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EVALUATION OF SOYBEAN RECOMBINANT INBRED LINES FOR YIELD POTENTIAL AND RESISTANCE TO SUDDEN DEATH SYNDROME

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by

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A Thesis Submitted in Partial

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for the Degree of

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in the field of Plant and Soil Agricultural Systems

Approved by:

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TITLE: EVALUATION OF SOYBEAN RECOMBINANT INBRED LINES FOR SEED WEIGHT YIELD, AGRONOMIC TRAITS, AND RESISTANCE TO SUDDEN DEATH SYNDROME

MAJOR PROFESSOR: Khalid Meksem and Stell Kantartzi

Sudden death syndrome (SDS) caused by *Fusarium virguliforme* is a devastating disease in soybean (*Glycine max* (L.) Merr.) that causes up to 70% of yield losses depending on the developmental stage when the plant become infected. The characterization of resistance is greatly significant for disease management. Therefore, three populations were developed by crossing three resistant lines, 'Hamilton', LS90-1920 and LS97-1610 with a susceptible line to SDS, 'Spencer'. Ninety-four $F_{5:6}$ recombinant inbred lines from each population (Hamilton x Spencer, LS90-1920 x Spencer, and LS97-1610 x Spencer) were evaluated for two years (2009 and 2010) at two locations (Carbondale and Valmeyer) in southern Illinois. Population statistics, genotype x environment interaction, and broad-sense heritability were used to reveal any major resistance genes. Genetic correlation coefficients of SDS resistance with important agronomic traits such as lodging, pubescence, growth habit, and plant height were also calculated. The information from this study will be helpful to breeders in developing populations for genetic analyses and enforcing selection practices.

DEDICATION

I would like to dedicate this thesis to my late mother. I wish she could be present to see me achieve this level. May she rest in peace.

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I would like to thank many people who pushed me to graduate. First off I want to thank my fiancée Misty, who has supported me through thick and thin in this process.

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For the next bit I would like to quote a joke from one of my favorite authors.

"It is embarrassing to know that one is a god of a world that only exists because every improbability curve must have its far end;" -Terry Pratchett *The Color of Magic*

I would like to thank Terry Pratchett for the wonderful books that he has produced that have kept me sane in the writing process as well as the offhand statistical joke that gets thrown in there.

I would like to thank all my friends and family who have supported me and been kind enough to put up with my oddities while I have been working, it has not gone unnoticed.

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TABLE OF CONTENTS

LIST OF FIGURES

LIST OF FIGURES

Figure Page

CHAPTER 1: LITERATURE REVIEW

1. Genus *Glycine*

Glycine is a genus of legume that is found in wide varying regions of the world. It has been found in Africa as *G. javanica,* Australia as *G. canescens,* and China as *G.soja* (Herman, 1962: Fujita et al., 1997). *Glycine* presents a trifoliate leaf pattern and its fruits are pods (Newell and Hymowitz, 1980). Soybeans have developed a method to generate root nodules (Walter and Bien, 1990) which have the ability to initiate a symbiotic relationship with Rhizobiaceae in order to fixate nitrogen (Crespi and Galvez, 2000). Soybeans were used as an ancient agricultural crop, and formed an important part of the diet for the Asian people. The foods derived from soybeans include: miso, soy sauce, tempeh, and tofu (Hymowitz and Newell, 1981). The integration of these foods into the everyday diet of the entire continent of Asia has ensured the continued use of the soybean plant. This makes *G.soja* an economically important member of the *Glycine* family (Hymowitz, 1970).

There is little difference between the wild type *G.soja* and the commercial variety used today, *G.max*. There is less than a 0.2% divergence from *G.soja* and *G.max* based of nucleotide sequence (Kollipara et al., 1997). The different species still share many of the same alleles. There is about 92% similarity between *G.soja* and *G.max* (Powell et al., 1996)

2. *Glycine max*

Glycine max, (L.) Merr., otherwise known as soybean, is an important agriculture crop from the subgenus *Soja* (Hymowitz, 1970). Soybeans are a common agricultural crop of the United States, with over 90 million metric tons produced in the United States in 2010 (Wrather and Koening, 2006).

Soybeans generate both protein and oil, each of which can be utilized differently. The proteins are a source that contains all essential amino acids, which is vital to those on a vegetarian diet (Rackis et al., 1961). The oil from the soybean can be used as both a source of power as well as a source of cooking oil (Hossain and Al-Saif, 2010; Hayati et al, 2009)

Soybeans have a chromosome count of n=20, it is believed to be an ancient polyploid (Qui and Chang, 2010). There is evidence that soybeans are an allopolyploid species, where heterosis and gene redundancy might be of an advantage (Comai, 2005; Gill et al., 2009).

3. Origin, History, and Domestication

The origin of soybeans comes from China. While many people claim that the first mention of soybean came from the Emperor Shen Nung, this is not entirely true (Hymowitz, 1970). There is mention of soybean in the written record of the book *The Shijing*, which mentions the bean as *shu* (Shurtleff and Aoyagi, 2009). Since Hymowitz (1970) states that most of the written records before 841 B.C. are suspect and *The Shijing* is attributed between the 10^{th} and 7^{th} century, it may be truly the first mention of the plant. Archeological evidence points to the domestication of soybeans a bit further back (Rectors and Visitors, 1998). Recent studies show that the soybean may have been domesticated as far back as 3500 B.C.E. in different parts of Asia and were not exclusive to China (Barlow, 2011).

The plant itself is widely used across China as a cheap food. These soybeans were known as *Glycine soja* and were used in many different foods in Asia and play a vital role in the diet of the people there (Fujita et al, 1996; Gibson and Benson, 2005). It is used for the production of cooking oil, tofu, tempeh, edamame, and protein powder (Barlow, 2011).

The soybean was first introduced to the United States by Samuel Bowen in 1765 to Savannah, Georgia region after learning the benefits of the crops from his time imprisoned in

China (Hymowitz and Harlan, 1983). Soybeans were mostly used for forage and did not significantly expand in the United States until the 1920s (Gibson and Benson, 2005). A.E. Stanley would be a major reason for the expansion of the soybean market in the 1920. Stanley started a soy mill and, starting in 1922, would buy most of the soybean crop produced in Illinois. In 1925 alone, he purchased 70,000 bushels of soybeans (Shurtleff and Aoyagi, 2004)

One of the reasons for the increased use of soybeans was the interest of Henry Ford. Ford was interested in both the nutritional and industrial applications of soybeans (Meikle, 1997). Through his innovations, he was able to use soy in the production of plastic for his car Model T (Wyss, 1998). Ford was a big innovator for uses of soybeans. He was a big proponent of soybeans used for industrial products (Shurtleff and Aoyagi, 2011).

The domestication of soybeans does not come off without repercussions. The effect of domestication inevitably leads to a loss of genetic diversity (Bettina et al, 2009). This effect is known as bottlenecking and occurs when a population's size is limited for some reason (Hyten et al., 2006). Such a bottleneck effect has been noted in several soybean studies (Xu et al, 2002; Lee et al., 2008; Li et al., 2008; Li et al., 2009). The bottleneck in soybeans in currently considered moderate, and the soybeans in south China comprise a vast genetic resource for the future (Guo et al., 2010).

4. The Plant Soybean and its Products

Increasing the production of a crop with these unique attributes will be vital with the growing world population that will require more and more resources. Because of this, plant breeders need to increase the production from what arable land we have. To do this, we need to have an increase in versatile, multipurpose crop production such as soybean.

Glycine max is a member of the subgenus *Glycine soja* and is herbaceous, erect, and can reach a height of 1 m (Jin et al., 2010). The cultivars of soybean can have indeterminate, determinate, or semi-determinate growth (Bernard and Weiss, 1973).

The soybean plant generally bears between 100 and 150 pods each (Shurtleff and Aoyagi, 2007). Flower colors are generally either white or purple (Hartwig and Hinson, 1962). The flowering of soybeans is controlled by the day length, with short day length being the trigger for flowering (Major et al., 1975).

The soybean plant is a viable choice for increased production due to the multiple outputs that come from its crop (Wyss, 1998; Moser, 2011; Hayati et al., 2009). The oil that is derived from the plant has some unique properties that make it ideal for both cooking and industrial uses. Soybean oil can be used for a myriad of different industrial uses. They can be used to form a plastic that can be used in industrial processes (Wyss, 1998). Soybeans can also be used to create a fuel to power mechanical machines (Moser, 2011). Soybean oil can be used as cooking oil that is especially useful due to its high smoke point as well as printing ink (Man et al., 1999). Soybean oil is a very common packaged food oil source.

In order to extract the oil from soybeans, a press is usually utilized (Qui and Chang, 2010). The remaining pressing of the soybean that is left behind is referred to as soy meal. This product is high in protein and is commonly used for feed for animals (Cromwell, 1999).

5. Development, Selection, and Cultivation of Soybeans

Glycine max has several vegetative states and reproductive stages through out its life cycle (McWilliam et al., 2004). The growth stages for the vegetative stages are summarized as follow, emergence from the soil surface (VE), cotyledon leaves opening (VC), first trifoliate unfolded (V1), second trifoliate unfolded (V2), third trifoliate unfolded (V3), nth trifoliate unfolded

(V(n)), and pre-flowering stage (V6). The first three stages are illustrated in figure 1. The plant enters the reproductive stages shortly after reaching the V6 stage. The reproductive stages of the plant are the beginning bloom with at least one flower on it (R1), full bloom with an open flower on one of the two uppermost nodes (R2), beginning pod where pods are 5mm at one of the four uppermost nodes (R3), full pod where pods are 2cm at one of the four uppermost nodes (R4), beginning seed where the seed is 3mm long in the pod at one of the four uppermost nodes (R5), full seed where a pod containing a green seed that fills the pod capacity at one of the four uppermost nodes (R6), beginning maturity where one of the pods on the main stem reaches mature pod color (R7), and full maturity where 95% of the pods have reached mature color (R8).

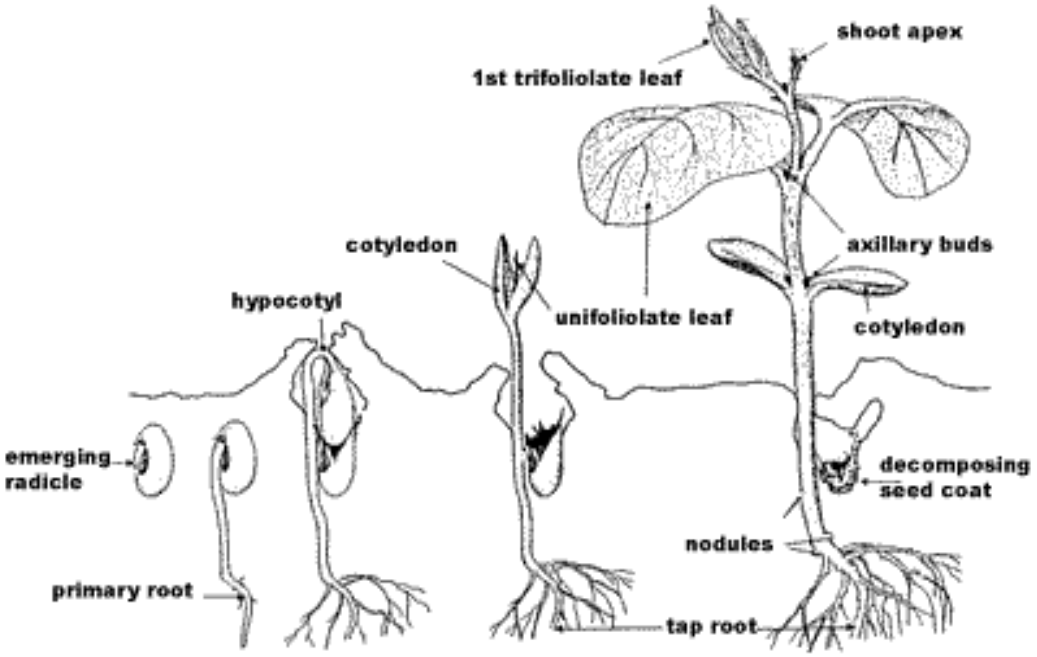


Figure 1 The Vegetative Stages of *G.max* (courtesy of University of Minnesota extension)

The soybean emerges from the soil, which completes the VE stage. The cotyledon of the plant quickly follows the emergence state and allows the plant to start to produce its own energy (Vines, 1913). The plant continues to grow and produces trifoliates as it progressed through the vegetative state. The reproductive stage starts whenever a flower is present on the plant (Wiatrak, 2012). The reproductive stage will eventually lead to the production of seed pods and the seeds itself.

Soybeans generate both protein and oil, each of which can be utilized differently. The oil extracted from soybeans could be used for the production of biodiesel (Ma and Hanna, 1999). The availability of biodiesel is becoming even more important, as the rising cost of fossil based fuel makes an increased production of soybean a cost effective solution. The oil in soybeans can also be used as cooking oil (Man et al., 1999).

In addition to the oil that can be acquired from soybeans, a large amount of protein can be obtained as well (Diftis and Kiosseoglou, 2003). The high level of protein in soybeans makes it an ideal source of food and feed. In addition to human use and consumption of soybean, the high protein content makes soybeans an ideal source for animal feed (Kerley and Allee, 2003). The versatility of being able to be used as a food and feed source for humans and animals, in addition to the ability to use the oil for both fuel as well as cooking, demonstrates the importance of the crop. Increasing the production of a crop with these unique attributes will be vital with the burgeoning world population that will require more and more resources (Tester and Langridge 2010). Because of this we need to have more production from what arable land we have. To do this, we need to have an increase in versatile, multipurpose crop production such as soybean.

Table 1 Detailed information on Pedigree Breeding (Used under creative commons license from theagricos.com)

Step	Details
Hybridization	Crossing between selected parent plants is the first step in pedigree method.
F_1**generation**	Seeds obtained by hybridization (F_1 seeds) are planted with proper sowing distance. Seeds of about 20-30 plants are harvested in bulk and forwarded to grow F_2 generation.
F_2**generation**	Selection is the main process carried in this step. About 10,000 plants are grown from F1 generation seeds (F2 seeds). With application of selection process about 500 plants are selected and harvested separately.
F_3**generation**	About 30 or more progenies are raised from each of the selected plant of F_2generation. About 100-400 superior plants (the number could be anything, preferably less than those selected in F_2 generation) are selected
F_4**generation**	Seeds from F_3 generation are space planted. Plants with desirable characters are selected in number much less than those selected in F_3 generation.
F_5 **generation**	Individual plant progenies planted in multi row (3 or more) plots so that superior plants (about 50 – 100) can be selected by comparison.
F_6**generation**	Individual plant progenies planted in multi row (3 or more) plots. Plants are selected based on visual evaluation, progenies showing segregation can be eliminated.
F_7**generation**	Preliminary yield trials with minimum 3 replications and a check. Quality tests are conducted.
F_8 **to** F_{12}**generation**	Multi-location yield trials with replications are conducted. Tests for quality and disease resistance are conducted.
F_{10} **or** F_{13}**generation**	Seed multiplication for distribution.

New work is constantly being done in order to increase soybeans yield. By selecting for different traits, such as drought tolerance, you can add new traits into different lines to produce plants with better agronomic traits (Hufstetler et al., 2007).

In order to do this, different methods of selection of the seeds must be undertaken. Methods such as single seed descent and/or bulk selection are utilized. Single seed descent is a method in which a single seed or pod are taken and replanted over several generations until they are selected for the trait that the researchers are interested in. During the 6^{th} generation, selection occurs for the trait that is desired (Miladinovic et al., 2010)

In bulk selection, all the seeds are collected from the plants that contain the trait that is desired. The seeds are replanted and then, during the 6^{th} generation, selection for the desired trait occurs. This method is easier than single seed, as it can be done in conjunction with harvest, and therefore, it does not need more labor. (Burton, 1990)

The method of pedigree selection varies from bulk and single seed descent in that only a handful of plants are chosen in the F_1 generation to forward to the F_2 generation. Selection for traits begins at the F_2 generation (Table 1) (Percy, 2003).

Pedigree breeding can be combined with mass selection or single-seed descent (Wang et al., 2003). This method is not commonly used due to the decreased efficiency in the pedigree system.

Once the plants which have desirable traits are identified from the selection methods, they have to be bred into elite lines which are desirable for agronomic traits. This is done via backcrossing, it is the process of crossing the individuals from the selection process with the elite lines used in the original cross (Schneider, 2005). The offspring is then crossed once again with the elite line and this process is repeated several times to allow for the largest amount of traits

from the elite line to be present while retaining the desirable(s) trait(s) from the line that was selected. This method is achieved in a quicker fashion with the use of marker assisted selection.

6. Genetic Improvement

Through the ages, farmers have selected what they thought was the best seed from their crop to plant in the following year (Guo et al., 2009). This idea is carried out through more rigorous methods today in order to obtain a more consistent plant in the next season. The most sought after improvement is the increase in yield. Also important factors to consider are the increase in performance for the plant, especially for those under adverse conditions. Resistance to disease is also of vital importance to the breeding process. All of these together are targets for breeding projects.

6a. Yield and Yield component

The goal for most breeding programs is to increase the crop yield of plants. Crop yield is defined as a measurement of the amount of a crop that was harvested per unit of land area one of the standard units of measurement for this is kilogram/hectare (Investopia, 2012). In order to achieve this, lines are developed in order to increase the amount produced per plant. (Cober and Voldeng, 2000) While this is the goal, it is not an easy one to achieve. Studies have shown that yield is attached to several different genes, which make backcrossing into the elite lines necessary (Yuan et al., 2002).

Yield has steadily increased over the years, with an increase from 25 to 30 kg/hectare per year due to increased genetic gain and paired with better resistance to pathogens (DeBruin and Pedersen, 2009). The effect of disease on yield is clear (Wrather and Koening, 2006). The economic advantage of having higher yield will push discoveries for higher yields in genetic gains (Cober and Voldeng, 2000). The combination of yield and disease resistance is also vital.

The adation of high yield lines with resistance resistance is also vital for development of soybeans. (Yuan et al., 2002)

In order to increase yield, improved growth of the plant must be considered. To do this, the overall growth and agronomic performances of the plants must be looked at. One of the key deciding factors of growth is the availability of water. To this end, drought tolerance is a key factor to the growth of plants (Bouslama and Schapaugh, 1984). If lines were available that would allow for more drought tolerant plants, less water would be needed for the fields.

Other agronomic traits that are important would be the germination rate of the plants, with lines with higher germination rates being favorable (Edwards and Hartwig, 1971). Time to maturity is also a valuable trait to look for, as being able to produce a quick or slow crop, depending on the environmental situation, it can be vital to the health of a crop (TeKrony et al., 1978).

The height of the soybean can also play a factor, as larger plants have the ability to produce more of a crop. The height of soybean is dependent on several different factors, with the seeding rate, row spacing, planting date, soil composition, fertilization, herbicide use, and genetics all playing a role in the final height (Peterson and Ikard, 2004).

6b. Disease Resistance

One of the key factors that are looked for in cultivars is their ability to resist disease. This is done through traditional methods, through mapping, and through genetic modification. (Aruna et al., 2011, Meksem et al., 2000: Roh et al., 2007) This is important due to the increased vast amount of loss that occurs yearly. In 2005, there were losses of nearly 7 million tons of soybeans due to various diseases (Wrather and Koenning, 2006). With the average cost of around $500 a metric ton in 2012, (World Bank, 2012) the total amount lost was $1.4 billion dollars for the year.

Resistance for disease is done through either vertical or horizontal resistance. Vertical resistance is resistance based off of one gene while horizontal resistance is resistance based off of several genes (Parleviet and Zadoks, 1977). A combination of the resistance types would be ideal, since horizontal resistance slows down the rate by which a disease spreads through a field while vertical resistance reduces the initial inoculum in a field (Poland et al., 2009; Van Der Plank, 1965).

Diseases have the ability to devastate a field, and different resistances for the different pathogens that can attack the plants are important. Sudden death syndrome is a disease that can cause chlorosis and necrosis on the plant leaf (Figure 2; Leandro et al., 2011). Brown stem rot shows very similar characteristics to sudden death syndrome (SDS), with chlorosis and necrosis of the leaves. The main difference between the two is the internal browning of the stems (Figure 3; Pederson, 2006).

Soybean cyst nematodes (SCN) can also cause severe damage to a field and spread unchecked due to the fact the disease survives in the soil overwinter and there is little that can be done chemically to deal with the pest, resistance and crop rotation are key to the management practices for SCN (Yu et al., 2009) The symptoms of SCN are dwarf plants and chlorosis of the leaves (Figure 4).

Figure 2 Soybean Sudden Death Syndrome (picture Courtesy Agriculture in Ohio)

Figure 3 Stems affected by Brown Stem Rot (picture Courtesy University of Illinois Extension)

Figure 4 Stunting and chlorosis caused by soybean cyst nematodes (picture Courtesy University of Minnesota Extension)

SDS is a fungal disease of soybean that is caused by *Fusarium solani* f.sp. *glycines* (Aoki et al., 2003). Its presence in soybeans can cause lower yield, so improvements in detecting lines that are resistant are vital (Rupe et al., 1993). The only way to imbue the field with resistance to the pathogen is to do it through resistant varieties (Leandro et al., 2011). When selecting resistant seeds, it is important to select seeds that has multiple resistances as well as, if possible, horizontal resistance (Leandro et al., 2011). In order to do this, modern technique as well as classical methods for determining plants that will contain resistance should be utilized. Molecular markers have been used to help identify resistance to SDS in soybeans (Hnetkovsky et al., 1995; Kazi et al., 2008).

With the production of SNP maps for soybean resistance to SDS, analysis of maps to identify SNPs for specific traits is possible (Kassem et al., 2012). This will allow for detection of individuals who have the traits for genetic resistance using marker assisted breeding.

7. Genetic Diversity and Bottleneck

Genetic diversity is important for the survival of species. Since humans started to domesticate plants instead of being hunter-gatherers, they started to alter the growth of plants (Haviland et al., 2010). The rapid change of the genetic material created different species of the plant and resulted in different outcome of the plant. By choosing a landrace that has adapted to an area and crossing them with current elite lines, plant breeders are able to bring traits from a line that has been exposed to the environment of a certain area together with the valuable genetics of elite lines. This is because the landraces are exposed every day to the pathogens and the environment of their area (Harlan, 1975). Further diversity can be established into lines which are not exposed to the same level of external sources. This will enable the production of lines which will benefit individual regions.

Molecular markers are used to determine the genetic diversity of soybean lines (Guo et al., 2010). By using RAPD and Microsatellites, a genetic distance map can be created in order to show how closely related different lines are from each other (Doldi et al., 1997). Once the genetic profile has been determined, lines can be identified for crossing in order to increase diversity (Cicek et al., 2006). While crosses can be done to incorporate different traits into elite lines, recent findings show that using landraces from China would do little to increase diversity in the lines in the United States due to the similarity of the lines (Suszkiw, 2007).

8. Recombinant Inbred Lines

Recombinant inbred lines (RIL) are a common practice in plant breeding. It is achieved by self-pollinating a line while at the same time ensuring that another source of pollen does not let a cross-pollination occur. Through the use of back crossing and the use of marker assisted

selection, this process has gotten significantly easier with a higher chance of success (Welsh and McMillan, 2012).

One of the major ways to increase production of soybeans is to, first create a RIL from a base population, it is generally done in order to produce a genetic map, the genetic map is then used to detect the presence of certain alleles that will have desirable traits in the offspring (Cregan et al., 1999). With RILs, a self pollinating species is the easiest way to ensure development. (Schneider, 2005)

8a. Recombinant Inbred Lines-Development

The RILs are created by crossing plants with themselves or a close relative when a plant cannot be self pollinated. The offspring that are produced (F_1) will contain a combination of the alleles from the parent(s) (P). This process is repeated five more times in order to produce an F_6 generation that will contain mostly homozygous individuals for the desirable traits. (Figure 5)

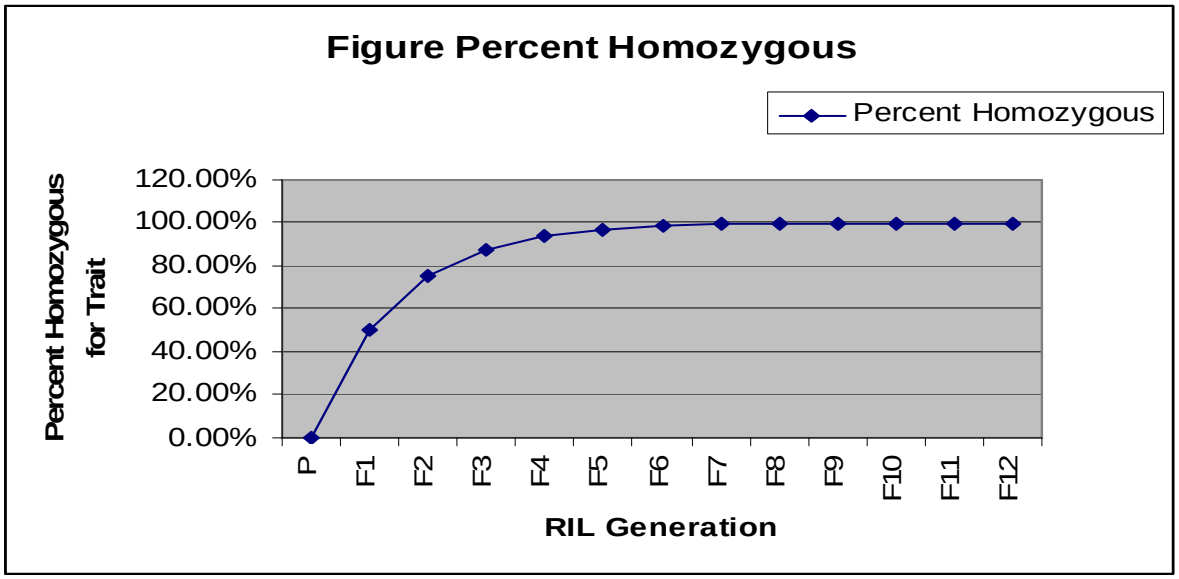


Figure 5 Percent of Homozygous for Traits for RIL-Single Trait

At the F_6 generation, there is a very high chance of choosing an individual that is either homozygous dominant or recessive. The more iterations are followed, the higher the percent that the trait of interest will either be dominant or recessive with little chance of having a heterozygous individual present.

8b. Recombinant Inbred Line-Description

The purpose of creating a RIL is that the progeny of the plants will generally produce the same offspring. The phenotypic traits as well as the genotypic traits should be nearly identical. Eventually, the RILs will start segregating for different traits, allowing for specific traits to be selected for further breeding programs (Shindo et al., 2003). Using this method, traits for disease resistance can be identified and incorporated into elite lines. (Graichen et al., 2010: Kassem et al., 2012)

8c. Advantages of Recombinant Inbred Line

When the segregation for specific trait occurs, one is able to have confidence that the genes governing that trait will be either homozygous dominant or recessive Schneider, 2005). This allows for ease of use when doing a breeding program with the RIL.

