ABSTRACT

MACHACEK, JEREMY LEE. Genotypic Variation in Soybean for Early Season Ground Cover and Relation to Agronomic Traits of Soybean in Ultra-narrow, Narrow, and Wide Row-spacing and High Density Plant Populations. (Under the direction of Thomas E. Carter Jr. and S. Chris Reberg-Horton.)

Globally, organic soybean production has continued to rise, with increased usage as food, feed, and oils. Weed control remains an over whelming problem in organic production. Growing soybean in ultra-narrow rows at high plant population densities is a potentially effective means of weed control in organic soybean production. During 2014 and 2015 in North Carolina, genotypic variation in soybean was evaluated for enhanced ground cover at 3 weeks after emergence (3WAE), seed size, lodging resistance, and seed yield, at high plant population densities in ultra-narrow, narrow, and wide row-spacings. The first objective was to compare the agronomic performance of 24 diverse southern soybean genotypes of maturity groups (MG) V through VII and assess their potential impact on the efficacy of ultra-narrow (11cm) and wide (97 cm) row-spacing production under high plant population densities (231 and 41 seeds m^{-2}, respectively). Lodging at maturity and percent ground cover at 3WAE were greater ($p<0.05$) in the ultra-narrow compared to wide row-spacing and yield was greater ($p<0.05$) in two of the three test environments. Genotypic differences were evident for all agronomic traits, and genotype x row-spacing interaction was significant ($p<0.05$) for lodging at maturity, and seed yield for the MG VI genotypes. Some genotypes appeared to yield relatively more and lodge relatively less in ultra-narrow than wide rows. For example, breeding lines N06-6 and NCC09-135 yielded 1,280 and 1,000 $kgha^{-1}$ more in ultra-narrow than wide rows, while the average response of all genotypes was only 332 $kgha^{-1}$. These two also had among the lowest lodging scores in the study. Estimated profit returns were also greater ($1082 and $790 ha^{-1}) in ultra-narrow vs. wide rows for these two genotypes as compared to a profit increase of only $143 ha^{-1} for the mean of all genotypes. Thus, soybean production in ultra-narrow rows at high plant

densities may have merit as a method to enhance canopy closure and potentially suppress weeds in organic production.

The second objective was to determine the impact of seed size (large vs. small) and plant population density (10 and 26 beans m^{-1}) on early season ground cover in ultra-narrow (11 cm) and narrow (23 cm) row-spacing for seven contrasting soybean genotypes. Mean percent ground cover at 3WAE was increased 7 percentage units by planting larger seed, 11 percentage units by employing higher seeding rate, and 15 percentage units in ultra-narrow vs. narrow row-spacing. These effects were additive and the greatest ground cover was observed in the ultra-narrow rows when planting larger seed at higher plant densities. Genotypic means for 3WAE ranged from 60 to 78% ($p<0.05$) for this combination of treatments. Genotype x plant-population interactions were detected ($p<0.05$) for most traits except seed yield and maturity date. Genotypes which exhibited greater ground cover at 3WAE in ultra-narrow rows production also tended to have greater unifoliate size and 100-seed weight for planting seed. The higher seeding rate reduced ($p<0.01$) yield 9 %. The interaction of treatment variables with genotype was more apparent for seed yield than for ground cover. However, genotype x treatment interactions for both traits suggest that identification of genotypes adapted to ultra-narrow production should be accomplished by evaluation in the specific row-spacing-planting-density and seed size combination targeted for production. A potential problem with respect to the ultra-narrow rows was a negative correlation among genotypic means for percent ground cover at 3WAE and lodging resistance. The two genotypes with the greatest percent ground cover in the ultra-narrow row-high-planting-density-large seed size management combination were also the poorest for lodging resistance. Although no one particular genotype seemed to fit all the criteria needed to be an excellent cultivar for the ultra-narrow system, the elements of an ideal cultivar for ultra-narrow row production were clearly present in the collection of genotypes in the study.

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Genotypic Variation in Soybean for Early Season Ground Cover and Relation to Agronomic Traits of Soybean in Ultra-narrow, Narrow, and Wide Row-spacing and High Density Plant Populations

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DEDICATION

I wish to dedicate this thesis to my fabulous family. My debonair daughter and wonderful wife, you are the best things in my life. Colleen, thank you for the encouragement and help throughout the many years of school. Thank you for your patience, love, and guidance during my college career. I also want to dedicate this to my brother, Brian. I look up to you more than you may know and you have been my inspiration from the beginning, a genuine gentleman. Additionally to my superb sisters, Lisa and Renee, for always having time to look out for me. Finally I dedicate this thesis to my perfect parents, Darlene and Ron, for always having faith in me, and for their love and support.

BIOGRAPHY

Jeremy Lee Machacek was born in 1980 and raised in Wisner, Nebraska. After completing a B.S. in Horticultural Science at North Carolina State University in 2013, he began his M.S. in Crop Science at North Carolina State University. His research under Dr. Carter was focused on improvement and development of an organic soybean. After graduation, Jeremy will begin work as a sweetpotato field breeder at North Carolina State University.

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Literature Review

Introduction

Although soybean [*Glycine max (*L.) Merrill] is an ancient crop in Asia, it has been an important seed crop in the global seed trade market only since the 1950s. Global soybean production is predicted to be 324 million metric tons for 2016-2017 (USDA ERS, 2016) with South America leading the way as the largest producer of soybean. Brazil and Argentina harvested an estimated 103 and 57 million metric tons, respectively in 2016 (USDA ERS, 2016). In the USA soybean production is forecast to be 103 million tons, and oil exports were near 1.1 million tons in 2015 (USDA Foreign Agricultural Service [FAS], 2016). The USA crushes over 41 million metric tons of soybean annually (USDA, 2016).

Dry soybean seed, on average, are approximately 40% protein, 20% oil, 35% carbohydrates, and 5% ash (Liu, 2005), making them higher in seed protein content than most other seed crops and a major protein feed source for animal production (USDA-ERS, 2016). Approximately 70% of high protein feed comes from soybean meal, globally (USDA ERS, 2016). In addition to high protein content, soybean has the second highest oil content compared to other oilseed crops. Soybean oil production is expected to grow to over 300 million metric tons of oilseed in 2016 (USDA FAS, 2016).

Origin of Soybean

Glycine max, the domesticated soybean, originated in the eastern part of Northern China approximately 3,000 to 5,000 years ago, and is one of the older domesticated commodity agricultural crops (Hymowitz and Bernard, 1991; Gai et al., 1999). The wild annual soybean *Gylcine soja* (Seib. and Zucc.) is believed to be the progenitor and it exists

throughout much of Asia, including China, eastern Russia, Vietnam, Korea, and Japan (Hymowitz and Bernard, 1991). Although the wild soybean is viny, small seeded, and at first glance strikingly different in architecture from the domesticated plant, both *G. max* and *G. soja* have 40 chromosomes (2n=2x=40), and freely hybridize to produce fertile progeny (Palmer et al., 1996). Approximately 700 unique accessions of wild soybean are preserved in the USDA soybean germplasm collection (Song, personal comm., 2016) and as a group are more diverse for single nucleotide polymorphisms (SNPs) than is the domesticated collection of more than 20,000 accessions (Carter et al., 2004). Delheimer (2012), and Ruff (2013) have indicated that wild soybean may be a source of yield quantitative trait loci (QTL).

Although wild soybean is freely compatible with the domesticate and exhibits traits of economic interest, thus far only a few USA specialty soyfoods (natto) varieties trace their pedigree to the wild soybean, primarily as a source of small seed size (Carter and Shanmugasundaram, 1993). The major limitation of using wild soybean in applied breeding is the large number of genes that control upright growth habit. Most breeding populations derived from wild soybean have a canopy architecture that resembles the wild soybean more than cultivars (Weber, 1950; Delheimer, 2012).

Production in the United States and North Carolina

Soybean (referred to as ‘Chinese vetches’ in older literature) was introduced to America in the 1700s by ex-mariner Samuel Bowen into the Colony of Georgia where he grew soybean on Skidaway Island near Savannah. Bowen received numerous royal patents for the production of American soy sauce and marketed this product to England extensively

for more than two decades (Hymowitz and Shurtleff, 2005). In 1804, Dr. James Mease coined the word “soybean” referring to the bean which produced soy sauce (Mease, 1804). Soybean was reintroduced in North America in the 1870s as a forage crop and as a rotational or green manure legume to replenish soil nitrogen. The first commercial extraction of soybean oil from seed was commenced in Elizabeth City, North Carolina in 1915, by modifying cotton seed presses already in use (Carter and Shanmugasundaram, 1993). North Carolina was the USA’s leading soybean producer in 1924. By the 1930s soybean was grown in the USA about equally for forage and seed in the southern USA. With the release of the productive cultivar ‘Lee’ soybean by USDA in 1953, soybean forage production virtually disappeared in the South and has remained a seed crop to the present (Carter and Shanmugasundaram, 1993). However, the center of production quickly expanded to the Midwest and by the 1990s nearly 80% of USA soybean production was in the Midwest, which is current today (Goldberg, 1952).

North Carolina planted 728, 745 hectares of soybean in 2015 (USDA-NASS, 2016), with the majority of soybean production located east of Interstate 95 in North Carolina, with the exception of Union County (USDA-NASS, 2012).

Organic Soybean

National standards define certified organic production in the USA as production on land that has been free of synthetic chemicals (e.g. pesticides and refined fertilizers) for a period of three years and that the harvested crop itself is free of synthetic chemicals and not genetically modified (GMO Electronic Code of Federal Regulations, 2016). Total organic soybean hectarage in the USA is 53,418 or less than 2% of soybean production (USDA,

2016). Consumer demand for organic products has increased 11% since 2011, and future demand is expected to follow the same growth trend (USDA-EMS, 2016). Some of the increased demand has been driven by increased consumption of organic livestock, which require organic feed sources for organic certification. North Carolina is estimated to produce 901,376 organic chicken hens for 2016 (USDA-AMS, 2016).

North Carolina organic soybean production is low (647 hectares in 2011; USDA 2012), and this may be a reflection that soybean cultivars are not well adapted for an organic cropping system in the state, especially in terms of weed control. Organic farmers reported weed management as the most challenging role in organic production (Cavigelli et al., 2008; Walz, 1999).

Introduction to Weeds

Weeds are often thought of as a plant out of place and as defined by the Weed Science Society of America, “any plant that is objectionable or interferes with the activities or welfare of man” (Weed Science Society of America, 2014). Weeds can survive and often thrive under poor environmental conditions such as excess heat, drought, and flooding. This plastic nature of weeds has also made control difficult for farmers. For example, the weed species Palmer amaranth (A*maranthus palmeri)* is able to produce half a million seeds per plant annually. Its optimal growing temperature is 42 degrees Celsius (C), much greater than soybean which has an optimum of less than 32 degrees C, and can reproduce from seed to seed in 45 days (a much shorter life cycle than for soybean) (Everman personal comm., 2015). However, despite advantages that weed species may have in crop production weeds are relatively intolerant to shading.

In soybean, weed pressure can reduce yield drastically. A comparison of weedy and weed-free experimental plots showed that six weeks of weed competition may reduce soybean yield 36% (Rose et al., 1984). In a weed comparison study (broadleaf vs. grass weeds), it was reported that broadleaf weeds cause the greater yield reduction in soybean (Bussan et al., 1997). Yield in soybean was reduced 22% from 16 pigweed (*Amaranthus*) plants per 10 m of row (Shurtleff and Coble, 1985). Provided soybean plants are weed-free for the first few weeks of the season, they are able to compete well and provide enough weed suppression to minimize weed impacts on seed yield (Burnside, 1979; Van Acker et al., 1993).

Organic Breeding

Typical non-organic soybean breeding programs (both GMO and conventional) target seed yield improvement under minimal stress and nematode and disease resistance as primary traits for genetic advance. Although these traits have obvious utility in organic production just as in conventional production, additional genetic traits are also potentially important to organic farmers but are paid little attention. One example is resistance to lodging under high plant population densities. Decreased row-spacing and increased plant density is a common weed suppression strategy in organic production, but seldom evaluated in other production systems (Hoad et al., 2012) but may lead to the problem of increased or excessive lodging at maturity.

A second often overlooked trait potentially important to organic production is enhanced early season canopy cover and competitiveness with weeds. Genetic variations for weed competition has been identified in soybean and component traits of interest may

include rate and success of soybean seed emergence, production of large leaves, rapid leaf expansion, vigorous growth, and early season increased plant height (Place et al., 2011b; Hoad et al., 2012). Given that breeding targets can differ for organic vs. other soybean production systems, initiation of a breeding program specifically for organic systems may result in faster adaptation of cultivars to organic production than reliance solely upon current conventional breeding programs (Murphy et al., 2008; Hoad et al., 2012). At present, no commercial, USDA, or university soybean breeding programs specifically target organic production in the USA (Carter, personal comm., 2016).

Breeding for Enhanced Ground Cover

An organic breeding program may approach weed suppression ability (WSA) conceptually in the same manner as a conventional program would integrate disease resistance into an overall breeding strategy. Early growth traits and greater plant height should be considered component traits of WSA for selection and breeding (Jannink et al., 2000). Early season percent ground cover is often used as a surrogate of WSA (Place et al., 2001b). Digitized images of canopy ground cover have been found to be a good measure of shading ability and suppression potential (Hoad et al., 2012). The initial screening for this ground cover can be performed in weed-free plots (Place et al., 2011b; Worthington, 2013).

Planting later maturing cultivars for a locality has historically been the only genetic trait used to improve weed competition in soybean (Place et al., 2011a). Later maturing soybean cultivars can shade the ground for as much as three weeks longer than early maturing cultivars during the growing season (Place et al., 2011a; Hoad et al., 2012). Rose

et al. (1984) tested 280 soybean cultivars and found later maturity groups were more competitive with weeds, and that later maturing soybean genotypes were able to recover from weed pressure better than earlier maturing types. Later maturity soybean groups were reported as having better early season competition and greater season long weed suppression (Knezevic et al., 2002), resulting in higher yield. Soybean weed management research showed that later maturing soybean demonstrated 94% weed control compared to 30% in early maturing soybean at harvest and that differences in weed suppression were related to incident light interception (Nordby et al., 2007).

Breeders interested in developing new soybean breeding lines with superior weed suppression capability should consider growth habit, speed of early development, plant height, and leaf size (Hoad et al., 2012). Soybean cultivars differ for speed of emergence, speed of ground cover development, and ability to control weed growth (Rose et al., 1984). A wider leaf width may be a potential trait for improving ground cover (Huel and Huel, 1996). Additionally, tall or very tall soybean lines appeared most competitive when established in high plant populations (Hoad et al., 2012). Heritability was shown to be high for early season height and that height was correlated with WSA, suggesting this trait may have utility in breeder selection (Jannink et al., 2000). However, the presence of a negative correlation of WSA with lodging and soybean seed yield may cause breeding for WSA to be a challenging task (Jannink et al., 2000). The negative correlation of yield with ground cover is not always present for each crop and weed combination (Caton et al., 2001).

Seed Size and 100-seed weight

100-seed weight is an agronomic trait commonly used to describe soybean cultivars (Gillen and Shelton, 2013). Soybean 100-seed weight ranges from less than 4g for most

wild soybean accessions to well over 40g for some domesticated types (USDA-GRIN, 2015). Commodity cultivars in the USA vary typically from 13 to 19 grams per 100-seed weight. A specialty Japanese breakfast soyfoods product, natto, requires a 100-seed weight less than 10g for processing (Carter and Shizerimdum, 1993). The small size is prized traditionally because the mature bean is relatively intact in the fermented product and affects 'mouthfeel'. Tofu generally requires a 100-seed weight greater than 20g for good processing. Larger seed have a lower seed to seed coat weight ratio and, thus, the unusable seed coat in tofu processing is minimized as a by-product when using larger seed. Edamame or vegetable soybean seed are typically greater than 24g 100 seed^{-1} at maturity and is eaten as whole bean shelled from the pod (Carter and Shizerimdum, 1993).

To clean harvested seed, soybean are sieved using metal round hole screens to sort and remover trash and broken seed (splits) and often to size the seed (e.g. remove large or small seed) to make the seed appear more uniform. Screen types are round (scalping screen) or slotted (sifting screen) holes ranging in size from 4/64 to 26/64 inches.

In soybean, grams 100-seed^{-1} may be used as an easily measured surrogate for the more traditional seed size descriptor of soybean. Seed size and 100-seed weight generally correlate well when comparing genotypes, because genotypes do not vary drastically for seed density under normal growing conditions. In general, increasing the hole in a sieving screen by 1/64th screen equates to about 1g increase for small seed to 4g for large seed. A typical soybean which exhibits 14g 100-seed^{-1} contains about 3,000 seed pound^{-1}.

There is greater energy and nitrogen reserve in a larger seed compared to smaller seed, as larger seed have a larger cotyledon which provides extra nutrient reserves for emergence and early growth (Burris et al., 1971). In early growth stages many crops have a seed size advantage over weed seed due to large reserves and a relatively large seedling

(Mohler, 1996). Previous research in soybean has shown that larger seed tend to produce taller plants early in the season and, thus, a larger seed size at planting may enhance early season weed control (Place et al., 2011a). A comparison of soybean genotypes under weed-free and weedy conditions showed that larger seed competed better against weeds, than did smaller seed, suggesting that sorting and saving of larger seed for planting may be a cost-effective tactic that organic farmer can implement as a part of organic weed management (Place et al., 2011a). Smith and Camper (1975) reported that larger seed size may translate to increased yield in soybean, in that larger seed from a larger seed genotype had 5.4% higher yield compared to a smaller seed genotype in ten experiments.

Suppression from Shading

Increasing the amount of shade to reduce weed growth has been thought of as a form of organic weed control. Producing greater soybean canopy faster led to suppressed weed growth, such that three weeks of weed-free conditions maximized seed yield (Murphy and Gossett, 1981). Stoller and Myers (1989) evaluated plots in full sunlight to 94% shade treatments using artificial shade in the field and showed that increased shade reduced growth and the number of shoots and berries in eastern black nightshade (*Solanum ptycanthum*). Decreasing the soybean row-spacing from 76 to 37.5 cm rows produced eight times fewer berries per nightshade plant. Additionally, shoot growth was reduced by 83% in 80% shade. Employing narrow row-spacing resulted in 40% weed mortality by the last harvest, and weeds were weaker and unable to support continued growth.

Decreased row-spacing in soybean combined with higher seeding rates prevented reproduction and suppressed growth in sicklepod (*Senna obtusifolia)* (Nice et al., 2001).

Comparing 76, 38, and 19 cm row-spacing, decreasing row width reduced sicklepod population up to 80%, and 65 or higher percent shade reduced weed height and dry weight. Planting at a higher seeding rate had no additional effect of sicklepod reduction while the 19 cm row-spacing led to the greatest reduction in sicklepod growth. Shade of 80 to 95% inhibited growth and reduced sicklepod growth 69%, which implies that denser soybean canopies can be an effective weed control method. Additionally, late emerging sicklepod were suppressed by soybean canopy. Rapid ground cover was enhanced with narrow row-spacing and demonstrated enough shade to suppress sicklepod (Nice et al., 2001).

Seeding Rate

The average North Carolina organic soybean farmer plants approximately, 494,210 seed ha^{-1} (Reberg-Horton, personal comm., 2014). Increased seeding rate or plant density has been explored as a weed control option. One hypothesis to explain an advantage of elevated seeding rate of weed control is that a crop may simply consume more available resources in the field and, thus, deprive the weed of needed nutrients, water, and space (Johnson, 1987). Another hypothesis is that weed control is primarily a function of competition for light (Johnson 1987; DeWerff et al., 2014). In North Carolina seeding rate 185, 309, 432, and 556 thousand live seeds ha^{-1} were evaluated for weed control in organic soybean production and at 556,000 live seed ha^{-1} results showed increased seeding rate to have greater weed control in the organic systems than in the conventional systems (Place et al., 2009). The results suggest the highest seeding rate may improve weed control in organic soybean production. Soybean grown in high density populations may have fewer

branches, greater lodging, fewer pods, and fewer seed per plant (Weber et al., 1966), and yet seed yield may not be affected (Seadh and Abids, 2013). Higher seeding rate alone may not have sufficient merit to be a standalone weed control option, and it has been suggested that new cultivars may need to be developed which are better able to take advantage of increased planting density to boost the potential cultural weed control in organic production (Place et al., 2009).

Seeding rate has also been evaluated for optimal density and yield return. A seeding rate up to 556,000 live seed ha^{-1} in 76 cm rows has been reported to have greater weed control, higher seed yields, and increased profit for organic growers compared to lower seeding rates (Place et al., 2009). The yield boost may be a response to greater weed control. Higher plant populations did not increase lodging effects (Place et al., 2009).

Row-spacing

Row-spacing in soybean production can greatly vary, ranging from 18 to 97 cm row width. In North Carolina, the current organic soybean row-spacing average is 76 cm, which is sufficiently wide to support between row cultivation as mechanical weed control. Decreasing the row-spacing may speed the rate of canopy closure, increasing between–row shading, which may improve weed control in organic systems but may also reduce or eliminate the possibility of cultivation (Cooper, 1977; Jannink et al., 2000; Nordby et al., 2007; Hoad et al., 2012). Wide row-spacing in soybean have been reported to require a longer critical weed-free period than narrow rows to realize seed yield potentials (Knezevic et al., 2002).

Soybean canopies have been shown to reduce weed growth in narrow vs. wide rows, suggesting that reduced light reaching soil results in less weed re-growth (Yelverton and Coble, 1991). Decreasing row width showed an effect on ground cover, but of the two tested soybean cultivars there were no ground cover differences (Yelverton and Coble, 1991). Narrow row-spacing in soybean may reduce weed growth while showing no impact on plant maturity date and height (Seadh et al., 2013; DeWerff et al., 2014). Additionally, lodging was relatively unaffected by row width, although lodging tended to increase at higher soybean plant density (Seadh et al., 2013). Higher soybean plant density in narrow rows did not produce additional yield in Louisiana (Board et al., 1990). Row-spacing has been reported as more critical than plant spacing in terms of influencing seed yield in soybean (Aslam et al., 1993). Board et al. (1990) showed significant seed yield increase in narrow rows, and more so when planted at later dates. The increase in seed yield is related to narrow rows having greater light interception and duration. Studies reported 95% light interception prior to the soybean R5 growth stage in the narrow rows (Board et al., 1990).

Narrow row-spacing had higher heritability for seed yield of 37 soybean lines compared to wide rows, suggesting yield trials are more informative when performed in narrow rows (Weaver and Wilcox, 1982). However, Weaver and Wilcox also reported there is no penalty for early generation selection and evaluation in wide rows with later evaluation and production in narrow rows. De Bruin and Pedersen (2008) reported higher soybean seed yield in narrow vs. wide rows, but increased production cost for narrow rows and high seeding rate was not offset by higher yield. In addition, the highest mean yield was reported in 10 cm row-spacing compared to the other treatments (Safo-Kantanka and Lawson, 1980). Ethredge et al. (1989) showed that seed yield increased as row spacing decreased and that the response for cultivar ‘Essex’ was greater than for cultivar ‘Detapine 105’ demonstrating a

cultivar x row-spacing interaction. This cultivar x row-spacing interaction suggested the treatment combination response is dependent on the cultivar (Burnside, 1979).

