	R3	Rod	18.70	22.29	36.41	12.00	11.28	0.50	2.73	0.39
Corvallis	R3	Rosalyn	15.80	17.43	38.52	12.19	11.34	0.41	2.88	0.39
Corvallis	R3	Rosalyn	16.14	18.99	39.22	12.01	11.39	0.66	2.91	0.40
Corvallis	R3	Skiles	10.55	17.83	40.70	11.10	11.12	0.33	2.84	0.36
Corvallis	R3	Skiles	13.22	18.32	38.50	11.25	11.10	0.41	2.77	0.39
Corvallis	R3	Stephens	23.74	18.15	39.19	13.54	10.94	0.39	2.90	0.45
Corvallis	R3	Stephens	25.86	19.65	39.44	13.46	10.92	0.39	2.87	0.41
Corvallis	R3	Tubbs	27.35	15.90	46.91	13.00	11.28	0.28	3.11	0.41
Corvallis	R3	Tubbs	28.95	16.51	46.64	13.16	11.25	0.26	3.09	0.41
Corvallis	R3	Tubbs-06	31.66	17.08	43.37	13.03	11.03	0.42	3.04	0.42
Corvallis	R3	Tubbs-06	30.33	16.65	42.51	13.75	11.00	0.41	3.01	0.43
Corvallis	R3	Xerpha	32.37	16.68	44.08	11.27	11.07	0.31	3.03	0.39
Corvallis	R3	Xerpha	31.95	17.44	44.15	11.30	11.07	0.34	3.01	0.38
Pendleton	R1	11-225-1C	22.61	16.04	31.79	8.81	8.68	0.82	2.61	0.32
Pendleton	R1	11-225-1C	23.89	14.71	30.74	8.82	8.58	0.83	2.57	0.30
Pendleton	R1	11-225-2C	30.59	15.11	33.79	8.22	8.86	0.82	2.64	0.28
Pendleton	R1	11-225-2C	31.35	15.11	33.30	7.69	8.84	0.87	2.66	0.30
Pendleton	R1	11-225-3C	27.60	16.59	31.34	8.64	7.64	0.60	2.62	0.31
Pendleton	R1	11-225-3C	24.66	15.86	31.28	9.64	7.69	0.61	2.58	0.31
Pendleton	R1	11-225-5C	29.11	15.63	27.74	7.89	7.84	0.65	2.48	0.28
Pendleton	R1	11-225-5C	27.22	17.16	28.16	8.24	7.81	0.61	2.47	0.27

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Pendleton	R1	11-225-6H	24.33	15.66	30.54	8.89	9.55	0.79	2.58	0.32
Pendleton	R1	11-225-6H	25.36	16.10	29.90	7.74	9.58	0.79	2.54	0.29
Pendleton	R1	11-225-7H	25.79	15.16	30.20	8.38	8.54	0.83	2.53	0.30
Pendleton	R1	11-225-7H	26.70	15.33	30.97	7.99	8.53	0.86	2.56	0.28
Pendleton	R1	Alba	36.28	15.21	28.06	6.11	7.73	0.72	2.58	0.23
Pendleton	R1	Alba	34.99	14.00	29.66	7.09	7.85	0.72	2.62	0.28
Pendleton	R1	Bitterroot	39.44	16.61	26.49	6.64	7.88	0.57	2.44	0.25
Pendleton	R1	Bitterroot	37.36	17.94	26.77	6.86	7.91	0.62	2.46	0.23
Pendleton	R1	Bobtail	38.09	14.02	26.09	5.99	7.46	0.40	2.40	0.23
Pendleton	R1	Bobtail	42.81	16.92	25.77	7.03	7.50	0.47	2.40	0.26
Pendleton	R1	Brevor	32.00	15.63	32.61	6.94	8.01	0.80	2.68	0.25
Pendleton	R1	Brevor	31.31	14.29	32.11	6.43	8.04	0.79	2.69	0.26
Pendleton	R1	Bruehl	40.62	15.42	29.61	7.73	7.85	0.58	2.44	0.26
Pendleton	R1	Bruehl	41.34	13.47	30.61	8.26	7.89	0.66	2.47	0.26
Pendleton	R1	Brundage	26.64	17.33	27.03	7.72	8.37	0.78	2.46	0.28
Pendleton	R1	Brundage	23.99	16.28	28.31	8.06	8.46	0.80	2.47	0.23
Pendleton	R1	Brundage 96	30.50	17.69	28.52	7.53	7.92	0.72	2.49	0.28
Pendleton	R1	Brundage 96	27.35	16.56	27.54	7.42	7.96	0.69	2.43	0.24
Pendleton	R1	Bruneau	37.90	17.09	27.62	6.49	7.50	0.55	2.44	0.27
Pendleton	R1	Bruneau	39.06	18.62	26.90	7.62	7.54	0.53	2.41	0.26
Pendleton	R1	Cara	44.95	17.96	26.00	7.72	7.37	0.39	2.40	0.26
Pendleton	R1	Cara	46.77	18.18	25.28	8.16	7.38	0.38	2.38	0.24
Pendleton	R1	Cayuga	27.79	14.47	29.97	6.52	8.40	0.80	2.53	0.25
Pendleton	R1	Cayuga	28.37	15.62	29.42	6.78	8.30	0.80	2.51	0.27
Pendleton	R1	Coda	57.40	14.69	24.35	5.46	7.32	0.43	2.46	0.22
Pendleton	R1	Coda	54.88	15.74	25.24	6.93	7.33	0.47	2.45	0.22
Pendleton	R1	Daws	44.81	16.99	27.58	7.98	7.53	0.60	2.50	0.25
Pendleton	R1	Daws	46.05	16.59	26.35	6.53	7.46	0.55	2.45	0.25
Pendleton	R1	Elmar	50.21	15.07	26.89	7.41	8.09	0.89	2.49	0.27
Pendleton	R1	Elmar	51.96	16.63	26.57	6.78	8.07	0.92	2.45	0.24
Pendleton	R1	Eltan	34.94	13.64	30.83	7.76	7.41	0.56	2.57	0.28
Pendleton	R1	Eltan	36.65	14.50	30.67	7.69	7.42	0.56	2.55	0.28
Pendleton	R1	Gaines	36.91	16.99	25.40	7.22	7.85	0.64	2.41	0.22
Pendleton	R1	Gaines	37.58	17.70	26.46	7.80	7.84	0.72	2.45	0.26
Pendleton	R1	Gene	44.00	16.15	27.78	7.95	8.38	0.88	2.45	0.27
Pendleton	R1	Gene	45.43	15.78	27.38	7.46	8.34	0.85	2.43	0.27
Pendleton	R1	Goetze	42.42	15.29	29.00	7.58	7.73	0.46	2.59	0.28
Pendleton	R1	Goetze	43.77	15.34	27.42	6.95	7.79	0.42	2.49	0.25
Pendleton	R1	Hill 81	42.78	14.43	28.37	7.01	7.84	0.68	2.47	0.23
Pendleton	R1	Hill 81	43.37	16.15	27.78	7.44	7.74	0.70	2.43	0.22