With the isolation of RIL genotypes to ensure that similar phenotypic trait comes the side effect of producing a similar genotype. This allows for the production of genetic maps from a RIL through the use of recombinant frequency, or the frequency of a single chromosomal crossover occurring (Singer et al., 2006). Genetic maps are important because they can be used to determine if other individuals would have the same trait through the use of markers. (Michelmore et al, 1991)

9. Genotype x Environment Interactions

Even when a trait is present in an individual, it may not express itself. In cases such as disease resistance, without the presence of the disease, the resistant gene will not show itself. While it may not be the chief driving force in an environment, it is a much bigger influence than just the genes (Aruna et al., 2011).

While genetic markers have the ability to ensure that traits are present at any given time, other factors may end up affecting the growth of plants (Hao et al., 2011), while DNA does play a large role in what is expressed in plants, not everything can be attributed to DNA expression (Eichten et al., 2011). The concept of epigenetics, or the expression of traits not influenced by DNA, is a vital reason why multiple environments should still be studied even with the emergence of molecular markers onto the scene.

In order to determine the extent of a resistance for a specific trait such as drought tolerance, it must be exposed to a range of environments. This is known as norm of reaction (Griffiths et al., 2000).

10. Molecular Markers

There are several types of molecular markers. Single nucleotide polymorphism (SNP), simple sequence repeats (SSR), random amplification of polymorphic DNA (RAPD), and restriction fragment length polymorphism (RFLP) are some of the major marker types used in plant breeding (Young, 1999: Collard and Mackill, 2008). They are used for a wide variety of different applications, from diversity studies with RAPD, mapping with SSR, and SNP for genotyping (Doldi et al, 1997; Meksem et al., 2001; Hao et al, 2012)

11. Single Nucleotide Polymorphisms

A SNP is a point mutation in the base pairs of the DNA. The SNP can be run through a gel electrophoresis (Ngyuyen and Wu, 2005). A determination can be made whether or not an

individual being screened contains the SNP of interest based on the presence of a band at the same location(s) as the SNP. A screening of the entire population against the SNP markers is used to determine whether or not they are positive or negative against the markers. Statistical analysis is then done against a trait of interest to see if there is a suite of markers that could identify the desired trait (Hao et al., 2012).

CHAPTER 2: MATERIALS AND METHODS

1. Plant material

Three recombinant inbred lines (RIL) (*n*=94 each) were used for this study: 'Hamilton' x 'Spencer', LS90-1920 x Spencer, and LS97-1610 x Spencer. They were a combination of a susceptible line (Spencer) and a resistant line (Hamilton, LS90-1920, and LS97-1610)

The line 'Hamilton' was developed by Nickell et al. 1990 and was derived from a F_4 plant that originated from a cross between the lines 'Sprite' and L75-3632. It was developed at the Illinois Agricultural Experiment Station via single seed descent method and evaluated under the experimental designation LN82-2366 (Nickell et al., 1990). Hamilton was classified as maturity group (MG) IV with white flowers, gray pubescence, brown pods at maturity, and shiny yellow seeds. It was released to seed foundations in Missouri, Illinois, Indiana, Nebraska, and Ohio (Nickell et al., 1990).

Wilcox et al. 1989 developed the Spencer variety (Wilcox et al., 1989). It was derived from a F_5 plant that originated from a cross between the A75-305022 and 'Century'. (Wilcox et al., 1989) It was crossed in 1978 and developed at the Purdue University Agricultural Experiment Station. Line A75-305022 was derived from an F_3 cross of 'Wye' x ('Amsoy x 'Wayne'). Wilcox et al. 1989 grew it at the Iowa Agricultural and Home Economics Improvement Station. Lines F_2 through F_5 were generated through single-seed descent and were replication tested in Indiana. Initial tests were done in Indiana in 1982 and 1983. Spencer is an indeterminate, MG IV cultivar that matures three days later than 'Williams 82' (Bernard and Cremeens, 1988). It has white flowers, tawny pubescence, with brown pods at maturity, and dull yellow seeds. Spencer was released to seed foundations in Illinois, Indiana, Ohio, and Kansas. The Purdue University is maintaining the breeding seed (Wilcox et al., 1989).

Schmidt et al. 1999 developed the line LS90-1920. It was derived from a F_5 plant that originated from a cross between the lines ‘Essex’ (Smith and Camper, 1973) and ‘Fayette’ (Bernard et al., 1988). The F_2 through F_5 generations were selected using single-pod descent (Fehr, 1991). A single F_5 plant was selected on a field infested with SCN HG Type 2.5.7 (Race 3). Soybean cyst nematode resistance was determined in greenhouse experiments by using soil collected in an SCN HG Type 2.5.7 (Race 3) infested field near Elkville, IL. Resistance was confirmed at the University of Arkansas by greenhouse evaluation against SCN HG Type 2.5.7 (Race 3) isolate maintained on Essex and the University of Missouri by greenhouse evaluation against SCN race 3 isolate maintained on ‘Hutcheson’ (Buss et al., 1988). LS90-1920 was tested in five *F. solani* infested environments from 1993 to 1997. LS90-1920 showed a high level of resistance to SDS. LS90-1920 is a MG IV cultivar that matures three days later than ‘Delsoy 4710’ (Anand, 1992) in a full season planting. It is determinate in growth habit, has purple flowers, tawny pubescence, and tan pod walls. LS90-1920 is resistant to stem canker and frogeye leaf spot. LS90-1920 was released in 1996 due to its high resistance to soybean cyst nematode and SDS (Schmidt et al., 1999).

The line LS97-1610 was released as germplasm due to it’s resistance to SDS and *H.glycines* Hg type 2.5.7. (Allen et al., 2005) It was chosen for this study for the disease resistance to SDS.

‘Saluki 4910’ and ‘Saluki 4411’ varieties were selected for yield checks due to their high yield potential as well as their disease resistance (Kantartzi et al., 2012, Kantartzi et al., 2012). Additionally, ‘Ripley’ was used as a resistant check for the SDS and Spencer as a susceptible check (Cooper et al., 1990).

2. Development of recombinant inbred lines

The crosses for the RIL genetic material development were made in 2002 at the ARC station, Carbondale, IL. The lines were developed over two years from an F_1 population to an F_2 population via single pod descent. Phenotypic traits were observed in order to determine if the cross between the parent and the donor took place. If the offspring exhibit a dominant trait from the donor parent that was not present in the acceptor, then the cross was considered successful (Campbell et al., 2003). Once the seeds from the F_2 population were collected it was shipped to the winter nursery in Puerto Rico, where it was advanced to the F_4 generation using single pod descent method. The seed was then returned to Carbondale, IL, where the F_5 population was grown.

Table 2 RILs development: Stages, locations and years (The tables and figures legends should all be under the table or figure, not sometime on top and sometime under, that's why I asked you to check for the guidance of the grad school), please modify all accordinally.

2005	F5 pop	Carbondale
	F4 pop	Puerto Rico
	F3 pop	Puerto Rico
2004	F2 pop	Carbondale
2003	F1 pop	Carbondale
2002	Cross	Carbondale

3. Field plot technique

There were two locations used for SDS testing and two locations used for agronomic and yield testing. SDS testing was done over a two years period. Agronomic and yield tests were done for one year. All locations used a randomized complete block design. Each location used two blocks which helped to minimize variation in the field. Each block had three different RIL lines planted.

4. Field locations

Locations for the experiment were located throughout southern Illinois. For the 2009 and 2010 season, two locations where used. Carbondale, IL (Figure 6) and Valmeyer, IL (no figure) were utilized for the SDS trials. Two locations were used for the agronomic trials in 2011. They were located in Dowell, IL (Figure 7) and Harrisburg, IL (Figure 8).

Figure 6 Location of Carbondale Plot (© 2012 Google)

Figure 7 Location of Dowell Plot (© 2012 Google © GeoEye)

Figure 8 Location for Harrisburg Plot (© 2012 Google)

5. Field treatment for weed control

The Harrisburg location was sprayed with 1.56 liters of S-Metolachlor per hectare, 0.44 liters of Sulfentrazone per hectare, and 1.16 liters of Glyphosate per hectare. Post emergence herbicide solutions were sprayed on July 1, 2011. They consisted of Clethodim at 0.59 liters per hectare and sodium salt of Fomesafen at a rate of 1.46 liters per hectare.

The Dowell location was pre-sprayed with Flumioxazin before planting. It was sprayed with a pendimethalin herbicide at a rate of 2.35 liters per hectare. Post emergence herbicide solutions were sprayed on June 30, 2011. They consisted of Clethodim at 0.59 liters per hectare and sodium salt of Fomesafen at a rate of 1.46 liters per acre.

6. Phenotyping

A. Phenotypic Traits

Several agronomic traits were taken in the Harrisburg and Dowell, IL locations. The methods for collecting the data were described in Crochet, 2010.

i. Maturity- the date when 95% of the pods have ripened, as indicated by their mature pod color. Delayed leaf drop and green stems are not considered in assigning maturity. Maturity is expressed as days earlier (-) of later (+) than the average date of the reference variety. To aid in maturity group classification, one earlier (E) and one later (L) check variety are given in the maturity column for each test, or a maturity check from an earlier or later maturity

ii. Height- Height is the average length in inches of mature plants from the ground to the tip of the main stem. The height reading is taken at the same time of maturity. The plants are measured in inches and the data is then converted to centimeters by multiplying by a 2.54 factor.

iii. Lodging- Lodging is rated at maturity. The rating system for lodging is scored according to the following scores:

1 = Almost all plants erect.

2 = All plants leaning slightly or a few plants down.

3 = All plants leaning moderately (45 degrees), or 25% to 50% of the plants down.

4 = All plants leaning considerably, or 50% to 80% of the plants down.

5 = Almost all plants down.

iv. Stand count-Stand count is the count of number of plants germinated between the 1st and 2nd meters in each row. Stand count is taken after the germination stage and is used as a measure of germination rate for the rows.

B. Screening for SDS

SDS leaf symptoms were rated and compared to two checks, one resistant, 'Ripley' (Cooper et al., 1990), and one susceptible, 'Spencer' (Wilcox et al., 1989), as close as possible to the R6 stage (Fehr et al., 1971) when seeds have filled the pod cavity, but have not yet begun to senesce. SDS was rated by two scores; disease incidence (DI), which is the percentage of plants with SDS symptoms in a plot, and disease severity (DS). DS is rated on a 1 to 9 scale with 1 describing mild symptoms and 9 being the premature death of the plant. More detailed, (1):0 to 10% where 1 to 5% of leaf surface chlorotic/necrotic, (2):10 to 20% where 6 to 10% of leaf surface chlorotic/necrotic,(3):20 to 40% where 10 to 20% of leaf surface

chlorotic/necrotic,(4):40 to 60% where 20 to 40% of leaf surface chlorotic/necrotic, (5): >60% where more than40% of leaf surface chlorotic/necrotic, (6):up to 33% premature defoliation, (7):up to 66% premature defoliation, (8): >66% premature defoliation, and (9):premature death of plant. These two scores are used to calculate a disease index (DX) with the formula (DI*DS)/9 (Njiti et al., 1996).

C. Post-harvesting

Yield is measured after the seeds have been dried to uniform moisture content and is recorded in bushels (60 pounds) per acre. To convert to kilograms/hectare multiply by 67.25.

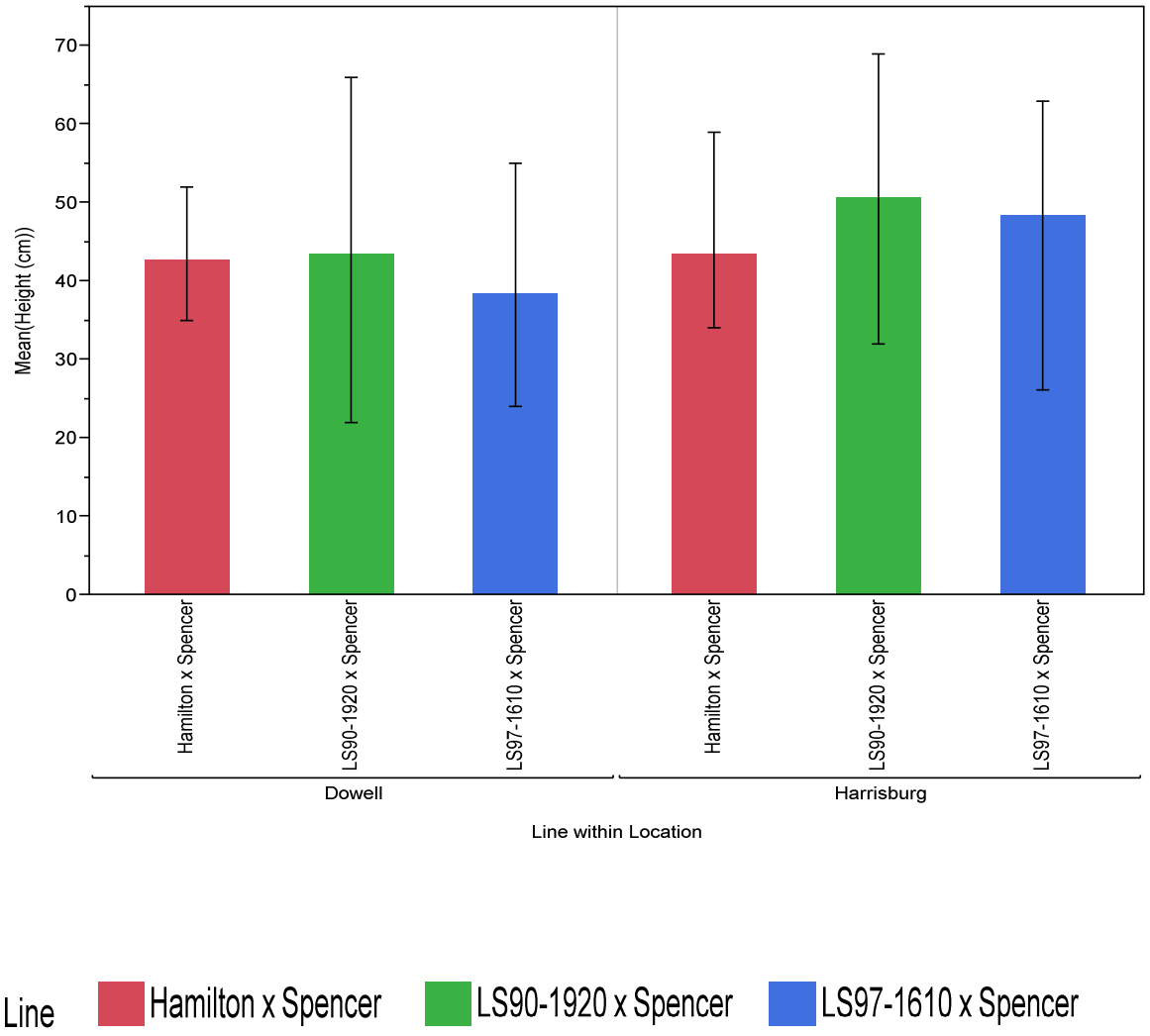
7. Statistical analysis

All traits for each line and field were analyzed as a randomized complete block design. Locations, replications, blocks, and lines were considered random effects. Error variance was treated as fixed effect. Analysis was done using the statistical programs R (R Development Core Team, 2011) as well as JMP 9.0 (SAS Institute Inc. 2007). Analysis of Variance (ANOVA) was done on DX for the plots planted in the year 2009 and 2010. ANOVA analysis was calculated for height, maturity, lodging, and yields for the plots planted in the year 2011. The results were considered significant if the (P) value was below 0.05. Distribution charts were created for the plots for the year 2011 for the traits flower color, pubescence, and growth habit.

CHAPTER 3: RESULTS

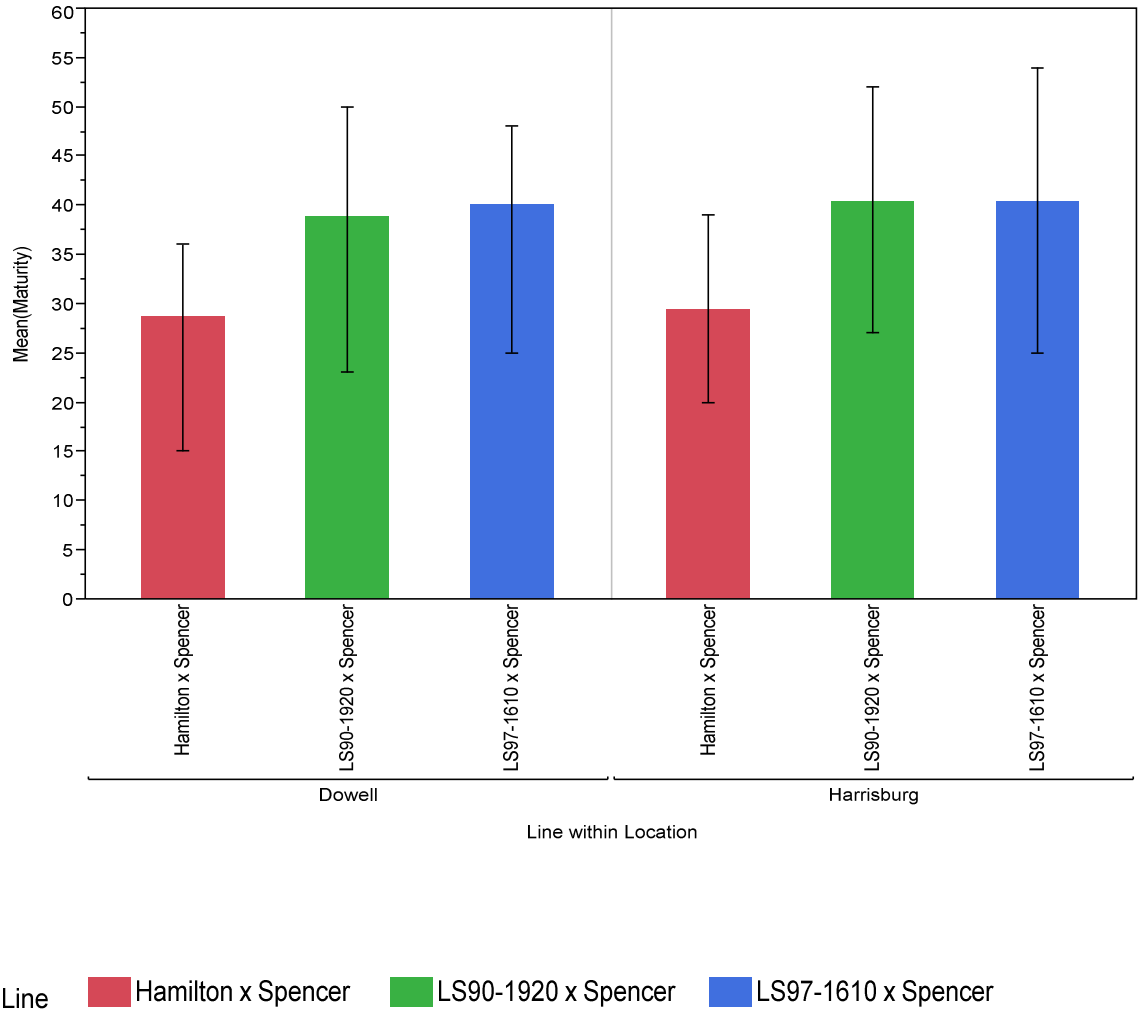
1. **Agronomic evaluation of three different recombinant inbred populations**

The RIL lines were planted in different locations in southern Illinois. Agronomic data was taken at each location. Mean average, standard deviation, range, and CV for the different RIL at different locations data are presented (Table3, Table 4, Table 5, Table 6, Table 7, and Table 8). The height (Figure 9) showed a grand mean for each line between 35 and 50 cm. Maturity date after September 1 (Figure 10) showed a grand mean for each line between 27.5 and 40 days. Lodging score (Figure 11) showed a grand mean for each line between 1.5 and 2.5. Yield (kg/hectare) (Figure 12) showed a grand mean between 2250 and 3250 kg/hectare.



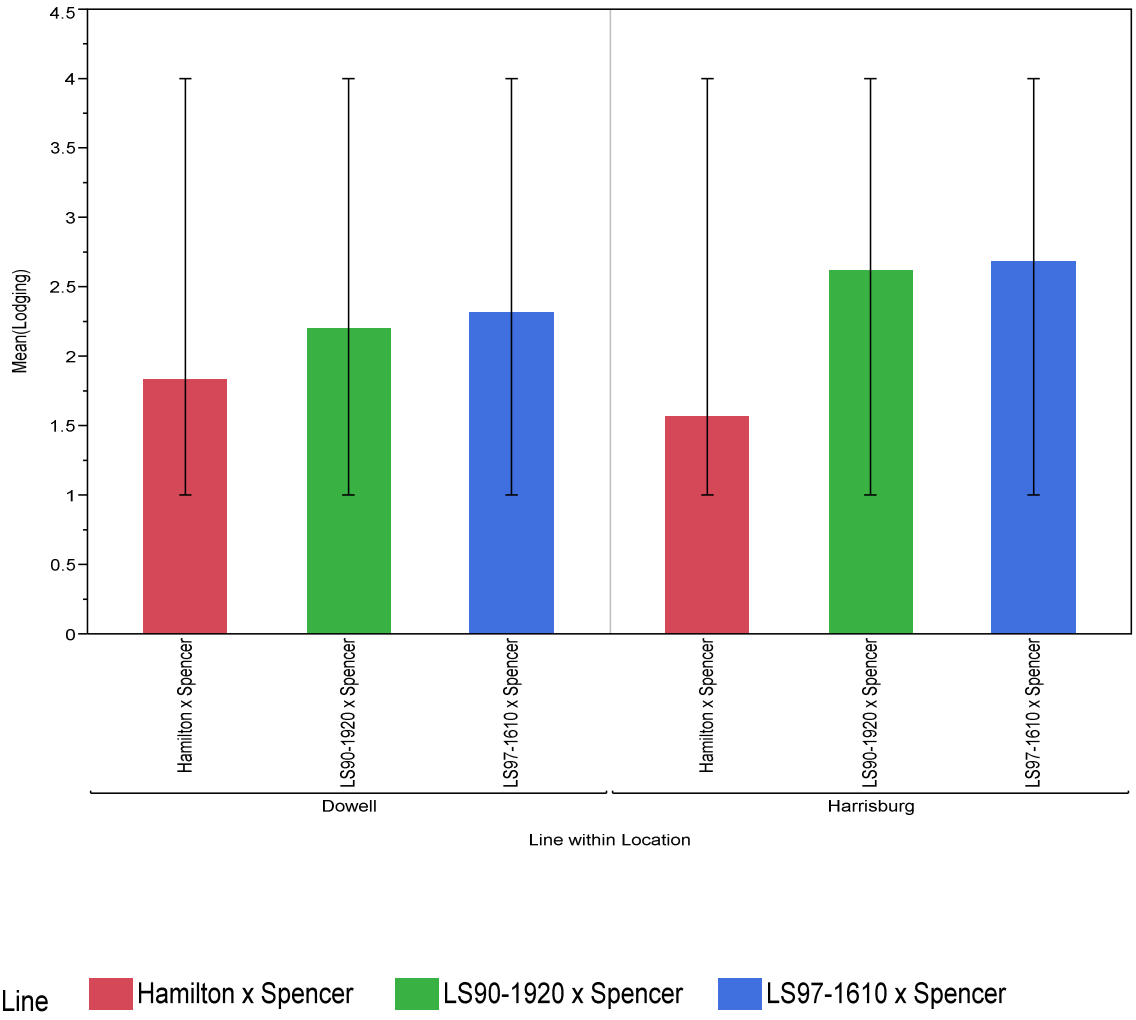
Each error bar is constructed using the min and max of the data.

Figure 9 Plant height of three recombinant inbred populations (Hamilton x Spencer, LS90-1920 x Spencer and LS97-1610 x Spencer) grown in Dowell and Harrisburg IL in 2011



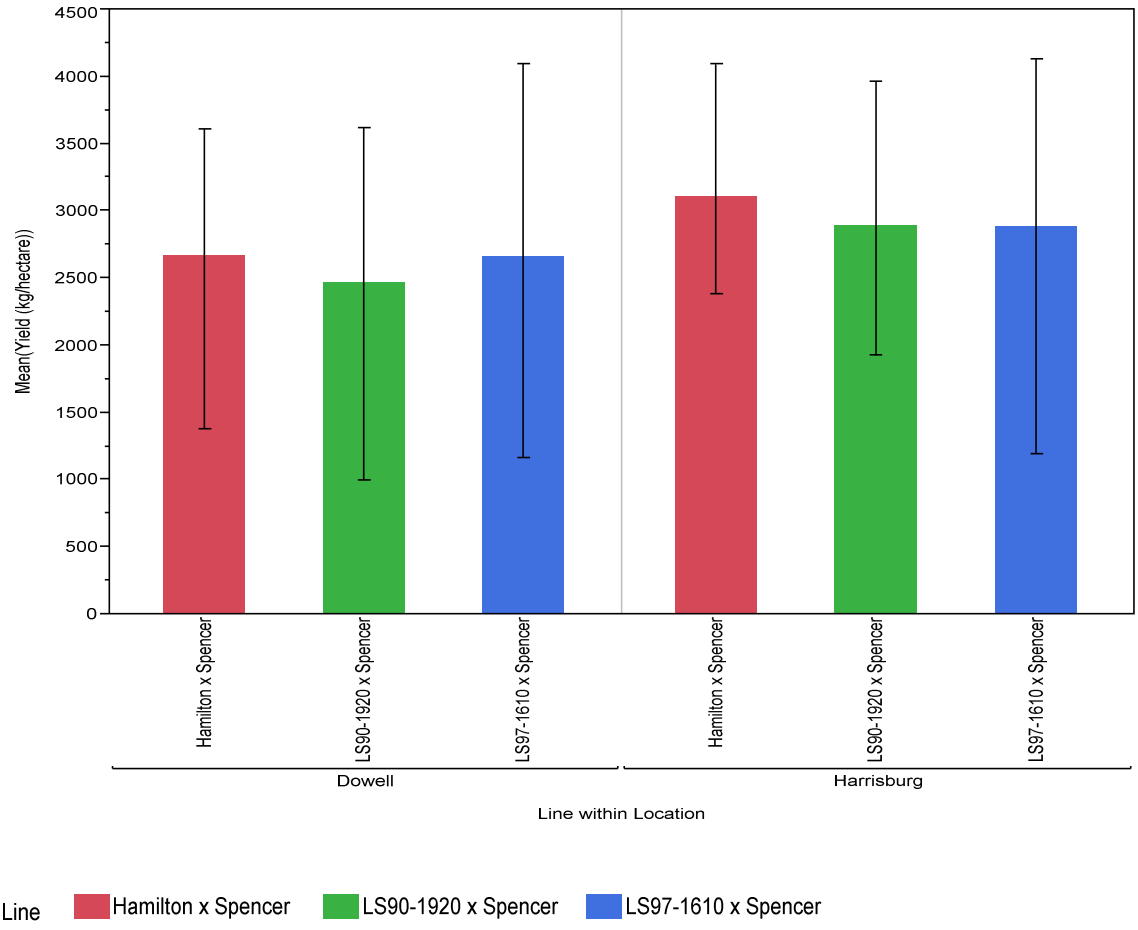
Each error bar is constructed using the min and max of the data.

