

2012

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Agronomic, seed traits and oleate stability of soybean lines containing the high-oleate transgene DP-305423-1 and the molecular characterization of the genomic region flanking the high-oleate transgene

by

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A dissertation submitted to the graduate faculty
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

Major: Plant Breeding

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2012

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ABSTRACT

To improve the oxidative stability of soybean [*Glycine max* (L.) Merr.] oil, it is desirable to increase the percentage of the monounsaturated fatty ester oleate. By altering the endogenous *FAD2-1* gene in soybean, oleate concentrations of greater than 750 g kg⁻¹ can be obtained. From a commercial perspective, it is important to understand the influence of this genetic alteration on agronomic and seed traits, as well as the stability of the increased oleate concentration across a range of environments.

Objective one of my research was to evaluate the influence of the DP-305423-1 high-oleate (HO) transgene on agronomic and seed traits in five populations evaluated across locations in Iowa, Illinois and Ohio during 2011. A total 27 high-oleate, normal-linolenate (HONL) and 27 normal-oleate, normal-linolenate (NONL) F_{3:5} lines from each population were evaluated. On average, the HONL lines yielded 4.6% less than the NONL lines, had 25 g kg⁻¹ greater protein and 13 g kg⁻¹ lower oil concentration. Of the top 10 yielding lines in each of the five populations, only 12% were HONL. These results suggested it may be difficult to develop HONL lines with seed yield and protein and oil concentration similar to NONL lines.

A second objective of my research was to evaluate the possible influence of undesirable linkage drag near the HO transgene as an explanation for the reduced yield of the HONL lines. All F_{3:5} lines were genotyped with a panel of single nucleotide polymorphism (SNP) markers flanking the HO transgene. Of the six HONL lines that had a mean yield not significantly different than the highest yielding NONL line, only one of them had a genetic recombination near the HO transgene. There were other HONL lines whose mean yield was significantly less than the highest yielding NONL line that had a recombination in the

genomic region. These results suggest that the reduction in yield of the HONL lines is not a result of linkage drag.

A third objective of my research was to evaluate the environmental stability of the increased oleate concentration in soybean lines homozygous for the DP-305423-1 HO transgene. A set of 15 lines with different combinations of alleles for alter fatty ester concentration, as well as three conventional lines were evaluated across 18 environments during 2010 and 2011. Stability was measured by the range in oleate concentration across environments as well as by regressing the mean oleate for each genotype on an environmental index for each environment. The HONL lines had the lowest mean range in oleate concentrations among environments at 73 g kg^{-1} and the lowest mean regression coefficient. These data indicated that the increased oleate concentration in lines homozygous for the DP-305423-1 transgene would be as stable as the oleate concentration of normal-oleate cultivars when produced across multiple environments.

CHAPTER 1

GENERAL INTRODUCTION

Conventional soybean [*Glycine max* (L.) Merr.] oil is comprised of about 600 g kg⁻¹ polyunsaturated fatty esters, including linoleate (18:2) and linolenate (18:3). The abundance of polyunsaturated fatty esters in the seed oil causes it to be highly unstable and susceptible to autoxidation (Cosgrove et al., 1987). To improve the oxidative stability, conventional soybean oil must either be saturated by a chemical process called hydrogenation or the soybean plant must be genetically altered to develop seed oil that has reduced levels of polyunsaturated fat. Chemical hydrogenation is a process by which free hydrogen atoms are supplied to an unstable double bond in order to saturate the bond and make it stable (Dutton, 1963). This chemical process can either be carried out to full saturation or to partial saturation. Most edible vegetable oil is partially hydrogenated. A consequence of partial hydrogenation is that *trans* fatty acid isomers will be produced (Ray and Carr, 1985). The amount of the *trans* isomer present in the oil is of nutritional importance because they have been linked to an increased risk of coronary heart disease (Hu et al., 1999). Extensive research has been conducted by both traditional breeding and biotechnology to alter the fatty ester concentrations in soybean oil as a means of increasing its oxidative stability (Fehr, 2007).

The first attempt to improve the oxidative stability of soybean oil was to decrease the linolenate (18:3) concentration (White et al., 1961). By reducing the concentration of highly unstable fatty ester in the oil, the need for chemical hydrogenation could be reduced or eliminated. One method of altering the linolenate concentration in soybean oil that has been by chemical mutagenesis (Fehr, 2007). By treating seeds of FA9525 with ethyl

methanesulfanate (EMS), Hammond and Fehr (1983) identified a mutant line A5 that had the *fan1*(A5) allele and contained 2 percentage units less linolenate than its parent. Wilcox et al. (1984) used EMS to develop a mutant line designated C1640 that had the *fan1*(C1640) allele and contained about 3 percentage units less linolenate than its parent Century. Chappell and Bilyeu (2006) reported that the reduced linolenate concentration in C1640 was due to a single base pair mutation in the *fan1*(C1640) allele, designated on a molecular basis as the *FAD3A* gene. The mutation introduced a premature stop codon that resulted in a non-functional enzyme. Stojisin et al. (1998) treated seeds of the mutant line C1640 with EMS and identified a line RG10 with less than 30 g kg⁻¹ linolenate. Reinprecht et al. (2009) identified a point mutation within the *FAD3B* gene designated *fan3*(RG10) that resulted in abnormal mRNA splicing and ultimately caused a reduction in linolenate concentration. RG10 also carries the same *fan1*(C1640) mutation within the *FAD3A* gene as C1640 (Reinprecht et al., 2009). Other examples of successful EMS programs include the development of A23 by treating seeds of FA47437 (Bubeck et al., 1989). When A23 was crossed to A5, transgressive segregates with about 25 g kg⁻¹ linolenate were observed indicating that A23 contained a mutation at a locus other than that of *fan1*(A5), which was designated *fan2*(A23) (Bubeck et al., 1989; Fehr et al., 1992). A third mutation identified in the line A26 that was obtained by treating seeds of A89-144033 with EMS was designated *fan3*(A26) (Fehr and Hammond, 2000). Ross et al. (2000) evaluated the agronomic performance of soybean lines containing the three mutant alleles from A5, A23, and A26. They reported that soybean lines homozygous for the three alleles contained a linolenate concentration of <20 g kg⁻¹. They indicated that it should be possible to develop soybean lines with the three alleles that have a

< 20 g kg⁻¹ linolenate and acceptable agronomic performance. Cultivars with the three alleles have been grown commercially for more than a decade (Fehr, 2007).

A second method to improve the oxidative stability of soybean oil has been to increase the concentration of oleate, a monounsaturated fatty ester. Rahman et al. (1994) treated the cultivar Bay with X-ray radiation and identified a mutant line designated M23. M23 contained about 500 g kg⁻¹ oleate (18:1) compared to Bay with 230 g kg⁻¹ oleate (Rahman et al., 1994; Takagi and Rahman, 1996). Devinder et al. (2007) reported that the oleate concentration in M23 was increased due to a deletion in the fatty acid desaturase gene, *FAD2-1A* that was designated *ol*. Dierking and Bilyeu (2009) utilized TILLING to identify a mutant *FAD2-1A* allele in the line designated 17D that caused an increase in oleate concentration. Pham et al. (2010) identified two plant introductions (PI) that had elevated levels of oleate concentration. They reported that PI 283327 and PI 567189A contained mutant *FAD2-1B* alleles that caused an increase in oleate concentration. They reported that by combining a mutant *FAD2-1A* allele with a mutant *FAD2-1B* allele, oleate concentrations of about 800 g kg⁻¹ could be obtained.

Biotechnology has been used to increase the amount of oleate in the seed oil. Knowlton (1999) developed a transgenic event, designated 260-05, which caused a suppression of the *FAD2-1* gene. This suppression was responsible for increasing the oleate concentration in the seed from 250 g kg⁻¹ to >800 g kg⁻¹. Commercialization of the cultivars with the 260-05 transgene was discontinued due to the presence of the *bla* gene for ampicillin resistance as the selectable marker (Fehr, 2007). This event was replaced with a second transgene developed by DuPont® designated DP-305423-1 (Kinney et al., 2008). DP-30542-1 contains a similar antisense copy of the endogenous *FAD2-1* gene as the previous 260-05

event but is linked to a different selectable marker. Instead of the *bla* gene as the selectable marker, a modified version of the *gm-hra* gene was used. Cultivars with the DP-305423-1 event are being commercialized by DuPont Pioneer. Buhr et al. (2002) developed a high-oleate transgene through the use of ribozyme termination in order to down regulate the endogenous *FAD2-1* gene. By inserting this transgene into soybean, they were able to identify transformed plants that had greater than 750 g kg⁻¹ oleate concentration.

Studies conducted to evaluate the influence of increasing the oleate concentration in the seed oil on agronomic and seed traits have reported differing results. Two studies have indicated that lines with increased oleate yield significantly less than normal-oleate lines from the same segregating population (Scherder and Fehr, 2008; Brace et al., 2011); while others have reported that high-oleate lines have similar yield to that of normal-oleate lines (Kinney and Clemente, 2005; Graef et al., 2009). One objective of my research was to determine if the negative influence of the DP-305423-1 transgene on seed yield reported by Brace et al. (2011) was unique to the populations they evaluated or generally would be expressed in segregating populations with multiple genetic backgrounds. A second objective of my research was to evaluate whether undesirable linkage to the DP-305423-1 transgene may be responsible for reducing the mean seed yield of high-oleate lines compared to normal-oleate lines.

Another important consideration regarding the commercial viability of the high-oleate trait is environmental stability of oleate concentration in lines with the DP-305423-1 transgene. It has been reported that oleate concentration is highly unstable across environments and is significantly affected by the mean daily temperature during the seed-fill period (Oliva et al., 2006; Scherder et al., 2008; Lee et al., 2009; Lee et al., 2012). These

studies, however, evaluated lines developed via traditional breeding that had a mean oleate concentration across environments of up to 799 g kg⁻¹. The third objective of my research was to evaluate the environmental stability of oleate concentration in soybean lines that contain the HO transgene DP-305423-1.

Literature Review

Agronomic and seeds traits of lines with elevated oleate

Brace et al. (2011) evaluated the agronomic and seed traits of soybean lines containing the DP-305423-1 event from DuPont Pioneer. They evaluated F_{3:5} lines from four single-cross populations across five North American environments in 2009. The HO parent for each of the four populations was restricted to SP16410155. SP16410155 was homozygous for the HO transgene as well as the *fan1*(C1640) and *fan3*(RG10) alleles that control reduced linolenate concentration. Four elite parents 92Y80, 93Y02, 93Y11 and 93Y20 were crossed to SP16410155 to develop the segregating populations. The four elite parents were cultivars developed by DuPont Pioneer. F_{3:5} lines from each of the four populations were divided into three genotypes: high oleate, low linolenate (HOLL), high oleate, normal linolenate (HONL), and normal oleate, normal linolenate (NONL). They reported that the oleate concentrations of the HOLL and HONL classes were not significantly different and that both classes had significantly higher oleate concentration than the NONL class in each of the four populations. The mean oleate concentration was 786 g kg⁻¹ for the HOLL class, 784 g kg⁻¹ for the HONL class and 226 g kg⁻¹ for the NONL class. They reported that the NONL class had a significantly higher mean yield than both the HOLL and the HONL classes. The mean yield of the NONL class averaged across the four populations was 4.5% greater than the HOLL class and 3.0 % greater than the HONL class. They

selected the top 10% of the lines in each population for mean yield. Averaged across the four populations, 60% were NONL, 25% were HOLL, and 15% were HONL. These results indicated that it should be possible to develop HO lines that have a yield performance equal to NONL lines; however, more progeny with the DP-305423-1 event would need to be evaluated to identify a superior genotype for seed yield. They found that the HONL lines had a mean protein concentration that was 7 g kg^{-1} greater than the NONL lines and an oil concentration that was 5 g kg^{-1} lower. Their results for the other agronomic and seed traits studied suggested that the development of a HO cultivar with acceptable performance would not be negatively impacted by the presence of the HO transgene. They also suggested that populations derived from multiple HO parents should be evaluated for agronomic performance to determine if the lower mean yield for the HOLL and HONL classes in their study was due to negative pleiotropic effects associated with the HO transgene per se or due to undesirable linkages between the HO transgene and other genes in the genome of the HO donor line SP16410155.

Scherder and Fehr (2008) evaluated 27 mid-oleate, low-linolenate and 27 normal-oleate, low-linolenate lines from three single-cross populations that were segregating for the *ol* allele from M23. Based on the performance of the lines across three Iowa locations in 2007, they reported that the mid-oleate lines had a mean seed yield that was 12% lower than that of the normal-oleate lines. The frequency of high yielding mid-oleate lines was significantly less than that of high yielding normal-oleate lines. Of the top 10 highest yielding lines in each of the three populations, only one was a mid-oleate line. They also reported that the protein concentration of the mid-oleate lines was significantly greater and the oil concentration was significantly less than the normal-oleate lines.

Kinney and Clemente (2005) reported that the insertion of the 260-05 transgene caused a significant increase in oleate concentration and that the yields of the high-oleate lines were not significantly reduced, indicating that it should be possible to develop a soybean cultivar with increased oleate concentration without sacrificing agronomic characteristics. Graef et al. (2009) reported that lines homozygous for the 335-13 event developed by Buhr et al. (2002) did not yield significantly less than the non-transformed parent 'A3237' across eight locations grown in Nebraska during 2004 and 2005.

Environmental stability of elevated oleate concentration

Previous research conducted by Scherder et al. (2008) evaluated the stability of oleate concentration in lines containing the mutant allele *ol* from M23. They evaluated three classes of genotypes that contained different combinations of other altered fatty ester alleles. This included a combination of the *ol* allele for mid-oleate concentration and the *fap1* (Erickson et al., 1988) and *fap3* (Fehr et al., 1991; Schnebly et al., 1994) alleles for low saturated fatty esters concentration (MO/LS). A second class they evaluated contained the *ol* allele for mid-oleate concentration and the *fan1*(A5), *fan2*(A23), and *fan3*(A29) alleles for reduced linolenate concentration (MO/LLN). Their third class was a combination of the mid-oleate, low-saturate, and low-linolenate traits (MO/LS/LLN). This set of lines was grown in five environments during each of two years. One of the environments was a normal planting date at Ames, IA, and a second environment was a second planting date 18 days following the first date at the same location. The other three environments were Kanawha, IA, Lewis, IA, and Portageville, MO. The oleate concentration of each plot was determined by analyzing by gas chromatography two five-seed bulk samples from each of the first five plants in each plot. They reported an inverse relationship between oleate concentration and

the stability of oleate concentration in lines across the 10 environments. However, they concluded that lines with the highest mean oleate concentration would be the most desirable from a commercial standpoint because they had $>500 \text{ g kg}^{-1}$ oleate in more environments than lines with a lower oleate concentration. They found that the earliest planting date had greater mean oleate concentration due to the greater daily temperature during seed-fill. They suggested that it would be most effective to plant the earliest mid-oleate lines that could be grown in a region to increase the oleate concentration.

Oliva et al. (2006) evaluated five mid-oleate lines across five locations with two planting dates at each location. The locations included, Columbia, MO, Portageville, MO, Portageville, MO, Sandhills, NC, and Stoneville, MS. Stability was determined by regressing oleate concentration at each location on mean daily temperature during the final 30 days of seed-fill. They reported that lines with increased oleate concentration were relatively less stable across multiple environments than lines with reduced oleate concentration and suggested that genotypes should be tested in multiple environments to ensure acceptable oleate stability.

Bachlava and Cardinal (2009) evaluated the influence of temperature during the seed-fill period in three populations segregating for oleate genes from two sister lines, N98-4445a and N97-3363-3. They reported that oleate concentration was positively correlated to average daily temperature during seed-fill for one of the populations, but was negatively correlated to average daily temperature in two of the populations. The two populations that showed a negative correlation were early maturing populations; whereas, the one population that showed results consistent with previous studies was late maturing. They also evaluated the influence of day length on oleate concentration and concluded that oleate concentration

was not significantly correlated to day length. They concluded that future research would need to be conducted to understand how temperature and photoperiod influence oleate concentration in lines grown in southern environments.

Primomo et al. (2002) evaluated the influence of locations and years on fatty acid concentration of 14 lines with differing fatty ester profiles. Two lines they evaluate contained elevated oleate concentration, RG9 and AN145-66. RG9 was developed by the treatment of Elgin 87 with EMS and AN145-66 was a selection from a cross between a recurrent selection population for elevated oleate concentration and A5. Their study was evaluated at four locations in southern Ontario, Canada during 1996-1998. The locations included Woodstock, Talbotville, Ridgetown and Tilbury. Three replications were grown at each location during each year. They reported that AN145-66 that had a mean oleate concentration among years of 313 g kg^{-1} was considered the least stable for oleate concentration because it had the largest *b*-value for oleate concentration of all lines evaluated, whereas RG9 that had a mean oleate concentration among years of 340 g kg^{-1} was relatively stable for oleate concentration. Neither elevated oleate line had a *b*-value as low as some of the normal-oleate lines.

Lee et al. (2009) evaluated the stability of oleate concentration in plant introductions (PI) that were identified as having increased oleate concentration. They evaluated 15 PIs with a mean oleate concentration ranging from 300 to 496 g kg^{-1} along with N98-4445A (573 g kg^{-1}) and M23 (512 g kg^{-1}) at five locations with two planting dates at each location. The locations included Columbia, MO, Portageville, MO, Clayton, NC, Stoneville, MS, and Knoxville, TN. The planting dates were about one month apart with the first being in mid May and the second date in mid June. There was a significant genotype x environment

interaction for oleate concentration. Maturity group II and III PIs generally had higher oleate concentration than group V PIs, which can be attributed to temperature during the seed-fill period. They reported a significant positive correlation of 0.59 between mean oleate and the range in oleate across locations, suggesting that the stability of oleate concentration is less for lines with greater oleate. However, they found that M23 was relatively stable across environments with a mean oleate concentration of 512 g kg⁻¹. They concluded that genes for elevated oleate concentration from these PIs could be used in combination with genes from M23 and or N98-4445A to develop commercially acceptable cultivars with elevated oleate.

Lee et al. (2012) studied the environmental stability of oleate concentration in lines with different combinations of mutant *FAD2* alleles. They evaluated 10 genotypes that contained both a mutant *FAD2-1A* allele and a mutant *FAD2-1B* allele. The mutant *FAD2-1A* allele was the *ol* allele from M23, while the mutant *FAD2-1B* alleles were from PI567189A and PI283327 as identified by Pham et al. (2010). They reported that mean oleate concentration increased as the mean daily temperature during the final 30 days of seed-fill increased. They concluded that lines with elevated oleate concentration generally had the greatest range in mean oleate among locations and would be considered less stable for oleate concentration than normal-oleate genotypes.

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CHAPTER 2**AGRONOMIC AND SEED TRAITS OF SOYBEAN LINES CONTAINING THE
HIGH-OLEATE TRANSGENE DP-305423-1**

Modified from a paper to be published in Crop Science

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Abstract

Soybean [*Glycine max* (L.) Merr.] lines homozygous for the transgene DP-305423-1 have elevated oleate concentrations. It has been reported that the mean seed yield of lines with the transgene was significantly less than that of lines without the transgene from the same populations. The objective of my study was to evaluate the DP-305423-1 transgene in multiple genetic backgrounds to determine if the yield reduction was unique to those populations previously studied. There were 27 high-oleate, normal-linolenate (HONL) and 27 normal-oleate, normal-linolenate (NONL) F_{3:5} lines from each of five single-cross populations evaluated in replicated trials in Iowa, Illinois, and Ohio in 2011. On average, the HONL lines had a mean oleate concentration of 821 g kg⁻¹ compared with 255 g kg⁻¹ for the NONL lines. The mean yield of the HONL lines was significantly less than the NONL lines in all of the populations by an average of 4.6%. Of the top 10 highest yielding lines in each of the populations, an average of 12% were HONL lines and 88% were NONL lines. The HONL lines also had significantly lower seed weight, higher protein, and lower oil, palmitate, stearate, linoleate, and linolenate concentrations than the NONL lines in all of the populations. The results indicated that the negative impact of the transgene on seed yield was consistent across multiple genetic backgrounds, which will have an influence on the development of HONL cultivars that yield as well as NONL cultivars.

Introduction

The relatively low oxidative stability of conventional soybean oil has been attributed to the multiple double bonds of two polyunsaturated fatty esters, linoleate (18:2) and linolenate (18:3) that are highly susceptible to autoxidation (Cosgrove et al., 1987). To improve oxidative stability, conventional soybean oil must be chemically hydrogenated (Dutton, 1963) or the soybean plant must be genetically altered to produce oil that has reduced concentrations of linoleate and linolenate (Fehr, 2007). The disadvantage of partial hydrogenation is that the *trans*-fatty esters produced by the process are considered undesirable for coronary health (Hu et al., 1999).

Genetic modifications have been made in soybean to reduce the amount of polyunsaturated fatty esters in the oil (Fehr, 2007). Multiple mutant alleles have been identified and characterized for reduced linolenate concentration in the seed oil. By reducing the amount of linolenate, the need for chemical hydrogenation was reduced or eliminated for preparation of food products.

A second genetic modification has been to increase the monounsaturated fatty ester oleate (18:1) and reduce the linoleate concentrations (Fehr, 2007). There are at least five members of the *Gm-FAD2* gene family in soybean that are responsible for the desaturation of oleate to linoleate (Schlueter et al., 2007). Pham et al. (2010) reported that by combining a mutant *FAD2-1A* allele with a mutant *FAD2-1B* allele, soybean lines with greater than 800 g kg⁻¹ oleate concentration could be obtained. The two mutant *FAD2-1A* alleles evaluated in their study were from the lines M23 and 17D. The oleate concentration of about 500 g kg⁻¹ in M23 is the result of a deletion of the *FAD2-1A* gene by X-ray radiation (Rahman et al., 1994, Devinder et al., 2007). Dierking and Bilyeu (2009) utilized reverse genetics to identify

the mutant *FAD2-IA* allele in 17D. Pham et al. (2010) identified two mutant *FAD2-IB* alleles in the soybean lines PI 283327 and PI 567189A. They found that by combining the mutant *FAD2-IB* allele from either PI 283327 or PI 567189A with either of the *FAD2-IA* alleles from M23 or 17D, it was possible to obtain an oleate concentration of about 800 g kg⁻¹.

Genetic engineering also has been used to increase the amount of oleate in the seed oil. Knowlton (1999) developed a transgene, designated 260-05, which caused a suppression of the endogenous *FAD2-1* gene. This suppression was responsible for increasing the oleate concentration in the seed oil to greater than 800 g kg⁻¹. Commercialization of cultivars with the 260-05 transgene was discontinued due to the presence of the *bla* gene for ampicillin resistance that was used as the selectable marker for transformation (Fehr, 2007). This transgene was replaced with a second one developed by DuPont® designated DP-305423-1 (Kinney et al., 2008). DP-305423-1 contains a similar antisense copy of the endogenous *FAD2-1* gene as the previous 260-05 transgene; however, it is coupled with a modified version of the *gm-hra* gene as the selectable marker for transformation. The *gm-hra* gene is responsible for the synthesis of the acetolactate synthase (ALS) enzyme. The insertion of the *gm-hra* polynucleotide confers tolerance to commercially available ALS-inhibiting herbicides. Cultivars with the DP-305423-1 transgene currently are being commercialized by DuPont Pioneer.

Additional transgenes have been used to elevated oleate and reduce linoleate in soybean. Buhr et al. (2002) used ribozyme termination to down regulate the endogenous *FAD2-1* gene to elevate oleate concentration and the *FatB* gene to reduce the concentration of saturated fatty esters. They identified transformed plants that had greater than 75% oleate

and less than 6% total saturated fatty ester concentrations. The Monsanto Co. utilized an RNA-based suppression technique to develop the transgene MON 87705 (United States Food and Drug Administration, 2011). This transgene caused a suppression of both the endogenous *FAD2-1* gene and the *FatB* gene. Transformed plants have elevated levels of oleate and reduced levels of saturated fatty esters (United States Food and Drug Administration, 2011).

Previous studies that evaluated the impacted of transgenes for elevated oleate on agronomic and seed traits have reported differing results. Kinney and Clemente (2005) reported that the 260-05 transgene had no negative effects on the seed yield of soybean lines. Graef et al. (2009) reported that lines containing the transgene for elevated oleate and reduced saturate concentrations developed by Buhr et al. (2002) had a mean yield that was not significantly different than the transformed cultivar A3237. Brace et al. (2011) evaluated the agronomic and seed traits of soybean lines with and without the transgene DP-305423-1 that were derived from four single-cross populations. The parent with the transgene for each of their four populations was SP16410155. SP16410155 was homozygous for the transgene, as well as the *fan1*(C1640) (Wilcox et al., 1984) and *fan3*(RG10) (Reinprecht et al., 2009) alleles that reduce linolenate concentration. Their F_{3:5} lines were divided into three genotypes: high oleate and low linolenate (HOLL), high oleate and normal linolenate (HONL), and normal oleate and normal linolenate (NONL). They reported that averaged across the four populations, the mean yield of the NONL lines was greater by 4.5% compared with the HOLL lines and 3.0% greater than the HONL lines. They found that of the top 10% of lines for seed yield in each population, an average of 60% of them were NONL, 25% were HOLL, and 15% were HONL. Their results indicated that it should be

possible to develop HONL lines that have a yield performance equal to NONL lines; however, more progeny with the DP-305423-1 transgene would need to be evaluated to identify HONL lines with seed yield comparable to NONL lines. The objective of my study was to determine if the negative influence of the DP-305423-1 transgene on seed yield reported by Brace et al. (2011) was unique to the populations they evaluated or generally would be expressed in segregating populations with multiple genetic backgrounds.

Materials and Methods

The soybean lines evaluated in my study were derived from five single-cross populations. Each population was developed by crossing one of two experimental lines that were homozygous for the high-oleate (HO) transgene DP-305423-1 (Kinney et al., 2008) to a DuPont Pioneer elite line without the transgene. The HO parents YR25C09 of maturity group 2 and YR37Y09 of maturity group 3 were homozygous for the transgene DP-305423-1 (Kinney et al., 2008); as well as the Roundup Ready® transgene (*Gly*^R) (Shah et al., 1993). YR25C09 was an F₃-derived line from the cross of XB21R05 x SP11520464 and YR37Y09 was an F₃-derived line from the cross of 93M11 x SP11520463. Both XB21R05 and 93M11 lack the HO transgene, whereas SP11520463 and SP11520464 are experimental lines that contained the transgene. The HO parents used in my study differed from the HO parent SP16410155 used by Brace et al. (2011) in three important aspects. First, neither of the HO parents in my study had major genes for reduced linolenate; whereas, SP16410155 had the *fan1*(C1640) and *fan3*(RG10) alleles. As a result, the five populations used in my study were not segregating for any major genes controlling linolenate concentration. Second, YR25C09 and YR37Y09 have smaller linkage blocks than SP16410155 around the transgene that were identical to that of the cultivar Jack that was used for transformation. YR25C09 has a region

on chromosome 16 whose DNA sequence is in common with that of Jack spanning from near Sat_350 (60.7 cM) to ss107913886 (76.2 cM) and YR37Y09 has a region spanning from Satt215 (47.4 cM) to ss107913886 (76.2 cM) (Hyten et al., 2010). SP16410155 has a larger region around the transgene from near Satt693 (38.0 cM) to ss107913886 (76.2 cM) (Hyten et al., 2010). Based on these map distances, SP16410155 has about 38.2 cM in common with Jack, YR37Y09 has 28.8 cM, and YR25C09 has 15.5 cM. Third, the seed yield of the two HO parents used in my study was greater than SP16410155. YR25C09 had a mean yield of 3945 kg ha⁻¹ compared with 3504 kg ha⁻¹ for SP16410155 averaged across three of my experiments grown in 2011. YR37Y09 had a mean yield of 3682 kg ha⁻¹ compared with 3564 kg ha⁻¹ for SP16410155 averaged across two of my experiments grown in 2011.

The five conventional parents used to develop the single-cross populations were 92Y30, 93Y20, YB26P09, RJS30006, and XB30C10. All of these parents developed by DuPont Pioneer lack the transgene DP-305423-1 and have normal concentrations of oleate and linolenate. They all are homozygous for the Roundup Ready® transgene (*Gly*^R) (Shah et al., 1993). 92Y30 and YB26P09 are of maturity group 2 and 93Y20, RJS30006, and XB30C10 are of maturity group 3. The yield of the conventional parent was greater than that of the HO parent with which it was mated to form a single cross population based on my experiments grown in 2011 (data not shown).

The five single-cross populations were formed at the DuPont Pioneer Research Station near Salinas, PR, during January 2009. The cross of 92Y30 x YR25C09 will be designated hereinafter as Pop1, YB26P09 x YR25C09 as Pop2, RJS30006 x YR25C09 as Pop3, 93Y20 x YR37Y09 as Pop4, and XB30C10 x YR37Y09 as Pop5. The F₁ seed of each population was harvested in bulk.

The F₁ seed was planted at the DuPont Pioneer Research Station near Salinas during March 2009. The F₁ plants of Pop1, Pop2, and Pop4 were confirmed as hybrids using a proprietary molecular marker of DuPont Pioneer associated with the HO transgene. Flower color was used to confirm F₁ plants from Pop3 and Pop5. F₁ plants from each population were harvested in bulk.

A random sample of 800 F₂ seeds from each population was planted in a two-row plot 11.28 m long at the DuPont Pioneer Research Station near Salinas during June 2009. The F₂ plants were sprayed with 0.035 kg a.e. ha⁻¹ of thifensulfuron-methyl (DuPont® Harmony GT™). This removed the F₂ plants that did not carry the HO transgene due to their lack of the *gm-hra* gene that was used as the selectable marker for transformation. Plants homozygous and heterozygous for the HO transgene were harvested in bulk.

A random sample of 1,400 F₃ seeds of each population was planted at the DuPont Pioneer Research Station near Johnston, IA, on 22 June 2010. The seeds of each population were planted in 16-row plots 5.33 m long with a row spacing of 0.76 m at a rate of 19 seeds m⁻¹. Leaf tissue from 252 F₃ plants of each population was collected and analyzed with a proprietary molecular marker of DuPont Pioneer associated with the HO transgene. A total of 398 F₃ plants homozygous for the transgene and 239 plants without the transgene were selected and harvested from the five populations. Homozygosity of the HO transgene was confirmed by the fatty ester concentrations of three five -seed bulks from each of the selected plants. The gas chromatography analysis was conducted with a Hewlett-Packard gas chromatograph (Hewlett-Packard Company) equipped with a ZB-wax column (Phenomenex) according to the methodology described by Butte et al. (1982) and Dolde et al. (1999). To be sure one normal seed could be identified in a five-seed bulk, check samples consisting of

different ratios of HONL to NONL seeds (0:5, 1:4, 2:3, 3:2, 4:1, 5:0) were randomly included in the analysis. The mean oleate concentration of the samples containing one NONL seed and 4 HONL seeds was 684 g kg^{-1} . The mean oleate concentration of the three five-seed bulk samples from the HONL plants considered homozygous for the transgene ranged from 779 g kg^{-1} to 839 g kg^{-1} in Pop1, 774 g kg^{-1} to 826 g kg^{-1} in Pop2, 780 g kg^{-1} to 832 g kg^{-1} in Pop3, 762 g kg^{-1} to 825 g kg^{-1} in Pop4, and 746 g kg^{-1} to 811 g kg^{-1} in Pop5. The oleate concentration of the NONL plants without the transgene ranged from 191 g kg^{-1} to 280 g kg^{-1} across the five populations with a mean of 234 g kg^{-1} .

The F_4 progeny of the F_3 plants confirmed to be HONL or NONL, the five parents of the populations, and SP16410155 were planted at the DuPont Pioneer Research Station in Viluco, Chile, during November 2010. There were 74 HONL and 36 NONL $F_{3,4}$ lines of Pop1; 79 HONL and 38 NONL lines of Pop2; 89 HONL and 51 NONL lines of Pop3; 52 HONL and 46 NONL lines of Pop4; and 79 HONL and 48 NONL lines of Pop5. Twenty-two F_4 seeds of each line, the parents, and SP16410155 were planted in one-row plots 0.91 m long with a 0.76 m spacing between rows. Maturity notes were taken on all plots and 27 HONL and 27 NONL lines of similar maturity in each population were selected. The selected lines, the parents and SP16410155 were harvested in bulk using a self-propelled plot combine (ALMACO).

Each of the five populations was a separate experiment for the replicated trials in 2011. Each experiment consisted of 27 HONL lines, 27 NONL lines, the two parents, and SP16410155. The experiments were grown as a randomized complete block design with two replications at each location. The plots were two-rows 4.57 m long with a row spacing of 0.76 m between rows and a seeding rate of 26 seeds m^{-1} . The locations for Pop1 and Pop2

were Conrad, Royal, and Pocahontas, IA, and Princeton, IL; for Pop3 were Cedar Falls and Conrad, IA, Princeton, IL, and Delphos, OH; for Pop4 were Hedrick, Atlantic, and Mount Pleasant, IA, and Delphos, OH; and for Pop5 were Hedrick, Atlantic, and Mount Pleasant, IA, Wyoming, IL, and Delphos, OH . The planting dates were 4 May at Conrad, 10 May at Pocahontas, 19 May at Royal, 10 May at Atlantic, 12 May at Hedrick, 16 May at Cedar Falls, 6 May at Princeton, 6 May at Wyoming, 19 May at Mount Pleasant and 6 June at Delphos. The soil type at Conrad is a Garwin silty clay loam (fine-silty, mixed, superactive, mesic Typic Endoaquolls); at Royal is a McCreath silty clay loam (fine-silty, mixed, superactive, mesic Aquic Hapludolls); at Pocahontas is a Webster clay loam (fine-loamy, mixed, superactive, mesic Typic Endoaquolls); at Cedar Falls is a Klinger silty clay loam (fine-silty, mixed, superactive, mesic Aquic Hapludolls); at Princeton is a Muscatune-Buckhart silt loam (fine-silty, mixed, superactive, mesic Aquic Argiudolls); at Hedrick and Mount Pleasant is a Taintor silty clay loam (fine, smectitic, mesic Vertic Argiaquolls); at Atlantic is a Melia silty clay loam (fine-silty, mixed, superactive, mesic Pachic Hapludolls); at Wyoming is a Tama silt loam (fine-silty, mixed, superactive, mesic Typic Argiudolls); and at Delphos is a Pewamo silty clay loam (fine, mixed, active, mesic Typic Argiaquolls). Seed yield was measured on all plots at all the locations. Maturity, plant height, lodging, seed size, and protein, oil, and fatty ester concentrations were measured on all plots at the three Iowa locations for Pop1, Pop2, Pop4, and Pop5. For Pop3, these data were obtained at the two Iowa locations and at Princeton, IL. Maturity was recorded as days after 31 August when 95% of the pods in a plot reached their mature color. Plant height was measured as the distance from the soil surface to the terminal node. Lodging was determined at maturity on a scale of 1 (all plants erect) to 5 (all plants prostrate). The plots were harvested with a self-

propelled plot combine (ALMACO) at all of the locations. The weight and moisture content of the seed were determined, and yield was expressed on a moisture basis of 130 g kg⁻¹. Seed size was obtained by weighing 400 random whole seeds from each plot and dividing by 400. Protein and oil were measured on a 454 g- sample using an Infratec™ 1241 grain analyzer (FOSS) and expressed on a moisture basis of 130 g kg⁻¹. Fatty ester concentration was measured on two five-seed bulk samples by gas chromatography (Butte et al., 1982 and Dolde et al., 1999). The mean of the two samples was used for data analysis.

All data were analyzed using the general linear model (GLM) procedure of SAS Enterprise Guide V4.3 (SAS institute Inc). Environments and replications within environments were considered random effects and genotypes were considered fixed effects. The sums of squares for genotypes were partitioned into variation among HONL lines, variation among NONL lines, and the orthogonal contrast between the two genotypic classes. The mean squares for the main effect x environment interaction were used to test the main effects and orthogonal contrast across environments by an F-test. The CORR procedure of SAS Enterprise Guide V4.3 (SAS institute Inc.) was used to calculate Pearson correlation coefficients among traits based on the entry means of the 27 HONL lines and 27 NONL lines across locations.

Results

The mean oleate concentration of the HONL lines was significantly greater than that of the NONL lines in all of populations (Table 1). Averaged across populations, the HONL lines had a mean oleate concentration of 821 g kg⁻¹ compared with 255 g kg⁻¹ for the NONL lines. There was significant variation for oleate concentration among the HONL lines in each of the populations, which was in agreement with the results of Brace et al. (2011). They

indicated that the variation among the HONL lines may be due to the segregation of modifying genes or other *FAD2* homologues that are not suppressed by the DP-305423-1 transgene. Due to the *FAD2-1* specificity of DP-305423-1, the *FAD2-2* family of genes could play a role in determining the oleate concentration of HONL lines (Heppard et al., 1996).

The mean yield of the HONL lines was significantly less than the NONL lines by 2.1% in Pop1, 6.0% in Pop2, 6.5% in Pop3, 2.5% in Pop4, and 5.3% in Pop5 (Table 1). Averaged across the populations, the difference in yield between the two classes was 4.6%. The majority of the 10 highest yielding lines in each population were from the NONL class (Table 2). There were two HONL lines in the top 10 for Pop1 and Pop4, one for Pop3 and Pop5, and none for Pop2. On the average, there were 88% NONL lines and 12% HONL lines in the top 10.

There were some significant differences between the means of the HONL and NONL lines for maturity, lodging score, and plant height; however, the differences were not consistent among the populations and there was considerable overlap in the distributions among lines of the two classes (Table 1). The results indicated that it should be possible to select HONL lines from a segregating population that are similar for these three agronomic traits to NONL lines. The mean seed weight of the HONL lines was significantly less than the NONL lines in all of the populations (Table 1). However, this should not prevent the selection of HONL lines that are similar to NONL lines in a breeding program because the largest difference between the mean of the two classes was only 4 mg sd⁻¹ and there was considerable overlap in the distributions among lines of the two classes.

The mean protein concentrations of the HONL lines were significantly greater and the mean oil concentrations were significantly less than the NONL lines in all of the populations (Table 1). Averaged across the populations, the mean protein concentration of the HONL lines was 25 g kg^{-1} greater than the NONL lines and all of the HONL lines had greater protein than any of the NONL lines in each of the populations. The HONL lines had an average oil concentration across populations that was 13 g kg^{-1} less than the NONL lines, and there was only a small overlap in the distribution among lines of the two classes. These results indicated that it may be difficult to select HONL lines from a segregating population that have protein and oil concentrations comparable to those of NONL lines.

The means of the HONL lines were significantly less than the NONL lines for palmitate, stearate, linoleate, and linolenate in all of the populations (Table 1). Averaged across the populations, the mean of the HONL lines was less by 36 g kg^{-1} for palmitate, 4 g kg^{-1} for stearate, 496 g kg^{-1} for linoleate, and 30 g kg^{-1} for linolenate than the NONL lines. There was overlap in the distributions among lines of the two classes for stearate but not for the other three fatty esters. The negative correlations between oleate concentration and the other fatty esters (data not shown) were in agreement with the results of Brace et al. (2011).

