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GERMPLASM

Registration of N6202 Soybean Germplasm with High Protein, Favorable Yield Potential, Large Seed, and Diverse Pedigree

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ABSTRACT

'N6202' soybean [*Glycine max* (L.) Merr.] (Reg. No. GP-366, PI 658498) was cooperatively developed and released by the USDA–ARS and the North Carolina Agricultural Research Service in October 2009 as a mid–Maturity Group VI germplasm with high-protein seed, favorable yield potential, large seed size, and diverse pedigree. The unusual combination of high protein and favorable yield in this germplasm, plus its diverse genetic background, makes it a potentially desirable breeding stock for both specialty and commodity breeding programs. N6202 was developed through conventional breeding and is adapted to the southern United States. Average seed protein level was 457 g kg^{-1} (zero moisture basis), which was 33 g kg^{-1} greater ($p < 0.05$) than that of the control cultivar NC-Roy. Average yield of N6202 was more than 90% of NC-Roy over 65 environments. The 100-seed weight of N6202 (21.4 g) was significantly greater ($p < 0.05$) than that of the largest-seeded control cultivar Dillon (15.2 g).Twenty-five percent of N6202's pedigree is derived from Japanese cultivar Fukuyataka. Fukuyataka is not known to be related to the genetic base of U.S. soybean. An additional 25% of N6202's pedigree traces to the Japanese cultivar Nakasennari, which appears in the pedigree of only one cultivar (its parent 'N6201'). Thus, the release of N6202 broadens the genetic range of materials adapted for soybean breeding in the United States. N6202 exhibits a moderate level of the bleeding hilum trait in some environments.

N6202 soybean [*Glycine max* (L.) Merr.] (Reg. No. GP-366, PI 658498) was developed by conventional breeding methods and tested as breeding line N01-10974 in North Carolina and across southern states from 2002 through 2007. N6202 was selected initially with the intent that it would be used in the tofu market. However, N6202 exhibited a moderate level of the bleeding hilum trait in some environments, which limits its potential in the tofu seed trade.

Despite its deficiency with respect to bleeding hilum, N6202 appears to be very promising as a parent for soybean breeding because it is a high seed-protein type that has favorable yield potential. A review of soybean registrations published by the CSSA from 1960 to the present reveals that a total of 19 high-protein public releases (defined here as having seed protein content greater than ~440 g kg^{-1}) were registered before the release of N6202 in Maturity Groups IV and later in the United States (Table 1). However, a favorable and well-documented combination of high seed protein content and good seed yield is rare among these releases and absent in Maturity Group VI. Most of these earlier releases were either yield-tested in too few environments to adequately estimate yield potential or yield levels proved to be below 90% of the control cultivars. Only the high-protein releases S97-1688 and BARC-7 (Maturity Groups V and IV-S) received a reasonable amount of yield testing (more than 10 environments) and also had yields near 90% of the controls or better (Anand et al., 2004; Leffel, 1992). In additional testing of BARC-7 over eight environments after its release, its yield was 87% of the Maturity Group IV control cultivar (Serretti et al., 1994). Despite the reported desirable yields of BARC-7, its potential to produce good-yielding prog-

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Abbreviations: OVT, Official Variety Testing; QTL, quantitative trait locus (loci); PR, Puerto Rico; RR, Roundup Ready; SAVE, Soybean Asian Variety Evaluation; USB, United Soybean Board.

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Table 1. Registrations reporting soybean releases having at least 440 g kg^{-1} seed protein content and a Maturity Group of IV and later.