Figure 10 Maturity date of three recombinant inbred populations (Hamilton x Spencer, LS90-1920 x Spencer and LS97-1610 x Spencer) grown in Dowell and Harrisburg IL in 2011



Each error bar is constructed using the min and max of the data.

Figure 11 Lodging score of three recombinant inbred populations (Hamilton x Spencer, LS90-1920 x Spencer and LS97-1610 x Spencer) grown in Dowell and Harrisburg IL in 2011



Each error bar is constructed using the min and max of the data.

Figure 12 Yield of three recombinant inbred populations (Hamilton x Spencer, LS90-1920 x Spencer and LS97-1610 x Spencer) grown in Dowell and Harrisburg IL in 2011

Table 3 Descriptive Statistics for Hamilton x Spencer planted in Dowell, IL in 2011

	Height	Lodging	Maturity	Yield
Mean	42.654	1.823	28.633	2667.052
SD	3.855	0.719	4.179	415.966
Range	17.000	39.270	21.000	2226.387
CV	9.037	3.000	14.595	15.596

Table 4 Descriptive Statistics for LS90-1920 x Spencer planted in Dowell, IL in 2011

	Height	Lodging	Maturity	Yield
Mean	43.457	2.202	38.936	2466.769
Std Dev	10.171	0.872	6.532	490.070
Range	44.000	3.000	27.000	2616.981
CV	23.404	39.616	16.777	19.867

Table 5 Descriptive Statistics for LS97-1610 x Spencer planted in Dowell, IL in 2011

	Height	Lodging	Maturity	Yield
Mean	38.399	2.319	40.059	2658.534
Std Dev	7.017	0.804	4.393	627.059
Range	31.000	3.000	23.000	2935.967
CV	18.273	34.664	10.966	23.587

Table 6 Descruptive Statistics for Hamilton x Spencer planted in Harrisburg, IL in 2011

	Height	Lodging	Maturity	Yield
Mean	43.415	1.569	29.447	3103.423
Std Dev	3.855	0.654	3.569	299.985
Range	25.000	3.000	19.000	1705.595
CV	8.880	41.709	12.121	9.666

Table 7 Descriptive Statistics for LS90-1920 x Spencer planted in Harrisburg, IL in 2011

	Height	Lodging	Maturity	Yield
Mean	50.660	2.622	40.346	2892.475
Std Dev	8.843	1.024	6.962	340.218
Range	37.000	3.000	25.000	2037.60
CV	17.456	39.059	17.255	11.762

Table 8 Descriptive Statistics for LS97-1610 x Spencer planted in Harrisburg, IL in 2011

	Height	Lodging	Maturity	Yield
Mean	48.394	2.686	40.367	2878.589
Std Dev	6.325	0.932	6.518	434.938
Range	37.000	3.000	29.000	2935.967
CV	13.070	34.702	16.146	15.109

A. Hamilton x Spencer

i. Descriptive statistics

In Table 9 and Table 10 the means, standard deviation, and range were compared to the parental lines in different locations (Dowell and Harrisburg, IL) for the RIL Hamilton x Spencer for agronomic traits. The mean height for the RIL for plant height at Dowell, IL was significantly different from the parents at ($P<0.0001$). Plant height at Harrisburg, IL for the RIL was not significantly different than the parent line at ($P<0.05$). Maturity date after September 1 in

Harrisburg and Dowell, IL for the Hamilton x Spencer was not significantly different than the parents at (P<0.05) for Dowell, IL and Harrisburg, IL. The lodging score in Dowell, IL was significantly different than the parental lines at (P<0.0432). The lodging score in Harrisburg, IL is significantly different than the parents at (P<.0001). Seed yield ($kgha^{-1}$) mean for Hamilton x Spencer in Dowell, IL was not significantly different than the parents mean average at (P<0.05). Seed yield (kg/hectare) mean for Hamilton x Spencer was significantly different at (P <0.020).

Table 9 Agronomic characteristics (plant height, maturity and lodging) and seed yield in Hamilton x Spencer recombinant inbred line population and parental lines evaluated at Dowell, IL in 2011.

	Hamilton x Spencer (*n*=94)			**Parental lines (*n*=4)**				***t* test**
Trait	**Mean**	**SD**	**Range**	**Hamilton Mean**	**SD**	**Spencer Mean**	**SD**	**RI mean-Midparent**
Plant height (cm)	42.650	3.855	17.000	36.000	1.414	38.000	1.414	<.0001***
Maturity (d)	28.633	4.179	21.000	27.000	1.414	29.667	2.944	0.734ns
Lodging	1.830	0.719	3.000	1.000	0.000	1.500	0.548	0.043*
Seed yield (kg ha^{-1})	2667.052	415.966	2226.390	3137.774	303.811	2155.863	317.738	0.213ns

Table 10 Agronomic characteristics (plant height, maturity and lodging) and seed yield in Hamilton x Spencer recombinant inbred line population and parental lines evaluated at Harrisburg, IL in 2011.

	Hamilton x Spencer (*n*=94)			**Parental lines (*n*=4)**				***t* test**
Trait	**Mean**	**SD**	**Range**	**Hamilton Mean**	**SD**	**Spencer Mean**	**SD**	**RI mean-Midparent**
Plant height (cm)	43.415	3.855	25.000	37.500	4.950	42.167	2.563	0.101ns
Maturity (d)	29.447	3.569	19.000	27.500	3.536	28.500	1.871	0.167ns
Lodging	1.569	0.654	3.000	1.500	0.707	1.000	0.000	<.0001***
Seed yield (kg ha^{-1})	3103.423	299.985	1705.600	3326.561	18.413	2659.296	238.470	0.002**

* Significant at P <0.05 probability level
** Significant at P < 0.01 probability level
*** Significant at P < 0.001 probability level

ii. Frequency Distributions

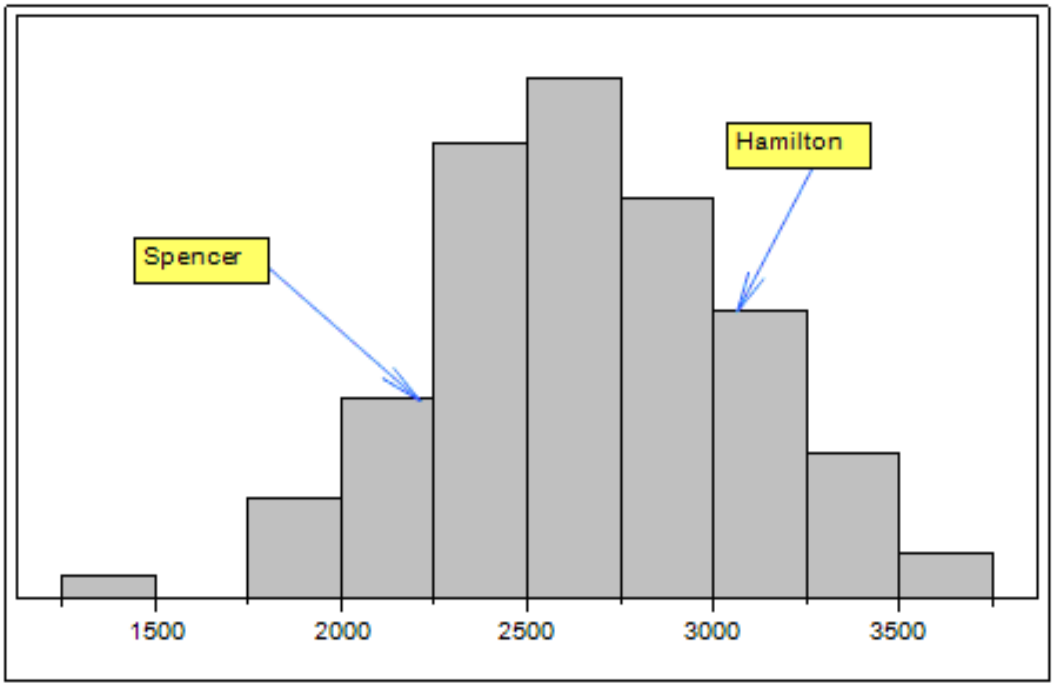


Figure 13 Frequency Distribution for Yield Hamilton x Spencer, Hamilton, and Spencer grown in Dowell, IL in 2011

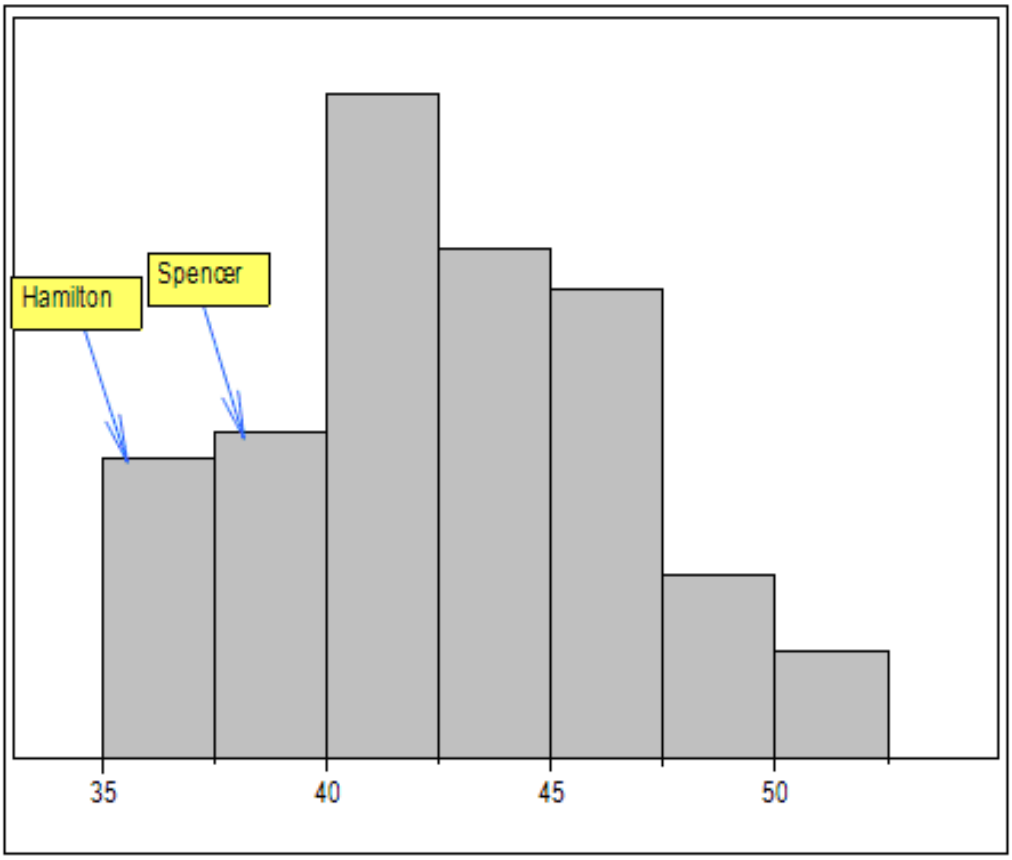


Figure 14 Frequency Distribution for Height (cm) Hamilton x Spencer, Hamilton, and Spencer grown in Dowell, IL in 2011

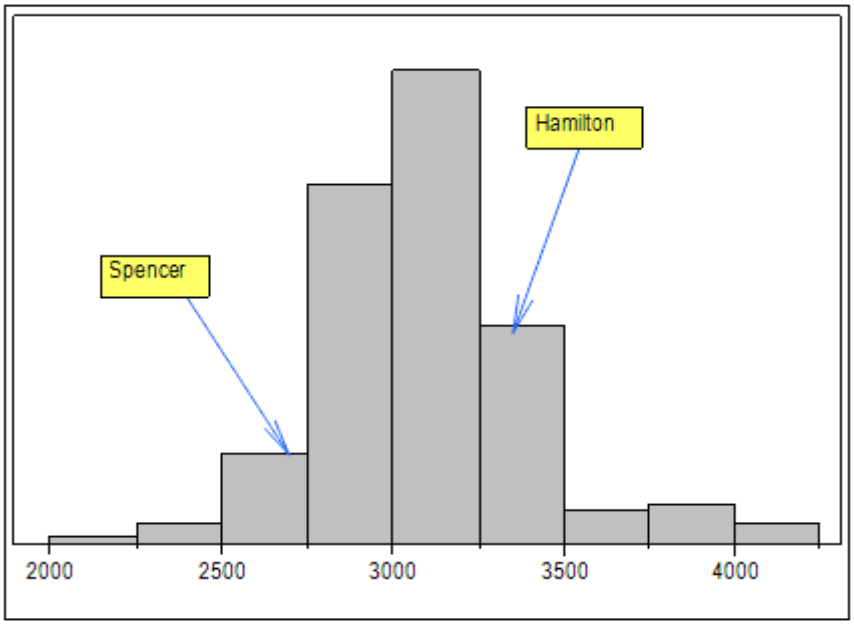


Figure 15 Frequency Distribution for Yield Hamilton x Spencer, Hamilton, and Spencer grown in Harrisburg, IL in 2011

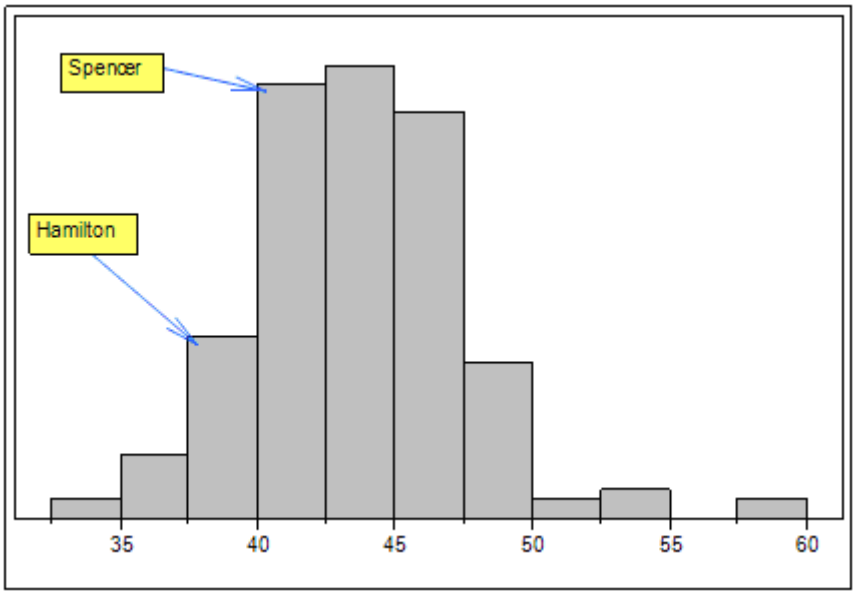


Figure 16 Frequency Distribution for Plant height in cm Hamilton x Spencer, Hamilton, and Spencer grown in Harrisburg, IL in 2011

iii. Genotype Differences and Genotype x Environment Interactions

There were significant differences in the genotype, location, and genotype x location for 'Hamilton x Spencer' for plant height in cm, maturity date, lodging, and seed yield (kg ha^{-1}) (Table 11). The heritability of 'Hamilton x Spencer' was driven by genetics with the broad sense heritability score above 70% for plant height, maturity date, and lodging. The seed yield was influenced more by a mixture of environment and genetics, with a heritability score of 46% (Table 11).

Table 11 Analysis of variance (*P* values) and heritability estimates of agronomic characteristics and seed yield in Hamilton x Spencer recombinant inbred population grown at Dowell and Harrisburg, IL in 2011

	Source of variation			
Trait	**Genotype**	**Location**	**Genotype x Location**	**h^2(%)**
Plant height (cm)	<.0001***	0.0059**	0.0409*	73.33
Maturity (d)	<.0001***	0.0001***	0.0011**	86.54
Lodging	<.0001***	<.0001***	0.1347ns	81.52
Seed yield (kg ha^{-1})	<.0001***	<.0001***	0.0001***	46.08

* Significant at P <0.05 probability level
** Significant at P < 0.01 probability level
*** Significant at P < 0.001 probability level

B. LS97-1610 x Spencer

i. Descriptive statistics

In Table 12 and Table 13, the means, standard deviation, and range were compared to the parental lines in different locations (Dowell and Harrisburg, IL) for LS97-1610 x Spencer. The mean height for LS97-1610 x Spencer for plant height at Dowell, IL was not significantly different than the parents at ($P<0.05$). Plant height at Harrisburg, IL for the LS97-1610 x Spencer was significantly different than the parental lines at ($P< 0.0002$). Maturity date after September 1 in Harrisburg and Dowell, IL for LS97-1610 x Spencer were significantly different from the parental lines at ($P<0.0035$) for Dowell, IL and a $P<0.0028$ for Harrisburg, IL. Lodging score in Dowell, IL was significantly different than the parental lines at ($P<0.0062$). The lodging score in Harrisburg, IL was significantly different than the parental lines at ($P<0.0001$). Seed yield ($kgha^{-1}$) mean for LS97-1610 x Spencer in Dowell, IL was significantly different from the parental lines at ($P<0.0047$). The seed yield ($kgha^{-1}$) in Harrisburg, IL for LS97-1610 x Spencer was not significantly different from the parental lines at ($P<0.05$).

Table 12 Agronomic characteristics (plant height, maturity and lodging) and seed yield in LS97-1610 recombinant inbred line population and parental lines evaluated at Dowell, IL in 2011.

	LS97-1610 x Spencer (*n*=94)			**Parental lines (*n*=4)**				***t* test**
Trait	**Mean**	**SD**	**Range**	**LS97-1610 Mean**	**SD**	**Spencer Mean**	**SD**	**RI mean-Midparent**
Plant height (cm)	38.90	7.02	31	22	2.83	38	1.41	0.148ns
Maturity (d)	40.06	4.40	23	39.5	2.12	29.67	2.94	0.0035**
Lodging	2.69	0.93	3	2	0	1.5	0.55	0.0062**
Seed yield (kg ha^{-1})	2658.53	627.06	2935.97	1220.61	188.73	2155.86	317.74	0.0047**

* Significant at P <0.05 probability level
** Significant at P < 0.01 probability level
*** Significant at P < 0.001 probability level

Table 13 Agronomic characteristics (plant height, maturity and lodging) and seed yield in LS97-1610 x Spencer recombinant inbred line population and parental lines evaluated at Harrisburg, IL in 2011.

	LS97-1610 x Spencer (*n*=94)			**Parental lines (*n*=4)**				***t* test**
Trait	**Mean**	**SD**	**Range**	**LS97-1610 Mean**	**SD**	**Spencer Mean**	**SD**	**RI mean-Midparent**
Plant height (cm)	48.394	6.33	37	37	2.83	42.17	2.56	0.0002***
Maturity (d)	40.37	6.52	29	40	4.25	28.5	1.87	0.0028**
Lodging	2.69	0.93	3	2	0	1	0	<.0001***
Seed yield (kg ha^{-1})	2878.59	299.99	2935.97	3831.078	59.84	2659.30	238.47	0.7332

* Significant at P <0.05 probability level
** Significant at P < 0.01 probability level
*** Significant at P < 0.001 probability level

ii. Frequency Distributions

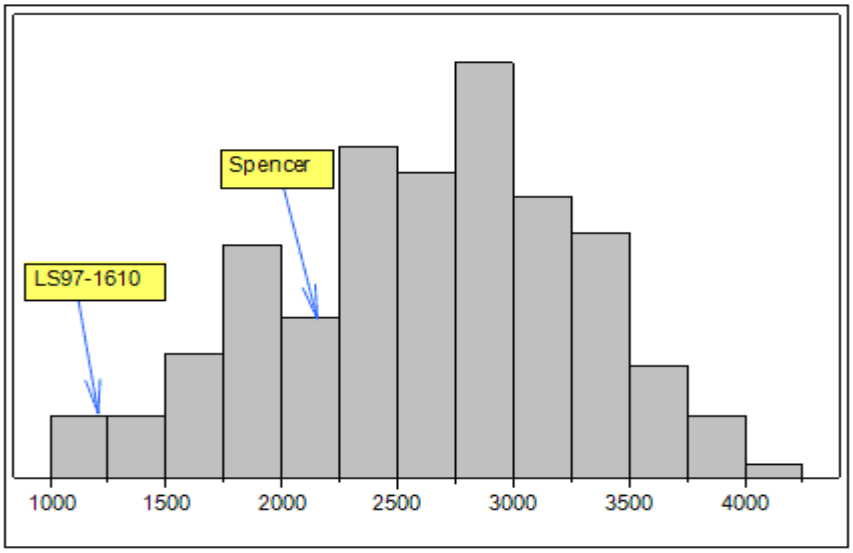


Figure 17 Frequency Distribution for Yield LS97-1610 x Spencer, LS97-1610, and Spencer grown in Dowell, IL in 2011

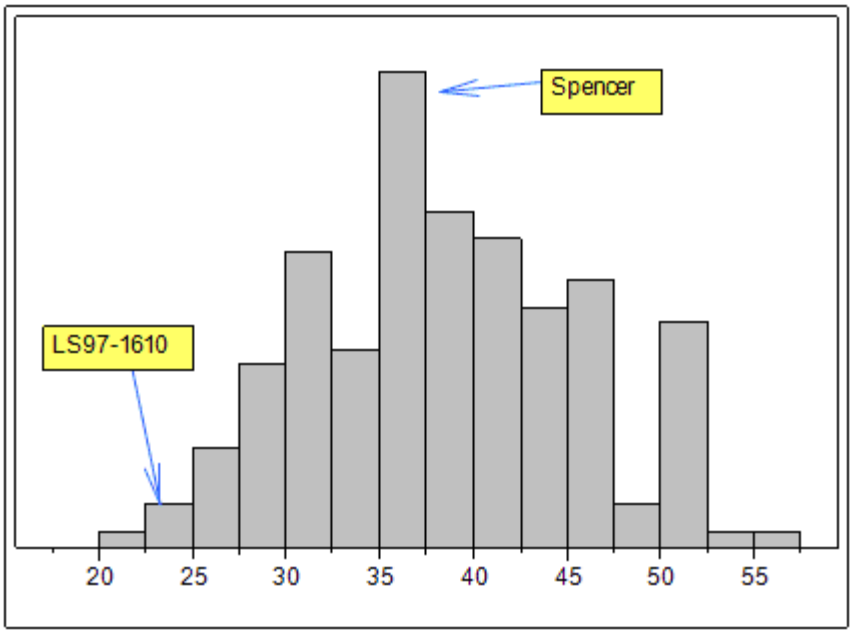


Figure 18 Frequency Distribution for Height (cm) LS97-1610 x Spencer, LS97-1610, and Spencer grown in Dowell, IL in 2011

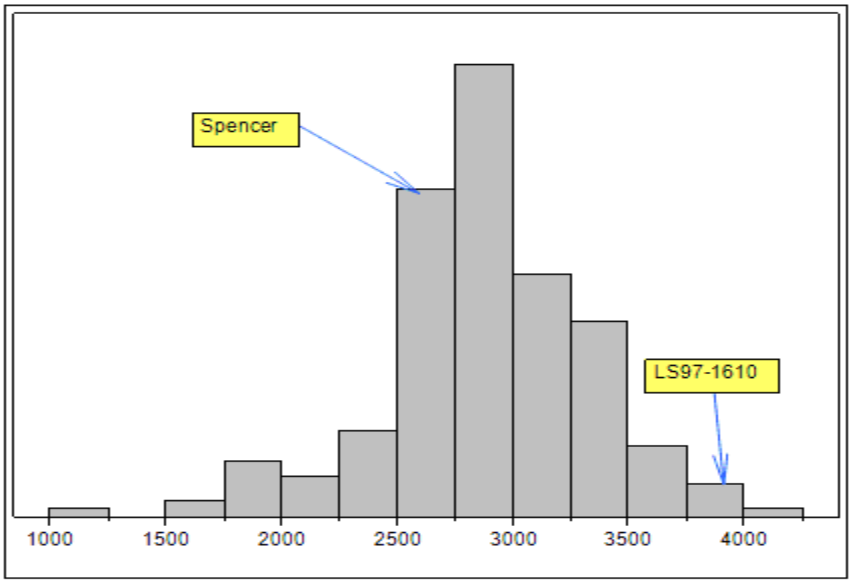


Figure 19 Frequency Distribution for Yield LS97 x Spencer, LS97-1610, and Spencer grown in Harrisburg, IL in 2011

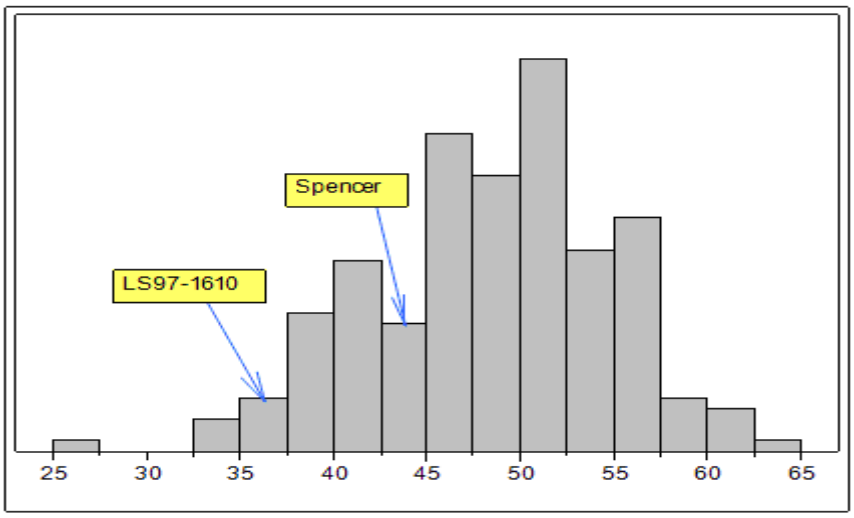


Figure 20 Frequency Distribution for Height (cm) LS97-1610 x Spencer, LS97-1610, and Spencer grown in Harrisburg, IL in 2011

iii. Genetic variation and correlation coefficients

The correlation between yield ($kgha^{-1}$) and height (cm) was significant at ($P<0.0001$). Maturity date and lodging can not be compared to plant height (cm) and yield ($kgha^{-1}$) as they are ordinal data and plant height and yield are continuous data. The R value for this correlation is 0.2457 and an R^2 value of 0.0604.