Discussion

The negative influence of the DP-305423-1 transgene on seed yield in my study agreed with the results reported by Brace et al. (2011) who evaluated HOLL, HONL, and NONL lines from four populations segregating for the transgene and for two major genes for reduced linolenate concentration. Of particular concern in both studies was the low frequency of HONL lines that were comparable in yield to the highest yielding NONL lines in the populations. In my study, only 12% of the 10 highest yielding lines averaged across

the five populations were HONL, and one population had no HONL lines in the top 10. Brace et al. (2011) found that of the 10 highest yielding lines in their four populations, 15% were HONL, 25% HOLL, and 60% NONL. The results of the two studies with the DP-305423-1 transgene indicated that for development of HO cultivars, a breeding program should use multiple HO and high-yielding conventional parents for developing segregating populations and that as many HONL lines should be evaluated from each population as possible.

The greater protein concentration of the HONL lines in my study was consistent with the increased protein of lines with elevated oleate in other studies. Scherder and Fehr (2008) reported that mid-oleate, low-linolenate (MOLL) lines homozygous for the *ol* allele from M23 had an average oleate concentration of 514 g kg⁻¹ compared with 273 g kg⁻¹ for NONL lines that were derived from the same three segregating populations. Averaged across the three populations, the MOLL lines yielded 12% less, had 1.4 percentage units greater protein, and 0.7 percentage units lower oil than the NONL lines. Lee et al. (2012) evaluated lines containing different combinations of mutant *Fad2* alleles for elevated oleate. They reported that the lines with elevated oleate concentration had greater mean protein concentrations than the conventional checks in the same experiment. They found that of the elevated oleate lines evaluated, the lines with the highest oleate concentration consistently had the highest protein concentration. Graef et al. (2009) reported that lines homozygous for the HO transgene developed by Buhr et al. (2002) had significantly greater protein concentrations than the transformed cultivar A3237.

The lower yield of the HONL lines may be associated with the lower oil and increased protein concentrations compared with the NONL lines. The negative correlation

between seed yield and protein concentration has been well documented in soybean. Simpson and Wilcox (1983) reported that three of the four single-cross populations they evaluated had a significant negative correlation between seed yield and protein concentration that ranged from -0.20 to -0.74. Wehermann et al. (1987) reported a range of correlation coefficients between seed yield and protein concentration of -0.54 to -0.86 across three BC₂F₂ populations. Wilcox and Shibles (2001) reported a correlation coefficient between seed yield and protein concentration of -0.45 among 43 breeding lines they evaluated. Chung et al. (2003) evaluated 76 F₅-derived lines from the cross PI 437088A x 'A3733' and reported a correlation between seed yield and protein concentration of -0.695. In my study, the Pearson correlation coefficients between seed yield and protein concentrations of -0.31 for Pop1, -0.65 for Pop2, -0.66 for Pop3, -0.42 for Pop4, and -0.62 for Pop5 were all significant (P<0.05). The correlation coefficients between seed yield and oil concentrations of 0.40 for Pop1, 0.70 for Pop2, 0.54 for Pop3, 0.40 for Pop4, and 0.45 for Pop5 also were all significant. Future research will be needed to determine the biochemical basis of the decrease in oil concentration of lines with elevated oleate that was observed in my study and that of Brace et al. (2011). It is possible that by suppression of the endogenous *FAD2-1* gene to increase the oleate concentration, other components of the oil synthesis pathway may be affected in a manner that reduces the total oil concentration in the seed.

The lower oil concentration of HO cultivars would have implications for their commercial production. If soybean growers are paid a premium to separate their production of HO cultivars from that of conventional cultivars during planting, harvest, transportation, and storage, that cost will increase the price of the HO oil compared with oil of conventional cultivars. The amount of the price increase will depend on the oil concentration in the HO

grain. As the number of units of oil obtained from a unit of grain decreases, the cost of each unit of oil associated with the grower premium will increase. Although it is expected that the protein concentration in the soybean meal will increase as the oil concentration decreases, this will only be an advantage if the grower is paid a premium for it.

In summary, my results and those of Brace et al. (2011) indicate that HONL lines with the DP-305423-1 transgene yield significantly less on the average than NONL lines across multiple populations formed with different parents. High yielding HONL lines were identified; however, their frequency was lower than that of high yielding NONL lines. The lower oil concentration and greater protein concentration of HONL lines may play a role in their lower yield. For development of HO cultivars with the DP-305423-1 transgene, it will be important to evaluate as many different populations and HO lines as possible.

Acknowledgements

The authors thank the staff at the DuPont Pioneer Dallas Center soybean research facility for assistance with field data collection; David Dolde and Karen Kratky at the DuPont Pioneer gas chromatography lab; Linda Byrum for her assistance with protein and oil analyses; and Ryan Brace for assistance with statistical analyses.

Table 1. Mean and range for agronomic and seed traits of high-oleate and normal-oleate lines from populations grown in 2011.

Trait	Class†	Population 1		Population 2		Population 3		Population 4		Population 5		
		Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	
Yield	HONL	3837	** 3507-4078	** 3815	** 3403-4048	** 4230	** 3919-4609	** 3789	** 3235-4019	** 3771	** 3455-4065	*
kg ha ⁻¹	NONL	3918	* 3586-4106	* 4058	* 3742-4323	* 4524	ns 4236-4955	ns 3887	** 3630-4086	** 3984	** 3574-4265	**
Maturity	HONL	26	ns 24-30	** 29	** 24-33	ns 27	** 21-33	** 30	** 19-32	** 26	** 20-31	**
d‡	NONL	26	** 22-31	** 28	** 23-31	** 27	** 20-33	** 29	** 26-32	** 29	** 20-34	**
Lodging	HONL	2.3	** 1.8-2.7	ns 2.2	ns 1.7-3.3	* 2.3	ns 2.0-2.75	* 1.9	* 1.3-2.5	* 1.5	ns 1.0-2.0	*
score§	NONL	2.1	* 1.8-2.8	* 2.2	* 1.8-3.0	* 2.1	ns 1.75-3.0	ns 1.8	* 1.3-2.3	* 1.5	1.0-1.8	ns
Height	HONL	114	ns 104-122	** 112	ns 104-126	** 115	ns 101-128	** 104	** 92-111	** 99	** 88-108	**
cm	NONL	113	** 105-122	** 113	* 104-118	** 115	** 102-132	** 102	** 97-111	** 101	** 89-109	**
Seed wt.	HONL	140	** 126-156	** 147	** 136-162	** 166	** 157-180	** 150	** 137-163	** 152	** 135-173	**
mg sd ⁻¹	NONL	144	** 123-171	** 148	** 139-162	** 170	** 159-184	** 151	** 135-166	** 155	** 133-178	**
Protein	HONL	362	** 353-370	** 372	** 363-381	** 368	* 363-373	** 352	** 346-362	** 356	** 339-369	**
g kg ⁻¹ ¶	NONL	338	** 327-349	** 346	** 333-356	** 344	** 331-362	** 327	** 318-342	** 327	** 310-337	**
Oil	HONL	171	** 163-177	** 166	** 155-175	** 174	** 166-181	** 182	** 176-190	** 181	** 171-190	**
g kg ⁻¹ ¶	NONL	183	** 177-191	** 178	** 170-188	** 184	** 173-192	** 197	** 192-201	** 196	** 184-206	**
Palmitate	HONL	64	** 60-67	** 64	** 58-71	** 68	** 61-76	** 60	** 57-66	** 62	** 59-68	**
g kg ⁻¹	NONL	97	** 91-104	** 100	** 93-106	** 104	** 94-111	** 96	** 91-100	** 103	** 97-107	**
Stearate	HONL	39	** 37-41	** 45	** 41-49	** 37	** 34-40	** 40	** 36-46	** 42	** 37-47	**
g kg ⁻¹	NONL	42	** 39-44	** 46	** 41-52	** 40	** 37-43	** 46	** 43-52	** 48	** 43-55	**
Oleate	HONL	814	** 794-830	** 804	** 788-822	** 823	** 805-844	** 828	** 801-841	** 834	** 793-856	**
g kg ⁻¹	NONL	258	* 231-287	* 242	** 223-270	* 260	* 231-290	* 259	ns 233-300	ns 257	** 230-325	**
Linoleate	HONL	33	** 23-44	* 35	** 30-47	** 28	** 19-47	ns 31	** 21-56	* 24	** 14-52	**
g kg ⁻¹	NONL	523	* 501-547	* 531	** 501-553	** 518	* 486-540	* 533	* 493-551	* 524	** 469-549	**
Linolenate	HONL	49	** 44-59	** 51	** 44-57	** 43	** 37-50	** 40	** 25-48	** 37	** 31-44	**
g kg ⁻¹	NONL	79	** 73-85	** 80	** 74-86	** 76	** 69-84	** 66	** 62-71	** 68	** 58-74	**

† = HONL = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

Table 2. Means and ranks of the top 10 yielding lines in each of five populations grown in 2011.

Population 1			Population 2			Population 3			Population 4			Population 5		
Rank	Class [†]	Yield kg ha ⁻¹	Rank	Class	Yield kg ha ⁻¹	Rank	Class	Yield kg ha ⁻¹	Rank	Class	Yield kg ha ⁻¹	Rank	Class	Yield kg ha ⁻¹
1	NONL	4106	1	NONL	4323	1	NONL	4955	1	NONL	4086	1	NONL	4265
2	NONL	4104	2	NONL	4223	2	NONL	4752	2	NONL	4036	2	NONL	4201
3	NONL	4098	3	NONL	4216	3	NONL	4743	3	HONL	4019	3	NONL	4175
4	NONL	4086	4	NONL	4208	4	NONL	4718	4	NONL	3996	4	NONL	4112
5	HONL	4078	5	NONL	4190	5	NONL	4699	5	NONL	3980	5	NONL	4112
6	NONL	4077	6	NONL	4177	6	NONL	4639	6	NONL	3978	6	NONL	4112
7	HONL	4040	7	NONL	4160	7	NONL	4616	7	NONL	3975	7	NONL	4081
8	NONL	4038	8	NONL	4153	8	HONL	4609	8	NONL	3957	8	NONL	4074
9	NONL	4033	9	NONL	4140	9	NONL	4576	9	HONL	3945	9	NONL	4071
10	NONL	4029	10	NONL	4139	10	NONL	4572	10	NONL	3939	10	HONL	4065
LSD [‡]		374			359			439			335			392

[†] = HONL = High oleate, normal linolenate lines, NONL = Normal oleate, normal linolenate lines.

[‡] = Least significant difference at the 0.01 probability level.

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CHAPTER 3

Molecular Characterization of the Genomic Region Flanking the High-Oleate

Transgene DP-305423-1

Abstract

Soybean [*Glycine max* (L.) Merr.] lines with the transgene DP-305423-1 have been reported to yield significantly less than lines that do not contain the transgene from the same population. One hypothesis is that the reduction in seed yield is a result of undesirable linkage drag from DNA flanking the transgene. The objective of my study was to evaluate the genomic region around the high-oleate (HO) transgene of the high-oleate, normal-linolenate (HONL) and normal-oleate, normal-linolenate (NONL) lines from the five single-cross populations described in chapter 2. DNA was bulked from eight random seedlings from each line as well as the parents. A panel of single nucleotide polymorphism (SNP) DNA markers genetically linked to the HO transgene were analyzed on each DNA sample. Of the six HONL lines that had a mean yield not significantly different than the highest yielding NONL line, only one of them had a genetic recombination near the HO transgene. There were other HONL lines that had a recombination in the genomic region evaluated; however, their mean yield was significantly less than the highest yielding NONL line. These data suggest that undesirable linkage drag is not the cause of the reduction in yield reported for lines that are homozygous for the DP-305423-1 transgene.

Introduction

Brace et al. (2011) reported that soybean lines containing the HO transgene DP-305423-1 yielded on average 3.0% less than NONL lines. They found that of the 10 highest yielding lines in their four populations, only 15% were HONL. In my study reported in chapter 2, the HONL lines yielded on average 4.6% less than NONL lines across five populations and of the top 10 highest yielding lines across five populations only 12% were HONL. Both studies suggested that HO lines with yield equivalent to NO lines could be identified; however, the frequency was lower than expected.

The HO transgene DP-305423-1 developed by Kinney et al. (2008) was inserted into the cultivar Jack. One hypothesis to explain the reduction in seed yield associated with the HO transgene is that there is undesirable linkage drag present around the transgene. It could be that Jack contained DNA near the insertion site that was deleterious to seed yield. This linked DNA would be inherited with the HO transgene when selecting for high-oleate concentration.

The two high-oleate donor parents used in my study differ in the length of the DNA sequence near the HO transgene that is in common with Jack. YR25C09 had a region of about 15.5 cM and YR37Y09 had about a 28.8 cM region in common with Jack around the HO transgene. Both of these parents have smaller regions in common with Jack than the HO donor parent SP16410155 used by Brace et al. (2011) that had about a 38.2 cM region. The objective of my study was to evaluate the genomic region around the HO transgene in all lines evaluated from the five single-cross populations reported on in Chapter 2. I hypothesized that the highest yielding HONL lines within each population would contain a recombination near the HO transgene that reduced the length of the DNA sequence in

common with Jack, which reduced or eliminated the influence of undesirable linkage drag on seed yield.

Materials and Methods

Twelve random F₅ seeds from each F₃-derived line and the parents evaluated during 2011 were rolled in ragdolls. The ragdolls were placed in a growth chamber at a 16-hour photoperiod for 14 days. Once plants reached the V1 stage of development (Fehr and Caviness, 1977), one unifoliate from eight random plants of each line were sampled in bulk to constitute the DNA sample for analysis. Leaf samples were freeze dried using a 24DX48 (VirTis SP Scientific) lyophilizer.

The single nucleotide polymorphism (SNP) genetic markers were selected based on their polymorphism between the parents as well as their genetic location relative to the HO transgene based on DuPont Pioneer's proprietary soybean genetic map. DNA from each sample was extracted using 315 mL of extraction buffer. Eleven mL of supernatant was transferred into a storage plate that contained 354 mL of a neutralization buffer. To generate the TaqMan (Applied Biosystems, ABI) PCR assay plates, 0.8 mL of neutralized DNA was placed into a plate containing 0.8 mL of the PCR assay mix. The PCR assay mix consisted of the forward and reverse primers, the allele 1 and allele 2 probes, along with the PCR mastermix that contained the buffer, ROX-internal control, dNTPs, 2x Klear kall (KBioscience LTD), and DNA polymerase. The PCR cycle was conducted as follows: 95° for 10 min, followed by 40 cycles of 95° for 30 sec, 60° for 60 sec, and 70° for 1 sec. The results were analyzed using a proprietary fluorescence reader.

Results

There were 23 SNPs evaluated on the lines from population 1 that ranged from about 12 cM left of the HO transgene to about 12 cM right of the transgene (Table 1). None of the top three highest yield NONL lines had a recombination in the 24 cM region because they had all SNPs in common with the NONL parent 92Y30. The three highest yielding HONL lines also did not have a recombination within this region because all of their SNPs were in common with the HONL parent YR25C09. There was only one HONL line, entry 12 that had SNPs from the NONL parent in the 24 cM region evaluated. This line had a mean yield that ranked 50th in population 1 and contained about 7.4 cM of DNA in common with the NONL parent 92Y30.

A total of 13 SNPs were evaluated for the lines and parents from population 2 that spanned about 51 cM around the HO transgene (Table 2). The three highest yielding NONL lines had DNA sequence in common with the HONL parent YR25C09 on the left side of the HO transgene. The nearest polymorphic SNP to the HO transgene was about 10.6 cM on the left side indicating that these lines must have had a recombination within 10.6 cM of the transgene. The top two ranked HONL lines did not contain any SNPs from the NONL parent YB26P09 within the genomic region evaluated; however, there were HONL lines that did have a recombination near the HO transgene. Entry 19, which had a mean yield that ranked 19th, contained SNPs from the NONL parent YB26P09 on the left side of the HO transgene indicating that this line had a recombination within 10.6 cM of the transgene. Entry 14 had a double recombination because it contained SNPs from YB26P09 on both sides of the HO transgene. This line had a mean yield that ranked 25th.

There were 23 SNPs spanning a 37 cM region around the HO transgene for the lines and parents of population 3 (Table 3). The top three highest yielding lines were NONL and two of them had DNA sequence in this region that was common to the HONL parent YR25C09. Entry 51, a NONL line which had a mean yield that ranked 2nd, contained about 13.8 cM of DNA sequence in common with the HONL parent YR25C09 on the left side of the transgene. Of the three highest yielding HONL lines, two of them contained SNPs from the NONL parent RJS30006. Entry 25 that had a mean yield rank of 8th and Entry 15 that had a mean yield rank of 22nd both contained about 14 cM of DNA in common with the NONL parent RJS30006 on the left side of the transgene. These data indicate that removing linkage drag around the transgene in HONL lines did not always result in a mean yield that was not significantly different than the highest yielding NONL line.

A region spanning about 20 cM around the HO transgene was evaluated utilizing 14 polymorphic SNPs on the lines and parents of population 4 (Table 4). Of the top 10 highest yielding lines in the population, two were HONL. Both of these HONL lines did not have a recombination in the region evaluated because all of their SNPs were from the HONL parent 93Y20. All of the eight highest yielding NONL lines had all of their SNPs in this region in common with 93Y20.

There were two HONL lines that ranked in the top 12 for mean seed yield in population 5 (Table 5). Neither of these lines were homozygous for any SNPs from the NONL parent within the 12 cM region evaluated.

Discussion

There were six HONL lines with a mean yield ranked in the top 10 across the five populations evaluated, of these six lines, only entry 25 from population 3 contained SNPs

from the NONL parent RJS30006, which indicated it had a recombination within the genomic region evaluated (Table 3). There were NONL lines ranked in the top 10 in two of the five populations that were homozygous for at least one SNP from the HONL parent within the region evaluated. If a breeder selected for the HO transgene as well as the nearest flanking SNP from the NONL parent, it only would have been effective in selecting the highest yielding HONL line in one population, which was entry 25 in population 3. Selection for the HO transgene and a flanking SNP from the NONL parent would have resulted in selecting two of the three highest yielding HONL lines from population 3, entry 25 and entry 15.

The lack of association between the highest yielding HONL lines and the presence of a recombination within 4.8 cM of the HO transgene did not support the hypothesis that the reduction in seed yield associated with the HO transgene was due to the undesirable linkage drag from DNA near the HO transgene in the HONL parents.

The results of the molecular analysis suggest that the reduction in seed yield associated with the HO transgene is more likely an affect of the increased protein and reduced oil concentrations of the HONL lines compared to the NONL lines or other pleiotropic effects.

Acknowledgements

I want to thank Molly Ryan-Mahmutagic at the DuPont Pioneer Dallas Center soybean research facility for assistance with tissue collection and Beau Brouillette, Barb Hobart, John Woodward, Josh Shendelman, and Becky Madsen at the DuPont Pioneer Molecular Analysis Lab for SNP development and analysis.

Table 1. Molecular markers used for the lines and parents of population 1.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	HO transgene																						
				SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14	SNP 15	SNP 16	SNP 17	SNP 18	SNP 19	SNP 20	SNP 21	SNP 22	SNP 23
53	NONL	4106	1	P1§	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
47	NONL	4104	2	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
50	NONL	4098	3	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
36	NONL	4086	4	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
25	HONL	4078	5	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	
43	NONL	4077	6	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
11	HONL	4040	7	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	
45	NONL	4038	8	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
33	NONL	4033	9	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
28	NONL	4029	10	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
31	NONL	4016	11	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
9	HONL	4013	12	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	
1	HONL	4011	13	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
6	HONL	4001	14	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	
5	HONL	3999	15	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	
23	HONL	3998	16	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	
37	NONL	3994	17	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
41	NONL	3991	18	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	
22	HONL	3990	19	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	

† = HONL = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Genetic location (cM) of SNP relative to the high-oleate transgene.

§ = P1 = 92Y30 SNP, P2 = YR25C09 SNP, 1/2 = Heterogeneous; SNPs underlined and in bold italic print are from alternative parent than the transgene.

Table 1. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14	SNP 15	SNP 16	SNP 17	SNP 18	SNP 19	SNP 20	SNP 21	SNP 22	SNP 23
				-12.3	-11.0	-10.6	-8.5	-8.3	-7.1	-5.0	-4.9	-4.6	-2.5	-1.4	0.0	1.8	3.6	4.5	4.6	4.8	5.3	5.3	8.2	8.6	11.3	11.9
54	NONL	3989	20	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
26	HONL	3971	21	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
34	NONL	3966	22	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
2	HONL	3963	23	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>
44	NONL	3931	24	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
42	NONL	3929	25	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
7	HONL	3920	26	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
35	NONL	3919	27	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
19	HONL	3905	28	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
40	NONL	3902	29	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	
4	HONL	3880	30	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>
3	HONL	3880	31	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
48	NONL	3866	32	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
49	NONL	3865	33	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
30	NONL	3835	34	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
24	HONL	3815	35	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
18	HONL	3803	36	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
17	HONL	3788	37	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
32	NONL	3787	38	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>

Table 1. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14	SNP 15	SNP 16	SNP 17	SNP 18	SNP 19	SNP 20	SNP 21	SNP 22	SNP 23	
				-12.3	-11.0	-10.6	-8.5	-8.3	-7.1	-5.0	-4.9	-4.6	-2.5	-1.4	0.0	1.8	3.6	4.5	4.6	4.8	5.3	5.3	8.2	8.6	11.3	11.9	
39	NONL	3775	39	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
10	HONL	3758	40	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
29	NONL	3747	41	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
52	NONL	3741	42	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
20	HONL	3735	43	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
16	HONL	3709	44	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
51	NONL	3698	45	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
27	HONL	3685	46	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
46	NONL	3675	47	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
8	HONL	3673	48	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
14	HONL	3673	49	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
12	HONL	3643	50	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
21	HONL	3598	51	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
38	NONL	3586	52	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
15	HONL	3573	53	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
13	HONL	3507	54	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
92Y30	NONL Parent	4168		P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
YR25C09	HONL Parent	3834		P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2

Table 2. Molecular markers used for the lines and parents of population 2.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1 -33.0‡	SNP 2 -32.2	SNP 3 -18.7	SNP 4 -12.3	SNP 5 -11.0	SNP 6 -10.6	HO transgene 0.0	SNP 8 5.3	SNP 9 11.3	SNP 10 11.9	SNP 11 16.1	SNP 12 18.6	SNP 13 18.3
54	NONL	4323	1	<u>P2</u> §	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>
51	NONL	4223	2	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1
33	NONL	4216	3	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1
40	NONL	4208	4	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1
41	NONL	4190	5	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1
44	NONL	4177	6	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>
38	NONL	4160	7	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	<u>1/2</u>
43	NONL	4153	8	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1
49	NONL	4140	9	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
48	NONL	4139	10	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
36	NONL	4131	11	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>
47	NONL	4124	12	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
50	NONL	4073	13	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>
31	NONL	4071	14	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
42	NONL	4059	15	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
16	HONL	4048	16	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
27	HONL	4043	17	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
34	NONL	4043	18	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>
19	HONL	4028	19	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Genetic location (cM) of SNP relative to the high-oleate transgene.

§ = P1 = YB26P09 SNP, P2 = YR25C09 SNP, 1/2 = Heterogeneous; SNPs underlined and in bold italic print are from alternative parent than the transgene.

Table 2. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	HO transgene	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13
39	NONL	4014	20	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
32	NONL	4000	21	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
30	NONL	3989	22	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>
10	HONL	3967	23	<u>1/2</u>	<u>1/2</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2	P2
35	NONL	3966	24	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
14	HONL	3954	25	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>
24	HONL	3948	26	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>
52	NONL	3948	27	P2	P2	P2	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
29	NONL	3940	28	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
53	NONL	3938	29	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>
2	HONL	3916	30	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2
45	NONL	3910	31	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
11	HONL	3896	32	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
46	NONL	3886	33	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
8	HONL	3870	34	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>
1	HONL	3853	35	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
3	HONL	3847	36	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
22	HONL	3845	37	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2
13	HONL	3829	38	P2	P2	P2	P2	P2	P2	P2	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>

Table 2. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	HO transgene	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13
37	NONL	3813	39	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
26	HONL	3807	40	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	<u>1/2</u>
5	HONL	3785	41	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	<u>1/2</u>
12	HONL	3777	42	<u>P1</u>	<u>P1</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2
21	HONL	3769	43	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>P1</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	<u>1/2</u>
6	HONL	3767	44	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	<u>1/2</u>
9	HONL	3763	45	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2
25	HONL	3751	46	P2	P2	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
23	HONL	3750	47	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
28	NONL	3742	48	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
15	HONL	3741	49	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
20	HONL	3722	50	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
18	HONL	3670	51	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
7	HONL	3643	52	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2
4	HONL	3623	53	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
17	HONL	3403	54	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
YB26P09	NONL Parent	4143		P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
YR25C09	HONL Parent	3901		P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2

Table 3. Molecular markers used for the lines and parents of population 3.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	HO transgene																						
				SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14	SNP 15	SNP 16	SNP 17	SNP 18	SNP 19	SNP 20	SNP 21	SNP 22	SNP 23
44	NONL	4955	1	P1§	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
51	NONL	4752	2	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>
37	NONL	4743	3	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>
41	NONL	4718	4	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
31	NONL	4699	5	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
54	NONL	4639	6	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
30	NONL	4616	7	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
25	HONL	4609	8	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
34	NONL	4576	10	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>
39	NONL	4572	11	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
49	NONL	4594	9	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
29	NONL	4545	12	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
43	NONL	4544	13	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>P2</u>	<u>P2</u>
27	HONL	4543	14	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
42	NONL	4539	15	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
32	NONL	4535	16	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
45	NONL	4518	17	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
53	NONL	4516	18	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
28	NONL	4493	19	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Genetic location (cM) of SNP relative to high-oleate transgene.

§ = P1 = RJS3006 SNP, P2 = YR37Y09 SNP, 1/2 = Heterogeneous; SNPs underlined and in bold italic print are from alternative parent than the transgene.

Table 3. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14	SNP 15	SNP 16	SNP 17	SNP 18	SNP 19	SNP 20	SNP 21	SNP 22	SNP 23
				-18.7	-15.8	-15.0	-8.5	-8.3	-5.0	-4.9	-4.6	-4.6	-1.3	-1.0	0.0	1.8	3.6	4.5	5.3	6.0	8.6	11.3	11.9	16.1	16.6	18.3
50	NONL	4493	20	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>
47	NONL	4469	21	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>
15	HONL	4461	22	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
35	NONL	4460	23	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
20	HONL	4428	24	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
52	NONL	4412	25	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>
2	HONL	4403	26	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>
48	NONL	4396	27	<u>1/2</u>	<u>1/2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
36	NONL	4380	28	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
14	HONL	4362	29	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>P1</u>	<u>P1</u>	<u>P1</u>
40	NONL	4357	30	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
26	HONL	4347	31	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
16	HONL	4317	32	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
33	NONL	4306	33	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
38	NONL	4302	34	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
18	HONL	4284	35	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>
24	HONL	4262	36	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>
21	HONL	4259	37	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>
8	HONL	4249	38	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2

Table 3. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14	SNP 15	SNP 16	SNP 17	SNP 18	SNP 19	SNP 20	SNP 21	SNP 22	SNP 23
				-18.7	-15.8	-15.0	-8.5	-8.3	-5.0	-4.9	-4.6	-4.6	-1.3	-1.0	0.0	1.8	3.6	4.5	5.3	6.0	8.6	11.3	11.9	16.1	16.6	18.3
22	HONL	4245	39	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
46	NONL	4236	40	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
13	HONL	4225	41	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
23	HONL	4220	42	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
9	HONL	4219	43	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
11	HONL	4205	44	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>
5	HONL	4197	45	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>P1</u>	<u>P1</u>	<u>P1</u>	<u>P1</u>
19	HONL	4145	46	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>
17	HONL	4117	47	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
4	HONL	4113	48	<u>P1</u>	<u>P1</u>	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
10	HONL	4043	49	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>P1</u>	<u>P1</u>	<u>P1</u>
1	HONL	4042	50	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>P1</u>
6	HONL	4040	51	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>
3	HONL	3994	52	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
7	HONL	3972	53	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	<u>1/2</u>	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
12	HONL	3919	54	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
RJS30006	NONL Parent	4690		P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
YR25C09	HONL Parent	4101		P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2

Table 4. Molecular markers used for the lines and parents of population 4.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1 -8.5‡	SNP 2 -7.1	SNP 3 -6.4	SNP 4 -5	SNP 5 -4.6	SNP 6 -2.5	SNP 7 -1.4	HO transgene 0	SNP 9 1.82	SNP 10 3.64	SNP 11 4.5	SNP 12 4.8	SNP 13 5.3	SNP 14 11.3
29	NONL	4086	1	P1§	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
34	NONL	4036	2	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
2	HONL	4019	3	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
46	NONL	3995	4	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
45	NONL	3980	5	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
49	NONL	3978	6	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
37	NONL	3975	7	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
42	NONL	3957	8	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
7	HONL	3945	9	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
36	NONL	3939	10	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
21	HONL	3938	11	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>
33	NONL	3931	12	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
1	HONL	3923	13	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
43	NONL	3911	14	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
48	NONL	3909	15	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
40	NONL	3907	16	P1	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	<u>P2</u>	P1	P1	P1	P1	P1	P1	P1
53	NONL	3904	17	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
50	NONL	3901	18	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
39	NONL	3901	19	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Genetic location (cM) of SNP relative to the high oleate transgene.

§ = P1 = 93Y20 SNP, P2 = YR37Y09 SNP, 1/2 = Heterogeneous; SNPs underlined and in bold italic print are from alternative parent than the transgene.

Table 4. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	HO transgene	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14
30	NONL	3898	20	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
13	HONL	3890	21	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
44	NONL	3886	22	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
35	NONL	3883	23	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
8	HONL	3883	24	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>
51	NONL	3870	25	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
23	HONL	3869	26	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>P1</u>
47	NONL	3861	27	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
25	HONL	3853	28	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
20	HONL	3847	29	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
38	NONL	3846	30	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
15	HONL	3841	31	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
10	HONL	3819	32	<u>P1</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
5	HONL	3817	33	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
6	HONL	3817	34	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
16	HONL	3811	35	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
24	HONL	3800	36	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
54	NONL	3799	37	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
31	NONL	3796	38	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>P2</u>	<u>P2</u>	<u>1/2</u>

Table 4. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	HO transgene	SNP 9	SNP 10	SNP 11	SNP 12	SNP 13	SNP 14
				-8.5	-7.1	-6.4	-5	-4.6	-2.5	-1.4	0	1.82	3.64	4.5	4.8	5.3	11.3
14	HONL	3787	39	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
26	HONL	3785	40	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
17	HONL	3781	41	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
28	NONL	3774	42	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
11	HONL	3769	43	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
12	HONL	3762	44	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
22	HONL	3742	45	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
27	HONL	3732	46	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
32	NONL	3721	47	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
19	HONL	3707	48	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
52	NONL	3677	49	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
3	HONL	3655	50	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
18	HONL	3645	51	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
41	NONL	3630	52	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
9	HONL	3623	53	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
4	HONL	3235	54	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
93Y20	NONL Parent	3777		P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
YR37Y09	HONL Parent	3557		P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2

Table 5. Molecular markers used for the lines and parents of population 5.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1 -8.5‡	SNP 2 -7.1	SNP 3 -5.0	SNP 4 -4.6	SNP 5 -4.6	SNP 6 -4.6	SNP 7 -1.4	SNP 8 -1.3	SNP 9 -1.0	SNP 10 -0.7	SNP 11 -0.5	HO transgene 0.0	SNP 13 1.2	SNP 14 1.8	SNP 15 1.8	SNP 16 3.9
29	NONL	4264	1	P1§	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
42	NONL	4201	2	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u><i>1/2</i></u>	<u><i>1/2</i></u>
44	NONL	4175	3	<u><i>1/2</i></u>	<u><i>1/2</i></u>	<u><i>1/2</i></u>	<u><i>1/2</i></u>	<u><i>1/2</i></u>	<u><i>1/2</i></u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
41	NONL	4112	4	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u><i>1/2</i></u>
52	NONL	4112	5	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
45	NONL	4112	6	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
28	NONL	4081	7	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
40	NONL	4074	8	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
39	NONL	4071	9	<u><i>1/2</i></u>	<u><i>1/2</i></u>	<u><i>1/2</i></u>	<u><i>1/2</i></u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
10	HONL	4065	10	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
35	NONL	4055	11	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
13	HONL	4044	12	<u><i>1/2</i></u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u><i>1/2</i></u>	<u><i>1/2</i></u>
43	NONL	4018	13	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
36	NONL	4018	14	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
33	NONL	3987	15	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
47	NONL	3968	17	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
37	NONL	3968	16	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
32	NONL	3956	18	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
34	NONL	3948	19	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Genetic location (cM) of SNP relative to the high oleate transgene.

§ = P1 = XB30C10 SNP, P2 = YR37Y09 SNP, 1/2 = Heterogeneous; SNPs underlined and in bold italic print are from alternative parent than the transgene.

Table 5. Molecular characterization of progeny and parents of population 5.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	HO transgene	SNP 13	SNP 14	SNP 15	SNP 16
				-8.5	-7.1	-5.0	-4.6	-4.6	-1.4	-1.3	-1.0	-0.7	-0.5	0.0	1.2	1.8	1.8	3.9	
38	NONL	3945	20	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
12	HONL	3942	21	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
49	NONL	3933	22	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>P2</u>
31	NONL	3919	23	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
11	HONL	3913	24	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
18	HONL	3906	25	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
51	NONL	3905	26	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
7	HONL	3903	27	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
30	NONL	3892	28	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
53	NONL	3891	29	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
54	NONL	3888	30	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
25	HONL	3886	31	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
4	HONL	3870	32	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
48	NONL	3866	33	<u>1/2</u>	<u>1/2</u>	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
24	HONL	3864	34	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
14	HONL	3835	35	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
16	HONL	3834	36	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
6	HONL	3800	37	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
21	HONL	3795	38	<u>1/2</u>	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>

Table 5. Continued.

Entry	Class†	Yield kg ha ⁻¹	Yield Rank	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10	SNP 11	HO transgene	SNP 13	SNP 14	SNP 15	SNP 16
15	HONL	3789	39	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
46	NONL	3742	40	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
5	HONL	3731	42	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
22	HONL	3724	43	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
23	HONL	3716	44	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>
3	HONL	3695	45	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	<u>1/2</u>	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>
27	HONL	3693	46	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
26	HONL	3689	47	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
9	HONL	3741	41	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
17	HONL	3649	48	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
2	HONL	3623	49	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
19	HONL	3613	50	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
8	HONL	3576	51	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
50	NONL	3574	52	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
1	HONL	3552	53	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	<u>1/2</u>	<u>1/2</u>
20	HONL	3455	54	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2
XB30C10 NONL Parent		4002		P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1	P1
YR37Y09 HONL Parent		3806		P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2	P2

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CHAPTER 4**STABILITY OF OLEATE CONCENTRATION IN SOYBEAN LINES CONTAINING****THE HIGH-OLEATE TRANSGENE DP-305423-1**

Modified from a paper to be published in Crop Science

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Abstract

Soybean [*Glycine max* (L.) Merr.] lines with the transgene DP-305423-1 produce oil with a high-oleate concentration that is desirable for oxidative stability. It is important for commercial production to understand the oleate concentration that can be expected when cultivars with the transgene are grown over a range of environmental conditions. The objective of my study was to evaluate the environmental stability of oleate concentration for lines with the transgene in comparison to that of lines without the transgene. Three high-oleate, normal-linolenate (HONL); six high-oleate, low-linolenate (HOLL); three mid-oleate, low-linolenate (MOLL); three normal-oleate, low-linolenate (NOLL); and three normal-oleate, normal-linolenate (NONL) lines were evaluated across 18 environments during 2010 and 2011. The mean oleate concentration of all the lines ranged from 529 to 643 g kg⁻¹ among the environments. The mean oleate concentration across environments was 842 g kg⁻¹ for HONL, 826 g kg⁻¹ for HOLL, 536 g kg⁻¹ for MOLL, 262 g kg⁻¹ for NOLL, and 238 g kg⁻¹ for NONL lines. The range in oleate concentrations among environments averaged 73 g kg⁻¹ for HONL, 128 g kg⁻¹ for HOLL, 148 g kg⁻¹ for MOLL, 153 g kg⁻¹ for NOLL, and 108 g kg⁻¹ for NONL lines. The results indicated that the consistency in oleate concentrations across a range of production environments for cultivars with the DP-305423-1 transgene would be equal or superior to cultivars without the transgene.

Introduction

Genetic modifications have been made in soybean to increase oleate concentration from about 250 g kg⁻¹ in conventional cultivars to greater than 800 g kg⁻¹ as a means of improving the oxidative stability of the oil (Fehr, 2007). An important consideration in the commercial production of the genetically modified cultivars is that their oleate concentration should be as consistent as possible across a range of environments. Scherder et al. (2008) evaluated the consistency of oleate concentration across environments for mid-oleate lines (492 to 625 g kg⁻¹) that contained the mutant allele *ol* from M23. They reported that the lines with the highest mean oleate generally had the greatest range in oleate concentrations across environment. However, the lines with the highest mean oleate concentration were considered to be the most desirable from a commercial standpoint because they met their standard of >500 g kg⁻¹ oleate in more environments than lines with lower mean oleate concentrations.

Oliva et al. (2006) evaluated five mid-oleate lines (383 to 533 g kg⁻¹) and 12 normal-oleate lines (195 to 343 g kg⁻¹) across five locations with two planting dates at each location during 2004. They reported that in general the mid-oleate lines were less consistent in their oleate concentrations across environments than lines with normal oleate concentrations. Lee et al. (2012) studied the environmental stability of oleate concentration for 18 lines with different combinations of mutant *FAD2* alleles that had from 252 to 799 g kg⁻¹ oleate. Their results indicated that lines with high oleate concentrations can have equal or greater environment stability than lines with lower oleate.

High-oleate soybean cultivars with the transgene DP-305423-1 have been developed that contain antisense copies of the endogenous *FAD2-1* gene (Kinney et al., 2008). The transgene causes a suppression of the *FAD2* gene that is responsible for the conversion of

oleate to linoleate. Lines homozygous for the transgene generally have an oleate concentration of greater than 750 g kg⁻¹ (Brace et al., 2011; Spear et al., in review). No studies have been reported on the environmental stability of high-oleate lines with the DP-305423-1 transgene in comparison to mid-oleate and normal-oleate lines. The objective of my study was to evaluate the consistency of oleate concentration of lines with and without the transgene over a broad range of environmental conditions.

