Registration of N6001 Soybean Germplasm with Enhanced Yield Derived from Japanese Cultivar Suzuyutaka

T. E. Carter Jr.,* S. M. Todd, and A. M. Gillen

Abstract
The genetic base of US soybean \[Glycine max\, (L.) Merr.\] is relatively narrow and derived primarily from Chinese ancestors. Since Japanese lines have been an underutilized resource, their incorporation into US breeding populations may aid soybean improvement. N6001 (Reg No. GP-396, PI 674170) is a conventional soybean germplasm of group VI maturity released by the USDA–ARS and the North Carolina Agricultural Research Service in September 2014. N6001 traces 25% of its pedigree to Japanese cultivar Suzuyutaka and 75% to US cultivar Young. This is the first release of a germplasm derived from Suzuyutaka, which is adapted to North America. N6001 was yield-tested across the southeastern United States in the United Soybean Board Southern Diversity Yield Trial Project and in the USDA Uniform Soybean Tests–Southern States. N6001 yielded 8.9% greater than, and had comparable protein content to, the adapted parent Young \((p < 0.05)\) in the Uniform Tests. N6001 also yielded 8.7% more than Young \((p < 0.05)\) in the Diversity Trials. Over 24 environments, N6001 yielded 98% of elite check cultivar NC-Roy. The improved performance of N6001 over its adapted parent, and near parity with NC-Roy, suggests that yield-enhancing alleles were transferred from Suzuyutaka to N6001. The maintenance of seed protein content with increased yield in N6001 suggests that these genetics may help mitigate the typical negative relation between seed protein content and seed yield.

SOYBEAN \[Glycine max\, (L.) Merr.\] breeders have been highly successful at developing improved North American cultivars for the past six decades (Orf et al., 2004). However, this progress rests on a relatively narrow genetic base that was formed early in the history of modern North American soybean breeding and has been very slow to expand (Carter et al., 2004; Gizlice et al., 1993; Gizlice et al., 1994; Hyten et al., 2006). The southern US germplasm pool is quite distinct from that of the Midwest and almost entirely defined by 17 ancestors, which were imported primarily from China (Gizlice et al., 1994). The coefficient of parentage \((CP, Malecot, 1948)\) of public southern cultivars released between 1979 and 1988 was 0.28 (Gizlice et al., 1993), indicating that their average relatedness is that of half-sibs.

While maintenance and utilization of broad genetic resources has traditionally been viewed as insurance against future biotic threats to crop production, recent economic research has suggested that broadening the genetic base has the additional inherent value of providing opportunities to improve yield potential (Simpson, 2005). Empirical evidence from Manjarrez-Sandoval et al. (1997b, 1997c) and Carter et al. (2004) supports this view by demonstrating that genetic variance for yield and predicted gain from selection are higher in soybean breeding populations when the CP for the parental stocks is low \((<0.27)\).

Previous studies have shown both substantial genetic diversity among Japanese cultivars and great divergence between them and Chinese or Korean types (Zhou et al., 2000; Zhou et al., 2002; Ude et al., 2003). However, relatively little of this Japanese diversity has been incorporated into North American breeding programs. The landrace ‘Tokyo’ \((PI 548493)\) is the only major contributor of Japanese genetics to southern US applied breeding programs. This genetic isolation makes the Japanese germplasm pool a good place to search for unique genetics to continue soybean improvement in the United States. The release

Abbreviations: CP, coefficient of parentage; SAVE, Soybean Asian Variety Evaluation Project; TARS, USDA–ARS Tropical Agricultural Research Station.
of N6001 (Reg No. GP-396, PI 674170) builds on previous efforts to expand the genetic base of US soybean breeding (Abdel-Haleem et al., 2013; Boerma et al., 2010; Boerma et al., 2011; Carter et al., 2003; Carter et al., 2007; Carter et al., 2008; Carter et al., 2010) by releasing the first high-yielding breeding line that incorporates genetics from the Japanese cultivar Suzuyutaka (PI 561395).