Early maturity soybean groups may respond better to narrow rows (Safo-Kantanka and Lawson, 1980). Cooper (1977) showed 17 cm narrow rows in combination with earlier maturity genotypes tended to have the highest yields while no differences in lodging were reported for the contrasting row-spacing. Maturity group had no effect on soybean canopy in wide vs. narrow rows (Nordby et al., 2007). However, early soybean maturity groups were found to have more weed issues later in the season compared to late soybean maturity groups (Yelverton and Coble, 1991).

Soybean 100-seed weight and seed per plant were not affected by row-spacing. However, average weed growth was higher in 76 vs. 38cm rows (Burnside, 1979). After the first month, the soybean were sufficiently established to provide their own weed control and the study reported some cultivars were more competitive against both early and late emerging weeds. Cooper (1977) suggested that the variety x row-spacing interaction is a critical component of selection.

Van Acker et al. (1993) showed that narrower row-spacing enhanced soybean competitiveness compared to wide row-spacing. Additionally, their results showed genotype differences in ground cover and leaf size. Weed suppression from genetic and management improvements in soybean canopy may have merit. However, more genetic variation may be needed for greater early ground cover and leaf area than exists in current cultivars (Vollmann et al., 2010).

Although past soybean research has tested a range of production systems under varying row-spacing, few studies have reported information on row-spacing narrower than 12 cm. A study conducted in 1966 evaluated soybean cultivar ‘Hawkeye’ under 13, 25, 51,

and 102 cm with four plant population (54, 128, 256, 516 thousands of plants per hectare), found the highest seed yield at 25 cm rows with 256,000 plants per hectare. Soybean dry weight was greatest in 13 cm rows at 516,000 plants per hectare (Weber et al., 1966). In Quebec in 1980, a study compared soybean cultivars 'Altona' and 'Clay' under four row-spacings (10, 15, 20 and 30 cm) at seeding rates from 11,000 to 4,000,000 plants per hectare. The results reported more rapid canopy cover in narrower rows, and the 10 cm row-spacing treatment showed the highest mean seed yield (Safo-Kantanka and Lawson, 1980). Additionally, in the treatment combination of 10 cm rows and 4,000,000 plants ha^{-1} seeding rate responded with the best soybean emergence of the study (Safo-Kantanka and Lawson, 1980). Early maturity genotypes responded better for seed yield under narrower row-spacing. Based on these outcomes, use of narrower row-spacing to enhance ground cover may require more investigation.

REFERENCES

Archer, David W; Jaradat, Abdullah A; Johnson, Jane MF; Weyers, Sharon Lachnicht; Gesch, Russ W; Forcella, Frank; Kludze, Hillarius K. Crop productivity and economics during the transition to alternative cropping systems. Agron.J., 2007, 99, 6, 1538-1547, American Society of Agronomy

Aslam, M., N. Khan, and M.S. Mirza. 1993. Effect of different row and plant spacings on soybean yield and its components. Pakistan Journal of Agricultural Research 14:143-148.

Board, J., B. Harville, and A. Saxton. 1990. Narrow-row seed-yield enhancement in determinate soybean. Agron. J. 82:64-68.

Burnside, O. 1979. Soybean (*Glycine max*) growth as affected by weed removal, cultivar, and row spacing. Weed Sci. 562-565.

Burris, JS; Wahab, AH; Edje, OT. Effects of seed size on seedling performance in soybeans. I. Seedling growth and respiration in the dark. Crop Sci., 1971, 11, 4, 492-496, Crop Science Society of America

Bussan, A.J., O.C. Burnside, J.H. Orf, and K.J. Puettmann. 1997. Field evaluation of soybean (*Glycine max*) genotypes for weed competitiveness. Weed Sci.31-37.

Carter Jr, TE; Hymowitz, T; Nelson, RL. Biogeography, local adaptation, Vavilov, and genetic diversity in soybean Source 2004, 47-59, Springer

Carter, T.E., R.L. Nelson, C.H. Sneller, and Z. Cui. 2004. Genetic diversity in soybean. Soybeans: Improvement, Production, and Uses 303-416, American Society of Agronomy, Crop Science Society of America, Soil Science Society of America

Caton, B., T. Foin, J. Hill and A. Mortimer. 2001. Measuring crop competitiveness and identifying associated traits in cultivar field trials. p. 139-145. In Measuring crop competitiveness and identifying associated traits in cultivar field trials. Proceedings from the 18th Asian pacific weed science society conference, Beijing, China, 2001.

Cavigelli, Michel A; Teasdale, John R; Conklin, Anne E. Long-term agronomic performance of organic and conventional field crops in the mid-Atlantic region. Agron.J., 2008, 100, 3, 785-794, American Society of Agronomy

Cooper, R. 1977. Response of soybean cultivars to narrow rows and planting rates under weed-free conditions. Agron. J. 69:89-92

De Bruin, J.L., and P. Pedersen. 2008. Effect of row spacing and seeding rate on soybean yield. Agron. J. 100:704-710.

Delheimer, J.C. 2012. Agronomic and molecular analysis of populations developed from a single cross of adapted x wild soybean. (Under the direction of Dr. Thomas E. Carter, Jr.). Ph.D. dissertation. North Carolina State University.

DeWerff, R.P., S.P. Conley, J.B. Colquhoun, and V.M. Davis. 2014. Can soybean seeding rate be used as an integrated component of herbicide resistance management? Weed Sci. 62:625-636.

Ecfr. 2016. Electronic Code of Federal Regulations (accessed 12 January 2016)

Ethredge, W., D. Ashley, and J. Woodruff. 1989. Row spacing and plant population effects on yield components of soybean. Agron. J. 81:947-951.

Gai, J., D. Xu, Z. Gao, T. Zhao, Y. Shimamoto, J. Abe, H. Fukushi and S. Kitajima. 1999. Genetic diversity of annual species of soybeans and their evolutionary relationship in china. p. 515. In Genetic diversity of annual species of soybeans and their evolutionary relationship in china. Proc. world soybean res. conf. VI, Chicago, IL, 1999.

Gillen, A.M., and G.W. Shelton. 2013. Uniform soybean tests, southern states, 2012. USDA-ARS, Stoneville, MS.

Goldberg, R. 1952. The soybean industry, Minneapolis. 1952, University of Minnesota Press

Hoad, S.P., N. Bertholdsson, D. Neuhoff, U. Köpke, E. van Bueren, and J. Myers. 2012. Approaches to breed for improved weed suppression in organically grown cereals. Organic Crop Breeding 61-76.

Huel, D., and P. Hucl. 1996. Genotypic variation for competitive ability in spring wheat. Plant Breeding 115:325-329.

Hymowitz, T., and R. Bernard. 1991. Origin of the soybean and germplasm introduction and development in North America. Use of Plant Introductions in Cultivar Development Part 1147-164.

Hymowitz, T; Shurtleff, WR. Debunking soybean myths and legends in the historical and popular literature. Crop Sci., 2005, 45 (2) 473-476.

Jannink, J., J. Orf, N. Jordan, and R. Shaw. 2000. Index selection for weed suppressive ability in soybean. Crop Sci. 40:1087-1094.

Johnson, William G; Kendig, J Andrew; Massey, Raymond E; Defelice, Michael S; Becker, Chad D. Weed control and economic returns with postemergence herbicides in narrow-row soybeans (*Glycine max*). Weed Technol., 1997, 453-459, JSTOR

Knezevic, S.Z., S.P. Evans, E.E. Blankenship, R.C. Van Acker, and J.L. Lindquist. 2002. Critical period for weed control: The concept and data analysis. Weed Sci. 50:773-786.

Liu, K. 2005. Soybeans as functional foods and ingredients.

Mease, J. 1804. The Domestic Encyclopedia, A. F. M. Willich, ed. 1st Amer. ed., Vol. 5: 13. Philadelphia

Mohler, C.L. 1996. Ecological bases for the cultural control of annual weeds. J. Prod. Agric. 9:468-474.

Murphy, K., J. Dawson, and S. Jones. 2008. Relationship among phenotypic growth traits, yield and weed suppression in spring wheat landraces and modern cultivars. Field Crops Res. 105:107-115

Murphy, T., and B. Gossett. 1981. Influence of shading by soybeans (*Glycine max*) on weed suppression. Weed Sci. 610-615.

Nice, G.R., N.W. Buehring, and D.R. Shaw. 2001. Sicklepod (*Senna obtusifolia*) response to shading, soybean (*Glycine max*) row spacing, and population in three management systems 1. Weed Technol. 15:155-162.

Nordby, D.E., D.L. Alderks, and E.D. Nafziger. 2007. Competitiveness with weeds of soybean cultivars with different maturity and canopy width characteristics. Weed Technol. 21:1082-1088

Palmer, R.G., T.Hymowitz, and R.L. Nelson. 1996. Germplasm diversity within soybean. p. 1–35. In D.P.S. Verma and R.C. Shoemaker (ed.) Soybean: Genetics, molecular biology and biotechnology. C.A.B. International, Wallingford, Oxon, UK

Place, G., S.C. Reberg-Horton, T. Carter, and A. Smith. 2011a. Effects of soybean seed size on weed competition. Agron. J. 103:175-181.

Place, G.T., D.A. Dickey, and T.E. Carter. 2011b. Identifying soybean traits of interest for weed competition. Crop Sci. 51:2642-2654.

Place, G.T., S.C. Reberg-Horton, J.E. Dunphy, and A.N. Smith. 2009. Seeding rate effects on weed control and yield for organic soybean production. Weed Technol. 23:497-502.

Rose, Steven J; Burnside, Orvin C; Specht, James E; Swisher, Beth A. Competition and allelopathy between soybeans and weeds. Agron.J., 1984, 76, 4, 523-528, American Society of Agronomy

Ruff, L.A. 2013. Heterosis as Evidence of Yield Alleles from Wild Soybean. (Under the direction of Dr. Thomas E. Carter, Jr.). Ph.D. dissertation. North Carolina State University.

Safo-Kantanka, O., and N.C. Lawson. 1980. The effect of different row spacings and plant arrangements on soybeans. Canadian Journal of Plant Science 60:227-231.

Seadh, S., and W. Abido. 2013. How soybean cultivars canopy affect yield and quality. Journal of Agronomy 12:46.

Seadh, S.E., Attia, A.N., El-Moursy, S.A., Said, E.M. and El-azab A.A.S. 2013. Productivity of maize as affected by organic, foliar and nitrogen fertilization levels. World Research Journal of Agronomy 2(1): 30-36.

Shurtleff, J.L., and H.D. Coble. 1985. Interference of certain broadleaf weed species in soybeans (*Glycine max*). Weed Sci.654-657.

Smith, T., and H. Camper. 1975. Effects of seed size on soybean performance. Agron. J. 67:681-684.

Stoller, E., and R. Myers. 1989. Effects of shading and soybean *Glycine max* (L.) interference on *Solanum ptycanthum* (dun.)(eastern black nightshade) growth and development. Weed Res. 29:307-316.

USDA, 2016. The United States Department of Agriculture (USDA). www.usda.gov (accessed 05 January 2016).

USDA-AMS, 2016. The USDA Agricultural Marketing Services. www. ams.usda.gov (accessed 10 November 2016).

USDA-ARS National Genetic Resources Program (USDA-ARS NGRP). 2012a. *Glycine max* (L.) Merr. PI 416937 Germplasm Resources Information Network (GRIN). National Germplasm Resources Lab., Beltsville, MD. http://www.ars-grin.gov/cgi-bin/npgs/acc/display. pl?1314868 (accessed 28 Sept. 2013).

USDA-ERS, 2016. The USDA Economic research Service. www.ers.usda.gov (accessed 15 January 2016)

USDA-FAS, 2016. The USDA Foreign Agricultral Service. www.fas.usda.gov (accessed 10 January 2016).

USDA-NASS, 2012. The USDA National Agricultural Statistics Service. Www.nass.usda.gov (accessed 21 January 2016)

Van Acker, R.C., C.J. Swanton, and S.F. Weise. 1993. The critical period of weed control in soybean [*Glycine max* (L.) merr.]. Weed Sci.194-200.

Vollmann, J., H. Wagentristl, and W. Hartl. 2010. The effects of simulated weed pressure on early maturity soybeans. Eur. J. Agron. 32:243-248.

Walz, E., 1999. Final Results of the Third Biennial National Organic Farmers' Survey. Organic Farming Research Foundation, Santa Cruz, CA, USA

Weaver, D., and J. Wilcox. 1982. Heritabilities, gains from selection, and genetic correlations for characteristics of soybeans grown in two row spacings. Crop Sci. 22:625-629.

Weber, C., R. Shibles, and D. Byth. 1966. Effect of plant population and row spacing on soybean development and production. Agron. J. 58:99-102.

Weber, Charles R. Inheritance and interrelation of some agronomic and chemical characters in an interspecific cross in soybeans, *Glycine max* × *G. ussuriensis*. Research Bulletin.Iowa Agricultural Experiment Station, 1950, 374

Worthington, M.L. 2013. Breeding Winter Wheat for Improved Powdery Mildew Resistance and Weed Suppressive Ability against Italian Ryegrass. (Under the direction of J. P. Murphy and S. Chris Reberg-Horton). Ph.D. dissertation. North Carolina State University.

WSSA, 2014. Weed Science Society of America. Www. Wssa.net (accessed 12 January 2016)

Yelverton, F.H., and H.D. Coble. 1991. Narrow row spacing and canopy formation reduces weed resurgence in soybeans *(Glycine max*). Weed Technol.169-174.

CHAPTER 2

Genotypic Variation in Soybean for Lodging Resistance, Canopy Ground Cover, and Yield in Ultra-narrow and Wide Row Spacing with High Density Plant Populations

Abstract

Growing soybean in ultra-narrow rows at high plant population densities is a potentially effective means of weed control in organic soybean production. Our objective was to compare the agronomic performance of 24 diverse southern soybean genotypes of maturity groups (MG) V through VII and assess their potential impact on the efficacy of ultra-narrow (11 cm) and wide (97 cm) row spacing production under high plant population densities (231 and 41 seeds m^{-2}, respectively). The experimental design was a split-plot employing four replications in three North Carolina environments during 2014-2015. Whole plots were assigned to row-spacing and sub-plots to genotype. Lodging at maturity and percent ground cover at three weeks after emergence (3WAE) were greater ($p<0.05$) in the ultra-narrow compared to wide row spacing and yield was greater ($p<0.05$) in two of the three environments. Genotypic differences were evident for all agronomic traits, and genotype x row spacing interaction was significant ($p<0.05$) for lodging at maturity, and seed yield among the MG VI genotypes. Some genotypes appeared to yield relatively more and lodge relatively less in ultra-narrow than wide rows. For example, breeding lines N06-6 and NCC09-135 yielded 1280 and 1000 $kgha^{-1}$ more in ultra-narrow than wide rows, while the average response of all genotypes was only 332 $kgha^{-1}$. These two also had among the lowest lodging scores in the study. Estimated profit returns were also greater ($1082 and $790 ha^{-1}) in ultra-narrow vs. wide rows for these two genotypes as compared to a profit increase of only $ 143 ha^{-1} for the mean of all genotypes. A potential problem with respect to weed control was the negative correlation among genotypic means for percent ground cover at 3WAE vs. seed yield and lodging resistance. The two genotypes with the greatest yield and lodging resistance in ultra-narrow rows were among the poorest for percent

ground cover. Breeding efforts may be needed to produce a cultivar which is desirable for all three traits in ultra-narrow row high-plant densities. Although no one particular genotype seemed to fit all the criteria needed to be an excellent cultivar for the ultra-narrow system, the elements of an ideal cultivar for ultra-narrow row production were clearly present in the collection of genotypes in the study.

Introduction

The organic sector has experienced double digit growth worldwide from 2014 to 2015, and projections are that these trends will continue in 2016. Globally, 31,160 certified organic farms are now in operation (U.S. Department of Agriculture, Economics Research Services [ERS], National Organic Program [NOP], 2016). The total retail market for organic products sold globally is over $75 billon, annually (USDA ERS, NOP 2016). The rapidly expanding organic market has been fueled by increased support for new producers to begin organic production and also by the high demand from consumers for organic foods (USDA AMS, 2016). More than $11.5 million was made available to assist organic operations with their certification costs through National Organic Certification Cost Share Program (NOCCSP) (USDA AMS 2016). A Consumer Reports survey showed that 84% of American consumers purchase organic food (Consumer Reports National Research Center [NRC] 2015). Moreover, the consumer survey reported that 75% of the consumers prefer not to purchase known genetically modified (GM) foods (Consumer Reports NRC 2015). Organic operations in the United States (USA) have grown 11% from 2014 to 2015, with 21,781 certified organic operations contributing to retail sales of $39 billon, annually.

In 2013, organic soybean production was reported in 30 US states, with organic soybean occupying 53,607 ha, or about 2% of production (USDA-ARS 2013). Organic soybean production has increased three percent from 2011 to 2014 in the USA, with Minnesota (7,616 ha) and Iowa (7,241 ha) as the leading producers of organic soybean (USDA ERS, 2013). In 2011, North Carolina organic soybean acreage was estimated at 683 ha (USDA ERS 2013).

The overall increase in demand for organic soybean is in part the result of increased consumer demand of organic meats, which are defined by organic standards as derived from livestock feed which is itself 100% organic (USDA ERS 2013). Organic beef cattle retail sales were over $15 million and retail sales of organic hogs were over $5 million in 2014 (USDA National Agriculture Statists Service [NASS], 2014). Soybean meal is the most important protein source of organic livestock feed, and producers command premiums for organically grown soybean meal (USDA ERS 2016). In that regard, organic soybean sold at \$459 MT^{-1} (average from 2011-2014) over the conventional soybean market price for both food and feed grade uses (USDA EMS NOP, 2016).

Research shows that some operational inputs for organic production are less than for conventional production, such as lower chemical and seed costs (USDA EMS NOP 2016). However, fuel costs associated with plowing are usually higher for organic production while final yields are usually lower. USA mean organic soybean production was 2085 kg ha^{-1} while conventional soybean production yielded 3161 kg ha^{-1} in 2011(Mcbride and Taylor, USDA 2015).

Weed control is the main problem in organic soybean production (Bond and Grundy, 2001; Hoad et al., 2012). Weeds are capable of reducing yield as much as a 70 percent (Zimdahi, 1980). Organic weed management options consist of harrowing after planting before crop emergence, plowing after emergence, cover crops before planting, rotations and fallow periods, no-till residues, and hand-weeding, all of which have a narrow window of effectiveness and are not usually cost effective. As a cultural management strategy, the rapid establishment of a crop canopy ground cover will help suppress weeds (Place et al 2011) in soybean and can be enhanced by planting in narrow rows, increasing the seeding rate and planting larger seed (Place et al. 2009). Yelverton and Coble (1991) also reported

that weed population decreased in narrow vs. wide row spacing. Choice of genotype for narrow cultivation may also affect weed suppression (Hoad et al., 2012). Soybean genotypes have been identified which spread canopies faster than typical cultivars and reduce weed growth (Place et al., 2011).

Machacek (2016, Chapter 3) suggested that employing ultra-narrow rows (11.4 cm), in combination with much higher than normal seeding rates, would be an additional means of controlling weeds in organic soybean production. However, establishing near 100% groundcover by three weeks after emergence (3WAE) (Knezevic and Datta 2015) may be critical for effective weed suppression in this system (Yelverton and Coble 1991). Jha (2008) reported 76% reduction in palmer amaranth (*Amaranthus palmeri*) emergence compared to plots with and without soybean. Achieving 100% ground cover at 3WAE with current soybean cultivars may not easily be attainable, even coupled with ultra-narrow rows. Thus, incorporating novel genotypes which potentially close canopies faster than normal into an ultra-narrow row system may provide the boost needed for effective weed suppression and increased yield in organic soybean production.

A potential problem with the ultra-narrow row system as seen in other species such as oat is that employing high seeding rates in ultra narrow rows can lead to excessive lodging in full season planting (Norden et al. 1959), in turn causing harvest issues which affect the overall yield of the crop (Vollmann et al., 2010). To address this issue, successful production in ultra-narrow row spacing may also require the adoption of cultivars which have at least partial resistance to lodging when planted in a high population density.

Few studies report agronomic comparisons of soybean genotypes in narrow vs. wide row conditions. Breeder selection for seed yield is suggested to be more efficient in narrow row plots when compared to wide row plots (Weaver and Wilcox, 1981). Cultivar selection

may not have an effect on agronomic performance in narrow vs. wide row spacing (Heatherly et al., 2001); however, there is insufficient information on soybean cultivar variation with respect to competitive ability with weeds (Vollmann et al., 2012). Thus, it is not clear what potential that choice of genotype may have to solve potential lodging problems, improve yields in narrow row and also suppress weeds (Hanson et al., 1961). Our objectives were to address this question by 1) evaluating an array of soybean genotypes for lodging resistance and other agronomic traits in ultra-narrow and wide row spacing, 2) evaluate soybean genotypes for canopy percent ground cover at 3WAE and other early season traits contributing to ground cover, and 3) determine genotypic associations among these traits and assess approaches for developing soybean cultivars adapted to ultra-narrow production.

Materials and Methods

Plant materials

24 soybean genotypes (Table 2.1) were selected to represent a range in canopy percent ground cover, lodging resistance, and maturity groups which are common for North Carolina. All genotypes were non-GM and either advanced breeding lines or cultivars. As a part of seed preparation before planting, seed grown in the previous season were cleaned with a Clipper 324 Eclipse (Bluffton, IN) to remove trash, soybean seed splits (broken seed), weed seed, and soybean seed with off-type seed sizes. After seed were cleaned, pre-plant 100-seed weight was recorded as the mean of six replications per genotype (Table 2.1). To further prepare the planting seed, they were passed through a seed spiral separator (Krussow Spiral, Hutchinson, MN) to remove non-round or heavily diseased soybean seed. Additionally, seed were passed over a slotted screen (3.97 and 4.77 mm) to remove any remaining split seed and then visually inspected for seed contaminants having off-type hilum color.

Field Trials.

Location and soil type. The experiment was conducted during the 2014 and 2015 growing seasons at the Central Crops Research Station in Clayton, NC (35.67°N, 78.49°W), and at the Caswell Research Station in Kinston, NC (35.16°N, 77.36°W) in 2015. Plots were planted on May 27, 2014 and May 27, 2015 at the Central Crops Research Station (hereafter referred to as Clayton) on a Dothan loamy sand and a Varina loamy sand/ Norfolk

loamy sand, respectively. At the Caswell Research Station (hereafter referred to as Kinston), plots were planted on June 10, 2015 on a Varina loamy sand soil. Planting sites were grown under conventional soybean production conditions.