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Pendleton	R1	Hyslop	47.25	17.51	27.93	8.91	7.67	0.69	2.50	0.29
Pendleton	R1	Hyslop	45.97	15.75	26.69	7.92	7.59	0.63	2.46	0.26
Pendleton	R1	Kaseberg	27.04	17.74	25.91	7.81	7.98	0.63	2.43	0.30
Pendleton	R1	Kaseberg	28.35	18.89	25.69	7.43	8.00	0.60	2.42	0.31
Pendleton	R1	Ladd	32.12	13.20	38.25	8.43	8.22	0.85	2.78	0.31
Pendleton	R1	Ladd	32.01	14.15	37.55	7.32	8.26	0.87	2.78	0.29
Pendleton	R1	Lewjain	37.12	18.41	26.26	7.19	7.75	0.65	2.41	0.25
Pendleton	R1	Lewjain	38.02	16.70	27.03	6.88	7.80	0.69	2.46	0.28
Pendleton	R1	Madsen	49.34	15.48	28.09	6.87	7.39	0.55	2.53	0.27
Pendleton	R1	Madsen	48.51	14.61	27.80	7.11	7.37	0.54	2.49	0.24
Pendleton	R1	Malcolm	42.53	16.09	30.54	7.44	9.53	0.79	2.57	0.28
Pendleton	R1	Malcolm	42.54	14.61	31.01	7.39	9.58	0.74	2.59	0.27
Pendleton	R1	Mary	37.36	14.21	31.07	6.57	7.59	0.67	2.58	0.26
Pendleton	R1	Mary	38.15	14.89	30.56	8.40	7.56	0.66	2.57	0.26
Pendleton	R1	Nugaines	39.13	16.96	27.08	7.58	8.36	0.75	2.48	0.26
Pendleton	R1	Nugaines	36.73	15.69	26.83	7.89	8.29	0.75	2.48	0.26
Pendleton	R1	Omar	44.99	15.15	28.65	6.60	7.84	0.79	2.51	0.29
Pendleton	R1	Omar	44.38	13.23	28.53	5.97	7.88	0.72	2.50	0.24
Pendleton	R1	ORCF-101	40.60	14.68	28.54	6.65	8.13	0.86	2.53	0.27
Pendleton	R1	ORCF-101	38.69	14.35	29.82	7.12	8.35	0.87	2.55	0.30
Pendleton	R1	ORCF-102	40.77	14.08	32.42	8.19	8.13	0.79	2.54	0.30
Pendleton	R1	ORCF-102	41.64	14.99	32.59	8.26	8.16	0.82	2.54	0.28
Pendleton	R1	ORCF-103	34.24	14.58	32.96	7.29	8.11	0.86	2.59	0.29
Pendleton	R1	ORCF-103	35.16	14.00	32.95	7.22	8.02	0.84	2.58	0.29
Pendleton	R1	ORSS-1757	25.19	14.46	32.50	7.53	8.62	0.78	2.61	0.29
Pendleton	R1	ORSS-1757	23.16	16.01	33.53	7.56	8.62	0.78	2.63	0.29
Pendleton	R1	Rely	46.68	15.84	24.96	6.97	7.75	0.51	2.41	0.22
Pendleton	R1	Rely	49.24	16.47	24.45	6.54	7.78	0.53	2.39	0.22
Pendleton	R1	Rod	39.26	16.46	31.84	8.51	7.95	0.63	2.63	0.30
Pendleton	R1	Rod	37.01	14.90	31.58	7.71	7.80	0.52	2.57	0.29
Pendleton	R1	Rosalyn	43.22	12.47	32.45	6.36	8.89	0.75	2.67	0.26
Pendleton	R1	Rosalyn	44.45	14.21	32.17	7.30	8.97	0.83	2.64	0.30
Pendleton	R1	Skiles	24.81	14.91	34.63	8.02	8.73	0.74	2.62	0.32
Pendleton	R1	Skiles	24.28	12.96	34.46	7.50	8.86	0.68	2.62	0.32
Pendleton	R1	Stephens	33.89	14.44	31.86	7.68	8.36	0.89	2.61	0.29
Pendleton	R1	Stephens	37.78	15.63	30.97	6.92	8.25	0.94	2.59	0.27
Pendleton	R1	Tubbs	39.83	13.88	33.37	9.94	8.52	0.94	2.69	0.33
Pendleton	R1	Tubbs	44.55	14.15	30.61	7.89	8.12	0.90	2.61	0.28
Pendleton	R1	Tubbs-06	47.44	13.91	31.07	7.90	7.48	0.57	2.63	0.30
Pendleton	R1	Tubbs-06	46.81	13.70	29.64	7.66	7.54	0.54	2.58	0.29

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Pendleton	R1	Xerpha	46.49	16.50	29.15	6.87	7.85	0.63	2.56	0.28
Pendleton	R1	Xerpha	47.36	16.65	29.39	7.41	7.80	0.60	2.58	0.29
Pendleton	R2	11-225-1C	20.03	13.22	37.41	9.79	8.10	0.76	2.80	0.37
Pendleton	R2	11-225-1C	21.45	12.26	37.85	8.58	8.13	0.72	2.83	0.32
Pendleton	R2	11-225-2C	29.15	13.07	36.07	7.01	8.71	0.78	2.75	0.31
Pendleton	R2	11-225-2C	28.60	12.37	37.96	7.98	8.95	0.66	2.80	0.30
Pendleton	R2	11-225-3C	24.25	13.40	38.44	10.21	8.73	0.78	2.87	0.38
Pendleton	R2	11-225-3C	22.40	13.90	37.96	9.24	8.83	0.77	2.82	0.34
Pendleton	R2	11-225-5C	23.66	12.54	38.50	8.09	7.83	0.68	2.81	0.33
Pendleton	R2	11-225-5C	23.23	14.38	38.43	8.40	7.80	0.75	2.82	0.33
Pendleton	R2	11-225-6H	23.06	15.32	32.77	6.79	7.74	0.67	2.64	0.29
Pendleton	R2	11-225-6H	25.03	17.01	32.52	8.25	7.83	0.66	2.62	0.29
Pendleton	R2	11-225-7H	19.33	16.32	35.60	7.69	7.56	0.66	2.71	0.28
Pendleton	R2	11-225-7H	22.53	16.01	35.65	7.12	7.56	0.64	2.74	0.29
Pendleton	R2	Alba	28.81	13.03	31.84	7.20	8.26	0.79	2.67	0.28
Pendleton	R2	Alba	30.61	13.73	31.83	7.04	8.22	0.78	2.69	0.28
Pendleton	R2	Bitterroot	32.93	13.86	33.44	7.98	8.14	0.81	2.68	0.29
Pendleton	R2	Bitterroot	32.89	14.14	34.36	7.20	8.12	0.78	2.71	0.29
Pendleton	R2	Bobtail	24.60	13.42	37.17	7.66	7.89	0.71	2.77	0.31
Pendleton	R2	Bobtail	24.57	14.48	35.80	7.86	7.87	0.72	2.71	0.32
Pendleton	R2	Brevor	32.00	15.46	34.65	7.77	8.67	0.91	2.78	0.31
Pendleton	R2	Brevor	31.50	15.04	35.81	8.19	8.71	0.87	2.80	0.30
Pendleton	R2	Bruehl	37.18	14.39	34.64	9.01	8.09	0.87	2.60	0.31
Pendleton	R2	Bruehl	35.61	13.77	35.18	7.94	8.19	0.91	2.62	0.30
Pendleton	R2	Brundage	22.92	17.70	31.57	7.68	7.72	0.65	2.58	0.29
Pendleton	R2	Brundage	20.50	16.71	32.86	7.93	7.89	0.71	2.59	0.28
Pendleton	R2	Brundage 96	23.98	15.47	33.27	8.40	9.04	0.78	2.60	0.27
Pendleton	R2	Brundage 96	22.91	14.82	34.66	8.07	9.04	0.80	2.64	0.31
Pendleton	R2	Bruneau	32.70	15.71	34.88	8.18	7.84	0.80	2.66	0.31
Pendleton	R2	Bruneau	35.15	14.54	34.28	8.19	7.77	0.77	2.67	0.30
Pendleton	R2	Cara	38.69	14.94	32.56	7.68	7.50	0.67	2.64	0.31
Pendleton	R2	Cara	37.30	13.63	32.17	7.34	7.50	0.67	2.60	0.30
Pendleton	R2	Cayuga	26.57	13.38	36.13	6.13	9.53	0.54	2.74	0.27
Pendleton	R2	Cayuga	26.52	13.07	35.19	7.28	9.58	0.59	2.72	0.30
Pendleton	R2	Coda	46.27	15.21	32.20	6.70	7.69	0.80	2.70	0.29
Pendleton	R2	Coda	46.64	13.55	33.34	6.32	7.75	0.88	2.76	0.27
Pendleton	R2	Daws	33.31	13.69	39.10	8.39	9.06	0.83	2.91	0.31
Pendleton	R2	Daws	35.27	14.33	37.75	9.60	8.96	0.89	2.83	0.36
Pendleton	R2	Elmar	50.05	14.40	29.56	6.90	7.49	0.67	2.53	0.24
Pendleton	R2	Elmar	49.56	14.73	28.49	6.18	7.51	0.64	2.55	0.27