Methods

Agronomic Performance of Japanese Antecedent Suzuyutaka

‘Suzuyutaka’ was evaluated via the United Soybean Board-sponsored Soybean Asian Variety Evaluation Project (SAVE), a cooperative public–private testing program to evaluate the performance of modern Asian cultivars in North America (Manjarrez-Sandoval et al., 1997a). Suzuyutaka was evaluated alongside 11 other Asian cultivars and 8 US checks in 14 environments across the southern United States in 1996 and 1997. Suzuyutaka was classified as having group IV maturity in these trials and yielded 75% of the appropriate maturity checks, which was higher than any other MG IV Asian genotype in the test.

Pedigree

N6001 is derived from a cross of USDA–ARS cultivar Young (Burton et al., 1987; PI 508266) × USDA–ARS breeding line N94-7350. Young is derived from a cross of cultivars Davis (Caviness and Walters, 1966; PI 553039) × Essex (Smith and Camper, 1973; PI 548667). N94-7350 was derived from a cross of Young × Suzuyutaka. Suzuyutaka is a Japanese cultivar derived from a cross of Karekei52 × Oku Shirome (PI 594243; Fig. 1, Shoji Miyazaki, personal communication, 1996). Oku Shirome is derived from a cross of ‘Nema Shirazu’ (PI 594231) × ‘Nangun Takedate’ (PI 594228). Nema Shirazu is a selection out of the Japanese landrace Geden Shirazu (PI 227557). Karekei52 is a Japanese breeding line developed from a cross of Nema Shirazu and the North American cultivar Harosoy (PI 548573; Weiss and Stevenson, 1955). Harosoy is a US cultivar derived from the backcross of ‘Mandarin (Ottawa)’ (PI 548379) to a selection from Mandarin (Ottawa) × ‘AK (Harrow)’ (PI 548298).

Suzuyutaka is descended from the Japanese landraces Geden Shirazu and Nangun Takedate and the northern US cultivar Harosoy (Fig. 1; Shoji Miyazaki, personal communication, 1996). Geden Shirazu is the most important ancestor of modern Japanese soybean germplasm (Zhou et al., 2000; Shoji Miyazaki, personal communication, 1996) but thus far, its pedigree has been incorporated into North American germplasm only via USDA–ARS germplasm release N6202 (PI 658498; Carter et al., 2010), which is a descendant of the Japanese cultivar Nakasennari (PI 507079). The relation of Suzuyutaka to Nakasennari is slight, with a CP of only 0.125 between the two (Fig. 1). For the purposes of calculation of CP, we arbitrarily assumed no relationship between Nema Shirazu, Nangun Takedate, and Houjaku. To our knowledge, this is the first incorporation of genetics from Nangun Takedate into North American germplasm. While Harosoy has been an important contributor to northern US germplasm, its relation to the southern germplasm pool is modest and derived from its coancestry with the southern US soybean ancestor ‘S-100’ (PI 548488; the CP is 0.25 between the two, Carter et al., 1993). To our knowledge, this is the first release descended directly from Harosoy that appears in the southern US germplasm pool (Gizlice et al., 1994). The CP of Harosoy and N6001 is 0.0742, with most of this relation (0.0625) occurring because N6001 is a grandchild of Harosoy. The remaining CP between the two (0.0117) is derived more indirectly from the relation between antecedents AK (Harrow) and Young (a descendant of S-100).