Wide row planting. Plots in wide rows consisted of three rows planted at 97 cm row spacing (hereafter referred to as wide row spacing) at 4.3 meter length using a John Deere 1700 MaxEmerge Plus Integral 3 row unit with Almaco cone planters. Seeding rate for the wide row spacing was 41 viable seed m^{-2} of row adjusted by rag doll germination results based on two replications. Rag dolls were constructed as follows. Wax paper (the outer covering of the rag doll) was laid flat and covered with a layer of wet germination paper. Fifty seed were placed on the wet paper and covered with dry germination paper. These materials were then rolled up and rubber banded, so that seed could not be lost. The rolled up rag doll was placed vertically into a 1000 ml plastic beaker holding approximately 100 ml of water, so that rag dolls could wick up water to keep the seed moist. Beakers were then placed in a controlled environment chamber (Hoffman Manufacturing Inc., Model SG30SS, Jefferson, OR) at 28 Celsius and 95% relative humidity for five days. At the end of five days, seedlings were evaluated for radical length and the presence of fungal hyphae. A seed was considered viable if the radical was at least three times the length of the imbibed seed. 80% germination was arbitrarily adopted as the minimum germination acceptable of inclusion in the study.

Ultra-narrow row planting. In 2014, planting was accomplished using a Hans-Ulrich Hege (Type 80,Germany) two cone drill with eleven rows at 11 cm row spacing (hereafter referred to as ultra narrow row spacing), with 4.3 m plot length. One cone supplied seed for six of

the row units, while the other cone distributed seed to the remaining five units. In 2015, we planted the experimental study using an Almaco Heavy Duty Grain Drill (Model HDGD: Nevada, IW) two cone drill with ten rows in ultra narrow row spacing at a 4.3 m plot length. Seeding rate for the ultra narrow row spacing was 231 viable seed m^{-2} and, adjusted through rag doll germination results in the manner described previously.

Traits measured

Stand counts were taken at 3WAE on three random 0.6 m row segments per plot and recorded as the plot mean. Stand counts were also taken at harvest in a similar manner.

Camera images were taken overhead and used to estimate soybean canopy percent ground cover at 3WAE at the two testing locations in 2015. Canopy images were captured with a PowerShot A360 digital camera (8.0 mega pixels; Canon USA Inc., Lake Success, NY) using a custom-built camera stand, which was placed over the center row in wide row spacing plots and within the narrow row spacing plots (Place et al., 2009). To avoid shadow effects in the image, the plots were shaded during the photography and no flash was used. The digital image captured a size of 1.3 x 1.8 m section of the photographed plot (Place et al., 2009). Digital image analysis of overhead photographs was conducted in a manner similar to that of Abramoff et al. (2004) and Place et al. (2009). To estimate percent ground cover, Image J pixel counting software was used to convert images of soybean leaves to black pixels while the background soil was converted to white. The hue, saturation, and brightness thresholds were adjusted manually per plot to differentiate soybean canopy pixels from the field background (Place et al. 2009). Thresholds for separating leaves from

background effects were dependent of the soil background and the light conditions present when the images were collected (Worthington et al. 2013). After calibration adjustments, the software produced a percentage ground cover value from the ratio of black pixels to the total number of the image pixels.

Lodging

In 2014, lodging was recorded at approximately the R5 reproductive growth stage (20, August 2014, Fehr and Caviness, 1977), at R6 reproductive growth stage (full seed fill: 17, October 2014), and at R8 reproductive growth stage (plant maturity), as the mean of three ratings on a 1-5 scale, where 1 indicates no lodging and 5 indicates a prostrate plant (Gillen and Shelton 2103). In 2015 at Clayton, lodging was recorded at approximately the R5 reproductive growth stage (28, September 2015), at R6 reproductive growth stage (8, October 2015), and at R8 reproductive growth stage, as the mean of three independent ratings on a 1-5 scale. In 2015 at Kinston, lodging was recorded at R5 reproductive growth stage (8, October 2015), at R6 reproductive growth stage (2, November 2015), and at R8 reproductive growth stage (December) and the mean of three independent ratings on a 1-5 scale.

Yield

Plots were harvested during the first two weeks of December 2014 and 2015. To remove end-row bias from yield estimates, all wide row plots were end trimmed mechanically to a uniform length of three m, after which the center row was harvested with

an Almaco SPC20 single plot combine, into #10 paper bags. In the ultra-narrow row plots, each plot was end trimmed by hand to a final harvest plot length of three m. After end-trimming, an outside border row was removed from each side of the plot by hand pulling. In 2014 and 2015 respectively, nine and eight rows, respectively, were harvested from each ultra-narrow row plot, using the same plot combine employed for wide rows. Seed were air dried to approximately eight percent moisture prior to determination of seed yield and 100-seed weight. Seed yield was converted to $kgha^{-1}$ prior to analysis with approximately eight percent seed moisture.

Maturity date.

Maturity date was recorded for each plot, and defined as the first day on which 95% of the pods in the plot were mature (Gillen and Shelton 2013). Once the first plot was rated for maturity data, plots were visited on approximately five day intervals until all plots were mature. Maturity was redefined as October 1= day 1 prior to analysis.

Experimental design and statistical analysis

The study was established as a split-plot design with ultra narrow and wide (1 and 97 cm, respectively) row spacing as whole plots, and subplots were assigned to soybean genotype. Four replications were employed in each environment. Genotype and row spacing were considered fixed effects, while environment and replication were treated as random effects. Statistical analyses were conducted using SAS 9.3 (SAS Institute Inc.,

Cary, NC). Analysis of variance and least squares means were calculated using the GLM procedure in SAS (Tables 2.3 and 2.2). A LSD was used to test for significant differences between genotypes for each trait. Genotypic means were subjected to correlation analysis using the correlation procedure in Excel (Microsoft Office Excel, 2007, Redmond, WA; Table 2.4). Linear regressions analysis of genotypic means was performed using the scatter plot function in Excel.

Prior to analysis of variance, plots with poor stands were deleted from the data set. Poor stand was defined arbitrarily as 75% or less than the target stand (173 and 31 plants m^{-2} as cutoff values for dropping a plot in ultra narrow and wide, respectively) at 3WAE or 50% or less than the target stand at harvest (116 and 21 plants m^{-2} as cutoff values, ultra narrow and wide, respectively). Using this approach, 112 plots were deleted from the percent ground cover data set of 400 plots (percent ground cover data not recorded at Clayton in 2014) based on the 3WAE stand count data (19% of the plots). Using the same approach, 96 plots (16% of the plots) were deleted for analysis of agronomic traits from the entire data set of 600 plots, based on the stand count data at harvest. Additionally, some plots were not used for percent ground cover measurements, but met the appropriate plants m^{-2} target and were used in their analysis for yield. The cutoff values at harvest (50% of target stand) was lower than at 3WAE (75% of target stand) because plant density decreased over the season.

Heterogeneity of error variance was detected for seed yield in wide vs. ultra-narrow row plots (99,048 for wide rows vs. 302,395 for ultra narrow rows) and transformation options were explored (squared, square root, and natural log). Transformation did not change the analysis of variance results appreciably, and arbitrarily chose to report results from the untransformed analysis of variance.

Broad sense heritability on an entry mean basis was calculated for percent ground cover, lodging at maturity, and yield for the wide and ultra narrow row spacing plots (Nyquist 1991; Holland et al. 2003).

Results

The mean yield in each of the three environments in this study was 3623, 2344, and 2979 $kgha^{-1}$ for Clayton in 2014 and 2015, and Kinston, 2015, respectively. The genotype x row spacing was significant ($p<0.05$) for seed yield, masking an overall statistical effect of row spacing (Tables 2.2 and 2.3). However, ultra-narrow row spacing produced significantly ($p<0.05$) greater yields than wide row spacing in two of the three environments (a response of 751 and 468 $kgha^{-1}$ at Clayton, 2014 and Kinston, 2015, respectively). At Clayton, 2015, yields in ultra-narrow and wide rows were essentially the same, with ultra-narrow rows yielding numerically 146 $kgha^{-1}$ less than wide rows. The contrasting yield response at Clayton in 2015 as compared to the other test sites may have been associated with a more variable germination rate associated with rain on the day after planting, and with lower rainfall (23.4 cm less) during pod filling in August and September than at Clayton, 2014. Over environments, plants in ultra-narrow rows were significantly (98 vs. 91 cm; $p<0.05$) taller and lodged more (3.8 vs. 2.2) at maturity than in wide rows (Table 2.2), and demonstrated greater percent ground cover at 3WAE (85 and 38%, respectively. By contrast, plant height at 3WAE and at the R5 growth stage, lodging at R6 stage, maturity date, and 100-seed weight were not affected significantly ($p>0.05$) by row-spacing, and numerical differences between the two row-spacings were small (Table 2.3).

Genotypes differed significantly ($p<0.01$) for most traits, including plant height (3WAE, R5 growth stage, and at maturity), lodging (at the R5 growth stage, R6 stage, and at maturity), 100-seed weight, maturity date, percent ground cover, and seed yield. Row spacing x genotype interaction was not significant ($p<0.05$) for most traits including percent ground cover, lodging at R5, 100-seed weight, maturity date, or plant height at any growth

stage. Row spacing x genotype interaction was significant for lodging at maturity, as well as row spacing x genotype interaction within maturity group ($p<0.01$ and $p<0.05$), respectively. N06-6 appeared to have greater lodging resistance at maturity than the other genotypes, as evidenced by regression of genotypic means for wide vs. ultra-narrow rows. For seed yield, the overall row spacing x genotype interaction and the orthogonal partition of row spacing x genotype interaction among MG VI entries resulted in P values of 0.17 and 0.04, respectively (Table 2.3). The interaction for MG VI entries could be attributed primarily to two genotypes, N06-6 and NCC09-135, which appeared to respond better than others for yield in ultra-narrow vs. wide as evidenced by regression of genotypic means for wide vs. ultra-narrow rows (Figure 2.1, Table 2.2). Analysis of variance showed that the contrast of these two genotypes vs. others accounted for 72% of the sums of squares for genotypes for yield in MG VI and 88% of the sums of squares for genotype x row spacing interaction. Genotype N06-6 was consistent in its positive response to ultra-narrow row spacing in all three environments of this study (1227, 985, and 1648 $kgha^{-1}$ in Clayton, 2014 and 2015 and Kinston, 2015, respectively). Genotype NCC09-135 also exhibited higher yield in ultra-narrow vs. wide rows at all three environments (780, 256, 2501 $kgha^{-1}$ in Clayton, 2014 and 2015 and Kinston, 2015, respectively; Table 2.2).

Maturity date was not significant ($p>0.05$) for row spacing and row spacing x genotype interaction. However, genotype was significant ($p<0.05$) for maturity date. Maturity date was significantly ($p<0.01$) different among maturity groups. Maturity date was not correlated with height at 3WAE, lodging (R5 and R6 growth stage), 100-seed weight, percent ground cover, or seed yield. Maturity date was positively correlated with height at R5 and at maturity.

Seed yield in ultra-narrow rows was negatively correlated with height at all three growth stages and lodging at R5 and at maturity. In the ultra-narrow rows, maturity date was not correlated ($p>0.05$) with lodging at the R5 growth stage or at maturity. Lodging at maturity and height at 3WAE were positively correlated ($p<0.05$) in ultra-narrow rows.

Genotypic means for 100-seed weight (pre-plant and harvested) were highly correlated ($p<0.01$) with plant height at maturity, lodging at the R6 growth stage and at maturity, and percent ground cover in wide row spacing. In wide rows, lodging at maturity was positively correlated ($r=0.36$) with percent ground cover. Place et al. (2009) identified 100-seed weight as a trait contributing positively to percent canopy ground cover, in wide row spacing.

Percent ground cover was positively correlated with 100-seed weight (pre-plant and harvest) and height at 3WAE for both row-spacings. Height at 3WAE was positively correlated with percent ground cover in wide ($r=0.48$) and ultra-narrow rows ($r=0.60$). In the ultra-narrow rows, percent ground cover was positively correlated with lodging at maturity ($r=0.41$) and negatively correlated with seed yield ($r=0.47$).

Discussion

Cultivation is a primary method for weed control in organic soybean production (Murphy et al., 2008; Knezevic 2013). An alternative approach is to forego cultivation and rely on high plant populations of closely spaced soybean plants to shade and control weeds. Place et al. (2009) reported that plant populations greater than 50% above normal planting recommendations would aid in weed suppression in organic systems and that a narrow-row high-plant population production system may have merit in organic production (Machacek, Chapter 3 2016). Potential lodging and harvestablility problems have hindered adoption of this management practice, however. In general, higher plant populations coupled with narrow row spacing lead to undesirable increases in plant lodging (Dunphy, personal communication). Currently, the mean row spacing of organic soybean in North Carolina is 88 cm, which is a much wider row spacing than used for GM soybean production in the Southern USA (NC Organic Grain Production Guide, 2013). The typical organic producer plants soybean at about 494,000 seed ha^{-1}, which was a common seeding rate for most soybean production in the USA prior to the 1990s and the advent of GM soybean production. Thus, current organic soybean production practices do not tend to employ sufficiently high population densities or narrow rows to create severe lodging problems for the farmer.

In assessing the potential utility of an ultra-narrow system, costs are an important consideration. The ultra-narrow system eliminates the cost of cultivation, but requires much more planting seed ha^{-1} than wide-row production, (2,295,321 vs. 516,230 seed ha^{-1}) for the ultra-narrow and wide row treatments in the present study, respectively. The higher seeding rate in the ultra-narrow system incurs an additional cost of \$176 ha^{-1} for organic producers,

assuming a cost \$74 ha^{-1} for seed and \$104 ha^{-1} for fixed production costs and \$6 $ha^{-1}$for seed processing (Appendix A). In our study, yield in ultra-narrow rows yielded significantly ($p<0.05$) greater than in wide rows in two of three test environments under relatively weed free conditions, with an overall numerical advantage of 332 kg ha^{-1}. This magnitude of yield advantage for ultra-narrow rows showed a \$39 ha^{-1} greater return for the average genotype, compared to wide rows. If one assumes a superior weed control in ultra-narrow vs. wide rows, and that at least three field cultivations would be necessary to control weeds in wide rows (at a fuel cost of \$34 of fuel ha^{-1} cultivation), then the ultra-narrow row system may well be cost effective. After subtracting planting seed cost and expenses for weed control, seed yield for genotypic means of \$143 ha^{-1} greater return in the ultra-narrow than in wide rows (Table 2.2; Appendix A).

Row spacing x genotype interactions for seed yield and lodging, in conjunction with inspection of genotypic means (Tables 2.2 and 2.3) suggest that some of the genotypes among the 24 in this study were better adapted to ultra-narrow rows than others. For example, N06-6, NCC09-135, and TCHM06-M-204 exhibited the lowest lodging scores at maturity (3.2, 3.7, and 3.6, respectively) and also displayed greater yield response in ultra-narrow vs. wide rows than most other genotypes (Table 2.2, Fig 2.1). Cost-benefit analyses for N06-6, NCC09-135, and TCHM06-M-204 suggested that they would be more profitable in ultra-narrow vs. wide rows production than most other genotypes (\$1,082 \$791, and \$834 ha^{-1}, respectively vs. mean response of \$143 ha^{-1}; Table 2.2). Comparison of the most profitable genotypes in ultra-narrow and wide rows showed that TCHM06-M-204 in ultra-narrow rows led to \$121 ha^{-1} greater profit than Osage in wide rows (Table 2.2; Appendix A).

Although genotypes N06-6, NCC09-135, and TCHM06-M-204 appeared to be superior for the ultra-narrow system in this study in that they lodged relatively less and yielded relatively more than others in ultra-narrow vs. wide rows, they were less desirable in terms of potential ability to compete with weeds, as indicated by percent ground cover at 3WAE (58, 51, and 62%, respectively) compared to a mean of 62% in ultra-narrow row (Fig. 2.2). Machacek (Chapter 3 2016) indicated that the cultivar NC-Raleigh has superior ground cover compared to other genotypes, and NC-Raleigh was also numerically the greatest for percent ground cover in ultra-narrow rows (93%) in this study as well, and significantly ($p<0.05$) better than the other three genotypes (Table 2.2). Place et al. (2009) has indicated that genotypes with greater percent ground cover at 3WAE are better able to suppress weeds and that genotypes tend to rank the same for percent ground cover at 3WAE both in the absence and presence of weed competition.

Implications to Breeding for Soybean Production in Ultra Narrow Rows

Plant breeding has increased the yield potential of most row crops in the USA over the past 50 years (Fehr et al., 1971). In the southern USA, commercial soybean breeding companies have greatly increased their breeding efforts since the deployment of herbicide resistant GM cultivars in the mid 1990s (Reddy and Nandula, 2012). Their intensified selection efforts have produced new cultivars which not only yield better, but also generally have altered plant architecture in the form of reduced height and lodging (DuPont Pioneer, 2016). One notable exception is cultivar development for the early (April) planting system in the Delta region of the USA, which appears to benefit from taller rather than shorter cultivars (Boerma and Specht, 2004). Recently developed non–GM breeding lines from North Carolina State University and the USDA-ARS at Raleigh, North Carolina are also following the trend toward high yield, shorter plant stature, and reduced lodging in MG V and VI cultivars (Gillen and Shelton, 2013). The superior agronomic performance of these North Carolina materials in the study highlights the potential importance of these newer architectural types in making ultra-narrow-row high-plant population organic production profitable.

An important question related to breeding cultivars adapted to ultra-narrow rows is, 'must selection be performed in ultra-narrow rows, or could selection be accomplished in wide rows more commonly grown by soybean breeders?' In that regard, an ideal cultivar for the ultra-narrow row system would be one which not only resists lodging and yields well, but also has superior weed suppressive ability. The genotype x row spacing interactions for seed yield and lodging in this study suggest that identifying superior genotypes for these

traits will require testing in ultra-narrow rows. By contrast, the lack of a significant row spacing x genotype interaction for percent ground cover suggests that this trait could be selected upon equally effectively in wide or ultra-narrow rows. Heritability for these three traits was similar in wide and ultra-narrow rows. The negative genotypic relations of percent ground cover with yield and lodging resistance (Table 2.4) were sufficiently large to suggest that developing a cultivar which is superior for all three traits in ultra-narrow rows may require a focused breeding program. However, none of the correlations was large enough to suggest that breeding progress would be difficult. Although no one particular genotype in this study seemed to fit all the criteria needed to be an excellent cultivar for the ultra-narrow system, the elements of an ideal cultivar for ultra-narrow row production were clearly present in the collection of genotypes investigated in the study.

The cultivar 'NC-Raleigh' appeared to be a good adapted parental source for improved percent ground cover and N06-6, NCC09-135, and TCHM06-M-204 appeared to be good parental sources for improved yield and lodging resistance in ultra-narrow rows. These genotypes may prove useful materials for initiation of southern breeding programs to improve ultra-narrow row organic production.

REFERENCES

Abràmoff, M.D., P.J. Magalhães, and S.J. Ram. 2004. Image processing with ImageJ. Biophoton Int. 11:36-42.

Boerma, H.R., and J.E. Specht. 2004. Soybeans: Improvement, production and uses. American Society of Agronomy. Inc. Crop Science Society of America, Inc., and Soil Science Society of America, Inc, 2004, 453-454

Bond, W., and A. Grundy. 2001. Non- chemical weed management in organic farming systems. Weed Res. 41:383-405.

DuPont Pioneer, 2016. DuPont Pioneer. www.pioneer.com (accessed 12 January 2016)

Fehr, WR; Caviness, CE; Burmood, DT; Pennington, JS. Stage of development descriptions for soybeans, *Glycine max* (L.) Merrill. Crop Sci., 1971, 11, 6, 929-931, Crop Science Society of America

Frey, Kenneth J; Norden, AJ. Lodging resistance studies in oats. II. Inheritance and heritability. Agron.J., 1959, 51, 9, 535-537, American Society of Agronomy

Gillen, A.M., and G.W. Shelton. 2013. Uniform soybean tests, southern states, 2012. USDA-ARS, Stoneville, MS.

Hamilton, M., & Reberg-Horton, C. 2013. North Carolina Organic Grain Production Guide. Raleigh: NC State University.

Hanson, W., C. Brim, and K. Hinson. 1961. Design and analysis of competition studies with an application to field plot competition in the soybean. Crop Sci. 1:255-258.

Heatherly, Larry G; Elmore, C Dennis; Spurlock, Stan R. Row width and weed management systems for conventional soybean plantings in the mid southern USA. Agron.J., 2001, 93, 6, 1210-1220, American Society of Agronomy

Hoad, S.P., N. Bertholdsson, D. Neuhoff, U. Köpke, E. van Bueren, and J. Myers. 2012. Approaches to breed for improved weed suppression in organically grown cereals. Organic Crop Breeding61-76.

Holland, James B; Nyquist, Wyman E; Cervantes-Martínez, Cuauhtemoc T. Estimating and interpreting heritability for plant breeding: an update. Plant Breed. Rev., 2003, 22, 9-11

Jha, Prashant; Norsworthy, Jason K; Bridges Jr, William; Riley, Melissa B. Influence of glyphosate timing and row width on Palmer amaranth *(Amaranthus palmeri*) and pusley (*Richardia* spp.) demographics in glyphosate-resistant soybean. Weed Sci., 2008, 56, 3, 408-415, Weed Science Society of America 810 East 10th Street, Lawrence, KS 66044-8897

Knezevic, S. (2013). Proof Positive-Research Shows Flaming and Cultivation Key to Weed Control. *Midwest Organic & Sustainable Education Service* P.O. Box 339, Spring Valley, WI

Knezevic, Stevan Z; Datta, Avishek. The critical period for weed control: revisiting data analysis. Weed Sci., 2015, 63, sp1, 188-202, Weed Science Society of America 810 East 10th Street, Lawrence, KS 66044-8897

McBride, William; Taylor, Curtia. USDA Economic Research Service-Price Premiums Behind Organic Field Crop Profitability. 2015

Murphy, K., J. Dawson, and S. Jones. 2008. Relationship among phenotypic growth traits, yield and weed suppression in spring wheat landraces and modern cultivars. Field Crops Res. 105:107-115

NRC, 2015. Consumer Reports National Research Center. www.consumerreports.org (accessed 10 January 2016).

Nyquist, Wyman E; Baker, RJ. Estimation of heritability and prediction of selection response in plant populations. Crit. Rev. Plant Sci., 1991, 10, 3, 235-322, Taylor & Francis

Place, G.T., D.A. Dickey, and T.E. Carter. 2011. Identifying soybean traits of interest for weed competition. Crop Sci. 51:2642-2654.