Materials and Methods

Eighteen soybean lines with different combinations of alleles for fatty ester concentration were evaluated during 2010 and 2011 (Table 1). Three lines were homozygous for the HO transgene DP-305423-1 and did not contain any mutant alleles for reduced linolenate concentration (HONL): YR25C09, YR26T09, and YR27E09. Three lines contained the HO transgene and the *fan1*(A5) (Hammond and Fehr, 1983) and *fan2*(A23) (Bubeck et al., 1989; Fehr et al., 1992) alleles for reduced linolenate concentration (HOLL): '92Y61', XR28K10, XR28L10. Three lines contained the HO transgene and the *fan1*(C1640) (Wilcox et al., 1984) and *fan3*(RG10) (Reinprecht et al., 2009) alleles for reduced linolenate concentration (HOLL): XR31C09, '93Y23', '93Y30'. There were three M23-derived, mid-oleate lines with the *fan1*(A5), *fan2*(A23), and *fan3*(A26) (Fehr and Hammond, 2000) alleles for reduced linolenate (MOLL): 'IA2088', 'IA3036', and 'IA3039'. Two lines without the HO transgene contained the *fan1*(A5) and *fan2*(A23) alleles for reduced linolenate (NOLL): '92M82' and '93Y03'. One normal-oleate, low-linolenate (NOLL) line '93M20' contained the *fan1*(C1640) and *fan3*(RG10) alleles for reduced linolenate concentration. There were three conventional lines with normal oleate and normal linolenate (NONL): '92Y60', '92Y80', and '93Y20'. All of the lines were developed by

DuPont Pioneer, except the three mid-oleate lines that were developed by Iowa State University.

The experiment was grown as a randomized complete block design with two replications at each of 18 environments during 2010 and 2011 (Table 2). To represent a double cropping system, there were two planting dates grown at Napoleon, OH, in 2010 and Napoleon, OH, and Mascoutah, IL, in 2011. Each planting date and environment combination was considered a different environment for the study. The North America environments had 35 seeds planted in a one-row plot 1.2 m long with a row spacing of 1.1 m. The Hawaii, Puerto Rico, and Chile environments had 22 seeds planted in a one-row plot 0.91 m long with a row spacing of 0.76 m. At maturity, five plants from each plot were individually harvested. Fatty ester concentration was measured on two five-seed bulk samples from each plant by gas chromatography (Butte et al., 1982; Dolde et al., 1999). The fatty ester analysis for each environment was conducted in plot order. The mean of the 10 seed samples from each plot was used for data analysis.

Weather stations at each environment recorded the daily mean temperature during the growing season. A maturity date was recorded for the earliest entry at an environment as well as the latest entry at an environment when 95% of the pods had reached their mature color. The mean daily temperature during the 30 d before maturity was calculated for the earliest entry and the latest entry at each environment. The mean of these two temperatures was used to characterize each location for mean daily temperature during the last 30 d of seed fill (Table 3).

All data were analyzed using the general linear model (GLM) procedure of SAS Enterprise Guide V4.3 (SAS institute Inc). Environments and replications within

environments were considered random effects and genotypes were considered fixed effects. To evaluate the environmental stability of oleate concentration for each entry, a regression analysis was conducted using the PROC REG procedure of SAS Enterprise Guide V4.3 (SAS institute Inc.). The mean oleate concentration of each entry at each environment was regressed on an environmental index as described by Scherder et al. (2008) to obtain the linear regression coefficients (b) and the coefficients of determination (r^2). The environmental index was calculated by subtracting the mean oleate of all entries across all environments from the mean oleate of all entries at the specific environment. The CORR procedure of SAS Enterprise Guide V4.3 (SAS institute Inc.) was used to calculate the correlation of mean daily temperature during the final 30 d of seed fill for a given environment to the mean oleate concentration of all entries at that environment.

Results and Discussion

There was significant variation among environments for the mean oleate concentration of the 18 entries (Table 3). This variation among environments was highly associated with the mean daily temperature during the last 30 d of seed fill. The correlation of 0.75 between the mean oleate concentration of all the entries at an environment and the mean daily temperature during the final 30 d of seed fill at the environment was highly significant ($P < 0.01$). The environment with the greatest mean oleate of 643 g kg^{-1} was Crawfordsville, AR, in 2010, which had the greatest mean daily temperature during seed fill of 25.4 C° . The second planting date at Napoleon, OH, in 2011 had the lowest mean oleate of 529 g kg^{-1} and the lowest mean daily temperature during seed fill of 13.8 C° . The positive association between oleate concentration and daily temperature during seed fill was

consistent with previous studies (Oliva et al., 2006; Scherder et al., 2008; Bachlava and Cardinal, 2009; Lee et al., 2009; Lee et al., 2012).

All of the HOLL and HONL lines with the DP-305423-1 transgene had a mean oleate concentration across the 18 environments of $>800 \text{ g kg}^{-1}$ (Table 3). The greater average oleate of the HONL class (842 g kg^{-1}) than that of the HOLL class (826 g kg^{-1}) was attributed to the genetic background of the particular lines used for each class and not to the influence of the alleles for low linolenate in the HOLL lines based on the research of Brace et al. (2011). They reported that the mean oleate of HOLL and HONL lines with the DP-305423-1 transgene was not significantly different in each of four populations.

The MOLL lines had mean oleate concentrations that were similar to those of the MOLL lines studied by Scherder et al. (2008) (Table 3). The mean oleate of the NOLL and NONL lines was representative of conventional soybean cultivars that lack the mutant allele for mid-oleate from M23 or the DP-305423-1 transgene (Fehr, 2007).

One measure of the environmental stability in oleate concentration for a line was the range in the trait among environments. The three HONL lines had the lowest range across environments with an average of 73 g kg^{-1} oleate (Table 3). The range in oleate for the HOLL lines varied from 96 g kg^{-1} for XR28K10 that had the highest mean oleate across environments for the six lines in that class to 166 g kg^{-1} for 93Y30 that had lowest mean oleate. The differences in the ranges of the nine HONL and HOLL lines indicated that it may be possible to select for environmental stability of oleate among lines with the DP-305423-1 transgene. The data suggested that HONL and HOLL lines with the greatest mean oleate also may have the greatest environmental stability for the trait. The lower range in oleate concentrations among environments for lines of the HONL class compared with lines of the

HOLL class may be due to the genetic background of the particular lines used for the study and not to the influence of the alleles for low linolenate in the HOLL lines. Additional research with random HOLL and HONL lines from a segregating population will be necessary to determine if the relationship between oleate concentration and environmental stability can be confirmed and if alleles for linolenate have an influence on oleate stability.

The ranges in oleate of the HOLL and HONL lines were equal to or superior to those of one or more of the lines in the other three classes (Table 3). None of the MOLL, NOLL, or NONL lines had a range as small as that of the three HONL lines. The range for 93Y30 that was the greatest of the nine lines with the HO transgene was less than the range of the MOLL line IA3036 and the NOLL line 92M82. These results indicated that the high oleate concentration of lines with the HO transgene does not result in less environmental stability for the trait than that of lines with substantially less oleate.

A second method used to evaluate the environmental stability of oleate concentration was to regress the mean oleate concentration of a line at an environment on an environmental index as described by Scherder et al. (2008) (Table 4). A low b -value and a high r^2 value indicated that a line was more environmentally stable for oleate concentration than one with a larger b -value and lower r^2 value. Only the NONL line 92Y60 had a lower b -value than the three HONL lines. The HOLL lines had b -values that were similar to one or more lines in the other four classes. These results indicated that lines with the DP-305423-1 transgene can have environmental stability for oleate that is equal or superior to lines with lower oleate concentrations.

From a commercial perspective, stability can be measured by the frequency with which a cultivar produces oil that meets a minimum standard value for oleate. Although

there is no official standard to define high-oleate oil in soybean, a value of 750 g kg^{-1} was used as the standard for my study, which was 250 g kg^{-1} greater than the standard used by Scherder et al. (2008) for mid-oleate oil. All of the HONL lines and three of the HOLL lines produced oil with greater than 750 g kg^{-1} oleate at all of the environments, including the second planting dates that simulated the planting of soybeans after the harvest of a small grains crop, such as wheat [*Triticum aestivum* (L.)] (Table 3). The data indicated that even with a later planting date and a reduced mean daily temperature during seed fill, HO lines can be identified that will produce oil with greater than 750 g kg^{-1} oleate concentration consistently across environments.

In summary, lines with the DP-305423-1 transgene had oleate concentrations that were equal or superior in consistency across environments to those of mid-oleate and normal-oleate lines without the transgene. There was variation in environment stability for oleate concentrations among lines with the transgene, which indicated that selection for stability could be considered in a breeding program. From a commercial perspective, HO lines with the greatest oleate concentration would be most likely to meet a minimum standard for the fatty ester.

Acknowledgements

The authors thank the staffs at each DuPont Pioneer soybean research facility for assistance with field data collection; David Dolde and Karen Kratky at the DuPont Pioneer gas chromatography lab; and Ryan Brace of Iowa State University for assistance with statistical analyses.

Table 1. Class, maturity group, and mean fatty ester concentration of lines grown in 18 environments during 2010 and 2011.

Entry	Class†	Maturity group	Palmitate	Stearate	Oleate	Linoleate	Linolenate
-----g kg ⁻¹ -----							
YR25C09	HONL	II	62	40	842	18	36
YR26T09	HONL	II	65	37	843	18	36
YR27E09	HONL	II	66	37	840	19	37
92Y61	HOLL	II	65	43	830	40	21
XR28K10	HOLL	II	59	41	840	38	20
XR28L10	HOLL	II	60	42	837	40	20
XR31C09	HOLL	III	62	44	830	44	18
93Y23	HOLL	III	61	46	812	60	21
93Y30	HOLL	III	61	45	808	65	21
IA2088	MOLL	II	86	47	521	334	10
IA3036	MOLL	III	84	50	552	304	10
IA3039	MOLL	III	86	52	535	317	10
93M20	NOLL	III	103	48	244	582	22
93Y03	NOLL	III	101	43	265	567	23
92M82	NOLL	II	100	40	277	557	25
92Y60	NONL	II	108	49	240	531	72
92Y80	NONL	II	110	45	240	530	74
93Y20	NONL	III	93	44	233	558	72
LSD‡			2	2	12	11	3

† = HONL = high oleate, normal linolenate; HOLL = high oleate, low linolenate; MOLL = mid oleate, low linolenate; NOLL = normal oleate, low linolenate; NONL = normal oleate, normal linolenate.

‡ = Least significant difference at the 0.05 probability level for comparisons among lines.

Table 2. Planting date and soil type of the 18 environments at which lines were grown during 2010 and 2011.

Environment	Latitude	Planting Date	Soil Type
Algona, IA 2010	43° 3' N	17-May-2010	Nicollet Loam (Fine-loamy, mixed, superactive, mesic Aquic Hapludolls)
Algona, IA 2011	43° 3' N	7-May-2011	Webster clay loam (Fine-loamy, mixed, superactive, mesic Typic Endoaquolls)
Dallas Center, IA 2010	41° 41' N	6-May-2010	Nicollet Loam (Fine-loamy, mixed, superactive, mesic Aquic Hapludolls)
Dallas Center, IA 2011	41° 41' N	11-May-2011	Wiota silty clay loam (Fine-silty, mixed, superactive, mesic Pachic Argiudolls)
Princeton, IL 2010	41° 25' N	7-Jun-2010	Buckhart silt loam (Fine-silty, mixed, superactive, mesic Oxyaquic Argiudolls)
Princeton, IL 2011	41° 25' N	7-May-2011	Buckhart silt loam (Fine-silty, mixed, superactive, mesic Oxyaquic Argiudolls)
Napoleon, OH 2010 Date 1	41° 25' N	8-Jun-2010	Lenawee silty clay loam (Fine, mixed, semiactive, nonacid, mesic Mollic Epiaquepts)
Napoleon, OH 2011 Date 1	41° 25' N	5-Jun-2011	Lenawee silty clay loam (Fine, mixed, semiactive, nonacid, mesic Mollic Epiaquepts)
Napoleon, OH 2010 Date 2	41° 25' N	2-Jul-2010	Lenawee silty clay loam (Fine, mixed, semiactive, nonacid, mesic Mollic Epiaquepts)
Napoleon, OH 2011 Date 2	41° 25' N	29-Jun-2011	Lenawee silty clay loam (Fine, mixed, semiactive, nonacid, mesic Mollic Epiaquepts)
Mascoutah, IL 2010	38° 28' N	14-Jun-2010	Downsouth silt loam (Fine-silty, mixed, superactive, mesic Mollic Oxyaquic Hapludalfs)
Mascoutah, IL 2011 Date 1	38° 28' N	12-May-2011	Herrick silt loam (Fine, smectitic, mesic Aquic Argiudolls)
Mascoutah, IL 2011 Date 2	38° 28' N	18-Jul-2011	Herrick silt loam (Fine, smectitic, mesic Aquic Argiudolls)
Crawfordsville, AR 2010	35° 15' N	17-Jun-2010	Dubbs silt loam (Fine-silty, mixed, active, thermic Typic Hapludalfs)
Crawfordsville, AR 2011	35° 15' N	7-Jun-2011	Dubbs silt loam (Fine-silty, mixed, active, thermic Typic Hapludalfs)
Waimea, HI	21° 57' N	8-Dec-2010	Makaweli silty clay loam (Fine, parasquic, isohyperthermic torroxidic Haplustolls)
Salinas, PR	17° 58' N	7-Dec-2010	Vives clay (Fine-loamy, mixed, superactive, isohyperthermic Fluventic Haplustepts)
Viluco, Chile	33° 43' S	16-Nov-2010	Maipo silt loam (Fine-loamy, mixed, thermal Fluventic Haploxerolls)

Table 3. Mean oleate concentration for lines grown at 18 environments in 2010 and 2011.

Entry	Class†	Algona, IA 2010	Algona, IA 2011	Princeton, IL 2010	Princeton, IL 2011	Dallas Center, IA 2010	Dallas Center, IA 2011	Napoleon, OH Date 1 2010	Napoleon, OH Date 2 2010	Napoleon, OH Date 1 2011	Napoleon, OH Date 2 2011	Mascoutah, IL 2010	Mascoutah, IL Date 1 2011	Mascoutah, IL Date 2 2011	Crawfordsville, AR 2010	Crawfordsville, AR 2011	Salinas, PR	Wainea, HI	Viluco, CH	Overall Mean	Range	LSD ‡
YR25C09	HONL	856	821	849	858	849	836	844	837	839	804	862	867	795	868	867	855	841	807	842	73	16
YR26T09	HONL	854	825	848	854	864	837	856	824	837	796	861	863	797	869	869	854	838	821	843	73	11
YR27E09	HONL	851	815	844	852	855	835	841	828	835	794	861	866	801	868	862	852	846	812	840	74	12
92Y61	HOLL	847	812	840	847	847	826	838	814	823	780	859	864	742	866	865	847	826	791	830	124	10
XR28K10	HOLL	856	818	841	855	857	832	848	827	832	778	865	874	794	874	871	855	845	805	840	96	9
XR28L10	HOLL	859	808	842	858	853	831	845	826	828	779	861	875	762	872	865	855	845	801	837	113	10
XR31C09	HOLL	842	807	844	848	840	829	841	808	825	754	854	863	771	871	866	847	846	794	830	117	12
93Y23	HOLL	819	772	819	834	834	813	815	790	791	713	837	854	758	863	847	846	827	782	812	150	9
93Y30	HOLL	823	773	820	832	827	804	819	767	779	695	848	850	739	861	852	843	825	779	808	166	10
IA2088	MOLL	504	464	551	562	541	571	521	518	477	443	556	498	485	573	576	486	533	525	521	133	34
IA3036	MOLL	568	473	577	580	575	540	564	526	504	476	601	599	452	614	615	508	638	518	552	186	41
IA3039	MOLL	532	467	556	585	539	540	570	507	517	486	547	591	477	579	577	535	522	512	535	124	40
93M20	NOLL	241	229	261	271	229	244	236	232	213	194	256	278	234	320	271	232	209	236	244	126	10
93Y03	NOLL	259	241	275	291	254	261	257	265	246	227	267	279	236	378	310	245	230	242	265	151	18
92M82	NOLL	268	257	289	296	276	281	262	270	253	216	292	312	237	398	343	251	232	247	277	182	20
92Y60	NONL	237	222	259	264	246	240	239	243	224	200	248	249	234	299	266	211	200	231	240	99	30
92Y80	NONL	233	210	248	270	238	238	228	241	214	196	259	264	212	307	290	218	204	241	240	111	30
93Y20	NONL	217	215	236	257	211	232	241	225	195	187	250	294	225	301	262	220	192	236	233	114	19
LSD§		23	29	13	14	22	19	15	13	18	21	17	15	23	45	28	12	22	13	12		
Mean		593	557	600	612	596	588	592	575	568	529	610	619	542	643	626	587	583	566	588	115	6
Mean C°¶		18.9	16.0	19.3	16.7	20.4	17.0	19.2	17.7	15.0	13.8	22.3	24.7	15.7	25.4	23.0	24.8	22.6	19.2			

† = HONL = High oleate, normal linolenate; HOLL = high oleate, low linolenate; MOLL = mid oleate, low linolenate; NOLL = normal oleate, low linolenate; NONL = normal oleate, normal linolenate.

‡ = Least significant difference at the 0.05 probability level for comparisons among environments.

§ = Least significant difference at the 0.05 probability level for comparisons among entries.

¶ = Mean daily temperature during the final 30 d of seed fill.

Table 4. Regression coefficients and coefficients of determination for oleate concentration regressed on an environmental index.

Entry	Class [†]	$b_{‡}$	r^2	Mean Oleate g kg ⁻¹
YR25C09	HONL	0.70	0.85	842
YR26T09	HONL	0.72	0.86	843
YR27E09	HONL	0.71	0.88	840
Mean	HONL	0.71	0.86	842
92Y61	HOLL	1.01	0.81	830
XR28K10	HOLL	0.88	0.88	840
XR28L10	HOLL	0.99	0.84	837
XR31C09	HOLL	1.04	0.88	830
93Y23	HOLL	1.22	0.87	812
93Y30	HOLL	1.41	0.87	808
Mean	HOLL	1.09	0.86	826
IA2088	MOLL	1.06	0.60	521
IA3036	MOLL	1.58	0.72	552
IA3039	MOLL	1.15	0.82	535
Mean	MOLL	1.26	0.71	536
93M20	NOLL	0.84	0.71	244
93Y03	NOLL	0.99	0.67	265
92M82	NOLL	1.29	0.77	277
Mean	NOLL	1.04	0.72	262
92Y60	NONL	0.65	0.61	240
92Y80	NONL	0.90	0.77	240
93Y20	NONL	0.84	0.61	233
Mean	NONL	0.80	0.66	238

[†] = HONL = High oleate, normal linolenate; HOLL = high oleate, low linolenate; MOLL = mid oleate, low linolenate; NOLL = normal oleate, low linolenate; NONL = normal oleate, normal linolenate.

[‡] = All of the regression coefficients were significant at the 0.01 probability level.

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CHAPTER 5

GENERAL CONCLUSIONS

Soybean lines homozygous for the high-oleate (HO) transgene DP-305423-1 have a significantly greater oleate concentration than lines that do not contain the HO transgene. The HONL lines had an average seed yield across five populations that was 4.6% lower than the NONL lines. Of the top 10 yielding lines within each population only 12% of them were HONL. Averaged across the five populations, the HONL lines had a protein concentration that was 25 g kg⁻¹ greater than that of the NONL lines and an oil concentration that was 13 g kg⁻¹ lower. There were no HONL lines with a mean protein concentration as low as the NONL lines. The increase in protein concentration may play a role in the reduction of seed yield identified in the HONL lines because it has been well documented in the literature that seed yield and protein concentration are negatively correlated.

There were only a total of six HONL lines across the five populations that had a mean yield ranked in the top 10 for the population. Only one of these six lines had a recombination within the genomic region that was evaluated and there were other HONL lines that had a recombination in this region, however their mean yield was significantly less than the highest yielding NONL lines. These results indicate that the reduction in seed yield associated with the HONL lines was not the result of undesirable linkage drag around the HO transgene.

The increased oleate concentration in the seed oil of soybean lines containing the HO transgene DP-305423-1 was as stable as the oleate concentration from soybean lines with normal-oleate across 18 environments in 2010 and 2011. The mean range of oleate concentration across environments for the HONL class was the least at 73 g kg⁻¹ followed by the HOLL class that had a mean range of 128 g kg⁻¹. The mean range of oleate concentration

for the normal-oleate lines was 131 g kg^{-1} . The HONL lines also were considered the most stable based on the regression analysis. The HONL class had the lowest regression coefficient and highest coefficient of determination when regressing the mean oleate concentration at a location onto an environmental index. These data indicate that the increased oleate concentration associated with the DP-305423-1 transgene was as stable across environments as the oleate concentration of normal-oleate commercial cultivars.

APPENDIX A

**ANALYSIS OF VARIANCE AND ENTRY MEANS FOR AGRONOMIC AND SEED
TRAITS ACROSS ENVIRONMENTS**

Table A1. Analysis of variance for yield of five populations across four environments for populations 1, 2, 3, and 4 and across five environments for population 5 in 2011.

Sources of variation†	<u>Mean Squares</u>														
	<u>Population 1</u>			<u>Population 2</u>			<u>Population 3</u>			<u>Population 4</u>			<u>Population 5</u>		
	df	Yield‡		df	Yield‡		df	Yield‡		df	Yield‡		df	Yield‡	
Environments (E)	3	56071539 **	3	60842014 **	3	28523958 **	3	2613905 ns	4	29572215 **					
Replications/E	3	10555 ns	4	184804 **	4	947895 **	4	561297 **	5	492729 **					
Genotypes(G)	53	178472 **	53	273435 **	53	393010 **	53	143775 **	53	325260 **					
HONL	26	183835 **	26	161448 **	26	236645 **	26	167090 **	26	219797 *					
NONL	26	151350 *	26	150894 *	26	205120 ns	26	85879 *	26	207606 **					
HONL vs NONL	1	744197 **	1	6371170 **	1	9343645 **	1	1042884 **	1	6126306 **					
G x E	159	71920 **	159	75730 **	159	113396 **	159	65951 ns	212	113485 **					
HONL x E	78	67881 **	78	70126 **	78	86572 ns	78	80563 ns	104	115858 **					
NONL x E	78	75594 **	78	83636 **	78	126296 **	78	46450 ns	104	105166 ns					
HONL vs NONL x E	3	81390 *	3	15865 ns	3	475402 **	3	193090 *	4	268103 **					
Error	159	29759	212	43430	212	63426	212	52780	265	71419					
CV (%)§		4.4		5.3		5.8		6.0		6.9					

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Coefficient of variation.

Table A2. Analysis of variance for population 1 across three Iowa environments in 2011.

Sources of variation†	df	Mean Squares											
		Maturity‡		Height§		Lodging¶		Seed wt. #		Protein††		Oil††	
Environments (E)	2	1580.8	**	4394.8	**	0.6	ns	4357.2	**	1237.5	**	9226.0	**
Replications/E	3	4.6	**	87.2	*	0.9	**	83.6	**	12.0	ns	15.9	*
Genotypes(G)	53	24.2	**	86.9	**	0.4	**	384.9	**	983.2	**	304.2	**
HONL	26	19.5	**	86.0	**	0.4	ns	231.1	**	116.3	**	81.5	**
NONL	26	29.9	**	90.3	**	0.3	*	493.3	**	202.6	**	99.1	**
HONL vs NONL	1	2.3	ns	21.8	ns	1.8	**	1565.1	**	43815.8	**	11427.6	**
G x E	106	6.4	**	25.4	ns	0.2	**	25.2	**	20.6	**	8.8	**
HONL x E	52	5.2	**	23.8	ns	0.2	ns	25.2	*	18.0	*	10.4	**
NONL x E	52	7.0	**	27.8	ns	0.2	ns	25.6	ns	19.2	ns	6.4	ns
HONL vs NONL x E	2	21.2	**	3.8	ns	0.1	ns	13.3	ns	126.9	**	28.7	**
Error	159	1.0		25.1		0.2		16.0		12.0		5.0	
CV (%)‡‡		3.8		4.4		20.1		2.8		1.0		1.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Maturity measured as days after 31 August.

§ = Height measured as the distance from the soil surface to the terminal node in cm.

¶ = Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

= Seed weight measured as mg sd⁻¹.

†† = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

‡‡ = Coefficient of variation.

§§ = Fatty esters measured as g kg⁻¹.

Table A2. Continued.

Sources of variation†	df	<u>Mean Squares</u>									
		Palmitate§§		Stearate§§		Oleate§§		Linoleate§§		Linolenate§§	
Environments (E)	2	522.4	**	160.1	*	12690.5	**	269.2	ns	3823.5	**
Replications/E	3	1.4	ns	6.2	ns	215.9	ns	132.6	ns	18.9	*
Genotypes(G)	53	1738.9	**	26.9	**	471769.5	**	366767.2	**	1370.3	**
HONL	26	18.0	**	9.8	**	413.1	**	139.3	*	50.9	**
NONL	26	56.7	**	13.5	**	935.1	*	705.2	*	56.3	**
HONL vs NONL	1	90220.1	**	822.4	**	24968732.0	**	19416703.7	**	69836.9	**
G x E	106	4.8	ns	2.5	ns	298.2	ns	213.7	ns	8.2	ns
HONL x E	52	4.6	*	2.4	ns	129.9	ns	74.5	ns	5.7	ns
NONL x E	52	4.2	ns	2.5	ns	441.5	ns	336.8	ns	10.3	ns
HONL vs NONL x E	2	29.7	**	2.7	ns	946.7	ns	629.2	ns	17.6	ns
Error	159	3.8		2.4		310.7		237.5		6.6	
CV (%)‡‡		2.4		3.9		3.3		5.5		4.0	

Table A3. Analysis of variance for population 2 across three Iowa environments in 2011.

Sources of variation†	df	Mean Squares											
		Maturity‡		Height§		Lodging¶		Seed wt. #		Protein††		Oil††	
Environments (E)	2	318.3	**	4027.6	*	0.1	ns	5196.2	**	311.4	**	8219.4	**
Replications/E	3	4.0	*	189.0	**	0.4	*	30.6	ns	6.3	ns	3.8	ns
Genotypes(G)	53	27.3	**	98.4	**	0.5	**	237.4	**	1174.1	**	353.2	**
HONL	26	25.7	**	110.1	**	0.6	**	256.0	**	104.2	**	125.3	**
NONL	26	25.5	**	89.3	*	0.4	*	221.5	**	240.5	**	98.7	**
HONL vs NONL	1	117.2	**	31.7	ns	0.1	ns	169.4	**	53263.5	**	12897.4	**
G x E	106	5.9	**	35.5	**	0.2	*	17.7	*	19.4	**	8.3	**
HONL x E	52	5.6	**	24.8	ns	0.2	ns	20.2	ns	17.8	*	7.0	ns
NONL x E	52	5.4	**	44.3	*	0.2	ns	15.1	**	17.0	ns	9.5	**
HONL vs NONL x E	2	25.6	**	82.9	*	0.2	ns	18.3	ns	123.3	**	8.8	ns
Error	159	1.0		23.0		0.1		11.8		11.6		4.8	
CV (%)‡‡		3.8		4.3		16.7		2.3		0.9		1.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Maturity measured as days after 31 August.

§ = Height measured as the distance from the soil surface to the terminal node in cm.

¶ = Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

= Seed weight measured as mg sd⁻¹.

†† = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

‡‡ = Coefficient of variation.

§§ = Fatty esters measured as g kg⁻¹.

Table A3. Continued.

Sources of variation†	df	<u>Mean Squares</u>								
		Palmitate§§		Stearate§§		Oleate§§		Linoleate§§		Linolenate§§
Environments (E)	2	435.1 *	531.4 **	22036.8 **	1586.5 **	4560.5 **				
Replications/E	3	30.6 **	6.5 ns	71.5 ns	38.1 ns	10.5 ns				
Genotypes(G)	53	2055.9 **	43.7 **	484482.3 **	376195.9 **	1399.8 **				
HONL	26	72.7 **	33.3 **	443.4 **	105.1 **	60.1 **				
NONL	26	74.2 **	50.0 **	1110.0 **	996.5 **	40.1 **				
HONL vs NONL	1	105145.3 **	149.9 **	25637175.7 **	19909741.5 **	71583.0 **				
G x E	106	5.8 ns	5.2 **	303.0 ns	224.9 ns	9.2 **				
HONL x E	52	3.7 ns	6.7 **	59.2 ns	34.6 ns	6.5 *				
NONL x E	52	4.4 ns	3.8 ns	435.9 ns	369.3 ns	9.5 ns				
HONL vs NONL x E	2	96.3 **	1.0 ns	3186.2 **	1416.3 **	72.6 **				
Error	159	4.6	3.4	284.9	214.4	5.9				
CV (%)‡‡		2.6	4.0	3.2	5.2	3.7				

Table A4. Analysis of variance for population 3 across three Iowa and one Illinois environments in 2011.

Sources of variation†	df	Mean Squares									
		Maturity‡		Height§		Seed wt.¶		Protein#		Oil#	
Environments (E)	2	4501.3	**	3345.7	*	9733.1	**	1209.4	*	5381.8	**
Replications/E	3	29.2	**	129.8	*	206.6	**	94.7	**	50.1	**
Genotypes(G)	53	82.7	**	258.9	**	253.2	**	1016.8	**	241.4	**
HONL	26	97.3	**	220.6	**	183.2	**	37.9	*	97.2	**
NONL	26	71.3	**	307.2	**	274.9	**	226.4	**	123.4	**
HONL vs NONL	1	1.1	ns	0.5	ns	1506.7	**	47016.7	**	7061.6	**
G x E	106	7.7	**	75.0	**	41.9	**	23.5	**	8.9	**
HONL x E	52	9.5	**	96.0	*	42.4	**	17.9	*	9.4	**
NONL x E	52	6.2	**	54.9	*	41.6	**	22.8	ns	8.1	**
HONL vs NONL x E	2	1.0	ns	52.1	ns	33.1	ns	186.3	**	19.7	**
Error	159	2.0		48.3		15.6		13.8		3.8	
CV (%)††		4.5		6.0		2.3		1.0		1.1	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Maturity measured as days after 31 August.

§ = Height measured as the distance from the soil surface to the terminal node in cm.

¶ = Seed weight measured as mg sd⁻¹.

= Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

†† = Coefficient of variation.

‡‡ = Fatty esters measured as g kg⁻¹.

Table A4. Continued.

Sources of variation†	df	<u>Mean Squares</u>									
		Palmitate‡‡		Stearate‡‡		Oleate‡‡		Linoleate‡‡		Linolenate‡‡	
Environments (E)	2	292.9	**	99.0	*	21069.6	**	5831.2	**	5749.6	**
Replications/E	3	1.6	ns	3.3	ns	32.7	ns	26.5	ns	44.8	**
Genotypes(G)	53	2049.3	**	33.6	**	485593.7	**	368474.8	**	1760.3	**
HONL	26	102.0	**	13.7	**	532.0	**	256.1	ns	57.2	**
NONL	26	107.4	**	9.9	**	1661.3	*	1130.8	*	83.2	**
HONL vs NONL	1	103169.4	**	1163.9	**	25679443.6	**	19493108.0	**	89643.7	**
G x E	106	6.5	**	3.5	ns	510.3	**	384.4	**	10.4	**
HONL x E	52	4.8	**	4.1	ns	224.8	ns	166.4	ns	7.7	*
NONL x E	52	5.4	ns	2.8	ns	794.3	*	611.4	**	12.7	*
HONL vs NONL x E	2	77.8	**	3.5	ns	547.2	ns	148.6	ns	21.2	*
Error	159	3.7		3.4		310.6		231.9		6.4	
CV (%)††		2.2		4.8		3.3		5.6		4.3	

Table A5. Analysis of variance for lodging score of population 3 across two Iowa environments in 2011.

Sources of variation†	df	Mean Squares	
		Lodging‡	
Environments (E)	1	0.0	ns
Replications/E	2	0.0	ns
Genotypes(G)	53	0.3	ns
HONL	26	0.2	ns
NONL	26	0.3	ns
HONL vs NONL	1	1.7	*
G x E	53	0.3	**
HONL x E	26	0.3	**
NONL x E	26	0.2	*
HONL vs NONL x E	1	2.9	**
Error	106	0.1	
CV (%)‡		15.5	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

Table A6. Analysis of variance for population 4 across three Iowa environments in 2011.

Sources of variation†	df	Mean Squares											
		Maturity‡		Height§		Lodging¶		Seed wt. #		Protein††		Oil††	
Environments (E)	2	324.7	**	4433.4	**	20.3	**	2977.6	*	13755.6	**	11029.7	**
Replications/E	3	1.7	ns	13.3	ns	0.0	ns	167.4	**	5.4	ns	8.5	ns
Genotypes(G)	53	29.3	**	74.6	**	0.4	**	301.3	**	1122.7	**	411.2	**
HONL	26	43.5	**	85.1	**	0.5	*	303.3	**	141.0	**	84.4	**
NONL	26	14.9	**	61.2	**	0.4	*	300.6	**	206.4	**	52.0	**
HONL vs NONL	1	32.2	**	150.9	**	1.1	*	265.1	**	50470.1	**	18244.5	**
G x E	106	1.8	*	20.5	ns	0.2	ns	28.0	ns	23.8	*	12.6	**
HONL x E	52	1.9	ns	25.0	ns	0.2	ns	16.6	ns	22.9	*	12.4	**
NONL x E	52	1.6	*	15.8	ns	0.2	*	35.7	ns	25.1	ns	9.1	ns
HONL vs NONL x E	2	4.3	*	22.0	ns	0.0	ns	124.3	*	13.1	ns	110.8	**
Error	159	1.0		17.0		0.2		28.0		16.0		7.9	
CV (%)‡‡		3.8		4.0		23.3		3.5		1.2		1.5	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Maturity measured as days after 31 August.

§ = Height measured as the distance from the soil surface to the terminal node in cm.

¶ = Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

= Seed weight measured as mg sd⁻¹.

†† = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

‡‡ = Coefficient of variation.

§§ = Fatty esters measured as g kg⁻¹.

Table A6. Continued.

Sources of variation†	df	Mean Squares									
		Palmitate‡‡		Stearate‡‡		Oleate‡‡		Linoleate‡‡		Linolenate‡‡	
Environments (E)	2	22.8	ns	507.2	**	9212.7	*	6339.4	*	1154.8	**
Replications/E	3	3.5	ns	1.0	ns	605.8	ns	371.5	ns	14.7	*
Genotypes(G)	53	1900.6	**	100.1	**	495629.9	**	385199.8	**	1079.3	**
HONL	26	19.6	**	44.9	**	636.8	**	408.0	*	86.3	**
NONL	26	26.6	**	33.5	**	1244.7	ns	1080.1	*	34.6	**
HONL vs NONL	1	99526.2	**	3265.5	**	26219463.4	**	20376898.2	**	54058.8	**
G x E	106	5.1	**	6.2	**	506.5	*	400.8	ns	7.1	**
HONL x E	52	2.1	ns	3.0	ns	252.1	ns	207.0	ns	4.7	ns
NONL x E	52	5.2	ns	4.5	ns	763.0	ns	577.3	ns	7.7	*
HONL vs NONL x E	2	82.1	**	135.3	**	448.3	ns	848.1	ns	55.1	**
Error	159	3.4		3.0		370.2		304.7		4.6	
CV (%)‡‡		2.4		4.1		3.5		6.2		4.1	

Table A7. Analysis of variance for population 5 across three Iowa environments in 2011.

Sources of variation†	df	Mean Squares											
		Maturity‡		Height§		Lodging¶		Seed wt. #		Protein††		Oil††	
Environments (E)	2	837.4	**	7035.6	**	7.3	*	6714.1	*	10323.6	*	7995.5	**
Replications/E	3	7.0	**	17.2	ns	0.6	*	326.0	**	504.3	**	95.3	**
Genotypes(G)	53	78.1	**	173.4	**	0.4	ns	403.8	**	1512.3	**	490.0	**
HONL	26	63.6	**	163.9	**	0.4	*	319.7	**	281.3	**	132.2	**
NONL	26	74.8	**	177.9	**	0.3	ns	476.3	**	285.2	**	134.2	**
HONL vs NONL	1	539.3	**	300.3	**	0.3	ns	706.4	**	65422.3	**	19044.0	**
G x E	106	2.0	ns	30.9	ns	0.3	ns	34.8	ns	34.9	*	15.2	**
HONL x E	52	2.2	ns	23.0	ns	0.2	ns	38.8	ns	35.4	*	11.3	**
NONL x E	52	1.1	ns	36.1	ns	0.3	*	29.9	ns	31.5	ns	12.6	**
HONL vs NONL x E	2	16.6	**	102.7	*	0.1	ns	57.1	ns	113.8	*	182.2	**
Error	159	2.0		28.9		0.2		27.7		24.3		5.9	
CV (%)‡‡		4.4		5.4		30.8		3.4		1.4		1.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Maturity measured as days after 31 August.

§ = Height measured as the distance from the soil surface to the terminal node in cm.

¶ = Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

= Seed weight measured as mg sd⁻¹.

†† = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

‡‡ = Coefficient of variation.

§§ = Fatty esters measured as g kg⁻¹.

Table A7. Continued.

Sources of variation†	df	Mean Squares									
		Palmitate‡‡		Stearate‡‡		Oleate‡‡		Linoleate‡‡		Linolenate‡‡	
Environments (E)	2	55.3	ns	524.0	**	5629.8	**	3913.0	**	1248.9	**
Replications/E	3	9.0	*	0.3	ns	59.2	ns	33.1	ns	1.9	ns
Genotypes(G)	53	2580.2	**	112.3	**	511309.7	**	383351.4	**	1499.2	**
HONL	26	28.4	**	51.9	**	857.1	**	344.6	**	46.6	**
NONL	26	51.7	**	62.7	**	2454.5	**	1937.1	**	61.7	**
HONL vs NONL	1	134668.6	**	2975.7	**	27013313.3	**	20258300.9	**	76642.8	**
G x E	106	4.9	**	8.0	**	305.6	ns	256.0	*	4.9	ns
HONL x E	52	2.9	ns	7.2	**	198.1	ns	130.4	ns	3.6	ns
NONL x E	52	4.1	ns	6.4	**	387.4	ns	337.2	ns	5.5	ns
HONL vs NONL x E	2	76.7	**	73.1	**	971.2	*	1408.9	**	22.5	*
Error	159	3.0		3.0		240.5		175.5		4.9	
CV (%)‡‡		2.1		3.9		2.8		4.8		4.2	

Table A8. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 1 grown at four Iowa and one Illinois environments in 2011.