Fig. 1. Pedigree of Japanese cultivars Suzuyutaka and Nakasennari (Shoji Miyazaki, personal communication, 1996). Japanese and US landraces are aligned on the left, first-generation cultivars i.e., cultivars derived from crossing two landraces from which modern breeding efforts originated) are aligned in the middle, and more modern genotypes are further to the right. N6002 is derived from a Young (Burton et al. 1987) × (Young × Suzuyutaka) backcross. This release notice represents the first incorporation of Suzuyutaka genetics into the US germplasm pool. Nakasennari is an ancestor of the earlier release N6202 (Carter et al. 2010) and is included to show pedigree differences and similarities among recent releases incorporating Japanese germplasm. Geden Shirazu, Mandarin (Ottawa), AK (Harrow), Houjaku, and Nangun Takedate are landraces from which modern breeding efforts in North America and Japan originate. Mandarin (Ottawa) and Nangun Takedate genetics have not previously been incorporated into southern US germplasm. Mandarin (Ottawa) and AK (Harrow) have contributed significantly to northern US and Canadian soybean cultivars. AK (Harrow) is related to Young via S-100. Geden Shirazu genetics have only recently been incorporated into southern US germplasm releases (Carter et al., 2010).
Breeding Line Development

The cross between Young and N94-7350 was made at the Central Crops Research Station in Clayton, NC, during summer 2003, and F₁ plants were grown at the USDA-ARS Tropical Agricultural Research Station (TARS) in Isabela, PR, during winter 2003–2004. The F₁ seed was advanced at the Central Crops Research Station during summer 2004 using the single seed descent procedure (Brim, 1966). Subsequently, F₂ plants were grown at TARS and subjected to single seed descent in the winter of 2004–2005. The F₂ plants were grown at the Sandhills Research Station at Jackson Springs, NC, during summer 2005 for individual plant selection. From these plants, 194 F₃-derived full-sib progeny rows were grown in one-row nursery plots at the Caswell Research Farm, Kinston, NC, in 2006. Visually superior breeding lines were retested in three-row nursery plots at the Caswell Research Farm in 2007. Progeny lines that were superior for overall agronomic performance and appearance were retained for further testing. One of the progeny lines, N07-14718, was identified as a promising breeding line and subsequently renamed N6001.

Breeding Line Evaluation

Forty-one full-sib breeding lines were tested in replicated yield trials at the Tidewater Research Station, Plymouth, NC, in 2008, with the best-performing lines selected for additional testing at the Caswell Research Farm during 2009 and 2011 (data not shown). Based on in-house test results, N6001 was entered into two regional collaborative trials: the United Soybean Board Southern Diversity Yield Trial Project, and the USDA Uniform Soybean Tests–Southern States. N6001 was evaluated in a total of 12 environments across North Carolina, South Carolina, and Georgia in the Diversity Trials during 2010, 2011, and 2012. N6001 was also tested in 12 environments in Alabama, Arkansas, Georgia, Mississippi, North Carolina, and South Carolina in the Uniform Tests, Preliminary Group VI in 2011 and 2012 (Gillen and Shelton, 2012, 2013).

Plot Technique

Plot technique was previously described (Carter et al., 2009; Carter et al., 2010). Briefly, in the Diversity Trials, plots consisted of three rows at North Carolina locations or four rows at all other locations. The outside two rows served as buffer, and the middle row(s) was harvested for yield determination. Row spacing ranged from 76 to 96 cm. Row lengths were planted to between 6 and 7 m and end trimmed at maturity to between 3.6 and 4.6 m long in Georgia and North Carolina, respectively. Plots were seeded at a rate of about 344,000 seeds ha⁻¹. Further agronomic details of the field trials in the Uniform Tests are described by Gillen and Shelton (2012, 2013).