Place, G.T., S.C. Reberg-Horton, J.E. Dunphy, and A.N. Smith. 2009. Seeding rate effects on weed control and yield for organic soybean production. Weed Technol. 23:497-502.

Reddy, K., and V. Nandula. 2012. Herbicide resistant crops: History, development and current technologies. Indian Journal of Agronomy 57:1-7.

Schweiger, P; Hofer, M; Hartl, W; Wanek, W; Vollmann, J. N2 fixation by organically grown soybean in Central Europe: method of quantification and agronomic effects. Eur.J.Agron., 2012, 41, 11-17, Elsevier

USDA-AMS, 2016. The USDA Agricultural Marketing Services. www. ams.usda.gov (accessed 10 January 2016).

USDA-ARS, 2013. The USDA Agricultural Research Service. www. ars.usda.gov (accessed 10 January 2016).

USDA-NASS, 2014. The USDA National Agriculture Statists Service. www.nass.usda.gov (accessed 10 January 2016).

USDA-NOP, 2016. The USDA National Organic Program. www.ams.usda.gov (accessed 10 January 2016).

Vollmann, J., H. Wagentristl, and W. Hartl. 2010. The effects of simulated weed pressure on early maturity soybeans. Eur. J. Agron. 32:243-248.

Weaver, D., and J. Wilcox. 1982. Heritabilities, gains from selection, and genetic correlations for characteristics of soybeans grown in two row spacings. Crop Sci. 22:625-629.

Worthington, M.L. 2013. Breeding Winter Wheat for Improved Powdery Mildew Resistance and Weed Suppressive Ability against Italian Ryegrass. (Under the direction of J. P. Murphy and S. Chris Reberg-Horton). Ph.D. dissertation. North Carolina State University.

Yelverton, F.H., and H.D. Coble. 1991. Narrow row spacing and canopy formation reduces weed resurgence in soybeans (*Glycine max*). Weed Technol.169-174.

Zimdahl, R.L. 2007. Weed-crop competition: A review. John Wiley & Sons

Table 2.1. 24 soybean genotypes with their maturity group and 100-seed weight used in the three test environments.

Genotype	Maturity Group	Seed Weight (g 100-seed^{-1})	Reference or Developer
Holladay	V	13.0	Burton et al., 1996
Hutcheson	V	12.0	Buss et al., 1988
Jake	V	15.9	Shannon et al., 2007
JTN-5203	V	12.6	Arelli et al., 2015
N02-7002	V	13.2	USDA-ARS‡
NC-Miller	V	16.2	Burton et al., 2012
Osage	V	12.6	Chen et al., 2007
Dillon	VI	19.2	Shipe et al., 1997
N06-10237	VI	18.9	USDA-ARS‡
N06-6	VI	10.4	USDA-ARS‡
N11-9298	VI	18.1	USDA-ARS‡
NCC06-1090	VI	17.7	NCSU†
NCC07-8138	VI	17.2	NCSU†
NCC09-135	VI	10.6	NCSU†
NC-Roy	VI	13.4	Burton et al., 2005
Young	VI	13.5	Burton et al., 1987
Benning	VII	16.0	Boerma et al., 1997
N09-13128	VII	14.4	USDA-ARS‡
N7003CN	VII	22.0	Carter et al., 2011
N7103	VII	12.3	Carter et al., 2003
NCC06-899	VII	13.5	NCSU†
NC-Raleigh	VII	19.1	Burton et al., 2006
TCHM06-M-204	VII	16.3	USDA-ARS‡
Woodruff	VII	17.3	Boerma, 2004
Mean		15.2	

†NCSU = North Carolina State University

‡USDA-ARS = US Department of Agriculture, Agricultural Research Serivices

Table 2.2 Least square means of the twelve traits, averaged over environment and replication. Comparison of cost analysis for ultra-narrow vs. wide rows.

Genotype	Maturity Group	Stand Count at 3WAE†		Height at 3WAE†		Height at R5‡		Height at Maturity	
		97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space
		------meter^{-2}-----		-------cm--------		-------cm--------		-------cm--------	
Holladay	V	36	203	14	15	62	65	74	85
Hutcheson	V	38	232	15	15	68	77	91	92
Jake	V	38	254	15	15	62	73	81	92
JTN-5203	V	45	289	15	16	61	70	76	86
N02-7002	V	35	231	17	15	70	78	88	95
NC-Miller	V	39	222	15	14	65	76	83	90
Osage	V	38	243	14	14	60	68	74	87
Dillon	VI	34	233	16	14	76	86	101	109
N06-10237	VI	41	242	19	17	75	77	94	98
N06-6	VI	36	244	13	12	67	71	83	93
N11-9298	VI	38	271	17	15	70	81	97	102
NCC06-1090	VI	36	229	16	16	71	78	92	99
NCC07-8138	VI	44	254	14	14	60	68	78	86
NCC09-135	VI	31	262	12	12	60	64	76	88
NC-Roy	VI	34	239	16	15	77	80	99	108
Young	VI	34	216	15	16	86	92	113	108
Benning	VII	36	227	16	16	80	86	109	110
N09-13128	VII	30	227	14	12	78	82	100	102
N7003CN	VII	41	247	17	16	80	80	102	101
N7103	VII	38	247	15	15	72	81	90	96
NCC06-899	VII	34	234	14	14	78	82	97	108
NC-Raleigh	VII	37	222	14	15	76	79	104	103
TCHM06-M-204	VII	39	225	15	14	69	76	90	96
Woodruff	VII	42	248	17	16	80	86	103	107
Mean		37	239	15	15	71	77	91	98
LSD		4	30	1	1	6	6	5	5

Table 2.2 Continued

Genotype	Maturity Group	Percent Ground Cover at 3WAE[†]		Lodging at R5[‡]		Lodging at R6[§]		Lodging at Maturity	
		97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space
		---------%---------		-------1-5 scale--------		-------1-5 scale--------		-------1-5 scale--------	
Holladay	V	35	86	1.3	2.2	1.5	3.1	1.9	3.8
Hutcheson	V	38	87	1.1	2.2	1.5	3.2	2.2	4.0
Jake	V	37	88	1.1	2.3	1.2	2.5	1.7	3.5
JTN-5203	V	39	84	1.0	2.2	1.1	3.1	1.6	3.8
N02-7002	V	37	85	1.1	1.7	1.3	2.7	1.9	3.6
NC-Miller	V	40	84	1.0	2.1	1.6	2.9	1.8	4.1
Osage	V	37	81	1.0	1.8	1.2	3.3	1.5	3.6
Dillon	VI	37	80	1.1	2.0	1.8	2.8	2.1	3.6
N06-10237	VI	42	88	1.1	2.3	1.9	3.1	2.4	4.1
N06-6	VI	33	83	1.0	1.8	1.3	2.7	1.6	3.2
N11-9298	VI	38	86	1.1	1.8	1.8	2.3	2.0	3.5
NCC06-1090	VI	42	90	1.1	1.9	1.8	2.7	2.0	3.9
NCC07-8138	VI	45	89	1.0	2.0	1.6	3.2	2.2	3.9
NCC09-135	VI	31	72	1.0	1.3	1.3	3.1	1.6	3.7
NC-Roy	VI	36	87	1.3	3.2	2.6	3.8	3.0	4.3
Young	VI	37	87	1.2	1.7	2.1	2.9	2.7	4.0
Benning	VII	38	89	1.0	2.3	2.3	2.9	2.9	3.7
N09-13128	VII	36	85	1.0	2.0	1.9	2.7	1.9	3.5
N7003CN	VII	41	87	1.2	2.0	2.3	2.9	2.4	3.7
N7103	VII	34	76	1.0	1.4	1.9	2.8	2.3	3.8
NCC06-899	VII	34	83	1.4	1.7	2.4	3.3	2.8	3.8
NC-Raleigh	VII	47	93	1.4	2.2	2.5	3.2	3.1	4.3
TCHM06-M-204	VII	39	85	1.0	1.9	2.0	3.0	2.3	3.6
Woodruff	VII	43	91	1.1	1.9	2.2	3.2	2.6	4.3
Mean		38	85	1.1	2.0	1.8	3.0	2.2	3.8
LSD		4	5	0.3	0.5	0.4	0.5	0.3	0.4

Table 2.2 Continued

Genotype	Maturity Group	Stand Count at Harvest		Maturity Date		Harvest 100-Seed Weight		Seed Yield		Profit Wide Rows ha^{-1}¶	Profit Ultra-narrow Rows ha^{-1}#	Profit Ultra-narrow vs. Wide Rows ha^{-1}
		97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space	97 cm row-space	11 cm row-space	Overall	96.5 cm row-space	11.4 cm row-space
		------meter^{-2}-----		-----Oct1=1-------		---g 100 seed-1---		------Kg ha^{-1}-------		----$----	----$----	----$----
Holladay	V	29	203	19	19	15.4	15.2	2750	3185	3041	2174	234
Hutcheson	V	27	196	18	21	15.6	16.2	2413	2880	2750	1868	254
Jake	V	32	203	15	17	15.6	15.8	2691	3020	2884	2006	125
JTN-5203	V	35	234	16	19	13.2	12.8	2601	2413	2304	1491	-318
N02-7002	V	32	180	16	20	15.1	15.1	2827	2886	2756	1892	-122
NC-Miller	V	34	210	21	24	17.1	16.5	2939	3119	2979	2074	-38
Osage	V	31	196	18	22	13.9	13.6	3121	3794	3623	2792	490
Dillon	VI	28	190	24	26	15.9	15.4	2736	3060	2922	2045	121
N06-10237	VI	32	205	25	24	16.7	16.5	2918	3012	2876	1978	-115
N06-6	VI	31	207	24	27	13.1	13.2	2696	3976	3797	2981	1082
N11-9298	VI	30	200	26	28	15.6	16.2	2762	3089	2950	2067	120
NCC06-1090	VI	33	209	27	29	17.3	17.7	2826	2970	2836	1917	-84
NCC07-8138	VI	33	241	21	25	16.8	17.0	3009	3214	3069	2163	-15
NCC09-135	VI	29	217	20	24	14.1	14.6	3112	4111	3926	3081	791
NC-Roy	VI	29	215	23	25	13.7	13.3	2929	2897	2766	1941	-179
Young	VI	28	197	24	28	15.2	15.3	2641	2549	2434	1567	-268
Benning	VII	28	201	27	29	15.2	15.0	2617	2851	2723	1860	46
N09-13128	VII	27	196	25	26	14.6	15.0	2867	2816	2689	1833	-221
N7003CN	VII	38	251	31	31	16.5	16.0	2762	3011	2875	1984	38
N7103	VII	33	230	29	30	7.8	7.9	2465	2964	2830	2141	433
NCC06-899	VII	30	200	29	30	15.2	15.2	3107	3633	3469	2603	323
NC-Raleigh	VII	30	189	31	31	13.9	14.2	2796	3073	2935	2096	106
TCHM06-M-204	VII	32	191	28	29	14.8	15.0	3091	4145	3959	3101	834
Woodruff	VII	35	234	30	30	15.5	15.5	2723	2698	2577	1704	-209
Mean		31	208	24	26	14.9	14.9	2808	3140	2999	2140	143
LSD		4	31	2	3	0.5	0.5	280	504	-	-	-

†3WAE=3 weeks after emergence

‡R5=Reproductive growth stage 5

§R6=Reproductive growth stage 6

¶Profit wide rows, harvest total (Appendix A) minus total expenses (plowing 3 times at $34 ha^{-1}, seed at $74 ha^{-1}, $6 seed processing, $104 fixed production cost, and$64 ha^{-1} (2015 average organic soybean food grade and feed)

#Profit ultra-narrow rows, harvest total (Appendix A) minus total expenses (seed at $74 ha^{-1}, $6 seed processing, $104 fixed production cost, and$64 ha^{-1} (2015 average organic soybean food grade and feed)

Table 2.3 ANOVA of the twelve traits for the test enivornments.

Source of Variation	Stand Count at 3WAE‡ -----meter^{-2}------		Height at 3WAE‡ --------cm--------		Height at R5§ --------cm--------		Height at Maturity --------cm--------	
	DF†	Mean Square	DF†	Mean Square	DF†	Mean Square	DF†	Mean Square
Environment	2	1904	2	280.3	2	90307	2	3498
Rep(environment)	9	1392	9	28.8	9	218	9	336
Error 96.5cm	9	51	9	18.7	9	240	9	444
Error 11.4cm	9	2928	9	21.3	9	148	9	151
Rowspace	1	3571306 **	1	27.3 ns	1	4011 ns	1	3725 *
Environment*Rowspace	2	1020 ns	2	134.7 **	2	732 *	2	117 ns
Rep*Rowspace(environment)	9	1619	9	10.5	9	172	9	260
Genotype	23	1330 ns	23	30.9 **	23	985 **	23	1759 **
Maturity group	2	991 ns	2	5.3 ns	2	3963 **	2	8864 **
Genotype(maturity group)	21	1353 ns	21	32.1 **	21	682 **	21	1062 **
Genotype(maturity group V)	6	1917 ns	6	18.4 **	6	304 ns	6	420 **
Genotype(maturity group VI)	8	1368 ns	8	51.9 **	8	1346 **	8	1846 **
Genotype(maturity group VII)	7	907 ns	7	20.2 **	7	231 ns	7	601 **
Environment*Genotype	46	949 **	46	5.7 **	46	172 **	46	111 **
Environment*Maturity group	4	1591 **	4	5.7 *	4	898 **	4	395 **
Environment*Genotype(maturity group)	42	915 **	42	5.7 **	42	103 **	42	87 **
Environment*Genotype(maturity group V)	12	765 ns	12	5.6 **	12	99 *	12	60 *
Environment*Genotype(maturity group VI)	16	568 ns	16	6.1 **	16	151 **	16	63 *
Environment*Genotype(maturity group VII)	14	1396 **	14	4.7 *	14	40 ns	14	130 **
Rowspace*Genotype	23	732 ns	23	2.0 ns	23	43 ns	23	98 ns
Rowspace*Maturity group	2	201 ns	2	1.1 ns	2	136 ns	2	206 ns
Rowspace*Genotype(maturity group)	21	786 ns	21	2.0 ns	21	33 ns	21	85 ns
Rowspace*Genotype(maturity group V)	6	1112 ns	6	2.3 ns	6	33 ns	6	66 ns
Rowspace*Genotype(maturity group VI)	8	561 ns	8	2.2 ns	8	41 ns	8	121 ns
Rowspace*Genotype(maturity group VII)	7	748 ns	7	1.2 ns	7	32 ns	7	55 ns
Environment*Rowspace*Genotype	44	854 **	44	2.1 ns	45	55 ns	45	78 **
Enironment*Rowspace*Maturity group	4	1296 *	4	0.4 ns	4	22 ns	4	132 **
Enironment*Rowspace*Genotype(maturity group)	40	837 **	40	2.2 ns	41	59 ns	41	74 **
Environment*Rowspace*Genotype(maturity group V)	12	578 ns	12	1.6 ns	12	17 ns	12	34 ns
Environment*Rowspace*Genotype(maturity group VI)	14	572 ns	14	2.6 ns	15	74 ns	15	117 **
Environment*Rowspace*Genotype(maturity group VII)	14	1281 **	14	1.9 ns	14	98 **	14	55 ns
Error	300	471	299	2.4	305	50	307	34
Error 96.5cm	159	17	158	2.5	157	49	160	35
Error 11.4cm	141	983	141	2.4	148	50	147	33
Error Maturity group V	88	553	88	2.1	82	32	82	22
Error Maturity group VI	93	419	92	2.8	98	56	99	51
Error Maturity group VII	83	549	83	2.7	89	40	90	34

Table 2.3. Continued

Source of Variation	Percent Ground Cover at 3WAE		Lodging at R5[§]		Lodging at R6 [¶]		Lodging at Maturity	
	-------%--------		------1-5 scale-----		------1-5 scale-----		------1-5 scale-----	
	DF[†]	Mean Square	DF[†]	Mean Square	DF[†]	Mean Square	DF[†]	Mean Square
Environment	1	7	2	3.07	2	54.47	2	5.72
Rep(environment)	6	225	9	0.36	9	0.84	9	1.11
Error 96.5cm	6	179	9	0.22	9	0.94	9	1.23
Error 11.4cm	6	80	9	0.47	9	0.67	9	0.79
Rowspace	1	156634 *	1	64.87 **	1	140.26 ns	1	262.17 **
Environment*Rowspace	1	472 **	2	0.57 ns	2	14.95 **	2	3.65 *
Rep*Rowspace(environment)	6	24	9	0.32	9	0.79	9	0.87
Genotype	23	153 **	23	0.71 **	23	1.68 **	23	2.15 **
Maturity group	2	53 ns	2	0.03 ns	2	5.93 **	2	5.27 **
Genotype(maturity group)	21	156 **	21	0.75 **	21	1.29 ns	21	1.88 **
Genotype(maturity group V)	6	24 ns	6	0.28 ns	6	0.43 ns	6	0.81 ns
Genotype(maturity group VI)	8	185 **	8	1.30 **	8	2.34 **	8	2.72 **
Genotype(maturity group VII)	7	212 **	7	0.35 ns	7	0.41 ns	7	1.66 **
Environment*Genotype	23	27 ns	46	0.30 **	46	0.76 **	46	0.51 **
Environment*Maturity group	2	33 ns	4	0.34 ns	4	2.34 **	4	1.73 **
Environment*Genotype(maturity group)	21	25 ns	42	0.29 **	42	0.60 **	42	0.39 **
Environment*Genotype(maturity group V)	6	9 ns	12	0.17 ns	12	0.80 **	12	0.42 **
Environment*Genotype(maturity group VI)	8	22 ns	16	0.38 **	16	0.40 **	16	0.44 **
Environment*Genotype(maturity group VII)	7	43 **	14	0.27 ns	14	0.73 **	14	0.31 **
Rowspace*Genotype	23	27 ns	23	0.36 ns	23	0.79 *	23	0.71 **
Rowspace*Maturity group	2	0 ns	2	0.31 ns	2	5.37 **	2	4.43 **
Rowspace*Genotype(maturity group)	21	29 ns	21	0.36 ns	21	0.34 ns	21	0.37 *
Rowspace*Genotype(maturity group V)	6	38 ns	6	0.14 ns	6	0.42 ns	6	0.24 ns
Rowspace*Genotype(maturity group VI)	8	30 ns	8	0.61 *	8	0.43 ns	8	0.37 ns
Rowspace*Genotype(maturity group VII)	7	17 ns	7	0.23 ns	7	0.15 ns	7	0.43 *
Environment*Rowspace*Genotype	22	22 ns	44	0.25 ns	45	0.40 **	45	0.20 *
Enironment*Rowspace*Maturity group	2	98 **	4	0.18 ns	4	0.69 **	4	0.26 ns
Enironment*Rowspace*Genotype(maturity group)	20	15 ns	40	0.24 ns	41	0.37 **	41	0.19 ns
Environment*Rowspace*Genotype(maturity group V)	6	3 ns	12	0.23 ns	12	0.34 ns	12	0.22 ns
Environment*Rowspace*Genotype(maturity group VI)	7	17 ns	14	0.32 *	15	0.50 **	15	0.23 ns
Environment*Rowspace*Genotype(maturity group VII)	7	21 ns	14	0.24 ns	14	0.31 ns	14	0.15 ns
Error	225	17	297	0.18	307	0.21	308	0.14
Error 96.5cm	123	16	156	0.09	160	0.17	161	0.13
Error 11.4cm	102	19	141	0.28	147	0.25	147	0.16
Error Maturity group V	60	21	87	0.14	81	0.18	82	0.16
Error Maturity group VI	79	15	93	0.16	99	0.20	98	0.11
Error Maturity group VII	62	15	81	0.24	91	0.20	92	0.12

Table 2.3. Continued

Source of Variation	Stand Count at Harvest -----meter^{-2}-----		Maturity Date -----Oct 1=1-----		Harvest 100-Seed Weight ---g 100 seed^{-1}----		Yield -----Kg ha^{-1}-----	
	DF†	Mean Square	DF†	Mean Square	DF†	Mean Square	DF†	Mean Square
Environment	2	9085	2	601	2	119.53	2	61195791
Rep(environment)	9	1168	9	42	9	3.09	9	2135519
Error 96.5cm	9	71	9	21	9	0.78	9	396675
Error 11.4cm	9	2008	9	34	9	3.50	9	3494246
Rowspace	1	3322820 **	1	406 ns	1	0.01 ns	1	12596813 ns
Environment*Rowspace	2	4457 *	2	114 **	2	0.92 ns	2	8060643 *
Rep*Rowspace(environment)	9	953	9	11	9	1.28	9	1683764
Genotype	23	2043 **	23	365 **	23	66.22 **	23	1597087 **
Maturity group	2	626 ns	2	3540 **	2	54.77 **	2	573647 ns
Genotype(maturity group)	21	2165 **	21	60 ns	21	67.26 **	21	1697743 **
Genotype(maturity group V)	6	1613 ns	6	80 ns	6	32.06 **	6	1803354 **
Genotype(maturity group VI)	8	1772 ns	8	34 ns	8	35.36 **	8	1527310 **
Genotype(maturity group VII)	7	3240 **	7	64 ns	7	128.84 **	7	1843226 **
Environment*Genotype	46	977 **	46	42 **	46	1.40 **	46	512976 **
Environment*Maturity group	4	904 ns	4	249 **	4	8.03 **	4	373519 ns
Environment*Genotype(maturity group)	42	962 **	42	24 **	42	0.75 **	42	507676 **
Environment*Genotype(maturity group V)	12	468 ns	12	7 ns	12	0.57 *	12	679136 **
Environment*Genotype(maturity group VI)	16	829 ns	16	19 **	16	0.92 **	16	470235 **
Environment*Genotype(maturity group VII)	14	1520 **	14	40 **	14	0.69 **	14	489635 **
Rowspace*Genotype	23	1292 *	23	12 ns	23	0.54 ns	23	654712 ns
Rowspace*Maturity group	2	813 ns	2	38 **	2	0.35 ns	2	80264 ns
Rowspace*Genotype(maturity group)	21	1344 *	21	9 ns	21	0.56 ns	21	720408 ns
Rowspace*Genotype(maturity group V)	6	1061 ns	6	9 ns	6	0.62 ns	6	560908 ns
Rowspace*Genotype(maturity group VI)	8	1176 ns	8	16 ns	8	0.57 ns	8	1170611 *
Rowspace*Genotype(maturity group VII)	7	1949 **	7	4 ns	7	0.45 ns	7	494729 ns
Environment*Rowspace*Genotype	45	698 ns	45	8 ns	45	0.40 ns	45	509535 **
Enironment*Rowspace*Maturity group	4	768 ns	4	5 ns	4	0.35 ns	4	684953 **
Enironment*Rowspace*Genotype(maturity group)	41	670 ns	41	8 ns	41	0.39 ns	41	471758 **
Environment*Rowspace*Genotype(maturity group V)	12	324 ns	12	8 ns	12	0.37 ns	12	591328 **
Environment*Rowspace*Genotype(maturity group VI)	15	420 ns	15	16 **	15	0.56 *	15	543292 **
Environment*Rowspace*Genotype(maturity group VII)	14	1287 **	14	5 ns	14	0.25 ns	14	310936 ns
Error	315	566	303	7	308	0.32	309	197067
Error 96.5cm	163	17	157	6	160	0.34	161	98947
Error 11.4cm	152	1156	146	9	148	0.30	148	303805
Error Maturity group V	82	469	81	6	82	0.30	82	153602
Error Maturity group VI	102	670	98	8	98	0.39	99	216606
Error Maturity group VII	95	507	88	8	92	0.27	92	195474

†DF=Degrees of Freedom

‡3WAE=3 weeks after emergence

§R5=Reproductive stage 5

¶R6=Reproductive stage 6

#ns=No significant difference between genotypes

*,** significantly different from zero at P ≤ 0.05 and P ≤ 0.01 respectively

Table 2.4. Phenotypic correlation coefficients (n=24) of genotypic means for 97 and 11 cm row-spacings of the three test environments.