Germplasm[†‡]	Maturity group	Protein content of germplasm release	Protein content of control cultivar	Yield compared to control cultivar	Environments for which yield was evaluated[§]	Reference
		g kg^{-1}		%	No.	
BARC-7	IVS	491	–	89	19	Leffel (1992)
BARC-8	V	528	–	73	19	Leffel (1992)
BARC-9	IVS	529	–	73	19	Leffel (1992)
D76-8070	V	495	402	93	8	Hartwig (1990)
D90-7256	V	505	413	102	3	Hartwig (1996)
DMK93-9048	VII	462	440	67	7	Kenty et al. (2001)
N6202	VI	456	424	92	43	
NC 101	VI	468	432	95	2	Carter et al. (1986)
NC 102	VI	465	432	88	2	Carter et al. (1986)
NC 103	VII	449	419	88	2	Carter et al. (1986)
NC 104	VI	507	432	73	2	Carter et al. (1986)
NC 105	VI	487	432	79	2	Carter et al. (1986)
NC 106	VI	504	432	75	2	Carter et al. (1986)
NC 108	VII	459	419	88	2	Carter et al. (1986)
NC 110	VII	478	419	73	2	Carter et al. (1986)
NC 111	VII	489	419	74	2	Carter et al. (1986)
NC 112	VII	505	419	86	2	Carter et al. (1986)
Prolina[¶]	VI	461	428	87	7	Burton et al. (1999)
R95-1705	V	467	408	82	43	Chen et al. (2008)
S97-1688	V	445	419	98	25	Anand et al. (2004)

[†]Pedigrees—BARC-7: CX797-21 × D80-6931; BARC-8 and BARC-9: CX797-21 × NC-2-62; D76-8070: multiple crossing program involving Hill, Sioux, FC31745, D492510, PI96983, D49-2491, and PI 163453; D90-7256: Forrest × D76-8070; DMK93-9048: D86-3429 × Braxton; N6202: N6201 × N95-7390; NC101-NC 106: lines from a recurrent selection population named IA and derived from D55-4110 × N56–4071; NC108–NC112: lines from recurrent selection population named IIA and derived from D49-2491 × 9 unadapted plant introductions; Prolina: line derived from recurrent selection population NRS4. Population derived from intermating lines from population IA with Bragg, Ransom, and Davis; R95-1705: Hutcheson × BARC-7; S97-1688: S91-1381 × Hartz 5810.

[‡]Recently released cultivar 'KS4607' appears to exhibit a favorable combination of high seed protein content and good seed yield. This group IV cultivar has 453 g kg^{-1} seed protein (zero moisture basis) and a seed yield that was 103% of the checks over 19 environments (Graef, 2007).

[§]The number of environments for protein assay may have been less than the number used for yield evaluation.

[¶]Subsequent testing of Prolina in North Carolina indicated lower yield potential than current varieties. Over 12 additional environments during 2002 to 2007, Prolina yielded only 82% of control cultivar NC-Roy, which was significantly less ($p > 0.05$, 2258 vs. 2755 kg ha^{-1}).

eny may be limited. The recent release of a high-protein progeny from BARC-7, R95-1705, had low yield (Table 1) (Chen et al., 2008). The low yield of the progeny R95-1705 may be attributed to the well-established negative genetic relation that occurs between seed protein content and seed yield in most breeding populations (Burton, 1985, 1987). A review of United Soybean Board (USB)–sponsored Regional Soybean Quality Trait Tests for southern maturity germplasm revealed that one other recently released cultivar, KS4607 (formerly K03-3281, developed in Kansas; William Schapaugh, personal communication, 2009), appears to exhibit a favorable combination of high seed protein content and good seed yield. This Maturity Group IV cultivar has 453 g kg^{-1} seed protein (zero moisture basis) and a seed yield that was 103% of the checks over 19 environments (Graef, 2007). KS4607 has not been tested in USDA regional yield trials. In view of these previous releases and because of N6202's extensively documented seed yield potential and seed protein levels, N6202 may be considered as one of the few high seed protein content germplasm releases in the southern United States that has favorable yield potential (Tables 2, 3, and 4).