Traits Evaluated

For the Diversity Trials, seed yield was harvested for each plot. Lodging was rated visually within each yield trial using a scale of 1 to 5 (Fehr 1987), in which 1 indicates no lodging and 5 indicates all plants in the plot were prostrate. Height was determined as the mean of three randomly selected plants per plot. Observational tests for two additional traits of interest were conducted as part of the Diversity Trials. Pod dehiscence was rated in single-row plots at Sandhills Research Station, Jackson Springs, NC, using a scale of 0 to 10, with 0 indicating no dehiscence and 10 indicating all pods dehisced. Resistance to root-knot nematodes [Meloidogyne incognita (Kofoid and White) Chitwood] was rated in greenhouses at the University of Georgia, Athens, GA, using a scale of 1 (no galls) to 5 (many galls) (Hussey and Boerma, 1981). Trait evaluation methodologies for the Uniform Tests are described in Gillen and Shelton (2012, 2013). Herein, maturity date (the estimated first date on which 95% of pods were mature) is reported using the convention that 1 October is day one. Seed quality was rated visually using a 1-to-5 scale in which 1 indicates good seed quality and 5 indicates poor seed quality (Green et al., 1965).

Statistical Analysis

As is common in advanced regional yield trials, the entries for the Diversity Trials changed each year, with low-performing entries being eliminated and replaced with new entries. This caused a nonrandom pattern of missing entries for combined analyses over years, posing special challenges for statistical analysis (Piepho and Möhring 2006). To achieve a balanced data set, we retained data from only those genotypes grown in all 3 yr in which N6001 was grown. Data were analyzed in a manner previously described (Carter et al., 2009; Carter et al., 2010). Briefly, SAS Enterprise Guide v4.2 (SAS Institute, Cary, NC) was used in a two-stage analysis in which PROC MIXED was used to determine adjusted means of each genotype within each environment, followed by PROC ANOVA on the adjusted means to identify differences among genotypes across environments. This procedure produced a final output in which the error term produced by PROC ANOVA was the equivalent of the genotype × environment mean square. Fischer’s protected least significant difference (LSD) was used to compare N6002 to each check line.

Analysis of raw data from the Uniform Tests was performed only on data from entries and checks that were present in all years. Note that the cultivar Young was designated as ‘YoungBC4LX’ in these trials. The published analysis of each location in each year was used to obtain the location’s coefficient of variation (CV) for yield. All data from individual trials with a CV of ≥15% for yield were omitted from the analysis. Analysis of variance was performed to obtain adjusted means using the MIXED procedure of SAS Version 9.3_M1 for Windows (SAS Institute Inc.). Yield, maturity, lodging, height, seed size, and seed quality were analyzed with a model with genotype as fixed effect and location, year, location × year, replication (location year), location × genotype, year × genotype, and location × year × genotype as random effects. Protein and oil data were analyzed with a model with genotype as a fixed effect and location, year, and location × year, location × genotype, and year × genotype as random effects. Fisher’s protected LSD was calculated at $\alpha = 0.05$.

Trial data were analyzed for each trial as described above; results are presented in Tables 1 and 2. For in-text presentation of the results, results of multiple trials were weighted by the number of environments each trial was grown in and then averaged over the total number of environments.
Seed Purification and Increase

Increase and purification of N6001 began in 2011 when seed from 2010 yield trials (F10 seed) were planted in six-row plots at the Sandhills Research Station. Seed was cleaned on a Clipper Eclipse 324 (A.T. Ferrell Company Inc.) to remove the largest and smallest 5% of seed to minimize off-types for seed size. Seed was further cleaned by hand to remove off-types for hilum color or other visual traits. Seed was planted at ~5 beans per foot and rogued for off-types at flowering and maturity. The outside rows served as border and the inner four rows were harvested for seed increase. The combine was cleaned between harvesting of each increase plot using a leaf blower, and, the first 3 kg of seed harvested from each increase plot was discarded to further reduce chances of contamination between plots. The same procedure was followed again in 2012 using seeds from the 2011 increase. Several years of observation indicated that border rows provided little benefit for reducing cross-contamination, so in 2013, the plot shape was altered from six-rows to three-rows wide with all seeds being harvested for increase.

Plant Characteristics

Agronomic and Botanical Description

N6001 is a determinate, mid-MG VI soybean with purple flowers and gray pubescence. N6001 matured on the same day as Young and 3 d earlier than ‘NC-Roy’ (PI 617045; Burton et al., 2005) over 18 environments (Tables 1–2). In nine environments of the Diversity Trials, N6001 matured 4 d earlier than AGS758RR. In the Uniform Tests, N6001 matured 5 and 3 d later than ‘AGS 606RR’ and ‘Dillon’ (PI 592756; Shipe et al., 1997), respectively.