			Height at 3WAE†		Height at Maturity		Percent Ground Cover at 3WAE†		Lodging at R5‡		Lodging at R6§		Lodging at Maturity		Maturity Date		Harvest 100-Seed Weight		Seed Yield	
			97 cm	11 cm	97 cm	11 cm	97 cm	11 cm	97 cm	11 cm	97 cm	11 cm	97 cm	11 cm	97 cm	11 cm	97 cm	11 cm	97 cm	11 cm
			-------cm--------		-------cm--------		---------%----------		----------1-5 scale----------		----------1-5 scale----------		----------1-5 scale----------		-----Oct1=1-------		---g 100 seed^{-1}---		------Kg ha^{-1}-------	
Height at 3WAE†	97 cm	----cm-----		0.77	0.42	0.36	0.49	0.47	-0.02	0.31	0.27	-0.11	0.27	0.30	0.25	0.11	0.34	0.29	-0.23	-0.56
	11 cm				0.37	0.27	0.55	0.60	0.22	0.28	0.29	0.02	0.42	0.47	0.22	0.10	0.25	0.21	-0.38	-0.62
Height at Maturity	97 cm	----cm-----				0.94	0.24	0.42	0.37	0.15	0.81	-0.05	0.77	0.28	0.69	0.68	0.11	0.11	-0.26	-0.42
	11 cm						0.10	0.32	0.41	0.18	0.82	0.00	0.75	0.22	0.67	0.66	0.08	0.07	-0.12	-0.31
Percent Ground Cover at 3WAE†	97 cm	-----%------						0.75	0.06	0.29	0.31	0.14	0.36	0.54	0.34	0.25	0.43	0.42	-0.01	-0.36
	11 cm								0.33	0.57	0.41	0.09	0.50	0.42	0.27	0.15	0.48	0.49	-0.18	-0.48
Lodging at R5‡	97 cm	1-5 scale-								0.28	0.58	0.37	0.60	0.43	0.30	0.21	0.05	0.03	0.05	-0.15
	11 cm										0.30	0.45	0.36	0.44	-0.11	-0.25	0.26	0.19	-0.10	-0.39
Lodging at R6§	97 cm	1-5 scale-										0.34	0.93	0.51	0.81	0.76	0.04	0.02	0.05	-0.19
	11 cm												0.44	0.68	0.01	-0.03	-0.06	-0.12	0.30	0.05
Lodging at Maturity	97 cm	1-5 scale-												0.61	0.66	0.62	0.03	0.01	-0.08	-0.28
	11 cm														0.22	0.15	0.14	0.11	-0.03	-0.45
Maturity Date	97 cm	·Oct1=1---														0.96	-0.06	-0.05	0.01	0.02
	11 cm																-0.12	-0.10	0.06	0.10
Harvest 100-Seed Weight	97 cm	100 seed·																0.98	0.30	-0.08
	11 cm																		0.28	-0.05
Seed Yield	97 cm	-Kg ha^{-1}--																		0.63
	11 cm																			

†3WAE=3 weeks after emergence

‡R5=Reproductive stage 5

§R6=Reproductive stage 6

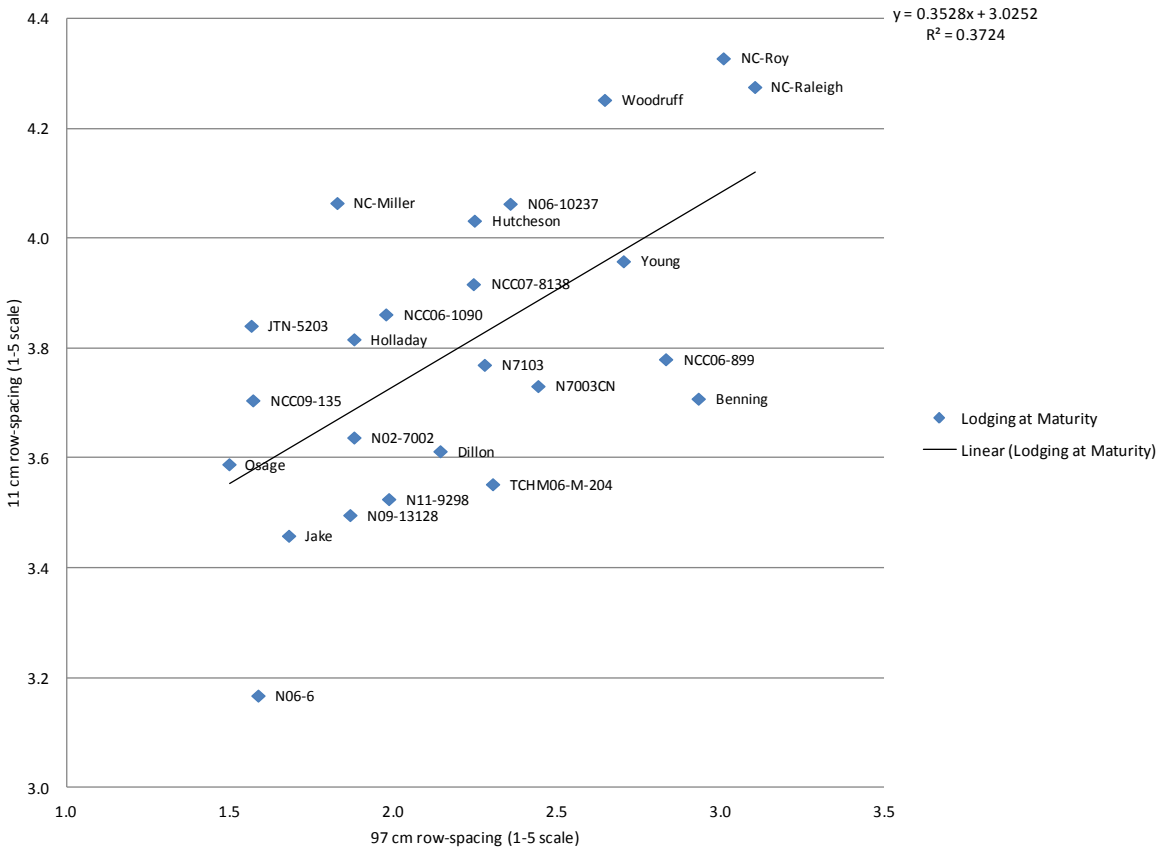

Figure. 2.1. Genotypic means for 97 cm row-spacing are regressed against 11 cm row-spacing for lodging at maturity (1-5 scale).

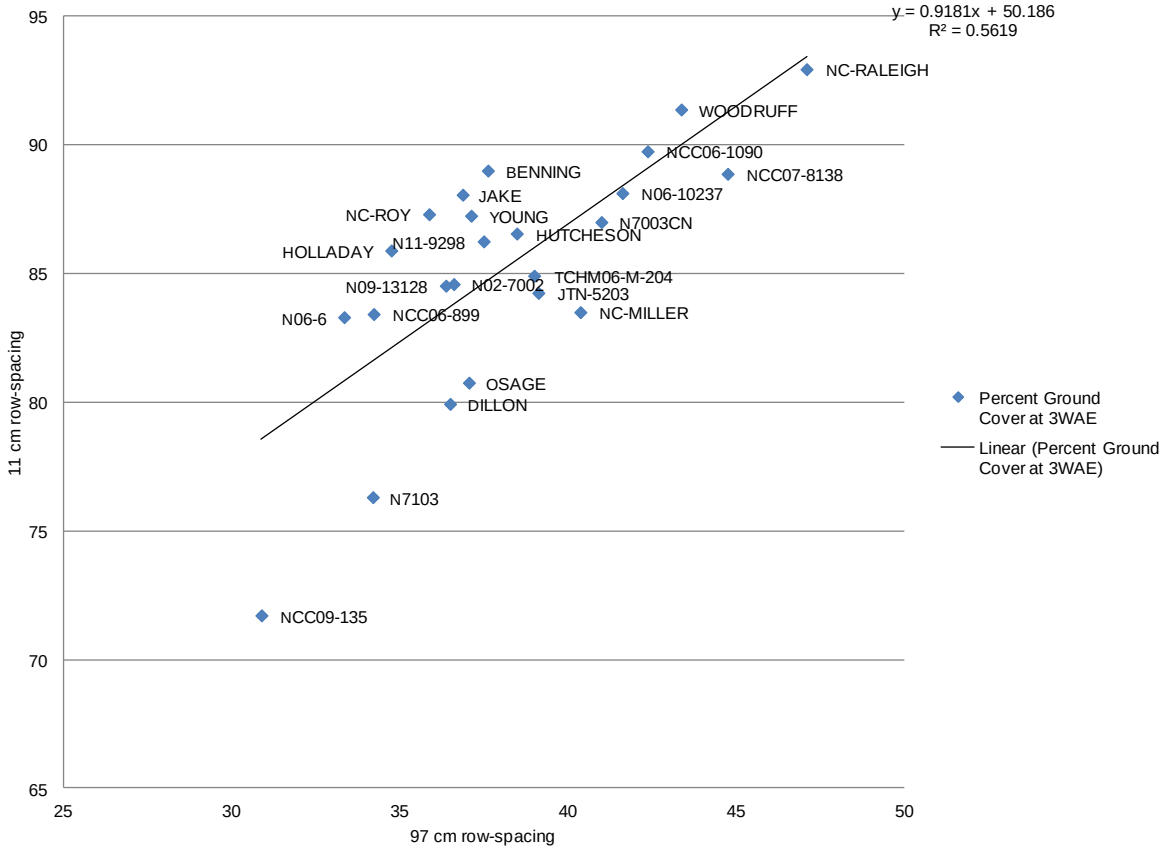

Figure. 2.2. Genotypic means for 97 cm row-spacing are regressed against 11 cm row-spacing for percent ground cover at 3 weeks after emergence (3WAE).

Chapter 3

Seed Size, Population Density, and Genotypic Effects on Ground Cover of Soybean at 3 weeks after emergence in Ultra-narrow and Narrow Row Spacing

Abstract

Soybean production in ultra-narrow rows at high plant densities may have merit as a method to enhance canopy closure and potentially suppress weeds in organic production. Our objective was to determine the impact of seed size (large vs. small) and plant population density (10 and 26 beans m^{-1}) on early season ground cover in ultra-narrow (11 cm) and narrow (23 cm) row spacing for seven contrasting soybean genotypes. The experimental design was a split-plot with whole plots assigned to row-spacing and sub-plots to factorial combinations of remaining treatments. The experiment was grown in three North Carolina environments during 2014-2015 employing four replications. Plant population effects were evaluated only in 2014. Mean percent ground cover at three weeks after emergence (3WAE) was increased 7 percentage units by planting larger seed, 11 percentage units by employing higher seeding rate, and 15 percentage units in ultra-narrow vs. narrow row-spacing. These effects were additive and the greatest ground cover was observed in the ultra-narrow rows when planting larger seed at higher plant densities. Genotypic means for percent ground cover at 3WAE ranged from 60 to 78 % ($p<0.05$) for this combination of treatments. Genotype x plant population interactions were detected ($p<0.05$) for most traits except seed yield and maturity date. However, genotypic changes in ranking were substantial only for percent ground cover. Cultivars 'N7103' and 'N7003CN' increased ground cover very little in response to higher seeding rates while 'NC-Raleigh' increased 18 percentage units. Genotypes which exhibited greater ground cover at 3WAE in ultra-narrow rows production also tended to have greater 100-seed weight and unifoliate size. Overall effects of row spacing and seed size on seed yield were masked by 2 and 3 way interactions involving genotype. The higher seeding rate reduced ($p<0.01$) yield 9 %.

The interaction of treatment variables with genotype was more apparent for seed yield than for ground cover. However, genotype x treatment interactions for both traits suggest that identification of genotypes adapted to ultra-narrow production should be accomplished by evaluation in the specific row spacing-planting density and seed size combination targeted for production. A potential problem with respect to the ultra-narrow rows was a negative correlation among genotypic means for percent ground cover at 3WAE and lodging resistance. The two genotypes with the greatest percent ground cover in the ultra ultra-narrow row-high planting density-large seed size management combination were also the poorest for lodging resistance.

Introduction

Organic farm production is expanding worldwide as evidenced by an almost 300% increase in the number of organic farm operations from 2002 to 2016 (U.S. Department of Agriculture, Economics Research Services [ERS], National Organic Program [NOP], 2016). Annually, the organic market produces $75 billion in global retail sales (USDA ERS, NOP 2016). In the USA, organic livestock and poultry sales are an important component of the organic market and increased 108% from 2008 to 2014 (USDA NASS, 2015). Organic soybean is the major high quality protein feed source for the organic market, and has commanded a market price that is approximately twice that of conventional soybean meal for the last decade (Hamilton and Rzewnicki, 2007).

Farmers have reported weed control to be the greatest challenge in organic soybean production (Bond and Grundy, 2001; Hoad et al., 2012). The average North Carolina organic farmer plants soybean in wide rows (76 cm rows) to facilitate between-row cultivation to combat weeds. However, research has shown that narrow row-spacing can lead to faster canopy closing, greater shading of weeds and higher yields as compared to wide row production (Weber et al., 1966; Yelverton and Coble, 1991; Alsam et al., 1993; Epler, M., and Staggenborg, S. 2008; Bruin and Pedersen, 2008). Many conventional farmers in the Midwest and South often plant soybean in narrow rows (approximately 19 cm) for these reasons.

Ultra-narrow (11 cm) rows and high population densities (26 viable seed m^{-1}) have been proposed as a means to partially suppress weeds in organic soybean farming. Machacek (Chapter 2 2016) showed that a mean of 85 percent ground cover could be achieved in ultra-narrow rows at 3WAE when planting at 26 live seed m^{-1}. Genotypic means

ranged from 72 to 93 percent ground cover in that study. This degree of canopy coverage has been suggested as sufficient to retard weed growth and reduce weed competition (Stoller and Myers, 1989; Shilling et al., 1995; Nice et al., 2001).

Although previous studies suggest that greater plant densities and larger planting seed lead to greater ground cover at 3WAE in wide rows, the impact of these variables and their interaction with genotype have not been investigated for ultra-narrow rows (Harder et al., 2007; Place et al., 2009; Place et al., 2011a). Row-spacing x soybean cultivar interaction for sicklepod suppression has been reported (Burnside, 1979). Knowledge of genotype x treatment (or management) interactions would facilitate development of screening programs to identify soybean germplasm and develop cultivars for narrow row production (Murphy et al., 2007). The objectives of this study were to 1) evaluate the effect of selection for large and small seed within seed lots of soybean on percent ground cover at two contrasting planting densities and row-spacings for seven soybean genotypes and 2) determine genotypic interactions with plant density and seed size and assess their impact on ground cover, and other agronomic traits in ultra-narrow and narrow row soybean production.

Materials and Methods

Plant materials

Seven soybean genotypes (Table 3.1) were selected to represent a range in 100-seed weight and their potential capacity to produce canopy ground cover at 3WAE. The genotypes were all non-GM advanced breeding lines or cultivars. As a part of seed preparation before planting, seed grown in the previous season were cleaned as described by Machacek (2016). Briefly, seed were passed through a Clipper 324 Eclipse (A.T. Ferrell, Bluffton, IN) to remove contamination and then separated into 100-seed weight classes using cleaning screens with various hole diameters, ranging from 5.16 mm to 7.15 mm and 5.95 mm to 7.94 mm for small and large seed categories, respectively. The largest and smallest seed were retained for the study. Seed were passed through a seed spiral separator (Krussow Spiral, Hutchinson, MN) to remove damaged non-round seed and then passed over a slotted screen (3.97 and 4.77 mm, respectively) to remove any remaining split seed. For each genotype, 100-seed weight of the two classes differed by at least four grams 100-seed^{-1}.

Field Trials

Location and soil type. The experiment was conducted during the 2014 and 2015 growing seasons at the Central Crops Research Station in Clayton, NC (35.67°N, 78.49°W), and at the Caswell Research Station in Kinston, NC (35.16°N, 77.36°W) in 2015. Plots were planted on May 27, 2014 and May 27, 2015 at the Central Crops Research Station (hereafter referred to as Clayton) on a Dothan loamy sand and a Varina loamy sand/ Norfolk

loamy sand, respectively. At the Caswell Research Station (hereafter referred to as Kinston), plots were planted on June 10, 2015 on a Varina loamy sand soil.

Ultra-narrow row planting. Plots were grown in 11 cm row-spacing and consisted of eleven or ten rows per plot (hereafter referred to as ultra-narrow row-spacing) at 3.7 and 4.3 m row length using a Hans-Ulrich Hege (Type 80,Germany) and Almaco Heavy Duty Grain Drill (Model HDGD: Nevada, IW) two cone drills in 2014 and 2015, respectively. Seeding rates for the ultra-narrow row-spacing were 91 and 231 viable seed m^{-2} (or 10 and 26 seed m^{-1}, of row, respectively), and adjusted through rag doll germination results based on two replications. Rag dolls were constructed as previously described in Chapter 2. Briefly, fifty seed were rolled up in germination paper and placed vertically into a 1000 ml plastic beaker holding approximately 100 ml of water. Beakers were placed in a controlled environment chamber (Hoffman Manufacturing Inc., Model SG30SS, Jefferson, OR) at 28 Celsius and 95% relative humidity for five days. At the end of five days, seedlings were evaluated for radical length and considered viable if the radical was at least three times the length of the imbibed seed. 80% germination was arbitrarily adopted as the minimum germination acceptable of inclusion in the study.

Narrow row planting. Planting equipment and plot length was the same as that described for ultra-narrow rows. A row-spacing of 22 cm (hereafter referred to as narrow row spacing) was achieved by shutting off alternate planters so that six or five rows were planted at 3.7 and 4.3 m plot length. Two seeding rates were employed (50 and 117 viable seed m^{-2} of plot or 10 and 26 viable seed m^{-1}, respectively), and adjusted by rag doll germination results in the manner described previously.

Traits measured

Stand counts were taken at 3WAE and at maturity on three random 0.6-m row segments per plot and recorded as the plot mean.

Unifoliates

For each plot, ten unifoliates were randomly collected, placed into a labeled plastic bag and stored on ice. The unifoliates were analyzed subsequently for surface area using a Li-Cor 3100 (Li-Cor Environmental, Lincoln, NE) leaf area meter.

Camera images were taken overhead and used to estimate soybean canopy percent ground cover at 3WAE at the three testing environments as described by Machacek (Chapter 2 2016). Canopy images were captured with a PowerShot A360 digital camera (8.0 mega pixels; Canon USA Inc., Lake Success, NY) using a custom-built camera stand, which was placed within the narrow and ultra-narrow row spacing plots (Place et al. 2009). The digital image captured a size of 1.37 x 1.87 m section of the photographed plot (Place et al. 2009) and conducted in a manner similar to that of Abramoff et al. (2004) and Place et al. (2009). Image J a pixel counting software was used to estimate percent ground cover, adjusting the thresholds for hue, saturation, and brightness manually per plot to differentiate soybean canopy pixels from the field background (Place et al., 2009). After threshold adjustments, the software produced a percentage ground cover value from the ratio of black pixels (converted soybean canopy) to the total number of the image pixels.

Lodging

Lodging was recorded at the R5 and R8 growth stages in all three environments for all plots, as the mean of three independent ratings on a 1-5 scale, where 1 indicates no lodging and 5 indicates a prostrate plant (Fehr and Caviness, 1977). The R5 lodging scores were recorded during the first week of October.

Plant Height

Plant height was recorded at 3WAE (on the same day as percent ground cover) and at harvest as the mean of three random plants per plot. Plant height was defined as distance from ground level to the apical meristem.

Maturity date was recorded for each plot, and defined as the first day on which 95% of the pods in the plot were mature (Fehr and Caviness, 1977). Once the first plot was rated for maturity date for an environment, plots were visited on approximately five day intervals until all plots were mature. Maturity was redefined as October 1= day 1 prior to analysis.

Yield

Prior to harvest, each plot was end trimmed by hand to a final harvest plot length of 2.4 and 3 m in 2014 and 2015, respectively. After end-trimming, an outside border row was removed from each side of all plots by hand pulling. In 2014 and 2015 six and five rows, respectively, were harvested from each narrow row plot, using an Almaco SP20 single plot

combine. In 2014 and 2015, nine and eight rows, respectively were harvested from each ultra-narrow row plot, using the same plot combine employed for narrow rows. Seed were air dried to approximately eight percent moisture prior to determination of seed yield and 100-seed weight. Prior to analysis, seed yield was converted to $kgha^{-1}$.

Experimental design and statistical analysis

In 2014, treatments consisted of two row-spacings (11 and 23 cm), two planting densities (10 and 26 m^{-1}), two seed size categories selected from within seed lots of genotypes, and seven genotypes adapted to the southern USA. In 2015, the experiment was repeated at two additional locations with the exception that seeding rate was eliminated as a variable. The study was established as a split-plot design with narrow and ultra-narrow row-spacing as whole plots, and subplots were assigned to factorial combinations of the remaining treatments. Four replications were employed in each environment. Genotype, seed size, population density, and row-spacing were considered fixed effects, while environment and replication were treated as random effect. Statistical analyses were conducted using SAS 9.4 (SAS Institute Inc., Cary, NC). Analysis of variance and least squares means were calculated using the GLM procedure in SAS (Tables 3.2 and 3.3). A LSD was used to test for significant differences between genotypes for each trait. For detection of row-spacing and seed size effects, one-tailed significance tests were employed in the analysis of percent ground cover, based on preplanned comparisons that narrow rows and larger seed would increase percent ground cover as compared to the alternative treatments. Means were subjected to correlation analysis using the correlation procedure in

Excel (Microsoft Office Excel, 2007, Redmond, WA; Table 3.2). Linear regression analysis of genotypic means was performed using the scatter plot function in Excel.