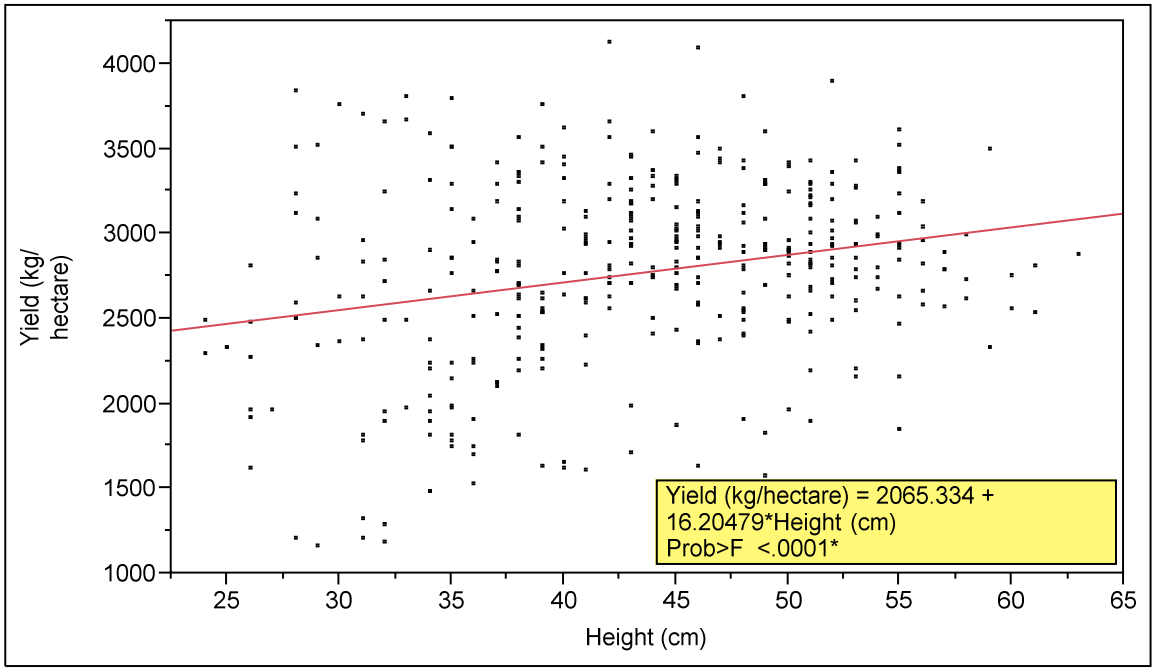


Figure 21 Line fit Yield (kg/hectare) by Height cm for LS97-1610 x Spencer

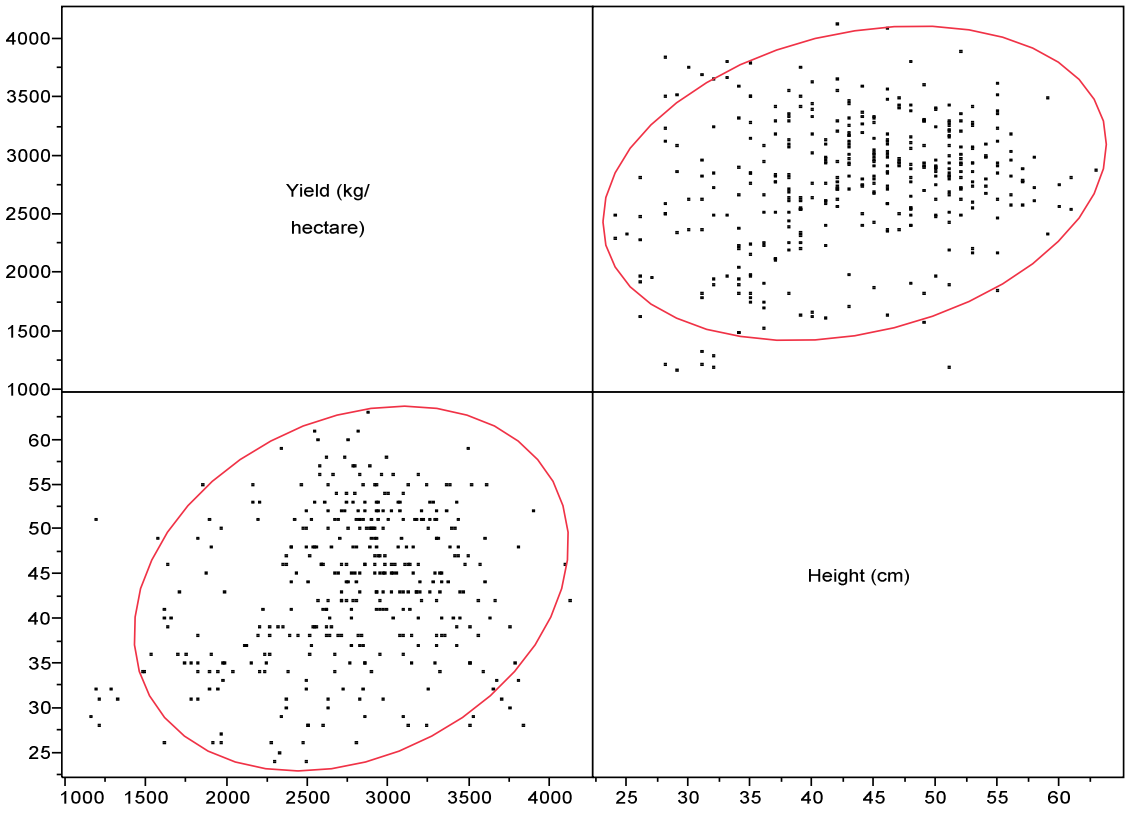


Figure 22 Multivariate Plot of Yield (kg/hectare) to Height (cm) in LS97-1610 x Spencer

iv. Genotype Differences and Genotype x Environment Interactions

Table 14 Analysis of variance (*P* values) and heritability estimates of agronomic characteristics and seed yield in LS97-1610 x Spencer recombinant inbred population grown at Dowell and Harrisburg, IL in 2011.

	Source of variation			
Trait	**Genotype**	**Location**	**Genotype x Location**	**H^2(%)**
Plant height (cm)	<.0001*	<.0001*	0.2306	70.37
Maturity (d)	<.0001*	0.0727	<.0001*	90.83
Lodging	<.0001*	<.0001*	<.0001*	80.23
Seed yield (kg ha^{-1})	<.0001*	<.0001*	<.0001*	34.85

There were significant differences in the genotype, location, and genotype x location for LS97-1610 x Spencer for maturity date, lodging, and seed yield (kg ha^{-1}). There were significant differences in genotype and location for plant height in cm. The heritability of LS97-1610 x Spencer was driven by genetics with the broad sense heritability score above 70% for the trait of plant height in cm, maturity date, and lodging. The seed yield was influenced mostly by environment, with a heritability score of 34%.

C. LS90-1920 x Spencer

Table 15 Agronomic characteristics (plant height, maturity and lodging) and seed yield in LS90-1920 recombinant inbred line population and parental lines evaluated at Dowell, IL in 2011.

	LS90-1920 x Spencer (*n*=94)			**Parental lines (*n*=4)**				***t* test**
Trait	**Mean**	**SD**	**Range**	**LS90-1920 Mean**	**SD**	**Spencer Mean**	**SD**	**RI mean-Midparent**
Plant height (cm)	43.46	10.17	44	28	4.25	38	1.41	0.0023*
Maturity (d)	38.94	6.53	27	41	0	29.67	2.94	0.0163*
Lodging	2.20	0.87	3	1	0	1.5	0.55	0.0022*
Seed yield (kg ha^{-1})	2466.77	490.07	2616.99	2766.71	46.03	2155.86	317.74	0.3059

Table 16 Agronomic characteristics (plant height, maturity and lodging) and seed yield in LS90-1920 x Spencer recombinant inbred line population and parental lines evaluated at Harrisburg, IL in 2011.

	LS90-1920 x Spencer (*n*=94)			**Parental lines (*n*=4)**				***t* test**
Trait	**Mean**	**SD**	**Range**	**LS90-1920 Mean**	**SD**	**Spencer Mean**	**SD**	**RI mean-Midparent**
Plant height (cm)	50.66	8.84	37	38.5	0.71	42.17	2.56	<.0001*
Maturity (d)	40.35	6.96	25	35	0	28.5	1.88	<.0001*
Lodging	2.62	1.02	3	2	0	1	0	<.0001*
Seed yield (kg ha^{-1})	2892.48	340.22	2037.60	3404.68	9.21	2659.30	238.47	0.7531

i. Descriptive statistics

In Table 15 and Table 16, the means, standard deviation, and range were compared to the parental lines in different locations (Dowell and Harrisburg, IL) for the RIL LS90-1920 x Spencer. The plant height for the LS90-1920 x Spencer at Dowell and Harrisburg, IL were significantly different from the parents at ($P<0.0023$) for Dowell, IL and $P<.0001$) for Harrisburg, IL. Maturity date after September 1 in Dowell and Harrisburg, IL for the LS90-1920 was significantly different from the parental lines at ($P<0.0163$) for Dowell, IL and $P<.0001$) for Harrisburg, IL. Lodging score in Dowell and Harrisburg, IL was significantly different from the parental lines at ($P<0.0022$) for Dowell, IL and $P<.0001$) for Harrisburg, IL. The seed yield ($kgha^{-1}$) in Dowell and Harrisburg, IL for LS90-1610 was not significantly different from the parental lines at ($P<0.05$).

ii. Frequency Distributions

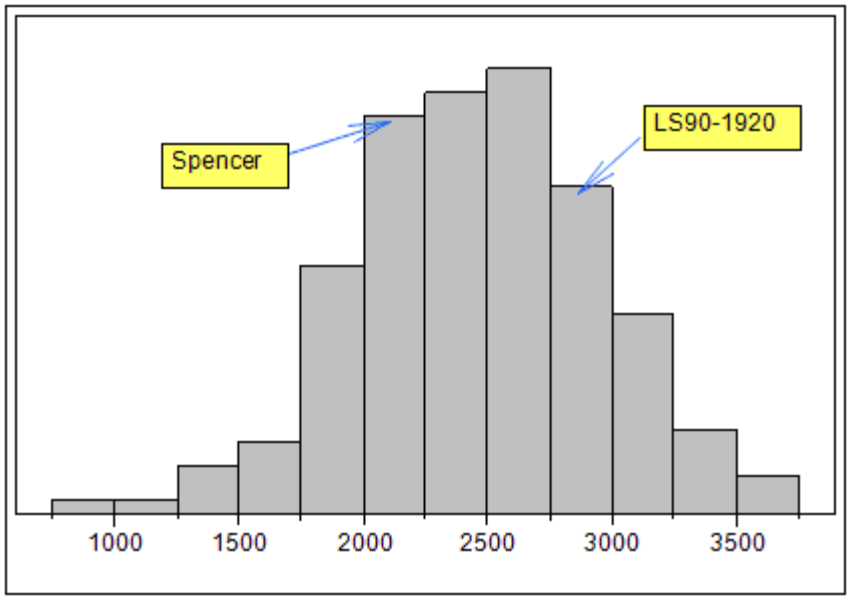


Figure 23 Frequency Distribution for Yield LS90-1920 x Spencer, LS90-1610, and Spencer grown in Dowell, IL in 2011

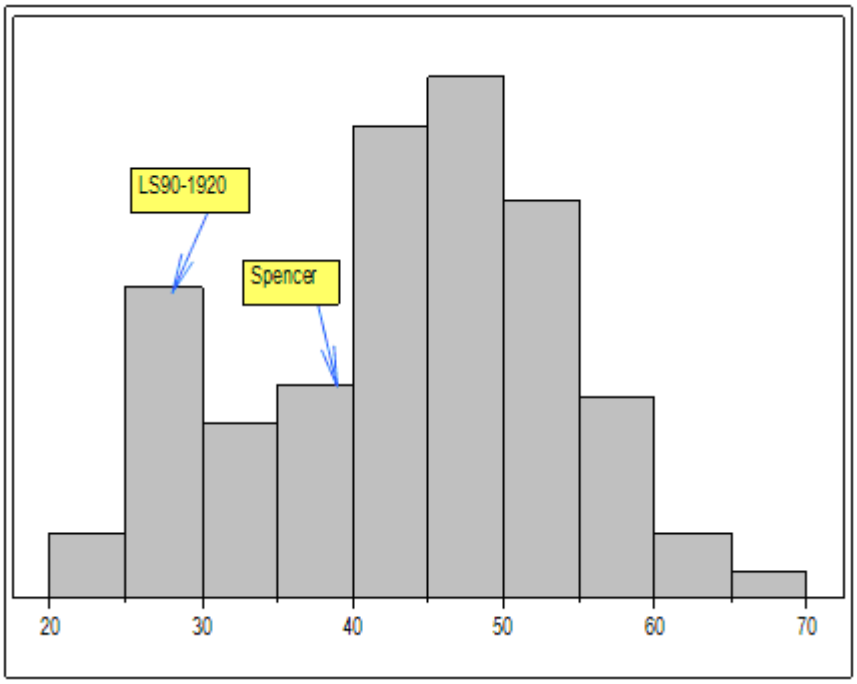


Figure 24 Frequency Distribution for Height (cm) LS90-1920 x Spencer, LS90-1920, and Spencer grown in Dowell, IL in 2011

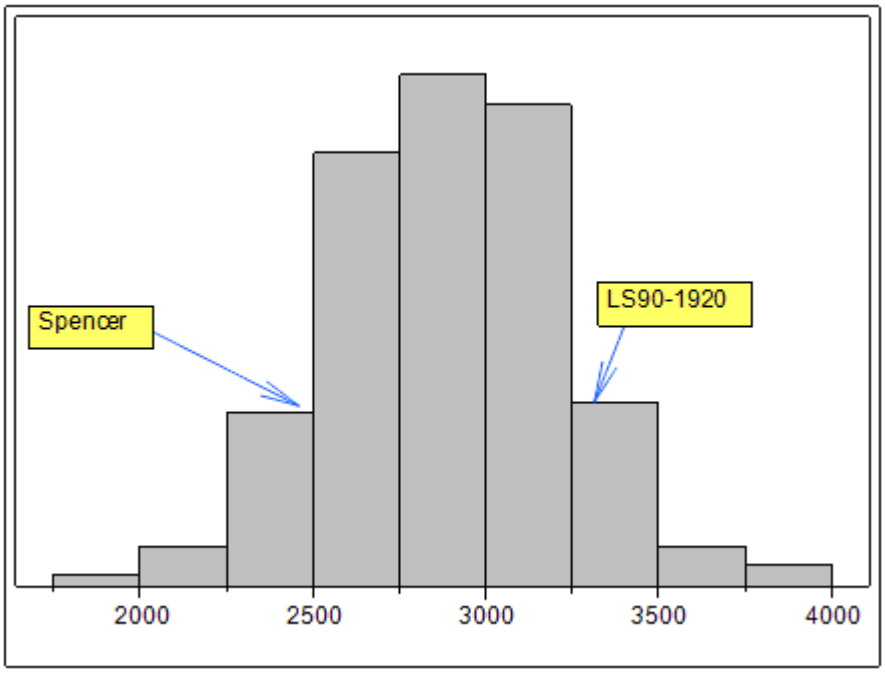


Figure 25 Frequency Distribution for Yield LS90-1920 x Spencer, LS90-1920, and Spencer grown in Harrisburg, IL in 2011

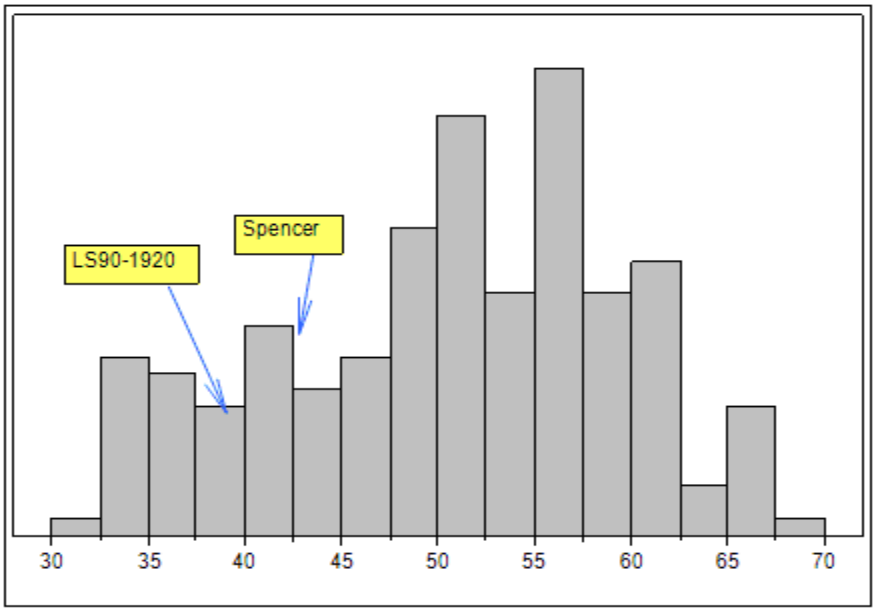


Figure 26 Frequency Distribution for Height (cm) LS90-1920 x Spencer, LS90-1920, and Spencer grown in Harrisburg, IL in 2011

iii. Genetic variation and correlation coefficients

The correlation between yield ($kgha^{-1}$) and height (cm) was significant at ($P<0.0001$). Maturity date and lodging can not be compared to plant height (cm) and yield ($kgha^{-1}$) as they are ordinal data and plant height and yield are continuous data. The R value for this correlation is 0.2716 and an R^2 value of 0.0738.

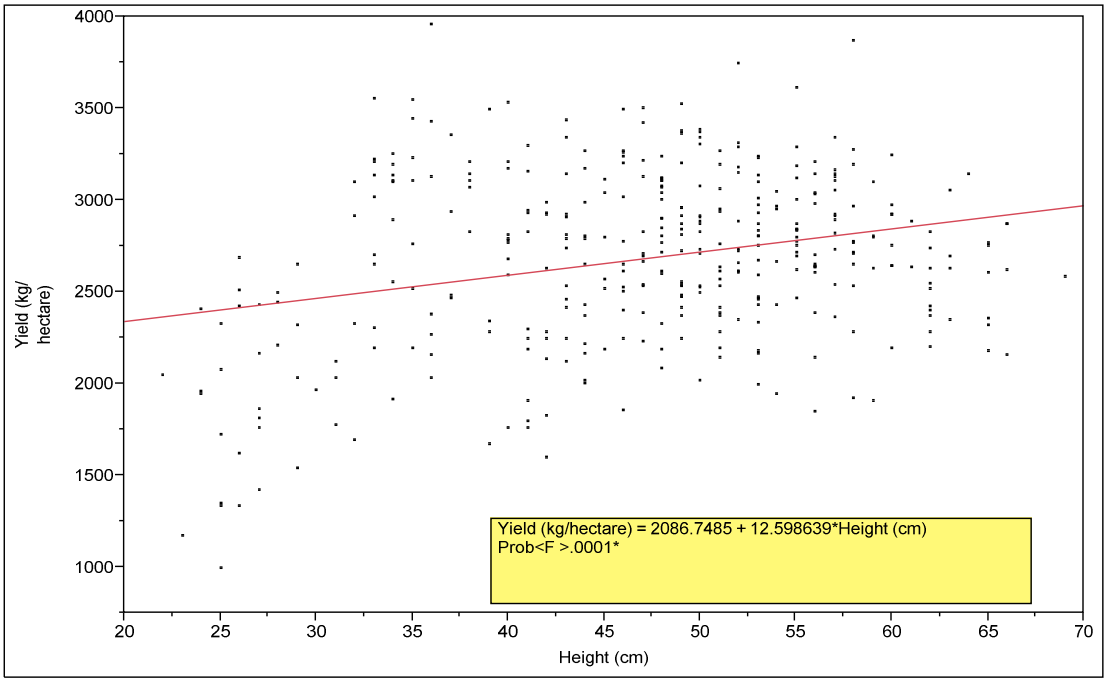


Figure 27 Line fit Yield (kg/hectare) by Height cm for LS90-1920 x Spencer

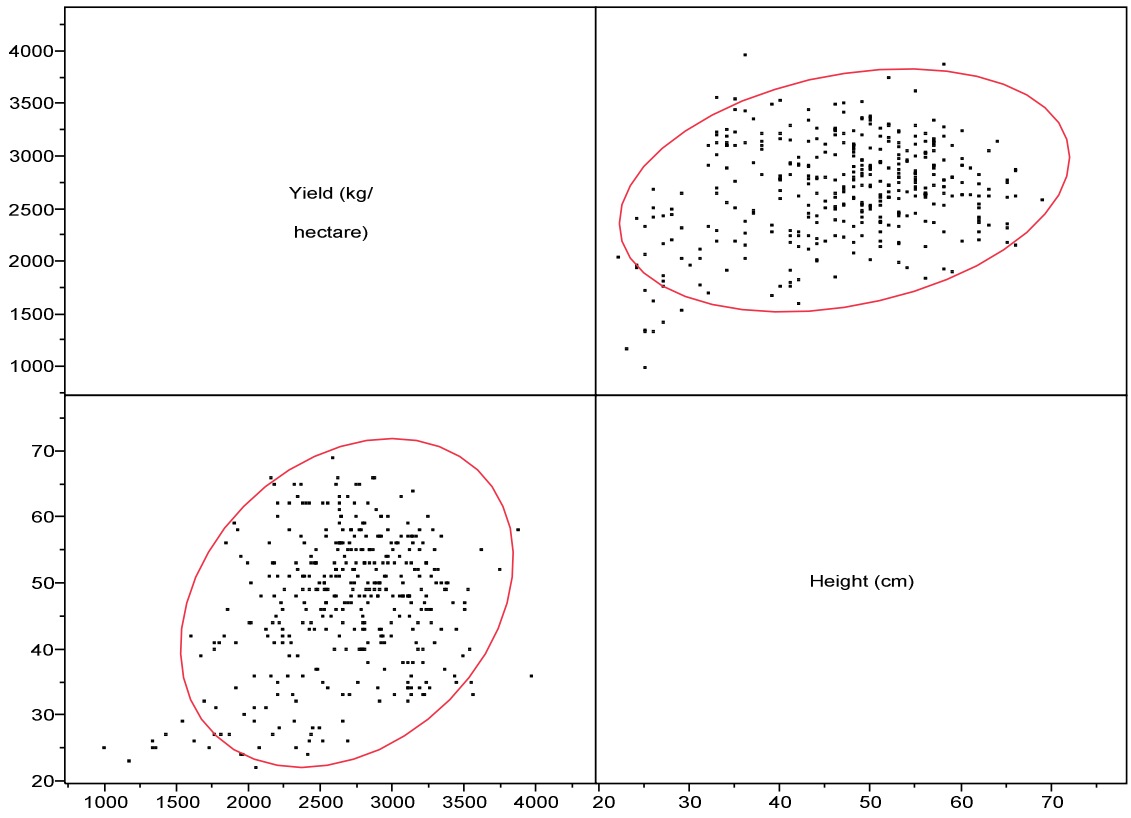


Figure 28 Multivariate of Yield (kg/hectare) to Height (cm) in LS90-1920 x Spencer

iv. Genotype Differences and Genotype x Environment Interactions

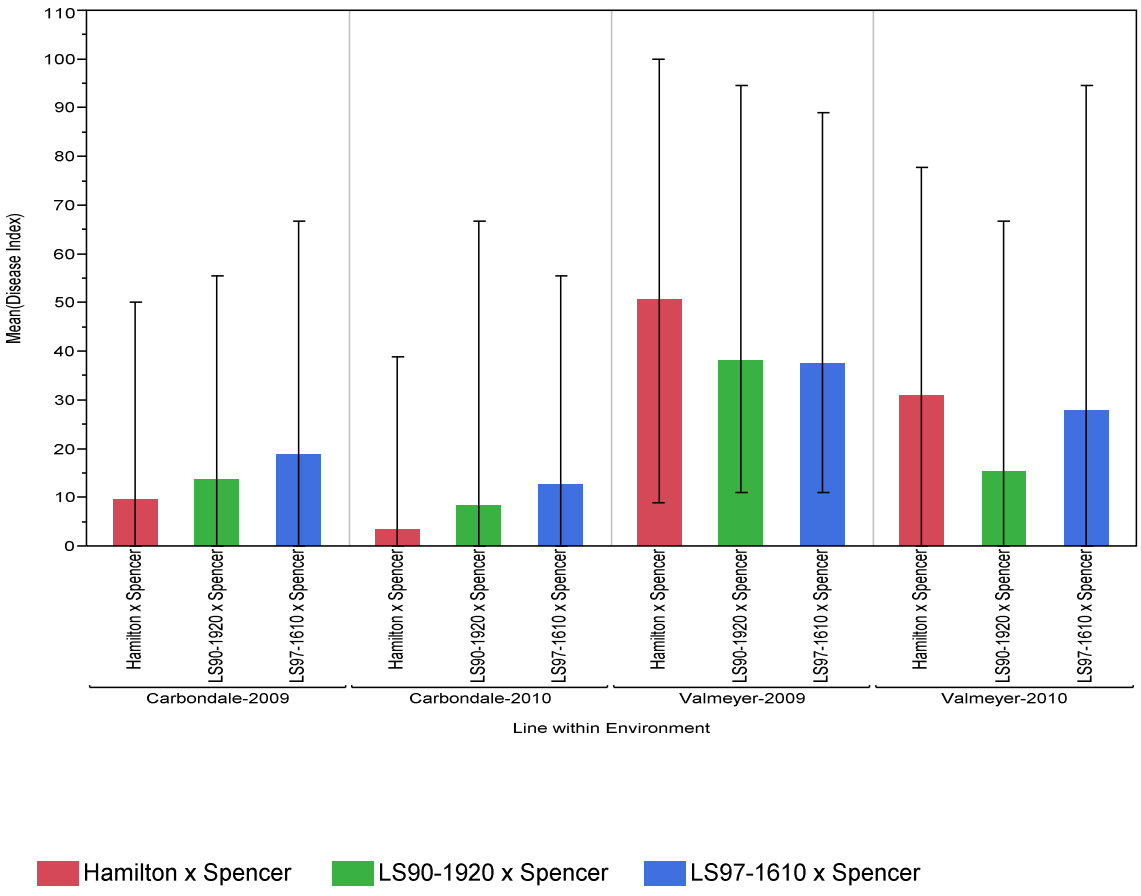
Table 17 Analysis of variance (*P* values) and heritability estimates of agronomic characteristics and seed yield in LS97-1610 x Spencer recombinant inbred population grown at Dowell and Harrisburg, IL in 2011.