N6001 averaged 16 cm shorter than the adapted parent Young and 9 cm shorter than NC-Roy over the 24 environments encompassed by the Diversity Trials and the Uniform Tests (Tables 1–2). In the Diversity Trials, N6001 was 15 cm shorter (p < 0.05) than the check line ‘AGS 758RR’, while in the Uniform Tests, N6001 (89 cm) was similar (not significant at p = 0.05) in height to the checks AGS 606RR (84 cm) or Dillon (96 cm). Over 23 environments, the lodging score for N6001 was 1.8, which was slightly less than that of Young (2.5) and NC-Roy (2.4) (Tables 1–2). In the Diversity Trials, lodging of N6001 was similar to that of AGS 758RR. In the Uniform Tests, the lodging of N6001 was similar to that of check cultivars AGS 606RR and Dillon.

Table 1. Performance of N6001 in the United Soybean Board Southern Diversity Yield Trial Project Maturity Group VII in 2010, 2011, and 2012. Trials were grown in 12 environments in North Carolina, South Carolina, and Georgia. Checks NC-Roy and AGS 758RR are late maturity group VI cultivars. Young is the adapted parent of N6001.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Yield (kg ha⁻¹)</th>
<th>Maturity (d 1 Oct. = 1)</th>
<th>Height (cm)</th>
<th>100-seed weight (g)</th>
<th>Lodging 1–5†</th>
<th>Root-knot nematodes 1–5‡</th>
<th>Pod dehiscence 0–10§</th>
</tr>
</thead>
<tbody>
<tr>
<td>N6001</td>
<td>2634</td>
<td>18</td>
<td>86</td>
<td>15.6</td>
<td>1.6</td>
<td>4.7</td>
<td>0.3</td>
</tr>
<tr>
<td>Young</td>
<td>2917</td>
<td>20</td>
<td>101</td>
<td>16.2</td>
<td>2.1</td>
<td>5.0</td>
<td>0.3</td>
</tr>
<tr>
<td>NC-Roy</td>
<td>2915</td>
<td>21</td>
<td>98</td>
<td>13.5</td>
<td>1.8</td>
<td>5.0</td>
<td>0.0</td>
</tr>
<tr>
<td>AGS758RR</td>
<td>2728</td>
<td>22</td>
<td>103</td>
<td>12.9</td>
<td>1.8</td>
<td>1.8</td>
<td>0.0</td>
</tr>
<tr>
<td>No. of environments</td>
<td>12</td>
<td>9</td>
<td>12</td>
<td>11</td>
<td>12</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>LSD (0.05)</td>
<td>175</td>
<td>3</td>
<td>5</td>
<td>0.7</td>
<td>0.2</td>
<td>0.5</td>
<td>0.8</td>
</tr>
</tbody>
</table>

† 1 = no lodging, 5 = complete lodging (Fehr, 1987).
‡ 1 = no galls, 5 = many galls (Hussey and Boerma, 1981).
§ 0 = no shattering, 1 = 1–10% shattering, 10 = 100% shattering.