Entry	Class [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging score [§]	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4011	25	2.0	110	141	364	173	63	39	830	23	44
2	HONL	3963	26	2.3	114	134	362	169	63	38	812	35	50
3	HONL	3880	25	2.0	113	145	362	170	63	38	816	31	51
4	HONL	3880	24	2.0	112	135	353	175	66	41	802	39	52
5	HONL	3999	25	2.0	114	138	363	171	65	41	809	34	50
6	HONL	4001	24	2.0	109	142	355	171	62	39	825	26	46
7	HONL	3920	25	2.2	110	138	358	172	65	37	813	34	50
8	HONL	3673	27	2.5	115	143	357	170	65	40	813	32	50
9	HONL	4013	26	2.7	113	142	364	172	63	37	822	28	49
10	HONL	3758	27	2.5	111	156	367	168	64	38	820	30	47
11	HONL	4040	24	1.8	104	149	367	173	66	37	814	37	44
12	HONL	3643	28	2.3	116	133	363	165	65	40	796	43	53
13	HONL	3507	30	2.7	117	136	362	163	63	38	794	44	59
14	HONL	3673	30	2.3	113	139	370	165	66	38	814	30	50
15	HONL	3573	29	2.5	122	133	361	170	62	38	810	37	52
16	HONL	3709	26	2.3	119	143	363	174	63	40	818	30	48
17	HONL	3788	25	2.0	117	140	358	174	63	38	820	30	48
18	HONL	3803	25	2.5	112	135	363	170	63	39	812	35	50
19	HONL	3905	27	2.3	111	126	354	176	64	38	818	33	46

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table A8. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3735	29	2.5	116	138	369	164	63	39	822	28	48
21	HONL	3598	27	2.0	114	137	368	166	67	38	808	36	51
22	HONL	3990	26	2.3	113	138	365	168	60	39	822	29	49
23	HONL	3999	27	2.2	114	147	358	172	64	40	811	35	49
24	HONL	3815	25	2.7	109	133	359	174	60	40	819	33	48
29	NONL	3747	24	2.2	116	133	331	188	92	41	287	501	78
30	NONL	3835	26	2.8	108	133	332	180	96	44	252	527	81
31	NONL	4016	25	2.0	110	137	334	183	97	42	250	527	83
32	NONL	3787	26	2.2	115	148	340	184	97	41	274	511	76
33	NONL	4033	24	2.5	105	135	327	186	96	44	273	513	73
34	NONL	3966	28	2.2	120	171	349	177	94	42	261	527	75
35	NONL	3919	29	2.2	111	145	346	177	99	43	261	518	78
36	NONL	4086	27	1.8	112	147	340	179	97	40	242	537	83
37	NONL	3994	26	2.0	114	153	342	182	95	40	260	528	77
38	NONL	3586	29	2.3	119	146	346	178	98	39	231	547	85
39	NONL	3775	28	2.0	116	159	348	177	99	42	248	530	80
40	NONL	3902	23	2.0	108	141	338	189	104	44	265	513	74
41	NONL	3991	28	2.3	118	149	340	185	101	40	250	528	80

Table A8. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3929	24	2.0	111	148	343	186	97	42	282	502	75
43	NONL	4077	22	2.0	112	143	333	191	97	42	268	516	76
44	NONL	3931	24	2.2	110	141	336	188	96	42	270	518	74
45	NONL	4038	24	2.0	110	147	342	179	94	42	259	526	79
46	NONL	3675	24	2.0	113	139	341	181	97	44	258	524	76
47	NONL	4104	29	2.0	115	137	333	182	101	40	268	509	81
48	NONL	3866	24	2.0	113	151	343	179	103	44	252	519	82
49	NONL	3865	27	2.3	112	123	331	184	96	42	253	526	82
50	NONL	4098	27	1.8	115	147	343	181	97	42	254	526	80
51	NONL	3698	31	1.8	122	144	339	177	103	44	245	527	81
52	NONL	3741	28	2.5	117	138	330	183	99	43	261	519	78
53	NONL	4106	27	2.2	110	147	336	182	97	41	255	524	82
54	NONL	3989	25	2.0	110	138	338	186	94	40	257	529	80
SEM		101	1	0	2	2	2	1	1	1	7	6	1
LSD 0.05		283	3	1	6	6	5	3	3	2	20	17	3
LSD 0.01		374	4	1	8	8	7	4	3	2	26	22	4
YR25C09	Parent	3834	26	2.0	111	150	367	165	63	39	821	29	48
92Y30	Parent	4168	24	2.2	105	133	327	197	99	42	265	520	74
SP16410155	Check	3222	32	3.3	110	145	375	151	66	43	785	81	24
YB26P09	Check	3876	27	2.5	114	140	357	180	105	52	239	526	77
92Y51	Check	3964	25	2.0	110	145	336	189	100	54	252	520	74
92Y80	Check	3916	27	2.0	108	141	355	182	109	47	235	531	78

Table A9. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 2 grown at four Iowa and one Illinois environments in 2011.

Entry	Class [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging scores [§]	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3853	27	2.0	116	151	376	170	65	47	810	30	48
2	HONL	3916	29	2.0	109	150	378	161	65	47	795	39	54
3	HONL	3847	30	2.2	110	150	375	166	71	43	804	33	49
4	HONL	3623	28	1.7	108	157	373	168	65	45	809	32	48
5	HONL	3785	28	2.3	110	156	374	164	59	41	822	30	47
6	HONL	3767	29	2.0	116	144	372	165	70	47	795	36	51
7	HONL	3643	32	2.3	113	145	381	160	61	44	799	40	55
8	HONL	3870	25	2.0	114	155	370	175	69	47	802	34	46
9	HONL	3763	30	2.3	111	137	373	166	59	48	801	37	53
10	HONL	3967	24	2.0	113	147	369	172	66	44	807	33	49
11	HONL	3896	28	2.0	111	145	372	167	60	45	801	38	55
12	HONL	3777	27	2.5	112	143	371	167	66	43	810	31	49
13	HONL	3829	29	2.2	113	162	373	166	61	41	817	32	48
14	HONL	3954	28	2.0	118	146	371	169	58	47	815	31	48
15	HONL	3741	29	2.0	111	142	377	165	68	42	807	33	50
16	HONL	4048	28	2.3	114	148	374	167	62	42	811	34	50
17	HONL	3403	32	3.3	114	136	369	157	63	42	807	34	52
18	HONL	3670	32	2.3	110	142	365	163	65	47	788	42	57
19	HONL	4028	28	2.2	104	145	367	165	61	42	808	34	53

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table A9. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3722	30	2.2	113	139	370	159	63	48	790	42	55
21	HONL	3769	31	2.8	115	144	363	167	62	47	799	40	51
22	HONL	3845	30	2.2	113	150	372	169	64	45	806	33	50
23	HONL	3750	33	2.0	126	136	373	155	68	49	790	47	44
24	HONL	3948	26	2.2	108	145	376	163	67	45	798	36	53
25	HONL	3751	31	2.5	108	144	367	171	60	43	813	32	51
26	HONL	3807	27	2.2	111	156	378	168	64	42	812	34	47
27	HONL	4043	29	2.0	105	146	367	169	68	46	797	36	53
28	NONL	3742	26	3.0	111	141	346	181	102	45	233	541	80
29	NONL	3940	27	2.0	116	149	350	177	97	46	258	519	79
30	NONL	3989	31	2.3	113	150	352	170	98	43	240	535	83
31	NONL	4071	27	2.2	115	148	333	184	101	49	240	529	80
32	NONL	4000	26	2.2	115	141	341	181	106	44	224	545	81
33	NONL	4216	23	2.0	104	151	349	179	105	50	242	520	82
34	NONL	4043	29	2.3	118	156	355	178	100	44	256	524	74
35	NONL	3966	30	2.0	117	148	355	171	95	45	237	536	86
36	NONL	4131	27	2.3	108	147	351	178	102	46	227	544	80
37	NONL	3813	29	2.2	112	151	350	174	106	44	232	537	80
38	NONL	4160	29	2.0	108	149	342	177	102	46	243	526	82
39	NONL	4014	30	2.5	114	146	342	180	96	49	250	524	80
40	NONL	4208	25	1.8	111	158	348	179	104	47	264	508	76
41	NONL	4190	26	2.0	106	144	350	175	102	43	239	539	76

Table A9. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4059	27	1.8	110	149	345	179	100	49	228	541	82
43	NONL	4153	27	2.2	109	162	356	176	103	42	254	522	78
44	NONL	4177	28	2.2	117	139	338	188	98	52	228	541	81
45	NONL	3910	30	2.2	118	143	345	174	93	47	223	553	84
46	NONL	3886	29	2.0	116	157	353	179	96	51	270	501	82
47	NONL	4124	30	2.0	113	152	349	174	98	47	246	527	81
48	NONL	4139	29	2.0	109	140	344	179	97	41	225	551	85
49	NONL	4140	26	2.2	113	156	348	181	98	44	247	531	79
50	NONL	4073	24	2.7	110	143	339	185	105	49	228	539	78
51	NONL	4223	27	2.0	114	147	344	181	100	48	248	522	79
52	NONL	3948	28	2.5	113	141	337	179	97	48	228	545	82
53	NONL	3938	26	2.3	117	147	354	176	99	43	263	514	80
54	NONL	4323	31	2.0	118	143	336	178	99	43	251	525	81
SEM		97	1	0	2	2	2	1	1	1	7	6	1
LSD 0.05		272	3	1	7	5	5	3	3	3	20	17	3
LSD 0.01		359	4	1	9	6	7	4	4	3	26	23	5
YR25C09	Parent	3901	26	2.2	110	152	366	167	62	39	823	28	47
YB26P09	Parent	4143	27	2.2	113	143	355	182	104	50	235	533	78
SP16410155	Check	3421	32	3.2	109	147	369	153	66	45	783	82	24
92Y30	Check	4196	23	2.0	111	136	329	195	99	41	263	521	75
92Y51	Check	4082	25	2.2	111	149	336	189	99	52	247	526	75
92Y80	Check	4046	27	2.2	110	143	350	185	109	46	227	536	81

Table A10. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 3 grown at two Iowa, one Illinois, and one Ohio environments in 2011.

Entry	Class [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging scores [§]	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4042	23	2.0	109	174	370	179	68	36	829	25	41
2	HONL	4403	30	2.3	116	160	370	173	68	37	831	22	41
3	HONL	3994	21	2.0	101	167	365	181	72	38	831	19	39
4	HONL	4113	31	2.3	115	163	370	172	64	35	830	27	42
5	HONL	4197	26	2.3	113	159	367	178	64	36	816	37	46
6	HONL	4040	23	2.5	104	165	368	176	69	34	820	36	40
7	HONL	3972	22	2.3	112	175	369	176	67	35	818	39	40
8	HONL	4249	33	2.8	121	180	369	166	69	38	822	25	45
9	HONL	4219	31	2.0	122	157	370	172	76	38	810	29	47
10	HONL	4043	22	2.5	111	173	371	172	67	35	834	20	43
11	HONL	4205	32	2.8	125	168	364	174	72	38	810	34	46
12	HONL	3919	26	2.0	118	169	364	173	62	36	810	47	44
13	HONL	4225	25	2.5	112	160	363	179	67	37	831	24	39
14	HONL	4362	22	2.3	113	165	368	180	71	38	827	24	38
15	HONL	4461	23	2.0	109	164	368	181	72	38	830	21	38
16	HONL	4317	31	2.3	115	164	373	172	66	35	828	27	43
17	HONL	4117	29	2.3	116	168	369	171	61	36	837	23	42
18	HONL	4284	29	2.5	124	168	372	174	73	39	816	26	45
19	HONL	4145	23	2.5	116	169	369	177	68	36	825	27	43

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table A10. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	4428	27	2.5	114	173	370	175	65	35	844	19	37
21	HONL	4259	32	2.5	128	163	366	169	74	37	805	33	50
22	HONL	4245	24	2.3	109	162	364	173	64	38	822	30	45
23	HONL	4220	30	2.0	117	159	368	167	67	37	826	24	44
24	HONL	4262	26	2.3	116	167	367	177	76	38	816	25	44
25	HONL	4609	31	2.3	120	166	367	176	74	38	816	27	45
26	HONL	4347	32	2.3	116	165	371	171	65	35	823	28	47
27	HONL	4543	31	2.3	117	160	372	170	71	40	815	29	44
28	NONL	4493	29	2.0	116	169	346	186	100	42	264	518	77
29	NONL	4545	25	2.0	108	163	338	187	106	40	255	521	77
30	NONL	4616	21	2.3	108	173	339	188	97	39	274	514	75
31	NONL	4699	28	2.0	110	162	338	184	106	41	254	522	77
32	NONL	4535	23	2.0	102	161	343	190	107	40	270	507	75
33	NONL	4306	27	2.0	116	170	362	174	104	42	271	507	74
34	NONL	4576	24	2.0	113	177	349	181	102	40	288	498	71
35	NONL	4460	28	2.0	115	168	347	183	94	38	257	535	76
36	NONL	4380	30	3.0	116	160	331	186	109	41	256	512	81
37	NONL	4743	33	2.0	122	171	344	179	105	41	239	534	79
38	NONL	4302	30	2.0	132	174	343	183	108	42	246	524	78
39	NONL	4572	28	2.0	119	177	342	186	98	42	281	503	75
40	NONL	4357	29	2.0	113	159	342	185	104	37	261	520	76
41	NONL	4718	31	2.5	124	176	350	182	106	40	231	540	82

Table A10. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4539	30	2.0	126	166	342	181	102	41	249	531	75
43	NONL	4544	31	2.3	119	180	345	182	109	40	235	538	77
44	NONL	4955	26	2.0	110	171	335	192	107	40	247	531	74
45	NONL	4518	30	2.8	122	167	342	183	111	41	239	529	81
46	NONL	4236	20	2.0	110	168	341	192	103	41	273	512	69
47	NONL	4469	25	2.0	109	176	352	182	108	43	287	491	71
48	NONL	4396	31	2.0	120	184	354	173	100	40	248	526	84
49	NONL	4389	24	2.3	110	160	348	181	109	41	290	486	74
50	NONL	4493	23	2.0	111	170	342	187	102	40	268	516	73
51	NONL	4752	23	1.8	103	176	343	186	100	41	277	512	71
52	NONL	4412	31	2.5	124	176	347	179	110	42	247	519	81
53	NONL	4516	30	2.0	118	179	348	179	102	40	264	517	75
54	NONL	4639	30	2.0	115	166	343	183	104	39	246	530	80
SEM		119	1	0	4	3	2	1	1	1	9	8	1
LSD 0.05		333	3	1	10	7	6	3	3	2	26	22	4
LSD 0.01		439	4	1	13	10	7	5	4	3	34	30	5
YR25C09	Parent	4101	23	2.3	109	169	375	169	61	37	838	23	40
RJS30006	Parent	4690	27	2.0	116	180	347	185	112	39	257	516	75
SP16410155	Check	3868	32	2.8	117	165	369	168	65	42	802	69	22
92Y30	Check	4332	19	1.8	103	144	331	203	98	39	307	487	67
92Y51	Check	4295	20	2.3	108	162	339	195	100	49	271	511	69
92Y80	Check	4470	25	2.5	108	160	351	191	110	43	238	534	75

Table A11. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 4 grown at three Iowa and one Ohio environments in 2011.

Entry	Class [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging scores [§]	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3923	29	1.7	104	152	354	184	61	40	822	37	39
2	HONL	4019	28	2.3	103	139	347	184	57	39	837	29	37
3	HONL	3655	32	2.5	111	147	356	180	60	38	832	28	41
4	HONL	3235	19	1.3	92	161	358	181	58	37	838	42	25
5	HONL	3817	31	1.8	103	145	347	183	62	37	815	40	44
6	HONL	3817	30	1.7	102	162	350	181	59	42	819	40	39
7	HONL	3945	27	2.0	102	149	358	183	61	38	837	25	38
8	HONL	3883	31	2.0	102	140	347	181	61	39	826	30	43
9	HONL	3623	31	1.7	101	137	348	190	60	43	839	21	37
10	HONL	3819	32	1.7	103	142	347	187	61	43	823	32	40
11	HONL	3769	31	2.3	100	137	350	181	58	39	838	25	39
12	HONL	3762	30	2.0	101	144	346	188	63	37	808	56	41
13	HONL	3890	31	2.2	108	153	350	179	63	39	835	23	39
14	HONL	3787	32	1.8	110	149	360	183	62	46	817	32	42
15	HONL	3841	31	2.2	99	150	356	183	61	46	826	26	40
16	HONL	3811	28	2.0	103	163	362	176	61	38	825	36	39
17	HONL	3781	32	1.7	106	148	355	181	59	41	833	25	41
18	HONL	3645	32	1.8	110	159	352	178	62	39	828	29	41
19	HONL	3707	32	2.2	103	149	352	179	61	43	813	38	44

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table A11. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3847	30	2.0	103	148	353	180	60	36	833	28	42
21	HONL	3938	28	1.8	102	151	346	188	59	37	835	28	40
22	HONL	3742	27	2.0	106	148	355	186	58	41	835	25	40
23	HONL	3869	30	1.5	104	160	348	185	61	39	832	27	39
24	HONL	3800	31	1.8	105	152	358	176	60	41	830	27	40
25	HONL	3853	32	2.2	106	150	351	183	60	40	834	25	40
26	HONL	3785	30	1.8	104	150	359	186	60	37	841	23	37
27	HONL	3732	32	1.5	102	153	350	176	66	38	801	47	48
28	NONL	3774	28	2.0	99	152	327	197	94	44	264	532	64
29	NONL	4086	29	2.0	102	145	323	199	93	43	257	539	67
30	NONL	3898	29	1.7	105	146	321	199	97	49	243	541	68
31	NONL	3796	27	2.3	111	149	327	200	98	45	248	543	65
32	NONL	3721	27	1.7	102	153	325	201	98	43	272	523	63
33	NONL	3931	28	1.5	98	158	330	200	96	51	260	531	62
34	NONL	4036	31	1.7	102	150	323	199	95	48	259	531	65
35	NONL	3883	28	1.7	100	158	324	198	93	45	280	517	65
36	NONL	3939	29	1.5	100	158	327	197	95	43	246	551	64
37	NONL	3975	30	2.2	103	149	324	200	91	52	282	511	63
38	NONL	3846	30	1.3	97	160	342	194	95	48	300	493	64
39	NONL	3901	32	2.3	105	151	334	193	93	45	245	548	67
40	NONL	3907	31	1.5	103	135	325	200	94	49	263	524	68
41	NONL	3630	31	1.7	102	147	326	193	95	44	252	541	67

Table A11. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3957	30	1.7	101	156	337	195	100	44	244	541	70
43	NONL	3911	29	2.0	104	159	329	196	96	46	256	536	65
44	NONL	3886	31	1.7	108	147	334	193	96	46	253	539	66
45	NONL	3980	31	1.7	98	146	322	198	97	50	247	536	68
46	NONL	3996	32	1.7	101	143	322	192	100	44	233	551	71
47	NONL	3861	29	2.0	99	148	324	200	96	46	255	539	63
48	NONL	3909	28	1.8	99	160	318	201	94	46	262	530	68
49	NONL	3978	28	1.7	103	154	333	196	98	47	258	533	63
50	NONL	3901	28	1.8	100	138	318	201	98	48	266	519	68
51	NONL	3870	31	1.7	105	166	334	198	94	44	248	547	65
52	NONL	3677	31	1.7	104	155	331	194	97	45	280	514	64
53	NONL	3904	26	1.8	100	156	327	200	94	46	254	539	65
54	NONL	3799	30	2.2	105	147	333	195	94	45	260	535	66
SEM		91	1	0	2	2	2	1	1	1	9	8	1
LSD 0.05		254	2	1	5	6	6	4	3	3	26	23	3
LSD 0.01		335	2	1	7	8	7	5	3	4	34	30	4
YR37Y09	Parent	3557	32	1.5	104	153	358	179	61	43	831	25	40
93Y20	Parent	3777	25	2.3	105	146	318	203	90	41	242	560	66
SP16410155	Check	3449	26	2.8	98	151	357	178	62	43	825	50	20
93Y05	Check	3701	23	1.2	91	151	316	207	102	41	250	543	64
93Y40	Check	3954	27	1.7	97	152	332	193	102	41	227	555	74
93Y82	Check	4166	30	1.5	101	169	315	195	98	42	252	531	75

Table A12. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 5 grown at three Iowa, one Illinois, and one Ohio environments in 2011.

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3552	20	2.0	97	135	358	186	61	47	836	19	36
2	HONL	3623	20	1.0	88	152	351	190	61	42	842	18	36
3	HONL	3695	28	1.8	104	154	361	179	61	43	828	29	38
4	HONL	3870	25	1.5	90	149	351	184	63	39	846	18	34
5	HONL	3731	24	1.3	102	155	356	184	63	42	839	21	34
6	HONL	3800	29	1.5	102	149	350	182	59	42	838	22	37
7	HONL	3903	31	1.2	98	152	346	177	60	43	837	23	37
8	HONL	3576	23	1.3	92	141	358	188	59	37	854	15	34
9	HONL	3664	29	1.7	93	144	364	175	64	44	835	20	36
10	HONL	4065	28	1.5	94	147	359	183	62	37	829	33	38
11	HONL	3913	30	1.5	98	143	368	173	61	37	833	26	42
12	HONL	3942	27	1.3	100	148	359	178	62	44	831	22	39
13	HONL	4044	29	1.5	101	153	352	180	61	39	846	18	35
14	HONL	3835	31	2.0	105	165	348	180	68	44	793	52	42
15	HONL	3789	24	1.7	94	151	357	181	61	37	856	14	31
16	HONL	3834	31	1.8	101	173	361	174	65	46	833	20	35
17	HONL	3649	26	1.7	106	149	348	182	64	43	827	28	36
18	HONL	3906	25	1.2	94	153	339	190	59	42	833	27	38
19	HONL	3613	28	1.5	102	155	364	178	60	45	822	28	44

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table A12. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3455	30	1.3	104	150	357	171	61	41	832	25	40
21	HONL	3795	26	1.5	101	154	358	180	64	38	837	21	38
22	HONL	3724	27	1.5	108	156	356	181	64	45	829	22	37
23	HONL	3716	20	2.0	97	154	369	179	61	41	844	16	36
24	HONL	3864	29	1.3	107	158	350	178	59	39	841	23	37
25	HONL	3886	29	1.7	100	160	359	181	64	39	836	23	37
26	HONL	3689	24	1.2	96	151	352	181	61	43	827	28	40
27	HONL	3693	26	1.5	97	153	351	183	65	44	818	35	39
28	NONL	4081	30	1.5	109	164	332	195	107	47	230	548	68
29	NONL	4265	33	1.5	104	164	319	191	100	48	245	536	71
30	NONL	3892	28	1.0	97	162	322	204	101	45	276	513	64
31	NONL	3919	34	1.5	109	154	333	193	100	48	246	536	69
32	NONL	3956	25	1.3	93	146	337	196	105	47	278	499	70
33	NONL	3987	31	1.2	102	158	330	194	103	48	257	522	68
34	NONL	3948	31	1.8	106	144	326	197	99	51	230	549	70
35	NONL	4055	31	1.7	96	153	332	198	106	48	245	531	70
36	NONL	4018	26	1.8	97	143	332	195	105	53	263	510	70
37	NONL	3968	25	1.5	96	162	333	196	102	46	263	520	69
38	NONL	3945	32	1.2	102	133	310	200	107	43	237	540	71
39	NONL	4071	31	1.7	105	153	319	195	97	52	248	534	67
40	NONL	4074	28	1.7	104	159	329	192	106	44	262	522	66
41	NONL	4112	28	1.5	103	153	326	192	107	45	258	522	68

Table A12. Continued

Entry	Class†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4201	31	1.7	106	164	327	196	103	55	269	505	67
43	NONL	4018	33	1.2	100	152	326	193	105	44	247	532	70
44	NONL	4175	29	1.7	102	152	321	197	105	44	232	544	74
45	NONL	4112	31	1.3	107	143	316	206	99	49	234	548	69
46	NONL	3742	20	1.5	89	178	332	202	100	47	325	469	58
47	NONL	3872	31	1.5	99	153	316	201	102	48	257	525	68
48	NONL	3866	27	1.3	102	150	331	195	102	52	277	503	64
49	NONL	3933	33	1.8	107	157	329	184	102	46	238	542	72
50	NONL	3574	23	1.3	91	153	329	198	107	48	260	519	66
51	NONL	3905	25	1.5	96	154	336	201	102	46	279	509	64
52	NONL	4112	32	1.2	100	159	323	192	103	51	252	525	67
53	NONL	3891	28	1.3	94	154	333	198	102	43	253	532	69
54	NONL	3888	33	1.3	105	167	335	189	98	49	266	514	71
SEM		107	1	0	2	2	2	2	1	1	7	7	1
LSD 0.05		297	2	1	6	7	7	4	3	3	20	18	3
LSD 0.01		392	2	1	8	9	9	6	3	4	26	24	3
YR37Y09	Parent	3806	32	1.8	101	154	358	180	60	44	828	26	40
XB30C10	Parent	4002	22	1.5	96	156	327	197	106	45	275	508	65
SP16410155	Check	3678	26	2.7	101	152	355	179	60	42	834	45	18
93Y05	Check	3917	24	1.3	88	150	317	204	102	40	250	544	64
93Y40	Check	4022	26	1.2	92	152	331	196	101	42	242	543	71
93Y82	Check	4266	30	1.7	101	169	312	197	96	42	250	537	74

Table A13. Entry means for the parents and SP16410155 of each population across locations grown in 2011.

Entry	Genotype†	Population	Yield kg ha ⁻¹ ‡	Maturity d§	Lodging score¶	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ #	Oil g kg ⁻¹ #	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
YR25C09	HONL	1	3834 ab	26 a	2 a	111 a	150 a	367 a	165 a	63 a	39 a	821 a	29 a	48 a
SP16410155	HOLL	1	3222 a	32 a	3 a	110 ab	145 a	375 a	151 b	66 a	43 b	785 b	81 b	24 b
92Y30	NONL	1	4168 b	24 a	2 a	105 b	133 a	327 b	197 c	99 b	42 b	265 c	520 c	74 c
YR25C09	HONL	2	3901 ab	26 a	2 a	110 a	152 a	366 a	167 a	62 a	39 a	823 a	28 a	47 a
SP16410155	HOLL	2	3421 a	32 a	3 a	109 a	147 a	369 a	153 b	66 a	45 b	783 b	82 b	24 b
YB26P09	NONL	2	4143 b	27 a	2 a	113 a	143 a	355 a	182 c	104 b	50 c	235 c	533 c	78 c
YR25C09	HONL	3	4101 ab	23 a	2 a	109 a	169 a	375 a	169 a	61 a	37 a	838 a	23 a	40 a
SP16410155	HOLL	3	3868 a	32 b	3 a	117 a	165 a	369 a	168 a	65 b	42 b	802 b	69 b	22 b
RJS30006	NONL	3	4690 b	27 ab	2 a	116 a	180 b	347 b	185 b	112 c	39 ab	257 c	516 c	75 c
YR37Y09	HONL	4	3557 a	32 a	2 a	104 ab	153 a	358 a	179 a	61 a	43 a	831 a	25 a	40 a
SP16410155	HOLL	4	3449 a	26 b	3 b	98 a	151 a	357 a	178 a	62 a	43 a	825 a	50 a	20 b
93Y20	NONL	4	3777 a	25 b	2 ab	105 b	146 a	318 b	203 b	90 b	41 a	242 b	560 b	66 c
YR37Y09	HONL	5	3806 a	32 a	2 a	101 a	154 a	358 a	180 a	60 a	44 a	828 a	26 a	40 a
SP16410155	HOLL	5	3678 a	26 b	3 a	101 a	152 a	355 a	179 a	60 a	42 a	834 a	45 a	18 b
XB30C10	NONL	5	4002 a	22 c	2 a	96 a	156 a	327 b	197 b	106 b	45 a	275 b	508 b	65 c

† = High oleate, normal linolenate parent, NONL = normal oleate, normal linolenate parent, HOLL = high oleate, low linolenate line.

‡ = Means followed by the same letter were not significantly different based on Tukey's honestly significant difference at the 0.05 probability level (Tukey, 1949).

§ = Days after 31 August.

¶ = Score of 1 (all plants erect) to 5 (all plants prostrate).

= Expressed on a 13 g kg⁻¹-moisture basis.

APPENDIX B

**ANALYSIS OF VARIANCE AND ENTRY MEANS FOR AGRONOMIC AND SEED
TRAITS AT INDIVIDUAL ENVIRONMENTS**

Table B1. Analysis of variance for population 1 grown at Pocahontas, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	14964.8	ns	1.3	ns	252.7	**	1.8	**	213.9	**	0.2	ns
Genotypes	53	107862.9	**	3.2	**	51.7	**	0.3	ns	146.7	**	293.9	**
HONL	26	130067.3	**	2.0	**	47.2	**	0.3	ns	102.6	**	34.8	*
NONL	26	89513.4	**	4.7	**	57.4	**	0.2	ns	176.0	**	55.7	**
HONL vs NONL	1	7632.2	ns	0.1	ns	17.3	ns	0.9	*	530.7	**	13220.2	**
Error	53	39823.1		0.5		15.4		0.2		12.6		12.3	
CV (%)§§		6.0		2.4		3.5		20.9		2.6		1.0	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	16.3	ns	3.2	ns	5.6	ns	322.1	ns	57.8	ns	46.7	*
Genotypes	53	99.3	**	561.8	**	10.8	**	154384.5	**	120330.7	**	446.4	**
HONL	26	31.9	**	9.6	**	4.9	**	199.3	**	63.1	**	27.6	**
NONL	26	44.7	**	20.5	**	5.7	**	722.0	ns	469.2	ns	37.7	**
HONL vs NONL	1	3270.3	**	28991.9	**	298.3	**	8158427.5	**	6363691.3	**	21959.3	**
Error	53	6.8		3.3		1.5		325.1		239.9		9.3	
CV (%)§§		1.5		2.2		3.0		3.4		5.6		4.5	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B2. Analysis of variance for population 1 grown at Royal, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	12677.2	ns	10.1	**	8.6	ns	0.6	ns	23.6	ns	25.6	ns
Genotypes	53	107946.2	**	4.2	**	34.0	**	0.3	ns	122.0	**	311.8	**
HONL	26	110034.0	**	4.0	**	27.4	**	0.3	ns	64.6	*	51.2	**
NONL	26	102342.5	**	4.2	**	41.9	**	0.3	ns	170.1	**	86.8	**
HONL vs NONL	1	199356.7	*	8.9	**	0.2	ns	0.1	ns	364.8	**	12936.3	**
Error	53	33108.3		0.9		10.7		0.3		27.3		11.8	
CV (%)§§		5.5		3.5		2.7		23.2		3.7		1.0	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	16.4	*	0.8	ns	12.7	*	310.1	ns	325.5	ns	9.5	ns
Genotypes	53	103.4	**	560.2	**	12.1	**	156961.3	**	121735.9	**	484.6	**
HONL	26	32.7	**	9.0	**	6.6	**	204.1	**	69.8	**	22.0	**
NONL	26	38.1	**	17.9	**	5.9	**	502.1	ns	358.2	ns	23.0	**
HONL vs NONL	1	3641.2	**	28991.9	**	313.5	**	8300587.8	**	6440872.7	**	24510.5	**
Error	53	3.9		3.0		2.0		166.2		128.8		4.8	
CV (%)§§		1.1		2.1		3.5		2.4		4.1		3.2	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B3. Analysis of variance for population 1 grown at Conrad, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	4023.6	ns	2.4	ns	0.3	ns	0.1	ns	13.4	ns	10.1	ns
Genotypes	53	59479.0	**	29.6	**	52.0	ns	0.2	ns	166.6	**	418.8	**
HONL	26	47568.4	*	23.9	**	59.0	ns	0.2	ns	114.3	**	66.4	**
NONL	26	65419.3	**	35.0	**	46.5	ns	0.1	ns	198.4	**	98.4	**
HONL vs NONL	1	214704.4	**	35.6	**	11.9	ns	0.9	**	696.2	**	17913.0	**
Error	53	16346.8		1.4		49.1		0.1		8.0		12.0	
CV (%)§§		2.8		5.5		6.5		15.3		1.9		1.0	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	15.1	ns	0.1	ns	0.4	ns	15.4	ns	14.5	ns	0.6	ns
Genotypes	53	119.1	**	626.6	**	9.1	**	161020.0	**	125127.9	**	455.6	**
HONL	26	37.8	**	8.5	*	3.2	ns	269.5	ns	155.5	ns	12.6	*
NONL	26	29.1	**	26.6	**	6.9	ns	594.0	ns	551.4	ns	16.1	**
HONL vs NONL	1	4573.4	**	32295.6	**	215.9	**	8511610.1	**	6613398.2	**	23402.4	**
Error	53	4.3		5.0		3.8		440.9		343.9		5.8	
CV (%)§§		1.1		2.9		5.0		3.8		6.7		4.2	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B4. Analysis of variance for population 2 grown at Pocahontas, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	234072.0	*	1.4	ns	501.4	**	1.2	**	23.5	ns	1.2	ns
Genotypes	53	99390.9	**	3.4	**	44.6	**	0.3	**	76.8	**	412.6	**
HONL	26	79862.6	**	3.8	**	38.1	**	0.3	**	92.1	**	54.1	**
NONL	26	63716.9	ns	3.0	**	50.7	**	0.2	ns	60.9	**	84.8	**
HONL vs NONL	1	1534652.3	**	16.1	**	54.5	*	0.0	ns	93.0	**	18254.6	**
Error	53	37478.1		0.7		11.9		0.1		8.9		17.4	
CV (%)§§		5.7		2.8		3.2		14.5		2.1		1.2	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	0.1	ns	90.6	**	5.3	ns	110.2	ns	1.6	ns	10.2	ns
Genotypes	53	140.3	**	649.9	**	19.0	**	161052.5	**	125579.6	**	475.2	**
HONL	26	55.0	**	26.5	**	16.7	**	214.1	**	71.7	**	30.9	**
NONL	26	50.0	**	21.9	**	20.2	**	700.4	**	611.0	**	23.0	**
HONL vs NONL	1	4707.1	**	33183.6	**	45.24	**	8512003.1	**	6637968.8	**	23786.7	**
Error	53	6.5		4.3		3.4		158.0		120.8		4.4	
CV (%)§§		1.5		2.5		4.0		2.4		3.8		3.1	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B5. Analysis of variance for population 2 grown at Royal, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	121645.6	*	9.5	**	10.1	ns	0.0	ns	3.3	ns	0.6	ns
Genotypes	53	176341.4	**	4.1	**	37.3	**	0.4	**	102.7	**	352.6	**
HONL	26	160042.9	**	4.1	**	34.0	ns	0.5	**	100.9	**	47.0	**
NONL	26	120401.4	**	4.0	**	28.5	**	0.4	ns	104.4	**	105.5	**
HONL vs NONL	1	2054544.6	**	7.3	*	91.3	*	0.2	ns	106.4	**	14721.0	**
Error	53	29809.1		1.3		15.7		0.2		8.9		8.7	
CV (%)§§		5.4		3.9		3.3		19.5		2.1		0.8	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	9.0	ns	1.0	ns	13.0	*	89.7	ns	112.6	ns	15.6	ns
Genotypes	53	118.3	**	643.2	**	19.8	**	155803.0	**	121873.1	**	422.4	**
HONL	26	50.6	**	22.0	**	17.5	**	173.4	*	51.7	ns	21.1	**
NONL	26	39.4	**	29.8	**	21.3	**	627.8	ns	558.4	ns	19.5	ns
HONL vs NONL	1	3928.9	**	32743.3	**	39.7	**	8236726.1	**	6443412.7	**	21336.3	**
Error	53	5.3		3.3		3.2		367.6		279.3		7.1	
CV (%)§§		1.4		2.2		3.8		3.7		5.9		3.8	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B6. Analysis of variance for yield of population 2 grown at Princeton, IL, in 2011.

Sources of variation†	df	Mean Squares	
		Yield‡	
Replications	1	372522.0	*
Genotypes	53	155497.8	*
HONL	26	80103.4	ns
NONL	26	177150.6	ns
HONL vs NONL	1	1552776.9	**
Error	53	87639.7	
CV (%)§		6.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Coefficient of variation.

Table B7. Analysis of variance for population 2 grown at Conrad, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	10976.7	ns	1.2	ns	55.6	ns	0.0	ns	64.9	ns	17.0	ns
Genotypes	53	69394.0	**	31.3	**	87.5	**	0.2	ns	93.3	**	447.8	**
HONL	26	51816.9	**	28.9	**	87.6	**	0.1	ns	10.3	**	38.8	**
NONL	26	40532.9	ns	29.4	**	88.8	ns	0.2	ns	86.5	**	84.2	**
HONL vs NONL	1	1276790.3	**	145.1	**	51.7	ns	0.0	ns	6.7	ns	20534.4	**
Error	53	18803.2		1.5		41.3		0.1		17.7		8.8	
CV (%)§§		3.1		4.7		5.9		15.5		2.7		0.8	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	2.4	ns	0.1	ns	1.3	ns	14.7	ns	0.2	ns	5.7	ns
Genotypes	53	111.2	**	774.5	**	15.3	**	168232.9	**	129192.9	**	520.5	**
HONL	26	33.8	**	31.6	**	12.4	*	174.4	**	50.8	**	21.2	**
NONL	26	28.4	**	31.3	**	16.1	**	653.5	ns	565.7	ns	16.5	ns
HONL vs NONL	1	4279.0	**	39410.9	**	66.9	**	8894818.8	**	6831192.7	**	2665.2	**
Error	53	2.5		6.4		3.5		329.1		243.1		6.3	
CV (%)§§		0.9		3.2		4.4		3.4		5.6		4.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B8. Analysis of variance for population 3 grown at Cedar Falls, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	14476.9	ns	0.2	ns	6.1	ns	0.0	ns	24.5	ns	1.3	ns
Genotypes	53	236486.3	**	8.1	**	111.3	**	0.4	**	99.3	**	283.9	**
HONL	26	112611.4	*	8.2	**	94.1	*	0.3	*	79.0	**	29.9	**
NONL	26	146390.3	ns	8.2	**	132.8	**	0.2	**	95.1	**	87.4	**
HONL vs NONL	1	5799729.2	**	0.2	ns	0.0	ns	4.5	**	733.2	**	11999.6	**
Error	53	63599.9		0.6		31.2		0.1		8.2		6.4	
CV (%)§§		5.7		2.2		4.6		16.4		1.7		0.7	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	0.1	ns	0.2	ns	0.6	ns	31.5	ns	24.4	ns	1.1	ns
Genotypes	53	99.6	**	652.9	**	11.8	**	160859.0	**	122377.3	**	616.6	**
HONL	26	46.0	**	39.5	**	6.3	**	304.3	ns	170.7	ns	30.7	**
NONL	26	60.1	**	36.7	**	5.3	**	1307.5	*	925.7	*	48.9	**
HONL vs NONL	1	2522.0	**	32621.6	**	325.2	**	8483615.9	**	6457489.6	**	30613.1	**
Error	53	2.8		3.5		1.2		382.6		272.3		8.2	
CV (%)§§		1.0		2.1		2.9		3.7		5.9		4.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B9. Analysis of variance for population 3 grown at Princeton, IL, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Seed wt. #		Protein††		Oil††	
Replications	1	3122696.2	**	85.7	**	73.0	ns	594.6	**	280.0	**	145.4	**
Genotypes	53	228498.1	*	41.1	**	171.3	**	165.6	**	407.9	**	64.2	**
HONL	26	256026.3	ns	51.8	**	218.4	**	142.6	**	22.9	ns	22.7	**
NONL	26	180633.3	**	32.0	**	129.1	**	172.5	**	111.1	**	35.4	**
HONL vs NONL	1	757250.8	*	0.6	ns	43.6	ns	584.3	**	18135.2	**	1890.9	**
Error	53	123930.0		2.5		26.2		29.3		26.8		6.2	
CV (%)‡‡		7.2		7.7		4.6		3.0		1.5		1.3	

Sources of variation†	df	Mean Squares											
		Palmitate§§		Stearate§§		Oleate§§		Linoleate§§		Linolenate§§			
Replications	1	0.0	ns	6.6	ns	66.6	ns	30.6	ns	133.1	**		
Genotypes	53	759.5	**	15.1	**	165102.8	**	124396.6	**	609.8	**		
HONL	26	37.5	**	11.1	ns	369.4	ns	260.6	*	21.1	**		
NONL	26	38.7	**	5.3	*	856.5	**	645.0	**	30.0	**		
HONL vs NONL	1	38269.3	**	374.5	**	8718574.5	**	6569473.4	**	30991.4	**		
Error	53	3.9		4.5		263.1		187.1		5.7			
CV (%)‡‡		2.2		5.5		2.9		5.1		4.5			

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Seed weight measured as mg sd⁻¹.

†† = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

‡‡ = Coefficient of variation.

§§ = Fatty esters measured as g kg⁻¹.

Table B10. Analysis of variance for population 3 grown at Conrad, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	4025	ns	1.8	ns	310.4	ns	0.0	ns	0.8	ns	2.9	ns
Genotypes	53	134147	**	49.1	**	126.3	ns	0.2	**	72.0	**	371.8	**
HONL	26	60072.4	ns	56.4	**	100.0	ns	0.2	*	46.5	**	20.9	**
NONL	26	98384.0	**	43.5	**	155.1	*	0.2	*	90.5	**	73.4	**
HONL vs NONL	1	2989908.5	**	2.4	ns	61.2	ns	0.1	ns	255.5	**	17254.6	**
Error	53	30964		1.5		87.3		0.1		9.3		8.1	
CV (%)§§		3.9		4.4		8.3		14.7		1.9		0.8	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	4.9	ns	4.5	ns	2.8	ns	0.1	ns	24.5	ns	0.1	ns
Genotypes	53	95.5	**	650.0	**	13.5	**	160652.5	**	122459.8	**	554.7	**
HONL	26	47.1	**	34.6	**	4.5	ns	307.9	**	157.6	*	20.9	**
NONL	26	44.2	**	42.9	**	4.9	ns	1085.8	*	782.9	*	29.7	**
HONL vs NONL	1	2688.0	**	32434.1	**	471.3	**	8478347.7	**	6466442.2	**	28081.7	**
Error	53	2.5		3.7		4.4		286.1		236.4		5.3	
CV (%)§§		0.9		2.3		5.3		3.1		5.6		3.9	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B11. Analysis of variance for population 4 grown at Atlantic, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	537534.6	**	2.1	ns	34.7	ns	0.0	ns	472.9	**	2.1	ns
Genotypes	53	108953.3	**	6.8	**	34.9	**	0.3	**	143.7	**	377.1	**
HONL	26	127237.0	*	9.4	**	43.9	**	0.3	ns	128.2	**	44.6	**
NONL	26	74256.3	*	4.3	**	26.6	*	0.3	*	146.6	*	108.5	**
HONL vs NONL	1	535701.8	**	5.0	ns	15.3	ns	0.3	ns	472.1	**	16001.6	**
Error	53	43630.9		1.3		12.5		0.2		43.9		16.3	
CV (%)§§		5.6		3.7		3.3		18.1		4.2		1.1	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	7.1	ns	0.2	ns	1.3	ns	700.7	ns	378.6	ns	29.6	**
Genotypes	53	122.5	**	566.9	**	24.7	**	164477.4	**	130806.1	**	336.3	**
HONL	26	32.2	**	8.0	**	20.8	**	323.2	**	320.0	**	46.2	**
NONL	26	35.3	**	13.0	**	11.9	**	839.9	ns	610.8	ns	20.3	**
HONL vs NONL	1	4736.2	**	29502.1	**	456.3	**	8687065.1	**	6908519.9	**	16096.7	**
Error	53	3.8		2.8		3.0		322.6		260.7		3.5	
CV (%)§§		1.1		2.2		4.2		3.4		5.6		3.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B12. Analysis of variance for population 4 grown at Hedrick, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	100961.7	ns	2.7	ns	2.2	ns	0.1	ns	23.0	ns	6.1	ns
Genotypes	53	78182.6	ns	15.2	**	32.4	*	0.3	ns	105.8	**	408.7	**
HONL	26	97705.9	ns	22.5	**	38.3	ns	0.2	ns	89.6	**	54.7	**
NONL	26	60880.1	ns	7.2	**	26.9	ns	0.3	**	126.1	**	91.5	**
HONL vs NONL	1	20443.5	ns	32.2	**	23.9	ns	0.5	ns	0.0	ns	17858.9	**
Error	53	101743.1		1.2		18.4		0.3		34.1		16.7	
CV (%)§§		8.7		3.9		4.5		24.6		4.0		1.2	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	10.0	ns	0.5	ns	0.6	ns	32.2	ns	2.7	ns	8.9	ns
Genotypes	53	176.2	**	663.5	**	53.3	**	163811.7	**	125409.1	**	358.4	**
HONL	26	31.0	**	7.3	**	15.8	**	288.8	*	165.6	ns	24.6	**
NONL	26	20.3	ns	12.2	*	16.3	**	944.5	ns	802.3	ns	14.3	**
HONL vs NONL	1	8006.6	**	34661.6	**	1991.8	**	8649951.6	**	6621517.3	**	17987.8	**
Error	53	13.8		3.5		2.3		371.3		293.6		5.5	
CV (%)§§		1.9		2.4		3.3		3.5		6.2		4.7	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B13. Analysis of variance for population 4 grown at Mount Pleasant, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	11589.9	ns	0.3	ns	2.9	ns	0.0	ns	6.2	ns	8.1	ns
Genotypes	53	66199.1	**	11.0	**	48.2	**	0.3	**	107.7	**	384.6	**
HONL	26	81825.9	*	15.5	**	52.9	**	0.4	**	118.6	**	87.4	**
NONL	26	36507.5	*	6.7	**	39.3	ns	0.2	ns	99.4	**	56.7	**
HONL vs NONL	1	431883.7	**	3.7	ns	155.8	**	0.3	ns	41.7	*	16635.9	**
Error	53	24898.4		1.3		20.2		0.2		6.0		15.1	
CV (%)§§		4.0		3.8		4.3		28.7		1.7		1.2	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	8.6	ns	10.0	ns	1.2	ns	1084.3	ns	733.2	ns	5.7	ns
Genotypes	53	137.8	**	680.4	**	34.5	**	168353.7	**	129786.1	**	398.8	**
HONL	26	46.1	**	8.6	*	14.1	**	529.1	ns	336.5	ns	24.9	**
NONL	26	14.7	*	12.0	**	14.3	*	986.4	ns	821.4	ns	15.5	**
HONL vs NONL	1	5723.2	**	35526.8	**	1088.1	**	8883343.2	**	6848557.2	**	20084.6	**
Error	53	6.1		3.9		3.8		416.5		359.7		4.7	
CV (%)§§		1.3		2.5		4.7		3.8		6.7		4.2	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B14. Analysis of variance for population 5 grown at Atlantic, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	25860.3	ns	2.1	ns	29.0	ns	0.5	ns	266.0	*	1409.1	**
Genotypes	53	166367.8	**	22.3	**	83.9	**	0.4	ns	184.9	**	455.8	**
HONL	26	141986.2	**	18.8	**	72.8	**	0.4	ns	142.9	**	127.6	**
NONL	26	95310.0	ns	23.5	**	81.3	**	0.3	ns	211.9	**	91.2	**
HONL vs NONL	1	2647792.8	**	80.1	**	440.8	**	0.1	ns	575.5	**	18468.4	**
Error	53	47821.8		1.2		25.1		0.2		41.6		20.6	
CV (%)§§		6.0		3.6		4.7		29.0		4.0		1.3	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	204.7	**	15.2	*	0.1	ns	6.3	ns	4.0	ns	3.0	ns
Genotypes	53	151.0	**	787.7	**	28.1	**	172773.3	**	131432.5	**	522.8	**
HONL	26	81.6	**	13.0	**	17.1	**	428.5	*	164.6	ns	23.7	**
NONL	26	67.4	**	20.1	**	22.1	**	1062.7	**	747.9	**	28.4	**
HONL vs NONL	1	4128.0	**	40891.7	**	468.8	**	9118214.5	**	6942199.0	**	26351.6	**
Error	53	5.6		2.6		1.7		276.7		205.5		5.4	
CV (%)§§		1.3		2.0		3.1		3.1		5.1		4.1	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B15. Analysis of variance for population 5 grown at Hedrick, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	653271.1	**	6.3	ns	13.9	ns	1.3	*	300.0	**	29.9	ns
Genotypes	53	123923.4	**	28.2	**	74.6	**	0.3	ns	177.0	**	570.5	**
HONL	26	86387.3	ns	23.7	**	75.5	**	0.3	ns	172.9	**	98.7	**
NONL	26	77054.7	ns	22.7	**	74.1	ns	0.3	*	184.0	**	120.0	**
HONL vs NONL	1	2318450.4	**	286.8	**	63.6	ns	0.3	ns	99.6	ns	24552.7	**
Error	53	51506.0		1.8		38.7		0.3		30.5		17.1	
CV (%)§§		6.0		5.1		6.8		33.8		3.6		1.2	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	62.0	**	1.8	ns	0.6	ns	57.8	ns	65.3	ns	2.1	ns
Genotypes	53	189.5	**	923.9	**	48.1	**	172392.5	**	128033.7	**	520.1	**
HONL	26	34.8	**	11.8	**	27.9	**	579.5	**	308.8	**	18.6	**
NONL	26	44.6	**	21.9	**	20.8	**	559.9	**	451.8	**	22.1	**
HONL vs NONL	1	7977.4	**	48091.1	**	1281.3	**	9107176.3	**	6766009.5	**	26508.0	**
Error	53	4.2		2.1		3.0		141.1		96.4		5.4	
CV (%)§§		1.1		1.8		3.7		2.2		3.6		4.5	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B16. Analysis of variance for population 5 grown at Mount Pleasant, IA, in 2011.

Sources of variation†	df	Mean Squares											
		Yield‡		Maturity§		Height¶		Lodging#		Seed wt.††		Protein‡‡	
Replications	1	1080100.0	**	12.7	**	8.6	ns	0.1	ns	412.2	**	73.8	ns
Genotypes	53	63069.9	ns	31.5	**	76.7	**	0.2	**	111.6	**	555.8	**
HONL	26	57834.2	ns	25.5	**	61.5	**	0.2	ns	81.6	**	125.7	**
NONL	26	63019.5	ns	30.9	**	94.7	**	0.2	*	140.2	**	137.0	**
HONL vs NONL	1	200509.8	ns	205.6	**	1.1	ns	0.0	ns	145.6	**	22628.8	**
Error	53	59168.1		1.5		22.9		0.1		10.8		35.2	
CV (%)§§		6.5		4.7		4.7		27.6		2.2		1.7	

Sources of variation†	df	Mean Squares											
		Oil‡‡		Palmitate¶¶		Stearate¶¶		Oleate¶¶		Linoleate¶¶		Linolenate¶¶	
Replications	1	19.2	ns	10.1	ns	0.1	ns	113.7	ns	30.0	ns	0.6	ns
Genotypes	53	179.8	**	878.3	**	52.3	**	166755.1	**	124397.2	**	466.1	**
HONL	26	38.3	**	9.4	**	21.3	**	245.3	ns	132.1	ns	11.6	**
NONL	26	47.4	**	17.9	**	32.5	**	1606.7	**	1411.9	**	22.2	**
HONL vs NONL	1	7303.0	**	45839.1	**	1371.7	**	8789864.8	**	6552910.1	**	23828.3	**
Error	53	7.7		4.2		4.3		303.7		223.3		4.0	
CV (%)§§		1.4		2.5		4.7		3.2		5.5		4.0	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Maturity measured as days after 31 August.

¶ = Height measured as the distance from the soil surface to the terminal node in cm.

= Lodging scores ranged from 1 (all plants erect) to 5 (all plants prostrate).

†† = Seed weight measured as mg sd⁻¹.

‡‡ = Protein and oil measured as g kg⁻¹ on a 13 g kg⁻¹-moisture basis.

§§ = Coefficient of variation.

¶¶ = Fatty esters measured as g kg⁻¹.

Table B17. Analysis of variance for yield of three populations grown at Delphos, OH, in 2011

Sources of variation†	df	Mean Squares		
		Population 3 Yield‡	Population 4 Yield‡	Population 5 Yield‡
Replications	1	650381.1 **	1595100.7 **	704350.0 *
Genotypes	53	134066.2 **	88294.4 **	234965.1 **
HONL	26	67651.7 *	102011.3 ns	278874.0 **
NONL	26	158600.1 **	53584.0 **	181829.3 ns
HONL vs NONL	1	1222961.6 **	634125.5 **	474867.1 *
Error	53	35309.3	40848.6	112538.9
CV (%)§		5.1	5.1	9.8

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Coefficient of variation.

Table B18. Analysis of variance for yield of population 5 grown at Wyoming, IL, in 2011.

Sources of variation†	df	Mean Squares	
		Yield‡	
Replications	1	65.2	ns
Genotypes	53	190875.1	**
HONL	26	118145.6	**
NONL	26	211057.7	ns
HONL vs NONL	1	1557096.6	**
Error	53	86059.5	
CV (%)§		6.1	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Yield measured as kg ha⁻¹.

§ = Coefficient of variation.

Table B19. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 1 grown at Pocahontas, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3648	29	2.0	109	135	365	168	66	39	817	28	50
2	HONL	3231	29	2.5	112	129	368	163	64	39	803	39	54
3	HONL	3443	29	2.0	113	140	367	165	64	38	808	35	54
4	HONL	3376	29	2.0	107	130	360	167	65	41	803	35	55
5	HONL	3726	29	2.0	117	134	363	167	67	41	800	38	53
6	HONL	3551	29	2.0	109	142	362	163	64	40	815	30	49
7	HONL	3342	28	2.0	109	130	361	167	67	37	802	40	53
8	HONL	3171	30	3.0	118	137	362	163	68	39	800	38	54
9	HONL	3423	29	3.0	109	136	371	166	64	36	815	32	52
10	HONL	3238	29	3.0	112	151	370	164	67	37	813	33	50
11	HONL	3732	28	2.0	99	149	369	169	67	37	817	31	47
12	HONL	2993	31	2.5	117	132	364	160	67	41	793	41	58
13	HONL	2747	32	2.5	116	126	368	156	66	38	773	56	66
14	HONL	3188	31	2.5	108	136	368	163	68	37	809	34	52
15	HONL	2993	30	2.0	122	125	365	163	63	37	803	41	55
16	HONL	3228	29	2.5	116	141	366	169	66	40	806	35	52
17	HONL	3131	29	2.0	116	135	362	167	65	37	812	36	50
18	HONL	3067	29	3.0	113	133	364	166	64	40	807	35	55
19	HONL	3242	28	3.0	103	117	356	172	66	37	815	32	48

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B19. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3356	31	2.5	112	128	370	159	65	40	813	31	51
21	HONL	3087	30	2.5	113	135	372	160	70	39	793	42	55
22	HONL	3591	29	2.5	111	135	370	163	61	37	817	31	53
23	HONL	3406	29	2.0	112	143	358	167	65	41	805	36	53
24	HONL	3231	29	2.5	105	129	362	169	59	41	820	31	47
25	HONL	3793	29	2.0	111	136	359	171	66	37	806	38	53
26	HONL	3544	29	2.5	116	134	361	166	67	41	799	38	54
27	HONL	3131	30	2.5	114	143	364	172	65	39	802	41	53
28	NONL	3416	29	2.5	112	139	337	181	91	41	244	543	81
29	NONL	3342	29	2.5	108	130	335	181	94	43	308	479	76
30	NONL	3137	28	3.5	100	127	341	170	98	44	252	522	84
31	NONL	3447	29	2.0	107	132	340	176	98	42	238	535	86
32	NONL	3100	29	2.5	116	146	345	177	97	40	271	513	78
33	NONL	3551	28	2.0	104	132	332	180	96	43	274	512	75
34	NONL	3120	32	2.5	122	167	352	172	97	42	256	528	77
35	NONL	3131	31	2.5	104	137	348	171	100	45	257	517	80
36	NONL	3689	29	2.0	111	145	339	173	98	40	238	537	86
37	NONL	3416	29	2.0	111	154	343	176	95	40	250	532	82
38	NONL	2915	31	2.5	114	138	351	170	100	39	220	549	92
39	NONL	3094	31	2.0	119	154	351	171	100	41	257	517	84
40	NONL	3383	28	2.0	104	138	343	183	103	45	258	518	76
41	NONL	3413	30	2.0	116	148	342	181	102	40	242	533	82

Table B19. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3517	29	2.0	109	141	342	183	97	41	292	492	77
43	NONL	3692	25	2.0	111	135	335	187	96	42	268	517	77
44	NONL	3510	28	2.0	104	138	340	182	96	43	290	497	75
45	NONL	3450	29	2.0	107	139	347	174	96	41	253	531	79
46	NONL	3275	29	2.0	113	137	345	175	98	44	255	526	77
47	NONL	3470	30	2.0	116	134	336	177	103	40	250	521	84
48	NONL	3346	29	2.0	113	146	347	172	104	44	240	525	87
49	NONL	2996	30	2.5	112	118	344	174	99	42	251	524	85
50	NONL	3510	29	2.0	113	143	345	176	99	43	241	533	84
51	NONL	3023	33	2.0	121	139	345	169	105	43	234	536	82
52	NONL	3164	30	2.5	113	133	337	174	101	43	266	508	82
53	NONL	3510	30	2.0	107	137	340	176	97	39	262	515	85
54	NONL	3443	28	2.0	111	133	346	180	94	42	257	525	81
SEM		141	1	0	3	3	2	2	1	1	13	11	2
LSD 0.05		400	1	1	8	7	7	5	4	2	36	31	6
LSD 0.01		533	2	1	10	9	9	7	5	3	48	41	8
YR25C09	Parent	3484	29	2.5	108	149	367	162	64	39	813	32	51
92Y30	Parent	3658	28	2.0	103	130	332	190	98	42	268	516	75
SP16410155	Check	2320	32	4.5	108	134	386	141	68	45	778	86	24
YB26P09	Check	3124	29	3.0	110	133	366	172	106	52	238	525	79
92Y51	Check	3480	29	2.0	109	137	343	180	100	56	246	521	77
92Y80	Check	3302	29	2.0	108	132	355	176	112	46	217	544	81

Table B20. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 1 grown at Royal, IA, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging scores [§]	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3447	26	2.0	117	137	360	169	63	39	828	25	44
2	HONL	3396	28	2.0	119	132	360	164	67	40	800	38	55
3	HONL	3302	28	2.0	118	145	361	166	65	39	807	34	55
4	HONL	3591	25	2.0	119	135	351	172	68	42	779	53	56
5	HONL	3437	27	2.0	121	138	364	167	68	44	797	37	54
6	HONL	3621	25	1.5	118	141	351	167	64	41	817	28	49
7	HONL	3376	26	2.5	116	139	358	165	67	37	805	38	53
8	HONL	2999	29	2.5	122	140	352	166	65	42	807	33	53
9	HONL	3477	27	2.5	118	138	362	167	65	38	811	31	54
10	HONL	3097	29	2.5	122	152	368	160	67	40	806	34	52
11	HONL	3500	26	1.5	113	144	368	167	69	37	815	31	48
12	HONL	3127	29	2.0	123	132	362	164	67	42	796	39	56
13	HONL	2734	30	3.0	127	133	362	154	65	40	783	48	63
14	HONL	2986	29	2.5	117	133	368	161	68	39	808	31	53
15	HONL	2848	28	2.5	128	133	362	165	63	38	804	39	55
16	HONL	3285	27	2.0	127	140	362	173	66	41	808	33	52
17	HONL	3490	26	1.5	121	138	357	169	64	39	812	33	51
18	HONL	3470	25	2.5	122	135	366	166	63	41	814	29	52
19	HONL	3363	28	2.0	118	128	356	170	65	38	819	28	49

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table B20. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3080	29	2.0	122	134	363	163	66	39	806	34	54
21	HONL	2983	27	1.5	118	136	370	162	70	39	798	38	54
22	HONL	3278	29	2.5	123	136	363	163	61	40	813	32	54
23	HONL	3289	28	2.5	121	143	359	169	65	41	809	32	52
24	HONL	3026	28	2.5	118	129	358	167	63	40	806	38	52
25	HONL	3231	29	2.5	117	148	356	168	66	36	811	34	53
26	HONL	3319	26	2.5	124	135	360	168	67	42	801	37	52
27	HONL	2983	26	2.5	124	142	360	172	65	40	801	39	54
28	NONL	3591	26	2.0	118	140	335	182	92	43	245	538	81
29	NONL	3551	26	2.0	121	133	331	184	93	43	268	515	81
30	NONL	3473	28	2.5	118	133	328	176	96	45	239	533	86
31	NONL	3457	27	2.0	117	136	333	178	99	44	232	538	87
32	NONL	3433	28	2.0	121	149	338	180	96	44	260	519	81
33	NONL	3228	27	3.5	111	130	328	182	97	46	270	510	77
34	NONL	3322	28	2.0	135	164	351	170	95	42	249	531	81
35	NONL	3211	29	2.0	117	142	344	173	100	43	256	518	81
36	NONL	3588	29	1.5	119	145	344	174	98	42	242	531	86
37	NONL	3339	28	2.0	119	149	343	177	96	40	257	527	79
38	NONL	2781	29	2.5	128	141	347	172	99	40	234	539	88
39	NONL	3131	29	2.0	121	157	349	170	100	44	236	536	83
40	NONL	3336	26	2.0	121	137	341	184	105	44	271	502	77
41	NONL	3322	29	2.5	126	141	341	179	101	41	251	523	83

Table B20. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3500	27	2.0	117	146	346	180	100	45	241	531	83
43	NONL	3813	27	2.0	121	144	337	183	96	44	290	490	80
44	NONL	3359	28	2.5	121	140	339	184	98	43	267	514	78
45	NONL	3547	26	2.0	118	148	341	173	96	44	239	533	87
46	NONL	3083	27	2.0	119	136	343	176	97	46	257	517	83
47	NONL	3352	31	2.0	121	132	334	177	101	41	273	500	84
48	NONL	3413	26	2.0	118	148	343	176	104	45	240	524	86
49	NONL	3144	28	2.5	116	119	327	181	100	43	225	545	87
50	NONL	3322	29	1.5	122	143	344	173	98	42	246	527	87
51	NONL	2936	31	1.5	127	137	338	172	103	45	236	528	87
52	NONL	2952	30	2.5	124	132	331	179	98	44	269	508	80
53	NONL	3416	28	2.5	119	153	333	177	99	42	236	536	86
54	NONL	3453	27	2.0	118	138	340	181	96	41	259	520	85
SEM		129	1	0	2	4	2	1	1	1	9	8	2
LSD 0.05		365	2	1	7	10	7	4	3	3	26	23	4
LSD 0.01		486	3	1	9	14	9	5	5	4	34	30	6
YR25C09	Parent	3305	28	1.5	122	147	365	162	65	41	810	32	52
92Y30	Parent	3830	26	2.0	113	131	327	191	99	43	264	517	76
SP16410155	Check	2434	31	3.0	122	140	370	147	66	44	780	84	25
YB26P09	Check	3396	28	2.0	118	139	355	177	105	54	233	528	80
92Y51	Check	3813	26	2.0	122	144	335	185	102	54	248	520	76
92Y80	Check	3231	28	2.0	113	137	357	177	108	51	243	518	80

Table B21. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 1 grown at Conrad, IA, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging scores [§]	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4708	20	2.0	105	152	367	183	61	37	847	17	37
2	HONL	4573	23	2.5	111	141	357	179	59	36	833	29	43
3	HONL	4586	19	2.0	107	150	358	179	60	37	835	25	43
4	HONL	4287	18	2.0	109	140	348	187	64	39	823	27	46
5	HONL	4516	19	2.0	105	140	363	180	61	38	830	27	44
6	HONL	4180	19	2.5	99	144	354	182	59	38	844	19	40
7	HONL	4452	20	2.0	105	144	355	183	61	36	833	26	43
8	HONL	4375	23	2.0	104	153	357	180	62	38	832	25	43
9	HONL	4543	22	2.5	112	151	358	184	61	35	839	21	42
10	HONL	4590	23	2.0	100	166	363	181	57	36	843	23	41
11	HONL	4422	18	2.0	99	155	366	182	63	37	811	51	38
12	HONL	4445	26	2.5	107	134	363	172	63	39	801	50	46
13	HONL	4519	29	2.5	109	148	357	178	58	37	826	30	47
14	HONL	4442	30	2.0	114	147	372	171	64	38	825	26	45
15	HONL	4328	28	3.0	117	142	357	183	61	38	824	30	46
16	HONL	4233	23	2.5	114	149	362	180	58	39	841	22	40
17	HONL	4344	21	2.5	116	148	356	184	62	37	836	23	42
18	HONL	4317	20	2.0	102	137	359	180	63	36	814	42	44
19	HONL	4526	25	2.0	112	134	351	186	61	40	819	39	41

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table B21. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	4492	29	3.0	116	150	375	171	57	38	845	19	39
21	HONL	4149	26	2.0	110	141	363	175	61	36	832	26	43
22	HONL	4553	21	2.0	105	144	362	180	59	38	837	24	41
23	HONL	4603	23	2.0	110	157	357	181	62	37	818	38	44
24	HONL	4513	20	3.0	104	142	357	186	58	38	831	29	43
25	HONL	4768	24	2.0	108	142	360	180	62	37	826	30	44
26	HONL	4617	20	2.0	109	144	358	183	63	41	811	40	44
27	HONL	4304	22	2.5	119	160	359	186	63	37	837	23	39
28	NONL	4630	16	2.5	105	159	335	194	91	38	240	555	76
29	NONL	4153	17	2.0	119	135	329	199	90	37	287	510	76
30	NONL	4412	22	2.5	107	140	327	195	93	42	265	526	73
31	NONL	4623	21	2.0	107	143	330	195	94	40	282	510	75
32	NONL	4365	21	2.0	108	151	338	193	96	40	292	502	69
33	NONL	4684	19	2.0	99	143	320	197	95	42	276	519	68
34	NONL	4751	25	2.0	103	182	345	190	91	42	279	521	67
35	NONL	4627	28	2.0	112	157	345	188	97	43	270	518	72
36	NONL	4738	23	2.0	107	151	338	189	94	37	247	545	76
37	NONL	4576	21	2.0	112	157	339	192	94	39	272	523	71
38	NONL	4385	26	2.0	114	159	340	191	94	38	240	553	75
39	NONL	4570	25	2.0	107	165	344	189	98	41	250	536	73
40	NONL	4328	17	2.0	100	149	331	201	104	43	265	519	68
41	NONL	4650	26	2.5	113	158	337	194	100	41	257	528	75

Table B21. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4398	17	2.0	105	157	341	194	95	41	312	485	67
43	NONL	4280	15	2.0	104	151	328	202	99	41	247	541	72
44	NONL	4402	17	2.0	107	146	330	200	93	39	254	543	70
45	NONL	4550	18	2.0	107	154	339	189	89	40	285	516	70
46	NONL	4284	17	2.0	108	145	333	192	96	42	262	531	69
47	NONL	4869	26	2.0	108	146	328	192	99	40	281	506	74
48	NONL	4570	18	2.0	107	160	339	189	101	42	275	509	72
49	NONL	4724	23	2.0	108	133	321	197	91	41	283	510	76
50	NONL	4802	24	2.0	111	156	340	193	95	41	275	518	70
51	NONL	4502	31	2.0	117	156	333	191	100	43	266	517	73
52	NONL	4563	26	2.5	113	148	324	195	98	42	248	541	71
53	NONL	4778	23	2.0	105	151	335	193	96	41	266	522	74
54	NONL	4580	20	2.0	100	142	329	198	92	37	257	542	72
SEM		90	1	0	5	2	2	1	2	1	15	13	2
LSD 0.05		256	2	1	14	6	7	4	5	4	42	37	5
LSD 0.01		342	3	1	19	8	9	6	6	5	56	50	6
YR25C09	Parent	4274	21	2.0	103	155	369	172	59	37	841	22	40
92Y30	Parent	4637	17	2.5	99	137	322	209	100	40	262	527	71
SP16410155	Check	3961	33	2.5	100	163	368	167	65	41	797	75	22
YB26P09	Check	4792	24	2.5	114	148	350	192	103	51	248	525	72
92Y51	Check	4338	20	2.0	99	155	330	200	98	52	261	520	69
92Y80	Check	4805	25	2.0	103	155	353	192	108	43	245	530	73

Table B23. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 2 grown at Pocahontas, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3275	29	2.0	111	146	380	166	65	49	803	32	50
2	HONL	3167	29	2.0	103	146	384	154	66	47	785	44	57
3	HONL	3366	32	2.0	105	147	376	161	73	41	797	36	51
4	HONL	3198	30	2.0	102	152	374	163	66	46	800	36	52
5	HONL	3201	30	2.0	111	155	374	160	62	43	810	34	50
6	HONL	3204	31	2.0	114	143	370	162	70	46	790	40	53
7	HONL	3188	32	2.0	108	146	379	156	63	46	784	46	60
8	HONL	3588	29	2.0	105	149	371	172	69	46	811	26	46
9	HONL	3127	31	2.0	108	134	372	162	59	50	794	40	56
10	HONL	3477	28	2.0	104	143	365	171	67	47	801	34	50
11	HONL	3420	29	2.0	103	142	373	165	58	50	803	36	52
12	HONL	3376	29	2.5	104	139	372	166	66	44	804	33	51
13	HONL	3174	29	2.5	108	158	376	162	63	42	811	34	50
14	HONL	3440	30	2.0	113	145	374	165	59	46	811	33	50
15	HONL	3134	31	2.0	108	138	379	162	68	41	803	36	52
16	HONL	3514	30	2.5	109	144	373	164	65	42	805	35	53
17	HONL	2751	33	3.5	108	132	373	151	63	43	803	35	55
18	HONL	3218	33	2.0	108	131	363	160	65	49	774	48	62
19	HONL	3578	29	2.0	102	145	367	162	62	46	802	36	53

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B23. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3171	31	2.0	105	134	375	156	65	50	779	45	59
21	HONL	3043	31	3.0	113	140	361	164	61	48	802	37	52
22	HONL	3258	30	2.0	108	146	374	163	65	46	798	37	53
23	HONL	2972	33	2.0	122	134	372	151	69	51	781	54	45
24	HONL	3346	29	2.5	105	141	375	162	66	46	792	40	54
25	HONL	3268	32	3.0	107	140	369	166	60	43	808	36	53
26	HONL	3376	29	2.0	109	151	379	168	63	41	800	47	48
27	HONL	3658	30	2.0	105	142	368	167	70	48	790	38	55
28	NONL	3242	28	3.5	111	140	346	180	103	46	229	541	81
29	NONL	3480	29	2.0	114	148	353	173	98	45	221	550	85
30	NONL	3413	32	2.5	112	146	351	167	99	44	235	536	86
31	NONL	3628	29	2.0	112	144	336	180	100	50	227	539	83
32	NONL	3393	29	2.0	116	136	341	178	104	44	219	549	84
33	NONL	3618	27	2.0	94	144	347	178	105	50	234	527	85
34	NONL	3231	30	2.5	114	153	354	174	100	46	253	525	77
35	NONL	3403	30	2.0	117	143	354	168	93	46	231	542	88
36	NONL	3554	29	2.0	108	143	355	172	104	49	232	534	81
37	NONL	3241	30	2.5	111	149	352	171	106	44	225	541	83
38	NONL	3726	29	2.0	104	146	338	175	102	48	236	528	85
39	NONL	3235	32	2.5	102	142	347	172	98	50	209	556	86
40	NONL	3807	29	1.9	107	154	345	177	105	47	251	519	77
41	NONL	3665	29	2.0	109	142	351	172	101	43	239	541	75

Table B23. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3521	29	2.0	100	146	346	176	99	52	224	542	84
43	NONL	3473	29	2.0	107	157	357	171	102	42	252	524	80
44	NONL	3796	29	2.0	109	138	338	186	98	53	221	545	83
45	NONL	3386	30	2.5	112	139	344	172	94	47	215	558	86
46	NONL	3440	30	2.0	114	154	352	176	97	53	265	500	84
47	NONL	3615	32	2.0	111	148	349	167	98	48	247	520	86
48	NONL	3581	31	2.0	105	140	346	175	98	43	214	561	84
49	NONL	3477	29	2.0	111	153	348	181	98	44	238	539	79
50	NONL	3759	28	2.0	107	141	341	186	101	51	228	538	80
51	NONL	3796	29	2.5	111	144	343	181	100	49	241	530	79
52	NONL	3584	29	2.0	108	140	336	179	96	49	238	534	83
53	NONL	3315	29	2.5	109	143	358	173	98	45	299	479	78
54	NONL	3544	32	2.0	114	139	337	174	97	45	256	517	84
SEM		137	1	0	2	2	3	2	1	1	9	8	1
LSD 0.05		388	2	1	7	6	8	5	4	4	25	22	4
LSD 0.01		517	2	1	9	8	11	7	6	5	34	29	6
YR25C09	Parent	3584	29	2.0	108	151	366	164	59	40	824	29	48
YB26P09	Parent	3447	29	2.5	112	137	353	180	103	49	227	541	81
SP16410155	Check	2535	31	3.5	107	140	378	147	67	48	773	88	24
92Y30	Check	3729	28	2.0	105	133	328	193	99	42	250	532	77
92Y51	Check	3722	29	2.0	104	143	336	186	99	54	237	530	79
92Y80	Check	3551	29	2.5	104	139	349	182	110	47	216	542	84

Table B24. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 2 grown at Royal, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3127	28	2.0	124	150	379	162	67	49	796	35	53
2	HONL	3305	30	2.0	113	147	378	154	67	51	779	43	59
3	HONL	3013	30	2.5	116	146	375	161	72	46	793	35	55
4	HONL	2989	30	1.0	117	150	372	164	68	44	798	35	54
5	HONL	3201	29	3.0	118	150	373	158	62	44	807	34	53
6	HONL	3016	28	2.0	121	138	371	157	72	50	779	42	57
7	HONL	2522	30	3.0	118	138	383	152	64	45	788	42	61
8	HONL	3423	26	2.0	123	157	373	169	71	50	781	46	52
9	HONL	3009	30	2.5	113	134	377	156	64	49	785	41	61
10	HONL	3581	26	2.0	122	142	369	166	69	43	787	42	58
11	HONL	3151	28	2.0	117	138	372	159	64	45	782	46	62
12	HONL	3077	29	2.5	121	139	372	158	70	45	795	35	55
13	HONL	2912	28	2.0	118	155	374	161	63	41	807	35	53
14	HONL	3208	28	2.0	123	140	371	163	61	49	795	39	55
15	HONL	2946	29	2.0	116	136	375	160	72	46	786	39	57
16	HONL	3124	29	2.0	119	141	375	160	64	43	793	45	55
17	HONL	2209	31	3.5	117	129	370	149	67	43	791	40	58
18	HONL	2535	31	2.5	114	135	371	156	65	48	781	44	61
19	HONL	3097	29	2.0	114	140	364	159	63	42	793	41	60

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B24. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	2892	28	2.5	119	135	368	153	66	51	772	49	62
21	HONL	2996	31	3.0	124	142	363	162	64	47	779	55	55
22	HONL	3319	29	2.5	121	145	370	163	66	48	792	37	56
23	HONL	3292	32	2.0	130	128	374	150	69	52	782	42	53
24	HONL	3161	28	2.0	116	143	377	155	72	49	776	42	61
25	HONL	3107	31	2.5	117	141	363	169	64	46	799	34	56
26	HONL	2949	29	2.5	118	150	376	161	66	44	801	35	53
27	HONL	3272	30	2.0	112	140	365	163	71	45	781	43	60
28	NONL	2905	28	3.0	117	139	350	173	100	47	231	536	85
29	NONL	3117	29	2.0	121	145	353	169	98	48	278	493	82
30	NONL	2983	31	2.0	122	145	353	164	99	43	240	531	87
31	NONL	3477	28	2.5	123	142	331	179	103	51	259	506	81
32	NONL	3400	27	2.5	122	136	341	176	110	46	221	540	83
33	NONL	3837	27	2.0	111	152	352	175	106	53	237	519	84
34	NONL	3057	29	2.5	127	152	358	171	103	47	241	530	79
35	NONL	3124	30	2.0	131	146	361	162	97	47	226	536	93
36	NONL	3265	28	2.5	113	141	352	174	103	50	222	540	85
37	NONL	3184	28	2.0	117	147	355	165	107	46	238	528	81
38	NONL	3292	29	2.0	116	142	344	170	103	46	229	535	86
39	NONL	3006	30	2.5	123	142	344	173	97	50	279	492	83
40	NONL	3779	26	1.5	119	160	349	172	106	50	256	507	82
41	NONL	3433	27	2.0	121	141	355	167	104	44	233	537	82

Table B24. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3648	29	1.0	119	147	346	172	100	49	221	544	86
43	NONL	3544	27	2.5	118	157	357	172	107	43	227	537	86
44	NONL	3487	29	2.0	121	132	340	181	100	54	223	540	83
45	NONL	3268	31	2.0	121	135	349	165	95	49	219	547	90
46	NONL	3087	30	2.0	124	150	356	171	96	52	270	496	86
47	NONL	3235	30	2.0	119	146	350	168	101	48	233	533	84
48	NONL	3201	30	2.0	118	132	348	173	98	43	208	560	90
49	NONL	3527	27	2.5	119	153	350	174	98	45	240	533	84
50	NONL	3709	27	3.0	118	138	346	176	107	53	225	533	82
51	NONL	3352	28	1.5	117	143	346	174	102	49	234	529	85
52	NONL	3188	29	2.5	121	133	337	172	99	51	223	541	85
53	NONL	3430	28	2.5	128	147	359	168	99	44	235	533	89
54	NONL	3346	31	2.0	125	138	339	172	102	44	237	530	87
SEM		122	1	0	3	2	2	2	1	1	14	12	2
LSD 0.05		346	2	1	8	6	6	5	4	4	38	34	5
LSD 0.01		461	3	1	11	8	8	6	5	5	51	45	7
YR25C09	Parent	3379	27	2.0	119	147	366	160	66	40	806	34	53
YB26P09	Parent	3420	28	2.0	118	140	358	174	106	50	229	533	82
SP16410155	Check	2646	32	4.0	118	139	365	146	68	44	774	87	26
92Y30	Check	3937	26	2.0	119	135	333	188	101	43	260	517	79
92Y51	Check	3746	26	2.5	122	147	334	185	101	53	244	523	78
92Y80	Check	3349	29	2.0	117	141	354	178	111	48	220	534	86