	Source of variation			
Trait	**Genotype**	**Location**	**Genotype x Location**	**H^2(%)**
Plant height (cm)	<.0001*	<.0001*	0.1184	85.18
Maturity (d)	<.0001*	<.0001*	<.0001*	94.80
Lodging	<.0001*	<.0001*	<.0001*	84.72
Seed yield (kg ha^{-1})	<.0001*	<.0001*	<.0001*	0.00

There were significant differences in the genotype, location, and genotype x location for LS90-1920 x Spencer for maturity date, lodging, and seed yield (kg ha^{-1}). There were significant differences in genotype and location for plant height in cm. The heritability of LS90-1920 x Spencer was driven by genetics with the broad sense heritability score above 80% for the trait of plant height in cm, maturity date, and lodging. The seed yield was driven by location, with a heritability score of 0%.

2. Evaluation of recombinant inbred populations for resistance to sudden death syndrome

The disease index (DX) grand mean for all RIL for Carbondale, IL in 2009 and 2010 was between 0 and 20. The DX grand mean for all RIL for Valmeyer, IL for 2009 and 2010 was between 15 and 50.



Each error bar is constructed using the min and max of the data.

Figure 29 Disease index of three recombinant inbred populations (Hamilton x Spencer, LS90-1920 x Spencer and LS97-1610 x Spencer) grown in Carbondale and Valmeyer IL in 2009 and 2010

A. Hamilton x Spencer

i. Resistance reaction

Table 18 shows the mean, P value, and CV of Hamilton x Spencer in Carbondale, IL and Valmeyer, IL for the years 2009, 2010, and the two year average for each site. There was significant differences within Hamilton x Spencer for 2009 in Carbondale, IL at (P<0.0287). There was not significant differences within Hamilton x Spencer for 2010 in Carbondale at (P<0.05). There was significant differences within Hamilton x Spencer for the two year average in Carbondale, IL at (P<0.0015). There was not any significant differences within Hamilton x Spencer for 2009 in Valmeyer, IL at (P<0.05). There was not any significant differences within Hamilton x Spencer for 2010 in Valmeyer at (P<0.05). There was significant differences within Hamilton x Spencer for the two year average in Valmeyer, IL at (P<0.0001).

Table 18 Means, coefficients of variation, and *P* values of DX in Hamilton Spencer recombinant inbred line population grown in Carbondale and Valmeyer, IL (2009 and 2010)

	Carbondale			**Valmeyer**		
Statistics	**2009**	**2010**	**2-yr combined**	**2009**	**2010**	**2-yr combined**
Mean (±SD)	**13.899**	**8.183**	**11.044**	**42.049**	**24.915**	**33.520**
***P* value**	**0.0287***	**0.1571**	**0.0015***	**0.0701**	**0.0908**	**<.0001***
CV	**96.652**	**141.025**	**116.271**	**50.035**	**83.039**	**67.270**

ii. Frequency Distribution

Frequency distributions for DX for Hamilton x Spencer are heavily skewed positively. In order to make the data more normal, a logarithmic transformation was suggested by Dr. Njiti. Frequency data unaltered and transformed are presented to show effect of the transformation.

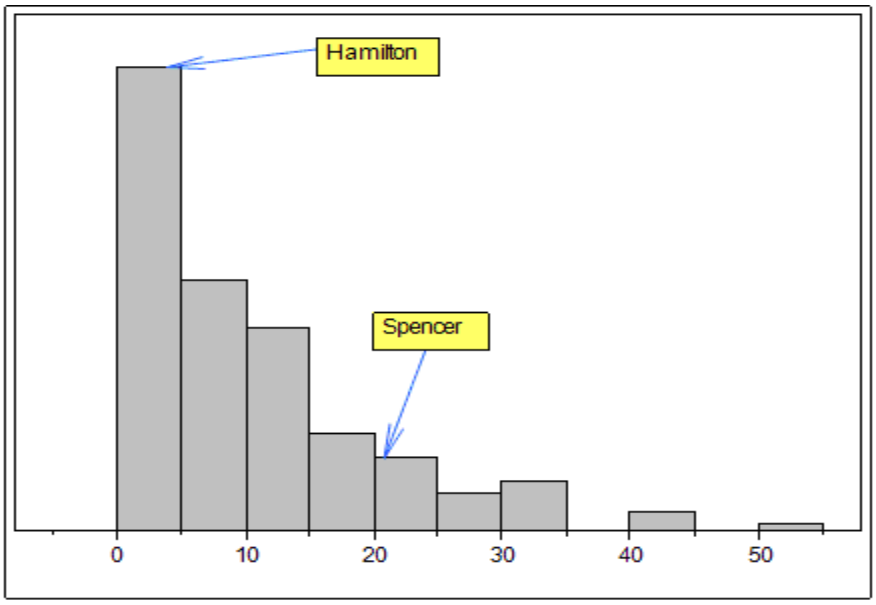


Figure 30 Frequency Distribution for DX not transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Carbondale, IL in 2009

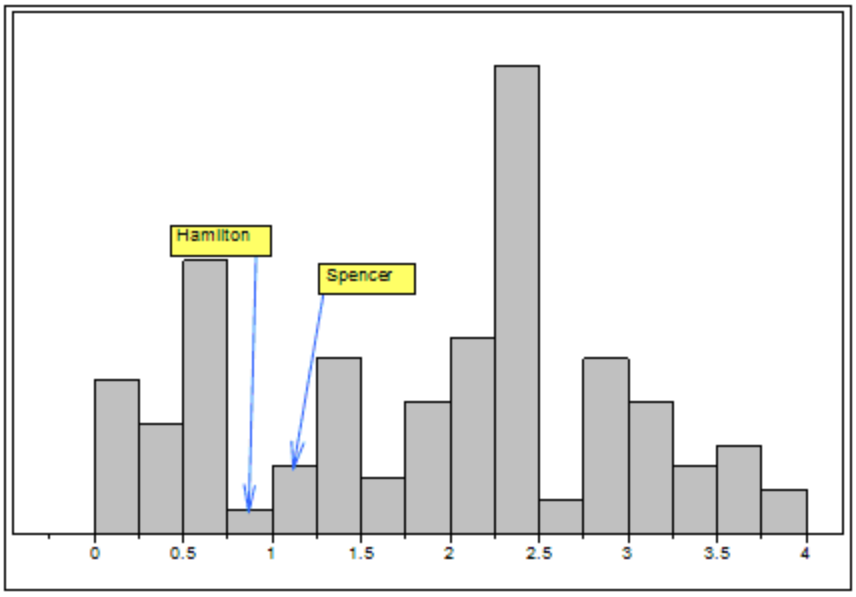


Figure 31 Frequency Distribution for DX log transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Carbondale, IL in 2009

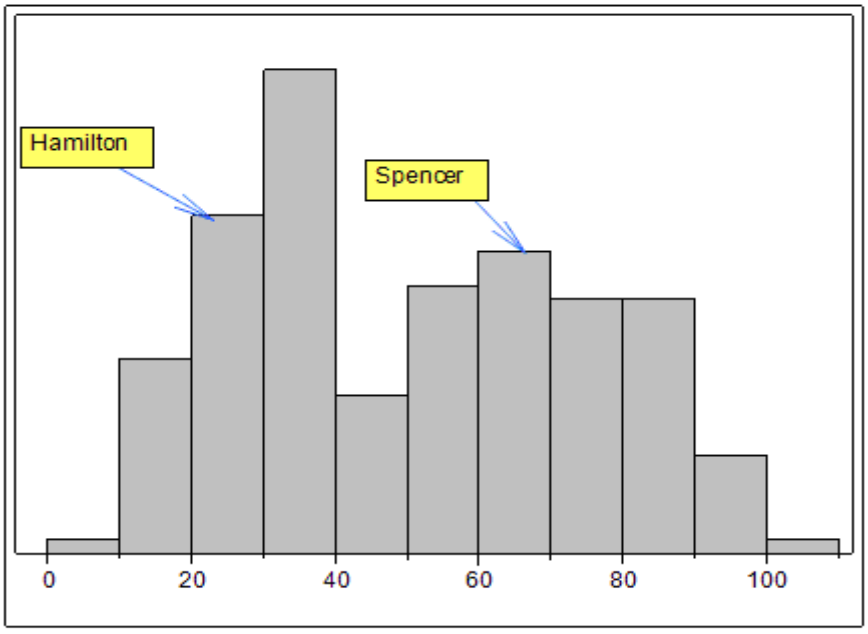


Figure 32 Frequency Distribution for DX not transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Valmeyer, IL in 2009

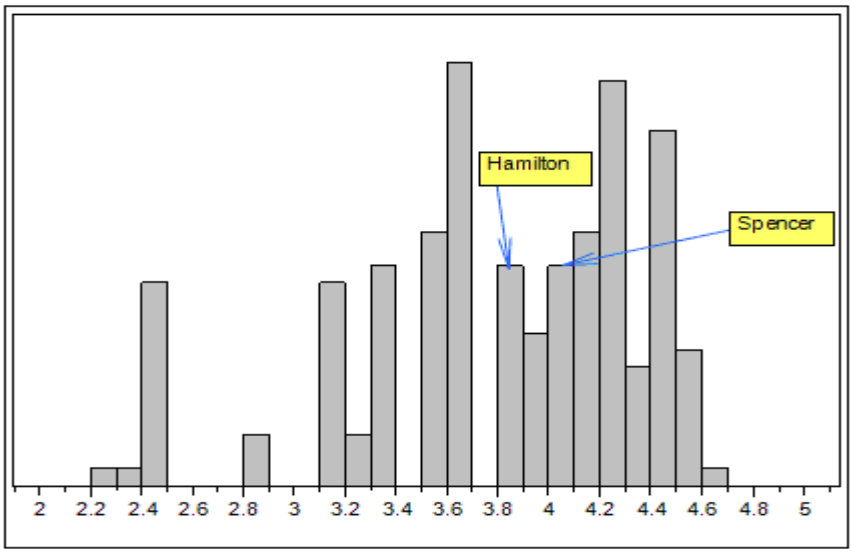


Figure 33 Frequency Distribution for DX log transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Valmeyer, IL in 2009

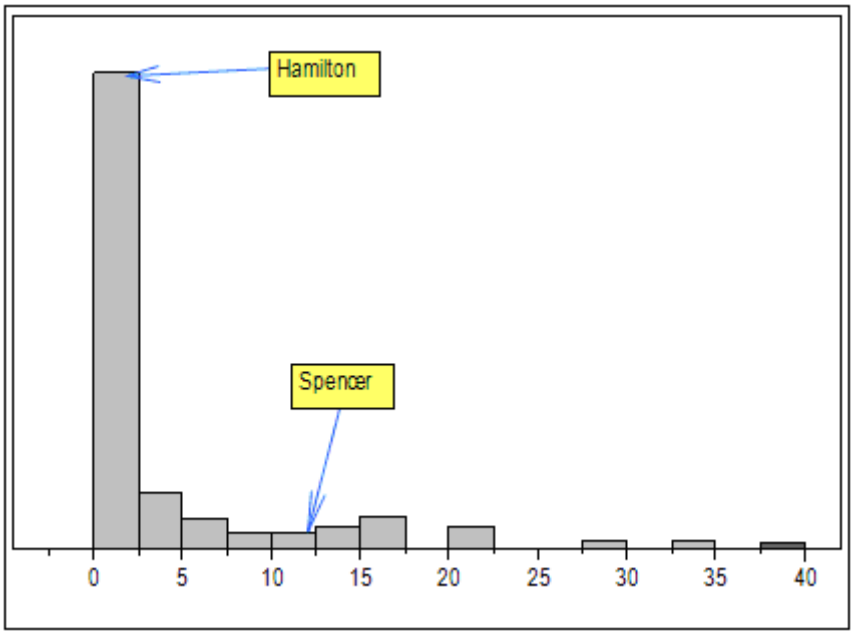


Figure 34 Frequency Distribution for DX not transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Carbondale, IL in 2010

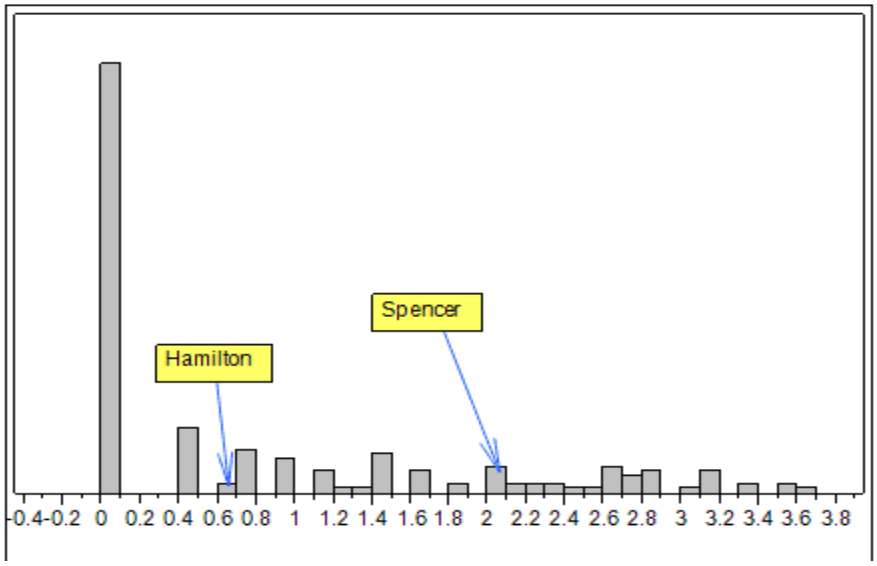


Figure 35 Frequency Distribution for DX log transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Carbondale, IL in 2010

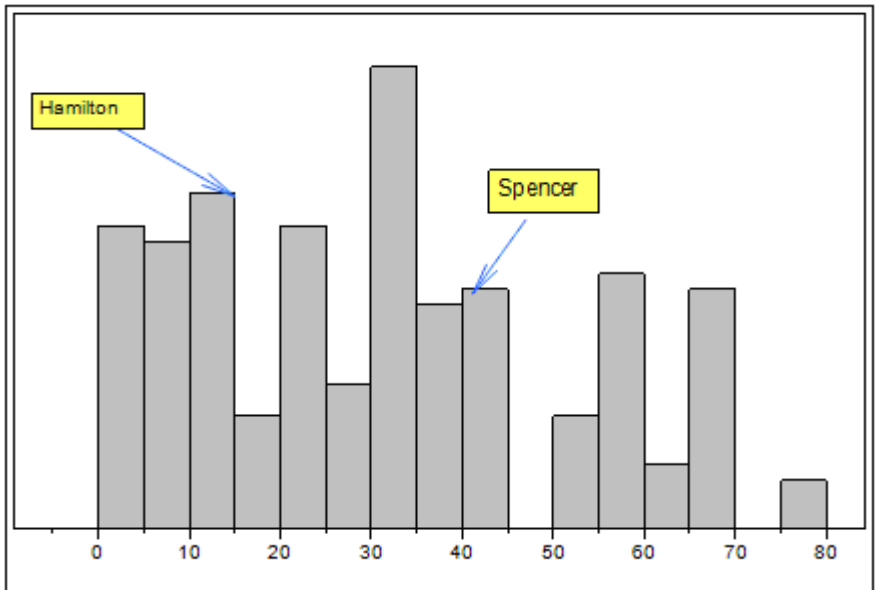


Figure 36 Frequency Distribution for DX not transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Valmeyer, IL in 2010

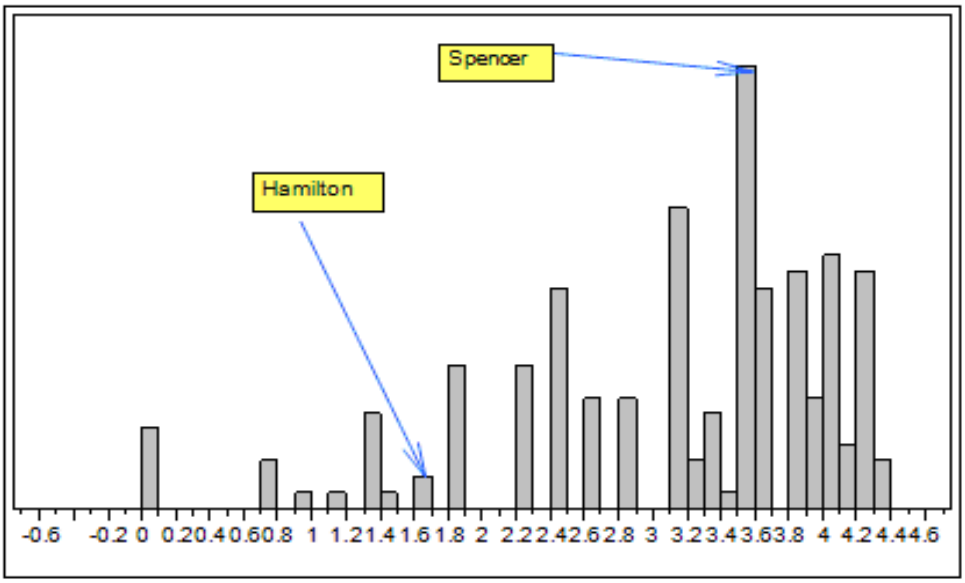


Figure 37 Frequency Distribution for DX log transformed for Hamilton x Spencer, Hamilton, and Spencer grown in Valmeyer, IL in 2010

Table 19 Mean, Standard Deviation, and Range for Transformed Data Hamilton x Spencer

	Carbondale 2009	**Carbondale 2010**	**Valmeyer 2009**	**Valmeyer 2010**
Mean	1.913	0.836	3.810	3.130
Std Dev	1.034	1.086	0.564	0.989
Range	3.932	3.686	2.324	4.367

Table 20 Mean, Standard Deviation, and Range for Hamilton x Spencer

	Carbondale 2009	Carbondale 2010	Valmeyer 2009	Valmeyer 2010
Mean	9.758	3.764	50.703	31.002
Std Dev	10.038	7.137	24.149	20.600
Range	50.000	38.889	91.111	77.778

iii. Genotypic Differences and Genotype x Environment Interactions

The genotype was significant for DX for the line Hamilton x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL at ($P<0.0001$). The location was significant for DX for the line Hamilton x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL at ($P<0.0001$). The interaction between genotype and location was significant for DX for the line Hamilton x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL at ($P<0.0001$). The broad sense heritability for the line Hamilton x Spencer was 0%.

Table 21 Analysis of variance (*P* values) and heritability estimates of Disease Index Hamilton x Spencer recombinant inbred population grown at Carbondale and Valmeyer, IL in 2009 and 2010.

	Source of variation DX			
Trait	**Genotype**	**Location**	**Genotype x Location**	**H^2(%)**
DX	<.0001*	<.0001*	<.0001*	0.00

H^2 broad sense heritability (%) estimated from ANOVA

B. LS97-1610 x Spencer

i. Resistance reaction

Table 22 shows the mean, P value, and CV of LS97-1610 x Spencer in Carbondale, IL and Valmeyer, IL for the years 2009, 2010, and the two year average for each site. There was significant differences within LS97-1610 x Spencer for 2009 in Carbondale, IL at (P<0.0001). There was significant differences within LS97-1610 x Spencer for 2010 in Carbondale at (P<0.0001). There was significant differences within LS97-1610 x Spencer for the two year average in Carbondale, IL at (P<0.0001). There was significant differences within LS97-1610 x Spencer for 2009 in Valmeyer, IL at (P<0.0212). There was significant differences within LS97-1610 x Spencer for 2010 in Valmeyer at (P<0.0001). There was significant differences within LS97-1610 x Spencer for the two year average in Valmeyer, IL at (P<0.0001).

Table 22 Means, coefficients of variation, and *P* values of DX in LS97-1610 x Spencer recombinant inbred line population grown in Carbondale and Valmeyer, IL (2009 and 2010)

	Carbondale			Valmeyer		
Statistics	**2009**	**2010**	**2-yr combined**	**2009**	**2010**	**2-yr combined**
Mean (±SD)	**18.610**	**12.572**	**15.591**	**37.530**	**27.816**	**32.673**
***P* value**	**<.0001***	**<.0001***	**<.0001***	**0.0212***	**<.0001***	**<.0001***
CV	**84.525**	**108.784**	**96.379**	**41.992**	**80.618**	**61.080**

ii. Frequency Distribution

Frequency distributions for DX for LS97-1610 x Spencer are heavily skewed positively. In order to make data more normal, a logarithmic transformation was suggested by Victor Njiti. Frequency data unaltered and transformed are presented to show effect of the transformation.

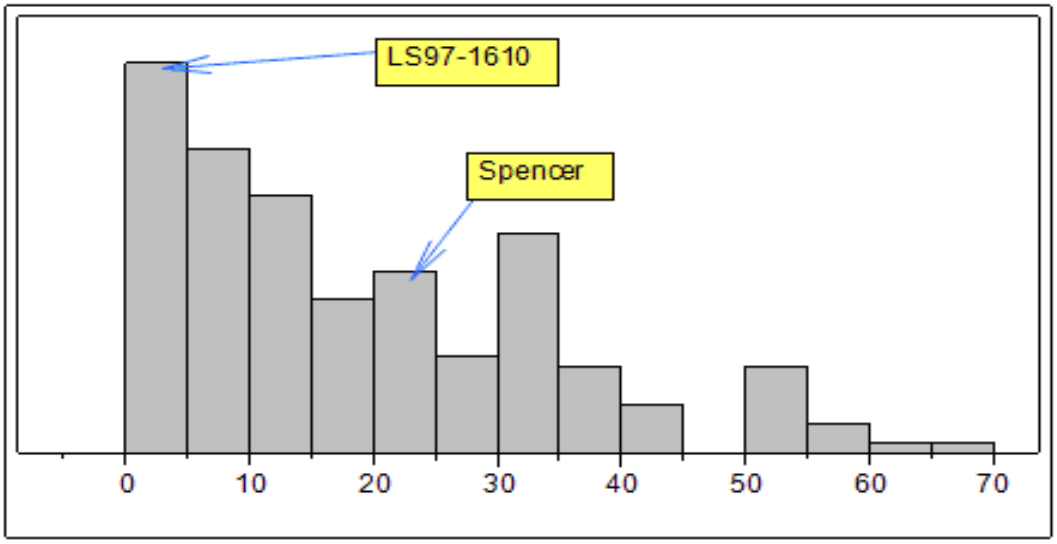


Figure 38 Frequency Distribution for DX not transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Carbondale, IL in 2009

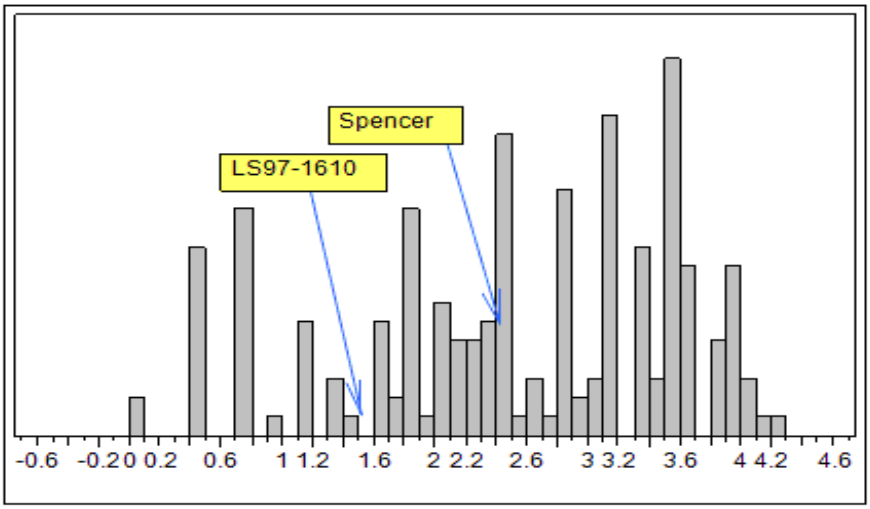


Figure 39 Frequency Distribution for DX log transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Carbondale, IL in 2009

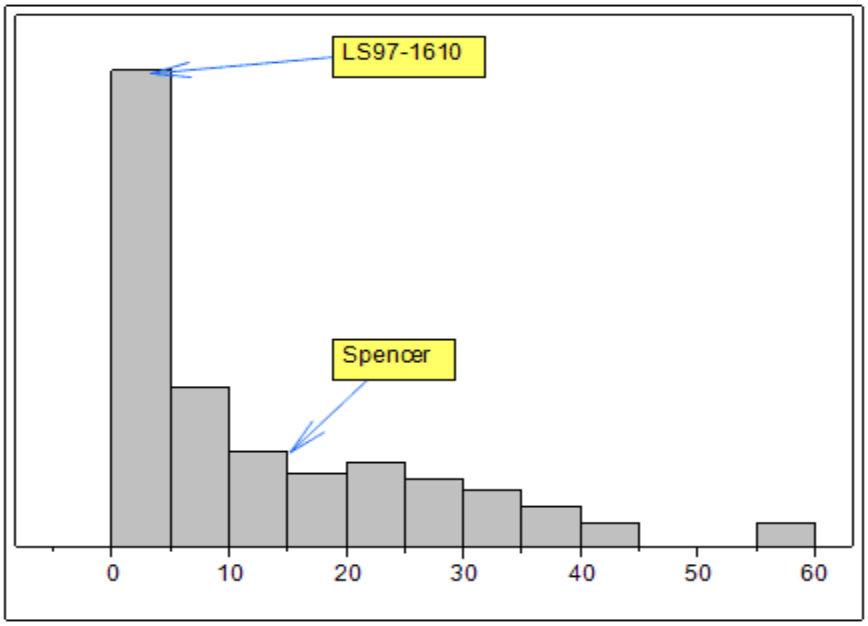


Figure 40 Frequency Distribution for DX not transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Carbondale, IL in 2010