Table 2. N6001 agronomic characteristics in USDA Uniform Soybean Tests–Southern States, Preliminary Group VI Trials in 2011 and 2012. Trials were grown in 12 environments in Alabama, Arkansas, Georgia, Mississippi, North Carolina, and South Carolina. Young is the adapted parent of N6001. AGS606RR, Dillon, and NC-Roy are maturity group VI check cultivars. Data analysis was performed on all lines that were grown in all environments alongside N6001; however, only the most relevant checks are shown.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Yield (kg ha⁻¹)</th>
<th>Maturity (d 1 Oct. = 1)</th>
<th>Height (cm)</th>
<th>100-seed weight (g)</th>
<th>Lodging 1–5†</th>
<th>Seed quality 1–5‡</th>
<th>Protein g kg⁻¹§</th>
<th>Oil kg ha⁻¹§</th>
</tr>
</thead>
<tbody>
<tr>
<td>N6001</td>
<td>4038</td>
<td>14</td>
<td>96</td>
<td>13.9</td>
<td>3</td>
<td>2.0</td>
<td>423</td>
<td>216</td>
</tr>
<tr>
<td>Young</td>
<td>3815</td>
<td>12</td>
<td>109</td>
<td>15.2</td>
<td>2</td>
<td>1.9</td>
<td>415</td>
<td>218</td>
</tr>
<tr>
<td>AGS606RR</td>
<td>3915</td>
<td>13</td>
<td>110</td>
<td>15.0</td>
<td>2</td>
<td>1.9</td>
<td>418</td>
<td>210</td>
</tr>
<tr>
<td>Dillon</td>
<td>3705</td>
<td>12</td>
<td>96</td>
<td>15.2</td>
<td>2</td>
<td>1.9</td>
<td>415</td>
<td>218</td>
</tr>
<tr>
<td>NC-Roy</td>
<td>3815</td>
<td>18</td>
<td>95</td>
<td>13.9</td>
<td>3</td>
<td>1.8</td>
<td>418</td>
<td>210</td>
</tr>
<tr>
<td>No. of environments</td>
<td>12</td>
<td>9</td>
<td>12</td>
<td>8</td>
<td>11</td>
<td>6</td>
<td>9</td>
<td>9</td>
</tr>
<tr>
<td>Mean</td>
<td>3637</td>
<td>14</td>
<td>90</td>
<td>16.2</td>
<td>2</td>
<td>1.9</td>
<td>420</td>
<td>216</td>
</tr>
<tr>
<td>LSD (0.05)</td>
<td>270</td>
<td>3</td>
<td>8</td>
<td>1.5</td>
<td>0</td>
<td>0.3</td>
<td>11</td>
<td>5</td>
</tr>
<tr>
<td>CV (%)</td>
<td>10.8</td>
<td>4.1</td>
<td>11.6</td>
<td>7.7</td>
<td>26.2</td>
<td>13.0</td>
<td>2.2</td>
<td>1.9</td>
</tr>
</tbody>
</table>

† 1 = no lodging, 5 = all lodged (Fehr, 1987).
‡ 1 = very good, 5 = very poor (Green et al., 1965).
§ Protein and oil measured on a zero moisture basis.
In observation nurseries at Sandhills Research Station in 2010, 2011, and 2012, N6001 (0.3) exhibited a very low incidence of pod dehiscence that was comparable to that of Young (0.3) and only slightly greater than that of NC-Roy (0.0) or AGS 758RR (0.0, Table 1). N6001 (4.7) was susceptible to root-knot nematodes, with visual ratings similar to that susceptible NC-Roy (5.0) and Young (5.0), but significantly more susceptible \((p < 0.05)\) than AGS 758RR (1.8, Table 1).

In tests conducted as part of the Uniform Tests in 2011 and 2012, N6001 was susceptible to soybean cyst nematode \((Heterodera glycines\) Ichinohe) Race 2 (HG type 2.5.7), Race 3 (HG Type 0), and Race 5 (HG type 2.5.7), with mean 2-yr ratings of 4.8, 5.0, and 4.9, respectively (Gillen and Shelton, 2012, 2013). N6001 was susceptible to southern stem canker \([\text{caused by Diaporthe phaseolorum}\) ( Cooke & Ellis) Sacc. var meridionalis Fernández] (Gillen and Shelton, 2012, 2013).