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Pendleton	R2	Eltan	35.00	15.43	30.80	8.19	7.67	0.71	2.51	0.29
Pendleton	R2	Eltan	36.32	13.90	32.23	7.40	7.79	0.78	2.59	0.29
Pendleton	R2	Gaines	32.35	16.48	29.22	8.37	8.33	0.82	2.53	0.27
Pendleton	R2	Gaines	33.78	14.44	28.62	7.08	8.35	0.81	2.51	0.25
Pendleton	R2	Gene	37.04	12.55	36.07	7.06	7.76	0.83	2.69	0.28
Pendleton	R2	Gene	38.32	13.17	36.14	6.91	7.74	0.80	2.69	0.27
Pendleton	R2	Goetze	33.48	15.80	36.44	9.17	7.50	0.71	2.82	0.34
Pendleton	R2	Goetze	35.76	14.31	35.37	8.92	7.51	0.70	2.80	0.36
Pendleton	R2	Hill 81	41.40	13.23	33.21	7.40	7.37	0.59	2.59	0.27
Pendleton	R2	Hill 81	41.45	14.91	32.90	7.26	7.40	0.65	2.62	0.30
Pendleton	R2	Hyslop	43.21	14.04	32.73	8.68	7.37	0.67	2.63	0.31
Pendleton	R2	Hyslop	42.90	13.88	32.54	7.73	7.26	0.62	2.64	0.27
Pendleton	R2	Kaseberg	22.87	18.49	27.85	7.58	7.76	0.61	2.46	0.27
Pendleton	R2	Kaseberg	22.40	17.61	27.55	7.86	7.68	0.51	2.45	0.28
Pendleton	R2	Ladd	33.50	13.70	34.15	7.61	7.47	0.69	2.67	0.31
Pendleton	R2	Ladd	32.69	15.47	34.80	7.55	7.43	0.74	2.67	0.32
Pendleton	R2	Lewjain	35.30	16.10	28.13	6.76	8.37	0.87	2.46	0.26
Pendleton	R2	Lewjain	35.79	15.19	27.88	7.08	8.30	0.86	2.49	0.27
Pendleton	R2	Madsen	46.54	14.43	34.79	7.10	7.72	0.88	2.76	0.29
Pendleton	R2	Madsen	43.54	13.84	35.80	6.63	7.78	0.82	2.79	0.29
Pendleton	R2	Malcolm	45.54	14.60	32.74	8.56	7.30	0.61	2.67	0.32
Pendleton	R2	Malcolm	43.26	13.68	35.35	8.17	7.24	0.60	2.76	0.32
Pendleton	R2	Mary	33.38	14.73	35.94	9.38	8.20	0.85	2.70	0.29
Pendleton	R2	Mary	35.07	13.44	35.99	8.59	8.20	0.82	2.72	0.29
Pendleton	R2	Nugaines	34.79	15.16	28.90	8.49	9.64	0.71	2.53	0.28
Pendleton	R2	Nugaines	33.03	16.70	29.91	8.14	9.63	0.72	2.55	0.26
Pendleton	R2	Omar	41.65	14.00	30.67	6.63	7.67	0.74	2.59	0.24
Pendleton	R2	Omar	41.31	15.24	31.02	6.24	7.67	0.77	2.61	0.28
Pendleton	R2	ORCF-101	36.12	15.30	34.23	8.79	8.11	0.85	2.70	0.36
Pendleton	R2	ORCF-101	37.27	12.12	32.71	8.34	8.06	0.81	2.69	0.35
Pendleton	R2	ORCF-102	42.58	13.40	40.62	8.49	7.49	0.83	2.79	0.31
Pendleton	R2	ORCF-102	41.66	13.41	40.23	8.72	7.46	0.81	2.77	0.32
Pendleton	R2	ORCF-103	34.99	13.82	34.56	7.61	7.58	0.73	2.61	0.29
Pendleton	R2	ORCF-103	33.47	13.73	35.61	7.53	7.53	0.74	2.64	0.29
Pendleton	R2	ORSS-1757	14.56	13.63	37.88	7.06	9.64	0.56	2.76	0.32
Pendleton	R2	ORSS-1757	17.30	14.14	37.65	8.09	9.49	0.58	2.76	0.32
Pendleton	R2	Rely	47.20	16.63	27.65	7.32	7.55	0.64	2.51	0.30
Pendleton	R2	Rely	47.48	14.83	27.80	6.83	7.52	0.61	2.50	0.27
Pendleton	R2	Rod	34.53	14.60	35.60	7.45	9.59	0.63	2.69	0.30
Pendleton	R2	Rod	34.03	14.49	35.91	7.23	9.59	0.59	2.69	0.27

Table 7.24 Continued. Data collected from the SKCS machine for Kernel hardness for every variety and field replication. Each field replication was replicated twice through the SKCS machine.

Location	Rep	Variety	Hardness Avg	S. Dev	Weight Avg	S.Dev	Moisture Avg	S.Dev	Diameter Avg	S.Dev
Pendleton	R2	Rosalyn	35.92	14.68	38.05	7.33	9.60	0.54	2.83	0.31
Pendleton	R2	Rosalyn	34.20	15.77	37.86	7.52	9.64	0.57	2.83	0.31
Pendleton	R2	Skiles	25.31	11.93	39.98	7.71	7.38	0.64	2.82	0.34
Pendleton	R2	Skiles	25.61	12.86	39.38	8.84	7.50	0.68	2.78	0.33
Pendleton	R2	Stephens	33.86	12.07	37.89	8.84	8.69	0.81	2.85	0.37
Pendleton	R2	Stephens	35.46	12.75	38.39	9.69	8.63	0.83	2.86	0.38
Pendleton	R2	Tubbs	41.69	12.95	37.07	8.15	8.44	0.92	2.80	0.32
Pendleton	R2	Tubbs	41.24	12.45	35.53	8.06	8.31	0.90	2.73	0.30
Pendleton	R2	Tubbs-06	44.47	12.03	34.51	8.37	9.09	0.78	2.74	0.32
Pendleton	R2	Tubbs-06	45.90	14.16	34.40	8.04	9.00	0.84	2.76	0.31
Pendleton	R2	Xerpha	38.47	15.95	41.13	6.40	8.86	0.76	2.90	0.30
Pendleton	R2	Xerpha	39.95	16.34	39.88	6.71	8.82	0.79	2.86	0.27

Appendix 10: DNA Concentration from NanoDrop

Table 7.25. Results from NanoDrop nucleic acid concentration converted to the DNA concentration and the amount of TE buffer needed for each individuals DNA working stock (Plants that died are highlighted).

Plant ID	Box Position	Nucleic Acid Conc.	DNA Concentration	TE Buffer
1-1	A1	243.4	8.2	91.8
1-2	B1	227.5	8.8	91.2
1-3	C1	262.1	7.6	92.4
1-4	D1	414.8	4.8	95.2
1-5	E1	380.9	5.3	94.7
1-6	F1	315.2	6.3	93.7
1-7	G1	475.5	4.2	95.8
1-8	H1	264.1	7.6	92.4
1-9	A2	281.6	7.1	92.9
1-10	B2	319.1	6.3	93.7
1-11	C2	417.5	4.8	95.2
1-12	D2	183.0	10.9	89.1
1-13	E2	218.3	9.2	90.8
1-14	F2	264.6	7.6	92.4
1-15	G2	289.0	6.9	93.1
1-16	H2	192.5	10.4	89.6
2-1	A3	340.9	5.9	94.1
2-2	B3	315.1	6.3	93.7
2-3	C3	429.8	4.7	95.3
2-4	D3	352.2	5.7	94.3
2-5	E3	531.7	3.8	96.2
2-6	F3	392.4	5.1	94.9
2-7	G3	401.8	5.0	95.0
2-8	H3	624.6	3.2	96.8
2-9	A4	319.6	6.3	93.7
2-10	B4	326.9	6.1	93.9
2-11	C4	299.0	6.7	93.3
2-12	D4	466.0	4.3	95.7
2-13	E4	450.8	4.4	95.6
2-14	F4	405.0	4.9	95.1
2-15	G4	335.7	6.0	94.0
2-16	H4	601.4	3.3	96.7
3-1	A5	523.0	3.8	96.2
3-2	B5	667.4	3.0	97.0
3-3	C5	488.0	4.1	95.9

Table 7.25 Continued. Results from NanoDrop nucleic acid concentration converted to the DNA concentration and the amount of TE buffer needed for each individuals DNA working stock (Plants that died are highlighted).