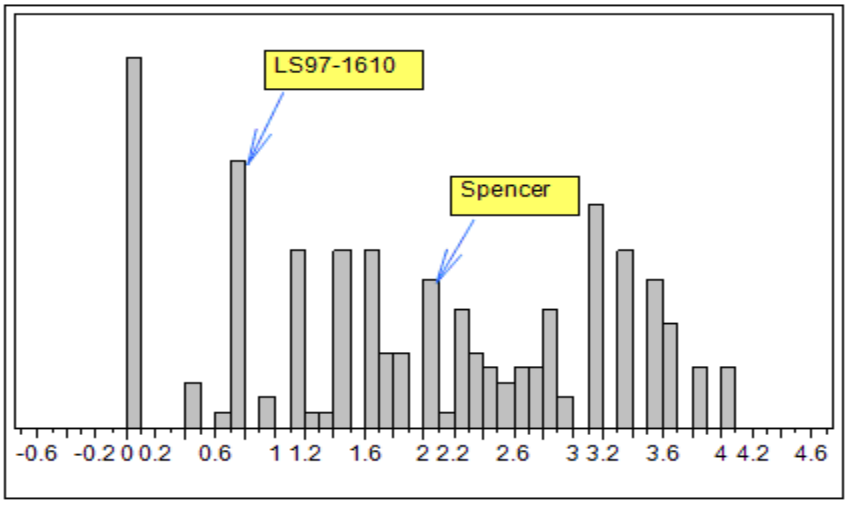


Figure 41 Frequency Distribution for DX log transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Carbondale, IL in 2010

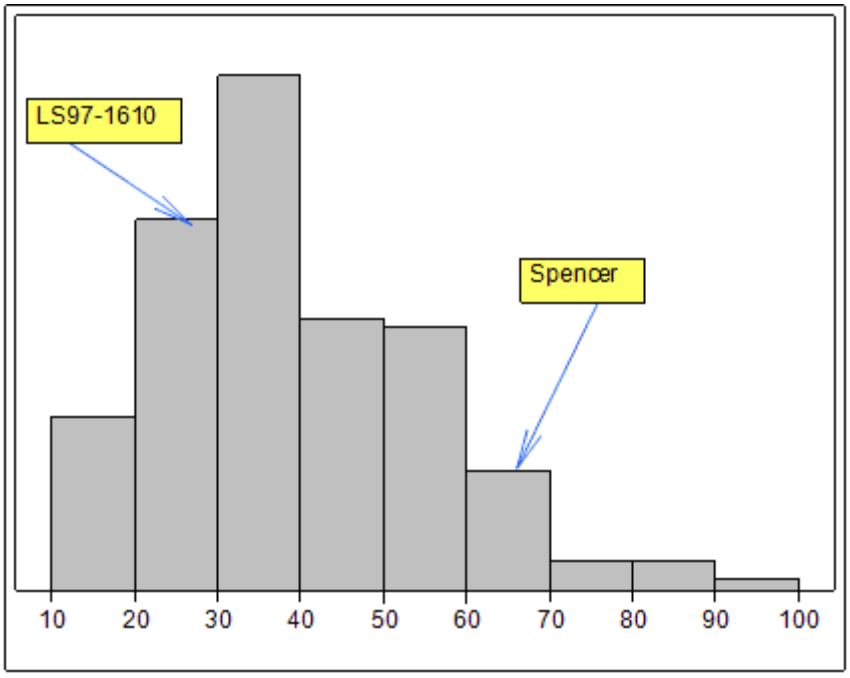


Figure 42 Frequency Distribution for DX not transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Valmeyer, IL in 2009

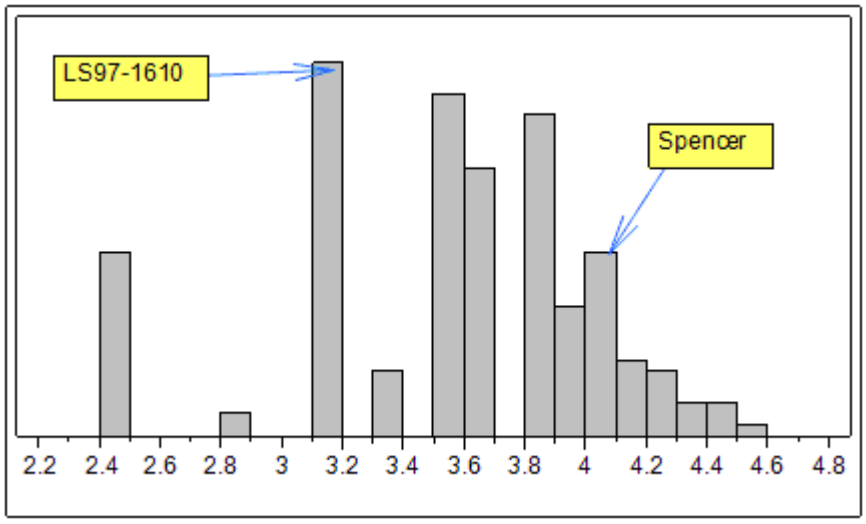


Figure 43 Frequency Distribution for DX log transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Valmeyer, IL in 2009

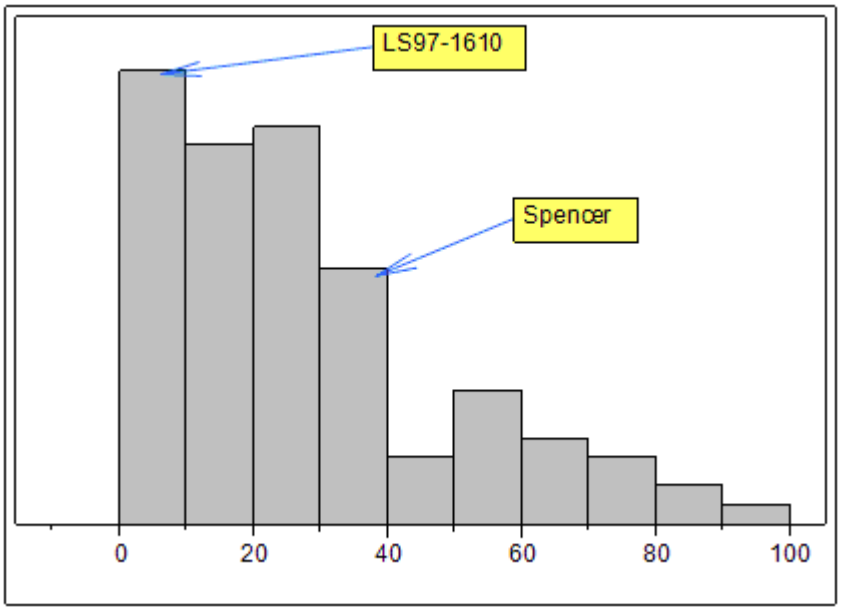


Figure 44 Frequency Distribution for DX not transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Valmeyer, IL in 2010

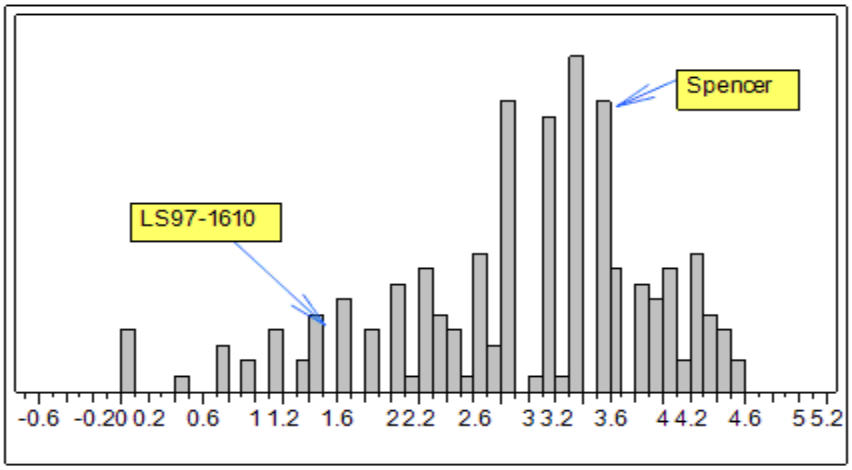


Figure 45 Frequency Distribution for DX log transformed for LS97-1610 x Spencer, LS97-1610, and Spencer grown in Valmeyer, IL in 2010

Table 23 Mean, Standard Deviation, and Range for Transformed Data LS97-1610

	Carbondale 2009	**Carbondale 2010**	**Valmeyer 2009**	**Valmeyer 2010**
Mean	2.538	1.975	3.568	2.970
Std Dev	1.053	1.200	0.479	0.998
Range	4.215	4.035	2.064	4.559

Table 24 Standard Deviation, and Range for LS97-1610

	Carbondale 2009	Carbondale 2010	Valmeyer 2009	Valmeyer 2010
Mean	18.510	12.280	38.265	27.564
Std Dev	15.689	13.610	16.839	22.339
Range	66.667	55.556	83.333	94.444

iii. Genotypic Differences and Genotype x Environment Interactions

The genotype was significant for DX for the line LS97-1610 x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL at (P<0.0001). The location was significant for DX for the line Hamilton x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL at (P<0.0001). The interaction between genotype and location was significant for DX for the line Hamilton x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL at (P<0066). The broad sense heritability for the line Hamilton x Spencer was 61.77%.

Table 25 Analysis of variance (*P* values) and heritability estimates of Disease Index LS97-1610 x Spencer recombinant inbred population grown at Carbondale and Valmeyer, IL in 2009 and 2010.

	Source of variation DX			
Trait	**Genotype**	**Location**	**Genotype x Location**	**H^2(%)**
DX	<.0001*	<.0001*	.0066*	61.77

H^2 broad sense heritability (%) estimated from ANOVA

C. LS90-1920 x Spencer

i. Resistance reaction

Table 26 shows the mean, P value, and CV of LS90-1920 x Spencer in Carbondale, IL and Valmeyer, IL for the years 2009, 2010, and the two years average for each site. There was significant differences within LS90-1920 x Spencer for 2009 in Carbondale, IL (P<0.0039). There was significant differences within LS90-1920 x Spencer for 2010 in Carbondale at (P<0.0033). There was significant differences within LS90-1920 x Spencer for the two years average in Carbondale, IL at (P<0.0001). There was significant differences within LS90-1920 x Spencer for 2009 in Valmeyer, IL at (P<0.0001). There was significant differences within LS90-1920 x Spencer for 2010 in Valmeyer at (P<0.0009). There was significant differences within LS90-1920 x Spencer for the two years average in Valmeyer, IL at (P<0.0001).

Table 26 Means, coefficients of variation, *P* values, and broad-sense heritability of DX in LS90-1920 x Spencer recombinant inbred line population grown in Carbondale and Valmeyer, IL (2009 and 2010)

	Carbondale			**Valmeyer**		
Statistics	**2009**	**2010**	**2-yr combined**	**2009**	**2010**	**2-yr combined**
Mean (±SD)	13.501	8.375	10.945	38.061	15.260	26.661
***P* value**	0.0039*	0.0033*	<.0001*	<.0001*	0.0009*	<.0001*
CV	93.448	134.380	111.590	52.766	98.793	79.106

ii. Frequency Distribution

Frequency distributions for DX for LS97-1610 x Spencer are heavily skewed positively. In order to make data more normal, a logarithmic transformation was suggested by Victor Njiti. Frequency data unaltered and transformed are presented to show effect of the transformation.

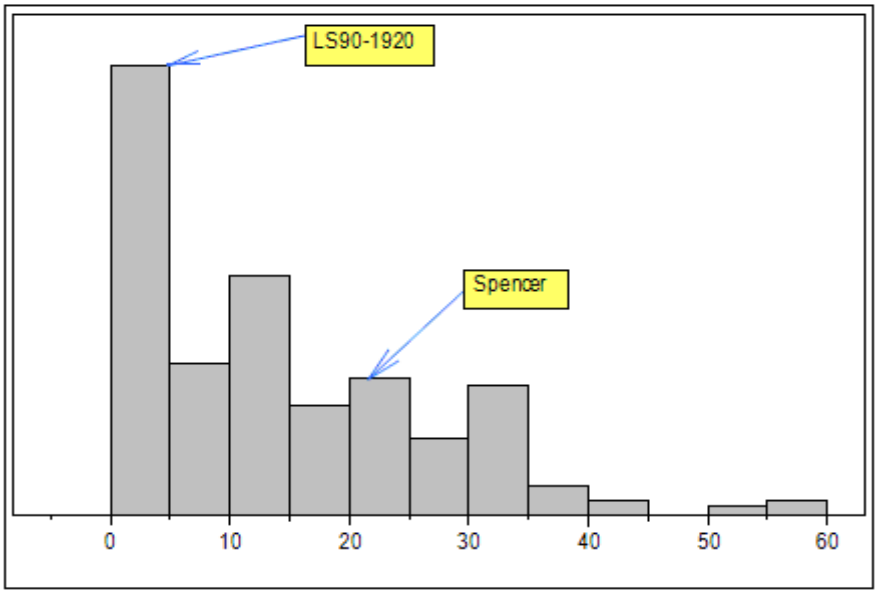


Figure 46 Frequency Distribution for DX not transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Carbondale, IL in 2009

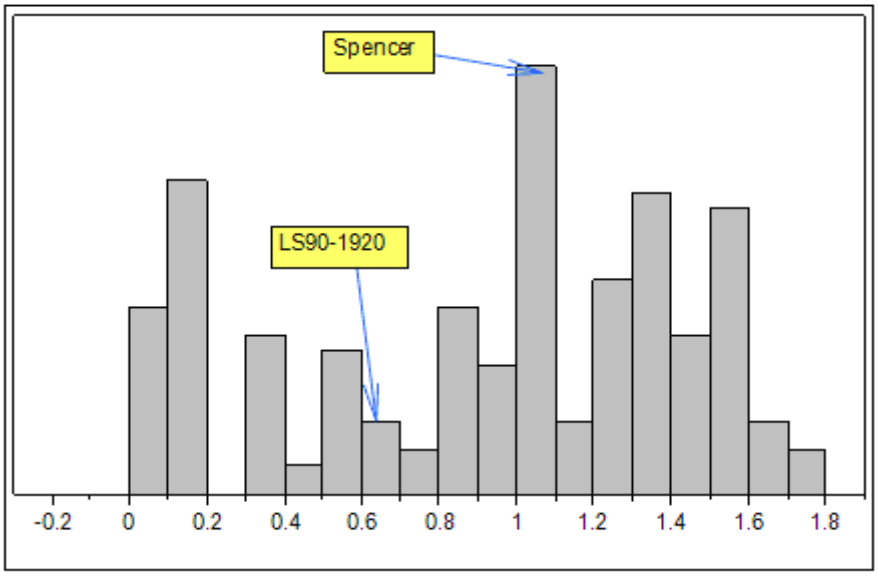


Figure 47 Frequency Distribution for DX log transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Carbondale, IL in 2009

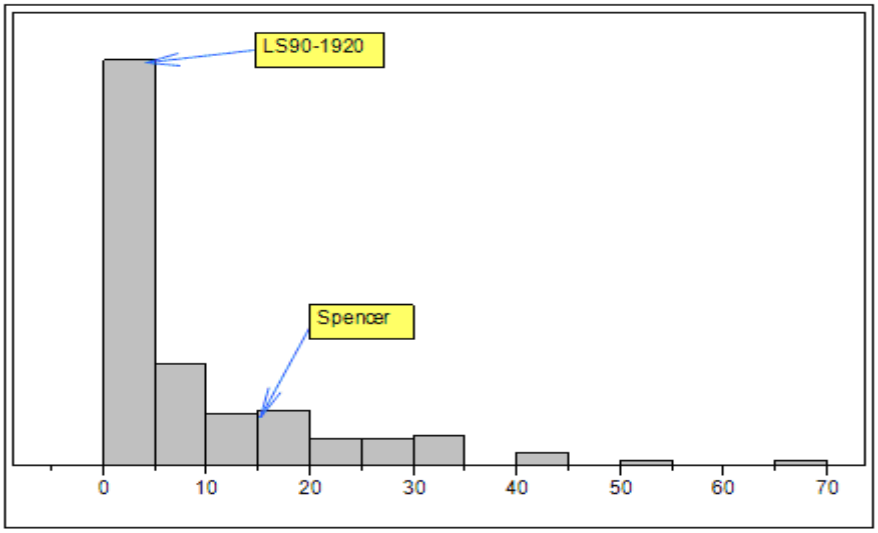


Figure 48 Frequency Distribution for DX not transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Carbondale, IL in 2010

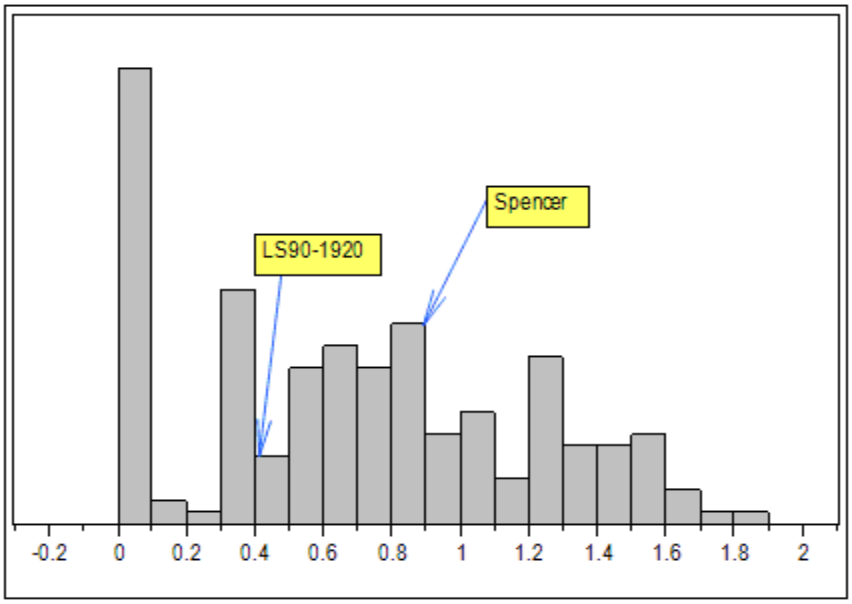


Figure 49 Frequency Distribution for DX log transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Carbondale, IL in 2010

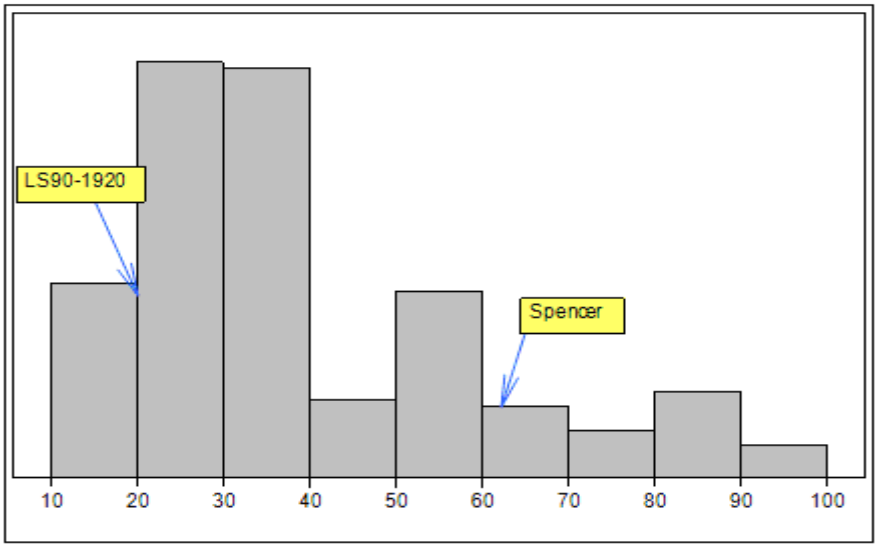


Figure 50 Frequency Distribution for DX not transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Valmeyer, IL in 2009

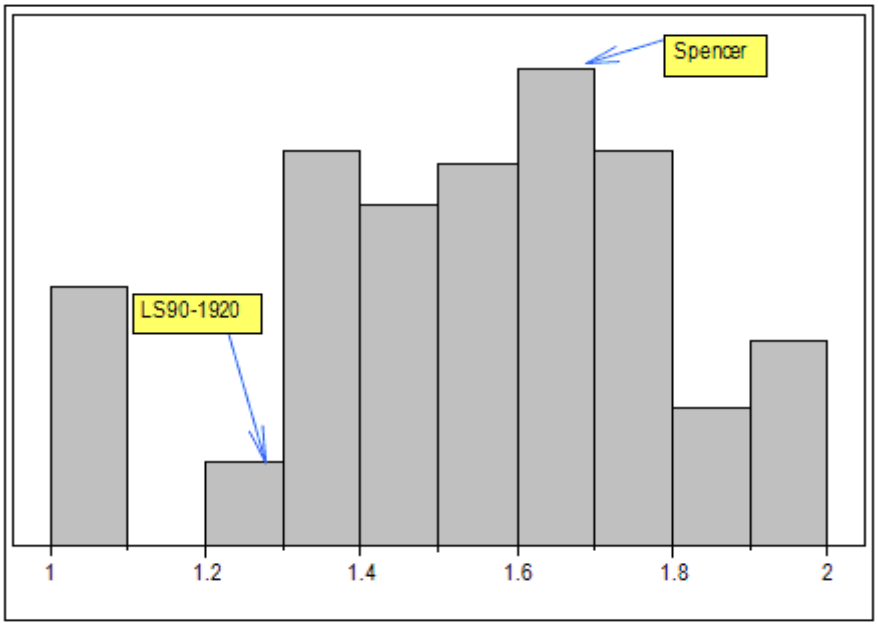


Figure 51 Frequency Distribution for DX log transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Valmeyer, IL in 2009

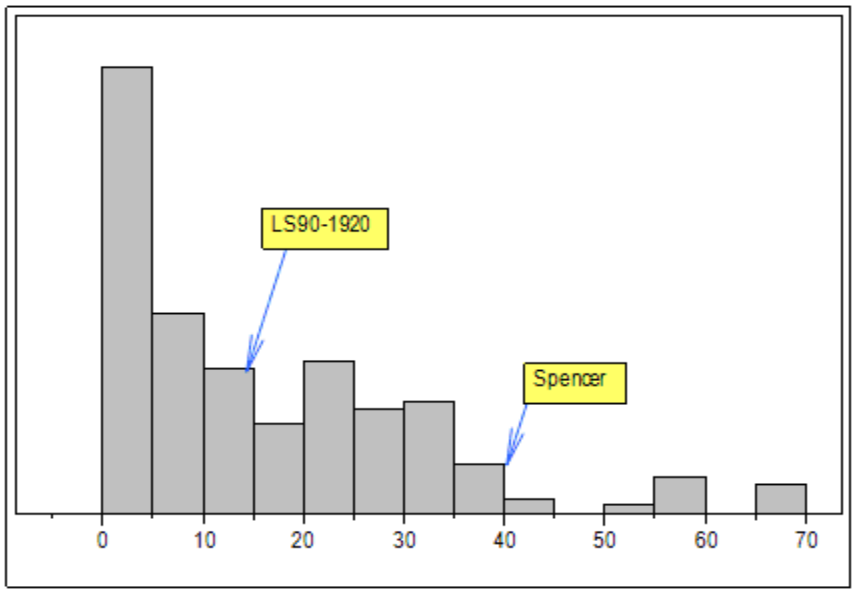


Figure 52 Frequency Distribution for DX not transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Valmeyer, IL in 2010

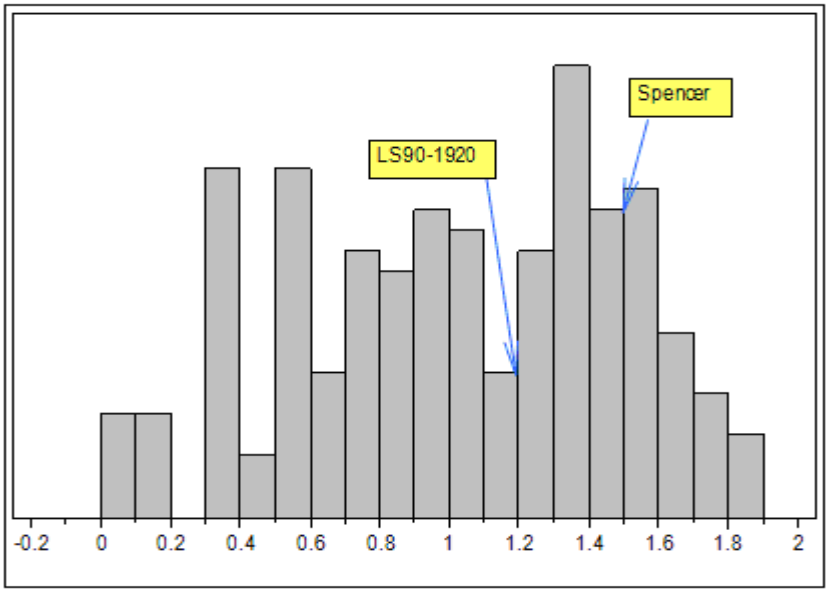


Figure 53 Frequency Distribution for DX log transformed for LS90-1920 x Spencer, LS90-1920, and Spencer grown in Valmeyer, IL in 2010

Table 27 Mean, Standard Deviation, and Range for Transformed Data LS90-1920

	Carbondale 2009	**Carbondale 2010**	**Valmeyer 2009**	**Valmeyer 2010**
Mean	0.932	0.688	1.540	1.017
Std Dev	0.508	0.505	0.231	0.470
Range	1.752	1.830	0.897	1.830

Table 28 Mean, Standard Deviation, and Range for LS90-1920

	Carbondale 2009	Carbondale 2010	Valmeyer 2009	Valmeyer 2010
Mean	13.532	8.302	38.690	15.983
Std Dev	12.681	11.234	20.782	15.480
Range	55.556	66.667	83.333	66.667

iii. Genotypic Differences and Genotype x Environment Interactions

The genotype was significant for DX for the line LS90-1920 x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL ($P<0.0001$). The location was significant for DX for the line Hamilton x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL ($P<0.0001$). The interaction between genotype and location was significant for DX for the line Hamilton x Spencer for the years 2009 and 2010 at Carbondale and Valmeyer, IL at ($P<0.0146$). The broad sense heritability for the line Hamilton x Spencer was 61.64%.

Table 29 Analysis of variance (*P* values) and heritability estimates of Disease Index LS90-1920 x Spencer recombinant inbred population grown at Carbondale and Valmeyer, IL in 2009 and 2010.

	Source of variation DX			
Trait	**Genotype**	**Location**	**Genotype x Location**	**H^2**
DX	<.0001*	<.0001*	0.0146*	61.64

H^2 broad sense heritability (%) estimated from ANOVA

3. Selection of Superior Lines

A. Hamilton x Spencer

The RIL Hamilton x Spencer was analyzed with an ANOVA test for yield to determine if there were significant differences between the individual lines of Hamilton x Spencer and the yield checks. A student t test was used to determine which lines were not significantly different from the yield checks ‘Saluki 4910’ and ‘Saluki 4411’. An ANOVA test for transformed DX was then run to determine if there were significant differences between the individual lines of Hamilton x Spencer and the DX check. The line within Hamilton x Spencer that was not significantly different from either the yield check or the DX check appears in Table 30.