Prior to analysis of variance, plots with poor stands were deleted from the data set as described by Machacek (Chapter 2 2016). In 2014, poor stand was defined arbitrarily as 75% or less than the target stand of 69 and 173 plants m^{-2} for the ultra-narrow and 38 and 88 plants m^{-2} for the narrow row-spacing as cutoff values for removing a plot at 3WAE or 50% or less than the target stand at harvest of 46 and 115 plants m^{-2} for ultra-narrow row-spacing and 25 and 59 plants m^{-2} for narrow row-spacing (10 and 26 seed m^{-1}, respectively) as cutoff values. Using this approach, 45 of 224 plots were deleted from the percent ground cover data set (20% of the plots) and 40 plots (18% of the plots) were deleted for analysis of agronomic traits. Using this protocol in 2015, poor stand was defined arbitrarily as 75% or less than the target stand of 173 and 88 plants m^{-2} cutoff values for removing a plot at 3WAE or 50% or less than the target stand at harvest of 115 and 59 plants m^{-2} cutoff values (ultra-narrow vs. narrow row-spacing, respectively). Using this approach 16 of 336 plots (5% of the plots) were deleted from the percent ground cover data set and 55 of 336 plots (16% of the plots) were deleted for analysis of agronomic traits. Because plant stands were estimated on row segments rather than the entire plots, agreement between lists of discarded plots at 3WAE and at maturity was not absolute. Some plots that were deemed unusable for percent ground cover measurements met the appropriate minimum plant stand target for analysis of agronomic traits. The cutoff values at harvest (50% of target stand) was lower than at 3WAE (75% of target stand), because plant density decreased over the season.

Results

Plant density effects

In 2014, the higher seeding rate (26 seed m^{-1}) affected most traits including significant ($p<0.01$) increases in height at 3WAE (1 cm), unifoliate size (1 cm^2), percent ground cover (11 percentage units), and lodging at maturity (0.6 units). Height at maturity, maturity date, and 100-seed weight were relatively unaffected by planting density. Although the seeding rate x row-spacing interaction for percent ground cover was not significant ($p>0.05$), response to the higher seeding rate was numerically greater in the ultra-narrow than narrow row spacing (increases of 15 vs. 6 percentage units, respectively). A percent ground cover of a least 70% was achieved only under the higher seeding rate (26 seed m^{-1}) conditions, except for breeding line N93-7133. This genotype exhibited 72% ground cover at the lower planting rate in the ultra-narrow row spacing.

A genotype x seeding rate interaction was detected for all traits except maturity date, 100-seed weight, and seed yield. However, the interactions were modest except for lodging at maturity and percent ground cover. Soybean cultivar 'N7003CN' ranked relatively more poorly for percent ground cover and better for lodging at maturity than did other genotypes under the higher vs. lower seeding rate (Table 3.2). Overall the higher planting density reduced yield 9 % ($p<0.01$) as compared to the lower planting density.

Seed size, genotype, and row-spacing effects

Data for all three environments were analyzed as a group, after eliminating the low seeding rate of 10 viable seed m^{-1} of row from the 2014 data set. Percent ground cover at 3WAE varied considerably among the three environments (74, 60, and 45 %, Kinston 2015, Clayton 2014 and 2015, respectively) and ground cover in ultra-narrow rows was less in comparison to Machacek Chapter 2 (2016). The reduced ground cover at 3WAE in the present study was primarily a function of slow emergence and poor early growth at Clayton, NC in 2015. Partitioning of the sums of squares for overall environmental effects on percent ground cover revealed that 55% of the sums of squares for environmental effects could be explained by the comparison of Clayton 2015 vs. the other two environments. A companion study was in the same Clayton 2015 environment (Machacek Chapter 2 2016) but had five times less error variance for ground cover (76 and 15 $units^2$, respectively).

The sorting of planting seed, *via* sieving produced large and small seed size treatments that differed by approximately 7 g 100-seed^{-1} (Table 3.1). Differences between treatments within genotypes ranged from approximately 4.8 to 9.5 g 100-seed^{-1}. The larger seed treatment significantly ($p<0.05$) increased height at 3WAE (2 cm), height at maturity (2 cm), size of unifoliate (2.3 cm^2), and percent ground cover (5 percentage units) as compared to smaller seed. Ultra-narrow row-spacing generally increased height at 3WAE (1 cm, $p<0.05$), lodging at maturity (0.8 units, $p<0.05$), and percent ground cover (15 percentage units, $p<0.065$) as compared to narrow rows. Seed size had no effect on lodging at maturity and row spacing x seed size interactions were generally undetectable ($p>0.05$).

Genotypes differed significantly ($p<0.01$) for most traits (Table 3.3). A genotype x seed size interaction was detected for unifoliate size (Table 3.3, $p<0.05$), in which USDA

breeding line N93-7133 responded the least, numerically, to increasing seed size and NC-Raleigh responded the most (1.3 vs. 3.6 cm^2, respectively). Despite this interaction, N93-7133 produced among the largest unifoliates in both seed size treatments and the greatest overall ground cover at 3WAE in both the large and small seed size treatments.

Main effects of row-spacing and seed size on yield were masked by a substantial row-spacing x genotype x seed size interaction ($p<0.01$). Narrow rows yielded significantly ($p<0.05$) better than ultra-narrow in two of the three test environments, but significantly worse in the third environment (4540 vs. 4986, 4715 vs. 3650, and 3090 vs. 2648 narrow vs. ultra- narrow rows, Clayton 2014, Clayton 2015, and Kinston 2015, respectively).

Overall genotypic differences for yield were masked by genotype x seed size and genotype x seed size x row-spacing interactions. Inspection of the seed yield means of genotypes for large and small seed size treatments indicated that genotypes 'Dillon', 'N7103', and N93-7133 responded positively to selection for large seed size, while the other genotypes had no response or responded negatively, numerically. Response to sorting of seed was also expressed as a numerical change in yield ranking for USDA cultivar N7103 and 'NC-Roy'. N7103 was the genotype with the smallest seed, greatest lodging resistance, and shortest height in this study, numerically, and was also the genotype most enhanced for seed yield by selecting and planting larger seed. N7103 increased its yield ranking from fourth to first in the large vs. small seed size treatments. NC-Roy, by contrast was the most favored by selection for small seed size, and increased its ranking for yield from fifth to second in the smaller vs. larger seed size treatment. Yield performance of N93-7133, USDA N6202, and USDA NC-Raleigh were generally stable across treatments for yield, with NC-Raleigh yielding numerically the greatest or near the highest performance in both seed size

treatments. N93-7133 yielded poorly in both seed size treatments, and N6202 yielded near the mean of the study.

Correlations among genotypic means

Correlation of genotypic means between maturity date and the other traits were not significant ($p>0.05$) for any row spacing-seed size combination. Unifoliate size was correlated with harvest 100-seed weight ($r=0.84$, $p<0.01$) over all combinations of row spacing and seed size. Previous soybean weed suppression studies found that early height and 100-seed weight were positively associated with canopy coverage when evaluated as selection criteria for organic breeding (Smith and Camper, 1974; Jannink et al., 2000; Place et al., 2011a; Soares et al., 2013). Correlations based on genotypic means over treatments, row-spacing, and seed size for the three environments revealed that height at 3WAE was highly correlated with 100-seed weight ($r=0.91$, $p<0.01$). Unifoliate size was positively correlated ($r=0.77$, $p<0.025$) with percent ground cover. Lodging at maturity was positively correlated with percent ground cover in the ultra-narrow rows for both the large ($r=0.79$, $p<0.05$) and small ($r=0.76$, $p<0.05$) seed size treatments and in the narrow rows with large seed size ($r=0.79$, $p<0.025$). Seed yield was not correlated with height at 3WAE or at maturity for any row spacing-seed size combinations. Yield was negatively correlated with unifoliate size ($r=-0.76$, $p<0.05$) and 100-seed weight ($r=-0.67$, $p<0.05$) for the narrow row-spacing and large seed treatment combination.

Discussion

In previous studies, a reduction in row spacing, increased planting density, larger planting seed, and appropriate genotype selection have all been shown to produce larger canopies early in the growing season, leading to reduced weed pressure in soybean (Burris et al., 1971; Burris et al., 1973; Smith and Camper, 1974; Place et al., 2011a; Place et al., 2011b; Soares et al., 2013). In the present study, these results were extended to ultra-narrow rows, where these same factors were combined to increase percent ground cover at 3WAE. Although environments varied in the absolute levels of ground cover at 3WAE, as a result of weather and emergence factors, the ultra-narrow row-high plant population-large planting seed combination always produced the greatest ground cover when combined with USDA large-seeded breeding line N93-7133. N93-7133 was previously identified as a superior genotype for percent ground cover in wide rows (Place et al., 2011b), and ranked number one among genotypes for ground cover in the ultra-narrow row-high plant population-large planting seed treatment combination in each of the three North Carolina environments studied. Mean percent ground cover for N93-7133 in this treatment combination was 78%, among the three environments its greatest ground cover was 93%. Eighty percent or greater of shading has been shown to suppress vegetative and reproductive growth in eastern black nightshade (*Solanum ptycanthum*) (83 and 87%, respectively) (Stoller et al., 1989), and reduce sicklepod populations (80%) (Nice et al., 2001).

Genotype x treatment interaction for percent ground cover was generally small in this study, except for genotype x planting rate, where changes in genotypic ranking were evident for USDA cultivar ‘N7003CN’, N7003CN was numerically the second best genotype at the

low planting rate but then dropped to sixth of seven genotypes at the high planting rate. N7003CN actually decreased two percentage units for ground cover at higher planting rate, while N93-7133 increased 18 percentage units, as compared to the lower planting rate. These observations suggested that if one is interested in identifying genotypes or developing new cultivars with superior canopy coverage at high planting densities, then evaluations under high density conditions may be required.

Both phenotypic recovery of larger seed from sieving seed lots of soybean and also direct breeder selection for larger seed (i.e. development of larger seeded breeding lines and cultivars) produced greater ground cover in ultra-narrow rows (Fig 3.1). The interaction between genotypes and seed size treatments was small for percent ground cover, suggesting that any management approach that increases the seed size of planting seed may have a positive effect on percent ground cover at 3WAE. Unifoliate size was correlated with percent ground cover and seed size (r=0.84 overall row spacing-seed size combinations), suggesting that unifoliate size may also have utility in identifying candidate soybean germplasm for evaluation in ultra-narrow row production. NC-Raleigh had good percent ground cover in this study (ranking number two among seven genotypes in ultra-narrow rows using high plant populations, and larger planting seed), but did not possess either large seed or large unifoliates. Thus, NC-Raleigh may carry an additional trait(s) which enhance ground cover at 3WAE, such as rapid leaf expansion or seed emergence, which may be useful in breeder selection for genotypes adapted to ultra-narrow production. NC-Raleigh has also been identified previously as having excellent ground coverage at 3WAE (Place et al., 2011b; Machacek Chapter 2 2016).

Seed Yield

Treatment effects on seed yield were varied, with selection for seed size having almost no overall impact on yield, while higher seeding rates decreased yield by 9 %. Ultra-narrow row spacing decreased yield over two environments by 22 %, but increased yield 10% in the third. Machacek (Chapter 2 2016) showed contrasting results in that a positive yield response was obtained in ultra-narrow vs. wide rows in two of the three same environments in a companion study which also had lower mean yields as compared to the present study. The presence of a substantial genotype x seed size interaction for yield, suggested that genotypic performance for yield was dependent upon specific treatment combinations. These results suggest that identification of genotypes best adapted for seed yield in ultra-narrow row-high density production using larger planting seed, will be most effective under those specific target conditions.

Lodging

A main purpose of ultra-narrow row high-plant population production is to increase percent ground cover as a potential means to combat weeds. Although percent ground cover and final seed yield did not appear to be correlated in this study, lodging at maturity was substantial in ultra-narrow rows and correlated with percent ground cover ($r=0.77$, $p<0.025$). Genotype N93-7133 exhibited the best ground cover of the seven genotypes tested in this study, but also, had the worst lodging score (4.4 units) in the ultra-narrow-high plant population larger seed size treatment combination. In a companion study, Machacek (Chapter 2 2016), the seed size and lodging correlation followed the same trend such that

genotypes with greater percent ground cover exhibited worse lodging scores. Thus, selection of genotypes with greater percent ground cover by breeders for the ultra-narrow row system may increase lodging problems unless care is taken to make simultaneous improvements in both.

Conclusions

Current land devoted to organic soybean is approximately two percent of total soybean production in the USA. This small hectarage may be indicative of market demand, but may also reflect that conventional cultivars are not well suited to high yield production under organic conditions. The results of the present study indicate that high-population planting density and larger planting seed, coupled with the appropriate genotype, can enhance early season ground cover in ultra-narrow rows, and potentially improve weed control and overall profitability. In organic systems, farmers often save or 'brown bag' their seed from one season to the next, because typically most non-GMO cultivars are not patented and, thus, no legal restrictions apply. If a farmer sorted out and saved the largest seed size of their cultivar for planting seed, then this tactic may offer an easy approach for optimizing an ultra-narrow row spacing and high density production system.

Specific traits such as enhanced ground cover, increased seed size, increased lodging resistance, and adaptation to ultra-narrow production, although potentially important to organic production, have received little breeding attention to date (Murphy et al., 2008). Vollmann et al. (2010) suggested that soybean germplasm should be evaluated to identity genotypes with superior weed suppressive ability. In ultra-narrow rows, Machacek (Chapter 2 2016) showed that some genotypes produce more ground cover than others at 3WAE in high-density ultra-narrow row spacing and that cultivar NC-Raleigh was superior for ground cover at 3WAE. The present study identified a breeding line N93-7133 as numerically superior to NC-Raleigh for ground cover and hints that breeding efforts may be able to develop new cultivars that are superior in early ground cover to those which now exist for

ultra-narrow production. Thus, breeding advances in this area could improve profitability in organic soybean production and expand organic markets.

The genotype x planting density interaction for percent ground cover, the substantial genotype x seed size and genotype x row-spacing x seed size interaction detected for seed yield, and the correlation between lodging at maturity and ground cover all suggested that identifying or screening genotypes adapted to the ultra-narrow high-population large seed-size production system should be conducted in that targeted management system.

In considering future breeding for organic soybean production, hybridization programs should include the mating of genotypes which are not only superior with respect to ground cover at 3WAE, but also diverse for other traits. Increased seed size appears to be related to increased ground cover in some genotypes, such as N93-7133, but other genotypes appear to be superior which have only typical seed size, e.g. NC-Raleigh. Hybridization of these two may produce progeny which have greater percent ground cover at 3WAE than either parent. Recombinant inbred lines from the cross may also aid in genetic studies aimed at elucidating the underlying genetic control of canopy development.

REFERENCES

Amoff, M.D., P.J. Magalhães, and S.J. Ram. 2004. Image processing with ImageJ. Biophoton Int. 11:36-42.

Aslam, M., N. Khan, and M.S. Mirza. 1993. Effect of different row and plant spacings on soybean yield and its components. Pakistan Journal of Agricultural Research 14:143-148.

Bond, W., and A. Grundy. 2001. Non-chemical weed management in organic farming systems. Weed Res. 41:383-405.

Burnside, O. 1979. Soybean (*Glycine max*) growth as affected by weed removal, cultivar, and row spacing. Weed Sci.562-565

Burris, JS; Edje, OT; Wahab, AH. Effects of seed size on seedling performance in soybeans: II. Seedling growth and photosynthesis and field performance. Crop Sci., 1973, 13, 2, 207-210, Crop Science Society of America

Epler, Michael; Staggenborg, Scott. Soybean yield and yield component response to plant density in narrow row systems. Crop Management, 2008, 7, 1, 0-0, Plant Management Network

Fehr, W., C. Caviness, D. Burmood, and J. Pennington. 1971. Stage of development descriptions for soybeans, *Glycine max* (L.) Merrill. Crop Sci. 11:929-931.

Hamilton, M; Rzewnicki, P. North Carolina Organic Grain Production Guide North Carolina State University, 2007

Harder, D.B., C.L. Sprague, and K.A. Renner. 2007. Effect of soybean row width and population on weeds, crop yield, and economic return. Weed Technol. 21:744-752.

Hoad, S.P., N. Bertholdsson, D. Neuhoff, U. Köpke, E. van Bueren, and J. Myers. 2012. Approaches to breed for improved weed suppression in organically grown cereals. Organic Crop Breeding61-76.

Jannink, J., J. Orf, N. Jordan, and R. Shaw. 2000. Index selection for weed suppressive ability in soybean. Crop Sci. 40:1087-1094.

Murphy, K., J. Dawson, and S. Jones. 2008. Relationship among phenotypic growth traits, yield and weed suppression in spring wheat landraces and modern cultivars. Field Crops Res. 105:107-115.

Murphy, K.M., K.G. Campbell, S.R. Lyon, and S.S. Jones. 2007. Evidence of varietal adaptation to organic farming systems. Field Crops Res. 102:172-177.

Nice, G.R., N.W. Buehring, and D.R. Shaw. 2001. Sicklepod *(Senna obtusifolia*) response to shading, soybean (*Glycine max*) row spacing, and population in three management systems 1. Weed Technol. 15:155-162.

Place, G., S.C. Reberg-Horton, T. Carter, and A. Smith. 2011a. Effects of soybean seed size on weed competition. Agron. J. 103:175-181.

Place, G.T., D.A. Dickey, and T.E. Carter. 2011b. Identifying soybean traits of interest for weed competition. Crop Sci. 51:2642-2654.

Place, G.T., S.C. Reberg-Horton, J.E. Dunphy, and A.N. Smith. 2009. Seeding rate effects on weed control and yield for organic soybean production. Weed Technol. 23:497-502.

Shilling, D.G., B.J. Brecke, C. Hiebsch, and G. MacDonald. 1995. Effect of soybean (*Glycine max*) cultivar, tillage, and rye (*Secale cereale*) mulch on sicklepod (*Senna obtusifolia*). Weed Technol.339-342.

Smith, T., and H. Camper. 1975. Effects of seed size on soybean performance. Agron. J. 67:681-684.

Soares, M.M., G.L. Oliveira, P.E. Soriano, M.C. Sekita, and T. Sediyama. 2013. Performance of soybean plants as function of seed size: II. nutritional stress. Journal of Seed Science 35:419-427.

Stoller, E., and R. Myers. 1989. Effects of shading and soybean *Glycine max* (L.) interference on *Solanum ptycanthum* (dun.)(eastern black nightshade) growth and development. Weed Res. 29:307-316.

USDA-NASS, 2015. The USDA National Agricultural Statistics Service. www.nass.usda.gov (accessed 21 January 2016)

USDA-NOP, 2016. The USDA National Organic Program. www.ams.usda.gov (accessed 10 January 2016).

Vollmann, J., H. Wagentristl, and W. Hartl. 2010. The effects of simulated weed pressure on early maturity soybeans. Eur. J. Agron. 32:243-248.

Weber, C., R. Shibles, and D. Byth. 1966. Effect of plant population and row spacing on soybean development and production. Agron. J. 58:99-102.

Yelverton, F.H., and H.D. Coble. 1991. Narrow row spacing and canopy formation reduces weed resurgence in soybeans (*Glycine max*). Weed Technol.169-174.

Table 3.1. Seven soybean genotypes with their 100-seed weight for large and small seed size treatment for the three test environments.

Genotype	Seed Treatment (g 100-seed^{-1})		Seed Treatment (g 100-seed^{-1})		Reference or Developer
	---------2014---------		---------2015----------		
	Large†	Small‡	Large†	Small‡	
Dillon	16.7	12.6	19	13.5	Shipe et al., 1997
N6202	25.0	16.0	27	17	USDA-ARS§
N7003CN	17.7	11.2	22	13	Carter et al., 2011
N7103	8.9	4.9	12.3	6.3	Carter et al., 2003
N93-7133	26.6	21.8	28	18.5	USDA-ARS§
NC-Raleigh	15.6	10	19.2	10.8	Burton et al., 2006
NC-Roy	15.5	9.1	18.7	10	Burton et al., 2005

†Large=Large seed size treatment

‡Small=Small seed size treatment

§USDA-ARS = US Department of Agriculture, Agricultural Research Services

Table 3.2. Least square means of the ten traits for 2014.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large‡------		------Small§------		------Large‡------		------Small§------	
	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#
	----------Stand at 3WAE† (m^{-2})----------							
Dillon	107	210	116	192	57	100	48	108
N6202	96	213	111	155	40	90	32	75
N7003CN	143	245	107	221	60	124	55	131
N7103	97	196	117	230	64	111	61	126
N93-7133	108	241	128	197	52	111	58	102
NC-Raleigh	129	260	95	286	45	103	48	96
NC-Roy	154	231	108	215	51	105	47	103
Mean	119	228	112	214	53	106	50	106
LSD	48	51	51	63	14	27	33	34

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large[‡]------		------Small[§]------		------Large[‡]------		------Small[§]------	
	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]
	----------Height at 3WAE[†] (cm)----------							
Dillon	15	17	14	15	14	16	14	14
N6202	18	19	17	18	16	21	17	19
N7003CN	16	16	14	13	15	16	13	14
N7103	14	15	11	12	12	13	10	12
N93-7133	16	21	16	18	16	17	14	17
NC-Raleigh	13	16	13	13	13	14	11	11
NC-Roy	14	16	11	14	14	14	12	12
Mean	15	17	14	15	14	16	13	14
LSD	1.6	2.7	1.6	2.4	1.4	2.8	2.3	2.3

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large[‡]------		------Small[§]------		------Large[‡]------		------Small[§]------	
	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]
	----------Height at Maturity (cm)----------							
Dillon	98	95	94	97	97	96	91	94
N6202	100	99	99	96	95	98	88	96
N7003CN	103	100	102	95	103	101	94	92
N7103	86	86	79	82	68	84	69	82
N93-7133	89	89	90	81	92	87	86	87
NC-Raleigh	98	94	96	95	90	99	88	93
NC-Roy	104	102	96	91	103	99	92	98
Mean	97	95	94	91	93	95	87	92
LSD	8.1	9.7	6.3	9.7	8.1	7.2	4.3	7.4

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large[‡]------		------Small[§]------		------Large[‡]------		------Small[§]------	
	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]
	----------Unifoliate at 3WAE[†] (cm^2)----------							
Dillon	12.3	12.6	10.5	11.3	11.5	12.8	9.9	11.3
N6202	13.9	15.3	11.0	10.1	11.4	13.0	9.7	10.8
N7003CN	9.2	9.6	7.5	7.3	9.2	9.4	7.0	7.2
N7103	5.5	6.2	3.9	4.5	4.8	5.8	3.7	4.6
N93-7133	13.0	14.0	11.0	12.7	12.0	14.6	12.0	13.0
NC-Raleigh	10.6	13.3	8.4	9.9	10.9	12.0	8.7	8.9
NC-Roy	8.3	9.3	5.7	6.4	7.5	8.6	5.8	6.6
Mean	10.4	11.5	8.3	8.9	9.6	10.9	8.1	8.9
LSD	1.1	1.4	0.8	1.2	1.6	1.8	1.4	1.1