Plant ID	Box Position	Nucleic Acid Conc.	DNA Concentration	TE Buffer
3-4	D5	431.5	4.6	95.4
3-5	E5	306.3	6.5	93.5
3-6	F5	321.5	6.2	93.8
3-7	G5	386.8	5.2	94.8
3-8	H5	231.9	8.6	91.4
3-9	A6	279.1	7.2	92.8
3-10	B6	413.8	4.8	95.2
3-11	C6	288.1	6.9	93.1
3-12	D6	319.0	6.3	93.7
3-13	E6	415.9	4.8	95.2
3-14	F6	341.4	5.9	94.1
3-15	G6	337.8	5.9	94.1
3-16	H6	452.2	4.4	95.6
4-1	A7	585.2	3.4	96.6
4-2	B7	386.4	5.2	94.8
4-3	C7	364.9	5.5	94.5
4-4	D7	375.5	5.3	94.7
4-5	E7	495.5	4.0	96.0
4-6	F7	505.7	4.0	96.0
4-7	G7	197.3	10.1	89.9
4-8	H7	465.0	4.3	95.7
4-9	A8	461.6	4.3	95.7
4-10	B8	285.8	7.0	93.0
4-11	C8	297.2	6.7	93.3
4-12	D8	430.7	4.6	95.4
4-13	E8	351.7	5.7	94.3
4-14	F8	447.9	4.5	95.5
4-15	G8	493.5	4.1	95.9
4-16	H8	471.4	4.2	95.8
5-1	A9	434.3	4.6	95.4
5-2	B9	494.9	4.0	96.0
5-3	C9	444.3	4.5	95.5
5-4	D9	452.3	4.4	95.6
5-5	E9	471.6	4.2	95.8
5-6	F9	507.5	3.9	96.1
5-7	G9	417.6	4.8	95.2
5-8	H9	353.4	5.7	94.3
5-9	A10	291.1	6.9	93.1

Table 7.25 Continued. Results from NanoDrop nucleic acid concentration converted to the DNA concentration and the amount of TE buffer needed for each individuals DNA working stock (Plants that died are highlighted).

Plant ID	Box Position	Nucleic Acid Conc.	DNA Concentration	TE Buffer
5-10	B10	656.8	3.0	97.0
5-11	C10	451.8	4.4	95.6
5-12	D10	458.5	4.4	95.6
5-13	E10	367.9	5.4	94.6
5-14	F10	393.7	5.1	94.9
5-15	G10	552.6	3.6	96.4
5-16	H10	458.3	4.4	95.6
6-1	A11	269.2	7.4	92.6
6-2	B11	365.6	5.5	94.5
6-3	C11	305.9	6.5	93.5
6-4	D11	427.9	4.7	95.3
6-5	E11	369.8	5.4	94.6
6-6	F11	372.8	5.4	94.6
6-7	G11	291.6	6.9	93.1
6-8	H11	244.4	8.2	91.8
6-9	A12	340.6	5.9	94.1
6-10	B12	323.8	6.2	93.8
6-11	C12	310.6	6.4	93.6
6-12	D12	350.1	5.7	94.3
6-13	E12	307.6	6.5	93.5
6-14	F12	313.3	6.4	93.6
6-15	G12	300.0	6.7	93.3
6-16	H12	310.4	6.4	93.6
7-1	A1	277.7	7.2	92.8
7-2	B1	252.0	7.9	92.1
7-3	C1	240.3	8.3	91.7
7-4	D1	273.8	7.3	92.7
7-5	E1	220.3	9.1	90.9
7-6	F1	279.7	7.2	92.8
7-7	G1	225.7	8.9	91.1
7-8	H1	181.0	11.0	89.0
7-9	A2	276.5	7.2	92.8
7-10	B2	264.9	7.6	92.4
7-11	C2	256.7	7.8	92.2
7-12	D2	273.7	7.3	92.7
7-13	E2	332.2	6.0	94.0
7-14	F2	400.0	5.0	95.0
7-15	G2	276.7	7.2	92.8

Table 7.25 Continued. Results from NanoDrop nucleic acid concentration converted to the DNA concentration and the amount of TE buffer needed for each individuals DNA working stock (Plants that died are highlighted).

Plant ID	Box Position	Nucleic Acid Conc.	DNA Concentration	TE Buffer
7-16	H2	276.0	7.2	92.8
8-1	A3	220.6	9.1	90.9
8-2	B3	275.3	7.3	92.7
8-3	C3	265.1	7.5	92.5
8-4	D3	269.9	7.4	92.6
8-5	E3	239.3	8.4	91.6
8-6	F3	365.1	5.5	94.5
8-7	G3	272.8	7.3	92.7
8-8	H3	328.5	6.1	93.9
8-9	A4	267.7	7.5	92.5
8-10	B4	290.2	6.9	93.1
8-11	C4	336.2	5.9	94.1
8-12	D4	221.5	9.0	91.0
8-13	E4	286.6	7.0	93.0
8-14	F4	264.6	7.6	92.4
8-15	G4	298.4	6.7	93.3
8-16	H4	273.5	7.3	92.7
9-1	A5	548.7	3.6	96.4
9-2	B5	476.2	4.2	95.8
9-3	C5	359.8	5.6	94.4
9-4	D5	437.8	4.6	95.4
9-5	E5	421.3	4.7	95.3
9-6	F5	299.4	6.7	93.3
9-7	G5	308.7	6.5	93.5
9-8	H5	347.6	5.8	94.2
9-9	A6	250.6	8.0	92.0
9-10	B6	367.4	5.4	94.6
9-11	C6	434.3	4.6	95.4
9-12	D6	458.5	4.4	95.6
9-13	E6	326.0	6.1	93.9
9-14	F6	290.0	6.9	93.1
9-15	G6	342.9	5.8	94.2
9-16	H6	280.4	7.1	92.9
10-1	A7	361.0	5.5	94.5
10-2	B7	299.5	6.7	93.3
10-3	C7	333.8	6.0	94.0
10-4	D7	0.1	20000.0	-19900.0
10-5	E7	261.1	7.7	92.3

Table 7.25 Continued. Results from NanoDrop nucleic acid concentration converted to the DNA concentration and the amount of TE buffer needed for each individuals DNA working stock (Plants that died are highlighted).

Plant ID	Box Position	Nucleic Acid Conc.	DNA Concentration	TE Buffer
10-6	F7	215.8	9.3	90.7
10-7	G7	258.0	7.8	92.2
10-8	H7	224.3	8.9	91.1
10-9	A8	227.9	8.8	91.2
10-10	B8	0.7	2857.1	-2757.1
10-11	C8	492.5	4.1	95.9
10-12	D8	239.4	8.4	91.6
10-13	E8	254.2	7.9	92.1
10-14	F8	302.6	6.6	93.4
10-15	G8	292.2	6.8	93.2
10-16	H8	250.3	8.0	92.0
11-1	A9	241.9	8.3	91.7
11-2	B9	456.2	4.4	95.6
11-3	C9	329.8	6.1	93.9
11-4	D9	492.2	4.1	95.9
11-5	E9	322.2	6.2	93.8
11-6	F9	196.7	10.2	89.8
11-7	G9	330.3	6.1	93.9
11-8	H9	322.2	6.2	93.8
11-9	A10	333.1	6.0	94.0
11-10	B10	259.6	7.7	92.3
11-11	C10	290.3	6.9	93.1
11-12	D10	283.6	7.1	92.9
11-13	E10	501.1	4.0	96.0
11-14	F10	467.7	4.3	95.7
11-15	G10	260.4	7.7	92.3
11-16	H10	285.5	7.0	93.0
12-1	A11	487.4	4.1	95.9
12-2	B11	229.0	8.7	91.3
12-3	C11	252.0	7.9	92.1
12-4	D11	338.1	5.9	94.1
12-5	E11	293.4	6.8	93.2
12-6	F11	239.2	8.4	91.6
12-7	G11	192.0	10.4	89.6
12-8	H11	151.8	13.2	86.8
12-9	A12	328.6	6.1	93.9
12-10	B12	357.2	5.6	94.4
12-11	C12	377.1	5.3	94.7

Table 7.25 Continued. Results from NanoDrop nucleic acid concentration converted to the DNA concentration and the amount of TE buffer needed for each individuals DNA working stock (Plants that died are highlighted).