Table 30 Top lines for both Yield and DX from Hamilton x Spencer recombinant inbred population from data obtained at Dowell and Harrisburg, IL in 2011 and Carbondale and Valmeyer, IL 2009 and 2010

Line	Flower Color	Pubesc.	Grow. Habit	Height (cm)	Mat.	Lod.	Yield (kg $^{ha-1}$)	DX
HxS_186	W	G	I	43	20	1.5	3652.06	23.68

B. LS90-1920 x Spencer

The RIL LS90-1920 x Spencer was analyzed with an ANOVA test for yield to determine if there were significant differences between the individual lines of LS90-1920 x Spencer and the yield checks. A student t test was used to determine which lines were not significantly different from the yield checks ‘Saluki 4910’ and ‘Saluki 4411’. An ANOVA test for transformed DX was then run to determine if there were significant differences between the individual lines of LS90-1920 x Spencer and the DX check. The lines within LS90-1920 x Spencer that was not significantly different from either the yield check or the DX check appears in Table 31.

Table 31 Top lines for both Yield and DX from LS90-1920 x Spencer recombinant inbred population from data obtained at Dowell and Harrisburg, IL in 2011 and Carbondale and Valmeyer, IL 2009 and 2010

Line	Flower Color	Pubesc.	Grow. Habit	Height (cm)	Mat.	Lod.	Yield (kg $^{ha-1}$)	DX
LS90xS_128	P	T	I	51	41.25	3.25	3131.26	7.01
LS90xS_232	W	T	I	47.75	48	2	3341.21	10

C. LS97-1610 x Spencer

The RIL LS97-1610 x Spencer was analyzed with an ANOVA test for yield to determine if there were significant differences between the individual lines of Hamilton x Spencer and the yield checks. A student t test was used to determine which lines were not significantly different from the yield checks ‘Saluki 4910’ and ‘Saluki 4411’. An ANOVA test for transformed DX was then run to determine if there were significant differences between the individual lines of LS97-1610 x Spencer and the DX check. There were no lines which were both not significantly different from Ripley for DX and Saluki 4411 and Saluki 4910 in LS97-1610 x Spencer.

CHAPTER 4: DISCUSSION

1. Agronomic Traits

The study of agronomic and seed weight yield of three RIL populations (Hamilton x Spencer, LS90-1920 x Spencer, and LS97-1610 x Spencer) was observed

The population means for Hamilton x Spencer for plant height in cm and lodging were significant from the mid-parental average ($P<0.05$) in Dowell, IL. The population means for Hamilton x Spencer for maturity date and seed weight yield were not significant from the mid-parental average ($P<0.05$) in Dowell, IL. The population mean for Hamilton x Spencer for lodging was significant from the mid parental average at ($P<0.05$) in Harrisburg, IL. The population means for Hamilton x Spencer for plant height in cm, maturity date, and seed weight yield were not significant from the mid-parental average at ($P<0.05$) in Harrisburg, IL.

The population means for LS97-1610 x Spencer for maturity date, lodging, and seed yield weight were significantly different from the mid-parental average at ($P<0.05$) in Dowell, IL. The population mean for LS97-1610 x Spencer for plant height in cm was not significantly different from the mid-parental average at ($P<0.05$) in Dowell, IL. The population means for LS97-1610 x Spencer for plant height in cm, maturity date, and lodging were significantly different from the mid-parental average at ($P<0.05$) in Harrisburg, IL. The population mean for LS97-1610 x Spencer for seed yield weight was not significantly different from the mid-parental average at ($P<0.05$) in Harrisburg, IL.

The population means for LS90-1920 x Spencer for plant height in cm, maturity date, and lodging were significantly different than the mid-parental average at ($P<0.05$) in Dowell, IL. The population mean for LS90-1920 x Spencer for seed yield weight was not significantly different from the mid-parental average at ($P<0.05$) in Dowell, IL. The population means for LS90-1920

x Spencer for plant height in cm, maturity date, and lodging were significantly different than the mid-parental average at (P<0.05) in Harrisburg, IL. The population mean for LS90-1920 x Spencer for seed yield weight was not significantly different from mid-parental average at (P<0.05) in Harrisburg, IL.

The mean plant height recorded at all locations varied from 38cm (LS97-1610 x Spencer at Dowell, IL) to 50 cm (LS90-1920 x Spencer at Harrisburg, IL). This is shorter than average height of 1 m for soybeans (Jin et al., 2010). It is closer to the lines tested in Sherrie et al., 2011. Environmental conditions such as temperature and sunlight may partially explain the reduced height (Major et al., 1975).

Lodging effects ranged between upright and a few plants down for the RIL Hamilton x Spencer. The RILs LS90-1920 x Spencer and LS97-1610 x Spencer had a mean score between a few plants down and up to 50% down. Lodging is a trait that can be associated with a lowering of yield as well as makes harvesting easier. The lodging scores for the RIL in the line appear similar to those of the RIL produced in Panthee et al., 2007.

1a. Correlation of Agronomic Traits

A correlation test was done for height versus seed yield for Hamilton x Spencer. The connection between plant height and seed yield was not significant significant at (P>F 0.05).

A correlation test was done for plant height versus seed yield for LS97-1610 x Spencer. The connection between plant height rank and maturity date is significant at (P <.0001). The relationship between plant height and seed yield weight is significant. The regression of the relationship is 0.0604. This means a very small amount of the seed yield weight is explained by the height of the plant (approximately 6%), with the remaining 94% being accounted for in other sources.

A correlation test was done for plant height versus seed yield for LS90-1920 x Spencer. The connection between plant height rank and maturity date is significant at (P<.0001). The relationship between plant height rank and maturity date is significant. The R^2 of the relationship is 0.0738. This means a small portion of the maturity is explained by the plant height rank (approximately 7%), with the remaining 93% being accounted for in other sources.

Sherrie, et al, 2011 reports that there is a significant negative correlation between plant height and seed yield. This contradicts the findings present here, which shows a significant positive correlation. Even so, the small correlation values (r<0.5) will do little to aid in the selection of new lines for high yield from the height trait. Instead, the RIL should be looked at for the individual trait and not how it interacts with another trait.

2. Disease Resistance

The frequency distribution for DX for the RIL lines Hamilton x Spencer, LS90-1920 x Spencer, and LS97-1610 x Spencer was heavily skewed positively at a value of 1.1134152. To deal with this issue, the data was transformed as recommended by Njiti with a log transformation. The distribution was not normal after the transformation, but the skew was lessened dramatically to -0.567926.

The mean value for different years for Hamilton x Spencer shows different DX for the each year in the different environment. Carbondale and Valmeyer, IL had a higher DX in 2009 than it did in 2010. All environments showed significant differences in the line, as did the two years combined for each location. The CV for Carbondale, IL was higher than that of Valmeyer, IL.

The mean value for different years for LS97-1610 x Spencer shows different DX for the each year in the different environment. Carbondale and Valmeyer, IL had a higher DX in 2009 than it did in 2010. All environments showed significant differences in the line, as did the two years

combined for each location. The CV for Carbondale, IL was higher than that of Valmeyer, IL. The mean value for different years for LS90-1920 x Spencer shows different DX for the each year in the different environment. Carbondale and Valmeyer, IL had a higher DX in 2009 than it did in 2010. All environments showed significant differences in the line, as did the two years combined for each location. The CV for Carbondale, IL was higher than that of Valmeyer, IL.

There were significant sources of variation for DX for Hamilton x Spencer in Harrisburg in Carbondale and Valmeyer, IL for the years 2009 and 2010. Genotype showed significance at (P <.0001). Location showed significance at (P<.0001), and Genotype x Location showed significance at (P <.0001). The broad sense heritability was calculated and shown to have 0%, meaning that the population was influenced 100% by the environment. This can be seen when observing both the high DX at the Valmeyer, IL location and the low DX at the Carbondale, IL location.

There were significant sources of variation for DX for LS97-1610 x Spencer in Harrisburg in Carbondale and Valmeyer, IL for the years 2009 and 2010. Genotype showed significance at (P<.0001), Location showed significance at (P <.0001), and Genotype x Location showed significance at (P<0.0066). The broad sense heritability was calculated and shown to be 61.77%, meaning that the population was influenced 61.77% by the genetics and 38.23% by the environment.

There were significant sources of variation for DX for LS90-1920 x Spencer in Harrisburg in Carbondale and Valmeyer, IL for the years 2009 and 2010. Genotype showed significance at (P <.0001), Location showed significance at (P <.0001), and Genotype x Location showed significance at (P< 0.0146). The broad sense heritability was calculated and shown to be 61.64%,

meaning that the population was influenced 61.64% by the genetics and 38.36% by the environment.

The environment was a key factor to the expression of the SDS resistance. The environment at the Carbondale location had a great impact, which can be seen by the broad sense heritability. Conversely the Valmeyer location had more of the genome playing a role in the resistance, with about 30% of the genome accounting for the resistance.

3. Selection of Superior Lines

The superior lines for Hamilton x Spencer would be those that are of the same level of yield potential as the yield checks Saluki 4910 and Saluki 4411 and have disease resistance similar to that of the disease resistant check Ripley. A student's t test to separate lines for yield was done. The check lines for yield were used for comparison. Lines in Hamilton x Spencer that did not differ significantly at ($P<0.05$) were selected. A student's t test to separate lines for transformed DX was done. The check line for DX was used for comparison. Lines in Hamilton x Spencer that did not differ significantly at ($P<0.05$) were selected. The list for yield was cross-referenced with the list for DX. Lines in Hamilton x Spencer that appeared in both lines were listed in Table 18.

The superior lines for LS90-1920 x Spencer would be those that are of the same level of yield potential as the yield checks Saluki 4910 and Saluki 4411 and have disease resistance similar to that of the disease resistant check Ripley. A student's t test to separate lines for yield was done. The check lines for yield were used for comparison. Lines in LS90-1920 x Spencer that did not differ significantly at ($P<0.05$) were selected. A student's t test to separate lines for transformed DX was done. The check line for DX was used for comparison. Lines in LS90-1920 x Spencer that did not differ significantly at ($P<0.05$) were selected. The list for yield was cross-

referenced with the list for DX. Lines in LS90-1920 x Spencer that appeared in both lines were listed in Table 19.

The superior lines for LS97-1610 x Spencer would be those that are of the same level of yield potential as the yield checks Saluki 4910 and Saluki 4411 and have disease resistance similar to that of the disease resistant check Ripley. A student's t test to separate lines for yield was done. The check lines for yield were used for comparison. Lines in LS97-1610 x Spencer that did not differ significantly at ($P<0.05$) were selected. A student's t test to separate lines for transformed DX was done. The check line for DX was used for comparison. Lines in LS97-1610 x Spencer that did not differ significantly at ($P<0.05$) were selected. The list for yield was cross-referenced with the list for DX. No lines were in both lists so there are no selected lines for LS97-1610 x Spencer.

4. Conclusions

One of the most important factors for soybean breeding is high-yield potential. Yield is a multi-factorial trait determined by several genetic traits and highly correlated with important agronomic traits. Agronomic characters such as plant height and maturity are highly correlated, in a positive or negative way with yield in soybean (Panthee et al., 2007; Li et al., 2008). Conversely, if a correlation is not significant for two traits, than those traits are not related. Therefore, the selection for each trait must be done independently.

Lines within each RIL population were selected for their yield potential and resistance independently. While there were a good number of lines within each population that were not significantly different than the seed weight yield or disease index check, there were few that were not significantly different from both checks. These lines can be advanced to further the germplasm development for the desired traits atSouthern Illinois.

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APPENDICIES

Appendix A Correspondence

Correspondence with Victor Njiti

Njiti, Victor

Mar 29

to David, me

Arcsine transformation. This consists of taking the arcsine of the square root of a number. (The result is given in radians, not degrees, and can range from $-\pi/2$ to $\pi/2$.) The numbers to be arcsine transformed must be in the range -1 to 1. This is commonly used for proportions, which range from 0 to 1, such as the proportion of female Eastern mudminnows that are infested by a parasite. Note that this kind of proportion is really a nominal variable, so it is incorrect to treat it as a measurement variable, whether or not you arcsine tranform it. For example, it would be incorrect to count the number of mudminnows that are or are not parasitized each of several streams in Maryland, treat the arcsine-transformed proportion of parasitized females in each stream as a measurement variable, then perform a linear regression on these data vs. stream depth. This is because the proportions from streams with a smaller sample size of fish will have a higher variance than proportions from streams with larger samples of fish, information that is disregarded when treating the arcsine-transformed proportions as measurement variables. Instead, you should use a test designed for nominal variables; in this example, you should do logistic regression instead of linear regression. If you insist on using the arcsine transformation, despite what I've just told you, the back-transformation is to square the sine of the number.

How to transform data

Spreadsheet

In a blank column, enter the appropriate function for the transformation you've chosen. For example, if you want to transform numbers that start in cell A2, you'd go to cell B2 and enter =LOG(A2) or =LN(A2) to log transform, =SQRT(A2) to square-root transform, or =ASIN(SQRT(A2)) to arcsine transform. Then copy cell B2 and paste into all the cells in column B that are next to cells in column A that contain data. To copy and paste the transformed values into another spreadsheet, remember to use the "Paste Special..." command, then choose to paste "Values." Using the "Paste Special...Values" command makes Excel copy the numerical result of an equation, rather than the equation itself. (If your spreadsheet is Calc, choose "Paste Special" from the Edit menu, uncheck the boxes labelled "Paste All" and "Formulas," and check the box labelled "Numbers.")

To back-transform data, just enter the inverse of the function you used to transform the data. To back-transform log transformed data in cell B2, enter =10^B2 for base-10 logs or =EXP^B2 for natural logs; for square-root transformed data, enter =B2^2; for arcsine transformed data, enter =(SIN(B2))^2

From: David Lightfoot [mailto:ga4082@siu.edu]

Sent: Thursday, March 29, 2012 12:58 PM

To: James Anderson; Njiti, Victor

Subject: Re: Arc Sin transformation

Correspondence with CP Smythe, Terry Pratchett’s agent

James Anderson Mar 10

Hello, My name is James Anderson and I am a great fan of Terry Pratchett's wo...

CPSmythe@aol.com

Mar 10

to me

Thanks for your email. If you would tell me the quotation and the context in which it is to be used, I'll be able to give you an answer. Normally we have no problem with the use of quotations in theses but we do expect to be told what they are. Being totally vague about what you plan to use does not help your request.

Colin Smythe

James Anderson

Mar 10

to CPSmythe

Colin Smythe,

Couldn't find the exact one that I wanted, but did find a correlation joke that I found humorous.

The context it will be used in will be on my page for acknowledgments. It would be as below (pending your approval as well as my committee).

I would like to thank Terry Pratchett for keeping me sane during my writing process, and making for reminding me that everything is relative and correlation does not imply causation.

"One interesting side effect of the fire in Ankh-Morpork concerns the inn-sewer-ants policy, which left the city through the ravaged roof of the Broken Drum, was wafted high into the Discworld's atmosphere on the ensuing thermal, and came to earth several days and a few thousand miles away on an uloruaha bush in the beTrobi islands. The simple, laughing islanders subsequently worshipped it as a god, much to the amusement of their more sophisticated neighbors. Strangely enough the rainfall and harvests in the next few years were almost supernaturally abundant, and this lead to a research team being dispatch to the islands by the Minor Religions faculty of Unseen University. Their verdict was that it only went to show." - Terry Pratchett The Color of Magic

Sorry about being vague but this was an exploratory email and I did not expect as quick as a response.

CPSmythe@aol.com

Mar 10

to me

I think you can take a little longer to choose your ideal quote... you gave the impression that you already knew which you wanted to use

Colin Smythe

James Anderson

Mar 14

to CPSmythe

Colin Smythe,

Yes, I did want to use another one. And, a bit or reading to relocate the quote I found humorous for no good reason, I found it. So here it goes again.

This would appear on the acknowledgments pages. I would start the part of with the quote

"It is embarrassing to know that one is a god of a world that only exists because every improbability curve must have its far end;" -Terry Pratchett The Color of Magic

I would like to thank Terry Pratchett for the wonderful books that he has produced that have kept me sane in the writing process as well as the offhand statistical joke that gets thrown in there.

I chose that line because I deal with far too many probability curves and statistical methods that I can't not laugh at any reference to it taken lightly. Please let me know if that is ok.

CPSmythe@aol.com

Mar 14

to me

That's fine. Thought you'd find a better one for yourself.

(And I'll allow you your curious American spelling of Colour :-))

Very best wishes

Colin Smythe

James Anderson

Mar 14

to CPSmythe

Colin Smythe,

Eh...I generally spell it Colour, but change it out of force of habit for people here.

CPSmythe@aol.com

Mar 14

to me

Whichever :-)

Correspondence with Neil Anderson

James Anderson

Mar 10

to mnext

Hello,

My name is James Anderson. I am email to request to use the picture http://www.extension.umn.edu/distribution/cropsystems/images/3935f03.jpg from the web page http://www.extension.umn.edu/distribution/cropsystems/components/DC3935b.html in my thesis on agronomic and disease traits in soybeans. If you can let me know one way or the other if I could use this picture I would appreciate it.

Neil Anderson ander706@umn.edu

Mar 13

to me

Hello James,

Please include in the photo caption "Courtesy University of Minnesota Extension" when you use the photo in your thesis. In your citations please include the article Title and web URL.

Sincerely,

Neil Anderson

Extension Copyright Manager

University of Minnesota Extension

Web page from University of Georgia Extension giving release of use for photo

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Correspondence with Michael Greifenkamp

Re: Message from the Bulletin web site

Inbox

x

Greifenkamp, Michael T grfnkmp@illinois.edu

Mar 12

to me

Good morning.

Dean Malvick actually works at the University of Minnesota now (I think).

Either way, you are more than welcome to use whatever photos you need for your thesis. If you would like to add a credit to the photo, something like "Courtesy of University of Illinois Extension" is more than sufficient.

Good luck with your thesis, and let us know if you need anything else.

Take care.

Mike

Michael Greifenkamp

Web Project and Database Specialist

University of Illinois

Department of Crop Sciences

grfnkmp@illinois.edu

On 3/10/12 8:12 PM, "jasper@siu.edu" <jasper@siu.edu> wrote:

>Hello,

>

>My name is James Anderson. I am writing my thesis and would like to use

>the picture http://bulletin.ipm.illinois.edu/photos/bsr_stems.jpg from

>the page http://bulletin.ipm.illinois.edu/article.php?id=185

>

>I attempted to contact the author, but the email came back unsendable so

>I am trying this method. Please let me know one way or another if I can

>use this picture.

>

>James Anderson

>

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Appendix B ANOVA tables and Student t separations

ANOVA for Hamilton x Spencer for Yield

Source	**DF**	**Sum of Squares**	**Mean Square**	**F Ratio**
Model	97	62803113	647455	7.1470
Error	318	28807836	90591	**Prob > F**
C. Total	415	91610949		<.0001*

Student's t test Hamilton x Spencer for Yield

Level		**Least Sq Mean**
97	A	3922.2169
81	A B	3702.5076
86	A B C	3652.0559
98	B C D	3392.7447
30	C D E	3272.8540
75	C D E	3269.5990
41	C D E F	3254.9518
7	D E F G	3184.9703
16	D E F G	3181.7153
42	D E F G H	3163.8131
20	D E F G H I	3152.4208
48	D E F G H I J	3144.2834
10	D E F G H I J K	3137.7735
23	D E F G H I J K	3128.0086

Level		Least Sq Mean
67	D E F G H I J K L	3124.7537
50	D E F G H I J K L	3118.2438
28	D E F G H I J K L	3111.7339
92	D E F G H I J K L	3103.5965
12	D E F G H I J K L	3103.5965
66	D E F G H I J K L	3097.0866
36	D E F G H I J K L M	3095.4591
47	D E F G H I J K L M	3093.8316
94	D E F G H I J K L M N	3085.6943
82	D E F G H I J K L M N O	3084.0668
90	D E F G H I J K L M N O	3074.3019
53	E F G H I J K L M N O P	3069.4195
69	E F G H I J K L M N O P Q	3053.1448
83	E F G H I J K L M N O P Q	3053.1448
80	E F G H I J K L M N O P Q R	3046.6348
72	E F G H I J K L M N O P Q R	3046.6348
40	E F G H I J K L M N O P Q R S	3033.6150
8	E F G H I J K L M N O P Q R S T	3015.7128
84	E F G H I J K L M N O P Q R S T	3015.7128
29	E F G H I J K L M N O P Q R S T	3014.0853
25	E F G H I J K L M N O P Q R S T U	2997.8106
88	E F G H I J K L M N O P Q R S T U V	2958.7511
60	E F G H I J K L M N O P Q R S T U V W	2952.2412
33	E F G H I J K L M N O P Q R S T U V W	2950.6138
4	E F G H I J K L M N O P Q R S T U V W	2945.7313
24	E F G H I J K L M N O P Q R S T U V W X	2931.0841
54	E F G H I J K L M N O P Q R S T U V W X	2929.4566

Level		Least Sq Mean
87	E F G H I J K L M N O P Q R S T U V W X	2921.3192
85	E F G H I J K L M N O P Q R S T U V W X	2911.5543
57	E F G H I J K L M N O P Q R S T U V W X	2901.7895
52	E F G H I J K L M N O P Q R S T U V W X	2892.0246
61	E F G H I J K L M N O P Q R S T U V W X	2890.3972
70	E F G H I J K L M N O P Q R S T U V W X	2880.6323
65	E F G H I J K L M N O P Q R S T U V W X	2874.1224
63	E F G H I J K L M N O P Q R S T U V W X	2872.4949
64	E F G H I J K L M N O P Q R S T U V W X	2869.2400
44	E F G H I J K L M N O P Q R S T U V W X	2864.3575
79	E F G H I J K L M N O P Q R S T U V W X	2864.3575
55	F G H I J K L M N O P Q R S T U V W X	2844.8278
37	F G H I J K L M N O P Q R S T U V W X	2839.9454
62	F G H I J K L M N O P Q R S T U V W X	2836.6905
32	G H I J K L M N O P Q R S T U V W X	2835.0630
73	G H I J K L M N O P Q R S T U V W X	2830.1806
91	G H I J K L M N O P Q R S T U V W X Y	2815.5333
93	G H I J K L M N O P Q R S T U V W X Y Z	2812.2783
89	G H I J K L M N O P Q R S T U V W X Y Z	2810.6508
71	G H I J K L M N O P Q R S T U V W X Y Z	2799.2585
18	G H I J K L M N O P Q R S T U V W X Y Z	2789.4937
34	G H I J K L M N O P Q R S T U V W X Y Z	2778.1013
74	G H I J K L M N O P Q R S T U V W X Y Z	2774.8464
3	H I J K L M N O P Q R S T U V W X Y Z	2761.8266
49	H I J K L M N O P Q R S T U V W X Y Z	2760.1991
43	H I J K L M N O P Q R S T U V W X Y Z	2755.3167
59	H I J K L M N O P Q R S T U V W X Y Z	2748.8068

Level		Least Sq Mean
26	I J K L M N O P Q R S T U V W X Y Z	2735.7870
1	J K L M N O P Q R S T U V W X Y Z	2732.5320
5	K L M N O P Q R S T U V W X Y Z	2724.3946
6	K L M N O P Q R S T U V W X Y Z	2722.7671
56	K L M N O P Q R S T U V W X Y Z	2719.5122
21	L M N O P Q R S T U V W X Y Z	2708.1199
46	M N O P Q R S T U V W X Y Z	2677.1978
9	N O P Q R S T U V W X Y Z	2673.9429
68	O P Q R S T U V W X Y Z	2665.8055
77	P Q R S T U V W X Y Z	2651.1582
38	Q R S T U V W X Y Z	2649.5307
76	Q R S T U V W X Y Z	2647.9033
51	Q R S T U V W X Y Z	2643.0208
17	Q R S T U V W X Y Z	2638.1384
78	R S T U V W X Y Z	2633.2560
14	R S T U V W X Y Z	2630.0010
22	S T U V W X Y Z	2616.9812
35	T U V W X Y Z	2600.7065
11	U V W X Y Z	2594.1966
19	U V W X Y Z	2589.3141
58	V W X Y Z	2569.7844
31	V W X Y Z	2561.6470
2	V W X Y Z	2561.6470
27	W X Y Z	2537.2349
39	W X Y Z	2533.9799
15	X Y Z	2516.0777
13	Y Z	2397.2720

Level		Least Sq Mean
45	Z	2394.0170

ANOVA for Hamilton x Spencer for DX

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	100	223.89212	2.23892	14.0006
Error	711	113.70065	0.15992	**Prob > F**
C. Total	811	337.59277		<.0001*

Student's t test Hamilton x Spencer for DX

Level		Least Sq Mean
89	A	1.4960428
77	A B	1.3829852
61	A B C D	1.3657715
43	A B C D E	1.3330610
99	A B C	1.3076228
45	A B C D E F	1.2916195
17	A B C D E F G	1.2769610
48	A B C D E F G	1.2717197
33	A B C D E F G H	1.2617567
3	A B C D E F G H	1.2612186
22	A B C D E F G H I	1.2570797
9	A B C D E F G H I J	1.2386886
36	A B C D E F G H I J K	1.2270821

Level		Least Sq Mean
26	A B C D E F G H I J K L	1.2182613
76	A B C D E F G H I J K L	1.2155360
67	A B C D E F G H I J K L M	1.2109508
80	A B C D E F G H I J K L M	1.2055209
49	A B C D E F G H I J K L M	1.2050747
82	A B C D E F G H I J K L M	1.2005895
10	A B C D E F G H I J K L M	1.1963364
19	A B C D E F G H I J K L M N	1.1782190
72	A B C D E F G H I J K L M N O	1.1654038
74	A B C D E F G H I J K L M N O	1.1651549
6	A B C D E F G H I J K L M N O	1.1629803
85	A B C D E F G H I J K L M N O	1.1607331
27	A B C D E F G H I J K L M N O	1.1537306
29	A B C D E F G H I J K L M N O P	1.1422133
11	A B C D E F G H I J K L M N O P Q	1.1407764
30	A B C D E F G H I J K L M N O P Q	1.1324166
78	A B C D E F G H I J K L M N O P Q	1.1310723
52	A B C D E F G H I J K L M N O P Q	1.1303831
53	A B C D E F G H I J K L M N O P Q R	1.1270169
12	A B C D E F G H I J K L M N O P Q R	1.1247885
60	A B C D E F G H I J K L M N O P Q R	1.1217410
18	A B C D E F G H I J K L M N O P Q R S	1.1207365
4	A B C D E F G H I J K L M N O P Q R S	1.1176274
46	A B C D E F G H I J K L M N O P Q R S	1.1062897
83	A B C D E F G H I J K L M N O P Q R S	1.1058755
35	A B C D E F G H I J K L M N O P Q R S	1.1057688
88	A B C D E F G H I J K L M N O P Q R S	1.1049192