Table B24. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 2 grown at Conrad, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4553	25	2.0	113	158	370	181	62	43	832	23	40
2	HONL	4519	28	2.0	112	157	371	174	62	42	821	29	46
3	HONL	4563	29	2.0	108	157	375	176	67	42	821	27	42
4	HONL	4200	26	2.0	107	171	373	177	61	44	829	25	39
5	HONL	4334	27	2.0	100	163	375	174	55	36	849	21	38
6	HONL	4341	29	2.0	113	151	374	174	67	44	816	26	45
7	HONL	4223	34	2.0	113	152	380	170	56	41	826	31	45
8	HONL	4351	21	2.0	113	158	367	184	68	45	814	31	41
9	HONL	4244	29	2.5	111	144	371	179	56	45	826	29	44
10	HONL	4476	18	2.0	114	155	373	180	61	43	834	22	40
11	HONL	4338	28	2.0	114	155	371	176	59	41	817	33	50
12	HONL	4244	23	2.5	111	150	370	178	63	39	831	24	42
13	HONL	4220	30	2.0	113	172	368	176	57	40	834	26	42
14	HONL	4580	28	2.0	117	154	369	180	53	46	839	22	40
15	HONL	4351	29	2.0	111	153	376	175	64	40	831	24	40
16	HONL	4637	26	2.5	113	158	375	176	59	42	834	23	42
17	HONL	4210	32	3.0	118	146	363	169	60	41	828	27	43
18	HONL	4267	32	2.5	108	160	361	174	63	43	809	35	49
19	HONL	4782	27	2.5	95	148	369	175	59	38	829	27	47

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B25. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	4324	30	2.0	116	149	366	170	60	44	820	32	44
21	HONL	4348	32	2.5	108	149	365	175	61	46	818	29	46
22	HONL	4422	30	2.0	109	158	370	180	62	42	828	24	42
23	HONL	4233	34	2.0	127	147	373	164	67	45	807	45	35
24	HONL	4539	23	2.0	103	151	376	173	63	41	825	26	44
25	HONL	4203	30	2.0	100	151	369	178	55	41	832	28	44
26	HONL	4318	24	2.0	107	168	378	176	62	40	836	22	39
27	HONL	4623	27	2.0	99	155	369	178	64	46	821	26	43
28	NONL	4459	23	2.5	104	145	344	190	102	41	239	545	73
29	NONL	4506	25	2.0	114	153	343	188	95	45	276	513	71
30	NONL	4681	30	2.5	104	159	354	178	96	42	246	539	77
31	NONL	4529	25	2.0	109	157	332	194	101	47	235	542	75
32	NONL	4422	22	2.0	108	150	342	189	106	41	231	547	75
33	NONL	4479	17	2.0	107	158	349	186	106	48	254	514	78
34	NONL	4560	28	2.0	112	163	352	189	99	41	274	517	67
35	NONL	4671	29	2.0	103	156	350	183	96	43	253	531	76
36	NONL	4704	24	2.5	104	157	347	188	100	40	228	557	74
37	NONL	4422	29	2.0	109	156	343	187	106	42	233	544	75
38	NONL	4822	28	2.0	104	161	343	184	102	44	264	515	74
39	NONL	4788	29	2.5	117	154	334	194	93	47	263	523	73
40	NONL	4624	20	2.0	108	160	349	189	102	46	287	497	69
41	NONL	4785	22	2.0	88	151	345	184	102	41	245	540	71

Table B25. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4348	25	2.5	110	154	342	190	101	46	239	539	75
43	NONL	4788	25	2.0	102	173	354	186	99	42	283	506	69
44	NONL	4738	26	2.5	121	146	337	197	96	50	239	538	76
45	NONL	4593	30	2.0	121	153	343	185	92	45	234	553	76
46	NONL	4597	28	2.0	109	169	351	189	94	48	274	507	76
47	NONL	4610	29	2.0	108	161	347	187	97	45	258	527	72
48	NONL	4657	28	2.0	104	148	337	190	96	39	253	532	79
49	NONL	4502	22	2.0	108	163	346	190	97	43	265	521	73
50	NONL	4435	18	3.0	107	151	331	194	106	44	231	547	73
51	NONL	4755	23	2.0	114	152	344	188	100	47	270	508	75
52	NONL	4465	26	3.0	110	150	337	188	96	44	223	559	77
53	NONL	4519	22	2.0	114	152	346	186	99	42	256	530	73
54	NONL	4855	32	2.0	116	151	333	189	98	41	259	527	74
SEM		97	1	0	5	3	2	1	2	1	13	11	2
LSD 0.05		275	2	1	13	8	6	3	5	4	36	31	5
LSD 0.01		366	3	1	17	11	8	4	7	5	48	42	7
YR25C09	Parent	4418	21	2.5	104	160	365	176	60	37	839	22	41
YB26P09	Parent	4842	23	2.0	110	151	352	191	104	49	250	526	71
SP16410155	Check	4005	33	2.0	103	161	365	168	63	42	802	71	21
92Y30	Check	4697	17	2.0	108	139	326	203	97	40	280	513	70
92Y51	Check	4449	19	2.0	108	156	337	196	97	50	262	525	67
92Y80	Check	4660	24	2.0	108	150	346	194	106	43	245	533	73

Table B26. Mean yield performance of 27 high-oleate and 27 normal-oleate lines from population 2 grown at Princeton, IL, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	
1	HONL	4455	23	HONL	4502	45	NONL	4391	
2	HONL	4674	24	HONL	4748	46	NONL	4422	
3	HONL	4445	25	HONL	4425	47	NONL	5037	
4	HONL	4106	26	HONL	4587	48	NONL	5118	
5	HONL	4405	27	HONL	4620	49	NONL	5054	
6	HONL	4506	28	NONL	4361	50	NONL	4388	
7	HONL	4640	29	NONL	4657	51	NONL	4990	
8	HONL	4120	30	NONL	4879	52	NONL	4553	
9	HONL	4672	31	NONL	4650	53	NONL	4489	
10	HONL	4334	32	NONL	4785	54	NONL	5548	
11	HONL	4677	33	NONL	4932				
12	HONL	4412	34	NONL	5323				
13	HONL	5010	35	NONL	4667	SEM		209	
14	HONL	4590	36	NONL	5000	LSD 0.05		594	
15	HONL	4533	37	NONL	4405	LSD 0.01		791	
16	HONL	4916	38	NONL	4799		YR25C09	Parent	4223
17	HONL	4442	39	NONL	5027		YB26P09	Parent	4866
18	HONL	4659	40	NONL	4623		SP16410155	Check	4499
19	HONL	4657	41	NONL	4876		92Y30	Check	4422
20	HONL	4502	42	NONL	4719		92Y51	Check	4412
21	HONL	4691	43	NONL	4805		92Y80	Check	4623
22	HONL	4381	44	NONL	4687				

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

Table B27. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 3 grown at Cedar Falls, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4097	32	2.0	114	175	374	171	70	34	815	33	47
2	HONL	4119	36	2.5	125	162	371	165	69	35	817	30	48
3	HONL	3887	30	2.0	107	163	366	176	73	40	819	24	45
4	HONL	3998	35	2.0	128	162	372	162	66	34	811	38	50
5	HONL	3732	33	2.0	117	157	373	170	64	34	811	35	55
6	HONL	4119	31	3.0	109	162	369	170	67	34	830	24	44
7	HONL	3931	31	2.5	128	170	369	171	68	34	784	63	50
8	HONL	4230	35	3.0	126	177	369	161	71	37	803	35	53
9	HONL	4116	36	2.0	130	152	373	164	76	38	794	37	53
10	HONL	4133	30	3.0	112	169	374	164	67	36	819	27	50
11	HONL	3954	36	3.0	127	157	366	163	75	36	794	39	56
12	HONL	3931	34	2.0	128	169	369	162	62	38	796	53	50
13	HONL	4264	32	2.0	112	158	364	173	70	37	800	44	48
14	HONL	4563	32	2.5	121	158	367	175	73	40	821	21	42
15	HONL	4660	32	2.0	117	156	370	175	74	38	817	24	46
16	HONL	4193	35	2.5	122	163	375	163	68	35	811	37	50
17	HONL	4102	36	2.5	124	167	370	163	64	36	814	34	51
18	HONL	4082	35	3.0	121	165	379	164	72	36	806	35	50
19	HONL	4059	32	3.0	124	169	371	169	70	35	809	37	50

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B27. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	4647	35	3.0	122	173	373	167	66	33	829	28	46
21	HONL	4112	36	2.0	135	157	365	163	76	35	784	45	59
22	HONL	4156	33	2.0	118	158	364	163	65	37	804	40	53
23	HONL	4428	35	2.0	119	158	371	159	69	36	814	31	49
24	HONL	4247	33	2.5	119	164	368	171	78	37	801	34	50
25	HONL	4516	36	2.5	124	158	369	168	76	37	794	38	54
26	HONL	4405	36	2.5	119	162	375	163	65	34	805	39	56
27	HONL	4465	36	2.5	131	160	377	161	74	37	790	45	53
28	NONL	4609	35	2.0	123	169	347	179	102	40	245	532	83
29	NONL	4721	32	1.5	113	160	343	182	108	40	236	530	86
30	NONL	4748	31	2.0	112	169	345	183	98	38	271	513	80
31	NONL	4859	35	2.0	116	158	342	178	108	40	238	532	82
32	NONL	5057	32	1.5	105	159	348	186	108	40	263	507	82
33	NONL	4412	33	2.0	121	173	367	165	104	42	252	519	83
34	NONL	4926	32	2.0	123	178	358	173	101	42	277	501	79
35	NONL	4657	35	2.0	117	167	354	176	96	36	238	550	84
36	NONL	4539	36	3.0	123	157	335	178	110	41	240	521	89
37	NONL	4718	35	2.0	130	162	349	169	104	39	214	549	92
38	NONL	4549	35	2.0	142	170	347	176	108	40	231	532	88
39	NONL	4768	34	2.0	114	173	348	178	97	41	299	482	80
40	NONL	4190	34	2.0	117	158	344	180	104	36	237	538	85
41	NONL	4829	35	2.0	127	172	352	174	108	39	215	548	90

Table B27. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4795	35	2.0	132	169	352	171	103	40	234	540	83
43	NONL	4513	36	2.0	126	176	354	170	109	38	213	552	87
44	NONL	5185	33	2.0	122	168	343	184	106	40	273	501	79
45	NONL	4637	36	2.5	128	164	347	176	112	40	214	545	92
46	NONL	4506	27	1.5	113	172	348	184	103	41	286	497	73
47	NONL	4724	32	2.0	117	179	359	174	107	43	280	491	80
48	NONL	4398	35	2.0	135	177	359	164	101	37	236	535	91
49	NONL	4546	32	2.0	117	159	351	175	109	40	282	487	82
50	NONL	4671	32	2.0	118	169	350	180	102	39	250	528	80
51	NONL	5024	32	1.5	112	174	348	180	102	39	267	514	77
52	NONL	3837	35	3.0	126	171	350	173	110	40	232	532	86
53	NONL	4499	35	2.0	123	176	353	172	101	39	234	538	85
54	NONL	4745	35	2.0	128	161	342	178	107	37	203	559	93
SEM		178	1	0	4	2	2	1	1	1	14	12	2
LSD 0.05		505	1	1	11	6	5	3	4	2	39	33	6
LSD 0.01		673	2	1	15	8	7	4	5	3	52	44	8
YR25C09	Parent	4143	32	2.0	117	166	377	165	64	38	821	30	48
RJS30006	Parent	4956	33	2.0	124	178	352	177	114	38	238	525	84
SP16410155	Check	3447	35	3.0	118	159	373	160	69	40	775	93	23
92Y30	Check	4475	30	1.5	110	146	341	191	96	37	369	425	73
92Y51	Check	4734	30	2.5	116	156	344	188	102	48	257	516	76
92Y80	Check	4849	34	3.0	113	154	359	182	110	41	218	544	86

Table B28. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 3 grown at Conrad, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4311	22	2.0	111	166	370	180	67	37	827	27	41
2	HONL	4418	32	2.0	112	155	371	170	66	38	833	22	40
3	HONL	4227	19	2.0	97	161	362	184	71	39	830	20	40
4	HONL	4237	33	2.5	102	156	368	172	62	37	830	27	43
5	HONL	4388	27	2.5	113	152	368	177	66	37	789	61	47
6	HONL	4361	21	2.0	108	163	365	177	68	35	812	44	41
7	HONL	4509	19	2.0	102	169	366	179	64	36	846	17	37
8	HONL	4085	34	2.5	114	167	368	165	67	38	823	25	45
9	HONL	4486	32	2.0	119	153	371	171	76	40	811	29	45
10	HONL	4112	20	2.0	109	161	367	174	66	36	828	23	46
11	HONL	4200	34	2.5	118	157	363	175	69	40	822	26	44
12	HONL	4106	29	2.0	121	169	362	174	60	37	829	28	46
13	HONL	4546	24	3.0	128	154	362	179	64	37	842	18	38
14	HONL	4543	21	2.0	113	156	364	182	69	38	814	39	40
15	HONL	4354	23	2.0	105	153	361	183	70	37	824	28	40
16	HONL	4539	34	2.0	105	158	371	172	63	37	829	26	43
17	HONL	4462	30	2.0	114	163	368	172	58	37	841	23	41
18	HONL	4334	29	2.0	122	162	369	176	72	40	814	28	45
19	HONL	4163	22	2.0	113	159	367	177	68	37	821	29	45

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B28. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	4489	28	2.0	113	159	366	176	66	36	844	18	36
21	HONL	4015	34	3.0	113	156	364	168	71	40	806	34	49
22	HONL	4539	25	2.5	111	159	359	173	65	38	819	33	45
23	HONL	4328	32	2.0	117	153	368	166	67	38	820	28	47
24	HONL	4600	26	2.0	116	158	364	177	75	37	814	29	45
25	HONL	4519	32	2.0	112	157	366	176	72	37	818	28	44
26	HONL	4533	34	2.0	118	157	368	172	64	37	825	27	46
27	HONL	4576	33	2.0	102	155	366	171	69	42	819	26	44
28	NONL	4852	30	2.0	108	162	335	188	96	42	276	510	75
29	NONL	4842	24	2.5	112	153	333	188	104	41	242	535	77
30	NONL	4943	19	2.5	107	163	337	188	93	39	279	514	74
31	NONL	4963	30	2.0	107	155	334	184	101	42	278	503	76
32	NONL	4993	21	2.5	102	149	338	192	105	42	280	498	74
33	NONL	4435	28	2.0	114	166	356	177	103	44	271	509	72
34	NONL	4792	26	2.0	105	171	344	183	102	41	270	515	71
35	NONL	4714	28	2.0	117	165	343	186	90	40	270	526	74
36	NONL	4563	31	3.0	117	151	328	187	105	42	272	500	80
37	NONL	4391	34	2.0	118	160	342	179	105	44	228	542	80
38	NONL	4402	30	2.0	135	163	341	184	108	43	241	531	76
39	NONL	4718	31	2.0	123	174	341	187	97	43	264	521	75
40	NONL	4657	30	2.0	118	153	342	185	99	39	313	478	71
41	NONL	4607	32	3.0	124	165	345	185	104	40	229	546	81

Table B28. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4694	32	2.0	118	160	340	180	99	43	255	529	74
43	NONL	4745	33	2.5	122	170	340	185	107	43	241	533	75
44	NONL	5155	25	2.0	100	158	332	194	105	39	230	550	75
45	NONL	4660	32	3.0	119	161	340	184	108	42	232	538	79
46	NONL	4439	19	2.5	113	158	336	194	101	42	276	512	69
47	NONL	4728	26	2.0	105	165	351	183	103	44	318	467	69
48	NONL	4217	34	2.0	111	172	349	175	99	43	239	534	85
49	NONL	4536	24	2.5	108	153	347	182	107	42	267	508	75
50	NONL	4879	21	2.0	116	161	339	189	100	42	263	522	72
51	NONL	4852	22	2.0	103	166	341	186	97	41	265	525	72
52	NONL	4482	33	2.0	130	169	346	179	109	43	251	517	80
53	NONL	4714	31	2.0	116	169	343	180	102	42	289	491	74
54	NONL	4993	32	2.0	100	158	338	186	102	41	259	521	77
SEM		124	1	0	7	2	2	1	1	1	12	11	2
LSD 0.05		353	2	1	19	6	6	3	4	4	34	31	5
LSD 0.01		470	3	1	25	8	8	4	5	6	45	41	6
YR25C09	Parent	4402	23	2.5	104	162	373	171	59	38	842	22	38
RJS30006	Parent	5030	28	2.0	110	172	345	185	111	41	262	512	73
SP16410155	Check	4048	32	2.5	116	160	369	168	63	45	807	64	21
92Y30	Check	4523	16	2.0	105	136	323	206	98	39	275	517	71
92Y51	Check	4408	19	2.0	104	157	337	195	98	53	305	478	66
92Y80	Check	4586	25	2.0	109	152	349	193	109	46	236	533	76

Table B29. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 3 grown at Princeton, IL, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ §	Oil g kg ⁻¹ §	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4428	15	103	181	367	186	67	36	846	16	35
2	HONL	5239	22	111	163	368	182	70	37	842	15	35
3	HONL	4523	13	99	178	369	184	74	36	843	13	33
4	HONL	4835	26	116	170	369	181	64	34	850	16	35
5	HONL	4936	20	108	168	361	187	63	37	848	14	36
6	HONL	4294	16	95	171	370	181	72	33	817	41	36
7	HONL	4220	16	105	186	372	180	68	34	825	38	35
8	HONL	5030	31	122	196	371	172	69	40	839	14	37
9	HONL	4775	25	117	167	368	181	76	37	824	21	42
10	HONL	4435	17	111	189	371	178	66	34	855	11	33
11	HONL	4718	28	131	190	364	183	71	39	813	38	38
12	HONL	4227	17	104	170	360	183	64	33	805	59	37
13	HONL	4623	19	95	168	364	184	69	37	851	11	32
14	HONL	4654	15	105	180	374	183	73	37	846	11	32
15	HONL	5343	15	104	182	374	186	72	39	850	10	29
16	HONL	4916	25	118	171	372	180	66	34	843	19	38
17	HONL	4365	22	109	176	368	177	61	35	857	13	34
18	HONL	4929	22	128	177	368	182	74	41	828	17	39
19	HONL	4745	15	111	179	368	184	66	37	846	16	35

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B29. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ §	Oil g kg ⁻¹ §	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	4983	19	108	188	370	183	64	36	860	9	29
21	HONL	5225	28	137	177	369	178	74	37	825	21	42
22	HONL	4748	16	99	169	370	183	62	41	845	16	36
23	HONL	4708	25	116	167	366	175	66	37	846	14	35
24	HONL	4748	20	113	179	370	182	75	39	834	14	36
25	HONL	5461	24	123	182	367	184	73	39	835	16	37
26	HONL	5044	26	109	178	369	179	67	34	841	19	40
27	HONL	5501	25	118	165	372	179	70	41	836	15	36
28	NONL	4671	21	116	176	356	190	103	44	270	511	72
29	NONL	5151	18	100	175	337	191	106	38	287	497	70
30	NONL	5145	14	104	188	336	194	101	40	272	516	70
31	NONL	5158	20	109	174	337	190	109	41	246	530	73
32	NONL	4825	17	98	174	342	193	108	39	266	516	70
33	NONL	4832	20	112	171	363	180	106	41	291	493	68
34	NONL	5017	16	111	181	344	187	103	39	316	478	63
35	NONL	4718	21	110	173	345	188	96	38	264	529	72
36	NONL	4684	25	109	173	330	194	113	41	258	514	74
37	NONL	5313	29	118	192	342	190	106	41	274	511	66
38	NONL	4694	25	121	189	343	187	109	43	267	509	71
39	NONL	4879	20	119	183	337	193	100	41	282	506	70
40	NONL	4993	23	104	165	339	192	109	36	235	545	73
41	NONL	4973	26	121	191	352	186	107	42	251	526	74

Table B29. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ §	Oil g kg ⁻¹ §	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4815	23	127	170	335	191	105	41	259	526	67
43	NONL	5155	24	108	195	343	191	111	39	252	528	69
44	NONL	5369	20	108	186	332	197	110	40	237	542	70
45	NONL	4950	23	118	176	338	190	112	40	270	504	73
46	NONL	4200	14	103	174	338	196	106	41	258	529	65
47	NONL	4677	18	104	184	346	189	113	42	265	515	65
48	NONL	4862	26	114	204	353	181	102	40	271	511	76
49	NONL	4701	16	104	168	346	187	111	40	322	463	64
50	NONL	4829	17	99	182	337	193	103	39	290	500	67
51	NONL	5367	17	95	187	340	193	101	42	298	496	63
52	NONL	5578	25	118	187	344	186	112	42	259	508	77
53	NONL	5383	23	114	191	348	185	103	40	269	522	66
54	NONL	5235	22	116	179	348	186	104	40	276	509	70
SEM		299	1	4	4	4	2	1	1	11	10	2
LSD 0.05		706	3	11	11	10	5	4	4	33	27	5
LSD 0.01		941	4	14	14	14	7	5	6	43	37	6
YR25C09	Parent	4435	16	107	178	376	173	61	36	851	16	35
RJS30006	Parent	5111	21	112	191	345	192	111	38	270	512	68
SP16410155	Check	4338	30	117	176	364	176	63	41	824	51	21
92Y30	Check	4475	13	94	150	329	211	100	42	278	520	59
92Y51	Check	4724	13	104	172	335	200	101	45	251	537	65
92Y80	Check	4671	16	100	172	346	198	111	41	259	525	64

Table B30. Mean yield performance of 27 high-oleate and 27 normal-oleate lines from population 3 grown at Delphos, OH, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	
1	HONL	3332	23	HONL	3415	45	NONL	3823	
2	HONL	3837	24	HONL	3453	46	NONL	3800	
3	HONL	3339	25	HONL	3941	47	NONL	3746	
4	HONL	3380	26	HONL	3406	48	NONL	4109	
5	HONL	3732	27	HONL	3628	49	NONL	3772	
6	HONL	3387	28	NONL	3840	50	NONL	3594	
7	HONL	3228	29	NONL	3467	51	NONL	3766	
8	HONL	3648	30	NONL	3628	52	NONL	3749	
9	HONL	3500	31	NONL	3816	53	NONL	3467	
10	HONL	3490	32	NONL	3263	54	NONL	3581	
11	HONL	3948	33	NONL	3544				
12	HONL	3413	34	NONL	3571		SEM	133	
13	HONL	3467	35	NONL	3753		LSD 0.05	377	
14	HONL	3689	36	NONL	3732		LSD 0.01	502	
15	HONL	3487	37	NONL	4551				
16	HONL	3618	38	NONL	3564		YR25C09	Parent	3423
17	HONL	3541	39	NONL	3924		RJS30006	Parent	3662
18	HONL	3790	40	NONL	3588		SP16410155	Check	3638
19	HONL	3615	41	NONL	4465		92Y30	Check	3853
20	HONL	3591	42	NONL	3853		92Y51	Check	3312
21	HONL	3682	43	NONL	3763		92Y80	Check	3773
22	HONL	3537	44	NONL	4110				

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

Table B31. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 4 grown at Atlantic, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3948	31	2.0	109	157	370	170	60	40	828	29	43
2	HONL	3901	30	3.0	107	147	359	173	59	39	814	46	42
3	HONL	3948	33	3.0	117	154	367	170	62	39	818	35	47
4	HONL	2966	24	1.5	97	169	363	178	62	34	802	78	26
5	HONL	3685	34	2.0	104	148	361	171	64	38	803	42	52
6	HONL	3790	30	2.0	107	171	363	171	61	40	823	32	43
7	HONL	3927	28	3.0	107	152	369	174	61	37	827	34	41
8	HONL	3901	32	2.0	107	142	360	170	62	38	819	34	47
9	HONL	3453	32	2.0	104	143	361	177	59	41	836	24	40
10	HONL	3810	33	2.0	109	146	360	176	62	45	820	29	43
11	HONL	3376	32	2.5	102	143	360	173	59	40	824	30	45
12	HONL	3342	32	2.5	107	151	363	176	66	37	776	74	47
13	HONL	3749	32	2.0	114	157	363	168	63	39	829	26	42
14	HONL	3551	34	2.0	117	149	374	170	64	48	800	40	46
15	HONL	3638	33	2.5	104	153	366	171	62	46	820	29	42
16	HONL	3571	30	2.5	107	169	376	165	62	37	814	44	43
17	HONL	4011	33	2.0	112	154	365	171	58	41	823	31	46
18	HONL	3655	34	2.0	114	166	366	164	64	38	818	32	46
19	HONL	3319	34	2.5	104	149	362	172	62	44	804	40	50

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B31. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3793	31	2.0	107	151	366	168	60	35	821	35	48
21	HONL	3642	31	2.0	107	159	360	176	60	37	824	32	46
22	HONL	3692	29	2.0	107	154	361	179	60	40	825	31	44
23	HONL	3860	32	2.0	112	167	361	173	61	39	824	31	43
24	HONL	3235	32	2.5	112	153	374	164	61	41	823	31	43
25	HONL	3635	33	2.5	109	154	363	172	61	39	823	30	45
26	HONL	3736	31	2.0	114	155	369	176	62	37	831	29	41
27	HONL	3453	33	1.5	107	156	365	167	66	37	799	44	53
28	NONL	3588	30	2.5	107	162	343	184	93	41	268	529	68
29	NONL	4163	31	2.0	109	154	338	184	91	42	273	525	70
30	NONL	3749	31	2.0	109	145	331	191	96	45	224	562	72
31	NONL	3813	30	3.0	117	158	343	187	98	44	246	544	67
32	NONL	3302	30	2.0	104	161	333	192	94	41	288	514	64
33	NONL	3890	30	2.0	99	166	343	187	96	48	249	541	65
34	NONL	3823	32	2.0	107	155	331	189	92	45	291	507	65
35	NONL	4015	30	2.0	104	169	332	188	93	41	243	553	70
36	NONL	3901	30	1.5	107	161	338	186	94	39	227	570	68
37	NONL	3944	31	2.0	107	157	340	187	90	49	271	525	65
38	NONL	3682	32	1.5	104	167	354	180	96	44	272	519	69
39	NONL	3823	34	2.0	112	156	352	178	92	43	228	563	74
40	NONL	3561	32	2.0	112	150	339	185	94	47	232	554	73
41	NONL	3756	33	2.0	109	155	343	177	94	43	234	559	70

Table B31. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4038	33	2.0	107	164	349	183	99	41	230	555	75
43	NONL	3746	31	2.5	109	178	347	183	96	42	247	548	68
44	NONL	3780	32	1.5	114	150	344	180	95	43	246	546	68
45	NONL	3820	33	2.0	107	149	335	183	98	46	228	554	73
46	NONL	3749	34	2.0	104	146	340	178	99	41	220	567	72
47	NONL	3864	30	2.5	107	156	336	187	94	43	282	517	63
48	NONL	4018	30	2.5	104	170	327	188	94	44	250	540	72
49	NONL	3981	31	2.0	104	160	347	184	97	46	240	550	66
50	NONL	3850	30	2.0	107	144	326	192	99	45	246	539	70
51	NONL	3796	31	2.0	107	171	347	189	93	43	246	552	66
52	NONL	3366	33	2.0	107	158	345	180	96	44	260	534	66
53	NONL	3773	29	2.0	107	166	339	188	93	41	237	560	70
54	NONL	3598	32	3.0	112	153	349	181	91	43	273	525	68
SEM		148	1	0	3	5	3	1	1	1	13	11	1
LSD 0.05		419	2	1	7	13	8	4	3	3	36	32	4
LSD 0.01		558	3	1	9	18	11	5	4	5	48	43	5
YR37Y09	Parent	3537	34	2.0	109	154	368	170	61	43	822	29	44
93Y20	Parent	3500	27	2.5	109	151	328	195	90	40	222	577	71
SP16410155	Check	3235	29	2.5	107	151	366	170	62	43	808	63	22
93Y05	Check	3363	25	1.5	99	157	326	201	101	38	229	564	68
93Y40	Check	3820	30	2.0	107	155	333	187	100	40	210	570	79
93Y82	Check	4065	32	1.5	104	175	336	180	97	41	244	539	80

Table B32. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 4 grown at Hedrick, IA, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging scores [§]	Height cm	Seed weight mg sd ¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3803	27	2.0	94	148	346	192	59	41	846	19	35
2	HONL	3981	26	2.0	95	135	336	193	56	40	853	19	32
3	HONL	3410	32	2.5	102	146	345	186	59	38	843	23	37
4	HONL	3262	15	1.5	94	154	347	185	57	39	854	25	24
5	HONL	3843	30	2.5	99	143	341	188	60	39	833	27	40
6	HONL	3349	28	1.5	91	153	341	188	58	45	814	45	37
7	HONL	3975	26	2.0	91	147	351	188	61	40	841	21	37
8	HONL	3601	29	2.5	91	140	340	186	60	41	831	27	41
9	HONL	3820	30	2.0	95	134	340	195	60	45	840	19	36
10	HONL	3558	30	2.0	95	142	344	192	62	44	813	43	38
11	HONL	3739	29	2.5	91	131	343	187	58	40	845	21	35
12	HONL	3356	28	2.5	89	137	334	198	63	40	821	54	39
13	HONL	3860	30	2.5	100	153	341	185	63	40	837	22	38
14	HONL	3776	31	2.5	107	149	350	188	62	46	823	28	40
15	HONL	3827	30	2.0	88	149	349	189	60	48	829	24	38
16	HONL	3517	25	1.5	93	157	352	184	59	40	844	21	36
17	HONL	3467	30	2.0	97	144	346	187	59	42	841	21	36
18	HONL	3396	31	2.0	99	152	337	186	61	41	831	28	39
19	HONL	3655	31	2.5	100	150	344	183	61	46	807	44	42

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table B32. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3850	29	2.0	98	147	343	187	59	37	838	26	40
21	HONL	4045	27	2.0	98	146	338	194	57	39	847	20	36
22	HONL	3558	25	2.0	102	142	350	189	58	42	841	22	37
23	HONL	3850	29	1.5	97	157	338	191	60	41	836	25	38
24	HONL	3746	30	2.0	99	151	348	183	60	42	833	25	39
25	HONL	3921	31	2.5	100	149	344	188	59	41	840	23	36
26	HONL	3887	30	2.5	94	148	353	190	59	39	846	21	35
27	HONL	3843	31	2.0	95	150	337	182	64	39	823	30	43
28	NONL	3537	26	2.0	89	145	311	207	94	48	260	537	62
29	NONL	3605	25	2.0	90	138	310	210	95	47	251	541	66
30	NONL	3843	28	2.0	99	148	315	204	98	52	266	517	66
31	NONL	3500	24	2.0	102	139	312	210	97	48	255	537	63
32	NONL	3712	25	2.0	97	149	320	207	99	47	279	513	62
33	NONL	3712	26	1.0	93	151	321	209	96	56	254	534	60
34	NONL	4028	30	2.0	97	145	318	204	98	52	245	543	63
35	NONL	3625	27	2.0	94	156	319	204	91	49	324	477	59
36	NONL	3857	28	1.5	91	154	319	203	96	48	251	544	61
37	NONL	3685	28	3.0	93	142	311	208	89	55	324	472	59
38	NONL	3756	28	1.5	90	156	335	202	96	54	290	496	62
39	NONL	3739	30	3.0	98	150	322	202	93	49	264	533	60
40	NONL	3662	29	1.5	94	130	312	210	95	51	270	517	66
41	NONL	3268	29	2.0	91	140	315	203	94	46	283	513	64

Table B32. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3813	29	2.0	98	152	331	201	101	47	245	538	69
43	NONL	3743	28	2.0	99	150	322	201	96	51	264	525	63
44	NONL	3648	29	2.5	102	145	328	201	96	52	266	523	63
45	NONL	3786	29	2.0	90	143	311	209	94	55	256	529	65
46	NONL	3968	30	2.0	95	140	308	201	99	47	259	527	68
47	NONL	3561	27	2.0	91	147	317	210	96	51	246	545	62
48	NONL	3339	26	1.5	97	152	310	210	96	50	256	533	64
49	NONL	3709	26	2.0	95	149	319	204	97	50	286	507	59
50	NONL	3578	24	2.0	93	129	312	208	97	51	283	503	64
51	NONL	3813	30	2.0	99	166	326	204	95	47	254	541	63
52	NONL	3426	28	2.0	98	150	320	204	95	48	304	491	61
53	NONL	3726	25	2.0	97	149	318	208	94	50	268	526	61
54	NONL	3510	28	2.0	99	143	319	205	94	48	262	534	62
SEM		226	1	0	3	4	3	3	1	1	14	12	2
LSD 0.05		640	2	1	9	12	8	7	4	3	39	34	5
LSD 0.01		852	3	1	11	16	11	10	5	4	51	46	6
YR37Y09	Parent	3447	30	1.5	97	151	346	186	60	44	836	23	37
93Y20	Parent	3917	25	3.0	100	146	313	206	91	46	262	539	63
SP16410155	Check	3060	24	3.5	90	150	349	182	62	43	831	45	19
93Y05	Check	3447	22	1.0	84	148	309	211	101	45	269	524	60
93Y40	Check	3497	25	2.0	91	148	330	197	102	43	237	547	71
93Y82	Check	4233	28	2.0	95	167	303	201	98	44	247	536	74

Table B33. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 4 grown at Mount Pleasant, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	4045	30	1.0	108	151	348	191	63	41	792	64	40
2	HONL	3988	29	2.0	107	135	345	187	57	40	845	21	37
3	HONL	3544	32	2.0	113	141	356	183	60	38	835	26	40
4	HONL	3225	19	1.0	86	159	363	179	56	38	859	24	25
5	HONL	3880	31	1.0	107	143	340	190	62	35	809	53	41
6	HONL	4045	31	1.5	108	163	345	185	59	40	820	42	39
7	HONL	4015	27	1.0	109	150	353	187	60	38	845	20	36
8	HONL	4015	32	1.5	107	138	341	187	61	40	829	28	42
9	HONL	4055	31	1.0	104	135	342	198	60	43	841	19	36
10	HONL	4112	33	1.0	105	139	336	194	60	41	836	24	39
11	HONL	3951	33	2.0	107	136	347	184	58	36	844	23	38
12	HONL	4096	31	1.0	107	143	341	191	62	36	826	39	37
13	HONL	3897	31	2.0	111	150	346	184	63	37	840	21	39
14	HONL	3722	31	1.0	108	151	356	190	61	44	827	27	40
15	HONL	3938	31	2.0	105	150	354	189	61	45	829	25	40
16	HONL	4126	29	2.0	109	162	359	179	63	37	816	45	39
17	HONL	3907	32	1.0	111	146	353	185	59	40	835	24	41
18	HONL	3574	32	1.5	117	158	352	183	62	37	835	27	39
19	HONL	3927	33	1.5	104	149	350	183	61	40	827	29	42

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 13 g kg⁻¹-moisture basis.

Table B33. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3998	30	2.0	104	145	349	186	60	36	840	24	40
21	HONL	4096	28	1.5	103	147	339	194	59	36	835	32	37
22	HONL	3911	28	2.0	109	148	354	190	58	41	838	24	38
23	HONL	3961	29	1.0	103	156	345	190	62	39	835	26	38
24	HONL	3988	31	1.0	104	153	352	183	60	41	833	25	39
25	HONL	3927	32	1.5	108	148	347	188	60	41	837	22	39
26	HONL	3699	30	1.0	103	146	355	191	59	37	848	20	35
27	HONL	3837	32	1.0	104	153	348	179	67	37	782	67	47
28	NONL	3833	28	1.5	103	150	327	201	96	45	265	530	64
29	NONL	4149	30	2.0	105	144	320	202	94	41	247	550	67
30	NONL	4001	30	1.0	107	145	319	202	98	51	240	543	67
31	NONL	4227	28	2.0	116	150	325	204	98	44	244	549	65
32	NONL	3890	27	1.0	105	151	322	205	101	42	249	544	64
33	NONL	3998	28	1.5	102	156	326	204	95	49	277	519	60
34	NONL	4079	31	1.0	104	151	319	205	96	49	243	544	67
35	NONL	3988	29	1.0	102	150	321	201	95	46	273	521	65
36	NONL	4045	29	1.5	102	160	325	200	95	43	258	540	62
37	NONL	4317	31	1.5	109	148	320	205	94	51	252	537	66
38	NONL	3907	30	1.0	98	156	338	200	92	46	338	463	60
39	NONL	3948	32	2.0	104	146	329	198	95	44	244	549	69
40	NONL	4176	32	1.0	104	127	323	204	94	48	289	503	66
41	NONL	3763	32	1.0	105	147	320	198	97	44	238	553	68

Table B33. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3991	29	1.0	99	152	331	201	101	45	255	532	67
43	NONL	4048	28	1.5	104	148	319	203	97	45	257	536	65
44	NONL	4082	32	1.0	108	147	330	197	96	43	248	547	65
45	NONL	4072	31	1.0	97	146	319	202	98	48	259	527	67
46	NONL	4163	32	1.0	104	144	319	197	101	44	221	559	74
47	NONL	4136	30	1.5	100	143	320	202	97	44	237	557	65
48	NONL	4099	29	1.5	98	158	316	205	94	44	278	516	67
49	NONL	3997	29	1.0	109	154	331	199	100	46	246	542	66
50	NONL	4173	30	1.5	100	140	318	204	99	48	268	514	71
51	NONL	3719	31	1.0	111	162	330	203	96	44	245	549	65
52	NONL	4042	32	1.0	107	156	328	197	100	42	276	518	64
53	NONL	4055	25	1.5	98	153	325	205	96	49	258	533	64
54	NONL	3995	31	1.5	105	144	329	199	97	43	246	547	67
SEM		112	1	0	3	2	3	2	1	1	14	13	2
LSD 0.05		316	2	1	9	5	8	5	4	4	41	38	4
LSD 0.01		422	3	1	12	7	10	7	5	5	55	51	6
YR37Y09	Parent	3870	33	1.0	105	155	359	180	61	42	834	24	40
93Y20	Parent	3880	25	1.5	105	140	313	209	91	39	241	564	65
SP16410155	Check	3978	25	2.5	97	151	356	182	62	42	835	42	19
93Y05	Check	3981	23	1.0	89	147	312	209	104	40	250	541	65
93Y40	Check	4496	28	1.0	94	152	332	196	104	42	234	547	72
93Y82	Check	4237	30	1.0	104	164	307	203	100	41	267	519	72

Table B34. Mean yield performance of 27 high-oleate and 27 normal-oleate lines from population 4 grown at Delphos, OH, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹
1	HONL	3897	23	HONL	3806	45	NONL	4240
2	HONL	4207	24	HONL	4233	46	NONL	4102
3	HONL	3719	25	HONL	3931	47	NONL	3886
4	HONL	3487	26	HONL	3820	48	NONL	4180
5	HONL	3860	27	HONL	3796	49	NONL	4227
6	HONL	4085	28	NONL	4139	50	NONL	4005
7	HONL	3863	29	NONL	4428	51	NONL	4153
8	HONL	4015	30	NONL	3998	52	NONL	3874
9	HONL	3165	31	NONL	3645	53	NONL	4062
10	HONL	3796	32	NONL	3981	54	NONL	4092
11	HONL	4011	33	NONL	4122			
12	HONL	4254	34	NONL	4213	SEM		143
13	HONL	4055	35	NONL	3904	LSD 0.05		405
14	HONL	4099	36	NONL	3954	LSD 0.01		540
15	HONL	3961	37	NONL	3954			
16	HONL	4032	38	NONL	4038	YR37Y09	Parent	3373
17	HONL	3739	39	NONL	4092	93Y20	Parent	3811
18	HONL	3954	40	NONL	4230	SP16410155	Check	3524
19	HONL	3927	41	NONL	3732	93Y05	Check	4015
20	HONL	3745	42	NONL	3985	93Y40	Check	4005
21	HONL	3971	43	NONL	4106	93Y82	Check	4129
22	HONL	3810	44	NONL	4035			

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

Table B35. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 5 grown at Atlantic, IA, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Maturity d [‡]	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3144	25	2.5	97	146	355	184	60	44	833	24	39
2	HONL	3571	24	1.0	97	153	357	184	62	38	834	24	41
3	HONL	3309	33	2.5	109	161	371	168	64	43	804	47	43
4	HONL	3433	28	2.0	102	157	361	177	63	38	841	21	37
5	HONL	3494	28	2.0	104	161	363	178	62	39	842	20	37
6	HONL	3322	32	2.0	107	152	364	172	60	43	828	26	41
7	HONL	3618	32	1.0	107	156	358	166	61	44	826	26	42
8	HONL	3642	26	1.5	99	151	366	182	58	34	855	17	36
9	HONL	3221	32	2.0	97	150	375	163	65	41	829	24	41
10	HONL	3588	32	1.5	94	152	369	174	61	37	833	25	43
11	HONL	3924	33	1.5	109	151	387	161	62	38	821	32	47
12	HONL	3648	34	1.5	107	171	368	169	63	41	822	28	44
13	HONL	3941	33	1.0	107	159	357	173	60	40	841	20	37
14	HONL	3628	33	2.5	109	175	367	168	69	46	790	49	45
15	HONL	3638	29	2.0	97	160	363	173	61	36	851	18	34
16	HONL	3161	34	1.5	104	185	371	163	66	43	831	22	38
17	HONL	3127	30	2.0	112	160	354	176	63	42	831	24	38
18	HONL	3608	30	1.0	102	159	348	182	60	40	830	26	43
19	HONL	3675	32	2.0	112	163	372	168	61	41	814	36	48

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

[‡] = Days after 31 August.