Plant ID	Box Position	Nucleic Acid Conc.	DNA Concentration	TE Buffer
12-12	D12	305.4	6.5	93.5
12-13	E12	168.7	11.9	88.1
12-14	F12	238.0	8.4	91.6
12-15	G12	385.0	5.2	94.8
12-16	H12	272.1	7.4	92.6
13-1	A1	196.5	10.2	89.8
13-2	B1	454.2	4.4	95.6
13-3	C1	424.5	4.7	95.3
13-4	D1	299.6	6.7	93.3
13-5	E1	529.0	3.8	96.2
13-6	F1	228.7	8.7	91.3
13-7	G1	295.1	6.8	93.2
13-8	H1	384.5	5.2	94.8
13-9	A2	527.3	3.8	96.2
13-10	B2	342.3	5.8	94.2
13-11	C2	262.9	7.6	92.4
13-12	D2	305.6	6.5	93.5
13-13	E2	357.5	5.6	94.4
13-14	F2	222.1	9.0	91.0
13-15	G2	218.6	9.1	90.9
13-16	H2	219.5	9.1	90.9
14-1	A3	271.4	7.4	92.6
14-2	B3	294.7	6.8	93.2
14-3	C3	219.0	9.1	90.9
14-4	D3	203.6	9.8	90.2
14-5	E3	1.0	2000.0	-1900.0
14-6	F3	215.1	9.3	90.7
14-7	G3	451.0	4.4	95.6
14-8	H3	250.9	8.0	92.0
14-9	A4	241.6	8.3	91.7
14-10	B4	293.8	6.8	93.2
14-11	C4	257.9	7.8	92.2
14-12	D4	356.2	5.6	94.4
14-13	E4	506.1	4.0	96.0
14-14	F4	454.4	4.4	95.6
14-15	G4	383.7	5.2	94.8
14-16	H4	274.8	7.3	92.7
15-1	A5	1.8	1111.1	-1011.1

Table 7.25 Continued. Results from NanoDrop nucleic acid concentration converted to the DNA concentration and the amount of TE buffer needed for each individuals DNA working stock (Plants that died are highlighted).

Plant ID	Box Position	Nucleic Acid Conc.	DNA Concentration	TE Buffer
15-2	B5	241.9	8.3	91.7
15-3	C5	351.5	5.7	94.3
15-4	D5	1.2	1666.7	-1566.7
15-5	E5	302.3	6.6	93.4
15-6	F5	212.9	9.4	90.6
15-7	G5	341.1	5.9	94.1
15-8	H5	341.2	5.9	94.1
15-9	A6	333.3	6.0	94.0
15-10	B6	281.0	7.1	92.9
15-11	C6	326.1	6.1	93.9
15-12	D6	281.9	7.1	92.9
15-13	E6	349.7	5.7	94.3
15-14	F6	335.0	6.0	94.0
15-15	G6	271.2	7.4	92.6
15-16	H6	297.5	6.7	93.3

Appendix 11: GeneMarker® System Settings

Settings used to examine the DNA data received from CGRB.

The data from each plate received from CGRB was imported into GeneScan and the Run function was used. In the Run Wizard, the Template Selection for the project was set up for the size standard to be GS500, Standard color: Orange, and the Analysis Type: Fragment (Plant). The parameters set up for calling the allele peaks for the allele range base pairs was set to start calling at 99 and ended at 300. The peak Detection threshold intensity was > 100 and the percentage > 15 with a local Region % >15 and Max Call Intensity 30,000. The Stutter Peak Filter (%) box was checked along with the Plus-A Filter box with Left set at 90 and Right set at 90. The Raw Data Analysis settings were left as default settings and the Size call was set for Local Southern. The additional settings for Fragment (Plant) Analysis for Allele Evaluation Peak Score was as follows: Reject < 1 Check 7 < Pass.

Appendix 12: Marker Results from GeneMarker®

Table 7.26. The results for each individual/line for each marker. These are the results from the GeneMarker® analysis. The highlighted boxes represent markers that were greater than 1.5 base pairs than Bobtail.

	Markers:	XGWM 169	XGWM 190	XGWM 194	XGWM 234	XGWM 261	XGWM 337	XGWM 437
		Fam	Fam	Fam	Fam	Hex	Hex	Fam
Phenotype	Lines	200	210.8	133.3	200.7/227.5	173.9	187.4	114.9/160.9
Awns	1-1	200.3	0	133.2	200.7/227.1	173.9	187.4	114.9
Awns	1-2	200.2	0	133.3	200.7/227.9	0	187.4	114.9
Awns	1-3	200.2	210.8	0	200.8/227.9	0	0	114.9
Awns	1-4	200.1	0	132.2	200.7/228	173.9	187.5	114.9/160.8
Awns	1-5	0	0	0	200.8/228	174	187.4	114.9
Awns	1-6	0	0	0	200.8/228	174	187.4	114.9/161.4
Awns	1-7	0	210.9	0	200.8/228.1	174	0	161.1
Awns	1-8	0	0	0	200.7/228.1	174	187.4	114.9/161.2
Awns	1-9	200	210.9	0	200.7/227.2	173.8	187.4	115
Awns	1-10	200.1	210.8	0	200.7/227.8	173.8	187.4	114.9/161.5
Awns	1-11	198.1	210.8	133.4	200.8/227.8	173.9	187.4	114.9/160.9
Awns	1-12	198	210.8	133.3	200.7/227.9	0	187.4	114.9/160.6
Awns	1-13	200.1	210.9	133.3	112.5/196.5	173.8	187.5	115
Awns	1-14	200.1	210.9	0	200.7/227.8	173.8	187.4	114.9
Awns	1-15	200.1	210.9	0	200.8/227.9	173.8	187.4	114.9/160.9
Awns	1-16	200.2	0	0	113.2/196.5	173.8	187.4	161.2
Awns	2-1	200.2	0	0	200.6/227.8	173.9	187.4	114.9/161.6
Awns	2-2	200.2	210.8	134.4	200.7/227.8	174.4	187.4	115/161.5
Awns	2-3	200.2	210.8	133.3	200.6/227.8	173.9	187.3	161.5
Awns	2-4	200.3	210.8	0	200.7/227.8	173.9	187.3	0
Awns	2-5	200	0	0	200.8/227.9	173.8	187.4	161.5
Awns	2-6	200.2	210.8	0	200.8/227.9	173.9	187.3	161.4
Awns	2-7	0	210.8	0	200.8/228	173.8	187.4	115/161.4
Awns	2-8	200.3	0	0	200.8/228	0	187.5	0
Awns	2-9	192.6	0	133.3	200.6/227.8	173.9	187.4	114.9
Awns	2-10	200.1	210.8	0	200.7/227.8	173.8	187.3	161.4
Awns	2-11	200	210.8	115	200.7/227.7	173.7	187.3	114.9
Awns	2-12	200	210.8	135.5	200.8/227.8	173.8	187.3	0
Awns	2-13	200	210.8	133.2	200.7/227.7	173.7	187.3	161.3
Awns	2-14	200	0	0	200.7/227.8	173.8	187.3	161.3
Awns	2-15	200.1	0	0	219.6/249.1	173.8	187.3	114.8/161.5
Awns	2-16	200.1	0	0	200.7/227.8	173.8	187.4	115/161.3
Awns	3-1	200.6	210.8	135.4	200.8/227.9	0	187.4	114.9/161.7
Awns	3-2	200.3	210.7	0	200.8/227.9	173.9	187.3	161.5
Awns	3-3	200.1	210.9	0	200.7/227.8	173.9	187.4	115/161.3
Awns	3-4	201.8	210.8	0	200.7/227.9	174.4	186.6	115/161.5
Awns	3-5	200.2	210.7	0	200.8/227.9	0	187.3	161.3
Awns	3-6	100	210.8	0	200.7/227.8	173.5	187.4	161.6
Awns	3-7	200.1	210.9	133.3	200.8/227.9	173.9	187.4	114.9
Awns	3-8	200.2	0	0	200.7/228	0	187.5	115
Awns	3-9	199.7	0	0	200.7/227.8	173.8	187.3	114.8
Awns	3-10	200	210.8	134.4	200.7/227.7	173.8	187.4	114.9

Table 7.26 Continued. The results for each individual/line for each marker. These are the results from the GeneMarker® analysis. The highlighted boxes represent markers that were greater than 1.5 base pairs than Bobtail.