Level		Least Sq Mean
39	B C D E F G H I J K L M N O P Q R S	1.1017211
5	B C D E F G H I J K L M N O P Q R S	1.0997844
42	B C D E F G H I J K L M N O P Q R S	1.0965505
69	B C D E F G H I J K L M N O P Q R S	1.0904732
15	B C D E F G H I J K L M N O P Q R S	1.0888154
20	B C D E F G H I J K L M N O P Q R S	1.0774251
71	B C D E F G H I J K L M N O P Q R S	1.0739592
66	B C D E F G H I J K L M N O P Q R S	1.0579739
55	B C D E F G H I J K L M N O P Q R S	1.0542208
37	B C D E F G H I J K L M N O P Q R S T	1.0375130
14	B C D E F G H I J K L M N O P Q R S T	1.0362440
2	B C D E F G H I J K L M N O P Q R S T	1.0299789
38	B C D E F G H I J K L M N O P Q R S T	1.0264541
70	B C D E F G H I J K L M N O P Q R S T	1.0187608
51	B C D E F G H I J K L M N O P Q R S T	1.0179672
24	B C D E F G H I J K L M N O P Q R S T	1.0055219
8	B C D E F G H I J K L M N O P Q R S T	1.0051840
57	B C D E F G H I J K L M N O P Q R S T	1.0035654
1	B C D E F G H I J K L M N O P Q R S T	0.9987642
47	B C D E F G H I J K L M N O P Q R S T	0.9965473
7	C D E F G H I J K L M N O P Q R S T	0.9842659
62	D E F G H I J K L M N O P Q R S T	0.9767145
44	D E F G H I J K L M N O P Q R S T	0.9739587
41	E F G H I J K L M N O P Q R S T	0.9692899
92	E F G H I J K L M N O P Q R S T	0.9629137
54	E F G H I J K L M N O P Q R S T	0.9603721
58	E F G H I J K L M N O P Q R S T	0.9595853

Level		Least Sq Mean
63	E F G H I J K L M N O P Q R S T	0.9558662
13	E F G H I J K L M N O P Q R S T	0.9542770
93	E F G H I J K L M N O P Q R S T	0.9530309
64	E F G H I J K L M N O P Q R S T	0.9456458
25	E F G H I J K L M N O P Q R S T	0.9425368
81	E F G H I J K L M N O P Q R S T	0.9413960
23	F G H I J K L M N O P Q R S T	0.9365715
56	F G H I J K L M N O P Q R S T	0.9297052
91	F G H I J K L M N O P Q R S T	0.9265395
34	F G H I J K L M N O P Q R S T	0.9150107
75	F G H I J K L M N O P Q R S T	0.9115438
87	G H I J K L M N O P Q R S T	0.8956771
73	G H I J K L M N O P Q R S T	0.8949076
28	G H I J K L M N O P Q R S T	0.8940175
79	G H I J K L M N O P Q R S T	0.8845885
31	H I J K L M N O P Q R S T	0.8702943
90	I J K L M N O P Q R S T	0.8679173
65	J K L M N O P Q R S T	0.8605030
68	K L M N O P Q R S T U	0.8427020
40	L M N O P Q R S T U	0.8286596
86	M N O P Q R S T U	0.8227973
50	N O P Q R S T U	0.8000646
95	R S T	0.7876926
21	O P Q R S T U	0.7828082
94	P Q R S T U	0.7561069
16	Q R S T U	0.7489493
59	Q R S T U	0.7489368

Level		Least Sq Mean
32	S T U	0.7283827
84	T U	0.6546917
98	U	0.5246558

ANOVA for LS90-1920 x Spencer for Yield

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	97	70914610	731078	4.7036
Error	318	49426751	155430	**Prob > F**
C. Total	415	120341361		<.0001*

Student’s t test LS90-1920 x Spencer for Yield

Level									Least Sq Mean
97	A								3922.2169
98		B							3392.7447
32		B	C						3341.2080
34		B	C	D					3170.3230
28		B	C	D	E				3131.2636
89		B	C	D	E	F			3031.9876
40		B	C	D	E	F	G		3005.9479
11		B	C	D	E	F	G	H	2975.0259
51		B	C	D	E	F	G	H	2975.0259
59			C	D	E	F	G	H	2965.2611
75			C	D	E	F	G	H	I	2948.9863

Level																Least Sq Mean
2	C	D	E	F	G	H	I									2947.3588
54	C	D	E	F	G	H	I	J								2931.0841
81	C	D	E	F	G	H	I	J								2927.8291
20	C	D	E	F	G	H	I	J								2926.2016
10	C	D	E	F	G	H	I	J	K							2916.4368
35	C	D	E	F	G	H	I	J	K							2914.8093
83	C	D	E	F	G	H	I	J	K							2911.5543
84	C	D	E	F	G	H	I	J	K							2909.9269
21	C	D	E	F	G	H	I	J	K							2905.0444
64	C	D	E	F	G	H	I	J	K	L						2885.5147
66	C	D	E	F	G	H	I	J	K	L						2879.0048
38	C	D	E	F	G	H	I	J	K	L	M					2839.9454
88	C	D	E	F	G	H	I	J	K	L	M					2838.3179
92	C	D	E	F	G	H	I	J	K	L	M					2836.6905
68	C	D	E	F	G	H	I	J	K	L	M	N				2830.1806
58	C	D	E	F	G	H	I	J	K	L	M	N				2828.5531
3	C	D	E	F	G	H	I	J	K	L	M	N				2817.1607
46	C	D	E	F	G	H	I	J	K	L	M	N	O			2810.6508
53	C	D	E	F	G	H	I	J	K	L	M	N	O			2810.6508
77	C	D	E	F	G	H	I	J	K	L	M	N	O			2809.0234
48	C	D	E	F	G	H	I	J	K	L	M	N	O			2807.3959
14	C	D	E	F	G	H	I	J	K	L	M	N	O	P		2796.0036
78		D	E	F	G	H	I	J	K	L	M	N	O	P		2769.9639
39		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	2755.3167
76		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	2752.0617
70		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	2748.8068
80		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	2739.0419

Level																	Least Sq Mean
6	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			2735.7870
47	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			2735.7870
24	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			2732.5320
86	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			2730.9045
93	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			2730.9045
17	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		2726.0221
8	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		2722.7671
71	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		2714.6298
90	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		2709.7473
15	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		2696.7275
1	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2688.5902
55	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2673.9429
67	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2662.5505
25	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2660.9231
52	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2660.9231
72	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2660.9231
23	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2656.0406
60	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2649.5307
29	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2649.5307
69	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2646.2758
33	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2646.2758
73	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2638.1384
61	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2633.2560
16	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2630.0010
43	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2625.1186
85		E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2605.5889
82		E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2603.9614

Level																Least Sq Mean
56	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2597.4515
19	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2584.4317
22		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2563.2745
79		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2558.3921
63		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2555.1371
94		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2553.5097
57		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2519.3327
65		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2517.7052
45		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2509.5678
13		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2506.3129
12		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2501.4304
27		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2496.5480
49		F	G	H	I	J	K	L	M	N	O	P	Q	R	S	2493.2930
42			G	H	I	J	K	L	M	N	O	P	Q	R	S	2481.9007
4			G	H	I	J	K	L	M	N	O	P	Q	R	S	2477.0183
74				H	I	J	K	L	M	N	O	P	Q	R	S	2452.6062
62				H	I	J	K	L	M	N	O	P	Q	R	S	2449.3512
41				H	I	J	K	L	M	N	O	P	Q	R	S	2441.2138
87				H	I	J	K	L	M	N	O	P	Q	R	S	2437.9589
50				H	I	J	K	L	M	N	O	P	Q	R	S	2431.4490
26					I	J	K	L	M	N	O	P	Q	R	S	2407.0368
5						J	K	L	M	N	O	P	Q	R	S	2384.2522
44							K	L	M	N	O	P	Q	R	S	2374.4873
9								L	M	N	O	P	Q	R	S	2345.1927
36									M	N	O	P	Q	R	S	2297.9959
31										N	O	P	Q	R	S	2284.9761
7											O	P	Q	R	S	2262.1915

Level		Least Sq Mean
91	P Q R S	2257.3090
30	Q R S	2206.8573
37	R S	2179.1902
18	S	2140.1308

ANOVA for LS90-1920 x Spencer for DX

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	100	124.94890	1.24949	7.4423
Error	713	119.70625	0.16789	**Prob > F**
C. Total	813	244.65515		<.0001*

Student’s t test LS90-1920 x Spencer for DX

Level		Least Sq Mean
44	A	1.6408855
9	A B	1.5837084
7	A B C	1.5323812
15	A B C	1.5284530
49	A B C D	1.5154900
3	A B C D E	1.5069401
47	A B C D E F	1.4709730
38	A B C D E F G	1.4105398
33	A B C D E F G H I	1.3402491
89	A B C D E F G H I	1.3397267

Level		Least Sq Mean
99	A B C D E F G H	1.3368635
92	A B C D E F G H I J	1.3264200
61	A B C D E F G H I J K	1.3116697
54	A B C D E F G H I J K L	1.2752101
60	A B C D E F G H I J K L M	1.2618285
64	B C D E F G H I J K L M N	1.2374378
13	B C D E F G H I J K L M N	1.2243973
83	B C D E F G H I J K L M N	1.2125563
2	B C D E F G H I J K L M N	1.2088770
59	B C D E F G H I J K L M N O	1.2003503
22	B C D E F G H I J K L M N O P	1.1867604
50	C D E F G H I J K L M N O P Q	1.1772885
14	C D E F G H I J K L M N O P Q	1.1760819
17	C D E F G H I J K L M N O P Q R	1.1656437
45	C D E F G H I J K L M N O P Q R S	1.1605532
55	C D E F G H I J K L M N O P Q R S	1.1601210
5	C D E F G H I J K L M N O P Q R S	1.1580100
53	C D E F G H I J K L M N O P Q R S	1.1576272
43	C D E F G H I J K L M N O P Q R S T	1.1500378
25	C D E F G H I J K L M N O P Q R S T	1.1472742
24	C D E F G H I J K L M N O P Q R S T	1.1397470
90	C D E F G H I J K L M N O P Q R S T	1.1378818
78	D E F G H I J K L M N O P Q R S T U	1.1144805
12	E F G H I J K L M N O P Q R S T U	1.1114727
36	F G H I J K L M N O P Q R S T U V	1.0904427
57	F G H I J K L M N O P Q R S T U V	1.0820126
48	F G H I J K L M N O P Q R S T U V	1.0711571

Level		Least Sq Mean
68	F G H I J K L M N O P Q R S T U V	1.0704720
34	G H I J K L M N O P Q R S T U V	1.0357535
79	G H I J K L M N O P Q R S T U V	1.0333144
71	G H I J K L M N O P Q R S T U V	1.0285708
41	G H I J K L M N O P Q R S T U V	1.0264440
80	G H I J K L M N O P Q R S T U V W	1.0220703
94	G H I J K L M N O P Q R S T U V W	1.0212929
29	G H I J K L M N O P Q R S T U V W	1.0170421
76	G H I J K L M N O P Q R S T U V W	1.0132274
30	H I J K L M N O P Q R S T U V W X	1.0074489
73	H I J K L M N O P Q R S T U V W X	1.0065657
19	I J K L M N O P Q R S T U V W X	0.9967773
88	I J K L M N O P Q R S T U V W X	0.9964199
39	I J K L M N O P Q R S T U V W X	0.9892171
85	I J K L M N O P Q R S T U V W X	0.9880401
6	I J K L M N O P Q R S T U V W X	0.9763085
52	I J K L M N O P Q R S T U V W X Y	0.9743875
20	I J K L M N O P Q R S T U V W X Y	0.9716873
27	I J K L M N O P Q R S T U V W X Y	0.9694071
77	I J K L M N O P Q R S T U V W X Y	0.9693342
46	I J K L M N O P Q R S T U V W X Y	0.9647532
21	I J K L M N O P Q R S T U V W X Y	0.9631815
58	I J K L M N O P Q R S T U V W X Y	0.9618922
37	I J K L M N O P Q R S T U V W X Y	0.9593527
74	I J K L M N O P Q R S T U V W X Y	0.9592894
75	I J K L M N O P Q R S T U V W X Y	0.9582217
86	J K L M N O P Q R S T U V W X Y	0.9365783

Level		Least Sq Mean
65	J K L M N O P Q R S T U V W X Y	0.9348013
69	J K L M N O P Q R S T U V W X Y	0.9342512
51	J K L M N O P Q R S T U V W X Y	0.9283650
23	K L M N O P Q R S T U V W X Y	0.9239943
40	K L M N O P Q R S T U V W X Y	0.9171847
84	K L M N O P Q R S T U V W X Y	0.9158602
63	L M N O P Q R S T U V W X Y	0.9078972
8	L M N O P Q R S T U V W X Y	0.9050293
11	L M N O P Q R S T U V W X Y	0.9046687
96	N O P Q R S T U V W X Y	0.9017551
26	L M N O P Q R S T U V W X Y	0.8978882
4	L M N O P Q R S T U V W X Y	0.8947930
56	L M N O P Q R S T U V W X Y Z	0.8827000
62	M N O P Q R S T U V W X Y Z	0.8617506
42	N O P Q R S T U V W X Y Z	0.8593595
35	N O P Q R S T U V W X Y Z	0.8574238
82	N O P Q R S T U V W X Y Z	0.8367234
32	O P Q R S T U V W X Y Z	0.7987157
18	P Q R S T U V W X Y Z	0.7895216
91	Q R S T U V W X Y Z	0.7841731
66	Q R S T U V W X Y Z	0.7796453
1	R S T U V W X Y Z	0.7688329
87	R S T U V W X Y Z	0.7672967
81	R S T U V W X Y Z	0.7659394
93	S T U V W X Y Z	0.7593288
16	T U V W X Y Z	0.7523903
70	U V W X Y Z	0.7339887

Level		Least Sq Mean
10	U V W X Y Z	0.7180246
67	V W X Y Z	0.7066986
28	W X Y Z	0.6232849
72	X Y Z	0.6072025
31	Y Z	0.5731833
98	Z	0.5538965

ANOVA for LS97-1610 x Spencer for Yield

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	97	85758595	884109	4.7826
Error	318	58784823	184858	**Prob > F**
C. Total	415	144543418		<.0001*

Student’s t test for LS97-1610 x Spencer for Yield

Level		Least Sq Mean
97	A	3922.2169
24	A B	3785.5089
18	A B C	3590.2118
26	A B C D E	3512.0929
55	B C D E F	3403.0521
72	B C D E F	3396.5422
98	B C D	3392.7447
77	B C D E F G	3363.9926

Level		Least Sq Mean
51	B C D E F G H	3329.8156
66	B C D E F G H I	3248.4419
52	B C D E F G H I J	3230.5396
49	B C D E F G H I J	3228.9121
25	B C D E F G H I J	3227.2847
91	C D E F G H I J K	3176.8329
93	C D E F G H I J K L	3132.8911
38	C D E F G H I J K L M	3129.6361
50	C D E F G H I J K L M N	3103.5965
29	C D E F G H I J K L M N	3080.8118
71	C D E F G H I J K L M N	3072.6745
39	C D E F G H I J K L M N	3067.7920
62	C D E F G H I J K L M N	3067.7920
6	C D E F G H I J K L M N	3053.1448
43	C D E F G H I J K L M N O	3002.6930
14	D E F G H I J K L M N O P	2991.3007
68	D E F G H I J K L M N O P	2991.3007
44	D E F G H I J K L M N O P	2988.0457
8	D E F G H I J K L M N O P Q	2963.6336
70	D E F G H I J K L M N O P Q R	2947.3588
85	E F G H I J K L M N O P Q R	2934.3390
42	E F G H I J K L M N O P Q R	2932.7115
60	E F G H I J K L M N O P Q R	2927.8291
54	E F G H I J K L M N O P Q R	2926.2016
13	E F G H I J K L M N O P Q R	2919.6917
53	F G H I J K L M N O P Q R	2909.9269
10	F G H I J K L M N O P Q R S	2888.7697

Level		Least Sq Mean
20	F G H I J K L M N O P Q R S	2888.7697
1	F G H I J K L M N O P Q R S T	2872.4949
7	F G H I J K L M N O P Q R S T U	2861.1026
78	F G H I J K L M N O P Q R S T U	2857.8476
57	F G H I J K L M N O P Q R S T U	2856.2202
69	F G H I J K L M N O P Q R S T U	2843.2004
92	F G H I J K L M N O P Q R S T U	2838.3179
40	F G H I J K L M N O P Q R S T U V	2812.2783
11	F G H I J K L M N O P Q R S T U V	2812.2783
16	F G H I J K L M N O P Q R S T U V	2810.6508
5	F G H I J K L M N O P Q R S T U V	2810.6508
63	F G H I J K L M N O P Q R S T U V W	2809.0234
23	G H I J K L M N O P Q R S T U V W	2797.6310
34	G H I J K L M N O P Q R S T U V W	2791.1211
46	G H I J K L M N O P Q R S T U V W	2781.3563
35	G H I J K L M N O P Q R S T U V W	2779.7288
73	G H I J K L M N O P Q R S T U V W	2778.1013
88	G H I J K L M N O P Q R S T U V W	2774.8464
17	H I J K L M N O P Q R S T U V W	2753.6892
21	H I J K L M N O P Q R S T U V W	2750.4342
84	H I J K L M N O P Q R S T U V W X	2747.1793
32	I J K L M N O P Q R S T U V W X	2727.6496
47	I J K L M N O P Q R S T U V W X	2721.1397
4	I J K L M N O P Q R S T U V W X	2721.1397
67	I J K L M N O P Q R S T U V W X Y	2690.2176
83	I J K L M N O P Q R S T U V W X Y	2685.3352
12	I J K L M N O P Q R S T U V W X Y	2685.3352

Level		Least Sq Mean
76	I J K L M N O P Q R S T U V W X Y	2682.0802
80	I J K L M N O P Q R S T U V W X Y	2677.1978
37	I J K L M N O P Q R S T U V W X Y	2673.9429
81	I J K L M N O P Q R S T U V W X Y	2664.1780
27	I J K L M N O P Q R S T U V W X Y	2662.5505
45	I J K L M N O P Q R S T U V W X Y Z	2657.6681
31	J K L M N O P Q R S T U V W X Y Z	2633.2560
90	K L M N O P Q R S T U V W X Y Z [	2612.0988
33	K L M N O P Q R S T U V W X Y Z [\	2603.9614
3	K L M N O P Q R S T U V W X Y Z [\	2595.8240
86	K L M N O P Q R S T U V W X Y Z [\	2592.5691
28	K L M N O P Q R S T U V W X Y Z [\	2590.9416
61	L M N O P Q R S T U V W X Y Z [\	2577.9218
48	L M N O P Q R S T U V W X Y Z [\ ]	2566.5295
58	M N O P Q R S T U V W X Y Z [\ ]	2533.9799
41	N O P Q R S T U V W X Y Z [\ ]	2517.7052
15	O P Q R S T U V W X Y Z [\ ]	2454.2336
64	P Q R S T U V W X Y Z [\ ]	2402.1544
87	Q R S T U V W X Y Z [\ ]	2387.5071
74	R S T U V W X Y Z [\ ] ^	2358.2125
82	R S T U V W X Y Z [\ ] ^	2351.7026
75	S T U V W X Y Z [\ ] ^	2293.1135
56	T U V W X Y Z [\ ] ^	2281.7212
89	T U V W X Y Z [\ ] ^	2276.8388
9	U V W X Y Z [\ ] ^	2270.3289
79	V W X Y Z [\ ] ^	2228.0145
94	W X Y Z [\ ] ^	2211.7397

Level		Least Sq Mean
22	X Y Z [\ ] ^	2151.5231
2	Y Z [\ ] ^	2118.9736
59	Z [\ ] ^	2060.3845
30	[\ ] ^	2016.4426
36	\ ] ^	2008.3052
19	] ^	1977.3832
65	^	1770.6938

ANOVA for LS97-1610 x Spencer for DX

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	100	106.67542	1.06675	7.5822
Error	711	100.03255	0.14069	**Prob > F**
C. Total	811	206.70798		<.0001*

Student’s t test for LS97-1610 x Spencer for DX

Level		Least Sq Mean
1	A	1.7525216
44	A B	1.6928132
22	A B C	1.6153499
25	A B C D	1.6115247
30	A B C D E	1.5988722
23	A B C D E F	1.5437690
9	A B C D E F G	1.5277581

Level		Least Sq Mean
17	A B C D E F G H	1.5047656
34	A B C D E F G H	1.4994758
50	A B C D E F G H	1.4941684
51	A B C D E F G H I	1.4831888
53	A B C D E F G H I J	1.4698799
33	A B C D E F G H I J K	1.4439313
43	A B C D E F G H I J K	1.4407109
72	A B C D E F G H I J K L	1.4319678
69	A B C D E F G H I J K L M	1.4242190
73	A B C D E F G H I J K L M N	1.4121180
41	A B C D E F G H I J K L M N	1.4079086
82	A B C D E F G H I J K L M N	1.4064946
18	A B C D E F G H I J K L M N O	1.3973774
47	A B C D E F G H I J K L M N O P	1.3898145
65	B C D E F G H I J K L M N O P Q	1.3742940
26	B C D E F G H I J K L M N O P Q R	1.3679114
80	B C D E F G H I J K L M N O P Q R S	1.3470431
99	C D E F G H I J K L M N O	1.3386643
14	B C D E F G H I J K L M N O P Q R S T	1.3337472
67	B C D E F G H I J K L M N O P Q R S T	1.3309894
66	B C D E F G H I J K L M N O P Q R S T	1.3304090
31	B C D E F G H I J K L M N O P Q R S T	1.3297454
32	C D E F G H I J K L M N O P Q R S T	1.3240363
88	C D E F G H I J K L M N O P Q R S T U	1.3151664
87	C D E F G H I J K L M N O P Q R S T U V	1.3057930
94	C D E F G H I J K L M N O P Q R S T U V	1.3046649
6	C D E F G H I J K L M N O P Q R S T U V W	1.2937734

Level		Least Sq Mean
56	C D E F G H I J K L M N O P Q R S T U V W	1.2846893
20	C D E F G H I J K L M N O P Q R S T U V W X	1.2782363
40	C D E F G H I J K L M N O P Q R S T U V W X	1.2766830
55	C D E F G H I J K L M N O P Q R S T U V W X Y	1.2673195
8	C D E F G H I J K L M N O P Q R S T U V W X Y	1.2658575
84	C D E F G H I J K L M N O P Q R S T U V W X Y	1.2639112
71	C D E F G H I J K L M N O P Q R S T U V W X Y	1.2627376
75	C D E F G H I J K L M N O P Q R S T U V W X Y Z	1.2607734
85	C D E F G H I J K L M N O P Q R S T U V W X Y Z	1.2551504
57	C D E F G H I J K L M N O P Q R S T U V W X Y Z	1.2544422
77	C D E F G H I J K L M N O P Q R S T U V W X Y Z	1.2534609
39	C D E F G H I J K L M N O P Q R S T U V W X Y Z	1.2516249
13	D E F G H I J K L M N O P Q R S T U V W X Y Z	1.2468674
24	E F G H I J K L M N O P Q R S T U V W X Y Z	1.2346416
92	E F G H I J K L M N O P Q R S T U V W X Y Z	1.2308968
78	F G H I J K L M N O P Q R S T U V W X Y Z	1.2293931
76	F G H I J K L M N O P Q R S T U V W X Y Z	1.2264731
29	F G H I J K L M N O P Q R S T U V W X Y Z	1.2016595
61	F G H I J K L M N O P Q R S T U V W X Y Z	1.1985793
2	F G H I J K L M N O P Q R S T U V W X Y Z	1.1869586
83	F G H I J K L M N O P Q R S T U V W X Y Z	1.1847043
68	F G H I J K L M N O P Q R S T U V W X Y Z	1.1766849
35	G H I J K L M N O P Q R S T U V W X Y Z	1.1706732
11	G H I J K L M N O P Q R S T U V W X Y Z	1.1650723
79	G H I J K L M N O P Q R S T U V W X Y Z	1.1611900
7	H I J K L M N O P Q R S T U V W X Y Z	1.1536952
59	H I J K L M N O P Q R S T U V W X Y Z [	1.1393568

Level		Least Sq Mean
91	I J K L M N O P Q R S T U V W X Y Z [\	1.1204995
70	I J K L M N O P Q R S T U V W X Y Z [\	1.1193713
90	I J K L M N O P Q R S T U V W X Y Z [\	1.1186898
42	I J K L M N O P Q R S T U V W X Y Z [\	1.1181200
36	J K L M N O P Q R S T U V W X Y Z [\	1.1141763
12	J K L M N O P Q R S T U V W X Y Z [\	1.1053595
38	K L M N O P Q R S T U V W X Y Z [\	1.0983370
93	K L M N O P Q R S T U V W X Y Z [\	1.0944175
16	K L M N O P Q R S T U V W X Y Z [\ ]	1.0799131
28	L M N O P Q R S T U V W X Y Z [\ ]	1.0670736
62	L M N O P Q R S T U V W X Y Z [\ ]	1.0658072
48	M N O P Q R S T U V W X Y Z [\ ] ^	1.0607598
52	N O P Q R S T U V W X Y Z [\ ] ^	1.0452388
60	O P Q R S T U V W X Y Z [\ ] ^ _	1.0377330
21	P Q R S T U V W X Y Z [\ ] ^ _ `	1.0267736
27	Q R S T U V W X Y Z [\ ] ^ _ `	1.0169532
10	R S T U V W X Y Z [\ ] ^ _ `	1.0023603
86	S T U V W X Y Z [\ ] ^ _ `	0.9828716
15	T U V W X Y Z [\ ] ^ _ `	0.9750407
49	T U V W X Y Z [\ ] ^ _ `	0.9718683
63	T U V W X Y Z [\ ] ^ _ `	0.9692619
46	U V W X Y Z [\ ] ^ _ ` a	0.9552219
64	V W X Y Z [\ ] ^ _ ` a	0.9397963
81	W X Y Z [\ ] ^ _ ` a	0.9282953
4	X Y Z [\ ] ^ _ ` a	0.9152513
58	Y Z [\ ] ^ _ ` a	0.9067822
3	Y Z [\ ] ^ _ ` a	0.9050601

Level		Least Sq Mean
54	Z [\ ] ^ _ ` a	0.8939829
74	[\ ] ^ _ ` a b	0.7842320
89	\ ] ^ _ ` a b	0.7644144
5	] ^ _ ` a b	0.7210873
37	^ _ ` a b	0.6933646
19	_ ` a b	0.6706431
45	` a b	0.6628633
97	a b	0.6402483
98	b	0.5556973

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APS annual meeting, August 4-8, 2012, Providence, RI

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