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large[‡]------		------Small[§]------		------Large[‡]------		------Small[§]------	
	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]	10 m^{-1}[¶]	26 m^{-1}[#]
	----------Percent Ground Cover at 3WAE[†] (%)----------							
Dillon	57	72	51	66	35	46	36	45
N6202	48	71	43	52	38	47	25	30
N7003CN	64	67	52	53	47	36	42	37
N7103	35	60	36	54	51	35	40	35
N93-7133	72	82	62	78	47	61	38	50
NC-Raleigh	63	75	52	71	31	64	36	46
NC-Roy	55	70	41	72	32	44	45	42
Mean	56	71	48	64	40	48	38	41
LSD	15	11	12	11	21	21	21	21

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large‡------		------Small§------		------Large‡------		------Small§------	
	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#
	----------Lodging at Maturity (1-5 scale)----------							
Dillon	2.7	3.9	2.2	4.0	2.0	2.9	2.2	2.6
N6202	3.1	3.8	3.3	3.6	3.3	3.2	3.1	4.1
N7003CN	3.5	4.0	3.6	4.1	3.4	3.2	3.6	3.3
N7103	3.1	3.8	2.9	3.7	2.2	3.3	2.8	3.4
N93-7133	4.0	4.7	4.0	4.7	3.6	4.3	3.5	4.4
NC-Raleigh	3.9	4.4	3.9	4.8	3.4	4.1	3.6	4.1
NC-Roy	3.9	4.3	3.9	4.4	3.5	3.9	3.6	4.0
Mean	3.4	4.1	3.4	4.2	3.0	3.5	3.2	3.7
LSD	0.6	0.6	0.8	0.7	0.7	0.6	0.9	0.5

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large‡------		------Small§------		------Large‡------		------Small§------	
	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#
	----------Stand at Harvest (m^{-2})----------							
Dillon	101	168	105	161	44	88	39	74
N6202	85	147	77	125	39	77	31	68
N7003CN	99	193	91	191	47	98	60	95
N7103	95	179	108	215	54	75	48	113
N93-7133	119	185	95	124	46	83	50	88
NC-Raleigh	92	189	100	147	42	80	48	85
NC-Roy	99	194	95	169	40	99	41	97
Mean	99	179	96	162	45	86	45	89
LSD	30	43	30	45	12	26	16	23

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large‡------		------Small§------		------Large‡------		------Small§------	
	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#
	----------Maturity Date (Oct 1=1)----------							
Dillon	25	26	25	25	25	26	25	25
N6202	29	27	26	27	28	27	26	27
N7003CN	30	28	28	28	30	28	28	28
N7103	27	27	27	26	26	26	27	27
N93-7133	29	31	31	30	30	29	30	30
NC-Raleigh	30	31	31	29	30	30	30	29
NC-Roy	25	25	24	26	24	25	24	25
Mean	28	28	27	27	28	27	27	27
LSD	2.8	1.8	2.3	2.1	1.9	1.5	2.9	1.7

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large‡------		------Small§------		------Large‡------		------Small§------	
	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#
	----------Harvest Seed Weight (g 100-seed^{-1})----------							
Dillon	17.9	17.2	16.6	16.8	17.2	17.3	17.7	17.0
N6202	25.9	25.3	25.9	27.0	25.6	24.4	24.4	25.0
N7003CN	17.8	17.4	17.6	17.0	18.4	17.5	17.5	17.7
N7103	8.7	8.6	8.7	8.3	8.4	9.0	8.8	8.8
N93-7133	24.3	25.0	24.8	22.8	25.4	24.3	23.8	24.0
NC-Raleigh	15.9	15.8	16.2	15.7	15.5	15.8	15.6	15.0
NC-Roy	15.4	14.2	14.5	14.6	14.6	14.9	14.7	14.3
Mean	18.0	17.6	17.7	17.5	17.9	17.6	17.5	17.4
LSD	0.9	0.8	1.4	1.2	0.9	1.0	0.9	1.0

Table 3.2. Continued.

Genotype	11 cm row spacing				23 cm row spacing			
	------Large‡------		------Small§------		------Large‡------		------Small§------	
	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#	10 m^{-1}¶	26 m^{-1}#
	----------Seed Yield ($kgha^{-1}$)----------							
Dillon	5663	5815	5923	4426	4628	4657	4790	4856
N6202	4936	5032	5925	5885	5110	4977	4040	3907
N7003CN	4699	3969	4936	3798	5530	4107	5788	4363
N7103	4270	5011	6216	5254	5579	5257	5193	3991
N93-7133	4620	5266	6073	3912	5630	3943	4789	3473
NC-Raleigh	6989	5082	5646	4702	5606	5481	5777	4999
NC-Roy	5689	4844	5664	6261	5178	5060	5813	4503
Mean	5267	5003	5769	4891	5323	4783	5170	4299
LSD	1605	1465	1613	1561	1243	1390	1129	1467

†3WAE=3 weeks after emergence

‡Large=Large seed size treatment

§Small=Small seed size treatment

¶10 m^{-1}=9.8 viable beans per meter

#26 m^{-1}=26.2 viable beans per meter

Table 3.3. ANOVA of the ten traits for 2014.

Source of Variation	Stand at 3WAE‡ (m^{-2})		Height at 3WAE‡ (cm)	
	DF†	Mean Square	DF†	Mean Square
Rep(Environment)	3	1035 ns	3	30.8 *
Row-spacing	1	282020 **	1	33.1 *
Error A	3	262 ns	3	3.6 *
Genotype	6	1861 **	6	71.3 **
Genotype*Row-spacing	6	1564 **	6	1.6 ns
Rate	1	233672 **	1	71.4 **
Rate*Row-spacing	1	24878 **	1	0.8 ns
Rate*Genotype	6	1101 *	6	4.1 **
Rate*Genotype*Row-spacing	6	1078 *	6	2.0 ns
Size	1	1390 ns	1	122.0 **
Size*Row-spacing	1	1164 ns	1	0.3 ns
Size*Genotype	6	654 ns	6	0.8 ns
Size*Genotype*Row-spacing	6	338 ns	6	0.2 ns
Size*Rate	1	2 ns	1	7.7 **
Size*Row-spacing*Rate	1	180 ns	1	0.5 ns
Size*Genotype*Rate	6	896 ns	6	2.5 ns
Size*Genotype*Row-spacing*Rate	6	863 ns	6	1.6 ns
Error B	109	569	110	1.4

Table 3.3. Continued.

Source of Variation	Height at Maturity (cm)		Lodging at Maturity (1-5 scale)	
	DF†	Mean Square	DF†	Mean Square
Rep(Environment)	3	129 ns	3	0.08 ns
Row-spacing	1	397 ns	1	6.72 **
Error A	3	119 **	3	0.23 ns
Genotype	6	1557 **	6	6.30 **
Genotype*Row-spacing	6	54 ns	6	0.25 ns
Rate	1	27 ns	1	15.34 **
Rate*Row-spacing	1	416 **	1	0.55 *
Rate*Genotype	6	119 **	6	0.63 **
Rate*Genotype*Row-spacing	6	35 ns	6	0.24 ns
Size	1	897 **	1	0.27 ns
Size*Row-spacing	1	11 ns	1	0.18 ns
Size*Genotype	6	38 ns	6	0.06 ns
Size*Genotype*Row-spacing	6	30 ns	6	0.07 ns
Size*Rate	1	8 ns	1	0.02 ns
Size*Row-spacing*Rate	1	44 ns	1	0.03 ns
Size*Genotype*Rate	6	13 ns	6	0.06 ns
Size*Genotype*Row-spacing*Rate	6	40 ns	6	0.24 ns
Error B	162	27	122	0.14

Table 3.3. Continued.

Source of Variation	Maturity Date (Oct 1=1)		Harvest Seed Weight (g 100-seed^{-1})	
	DF†	Mean Square	DF†	Mean Square
Rep(Environment)	3	11.21 ns	3	1.43 ns
Row-spacing	1	2.82 ns	1	0.73 ns
Error A	3	5.39 *	3	0.05 ns
Genotype	6	102.25 **	6	792.71 **
Genotype*Row-spacing	6	0.85 ns	6	1.45 **
Rate	1	0.92 ns	1	3.45 **
Rate*Row-spacing	1	0.11 ns	1	0.07 ns
Rate*Genotype	6	2.07 ns	6	0.30 ns
Rate*Genotype*Row-spacing	6	0.66 ns	6	0.15 ns
Size	1	2.89 ns	1	2.32 **
Size*Row-spacing	1	0.49 ns	1	0.10 ns
Size*Genotype	6	1.31 ns	6	0.64 ns
Size*Genotype*Row-spacing	6	0.69 ns	6	0.70 *
Size*Rate	1	0.10 ns	1	0.19 ns
Size*Row-spacing*Rate	1	3.03 ns	1	0.13 ns
Size*Genotype*Rate	6	2.36 ns	6	0.70 *
Size*Genotype*Row-spacing*Rate	6	1.58 ns	6	1.62 **
Error B	122	1.90	120	0.33

Table 3.3. Continued.

Sources of Variation	Stand at Harvest (m^{-2})		Seed Yield ($kgha^{-1}$)	
	DF†	Mean Square	DF†	Mean Square
Rep(Environment)	3	365 ns	3	1236484 ns
Row-spacing	1	179496 **	1	4251864 ns
Error A	3	956 **	3	1801140 *
Genotype	6	2256 **	6	2277185 **
Genotype*Row-spacing	6	344 ns	6	1570164 *
Rate	1	127618 **	1	15173444 **
Rate*Row-spacing	1	8434 **	1	365466 ns
Rate*Genotype	6	848 **	6	916795 ns
Rate*Genotype*Row-spacing	6	505 ns	6	600179 ns
Size	1	1002 ns	1	89624 ns
Size*Row-spacing	1	1737 **	1	3103402 *
Size*Genotype	6	1094 **	6	373415 ns
Size*Genotype*Row-spacing	6	603 *	6	1824730 **
Size*Rate	1	557 ns	1	2342963 ns
Size*Row-spacing*Rate	1	989 *	1	90644 ns
Size*Genotype*Rate	6	627 *	6	630414 ns
Size*Genotype*Row-spacing*Rate	6	166 ns	6	1499055 *
Error B	121	281	122	669875

†DF=Degrees of Freedom

‡3WAE=3 weeks after emergence

ns=No significant difference between genotypes

*,** significantly different from zero at P ≤ 0.05 and P ≤ 0.01 respectively

Table 3.4. Least square means of the ten traits for planting rate 26 soybean m^{-1} in the three environments.

Genotype	----------Stand at 3WAE† m^2----------				----------Height at 3WAE†(cm)----------			
	11 cm row-spacing		23 cm row-spacing		11 cm row-spacing		23 cm row-spacing	
	Large‡	Small§	Large‡	Small§	Large‡	Small§	Large‡	Small§
Dillon	208	208	112	114	16	15	16	14
N6202	215	187	116	95	20	17	19	16
N7003CN	235	220	119	119	16	13	16	13
N7103	224	250	108	126	14	12	13	11
N93-7133	235	205	114	101	18	16	16	16
NC-Raleigh	234	227	119	101	15	12	14	11
NC-Roy	217	222	109	112	16	13	15	11
Mean	224	217	114	110	16	14	16	13
LSD	33	41	16	17	2.9	2.5	1.8	0.9

Table 3.4. Continued.

Genotype	----------Unifoliate Size at 3WAE† (cm^2)----------				-----Percent Ground Cover at 3WAE† (%)-----			
	11 cm row-spacing		23 cm row-spacing		11 cm row-spacing		23 cm row-spacing	
	Large‡	Small§	Large‡	Small§	Large‡	Small§	Large‡	Small§
Dillon	13.4	11.8	13.6	11.1	68	67	55	53
N6202	13.6	11.6	13.6	10.5	72	62	58	46
N7003CN	10.0	7.6	9.7	7.5	71	59	52	41
N7103	6.7	4.4	6.1	4.6	57	50	42	33
N93-7133	13.3	12.0	13.2	11.9	78	69	62	51
NC-Raleigh	12.6	8.9	12.1	8.6	72	64	65	53
NC-Roy	9.1	6.4	8.6	6.1	69	66	54	46
Mean	11.3	8.9	11.0	8.6	69	63	55	46
LSD	1.5	1.6	1.5	0.9	9	16	11	8

Table 3.4. Continued.

Genotype	Height at Maturity (cm)				Lodging at Maturity (1-5 scale)			
	11 cm row-spacing		23 cm row-spacing		11 cm row-spacing		23 cm row-spacing	
	Large‡	Small§	Large‡	Small§	Large‡	Small§	Large‡	Small§
Dillon	101	99	100	102	3.5	3.7	2.5	2.3
N6202	101	99	102	100	3.6	3.5	3.0	2.9
N7003CN	101	100	107	101	3.6	3.2	2.6	2.7
N7103	94	90	94	86	3.2	3.3	2.6	2.5
N93-7133	96	90	93	94	4.4	4.3	3.5	3.3
NC-Raleigh	97	101	104	102	4.1	4.3	3.7	3.6
NC-Roy	106	102	108	106	4.1	4.0	3.3	3.4
Mean	99	97	101	99	3.8	3.7	3.0	2.9
LSD	7	5	5	4	0.35	0.38	0.66	0.72

Table 3.4. Continued.

Genotype	Stand at Harvest (m^{-2})				Maturity Date (Oct 1=1)			
	11 cm row-spacing		23 cm row-spacing		11 cm row-spacing		23 cm row-spacing	
	Large‡	Small§	Large‡	Small§	Large‡	Small§	Large‡	Small§
Dillon	176	185	99	86	26	25	25	26
N6202	167	162	102	86	30	29	29	30
N7003CN	201	186	102	102	33	33	33	33
N7103	182	204	92	104	31	31	31	30
N93-7133	193	163	93	91	35	34	34	34
NC-Raleigh	201	169	93	83	34	32	31	33
NC-Roy	184	176	99	96	27	28	27	26
Mean	186	178	97	93	31	30	30	30
LSD	27	29	17	18	3.7	4.2	3.8	3.3

Table 3.4. Continued.

Genotype	-----Harvest seed weight (g 100-seed^{-1})-------				----------Seed Yield (kgha^{-1})----------			
	11 cm row-spacing		23 cm row-spacing		11 cm row-spacing		23 cm row-spacing	
	Large‡	Small§	Large‡	Small§	Large‡	Small§	Large‡	Small§
Dillon	16.5	15.7	16.9	16.3	4126	3374	3978	4294
N6202	23.4	24.1	23.6	23.7	3668	4032	4208	4040
N7003CN	16.7	16.2	16.8	16.5	3392	3490	4139	4146
N7103	8.1	7.8	8.2	8.0	4008	4146	4465	3804
N93-7133	23.1	21.4	22.6	22.1	3619	2947	3459	3580
NC-Raleigh	14.8	14.3	14.8	14.2	4205	3911	4171	4806
NC-Roy	13.7	13.5	14.2	13.4	3359	4610	4417	4062
Mean	16.6	16.1	16.7	16.3	3768	3787	4120	4105
LSD	1.07	1.10	0.89	0.80	692	1008	875	1137

†3WAE=3 weeks after emergence

‡Large=Large seed size treatment

§Small=Small seed size treatment

Table 3.5. ANOVA of the ten traits for the three test environments.

Sources of Variation	Stand at 3WAE‡ (m^{-2})			Height at 3WAE‡ (cm)		
	DF†	Mean Square		DF†	Mean Square	
Environment	2	18028.5		2	508.88	
Rep(environment	9	1001.8		9	19.29	
Row-spacing	1	719403.5	*	1	44.36	ns
Environment*Row-spacing	2	1660.3	*	2	3.17	ns
Rep*Row-spacing(environment)	9	527.6		9	2.19	
Genotype	6	1889.1	*	6	132.17	**
Environment*Genotype	12	1450.5	**	12	10.47	**
Row-spacing*Genotype	6	933.3	ns	6	1.30	ns
Environment*Row-spacing*Genotype	12	1598.7	**	12	3.97	ns
Size	1	1796.1	ns	1	306.94	**
Environment*Size	2	141.2	ns	2	4.57	ns
Row-spacing*Size	1	201.4	ns	1	0.01	ns
Environment*Row-spacing*Size	2	564.1	ns	2	3.15	ns
Genotype*Size	6	1983.3	*	6	7.29	ns
Enivironment*Genotype*Size	12	517.1	ns	11	3.36	ns
Row-spacing*Genotype*Size	6	291.8	ns	6	1.26	ns
Environment*Row-spaincg *Genotype*Size	12	383.3	ns	11	1.58	ns
Error	182	576.8		181	2.77	
Error Kinston 2015	74	670.1		73	3.30	
Error Clayton 2014	46	587.0		46	1.85	
Error Clayton 2015	62	458.0		62	2.83	

Table 3.5. Continued.

Sources of Variation	Percent Ground Cover at 3WAE‡ (%)			Lodging at Maturity (1-5 scale)		
	DF†	Mean Square		DF†	Mean Square	
Environment	2	23086.1		2	15.37	
Rep(environment)	9	586.7		9	0.18	
Row-spacing	1	14452.6	ns	1	36.13	*
Environment*Row-spacing	2	2293.1	**	2	1.60	**
Rep*Row-spacing(environment)	9	103.5		9	0.18	
Genotype	6	1738.1	**	6	7.12	**
Environment*Genotype	12	388.1	**	12	0.71	**
Row-spacing*Genotype	6	99.5	ns	6	0.41	ns
Environment*Row-spacing*Genotype	12	50.7	ns	12	0.35	**
Size	1	5074.5	ns	1	0.21	ns
Environment*Size	2	613.7	**	2	0.44	ns
Row-spacing*Size	1	173.0	*§	1	0.09	ns
Environment*Row-spacing*Size	2	86.4	ns	2	0.14	ns
Genotype*Size	6	137.1	ns	6	0.04	ns
Enivironment*Genotype*Size	12	73.4	ns	12	0.08	ns
Row-spacing*Genotype*Size	6	10.2	ns	6	0.28	ns
Environment*Row-spaincg *Genotype*Size	12	67.6	ns	12	0.21	ns
Error	209	76.5		181	0.16	
Error Kinston 2015	75	99.0		62	0.18	
Error Clayton 2014	58	74.4		58	0.10	
Error Clayton 2015	76	55.9		61	0.19	

Table 3.5. Continued.

Sources of Variation	Stand at Harvest (cm^{-2})			Maturity Date Oct (1=1)		
	DF†	Mean Square		DF†	Mean Square	
Environment	2	8572.1		2	451.22	
Rep(environment)	9	653.8		7	22.05	
Row-spacing	1	449452.2	**	1	2.60	*
Environment*Row-spacing	2	2783.2	*	2	0.15	ns
Rep*Row-spacing(environment)	9	518.4		7	6.63	
Genotype	6	1583.6	ns	6	248.55	**
Environment*Genotype	12	928.6	ns	11	44.82	**
Row-spacing*Genotype	6	769.1	ns	6	1.22	ns
Environment*Row-spacing*Genotype	12	358.5	ns	11	2.13	ns
Size	1	3987.7	ns	1	2.33	ns
Environment*Size	2	11.6	ns	2	4.34	ns
Row-spacing*Size	1	626.6	ns	1	10.13	ns
Environment*Row-spacing*Size	2	758.3	ns	2	1.75	ns
Genotype*Size	6	1536.8	ns	6	0.73	ns
Enivironment*Genotype*Size	12	504.3	ns	11	2.47	ns
Row-spacing*Genotype*Size	6	797.6	ns	6	4.02	ns
Environment*Row-spaincg *Genotype*Size	12	409.0	ns	11	1.59	ns
Error	180	608.1		137	4.04	
Error Kinston 2015	62	790.3		18	3.35	
Error Clayton 2014	57	391.9		58	1.50	
Error Clayton 2015	61	624.8		61	6.65	

Table 3.5. Continued.

Sources of Variation	Harvest 100-seed weight (g 100-seed^{-1})			Seed Yield (kg ha^{-1})		
	DF†	Mean Square		DF†	Mean Square	
Environment	2	68.3		2	73298110	
Rep(environment)	9	0.8		9	1095925	
Row-spacing	1	1.1	ns	1	7344012	ns
Environment*Row-spacing	2	1.5	ns	2	11299709	**
Rep*Row-spacing(environment)	9	0.7		9	743075	
Genotype	6	967.3	**	6	2320656	ns
Environment*Genotype	12	2.4	**	12	1478305	*
Row-spacing*Genotype	6	0.4	ns	6	587570	ns
Environment*Row-spacing*Genotype	12	0.8	**	12	1143838	ns
Size	1	11.6	ns	1	13365	ns
Environment*Size	2	1.1	*	2	1216946	ns
Row-spacing*Size	1	0.1	ns	1	32015	ns
Environment*Row-spacing*Size	2	0.3	ns	2	668747	ns
Genotype*Size	6	1.4	**	6	800044	**
Enivironment*Genotype*Size	12	0.3	ns	12	265933	ns
Row-spacing*Genotype*Size	6	0.6	ns	6	2589300	**
Environment*Row-spaincg *Genotype*Size	12	0.3	ns	12	609549	ns
Error	181	0.4		181	812517	
Error Kinston 2015	62	0.3		62	603488	
Error Clayton 2014	58	0.3		58	733329	
Error Clayton 2015	61	0.4		61	1100267	

†DF=Degrees of Freedom

‡3WAE=3 weeks after emergence

§One-tailed significant test

ns=No significant difference between genotypes

*,** significantly different from zero at P ≤ 0.05 and P ≤ 0.01 respectively

Table 3.6. Phenotypic correlation coefficients (n = 7) of genotypic means for 11 and 23 cm row-spacings of the three test environments.