Phenotype	Lines	XGWM 169	XGWM 190	XGWM 194	XGWM 234	XGWM 261	XGWM 337	XGWM 437
Awns	3-11	200.1	0	0	200.7/221.6	174.3	187.3	161.1
Awns	3-12	199.6	0	133.3	200.7/227.7	0	187.3	114.9/161.5
Awns	3-13	200	0	0	200.7/227.8	0	187.4	114.9/161.7
Awns	3-14	197.9	0	0	200.7/227.8	173.7	187.4	161.4
Awns	3-15	197.8	210.8	133.3	200.7/227.8	173.8	187.4	114.9
Awns	3-16	0	0	0	200.7/227.9	173.9	187.4	115/161.3
Awnless	4-1	0	210.9	134.3	196.5/204.4	174	187.3	114.8
Awns	4-2	200.2	0	133.2	200.8/227.9	173.9	0	103.3
Awnless	4-3	200.1	210.8	0	200.9/227.9	0	187.4	114.9
Awnless	4-4	202.3	210.8	0	200.7/227.9	173.8	0	114.9/161.5
Awnless	4-5	200.2	210.8	0	200.7/227.9	173.9	0	0
Awns	4-6	200.1	210.8	133.3	200.7/228	174.4	187.4	114.9/161.6
Awns	4-7	200.2	210.8	134.3	200.7/228	173.9	187.4	162
Awnless	4-8	200.2	210.8	0	200.7/228	173.9	0	115
Awnless	4-9	0	0	133.3	196.5/216	173.8	187.3	114.9/161.0
Awnless	4-10	200.1	210.8	133.3	200.7/227.8	173.8	187.4	115/161.5
Awnless	4-11	200	210.8	0	196.5/218.1	0	187.4	161.4
Awnless	4-12	197.9	210.8	133.3	200.9/227.8	173.7	187.3	114.8/161.5
Awns	4-13	200.1	0	133.3	221.5/249	173.8	187.3	114.9/161.9
Awnless	4-14	200.2	210.9	133.3	200.7/227.8	173.7	187.4	161.6
Awns	4-15	99.8	0	133.3	200.8/227.8	173.8	187.4	114.9
Awnless	4-16	199.5	0	0	200.8/227.9	173.9	187.5	114.9
Awnless	5-1	200.1	0	133.2	200.8/228	174	187.5	115
Awnless	5-2	200.3	210.8	0	200.7/227.9	173.9	187.4	115/161.6
Awnless	5-3	200.2	210.8	0	200.8/228	0	187.3	114.8/161.5
Awnless	5-4	200.3	0	0	200.7/227.8	173.9	187.4	114.9/161.6
Awnless	5-5	200.1	0	132.2	200.8/228	174	187.4	115/161.6
Awnless	5-6	198.3	0	0	200.8/228	0	187.4	114.9/161.6
Awnless	5-7	200.2	210.9	132.2	200.8/228	173.9	187.4	114.9
Awnless	5-8	200.2	210.9	0	200.8/228.1	0	0	115/161.5
Awnless	5-9	200.1	0	133.3	200.7/227.9	173.9	187.5	115/161.5
Awnless	5-10	200.2	0	133.4	200.7/227.9	173.8	187.4	114.9
Awnless	5-11	200.2	210.8	0	200.6/227.7	173.7	187.4	115/161.7
Awnless	5-12	197.9	210.7	133.4	200.6/227.7	173.8	187.3	114.8
Awnless	5-13	200.2	210.8	133.3	200.7/227.8	173.7	187.3	114.8/161.5
Awnless	5-14	199.4	210.8	0	200.7/227.7	0	187.4	161.8
Awnless	5-15	200	210.9	0	200.7/227.8	173.8	187.4	114.9/161.5
Awnless	5-16	200.2	210.9	0	196.5/221.7	174.3	187.4	114.9/161.5
Awnless	6-1	200.2	211.1	133.3	221.8/249.5	174.1	187.5	114.9
Awns	6-2	200.2	210.9	133.3	216.1/221.8	174	187.5	115/161.7
Awnless	6-3	200.3	211	133.3	200.8/228.2	174	187.4	114.8/161.6
Awnless	6-4	200.2	210.9	0	196.5/216.1	173.9	187.4	114.8/161.6
Awnless	6-5	200.2	210.9	133.2	196.5/216.1	173.8	187.4	114
Awnless	6-6	198.3	210.9	0	196.5/221.8	173.9	187.5	115/161.8

Table 7.26 Continued. The results for each individual/line for each marker. These are the results from the GeneMarker® analysis. The highlighted boxes represent markers that were greater than 1.5 base pairs than Bobtail.

Phenotype	Lines	XGWM 169	XGWM 190	XGWM 194	XGWM 234	XGWM 261	XGWM 337	XGWM 437
Awnless	6-7	200.2	210.9	133.2	196.5/216.1	173.9	187.4	114.9/161.5
Awns	6-8	200.2	211	0	200.8/228.2	173.9	187.5	114.9/161.6
Awns	6-9	200.2	210.9	132.2	200.8/228.1	174	187.5	115/161.4
Awns	6-10	200	210.9	0	200.8/228	173.8	187.4	115
Awnless	6-11	200.1	210.9	0	200.7/228	173.8	187.5	161.4
Awns	6-12	200.2	210.9	0	200.8/228	173.8	187.3	114.9
Awnless	6-13	200.1	211	0	200.6/227.9	173.8	187.4	161.2
Awnless	6-14	200	210.9	133.3	200.8/227.9	173.8	187.5	114.9/161.6
Awns	6-15	200.1	210.9	132.3	200.7/227.9	173.9	187.4	115
Awnless	6-16	195.2	211	0	200.8/228	173.8	187.4	114.9
Awnless	7-1	200.1	210.9	133.3	200.8/227.9	0	187.4	114.9
Awnless	7-2	200.1	210.8	0	103.8/200.7	173.7	187.4	115/161.6
Awnless	7-3	200.1	210.8	133.3	200.7/227.7	173.8	187.4	114.9
Awnless	7-4	200.1	210.9	0	200.8/227.9	173.8	187.4	115
Died	7-5	200.1	210.8	0	200.7/227.9	173.8	187.4	114.9/161.5
Awnless	7-6	200.2	210.9	133.3	200.6/227.9	173.9	187.4	115
Awnless	7-7	200.1	0	0	200.8/227.9	173.9	187.5	0
Awnless	7-8	200.2	210.9	0	200.7/227.9	174	0	0
Awns	7-9	200.1	210.8	133.2	200.6/227.8	173.8	187.4	115/161.5
Awns	7-10	200	209.7	0	200.8/227.8	173.8	187.4	114.9
Awnless	7-11	200.1	210.8	133.2	200.6/227.8	0	187.4	114.9/160.9
Awnless	7-12	200.1	211	133.2	200.8/227.8	173.8	187.3	114.9
Awnless	7-13	200.1	210.8	0	200.6/227.8	173.8	187.5	114.9
Awnless	7-14	200.1	210.8	0	200.7/227.8	173.9	187.5	114.9/161.7
Awns	7-15	200.2	0	0	200.7/227.8	173.7	187.5	114.9/161.2
Awnless	7-16	200.2	210.9	131.1	103.8	173.8	105.6	114.9/161.4
Awns	8-1	99.9	116.1	0	200.9/227.8	173.8	0	114.9/161.7
Awnless	8-2	199.9	0	133.3	200.7/227.8	173.8	0	114.9/161.7
Awnless	8-3	0	0	0	200.7/227.7	173.8	187.3	114.9/161.7
Awnless	8-4	200.1	0	0	200.7/227.7	173.8	187.3	114.9/161.8
Awnless	8-5	199.9	0	0	200.7/227.7	0	0	114.9
Awnless	8-6	200	0	0	200.6/227.8	0	187.3	114.8
Awns	8-7	200.2	0	133.2	200.8/227.8	173.7	187.4	114.8/161.5
Awnless	8-8	100.8	210.9	0	200.8/227.9	173.8	0	114.9/161.6
Awns	8-9	200	210.9	0	200.8/227.7	173.7	187.3	114.8/161.6
Awnless	8-10	200	210.9	0	200.6/227.7	173.7	187.4	114.9/161.5
Awnless	8-11	200	210.8	133.3	200.6/227.7	173.8	187.4	161.7
Awnless	8-12	200	210.7	133.2	200.7/227.7	173.6	187.3	0
Awnless	8-13	200.1	210.7	0	200.7/227.7	173.7	187.3	114.9/161.2
Awns	8-14	198	210.8	133.2	200.8/227.8	173.7	187.3	114.8/161.2
Awnless	8-15	200.2	210.8	133.3	200.8/227.8	173.8	187.4	115
Awnless	8-16	200.2	210.9	0	200.8/227.9	173.7	187.4	115
Awnless	9-1	0	0	133.4	200.6/227.7	173.9	187.3	114.8/161.6
Awnless	9-2	0	210.8	0	200.9/227.8	173.7	0	114.9/161.6
Awnless	9-3	199.9	210.9	0	200.7/227.8	173.7	187.4	115/161.3