[§] = Score of 1 (all plants erect) to 5 (all plants prostrate).

[¶] = Expressed on a 13 g kg⁻¹-moisture basis.

Table B35. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3890	33	1.5	109	155	368	162	61	40	822	31	45
21	HONL	3904	31	1.5	109	166	370	170	65	38	828	25	43
22	HONL	3420	30	2.0	117	165	369	172	65	45	823	26	40
23	HONL	3006	23	2.0	104	160	372	174	61	37	843	20	39
24	HONL	3679	33	1.5	114	163	359	169	58	39	837	25	40
25	HONL	3473	32	2.0	109	170	369	171	64	39	826	28	41
26	HONL	3292	27	1.5	104	157	357	176	60	41	831	25	43
27	HONL	3110	29	2.0	99	160	362	175	66	40	797	53	44
28	NONL	3779	33	1.5	114	180	347	182	106	44	220	557	73
29	NONL	4181	36	2.0	117	176	333	175	97	43	235	548	77
30	NONL	3416	31	1.0	107	175	339	191	100	41	267	523	67
31	NONL	3806	37	2.0	122	158	350	179	98	46	244	539	72
32	NONL	3726	29	1.5	97	159	341	191	103	42	271	509	75
33	NONL	3537	34	1.5	109	172	343	181	102	44	238	541	75
34	NONL	3853	34	1.5	114	154	339	184	97	50	227	552	73
35	NONL	3975	34	2.0	97	159	341	188	107	46	234	539	74
36	NONL	3911	30	2.5	109	147	336	187	102	48	270	508	73
37	NONL	3621	27	1.5	102	171	342	189	100	44	267	519	71
38	NONL	4069	34	1.0	109	144	324	187	106	41	235	543	75
39	NONL	4181	33	2.0	114	170	336	183	97	49	233	549	72
40	NONL	3911	31	2.0	112	167	343	177	103	42	251	532	71
41	NONL	3951	31	1.5	109	162	335	181	105	41	246	535	72

Table B35. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3753	34	2.0	114	176	337	185	101	51	252	524	72
43	NONL	4022	36	1.5	109	159	336	181	104	41	235	546	74
44	NONL	4190	32	2.0	109	165	335	182	105	41	215	559	79
45	NONL	3749	32	1.0	117	149	322	196	98	46	225	558	73
46	NONL	3470	23	2.0	99	191	341	195	98	42	313	487	60
47	NONL	3598	34	1.5	104	159	327	189	100	46	239	542	73
48	NONL	3864	30	2.0	112	158	339	185	98	50	268	516	67
49	NONL	3938	37	2.0	117	166	345	172	100	44	223	555	77
50	NONL	3413	25	2.0	102	160	335	191	106	42	222	558	72
51	NONL	3689	29	2.0	109	163	346	190	101	42	258	531	69
52	NONL	3820	35	1.5	107	165	338	180	103	50	234	541	71
53	NONL	3732	32	1.0	104	166	347	187	98	41	264	525	71
54	NONL	3769	36	1.5	109	171	346	178	97	44	289	496	74
SEM		155	1	0	4	5	3	2	1	1	12	10	2
LSD 0.05		439	2	1	10	13	9	5	3	3	33	29	5
LSD 0.01		584	3	1	13	17	12	6	4	3	44	38	6
YR37Y09	Parent	3473	33	1.5	104	163	369	169	63	44	815	33	45
XB30C10	Parent	3584	25	1.5	107	165	331	192	106	41	250	534	69
SP16410155	Check	3332	29	3.0	104	163	370	167	62	39	820	60	19
93Y05	Check	3880	26	1.5	97	161	328	196	104	37	231	560	68
93Y40	Check	3958	30	1.5	97	161	335	187	100	40	212	568	80
93Y82	Check	4156	34	2.0	104	179	328	183	96	41	223	559	80

Table B36. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 5 grown at Hedrick, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3309	17	1.5	89	128	355	190	63	51	836	16	34
2	HONL	3339	18	1.0	76	162	347	194	63	45	845	14	33
3	HONL	3702	26	2.0	97	151	352	184	59	44	840	20	37
4	HONL	3847	24	1.0	79	147	340	188	62	40	849	16	32
5	HONL	3487	23	1.0	94	153	347	189	64	45	845	14	32
6	HONL	3766	27	1.5	94	148	338	188	59	42	842	20	36
7	HONL	3769	30	1.5	90	153	338	182	58	43	845	19	33
8	HONL	3423	23	1.5	81	133	348	192	60	39	852	15	35
9	HONL	3591	27	1.5	85	143	354	181	64	45	838	18	34
10	HONL	3961	26	2.0	88	144	350	188	62	36	827	36	37
11	HONL	3790	28	2.0	90	142	352	180	63	39	834	24	39
12	HONL	3682	24	1.5	94	140	351	183	62	48	834	19	36
13	HONL	4089	28	2.0	91	154	343	185	60	39	849	17	34
14	HONL	3927	29	2.0	100	166	335	186	70	46	761	79	44
15	HONL	3605	22	1.5	88	150	351	187	61	39	857	13	29
16	HONL	3618	29	2.5	94	173	353	179	64	49	834	19	34
17	HONL	3588	25	1.5	99	146	344	186	64	45	834	20	36
18	HONL	3672	23	1.5	84	150	333	191	59	43	848	15	34
19	HONL	3383	25	1.5	91	153	356	182	59	50	822	25	43

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

Table B36. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3413	28	1.5	97	147	349	176	62	41	840	21	37
21	HONL	3564	24	2.0	90	149	349	186	65	40	841	18	36
22	HONL	3675	27	1.5	98	155	347	185	63	46	830	23	37
23	HONL	3450	17	2.0	86	153	363	183	62	45	844	15	34
24	HONL	3981	27	1.5	98	160	339	184	60	39	841	23	37
25	HONL	3652	28	2.0	94	159	351	185	63	41	843	18	34
26	HONL	3373	22	1.0	86	151	351	182	61	46	836	18	38
27	HONL	3712	24	1.5	86	153	342	187	64	47	836	17	35
28	NONL	4052	29	1.5	102	160	321	201	109	50	229	544	68
29	NONL	4085	32	1.5	89	157	308	201	101	50	245	535	70
30	NONL	4038	27	1.0	94	158	310	211	101	49	286	502	61
31	NONL	3998	32	1.5	90	152	322	201	102	50	248	533	68
32	NONL	3568	24	1.5	90	142	331	199	107	51	274	500	68
33	NONL	3958	30	1.0	89	154	319	201	104	52	265	513	65
34	NONL	3776	30	2.0	97	139	314	204	100	52	232	545	71
35	NONL	4082	30	2.0	94	154	321	205	107	52	258	516	68
36	NONL	3726	24	1.0	85	145	324	202	108	56	246	521	69
37	NONL	4227	25	1.5	86	162	326	200	103	48	256	523	70
38	NONL	3951	31	1.5	95	127	294	210	109	46	242	534	68
39	NONL	4079	30	2.0	99	148	312	200	97	57	270	510	65
40	NONL	4106	27	2.0	97	158	322	199	108	47	270	513	63
41	NONL	4025	27	2.0	97	150	317	198	108	48	266	513	65

Table B36. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	3914	29	1.0	100	160	315	203	107	57	254	515	67
43	NONL	3901	31	1.0	84	147	316	201	105	48	245	534	67
44	NONL	3951	29	2.0	94	146	309	206	105	46	239	536	72
45	NONL	4213	30	2.0	99	143	310	212	99	52	238	543	68
46	NONL	3632	20	1.5	85	177	325	205	104	50	297	490	59
47	NONL	4106	30	1.5	94	151	306	208	104	49	260	520	67
48	NONL	3951	27	1.0	89	150	320	200	106	55	264	512	63
49	NONL	3877	32	2.0	99	155	321	191	104	47	243	535	71
50	NONL	3517	22	1.0	79	154	322	201	108	49	273	505	64
51	NONL	3618	23	1.0	83	153	325	209	103	49	278	508	62
52	NONL	4102	32	1.0	91	164	311	197	102	52	256	521	68
53	NONL	3722	26	2.0	85	147	321	204	105	44	238	544	68
54	NONL	4106	32	1.5	97	163	322	197	100	52	253	524	71
SEM		160	1	0	4	4	3	1	1	1	8	7	2
LSD 0.05		455	3	1	12	11	8	4	3	3	24	20	5
LSD 0.01		606	4	1	17	15	11	6	4	5	32	26	6
YR37Y09	Parent	3625	31	2.0	93	147	348	185	59	45	838	22	36
XB30C10	Parent	3840	22	1.0	84	157	320	200	108	47	286	496	63
SP16410155	Check	3699	26	3.0	98	147	345	184	60	44	840	39	17
93Y05	Check	3389	23	1.0	79	147	308	209	103	42	259	534	62
93Y40	Check	3742	24	1.0	89	148	327	201	103	44	237	549	67
93Y82	Check	4217	29	2.0	95	168	303	203	99	43	252	534	71

Table B37. Mean agronomic and seed performance of 27 high-oleate and 27 normal-oleate lines from population 5 grown at Mount Pleasant, IA, in 2011.

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging scores§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
1	HONL	3547	19	2.0	107	131	364	185	61	47	839	18	35
2	HONL	3685	18	1.0	90	140	349	194	60	43	846	16	34
3	HONL	3558	25	1.0	105	149	361	185	59	43	839	21	36
4	HONL	3938	22	1.5	90	143	352	188	64	40	849	16	32
5	HONL	3716	23	1.0	109	150	358	186	64	42	829	31	34
6	HONL	3601	28	1.0	105	146	349	186	59	42	844	21	34
7	HONL	3830	31	1.0	98	146	341	183	60	40	841	23	36
8	HONL	3615	20	1.0	95	140	361	190	59	38	855	15	33
9	HONL	3874	28	1.5	98	140	362	182	63	45	837	19	35
10	HONL	4207	26	1.0	100	144	359	186	61	37	827	38	35
11	HONL	3574	29	1.0	94	138	366	177	60	34	843	23	39
12	HONL	3608	24	1.0	99	133	358	182	61	43	839	20	37
13	HONL	3948	26	1.5	104	148	354	183	61	38	847	18	34
14	HONL	3662	30	1.5	107	154	343	187	65	39	828	29	38
15	HONL	3692	21	1.5	99	144	357	183	61	36	861	12	30
16	HONL	3692	29	1.5	105	162	358	181	64	46	836	20	34
17	HONL	3453	24	1.5	107	140	346	184	65	42	817	39	36
18	HONL	3692	24	1.0	97	150	335	196	58	43	822	39	37
19	HONL	3487	26	1.0	103	151	363	184	59	44	831	25	41

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

Table B37. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ⁻¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
20	HONL	3379	30	1.0	105	149	355	174	62	41	834	24	38
21	HONL	3840	24	1.0	103	147	355	185	63	38	843	18	37
22	HONL	3679	25	1.0	111	149	353	186	64	46	835	19	35
23	HONL	3679	19	2.0	100	148	371	181	62	42	844	15	36
24	HONL	3625	27	1.0	108	150	353	181	60	40	845	20	36
25	HONL	3702	28	1.0	97	149	355	187	63	38	840	22	36
26	HONL	3736	23	1.0	98	145	349	185	63	44	814	40	39
27	HONL	3786	24	1.0	104	147	351	185	65	45	820	34	37
28	NONL	3709	29	1.5	111	154	327	201	107	46	239	543	64
29	NONL	3890	33	1.0	105	158	316	198	101	51	257	524	67
30	NONL	3655	27	1.0	91	153	319	209	101	44	276	515	64
31	NONL	3961	32	1.0	114	153	328	200	100	50	247	536	68
32	NONL	3769	22	1.0	93	138	338	199	104	47	291	489	68
33	NONL	3847	29	1.0	109	147	327	200	102	49	270	514	65
34	NONL	3574	30	2.0	108	139	327	202	101	52	230	549	67
35	NONL	3729	30	1.0	97	145	333	202	104	45	245	539	67
36	NONL	3699	23	2.0	98	138	336	196	105	55	272	500	67
37	NONL	3944	23	1.5	99	155	333	199	102	46	268	517	66
38	NONL	3793	31	1.0	102	129	310	205	107	42	235	545	70
39	NONL	3897	31	1.0	103	140	309	201	99	49	242	544	66
40	NONL	4075	27	1.0	104	152	322	200	106	43	266	521	64
41	NONL	3864	27	1.0	103	146	326	197	108	45	261	519	66

Table B37. Continued

Entry	Genotype†	Yield kg ha ⁻¹	Maturity d‡	Lodging score§	Height cm	Seed weight mg sd ¹	Protein g kg ⁻¹ ¶	Oil g kg ⁻¹ ¶	Palmitate g kg ⁻¹	Stearate g kg ⁻¹	Oleate g kg ⁻¹	Linoleate g kg ⁻¹	Linolenate g kg ⁻¹
42	NONL	4109	29	2.0	104	155	329	201	103	58	302	477	61
43	NONL	3675	32	1.0	107	149	327	196	106	44	261	518	70
44	NONL	4159	26	1.0	103	144	318	204	105	44	243	536	71
45	NONL	3584	30	1.0	105	138	318	211	100	50	239	544	66
46	NONL	3389	18	1.0	84	166	329	207	97	50	364	432	56
47	NONL	3756	29	1.5	100	150	315	207	102	49	273	512	64
48	NONL	3544	26	1.0	105	141	333	199	103	53	301	482	61
49	NONL	3746	32	1.5	105	150	322	190	102	46	248	536	68
50	NONL	3605	21	1.0	93	144	330	203	107	54	285	494	61
51	NONL	3729	23	1.5	97	148	338	206	101	48	302	486	62
52	NONL	3820	30	1.0	102	148	319	199	104	51	268	514	62
53	NONL	3716	26	1.0	93	149	332	203	104	44	258	527	66
54	NONL	3890	32	1.0	109	166	337	191	97	52	257	524	69
SEM		172	1	0	3	2	4	2	1	1	12	11	1
LSD 0.05		488	2	1	10	7	12	6	4	4	35	30	4
LSD 0.01		650	3	1	13	9	16	7	5	6	47	40	5
YR37Y09	Parent	3685	31	2.0	107	151	357	185	59	45	832	25	39
93Y20	Parent	3833	19	2.0	97	146	330	200	106	46	289	496	63
SP16410155	Check	3346	23	2.0	102	146	352	185	59	44	842	36	19
93Y05	Check	4025	23	1.5	89	143	316	207	100	41	259	538	62
93Y40	Check	4126	25	1.0	91	147	329	199	100	44	276	512	68
93Y82	Check	3601	29	1.0	104	161	306	204	95	42	276	517	70

Table B38. Mean yield performance of 27 high-oleate and 27 normal-oleate lines from population 5 grown at Delphos, OH, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	
1	HONL	2847	23	HONL	3685	45	NONL	3816	
2	HONL	3077	24	HONL	3282	46	NONL	3312	
3	HONL	3517	25	HONL	3816	47	NONL	3491	
4	HONL	3457	26	HONL	3044	48	NONL	2919	
5	HONL	3588	27	HONL	3430	49	NONL	3312	
6	HONL	3467	28	NONL	3716	50	NONL	2747	
7	HONL	3615	29	NONL	4106	51	NONL	3578	
8	HONL	2939	30	NONL	3537	52	NONL	3729	
9	HONL	3359	31	NONL	3867	53	NONL	3278	
10	HONL	3601	32	NONL	3601	54	NONL	2966	
11	HONL	3621	33	NONL	3702				
12	HONL	3805	34	NONL	3473				
13	HONL	3611	35	NONL	3591	SEM		237	
14	HONL	3655	36	NONL	3667	LSD 0.05		673	
15	HONL	3254	37	NONL	3278	LSD 0.01		896	
16	HONL	3682	38	NONL	3673		YR37Y09	Parent	3470
17	HONL	3393	39	NONL	3529		XB30C10	Parent	3542
18	HONL	3645	40	NONL	3157		SP16410155	Check	3638
19	HONL	2603	41	NONL	3665		93Y05	Check	3658
20	HONL	2250	42	NONL	3642		93Y40	Check	3399
21	HONL	3201	43	NONL	3378		93Y82	Check	3689
22	HONL	3241	44	NONL	3531				

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

Table B39. Mean yield performance of 27 high-oleate and 27 normal-oleate lines from population 5 grown at Wyoming, IL, in 2011.

Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	Entry	Genotype [†]	Yield kg ha ⁻¹	
1	HONL	4913	23	HONL	4761	45	NONL	5195	
2	HONL	4442	24	HONL	4751	46	NONL	4909	
3	HONL	4391	25	HONL	4788	47	NONL	4412	
4	HONL	4674	26	HONL	5000	48	NONL	5054	
5	HONL	4371	27	HONL	4428	49	NONL	4792	
6	HONL	4842	28	NONL	5148	50	NONL	4586	
7	HONL	4684	29	NONL	5061	51	NONL	4909	
8	HONL	4264	30	NONL	4815	52	NONL	5088	
9	HONL	4277	31	NONL	3961	53	NONL	5007	
10	HONL	4970	32	NONL	5114	54	NONL	4711	
11	HONL	4657	33	NONL	4889				
12	HONL	4966	34	NONL	5061		SEM	207	
13	HONL	4630	35	NONL	4896		LSD 0.05	588	
14	HONL	4301	36	NONL	5088		LSD 0.01	784	
15	HONL	4758	37	NONL	4771				
16	HONL	5017	38	NONL	4241		YR37Y09	Parent	4775
17	HONL	4684	39	NONL	4667		XB30C10	Parent	5209
18	HONL	4913	40	NONL	5121		SP16410155	Check	4375
19	HONL	4916	41	NONL	5057		93Y05	Check	4634
20	HONL	4344	42	NONL	5589		93Y40	Check	4886
21	HONL	4465	43	NONL	5114		93Y82	Check	5666
22	HONL	4607	44	NONL	5044				

[†] = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

Table B40. Class means and ranges for agronomic and seed traits of 27 high-oleate, normal-linolenate and 27 normal-oleate, normal-linolenate lines from population 1 grown in 2011.

Trait	Class†	Pocahontas, IA		Royal, IA		Conrad, IA		Princeton, IL#	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Yield	HONL	3319 ns	2747-3793 **	3249 *	2734-3621 **	4459 **	4149-4768 *	4808	4291-5394
kg ha ⁻¹	NONL	3336	2915-3692 **	3335	2781-3813 **	4548	4153-4869 **	4988	4136-5494
Maturity	HONL	29 ns	28-32 **	27 **	25-30 **	22 **	18-30 **		
d‡	NONL	29	25-33 **	28	26-31 **	21	15-31 **		
Lodging	HONL	2.4 *	2.0-3.0 ns	2.2 ns	1.5-3.0 ns	2.3 **	2.0-3.0 ns		
score§	NONL	2.2	2.0-3.5 ns	2.1	1.5-3.5 ns	2.1	2.0-2.5 ns		
Height	HONL	112 ns	99-122 **	120 ns	113-128 ns	108 ns	99-119 ns		
cm	NONL	111	100-122 **	120	111-135 ns	108	99-119 ns		
Seed wt.	HONL	135 **	117-151 **	138 **	128-152 *	146 **	134-166 **		
mg sd ⁻¹	NONL	139	118-167 **	141	119-164 **	152	133-182 **		

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

= Unable to determine significance due to the loss of one replication.

Table B40. Continued.

Trait	Class†	Pocahontas, IA		Royal, IA		Conrad, IA		Princeton, IL	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Protein	HONL	365 **	356-372 *	361 **	351-370 **	360 **	348-375 **		
g kg ⁻¹ ¶	NONL	343	332-352 **	339	327-351 **	334	320-345 **		
Oil	HONL	165 **	156-172 **	166 **	154-173 **	181 **	171-187 **		
g kg ⁻¹ ¶	NONL	176	169-187 **	178	170-184 **	194	188-202 **		
Palmitate	HONL	65 **	59-70 **	66 **	61-70 **	61 **	57-64 *		
g kg ⁻¹	NONL	98	91-105 **	98	92-105 **	95	89-104 **		
Stearate	HONL	39 **	36-41 **	40 **	36-44 **	38 **	35-41 ns		
g kg ⁻¹	NONL	42	39-45 **	43	40-46 **	40	37-43 ns		
Oleate	HONL	806 **	773-820 **	806 **	779-828 **	829 **	801-847 ns		
g kg ⁻¹	NONL	256	220-308 ns	251	225-290 ns	268	240-312 ns		
Linoleate	HONL	36 **	28-56 **	35 **	25-53 **	29 **	17-51 ns		
g kg ⁻¹	NONL	522	479-549 ns	523	490-545 ns	524	485-555 ns		
Linolenate	HONL	53 **	47-66 **	53 **	44-63 **	43 **	37-47 *		
g kg ⁻¹	NONL	81	75-92 **	83	77-88 **	72	67-76 **		

Table B41. Class means and ranges for agronomic and seed traits of 27 high-oleate, normal-linolenate and 27 normal-oleate, normal-linolenate lines from population 2 grown in 2011.

Trait	Class†	Pocahontas, IA		Royal, IA		Conrad, IA		Princeton, IL	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Yield kg ha ⁻¹	HONL	3277 **	2751-3658 **	3053 **	2209-3581 **	4387 **	4200-4782 **	4545 **	4106-5010 ns
	NONL	3516	3231-3807 ns	3329	2905-3837 **	4604	4348-4855 ns	4785	4361-5548 ns
Maturity d‡	HONL	30 **	28-33 **	29 *	26-32 **	28 **	18-34 **		
	NONL	29	27-32 **	28	26-31 **	25	17-32 **		
Lodging score§	HONL	2.2 ns	2.0-3.5 **	2.3 ns	1.0-3.5 **	2.1 ns	2.0-3.0 ns		
	NONL	2.2	1.9-3.5 ns	2.2	1.0-3.0 ns	2.2	2.0-3.0 ns		
Height cm	HONL	108 *	102-122 **	119 *	112-130 ns	110 ns	95-127 **		
	NONL	109	94-117 **	120	111-131 **	109	88-121 ns		
Seed wt. mg sd ⁻¹	HONL	143 **	131-158 **	142 **	128-157 **	155 ns	144-172 **		
	NONL	145	136-157 **	144	132-160 **	156	145-173 **		

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

Table B41. Continued.

Trait	Class†	Pocahontas, IA		Royal, IA		Conrad, IA		Princeton, IL	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Protein	HONL	373 **	361-384 **	372 **	363-383 **	371 **	361-380 **		
g kg ⁻¹ ¶	NONL	347	336-358 **	349	331-361 **	344	331-354 **		
Oil	HONL	162 **	151-172 **	159 **	149-169 **	176 **	164-184 **		
g kg ⁻¹ ¶	NONL	175	167-186 **	171	162-181 **	188	178-197 **		
Palmitate	HONL	65 **	58-73 **	67 **	61-72 **	61 **	53-68 **		
g kg ⁻¹	NONL	100	93-106 **	101	95-110 **	99	92-106 **		
Stearate	HONL	46 **	41-51 **	46 **	41-52 **	42 **	36-46 *		
g kg ⁻¹	NONL	47	42-53 **	48	43-54 **	44	39-50 **		
Oleate	HONL	798 **	774-811 **	789 **	772-807 **	826 **	807-849 **		
g kg ⁻¹	NONL	236	209-299 **	236	208-279 ns	252	223-287 ns		
Linoleate	HONL	38 **	26-54 **	41 **	34-55 ns	27 **	21-45 **		
g kg ⁻¹	NONL	534	479-561 **	529	492-560 ns	530	497-559 ns		
Linolenate	HONL	53 **	45-62 **	57 **	52-62 **	43 **	35-50 **		
g kg ⁻¹	NONL	82	75-88 **	85	79-93 ns	74	67-79 ns		

Table B42. Class means and ranges for agronomic and seed traits of 27 high-oleate, normal-linolenate and 27 normal-oleate, normal-linolenate lines from population 3 grown in 2011.

Trait	Class†	<u>Cedar Falls, IA</u>		<u>Conrad, IA</u>		<u>Princeton, IL</u>		<u>Delphos, OH</u>	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Yield	HONL	4191 **	3732-4660 *	4370 **	4015-4600 ns	4802 *	4220-5501 ns	3559 **	3228-3948 *
kg ha ⁻¹	NONL	4654	3837-5185 ns	4702	4217-5155 **	4969	4200-5578 **	3772	3263-4551 **
Maturity	HONL	34 ns	30-36 **	28 ns	19-34 **	21 ns	13-31 **		
d‡	NONL	34	27-36	28	19-34 **	21	14-29 **		
Lodging	HONL	2.4 **	2.0-3.0 *	2.2 ns	2.0-3.0 *				
score§	NONL	2.0	1.5-3.0 **	2.2	2.0-3.0 *				
Height	HONL	121 ns	107-135 *	112 ns	97-128 ns	112 ns	95-137 **		
cm	NONL	121	105-142 **	114	100-135 *	110	95-127 **		
Seed wt.	HONL	163 **	152-177 **	159 **	152-169 **	177 **	163-196 **		
mg sd ⁻¹	NONL	168	157-179 **	162	149-174 **	181	165-204 **		

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

Table B42. Continued.

Trait	Class†	<u>Cedar Falls, IA</u>		<u>Conrad, IA</u>		<u>Princeton, IL</u>		<u>Delphos, OH</u>	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Protein	HONL	370 **	364-379 **	366 **	359-371 **	369 **	360-374 ns		
g kg ⁻¹ ¶	NONL	349	335-367 **	341	328-356 **	343	330-363 **		
Oil	HONL	167 **	159-176 **	175 **	165-184 **	181 **	172-187 **		
g kg ⁻¹ ¶	NONL	176	164-186 **	185	175-194 **	190	180-197 **		
Palmitate	HONL	70 **	62-78 **	67 **	58-76 **	69 **	61-76 **		
g kg ⁻¹	NONL	105	96-112 **	102	90-109 **	106	96-113 **		
Stearate	HONL	36 **	33-40 **	38 **	35-42 ns	37 **	33-41 ns		
g kg ⁻¹	NONL	40	36-43 **	42	39-44 ns	40	36-44 *		
Oleate	HONL	807 **	784-830 ns	823 **	789-846 **	839 **	805-860 ns		
g kg ⁻¹	NONL	247	203-299 *	263	228-318 *	271	235-322 **		
Linoleate	HONL	36 **	21-63 ns	28 **	17-61 *	19 **	9-59 *		
g kg ⁻¹	NONL	525	482-559 *	518	467-550 *	512	463-545 **		
Linolenate	HONL	50 **	42-59 **	43 **	36-49 **	36 **	29-42 **		
g kg ⁻¹	NONL	84	73-93 **	75	69-85 **	70	63-77 **		

Table B43. Class means and ranges for agronomic and seed traits of 27 high-oleate, normal-linolenate and 27 normal-oleate, normal-linolenate lines from population 4 grown in 2011.

Trait	Class†	<u>Atlantic, IA</u>		<u>Hedrick, IA</u>		<u>Mount Pleasant, IA</u>		<u>Delphos, OH</u>	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Yield	HONL	3651 **	2966-4011 *	3700 ns	3262-4045 ns	3907 **	3225-4126 *	3898 **	3165-4254 ns
kg ha ⁻¹	NONL	3792	3302-4163 *	3672	3268-4028 ns	4033	3719-4317 *	4051	3645-4428 **
Maturity	HONL	32 ns	24-34 **	29 **	15-32 **	30 ns	19-33 **		
d‡	NONL	31	29-34 **	27	24-30 **	30	25-32 **		
Lodging	HONL	2.2 ns	1.5-3.0 ns	2.1 ns	1.5-2.5 ns	1.4 ns	1.0-2.0 **		
score§	NONL	2.1	1.5-3.0 *	2.0	1.0-3.0 **	1.3	1.0-2.0 ns		
Height	HONL	108 ns	97-117 **	96.1 ns	88-107 ns	106 **	86-117 **		
cm	NONL	108	99-117 *	95.2	89-102 ns	104	97-116 ns		
Seed wt.	HONL	154 **	142-171 **	146 ns	131-157 **	148 *	135-163 **		
mg sd ⁻¹	NONL	159	144-178 *	147	129-166 **	149	127-162 **		

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

Table B43. Continued.

Trait	Class†	<u>Atlantic, IA</u>		<u>Hedrick, IA</u>		<u>Mount Pleasant, IA</u>		<u>Delphos, OH</u>	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range
Protein	HONL	365 **	359-376 **	344 **	334-353 **	349 **	336-363 **		
	NONL	340	326-354 **	318	308-335 **	324	316-338 **		
Oil	HONL	172 **	164-179 **	188 **	182-198 **	187 **	179-198 **		
	NONL	185	177-192 **	206	201-210 ns	202	197-205 *		
Palmitate	HONL	62 **	58-66 **	60 **	56-64 **	60 **	56-67 *		
	NONL	95	90-99 **	96	89-101 *	97	92-101 **		
Stearate	HONL	39 **	34-48 **	41 **	37-48 **	39 **	35-45 **		
	NONL	43	39-49 **	50	46-56 **	45	41-51 *		
Oleate	HONL	817 **	776-836 **	835 **	807-854 *	831 **	782-859 ns		
	NONL	250	220-291 ns	269	245-324 ns	257	221-338 ns		
Linoleate	HONL	37 **	24-78 **	27 **	19-54 ns	30 **	19-67 ns		
	NONL	543	507-570 ns	522	472-545 ns	534	463-559 ns		
Linolenate	HONL	44 **	26-53 **	37 **	24-43 **	39 **	25-47 **		
	NONL	69	63-75 **	63	59-69 **	66	60-74 **		

Table B44. Class means and ranges for agronomic and seed traits of 27 high-oleate, normal-linolenate and 27 normal-oleate, normal-linolenate lines from population 5 grown in 2011.

Trait	Class†	Atlantic, IA		Hedrick, IA		Mount Pleasant, IA		Delphos, OH		Wyoming, IL	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range
Yield kg ha ⁻¹	HONL	3499 **	3006-3941 **	3643 **	3309-4089 ns	3696 ns	3379-4207 ns	3359 *	2250-3816 **	4660 **	4264-5017 **
	NONL	3812	3413-4190 ns	3936	3517-4227 ns	3783	3389-4159 ns	3491	2747-4106 ns	4900	3961-5589 ns
Maturity d‡	HONL	30 **	23-34 **	25 **	17-30 **	25 **	18-31 **				
	NONL	32	23-37 **	28	20-32 **	28	18-33 **				
Lodging score§	HONL	1.7 ns	1.0-2.5 ns	1.6 ns	1.0-2.5 ns	1.2 ns	1.0-2.0 ns				
	NONL	1.7	1.0-2.5 ns	1.5	1.0-2.0 *	1.2	1.0-2.0 *				
Height cm	HONL	105 **	94-117 **	90 ns	76-100 **	101 ns	90-111 **				
	NONL	109	97-122 **	92	79-102 ns	102	84-114 **				
Seed wt. mg sd ⁻¹	HONL	160 **	146-185 **	150 ns	128-173 **	146 **	131-162 **				
	NONL	165	144-191 **	152	127-177 **	148	129-166 **				

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

¶ = Expressed on a 130 g kg⁻¹-moisture basis.

Table B44. Continued.

Trait	Class†	<u>Atlantic, IA</u>		<u>Hedrick, IA</u>		<u>Mount Pleasant, IA</u>		<u>Delphos, OH</u>		<u>Wyoming, IL</u>	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range
Protein	HONL	365 **	348-387 **	347 **	333-363 **	355 **	335-371 **				
	g kg ⁻¹ ¶	NONL	339	322-350 **	317	294-331 **	326	309-338 **			
Oil	HONL	172 **	161-184 **	185 **	176-194 **	185 **	174-196 **				
	g kg ⁻¹ ¶	NONL	185	172-196 **	202	191-212 **	201	190-211 **			
Palmitate	HONL	62 **	58-69 **	62 **	58-70 **	62 **	58-65 **				
	g kg ⁻¹	NONL	101	97-107 **	104	97-109 **	103	97-108 **			
Stearate	HONL	40 **	34-46 **	43 **	36-51 **	41 **	34-47 **				
	g kg ⁻¹	NONL	44	41-51 **	50	44-57 **	48	42-58 **			
Oleate	HONL	828 **	790-855 *	837 **	761-857 **	837 **	814-861 ns				
	g kg ⁻¹	NONL	247	215-313 **	256	229-297 **	267	230-364 **			
Linoleate	HONL	27 **	17-53 ns	21 **	13-79 **	24 **	12-40 ns				
	g kg ⁻¹	NONL	535	487-559 **	522	490-545 **	516	432-549 **			
Linolenate	HONL	41 **	34-48 **	36 **	29-44 **	36 **	30-41 **				
	g kg ⁻¹	NONL	72	60-79 **	67	59-72 **	65	56-71 **			

APPENDIX C

PHENOTYPIC CORRELATIONS BETWEEN AGRONOMIC AND SEED TRAITS

Table C1. Phenotypic correlation coefficients among traits on an entry-mean basis for population 1.

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Yield kg ha ⁻¹	HONL	-0.65**	-0.44*	-0.61ns	0.16ns	-0.25ns	0.47**	-0.05ns	-0.03ns	0.42*	-0.36**	-0.55**
	NONL	-0.24ns	-0.22ns	-0.44ns	0.10ns	-0.15ns	0.25ns	-0.20ns	-0.23ns	0.12ns	-0.04ns	-0.07ns
	ALL	-0.42**	-0.39**	-0.52ns	0.18ns	-0.31*	0.40**	0.23ns	0.11ns	-0.25ns	0.25ns	0.19ns
Maturity d‡	HONL		0.51**	0.51**	-0.17ns	0.38ns	-0.67**	0.04ns	-0.20ns	-0.30ns	0.23ns	0.50**
	NONL		0.00ns	0.65**	0.20ns	0.29ns	-0.69**	0.33ns	-0.22ns	-0.46*	0.32ns	0.49**
	ALL		0.24ns	0.59**	0.05ns	0.19ns	-0.42**	-0.03ns	-0.19ns	0.05ns	-0.06ns	0.03ns
Lodging score§	HONL			0.38ns	-0.15ns	0.09ns	-0.23ns	-0.41*	-0.01ns	-0.09ns	0.11ns	0.36ns
	NONL			-0.21ns	-0.30ns	-0.43*	0.12ns	-0.24ns	0.14ns	0.06ns	0.01ns	-0.10ns
	ALL			0.10ns	-0.29*	0.20ns	-0.28*	-0.34*	-0.18ns	0.30*	-0.30*	-0.27*
Height cm	HONL				-0.16ns	0.02ns	-0.17ns	-0.09ns	0.23ns	-0.33ns	0.23ns	0.53**
	NONL				0.43*	0.41*	-0.41*	0.20ns	-0.28ns	-0.26ns	0.21ns	0.26ns
	ALL				0.18ns	0.15ns	-0.21ns	-0.04ns	-0.08ns	0.04ns	-0.05ns	0.02ns
Seed wt. mg sd ⁻¹	HONL					0.27ns	0.09ns	0.13ns	-0.15ns	0.29ns	-0.31ns	-0.32ns
	NONL					0.80**	-0.44*	0.04ns	-0.17ns	-0.17ns	0.23ns	-0.12ns
	ALL					-0.01ns	0.11ns	0.28*	0.11ns	-0.27*	0.28*	0.23ns
Protein g kg ⁻¹	HONL						-0.61**	0.08ns	-0.25ns	0.11ns	-0.15ns	-0.05ns
	NONL						-0.60**	0.14ns	-0.16ns	-0.31ns	0.31ns	0.08ns
	ALL						-0.90**	-0.90**	-0.74**	0.91**	-0.91**	-0.90**
Oil g kg ⁻¹	HONL							-0.04ns	0.12ns	0.31ns	-0.19ns	-0.50**
	NONL							-0.20ns	-0.06ns	0.56**	-0.44*	-0.49*
	ALL							0.82**	0.64**	-0.83**	0.84**	0.77**

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

Table C1. Continued

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Palmitate g kg ⁻¹	HONL								0.02ns	-0.47*	0.38ns	0.11ns
	NONL								0.33ns	-0.18ns	-0.17ns	0.14ns
	ALL								0.77**	-0.99**	0.99**	0.97**
Stearate g kg ⁻¹	HONL									-0.26ns	0.15ns	0.09ns
	NONL									0.17ns	-0.31ns	-0.37*
	ALL									-0.75**	0.75**	0.72**
Oleate g kg ⁻¹	HONL										-0.95**	-0.81**
	NONL										-0.92**	-0.73**
	ALL										-1.00**	-0.98**
Linoleate g kg ⁻¹	HONL											0.70**
	NONL											0.56**
	ALL											0.98**

Table C2. Phenotypic correlation coefficients among traits on an entry-mean basis for population 2.