			---Height at 3WAE[†](cm)---				--Unifoliate Size at 3WAE[†] (cm^2)--				Percent Ground Cover at 3WAE[†] (%)				----Height at Maturity (cm)----			
			11 cm		23 cm		11 cm		23 cm		11 cm		23 cm		11 cm		23 cm	
			Large[‡]	Small[§]	Large[‡]	Small[§]	Large[‡]	Small[§]	Large[‡]	Small[§]	Large[‡]	Small[§]	Large[‡]	Small[§]	Large[†]	Small[‡]	Large[†]	Small[‡]
----------Height at 3WAE[†](cm)----------	11 cm	Large[‡]		0.94	0.97	0.92	0.69	0.76	0.71	0.73	0.62	0.43	0.43	0.33	0.23	-0.01	-0.11	0.16
		Small[§]			0.87	0.98	0.73	0.85	0.76	0.82	0.53	0.48	0.36	0.38	0.12	-0.17	-0.33	0.03
	23 cm	Large[‡]				0.87	0.72	0.76	0.74	0.70	0.61	0.42	0.44	0.36	0.34	0.20	0.10	0.33
		Small[§]					0.72	0.85	0.76	0.84	0.58	0.44	0.36	0.35	0.04	-0.23	-0.34	-0.02
-------Unifoliate Size at 3WAE[†] (cm^2)--------	11 cm	Large[‡]						0.97	1.00	0.95	0.79	0.76	0.83	0.85	0.07	0.22	-0.03	0.39
		Small[§]							0.98	0.99	0.74	0.73	0.70	0.76	0.05	0.05	-0.19	0.26
	23 cm	Large[‡]								0.96	0.76	0.74	0.78	0.83	0.08	0.20	-0.05	0.37
		Small[§]									0.77	0.74	0.71	0.76	-0.02	-0.03	-0.25	0.20
---Percent Ground Cover at 3WAE[†] (%)----	11 cm	Large[‡]										0.80	0.88	0.75	0.18	0.17	0.12	0.45
		Small[§]											0.80	0.93	0.40	0.30	0.13	0.61
	23 cm	Large[‡]												0.88	0.06	0.31	0.14	0.49
		Small[§]													0.23	0.39	0.15	0.60
----------Height at Maturity (cm)----------	11 cm	Large[†]														0.74	0.76	0.83
		Small[‡]															0.93	0.92
	23 cm	Large[†]																0.86
		Small[‡]																
-------Lodging at Maturity (1-5 scale)--------	11 cm	Large[†]																
		Small[‡]																
	23 cm	Large[†]																
		Small[‡]																
----------Maturity Date (Oct 1=1)----------	11 cm	Large[†]																
		Small[‡]																
	23 cm	Large[†]																
		Small[‡]																
----Harvest seed weight (g 100-$seed^{-1}$)------	11 cm	Large[†]																
		Small[‡]																
	23 cm	Large[†]																
		Small[‡]																
----------Seed Yield (kgha^{-1})----------	11 cm	Large[†]																
		Small[‡]																
	23 cm	Large[†]																
		Small[‡]																

Table 3.6. Continued.

			--Lodging at Maturity (1-5 scale)--				----Maturity Date (Oct 1=1)----				Harvest seed weight (g 100-seed^{-1})				------Seed Yield (kgha^{-1})--------			
			11 cm		23 cm		11 cm		23 cm		11 cm		23 cm		11 cm		23 cm	
			Large†	Small‡	Large†	Small‡	Large†	Small‡	Large†	Small‡	Large†	Small‡	Large†	Small‡	Large†	Small‡	Large†	Small‡
----------Height at 3WAE†(cm)----------	11 cm	Large‡	0.21	0.06	0.12	0.04	0.00	-0.02	0.02	0.15	0.93	0.96	0.94	0.95	-0.34	-0.31	-0.47	-0.32
		Small§	0.14	0.09	0.01	-0.15	-0.11	-0.14	-0.09	0.04	0.87	0.87	0.88	0.88	-0.15	-0.47	-0.60	-0.40
	23 cm	Large‡	0.12	-0.05	0.03	-0.01	-0.06	-0.09	-0.05	0.10	0.90	0.94	0.92	0.93	-0.32	-0.27	-0.37	-0.13
		Small§	0.14	0.04	-0.04	-0.18	0.04	0.01	0.07	0.19	0.90	0.89	0.90	0.91	-0.19	-0.61	-0.69	-0.42
-------Unifoliate Size at 3WAE† (cm^2)--------	11 cm	Large‡	0.43	0.47	0.37	0.19	0.04	-0.08	-0.08	0.16	0.83	0.81	0.83	0.82	0.19	-0.54	-0.67	0.25
		Small§	0.35	0.38	0.22	0.03	-0.02	-0.10	-0.09	0.12	0.87	0.84	0.87	0.86	0.12	-0.64	-0.75	0.02
	23 cm	Large‡	0.38	0.42	0.30	0.11	-0.01	-0.12	-0.11	0.12	0.83	0.81	0.84	0.83	0.19	-0.57	-0.67	0.21
		Small§	0.41	0.42	0.25	0.05	0.07	-0.01	0.00	0.20	0.86	0.82	0.86	0.85	0.12	-0.72	-0.83	-0.02
---Percent Ground Cover at 3WAE† (%)----	11 cm	Large‡	0.79	0.63	0.60	0.57	0.35	0.33	0.30	0.46	0.85	0.81	0.84	0.82	-0.29	-0.52	-0.75	0.06
		Small§	0.76	0.76	0.54	0.48	-0.17	-0.19	-0.23	-0.09	0.63	0.57	0.63	0.59	-0.11	-0.35	-0.63	0.14
	23 cm	Large‡	0.79	0.78	0.79	0.68	0.28	0.19	0.14	0.34	0.67	0.64	0.66	0.64	0.09	-0.33	-0.57	0.39
		Small§	0.66	0.75	0.56	0.43	-0.10	-0.19	-0.24	-0.04	0.55	0.50	0.55	0.52	0.21	-0.37	-0.57	0.43
----------Height at Maturity (cm)----------	11 cm	Large†	0.11	-0.05	-0.10	0.13	-0.66	-0.58	-0.59	-0.60	0.15	0.21	0.20	0.19	-0.58	0.40	0.26	0.14
		Small‡	0.06	0.01	0.07	0.23	-0.44	-0.48	-0.51	-0.42	0.01	0.08	0.06	0.04	-0.10	0.42	0.40	0.76
	23 cm	Large†	0.05	-0.11	0.00	0.26	-0.29	-0.27	-0.30	-0.28	-0.08	-0.02	-0.04	-0.05	-0.36	0.47	0.47	0.61
		Small‡	0.35	0.26	0.22	0.38	-0.41	-0.42	-0.45	-0.36	0.25	0.28	0.29	0.26	-0.27	0.22	0.09	0.58
-------Lodging at Maturity (1-5 scale)--------	11 cm	Large†		0.91	0.88	0.87	0.33	0.36	0.28	0.35	0.46	0.39	0.44	0.40	-0.25	-0.21	-0.56	0.02
		Small‡			0.89	0.78	0.20	0.17	0.08	0.18	0.30	0.23	0.27	0.24	0.13	-0.19	-0.52	0.16
	23 cm	Large†				0.94	0.40	0.37	0.27	0.37	0.31	0.27	0.28	0.26	0.03	0.04	-0.30	0.21
		Small‡					0.36	0.38	0.28	0.33	0.22	0.20	0.20	0.18	-0.23	0.21	-0.13	0.21
----------Maturity Date (Oct 1=1)----------	11 cm	Large†						0.98	0.97	0.99	0.20	0.15	0.15	0.16	-0.04	-0.42	-0.39	-0.10
		Small‡							0.99	0.96	0.17	0.12	0.12	0.13	-0.20	-0.38	-0.37	-0.23
	23 cm	Large†								0.97	0.19	0.15	0.15	0.16	-0.22	-0.42	-0.38	-0.27
		Small‡									0.35	0.31	0.31	0.32	-0.10	-0.51	-0.49	-0.14
----Harvest seed weight (g 100-seed^{-1})------	11 cm	Large†										0.99	1.00	1.00	-0.30	-0.53	-0.70	-0.20
		Small‡											0.99	1.00	-0.32	-0.43	-0.60	-0.17
	23 cm	Large†												1.00	-0.31	-0.50	-0.67	-0.18
		Small‡													-0.31	-0.49	-0.65	-0.19
----------Seed Yield (kgha^{-1})----------	11 cm	Large†														-0.11	0.02	0.48
		Small‡															0.90	0.22
	23 cm	Large†																0.30
		Small‡																

†3WAE=3 weeks after emergence

‡Large=Large seed size treatment

§Small=Small seed size treatment

11 cm = 11 cm row-spacing

23 cm = 23 cm row-spacing

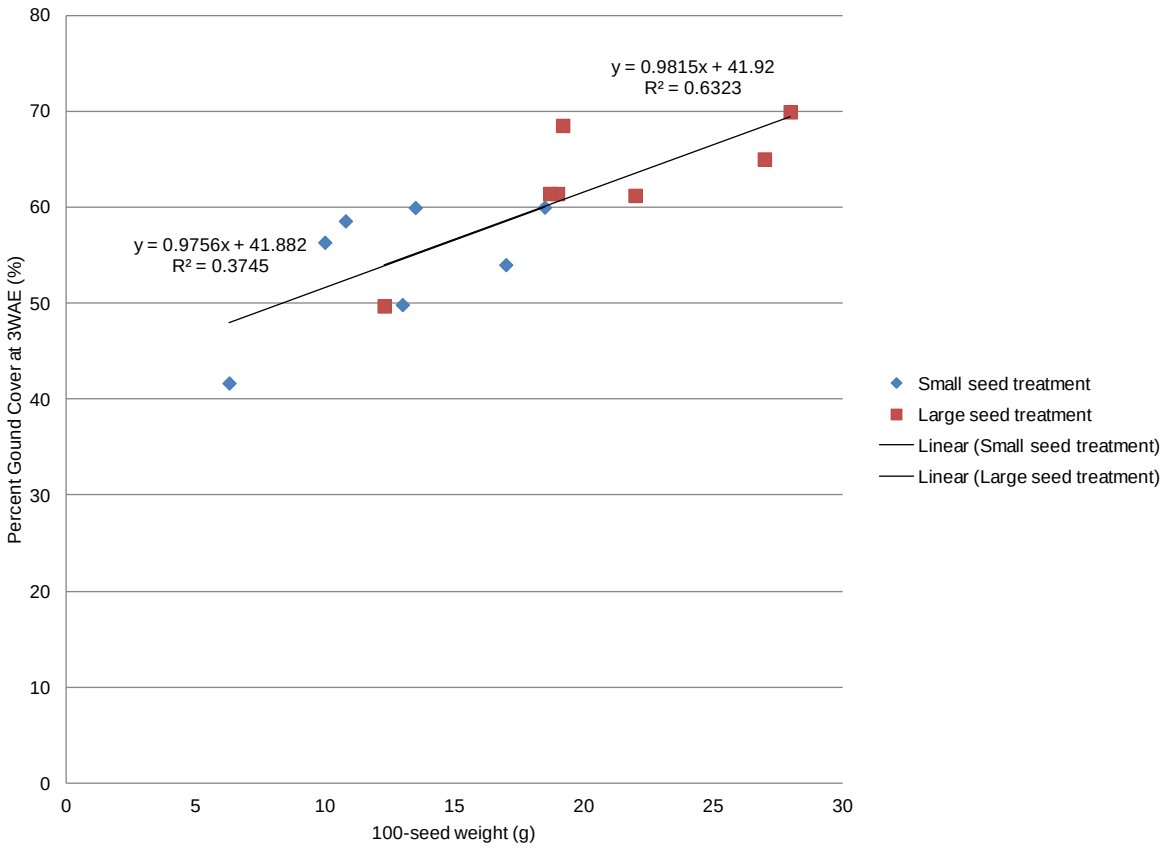

Figure. 3.1. Relationship between 100-seed weight and percent ground cover over three test environments based on genotypic means. Percent ground cover is regressed against the 100-seed weight for two seed size treatment combinations.

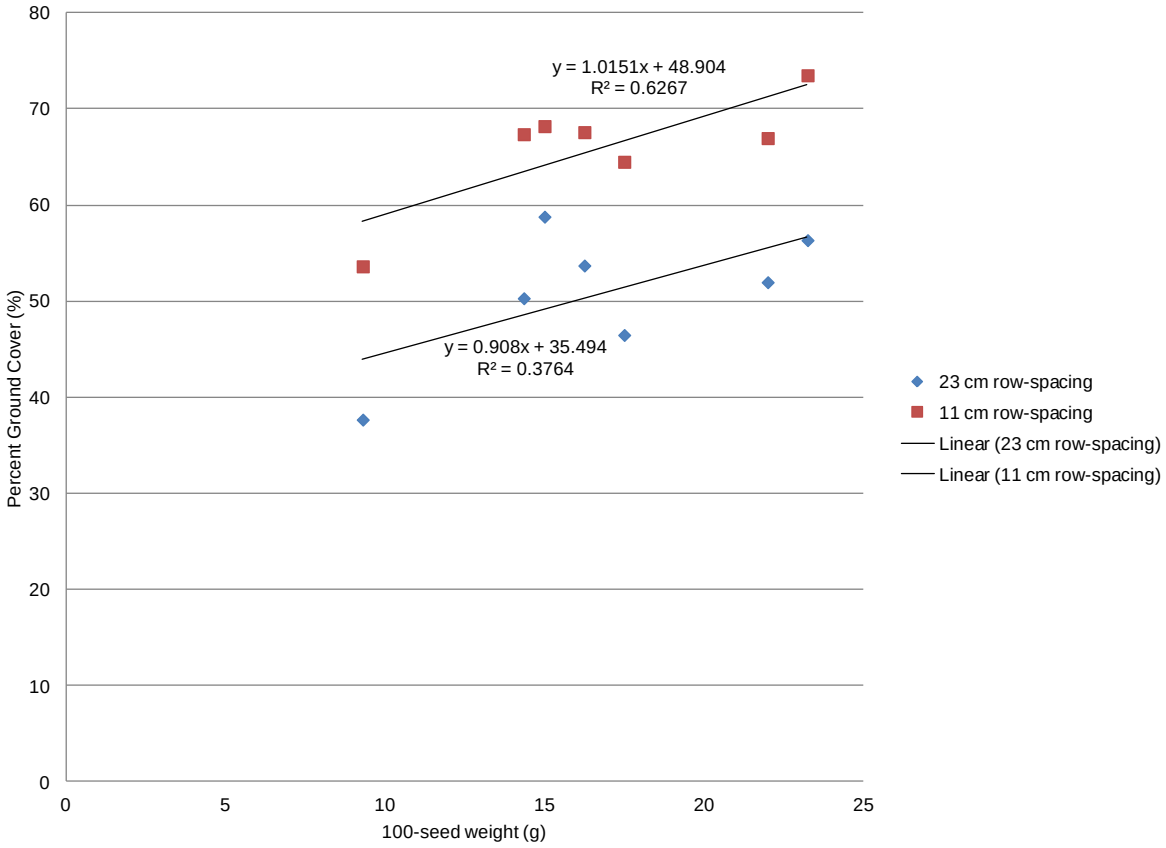

Figure. 3.2. The relationship between 100-seed weight and percent ground cover over the three environments. Genotypic means for percent ground cover are regressed against the 100-seed weight mean and for each row-spacing treatment.

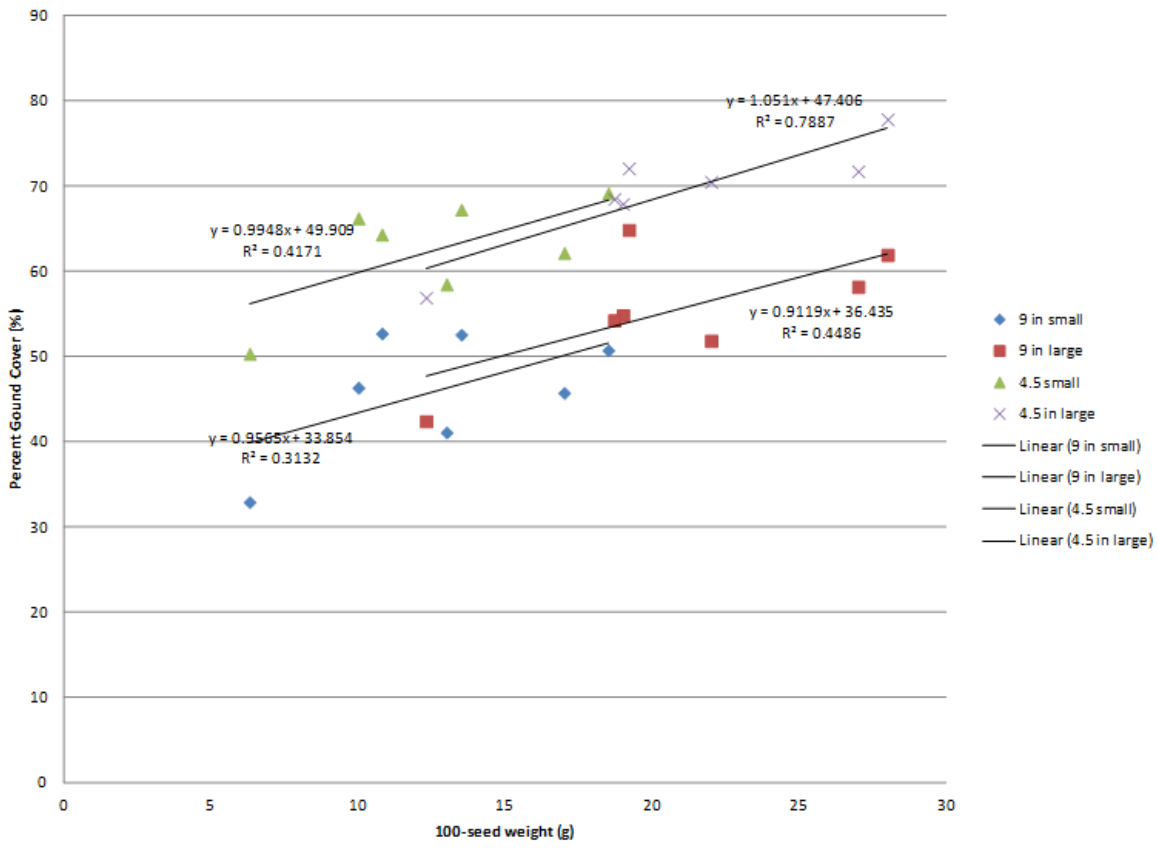

Figure. 3.3. The relationship for the interaction of 100-seed weight and percent ground cover over the three environments. Genotypic means for percent ground cover are regressed against 100-seed weight for each combination of row spacing and seed size treatments.

APPENDIX

Appendix A

Appendix A. Cost analysis for production in wide vs. ultra-narrow row-spacing and estimated profit returns.

Genotype	Maturity Group	100-seed weight	Wide rows (97 cm) planting population at 516,666 ha^{-1} (39 beans m^{-1})			Total Cost of Weed Control‡	Gross Harvest total @ $64 ha^{-1}¶	Profit Wide rows ha^{-1}†
		(g)	Total Planting Seed (kg ha^{-1})	Planting Seed Cost ha^{-1} @ $74 ha^{-1} ($)	Total Harvested (Kg ha^{-1})§	($)	($)	($)
Holladay	V	15.3	79	83	2750	104	2626	1939
Hutcheson	V	15.9	82	86	2413	104	2304	1614
Jake	V	15.7	81	85	2691	104	2570	1881
JTN-5203	V	13.0	67	70	2601	104	2483	1809
N02-7002	V	15.1	78	82	2827	104	2699	2013
NC-Miller	V	16.8	87	91	2939	104	2807	2112
Osage	V	13.8	71	74	3121	104	2981	2302
Dillon	VI	15.7	81	85	2736	104	2613	1924
N06-10237	VI	16.6	86	90	2918	104	2786	2093
N06-6	VI	13.1	68	71	2696	104	2574	1899
N11-9298	VI	15.9	82	86	2762	104	2637	1947
NCC06-1090	VI	17.4	90	94	2826	104	2698	2000
NCC07-8138	VI	16.9	87	91	3009	104	2873	2178
NCC09-135	VI	14.3	74	78	3112	104	2971	2290
NC-Roy	VI	13.5	70	73	2929	104	2797	2120
Young	VI	15.2	79	82	2641	104	2522	1835
Benning	VII	15.1	78	82	2617	104	2499	1814
N09-13128	VII	14.8	76	80	2867	104	2738	2054
N7003CN	VII	16.3	84	88	2762	104	2638	1946
N7103	VII	7.9	41	43	2465	104	2354	1708
NCC06-899	VII	15.2	79	82	3107	104	2967	2281
NC-Raleigh	VII	14.1	73	76	2796	104	2670	1990
TCHM06-M-204	VII	14.9	77	80	3091	104	2952	2268
Woodruff	VII	15.5	80	84	2723	104	2601	1913
Mean		14.9	77	81	2808	104	2682	1997

Appendix A. Continued.

Genotype	Maturity Group	100-seed weight	Ultra-narrow rows (11 cm) planting population at 2,296,297 ha^{-1} (26 beans m^{-1})			Total Cost of Weed Control‡	Gross Harvest total @ $64 ha^{-1}¶	Profit Ultra-narrow rows ha^{-1}†	Profit Ultra-narrow vs. wide rows ha^{-1}
		(g)	Total Planting Seed (kg ha^{-1})	Planting Seed Cost ha^{-1} @ $74 ha^{-1} ($)	Total Harvested (Kg ha^{-1})§	($)	($)	($)	($)
Holladay	V	15.3	351	219	3185	0	3041	2174	234
Hutcheson	V	15.9	365	202	2880	0	2750	1868	254
Jake	V	15.7	360	268	3020	0	2884	2006	125
JTN-5203	V	13.0	299	212	2413	0	2304	1491	-318
N02-7002	V	15.1	348	223	2886	0	2756	1892	-122
NC-Miller	V	16.8	386	273	3119	0	2979	2074	-38
Osage	V	13.8	316	212	3794	0	3623	2792	490
Dillon	VI	15.7	360	324	3060	0	2922	2045	121
N06-10237	VI	16.6	380	319	3012	0	2876	1978	-115
N06-6	VI	13.1	301	175	3976	0	3797	2981	1082
N11-9298	VI	15.9	366	305	3089	0	2950	2067	120
NCC06-1090	VI	17.4	400	298	2970	0	2836	1917	-84
NCC07-8138	VI	16.9	388	290	3214	0	3069	2163	-15
NCC09-135	VI	14.3	329	179	4111	0	3926	3081	791
NC-Roy	VI	13.5	311	226	2897	0	2766	1941	-179
Young	VI	15.2	350	228	2549	0	2434	1567	-268
Benning	VII	15.1	347	269	2851	0	2723	1860	46
N09-13128	VII	14.8	340	243	2816	0	2689	1833	-221
N7003CN	VII	16.3	373	371	3011	0	2875	1984	38
N7103	VII	7.9	181	208	2964	0	2830	2141	433
NCC06-899	VII	15.2	349	228	3633	0	3469	2603	323
NC-Raleigh	VII	14.1	323	322	3073	0	2935	2096	106
TCHM06-M-204	VII	14.9	341	275	4145	0	3959	3101	834
Woodruff	VII	15.5	356	292	2698	0	2577	1704	-209
Mean		14.9	343	257	3140	0	2999	2140	143

†Profit= harvest total minus total expenses (weed control, seed at $74 ha^{-1}, $6 seed processing, and $104 fixed production expense)

‡Weed control, assuming plowing 3 times at $34 ha^{-1}

§Machacek (2016) Chapter 2 yield data

¶Harvest seed gross, at $64 ha^{-1} (2015 average price of organic soybean food grade and feed)