Table 7.26 Continued. The results for each individual/line for each marker. These are the results from the GeneMarker® analysis. The highlighted boxes represent markers that were greater than 1.5 base pairs than Bobtail.

Phenotype	Lines	XGWM 169	XGWM 190	XGWM 194	XGWM 234	XGWM 261	XGWM 337	XGWM 437
Awnless	9-4	200.1	210.8	0	103.8	173.8	187.3	114.9
Awnless	9-5	200.2	0	0	200.7/227.8	173.7	187.3	114.9
Awnless	9-6	200.1	0	133.4	200.7/227.8	173.8	187.4	115
Awnless	9-7	200.1	0	133.3	200.6/227.7	173.8	187.4	114.9/161.6
Awnless	9-8	198.1	0	0	200.7/227.8	173.8	187.4	114.9/161.5
Awnless	9-9	0	117	133.3	200.7/227.8	0	187.4	115
Awnless	9-10	200	0	133.3	200.8/227.9	173.8	187.3	114.9/161.6
Awnless	9-11	200	210.7	0	200.7/227.7	0	187.3	114.9
Awnless	9-12	200	0	133.3	200.7/227.7	173.8	187.2	114.8/161.5
Awnless	9-13	200	210.8	133.2	200.7/227.7	0	187.4	114.9/161.6
Awnless	9-14	0	210.8	0	200.7/227.7	173.7	187.3	114.8
Awnless	9-15	200	0	133.3	200.6/227.8	173.8	187.4	115/161.7
Awnless	9-16	0	210.8	0	199.2/202.4	173.8	187.4	115
Awnless	10-1	0	0	133.2	200.8/227.8	177.5	0	115
Awnless	10-2	200	210.8	133.2	200.7/227.7	173.7	187.4	114.9/161.7
Awnless	10-3	0	210.8	133.3	199.7/200.8	173.8	0	114.9
Awnless	10-4	0	0	0	0	0	0	0
Awnless	10-5	200	210.9	0	200.7/227.7	173.8	0	114.9
Awnless	10-6	0	210.8	133.3	200.7/227.8	173.7	187.4	114.9/161.8
Awnless	10-7	0	210.9	133.2	200.7/227.8	173.8	187.3	114.9
Awnless	10-8	0	0	0	200.8/227.9	173.8	0	115/161.7
Awnless	10-9	0	0	0	200.7/227.8	173.8	187.4	115/161.7
Awnless	10-10	0	0	0	0	0	0	0
Awnless	10-11	0	210.8	133.3	200.7/227.7	173.8	187.3	114.8/161.4
Awnless	10-12	200	210.8	133.3	200.8/227.7	173.7	187.4	114.8
Awnless	10-13	199.8	210.8	133.4	200.6/227.8	173.7	187.4	114.9
Awnless	10-14	200	210.8	133.4	200.7/227.8	173.8	187.4	114.9
Awnless	10-15	200	210.9	133.2	200.8/227.8	173.8	187.4	114.9/162.4
Awnless	10-16	200.9	210.9	133.3	200.8/227.9	173.9	187.5	115
Awnless	11-1	0	210.8	133.3	200.8/227.9	173.8	187.4	115/161.8
Awnless	11-2	0	210.8	133.2	103.1	173.7	187.4	115/161.8
Awnless	11-3	200	210.8	133.2	102.9/204.4	173.8	187.4	114.9/161.8
Awns	11-4	200	210.8	133.3	200.7/227.7	173.8	187.3	114.9
Awnless	11-5	200	0	133.4	200.8/227.8	173.9	187.3	114.9/161.6
Awnless	11-6	201.5	210.8	133.3	200.6/226.7	173.8	187.4	114.9
Awnless	11-7	200.1	0	133.2	200.0/227.4	173.7	187.4	115
Awnless	11-8	200.2	0	0	200.8/228	173.9	187.5	114.9/161.7
Awnless	11-9	0	210.7	132.2	200.7/227.8	173.8	187.3	114.9
Awns	11-10	199	210.8	133.3	200.7/227.8	173.8	187.4	114.9/161.7
Awnless	11-11	200	210.6	133.3	200.6/227.6	173.8	187.4	115/161.7
Awnless	11-12	200	208.6	133.2	200.7/227.6	173.7	187.4	114.9
Awnless	11-13	199.9	210.8	133.4	200.7/227.7	173.6	187.4	115/161.7
Awnless	11-14	200.1	210.8	133.2	200.7/227.8	173.7	187.3	114.9/161.7
Awns	11-15	200.1	210.9	133.3	200.8/227.9	173.9	187.4	115
Awnless	11-16	200.1	210.9	135.3	200.7/227.9	173.8	187.4	115

Table 7.26 Continued. The results for each individual/line for each marker. These are the results from the GeneMarker® analysis. The highlighted boxes represent markers that were greater than 1.5 base pairs than Bobtail.

Phenotype	Lines	XGWM 169	XGWM 190	XGWM 194	XGWM 234	XGWM 261	XGWM 337	XGWM 437
Awnless	12-1	0	211	133.2	200.9/228	173.9	187.4	114.9/161.6
Awnless	12-2	0	211	0	200.9/227.9	173.9	187.4	115/161.7
Awnless	12-3	200.1	210.9	133.3	200.7/226.9	173.9	187.4	114.9
Awnless	12-4	200.1	211	133.3	200.7/228	173.8	187.4	115
Awnless	12-5	198.1	211	133.3	200/227.5	173.9	187.4	115/161.6
Awnless	12-6	200	213.8	133.2	200.6/227.8	173.4	187.4	161.7
Awnless	12-7	200.2	211	133.3	200.8/227.9	173.9	187.5	115/161.8
Awnless	12-8	200.2	210.9	0	200.8/228	173.9	187.5	115
Awnless	12-9	200.2	211	133.3	200/227.7	173.9	187.5	115
Awnless	12-10	200.1	211	133.2	200.7/228	173.8	187.4	115
Awnless	12-11	200.1	210.9	133.2	220.8/228	173.8	187.4	114.9/161.4
Awnless	12-12	200.2	210.9	133.3	200.8/227.9	173.7	187.3	114.9
Awnless	12-13	200.1	210.9	0	200.8/227.9	173.8	187.4	161.3
Awnless	12-14	200.1	208.7	0	200.7/227.9	0	187.5	161.6
Awnless	12-15	200.2	211	133.3	200.6/227.8	173.8	187.4	161.5
Awnless	12-16	200.4	211	132.2	200.7/225.8	173.8	187.4	161.4
Awnless	13-1	0	210.8	173.7	200.7/227.8	171.7	187.4	114.9/161.7
Awnless	13-2	200.2	210.8	133	200.6/227.8	173.8	0	115
Awnless	13-3	200.3	210.7	133	200.6/227.8	173.8	187.5	114.9
Awnless	13-4	200.2	211	132.9	200.7/227.9	173.9	187.4	114.9
Awnless	13-5	200.3	210.9	133	200.7/227.8	173.8	187.5	114.9
Awnless	13-6	200.1	210.9	132.9	200.7/227.8	173.7	187.5	114.9
Awnless	13-7	200.3	210.9	134	0	173.8	187.3	114.9/161.0
Awnless	13-8	0	211	0	200.8/228	173.8	187.5	115
Awnless	13-9	200.1	210.8	131.7	200.7/227.9	173.7	187.4	115
Awnless	13-10	200.2	210.8	132.8	200.7/227.8	173.6	187.3	114.8
Awnless	13-11	200.2	210.8	132.9	204.7	173.7	0	115
Awnless	13-12	200.2	210.7	0	200.7/227.9	173.8	187.4	115
Awnless	13-13	200.1	210.8	132.9	200.8/227.9	173.8	187.4	115
Awnless	13-14	200.2	210.9	133	200.7/227.9	173.7	187.4	114.9
Awnless	13-15	200.3	210.8	132.9	200.7/227.9	171.7	187.3	114.9
Awnless	13-16	200.2	208.8	133	116.5	173.9	187.5	114.9
Awns	14-1	200.2	210.9	131.8	200.7/227.8	173.8	105.4/168	114.9
Awns	14-2	200.1	211.1	134.1	200.7/227.7	173.9	187.4	114.9
Awns	14-3	198.2	211	132.8	200.8/227.7	173.8	187.4	114.8
Awns	14-4	200.2	210.8	132.9	200.8/227.8	173.9	187.4	114.8
Awns	14-5	0	0	0	0	0	0	0
Awns	14-6	200.2	210.9	132.9	200.7/227.5	173.8	187.3	115/161.7
Awns	14-7	0	211	0	200.8/227.8	173.8	187.4	115
Awns	14-8	0	0	131.8	200.8/227.9	173.9	187.3	112.9
Awns	14-9	200.1	210.9	132.9	200.8/227.8	173.9	187.4	114.9
Awns	14-10	200.1	210.8	132.9	200.8/227.8	173.8	187.3	0
Awns	14-11	200.1	210.8	0	200.6/227.7	173.7	187.3	0
Awns	14-12	200.2	210.7	0	200.7/227.7	173.8	187.3	114.9
Awns	14-13	200.1	210.8	133	200.7/227.7	173.8	187.4	115