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Yield kg ha ⁻¹	HONL	-0.57**	-0.49**	-0.21ns	0.27ns	-0.01ns	0.47*	0.04ns	0.01ns	0.12ns	-0.18ns	-0.07ns
	NONL	-0.14ns	-0.51**	-0.30ns	0.10ns	-0.23ns	0.22ns	0.18ns	0.01ns	0.11ns	-0.15ns	-0.21ns
	ALL	-0.45**	-0.41**	-0.13ns	0.22ns	-0.65**	0.70**	0.67**	0.17ns	-0.66**	0.66**	0.63**
Maturity d‡	HONL		0.42*	0.23ns	-0.49**	-0.13ns	-0.65**	-0.15ns	0.18ns	-0.39*	0.56**	0.30ns
	NONL		-0.12ns	0.51**	-0.06ns	0.02ns	-0.47*	-0.63**	-0.19ns	0.01ns	0.12ns	0.42*
	ALL		0.19ns	0.32*	-0.31*	0.24ns	-0.54**	-0.35*	-0.09ns	0.28*	-0.27*	-0.21ns
Lodging score§	HONL			0.02ns	-0.38*	-0.34ns	-0.31ns	-0.29ns	-0.30ns	0.10ns	0.02ns	0.21ns
	NONL			0.05ns	-0.35ns	-0.17ns	0.26ns	0.09ns	-0.01ns	-0.27ns	0.31ns	-0.13ns
	ALL			0.03ns	-0.37**	-0.04ns	-0.08ns	-0.07ns	-0.16ns	0.05ns	-0.05ns	-0.04ns
Height cm	HONL				-0.24ns	0.10ns	-0.26ns	0.08ns	0.41*	-0.15ns	0.32ns	-0.48*
	NONL				-0.09ns	-0.09ns	0.00ns	-0.56**	0.05ns	0.23ns	-0.12ns	0.10ns
	ALL				-0.16ns	-0.09ns	0.00ns	0.05ns	0.23ns	-0.08ns	0.09ns	0.04ns
Seed wt. mg sd ⁻¹	HONL					0.28ns	0.51**	-0.01ns	-0.38*	0.55**	-0.54**	-0.42*
	NONL					0.62**	-0.29ns	0.13ns	-0.07ns	0.68**	-0.68**	-0.37ns
	ALL					0.07ns	0.17ns	0.12ns	-0.18ns	-0.09ns	0.09ns	0.03ns
Protein g kg ⁻¹	HONL						-0.21ns	0.10ns	-0.18ns	0.15ns	-0.10ns	-0.16ns
	NONL						-0.64**	-0.04ns	-0.37ns	0.42*	-0.33ns	-0.14ns
	ALL						-0.86**	-0.91**	-0.34*	0.93**	-0.93**	-0.92**
Oil g kg ⁻¹	HONL							0.02ns	-0.10ns	0.45*	-0.63**	-0.29ns
	NONL							0.23ns	0.53**	-0.14ns	0.03ns	-0.26ns
	ALL							0.83**	0.32*	-0.83**	0.83**	0.79**

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

Table C2. Continued

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Palmitate g kg ⁻¹	HONL								0.19ns	-0.43*	0.12ns	-0.21ns
	NONL								-0.09ns	-0.10ns	-0.05ns	-0.47*
	ALL								0.25ns	-0.98**	0.98**	0.95**
Stearate g kg ⁻¹	HONL									-0.72**	0.60**	0.14ns
	NONL									-0.02ns	-0.18ns	0.07ns
	ALL									-0.26ns	0.25ns	0.26ns
Oleate g kg ⁻¹	HONL										-0.87**	-0.51**
	NONL										-0.95**	-0.42*
	ALL										-1.00**	-0.98**
Linoleate g kg ⁻¹	HONL											0.39*
	NONL											0.37ns
	ALL											0.98**

Table C3. Phenotypic correlation coefficients among traits on an entry-mean basis for population 3.

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Yield kg ha ⁻¹	HONL	0.45*	0.12ns	0.32ns	-0.32ns	0.25ns	-0.08ns	0.35ns	0.48*	0.02ns	-0.37ns	0.07ns
	NONL	0.05ns	-0.14ns	-0.21ns	0.13ns	-0.31ns	0.25ns	-0.06ns	-0.14ns	-0.24ns	0.34ns	0.02ns
	ALL	0.21ns	-0.26ns	0.04*	0.17ns	-0.66**	0.54**	0.68**	0.63**	-0.67**	0.67**	0.66**
Maturity d‡	HONL		0.27ns	0.77**	-0.22ns	0.24ns	-0.74**	0.10ns	0.20ns	-0.32ns	0.06ns	0.63**
	NONL		0.29ns	0.78**	0.18ns	0.13ns	-0.57**	0.23ns	0.04ns	-0.73**	0.59**	0.77**
	ALL		0.25ns	0.77**	0.00ns	0.03ns	-0.42**	0.06ns	0.10ns	-0.05ns	0.04ns	0.16ns
Lodging score§	HONL			0.37ns	0.36ns	-0.01ns	-0.26ns	0.04ns	-0.04ns	-0.07ns	0.01ns	0.18ns
	NONL			0.29ns	-0.16ns	-0.25ns	-0.04ns	0.51**	0.08ns	-0.33ns	0.10ns	0.53**
	ALL			0.30*	-0.08ns	0.28*	-0.35**	-0.29*	-0.28*	0.35**	-0.36**	-0.28*
Height cm	HONL				-0.05ns	0.09ns	-0.58**	0.28ns	0.32ns	-0.55**	0.22ns	0.70**
	NONL				0.33ns	0.19ns	-0.52**	0.17ns	0.23ns	-0.60**	0.48*	0.57**
	ALL				0.17ns	0.05ns	-0.36**	0.06ns	0.17ns	-0.03ns	0.02ns	0.13ns
Seed wt. mg sd ⁻¹	HONL					0.13ns	0.00ns	-0.12ns	-0.24ns	0.21ns	-0.05ns	-0.21ns
	NONL					0.46*	-0.40*	-0.24ns	0.23ns	-0.07ns	0.12ns	0.05ns
	ALL					-0.19ns	0.10ns	0.28*	0.27*	-0.33*	0.33*	0.31*
Protein g kg ⁻¹	HONL						-0.30ns	-0.02ns	-0.18ns	0.26ns	-0.31ns	-0.01ns
	NONL						-0.75**	-0.13ns	0.20ns	0.17ns	-0.19ns	-0.02ns
	ALL						-0.83**	-0.92**	-0.73**	0.93**	-0.93**	-0.92**
Oil g kg ⁻¹	HONL							0.18ns	0.01ns	0.20ns	-0.11ns	-0.60**
	NONL							-0.03ns	-0.17ns	0.17ns	-0.05ns	-0.41*
	ALL							0.73**	0.56**	-0.73**	0.74**	0.66**

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

Table C3. Continued

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Palmitate g kg ⁻¹	HONL								0.61**	-0.46*	-0.18ns	0.19ns
	NONL								0.34ns	-0.31ns	-0.03ns	0.26ns
	ALL								0.85**	-0.98**	0.97**	0.96**
Stearate g kg ⁻¹	HONL									-0.36ns	-0.19ns	0.21ns
	NONL									0.18ns	-0.38ns	-0.10ns
	ALL									-0.80**	0.80**	0.79**
Oleate g kg ⁻¹	HONL										-0.72**	-0.73**
	NONL										-0.92**	-0.75**
	ALL										-1.00**	-0.99**
Linoleate g kg ⁻¹	HONL											0.40*
	NONL											0.57**
	ALL											0.98**

Table C4. Phenotypic correlation coefficients among traits on an entry-mean basis for population 4.

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Yield kg ha ⁻¹	HONL	0.42*	0.37ns	0.33ns	-0.23ns	-0.27ns	0.13ns	0.07ns	0.03ns	-0.02ns	-0.25ns	0.48*
	NONL	0.08ns	-0.03ns	-0.18**	-0.10ns	-0.19ns	0.20ns	-0.06ns	0.31ns	-0.26ns	0.18ns	0.25ns
	ALL	0.25ns	0.12ns	0.05**	-0.12ns	-0.42**	0.40**	0.37**	0.37**	-0.38**	0.37**	0.45**
Maturity d‡	HONL		0.33ns	0.63**	-0.32ns	-0.26ns	-0.11ns	0.44*	0.36ns	-0.35ns	-0.17ns	0.80**
	NONL		-0.09ns	0.15ns	-0.24ns	0.23ns	-0.64**	-0.04ns	0.05ns	-0.19ns	0.12ns	0.41*
	ALL		0.20ns	0.47**	-0.29*	0.10ns	-0.22ns	-0.10ns	0.05ns	0.11ns	-0.13ns	0.04ns
Lodging score§	HONL			0.34ns	-0.42*	-0.01ns	-0.10ns	-0.17ns	0.04ns	0.17ns	-0.30ns	0.25ns
	NONL			0.49**	-0.18ns	-0.13ns	0.06ns	-0.26ns	-0.14ns	-0.19ns	0.27ns	-0.02ns
	ALL			0.43**	-0.32*	0.16ns	-0.20ns	-0.22ns	-0.18ns	0.20ns	-0.20ns	-0.16ns
Height cm	HONL				0.01ns	0.12ns	-0.17ns	0.22ns	0.15ns	-0.03ns	-0.33ns	0.50**
	NONL				-0.17ns	0.17ns	-0.17ns	0.06ns	-0.18ns	-0.29ns	0.32ns	0.05ns
	ALL				-0.09ns	0.24ns	-0.26ns	-0.19ns	-0.16ns	0.20ns	-0.20ns	-0.12ns
Seed wt. mg sd ⁻¹	HONL					0.42*	-0.44*	0.16ns	-0.12ns	-0.11ns	0.22ns	-0.22ns
	NONL					0.45*	-0.06ns	-0.14ns	-0.22ns	0.20ns	-0.06ns	-0.45*
	ALL					0.05ns	0.01ns	0.12ns	0.00ns	-0.12ns	0.13ns	0.05ns
Protein g kg ⁻¹	HONL						-0.40*	-0.09ns	0.14ns	0.19ns	-0.18ns	-0.27ns
	NONL						-0.58**	0.03ns	-0.15ns	0.18ns	-0.11ns	-0.25ns
	ALL						-0.92**	-0.92**	-0.73**	0.92**	-0.92**	-0.92**
Oil g kg ⁻¹	HONL							-0.26ns	0.11ns	0.23ns	-0.12ns	-0.22ns
	NONL							-0.18ns	0.34ns	0.15ns	-0.17ns	-0.26ns
	ALL							0.90**	0.77**	-0.91**	0.91**	0.87**

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

Table C4. Continued

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Palmitate g kg ⁻¹	HONL								-0.01ns	-0.71**	0.42*	0.58**
	NONL								-0.14ns	-0.37ns	0.21ns	0.31ns
	ALL								0.77**	-1.00**	0.99**	0.98**
Stearate g kg ⁻¹	HONL									-0.16ns	-0.20ns	0.13ns
	NONL									0.27ns	-0.43*	-0.14ns
	ALL									-0.78**	0.77**	0.77**
Oleate g kg ⁻¹	HONL										-0.80**	-0.62**
	NONL										-0.96**	-0.51**
	ALL										-1.00**	-0.98**
Linoleate g kg ⁻¹	HONL											0.13ns
	NONL											0.35ns
	ALL											0.97**

Table C5. Phenotypic correlation coefficients among traits on an entry-mean basis for population 5.

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Yield kg ha ⁻¹	HONL	0.40*	-0.05ns	-0.02ns	0.25ns	-0.17ns	-0.04ns	0.05ns	-0.37ns	0.02ns	0.12ns	-0.04ns
	NONL	0.51**	0.30ns	0.55ns	-0.03ns	-0.31ns	-0.24ns	0.03ns	0.14ns	-0.45*	0.40*	0.44*
	ALL	0.56**	0.02ns	0.32ns	0.18ns	-0.62**	0.45**	0.60**	0.36**	-0.61**	0.61**	0.62**
Maturity d‡	HONL		0.04ns	0.51**	0.41*	-0.04ns	-0.68**	0.24ns	0.01ns	-0.40*	0.43*	0.39*
	NONL		0.02ns	0.77**	-0.18ns	-0.41*	-0.41*	-0.20ns	0.09ns	-0.71**	0.69**	0.62**
	ALL		-0.01ns	0.65**	0.14ns	-0.42**	0.05ns	0.36**	0.29*	-0.39**	0.39**	0.44**
Lodging score§	HONL			0.25ns	0.13ns	0.41*	-0.23ns	0.47*	0.22ns	-0.26ns	0.18ns	-0.05ns
	NONL			0.26ns	0.00ns	0.13ns	-0.29ns	-0.03ns	0.30ns	-0.19ns	0.16ns	0.22ns
	ALL			0.23ns	0.04ns	0.22ns	-0.23ns	-0.09ns	0.10ns	0.10ns	-0.11ns	-0.10ns
Height cm	HONL				0.42*	-0.01ns	-0.47*	0.22ns	0.28ns	-0.43*	0.34ns	0.32ns
	NONL				-0.10ns	-0.29ns	-0.41*	-0.22ns	0.22ns	-0.64**	0.63**	0.42*
	ALL				0.15ns	-0.22ns	-0.07ns	0.17ns	0.30*	-0.20ns	0.20ns	0.24ns
Seed wt. mg sd ⁻¹	HONL					-0.13ns	-0.24ns	0.45*	0.19ns	-0.34ns	0.30ns	0.09ns
	NONL					0.35ns	-0.20ns	-0.26ns	0.03ns	0.50**	-0.44*	-0.46*
	ALL					-0.11ns	0.05ns	0.18ns	0.20ns	-0.17ns	0.17ns	0.14ns
Protein g kg ⁻¹	HONL						-0.48*	0.05ns	-0.09ns	0.15ns	-0.27ns	0.10ns
	NONL						-0.28ns	0.07ns	0.06ns	0.42*	-0.45*	-0.20ns
	ALL						-0.86**	-0.89**	-0.65**	0.91**	-0.91**	-0.89**
Oil g kg ⁻¹	HONL							-0.17ns	-0.06ns	0.19ns	-0.09ns	-0.35ns
	NONL							-0.06ns	-0.08ns	0.23ns	-0.17ns	-0.41*
	ALL							0.84**	0.59**	-0.85**	0.85**	0.81**

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = High oleate, normal linolenate lines, NONL = normal oleate, normal linolenate lines.

‡ = Days after 31 August.

§ = Score of 1 (all plants erect) to 5 (all plants prostrate).

Table C5. Continued

Trait	Class†	Maturity	Lodging	Height	Seed wt.	Protein	Oil	Palmitate	Stearate	Oleate	Linoleate	Linolenate
Palmitate g kg ⁻¹	HONL								0.28ns	-0.58**	0.48*	0.08ns
	NONL								-0.36ns	-0.13ns	0.03ns	0.15ns
	ALL								0.70**	-0.99**	0.99**	0.98**
Stearate g kg ⁻¹	HONL									-0.52**	0.24ns	0.25ns
	NONL									0.09ns	-0.19ns	-0.13ns
	ALL									-0.72**	0.71**	0.71**
Oleate g kg ⁻¹	HONL										-0.93**	-0.74**
	NONL										-0.98**	-0.78**
	ALL										-1.00**	-0.99**
Linoleate g kg ⁻¹	HONL											0.68**
	NONL											0.70**
	ALL											0.99**

APPENDIX D

ANALYSIS OF VARIANCE AND ENTRY MEANS ACROSS ENVIRONMENTS

AND WITHIN EACH ENVIRONMENT

Table D1. Analysis of variance for fatty ester concentration across 18 environments in 2010 and 2011.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Environments (E)	17	183.8	**	183.8	**	30656.5	**	16775.0	**	789.9	**
Replications/E	18	16.4	**	16.4	**	166.45	ns	152.5	*	6.9	**
Genotypes(G)	17	13099.7	**	13099.7	**	2607756.0	**	2069842.1	**	15966.7	**
G x E	289	13.8	**	13.8	**	680.4	**	605.8	**	32.3	**
Error	306	3.1		3.1		104.2		86.6		2.2	
CV (%)‡		2.2		2.2		1.7		3.6		4.9	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D2. Mean palmitate concentration for lines grown at 18 environments in 2010 and 2011.

Entry	Class†	Algona, IA 2010	Algona, IA 2011	Princeton, IL 2010	Princeton, IL 2011	Dallas Center, IA 2010	Dallas Center, IA 2011	Napoleon, OH Date 1 2010	Napoleon, OH Date 2 2010	Napoleon, OH Date 1 2011	Napoleon, OH Date 2 2011	Mascoutah, IL 2010	Mascoutah, IL Date 1 2011	Mascoutah, IL Date 2 2011	Crawfordsville, AR 2010	Crawfordsville, AR 2011	Salinas, PR	Wainea, HI	Viluco, CH	Overall Mean	Range	LSD ‡
YR25C09	HONL	62	64	61	60	64	62	61	60	60	63	62	61	61	64	62	67	69	61	62	9	3
YR26T09	HONL	65	63	65	65	60	66	59	65	65	65	67	65	63	64	63	69	71	62	65	12	4
YR27E09	HONL	67	67	69	63	64	65	66	68	63	69	65	63	67	64	65	68	66	64	66	6	5
92Y61	HOLL	64	66	65	61	62	67	62	67	64	68	63	61	73	63	62	67	70	68	65	11	3
XR28K10	HOLL	57	60	60	55	57	59	59	59	59	66	57	55	61	55	55	66	63	60	59	12	5
XR28L10	HOLL	57	62	60	56	58	61	58	60	61	66	59	55	66	56	55	62	62	62	60	11	3
XR31C09	HOLL	61	62	63	58	62	62	63	63	60	68	61	60	66	59	58	66	67	61	62	9	3
93Y23	HOLL	61	64	62	57	59	61	63	60	61	68	61	57	63	56	57	61	66	61	61	12	2
93Y30	HOLL	60	64	62	58	61	61	61	64	62	68	58	58	65	57	56	63	66	58	61	12	3
IA2088	MOLL	88	88	84	82	84	84	87	84	86	87	85	91	82	88	85	97	92	81	86	17	3
IA3036	MOLL	84	86	84	80	82	84	82	80	86	86	83	84	86	86	79	97	84	78	84	19	3
IA3039	MOLL	86	87	85	79	86	84	79	85	82	87	88	86	86	88	85	94	94	80	86	15	4
93M20	NOLL	105	102	105	101	105	104	105	104	102	103	107	102	97	101	105	111	106	97	103	15	6
93Y03	NOLL	104	100	103	101	103	102	100	99	100	100	104	104	94	98	100	109	107	96	101	15	5
92M82	NOLL	103	102	100	100	100	102	99	99	101	102	100	97	95	93	97	105	108	99	100	15	4
92Y60	NONL	112	106	107	107	109	109	108	103	105	105	110	113	99	112	112	118	106	102	108	19	6
92Y80	NONL	113	111	112	108	111	109	110	108	108	109	110	111	101	110	110	120	114	104	110	19	6
93Y20	NONL	95	93	95	89	93	94	94	92	94	94	94	90	86	91	92	98	96	88	93	12	3
Mean		80	80	80	77	79	80	79	79	79	82	80	78	78	78	78	86	84	77	80	9	2

† = HONL = High oleate, normal linolenate; HOLL = high oleate, low linolenate; MOLL = mid oleate, low linolenate; NOLL = normal oleate, low linolenate; NONL = normal oleate, normal linolenate.

‡ = Least significant difference at the 0.05 probability level for comparisons among environments.

Table D3. Mean stearate concentration for lines grown at 18 environments in 2010 and 2011.

Entry	Class†	Mean Stearate Concentration (g kg ⁻¹)																		LSD ‡		
		Algona, IA 2010	Algona, IA 2011	Princeton, IL 2010	Princeton, IL 2011	Dallas Center, IA 2010	Dallas Center, IA 2011	Napoleon, OH Date 1 2010	Napoleon, OH Date 2 2010	Napoleon, OH Date 1 2011	Napoleon, OH Date 2 2011	Mascoutah, IL 2010	Mascoutah, IL Date 1 2011	Mascoutah, IL Date 2 2011	Crawfordsville, AR 2010	Crawfordsville, AR 2011	Salinas, PR	Wamea, HW	Viluco, CH		Overall Mean	Range
YR25C09	HONL	37	40	38	42	36	37	40	44	35	37	37	35	54	35	34	41	39	61	40	27	7
YR26T09	HONL	33	38	36	38	32	36	37	40	33	35	35	33	50	34	31	37	35	53	37	22	5
YR27E09	HONL	32	37	36	38	32	35	37	38	31	36	33	32	50	33	34	38	32	54	37	23	4
92Y61	HOLL	38	43	43	44	36	44	42	49	38	40	38	37	65	38	36	42	41	62	43	29	5
XR28K10	HOLL	37	41	42	44	35	43	41	48	36	41	36	35	44	37	35	43	37	57	41	23	3
XR28L10	HOLL	36	43	45	44	37	41	42	46	33	40	38	35	64	39	36	41	36	57	42	31	4
XR31C09	HOLL	39	42	42	44	37	43	42	49	37	45	41	41	59	41	37	44	39	66	44	29	7
93Y23	HOLL	43	46	46	46	39	45	48	48	39	47	42	43	60	42	41	46	42	64	46	25	4
93Y30	HOLL	40	44	44	45	39	45	46	48	37	45	38	41	58	41	40	44	40	65	45	28	6
IA2088	MOLL	43	47	48	52	41	43	50	53	43	43	43	39	60	44	38	53	39	75	47	37	3
IA3036	MOLL	45	49	48	50	42	47	51	46	44	48	44	54	67	49	46	53	35	72	50	37	4
IA3039	MOLL	51	50	51	53	46	51	53	54	47	50	47	47	72	47	46	54	39	76	52	37	4
93M20	NOLL	45	49	50	50	42	49	48	50	36	44	46	45	72	48	44	50	41	59	48	36	5
93Y03	NOLL	39	42	43	44	38	41	43	48	36	44	39	37	53	40	36	44	38	62	43	26	5
92M82	NOLL	37	42	40	41	35	39	41	45	37	36	38	36	53	36	34	41	35	55	40	21	3
92Y60	NONL	46	49	50	49	43	47	51	56	43	47	43	45	67	44	44	50	40	65	49	27	6
92Y80	NONL	40	45	45	47	41	45	45	50	39	44	43	41	56	41	38	45	39	72	45	34	6
93Y20	NONL	42	46	43	41	37	46	45	47	35	42	41	40	57	40	40	45	39	65	44	30	4
Mean		40	44	44	45	38	43	45	48	38	42	40	40	59	40	38	45	38	63	44	25	2

† = HONL = High oleate, normal linolenate; HOLL = high oleate, low linolenate; MOLL = mid oleate, low linolenate; NOLL = normal oleate, low linolenate; NONL = normal oleate, normal linolenate.

‡ = Least significant difference at the 0.05 probability level for comparisons among environments.

Table D4. Mean linoleate concentration for lines grown at 18 environments in 2010 and 2011.

Entry	Class†	g kg ⁻¹																		LSD ‡		
		Algona, IA 2010	Algona, IA 2011	Princeton, IL 2010	Princeton, IL 2011	Dallas Center, IA 2010	Dallas Center, IA 2011	Napoleon, OH Date 1 2010	Napoleon, OH Date 2 2010	Napoleon, OH Date 1 2011	Napoleon, OH Date 2 2011	Mascoutah, IL 2010	Mascoutah, IL Date 1 2011	Mascoutah, IL Date 2 2011	Crawfordsville, AR 2010	Crawfordsville, AR 2011	Salinas, PR	Wainea, HI	Viluco, CH		Overall Mean	Range
YR25C09	HONL	13	27	15	11	15	26	18	20	25	43	10	10	34	8	10	9	12	22	18	35	4
YR26T09	HONL	14	27	15	13	11	21	13	25	24	46	9	13	35	9	10	9	13	21	18	38	4
YR27E09	HONL	14	31	15	13	14	23	17	23	27	45	10	12	30	12	11	10	14	23	19	35	4
92Y61	HOLL	31	53	31	29	34	44	37	47	52	87	22	21	87	17	21	22	37	52	40	70	9
XR28K10	HOLL	30	56	36	27	32	44	32	43	52	88	24	20	73	18	22	14	32	51	38	74	7
XR28L10	HOLL	29	61	32	25	32	45	35	45	57	88	24	19	79	17	27	21	35	53	40	72	6
XR31C09	HOLL	39	69	33	31	41	49	37	60	59	110	27	19	79	15	23	23	29	56	44	96	7
93Y23	HOLL	55	94	50	43	48	61	53	80	86	144	39	28	92	23	37	26	42	69	60	121	7
93Y30	HOLL	55	95	52	44	52	68	54	96	99	162	36	33	112	24	33	29	47	71	65	138	8
IA2088	MOLL	354	390	306	292	323	293	332	333	382	414	306	362	357	285	292	354	325	309	334	129	34
IA3036	MOLL	293	381	281	280	292	318	293	334	355	378	263	253	381	243	251	324	233	321	304	149	37
IA3039	MOLL	321	384	298	272	319	315	288	341	343	365	308	267	353	279	281	307	335	321	317	117	38
93M20	NOLL	585	595	561	554	602	580	588	591	626	635	569	554	570	511	558	586	622	585	582	124	17
93Y03	NOLL	574	589	555	542	583	572	576	562	594	599	569	560	587	465	534	576	600	572	567	134	19
92M82	NOLL	567	572	544	540	565	553	572	558	582	617	548	535	580	452	505	578	598	570	557	165	21
92Y60	NONL	533	539	513	516	535	532	533	524	551	560	534	534	516	488	519	544	569	523	531	81	27
92Y80	NONL	538	549	522	507	534	533	544	525	555	565	527	525	541	484	503	534	548	509	530	81	27
93Y20	NONL	570	563	553	545	583	556	554	557	593	591	551	519	551	515	544	564	589	538	558	78	16
Mean		256	282	245	238	256	257	254	265	281	308	243	238	281	215	232	252	260	259	257	93	6

† = HONL = High oleate, normal linolenate; HOLL = high oleate, low linolenate; MOLL = mid oleate, low linolenate; NOLL = normal oleate, low linolenate; NONL = normal oleate, normal linolenate.

‡ = Least significant difference at the 0.05 probability level for comparisons among environments.

Table D5. Mean linolenate concentration for lines grown at 18 environments in 2010 and 2011.

Entry	Class†	Algona, IA 2010	Algona, IA 2011	Princeton, IL 2010	Princeton, IL 2011	Dallas Center, IA 2010	Dallas Center, IA 2011	Napoleon, OH Date 1 2010	Napoleon, OH Date 2 2010	Napoleon, OH Date 1 2011	Napoleon, OH Date 2 2011	Mascoutah, IL 2010	Mascoutah, IL Date 1 2011	Mascoutah, IL Date 2 2011	Crawfordsville, AR 2010	Crawfordsville, AR 2011	Salinas, PR	Wainea, HI	Viluco, CH	Overall Mean	Range	LSD ‡
YR25C09	HONL	31	47	36	28	36	37	37	39	41	53	28	26	55	23	26	28	37	48	36	32	6
YR26T09	HONL	32	46	35	29	31	40	32	44	40	57	27	26	54	24	26	29	41	42	36	33	4
YR27E09	HONL	34	48	35	32	34	42	38	42	42	55	30	26	50	22	28	31	41	45	37	33	4
92Y61	HOLL	19	23	19	18	20	20	20	23	22	26	17	16	30	15	16	21	24	27	21	15	3
XR28K10	HOLL	18	24	20	18	19	21	19	22	20	26	17	15	28	15	16	22	22	26	20	13	2
XR28L10	HOLL	18	25	19	17	19	21	19	22	20	25	18	15	30	15	16	20	22	26	20	15	3
XR31C09	HOLL	17	19	17	16	18	16	15	19	18	23	17	15	23	13	14	19	17	22	18	9	1
93Y23	HOLL	20	23	22	18	19	19	20	22	21	27	20	17	25	15	18	19	22	22	21	12	2
93Y30	HOLL	20	23	21	19	21	20	20	24	23	28	18	17	25	16	18	19	22	25	21	12	2
IA2088	MOLL	9	11	10	9	9	9	10	11	10	11	9	9	15	9	8	10	9	10	10	6	2
IA3036	MOLL	9	10	9	9	8	10	9	12	9	11	8	8	14	8	8	16	8	9	10	8	1
IA3039	MOLL	9	10	10	9	9	9	9	12	10	11	8	8	11	8	9	9	9	10	10	4	1
93M20	NOLL	23	24	22	22	22	22	22	22	22	23	22	20	25	20	21	21	21	22	22	5	2
93Y03	NOLL	23	26	23	21	22	23	23	25	23	29	20	19	29	18	19	25	23	28	23	11	2
92M82	NOLL	24	27	25	22	22	24	25	27	25	28	22	19	33	21	20	24	25	28	25	14	2
92Y60	NONL	72	83	70	63	66	71	68	73	77	87	63	58	83	56	59	77	84	78	72	31	7
92Y80	NONL	75	84	72	67	75	75	72	76	84	86	60	58	89	57	58	81	94	72	74	37	5
93Y20	NONL	75	83	73	67	75	72	65	78	81	86	62	56	80	53	62	72	84	72	72	32	5
Mean		29	35	30	27	29	31	29	33	33	39	26	24	39	23	24	30	34	34	30	16	1

† = HONL = High oleate, normal linolenate; HOLL = high oleate, low linolenate; MOLL = mid oleate, low linolenate; NOLL = normal oleate, low linolenate; NONL = normal oleate, normal linolenate.

‡ = Least significant difference at the 0.05 probability level for comparisons among environments.

Table D6. Analysis of variance for fatty ester concentration at Algona, IA, in 2010.

Sources of variation	df	Mean Squares									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	0.4	ns	0.0	ns	935.3	*	845.8	*	6.7	ns
Genotypes	17	853.7	**	45.5	**	155920.0	**	121543.5	**	947.0	**
Error	17	1.6		2.1		113.9		101.8		1.7	
CV (%)‡		1.6		3.6		1.8		3.9		4.4	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D7. Analysis of variance for fatty ester concentration at Algona, IA, in 2011.

Sources of variation	df	Mean Squares									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	9.2	ns	2.6	ns	324.6	ns	203.2	ns	5.2	ns
Genotypes	17	685.7	**	29.6	**	144857.6	**	115866.8	**	1219.4	**
Error	17	2.1		1.5		193.0		147.0		4.4	
CV (%)‡		1.8		2.8		2.5		4.3		6.0	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D8. Analysis of variance for fatty ester concentration at Princeton, IL, in 2010.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	0.0	ns	1.6	ns	49.2	ns	55.3	ns	1.8	ns
Genotypes	17	736.4	**	38.7	**	142008.8	**	111733.8	**	854.6	**
Error	17	1.1		1.1		38.6		34.5		0.9	
CV (%)‡		1.3		2.3		1.0		2.4		3.2	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D9. Analysis of variance for fatty ester concentration at Princeton, IL, in 2011.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	9.3	*	0.1	ns	29.7	ns	77.1	ns	0.0	ns
Genotypes	17	772.9	**	39.7	**	140249.7	**	110330.3	**	718.4	**
Error	17	1.8		3.1		44.1		42.5		0.6	
CV (%)‡		1.7		3.9		1.1		2.7		2.9	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D10. Analysis of variance for fatty ester concentration at Dallas Center, IA, in 2010.

<u>Mean Squares</u>											
Sources of variation	df	Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	5.1	ns	2.6	ns	222.0	ns	91.5	ns	0.9	ns
Genotypes	17	521.5	**	28.6	**	156504.4	**	123679.1	**	896.9	**
Error	17	1.6		2.5		107.9		58.3		3.9	
CV (%)‡		1.6		4.1		1.7		3.0		6.8	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D11. Analysis of variance for fatty ester concentration at Dallas Center, IA, in 2011.

<u>Mean Squares</u>											
Sources of variation	df	Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	1.1	ns	11.8	ns	168.1	ns	33.2	ns	6.3	ns
Genotypes	17	731.9	**	38.0	**	142395.0	**	112768.4	**	923.9	**
Error	17	2.7		4.3		80.2		46.8		3.1	
CV (%)‡		2.0		4.8		1.5		2.7		5.8	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D12. Analysis of variance for fatty ester concentration at Napoleon, OH date 1 planting, in 2010.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	0.1	ns	0.2	ns	7.3	ns	19.4	ns	1.6	ns
Genotypes	17	763.5	**	44.8	**	150905.2	**	119791.6	**	791.4	**
Error	17	2.3		1.8		48.4		47.7		1.0	
CV (%)‡		1.9		3.0		1.2		2.7		3.5	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D13. Analysis of variance for fatty ester concentration at Napoleon, OH date 2 planting, in 2010.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	0.3	ns	1.8	ns	40.1	ns	55.3	ns	1.2	ns
Genotypes	17	650.8	**	38.3	**	138325.0	**	110761.1	**	947.2	**
Error	17	2.7		2.4		39.2		32.4		1.7	
CV (%)‡		2.1		3.3		1.1		2.2		4.0	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D14. Analysis of variance for fatty ester concentration at Napoleon, OH, date 1 planting, in 2011.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	10.4	ns	2.9	ns	13.3	ns	108.9	ns	3.7	ns
Genotypes	17	713.5	**	34.9	**	153656.0	**	122860.3	**	1169.6	**
Error	17	3.6		2.9		73.4		67.9		1.6	
CV (%)‡		2.4		4.5		1.5		2.9		3.9	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D15. Analysis of variance for fatty ester concentration at Napoleon, OH, date 2 planting, in 2011.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	45.5	*	51.8	**	9.3	ns	306.1	*	32.5	*
Genotypes	17	559.6	**	39.6	**	137105.1	**	112586.4	**	1326.9	**
Error	17	1.1		3.0		95.1		68.1		4.0	
CV (%)‡		1.3		4.1		1.8		2.7		5.2	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D16. Analysis of variance for fatty ester concentration at Mascoutah, IL, in 2010.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	3.1	ns	26.8	**	52.4	ns	213.0	ns	0.0	ns
Genotypes	17	822.0	**	28.0	**	150784.3	**	119259.9	**	625.0	**
Error	17	1.6		1.7		68.7		59.5		1.9	
CV (%)‡		1.6		3.2		1.4		3.2		5.3	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D17. Analysis of variance for fatty ester concentration at Mascoutah, IL date 1 planting, in 2011.

<u>Mean Squares</u>											
Sources of variation	df	Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	1.7	ns	0.2	ns	261.2	*	144.3	ns	4.5	*
Genotypes	17	888.0	**	61.0	**	147159.2	**	116168.9	**	530.9	**
Error	17	0.8		1.2		52.8		45.6		0.8	
CV (%)‡		1.1		2.8		1.2		2.8		3.8	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D18. Analysis of variance for fatty ester concentration at Mascoutah, IL date 2 planting, in 2011.

<u>Mean Squares</u>											
Sources of variation	df	Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	19.8	*	85.9	ns	14.5	ns	154.7	ns	24.6	**
Genotypes	17	440.9	**	126.0	**	128007.9	**	105345.5	**	1175.3	**
Error	17	4.3		21.4		119.9		77.8		2.3	
CV (%)‡		2.6		7.9		2.0		3.1		3.9	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D19. Analysis of variance for fatty ester concentration at Crawfordsville, AR, in 2010.

<u>Mean Squares</u>											
Sources of variation	df	Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	2.8	ns	5.1	*	421.9	ns	260.3	ns	0.0	ns
Genotypes	17	808.5	**	43.3	**	123425.3	**	95346.7	**	500.0	**
Error	17	4.9		1.0		447.5		346.1		2.0	
CV (%)‡		2.8		2.5		3.3		8.7		6.3	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D20. Analysis of variance for fatty ester concentration at Crawfordsville, AR, in 2011.

<u>Mean Squares</u>											
Sources of variation	df	Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	2.5	ns	6.5	ns	2.0	ns	18.3	ns	3.8	ns
Genotypes	17	856.0	**	39.7	**	140032.3	**	109555.3	**	587.8	**
Error	17	1.5		2.2		174.8		157.3		0.9	
CV (%)‡		1.6		3.9		2.1		5.4		3.9	

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D21. Analysis of variance for fatty ester concentration at Salinas, PR, in 2011.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	33.7	*	10.1	ns	3.6	ns	45.8	ns	0.7	ns
Genotypes	17	943.4	**	51.7	**	166168.1	**	128978.0	**	989.1	**
Error	17	5.6		2.8		32.4		44.1		2.0	
CV (%)‡		2.8		3.7		1.0		2.6		4.7	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D22. Analysis of variance for fatty ester concentration at Waimea, HW, in 2011.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	134.3	**	33.1	*	337.9	ns	10.2	ns	13.0	**
Genotypes	17	712.2	**	13.7	**	167610.0	**	134078.2	**	1398.7	**
Error	17	14.1		4.2		107.4		149.3		1.3	
CV (%)‡		4.5		5.3		1.8		4.7		3.4	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

Table D22. Analysis of variance for fatty ester concentration at Viluco, CH, in 2011.

Sources of variation	df	<u>Mean Squares</u>									
		Palmitate†		Stearate†		Oleate†		Linoleate†		Linolenate†	
Replications	1	16.8	*	73.5	ns	103.7	ns	102.3	ns	16.8	ns
Genotypes	17	573.8	**	98.4	**	134208.6	**	109487.6	**	914.4	**
Error	17	2.1		27.0		37.4		31.8		5.0	
CV (%)‡		1.9		8.2		1.1		2.2		6.6	

* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

ns = Not significant at the 0.05 probability level.

† = Fatty esters were measured in g kg⁻¹.

‡ = Coefficient of variation.

ACKNOWLEDGMENTS

I would like to thank my wife and children for being supportive and understanding during this time. I would like to especially thank Dr Fehr for the education and mentoring he has provided me, as well as being supportive and understanding. I would like to thank Steve Schnebly for giving me the opportunity to take time away from my job at DuPont Pioneer in order to successfully complete my degree. I would like to thank my fellow graduate students who I have had the privilege of working with during my time at Iowa State University, Ryan Brace, Shaylyn Wiarda, John Gill, Justin Mardorf, Brian De Vries, and Sheilah Oltmans. Lastly, I would like to thank the many employees at DuPont Pioneer who have helped me with trial execution and data collection.