### Seed Traits

Seed of N6001 has a yellow coat and buff hila. Seed weight of N6001 (15.8 g 100 seed\(^{-1}\)) averaged 0.6 and 2.1 g 100\(^{-1}\) greater than Young and NC-Roy, respectively, over 19 environments (Tables 1–2). In the Diversity Trials, 100-seed weight for N6001 (15.6 g) was significantly \((p < 0.05)\) larger than AGS 758RR (12.9 g) (Table 1). In the Uniform Tests, 100-seed weight of N6001 (16.0 g) was numerically larger than that of AGS 606RR (15.7 g) or Dillon (15.7 g). In six environments of the Uniform Tests, the average seed quality score for N6001 was 1.8, which was similar to that of the check cultivars (Table 2).

As part of the Uniform Tests, seed protein and oil content were measured on a zero moisture basis over 12 environments. Seed protein content of N6001 \((421\ \text{g kg}\^{-1})\) was very similar to \((\textit{not significant at} p = 0.05)\) that of Young \((423\ \text{g kg}\^{-1})\), Dillon \((415\ \text{g kg}\^{-1})\), and NC-Roy \((418\ \text{g kg}\^{-1})\) but was significantly less than AGS 606RR \((432\ \text{g kg}\^{-1})\) (Table 2). Seed oil content of N6001 \((220\ \text{g kg}^{-1})\) was similar to that of Young \((216\ \text{g kg}^{-1})\) and Dillon \((218\ \text{g kg}^{-1})\) but was significantly greater \((p < 0.05)\) than AGS 606RR \((211\ \text{g kg}^{-1})\) and NC-Roy \((210\ \text{g kg}^{-1})\).

### Yield Performance

Over 24 environments across the southern United States, N6001 yielded 108% of its adapted parent Young (or 268 kg ha\(^{-1}\) greater than Young), and 98% (62 kg ha\(^{-1}\) less than) the elite check cultivar NC-Roy (Table 1–2). In the Diversity Trials, N6001 (2834 kg ha\(^{-1}\)) yielded significantly \((p < 0.05)\) higher than Young (2607 kg ha\(^{-1}\)), while maintaining comparable seed protein content, suggesting that the genetics in this line may help reduce the effects of the frequently noted negative correlation between yield and seed protein content found in North American breeding programs (Wilson, 2004). Yield of N6001 was not significantly \((p < 0.05)\) different from that of either NC-Roy (2915 kg ha\(^{-1}\)) or AGS 758RR (2728 kg ha\(^{-1}\), Table 1). In the Uniform Tests, N6001 (3772 kg ha\(^{-1}\)) yielded significantly \((p < 0.05)\) greater than Young (3462 kg ha\(^{-1}\)). Yield was not significantly \((p < 0.05)\) different from that of AGS 606RR (3639 kg ha\(^{-1}\)), Dillon (3705 kg ha\(^{-1}\)), and NC-Roy (3815 kg ha\(^{-1}\)) (Table 2). Although the genotype \(\times\) location and genotype \(\times\) location \(\times\) year effects were significant \((p < 0.05)\), all genotype \(\times\) environment effects were small relative to the main effects.

### Conclusions

The release of N6001 opens up new opportunities for applied soybean breeding in North America and demonstrates that underutilized genetic resources may contain valuable alleles for crop improvement. The yield boost of N6001 over its adapted landmark parent Young indicates that yield-enhancing alleles were likely derived from Japanese cultivar Suzuyutaka. This yield increase was achieved without substantive loss of seed protein content, suggesting that the yield-enhancing alleles derived from Suzuyutaka may help in the mitigation of the widely recognized negative correlation between yield and seed protein. The unique pedigree and good agronomic performance of this release indicate the potential merit of incorporating N6001 into applied breeding programs.

### Availability

Small quantities of N6001 seed are available from the corresponding author for research and breeding purposes for a minimum of five years from the date of publication. Seed of N6001 has been deposited in the USDA NCGRP and is available for immediate release. Appropriate recognition is requested if this germplasm leads to new cultivar(s), germplasm release(s), and/or scientific discovery(s).

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### References


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