Table 7.26 Continued. The results for each individual/line for each marker. These are the results from the GeneMarker® analysis. The highlighted boxes represent markers that were greater than 1.5 base pairs than Bobtail.

Phenotype	Lines	XGWM 169	XGWM 190	XGWM 194	XGWM 234	XGWM 261	XGWM 337	XGWM 437
Awns	14-14	200.1	210.8	132.9	200.8/227.8	173.9	187.3	114.8
Awns	14-15	198.2	210.8	132.9	199.8/227.3	173.8	187.4	114.8
Awns	14-16	200.3	210.8	132.9	200.9/227.9	173.8	187.5	114.9
Awns	15-1	0	0	0	0	0	0	0
Awns	15-2	0	211.1	132.9	200.7/227.7	173.9	187.4	114.9
Awns	15-3	200.1	211.1	132.8	200.8/227.8	173.8	187.4	115
Awns	15-4	0	0	0	0	0	0	0
Awns	15-5	200.1	211	132.9	200.7/227.7	173.9	187.3	114.9
Awns	15-6	200.1	211.1	132.9	200.7/227.7	173.9	187.3	114.8
Awns	15-7	200.1	211.1	132.9	200.8/227.9	173.8	187.4	114.9
Awns	15-8	199.7	211.1	132.9	200.2/227.5	173.9	187.4	114.9
Awns	15-9	200.1	211	132.8	200.6/227.7	173.9	187.4	114.9
Awns	15-10	200.1	211	132.8	200.8/227.8	173.8	187.3	114.8
Awns	15-11	0	210.9	132.9	200.7/227.8	173.8	187.3	114.8
Awns	15-12	200	210.9	132.9	200.7/227.8	173.9	187.4	115
Awns	15-13	200.2	210.9	133	200.7/227.7	173.5	187.4	114.9
Awns	15-14	200.1	210.9	132.9	200.7/227.8	173.9	187.4	114.9
Awns	15-15	200.2	210.9	132.9	200.8/227.9	173.9	187.3	114.9
Awns	15-16	200.4	210.9	0	200.7/227.9	173.9	187.3	114.8

Appendix 13: ANOVA Results from Year 1 for 4°C Treatment

Table 7.27. ANOVA summary results from year 1 seed germination at 4°C.

Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	22276.95				
Rep	1.00	6.37	6.37	0.28	4.11	0.60
Variety	37.00	21417.95	578.86	25.12	1.73	0.00
Error	37.00	852.63	23.04			
Day 8						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	252.68				
Rep	1.00	3.37	3.37	1.84	4.11	0.18
Variety	37.00	181.68	4.91	2.69	1.73	0.00
Error	37.00	67.63	1.83			
Day 9						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	36.42				
Rep	1.00	0.05	0.05	0.18	4.11	0.68
Variety	37.00	25.42	0.69	2.32	1.73	0.01
Error	37.00	10.95	0.30			
Day 10						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	30.25				
Rep	1.00	0.01	0.01	0.07	4.11	0.80
Variety	37.00	22.75	0.61	3.04	1.73	0.00
Error	37.00	7.49	0.20			
Day 11						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	26.11				
Rep	1.00	0.05	0.05	0.33	4.11	0.57
Variety	37.00	20.11	0.54	3.38	1.73	0.00
Error	37.00	5.95	0.16			

Appendix 14: ANOVA Results from Year 2 for 4°C Treatment

Table 7.28. ANOVA summary results from year 2 seed germination at 4°C from Corvallis.

Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	14029.93				
Rep	2.00	1665.66	832.83	35.75	3.10	0.00
Variety	44.00	10314.37	234.42	10.06	1.51	0.00
Error	88.00	2049.90	23.29			
Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	23001.00				
Rep	2.00	562.59	281.30	6.22	3.10	0.00
Variety	44.00	18460.55	419.56	9.28	1.51	0.00
Error	88.00	3977.86	45.20			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	7001.41				
Rep	2.00	336.90	168.45	177.03	3.10	0.00
Variety	44.00	6580.77	149.56	157.18	1.51	0.00
Error	88.00	83.73	0.95			
Day 8						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	301.95				
Rep	2.00	7.57	3.79	4.69	3.10	0.01
Variety	44.00	223.30	5.08	6.28	1.51	0.00
Error	88.00	71.07	0.81			
Day 9						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	54.36				
Rep	2.00	3.51	1.76	6.97	3.10	0.00
Variety	44.00	28.67	0.65	2.59	1.51	0.00
Error	88.00	22.18	0.25			
Day 10						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	50.78				
Rep	2.00	4.46	2.23	8.78	3.10	0.00
Variety	44.00	23.97	0.54	2.15	1.51	0.00
Error	88.00	22.35	0.25			

Table 7.29. ANOVA summary results from year 2 seed germination at 4°C from Pendleton.

Day 5						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	750.40				
Rep	1.00	0.04	0.04	0.03	4.06	0.86
Variety	44.00	691.40	15.71	11.73	1.65	0.00
Error	44.00	58.96	1.34			
Day 6						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	8441.29				
Rep	1.00	12.84	12.84	0.74	4.06	0.39
Variety	44.00	7663.29	174.17	10.02	1.65	0.00
Error	44.00	765.16	17.39			
Day 7						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	29214.62				
Rep	1.00	499.38	499.38	6.59	4.06	0.01
Variety	44.00	25381.62	576.86	7.61	1.65	0.00
Error	44.00	3333.62	75.76			
Day 8						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	13909.96				
Rep	1.00	32.40	32.40	0.45	4.06	0.51
Variety	44.00	10682.96	242.79	3.34	1.65	0.00
Error	44.00	3194.60	72.60			
Day 9						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	145.12				
Rep	1.00	2.50	2.50	0.88	4.06	0.35
Variety	44.00	18.00	0.41	0.14	1.65	1.00
Error	44.00	124.62	2.83			
Day 10						
Source	df	SS	MS	F	Fcritical	P-value
Total	1.00	36.00				
Rep	1.00	0.40	0.40	0.49	4.06	0.49
Variety	44.00	0.00	0.00	0.00	1.65	1.00
Error	44.00	35.60	0.81			