The development of N6202 is an unusual story that highlights its uniqueness with respect to seed yield and protein. N6202 exhibited the highest seed protein content of any genotype tested in its maturity class in USDA Southern States Cooperative Uniform Soybean Yield Trials (USDA Southern Regional Tests) from 2005 to 2007 (Paris and Shelton, 2006; Gillen and Shelton, 2007, 2008). The high seed protein concentration was a surprising discovery, however, because seed composition was neither monitored nor selected on during the line's development or subsequent early testing stages. Agronomic performance, seed appearance, and seed weight were the primary selection criteria. Given the well-established negative genetic relationship between seed protein concentration and seed yield in soybean, it was unusual and perhaps unlikely that selection based primarily on seed yield and seed appearance would lead to development of a high-protein breeding line. This occurrence is theorized to be a product of its unique pedigree, of which 50% is derived from two Japanese grandparents that are not a part of most breeding populations in the United States. In that regard, N6202 is the first improved germplasm derived from 'Fukuyataka' to be released in the

United States and the second improved germplasm from 'Nakasennari'. The other 50% of the pedigree, the entire adapted portion, traces to only one genotype, the "double grandparent" cultivar Young (Burton et al., 1987). Over two environments in 2007, N6202 had numerically higher seed protein content (445 g kg^{-1}) than did Young (422 g kg^{-1}). We speculate that the Japanese grandparental stock passed on novel high-protein alleles that do not cause the normal seed yield reduction in soybean. Yates and Boerma (2006) recently discovered a quantitative trait locus (QTL) controlling seed protein that does not appear to impact yield. The QTL was found in 'Danbeakong', a Korean cultivar that is not part of the genetic base for U.S. breeding. It is possible that the same or other unique alleles may be present in N6202 and account for its unusually favorable combination of high seed protein content and high seed yield.

Methods

Parental Selection and Pedigree

N6202 is a F_4–derived selection from the cross of USDA–ARS cultivar N6201 (Carter et al., 2003) and USDA–ARS breeding line N95-7390. N6201 is derived from Young × Nakasennari. Breeding line N95-7390 is derived from Young × Fukuyataka. Nakasennari and Fukuyataka are Japanese cultivars. Fukuyataka is derived from the cross of landraces Oka Daizu and Shiro Daizu 3 (Shoji Miyazaki, personal communication, 1996). Nakasennari is derived from the cross of landrace Houjaku and Nema Shirazu (Shoji Miyazaki, personal communication, 1996). Nema Shirazu is a selection from landrace Geden Shirazu, the most important ancestor of Japanese breeding in terms of pedigree contribution (Zhou et al., 2000).

Agronomic Performance of Antecedents of N6202

Fukuyataka and Nakasennari, grandparents of N6202, are Japanese cultivars adapted for tofu manufacture (Zhou et al., 2002). Agronomic performance of these two cultivars was evaluated over 13 environments in the United States as a part of Project SAVE (Soybean Asian Variety Evaluation) in 1996 and 1997. Project SAVE was a farmer–public sector–private sector initiative to identify high-yielding Asian soybean cultivars for use in U.S. cultivar development programs (Manjarrez-Sandoval et al., 1998). Nakasennari and Fukuyataka exhibited elevated levels of seed protein content compared with the control commodity-type cultivars in these tests, (435 vs. 411 and 444 vs. 420 g kg^{-1}, respectively) and larger 100-seed weight (18.4 vs. 13.8 and 23.9 vs. 14.6 g, respectively). Seed yields of the two Japanese cultivars were 86 and 76% of control cultivars, respectively. N95-7390, the male parent of N6202 and progeny of Fukuyataka, was tested in the Maturity Group VI Preliminary tests of the USDA Southern Regional Tests in 1997 (Tyler and Bell, 1998). Over 10 environments, N95-7390 yielded 86% of the control cultivars and had a seed protein content that was only slightly greater than that of the controls (430 vs. 425 g kg^{-1}). N6201, the female parent of N6202 and progeny of Nakasennari, was evaluated in USDA regional trials in 1994 and 1995, where it exhibited a seed yield that was 85% of control cultivars and a seed protein content (423 g kg^{-1}) that was slightly less than that of the check Brim (429 g kg^{-1}) (Kenty and Mosley, 1995; Tyler and Bell, 1996). Seed protein content of Young (formerly N75-2213), the adapted "double" grandparent, was 432 g kg^{-1} compared with 410 g kg^{-1} for the control cultivar in the USDA Southern Regional Tests from 1978 through 1981 (Hartwig and Lappas, 1979, 1980, 1981, 1982).

Development of Breeding Line

The cross between N6201 and N95-7390 was made in the field at the Central Crops Research Station near Clayton, NC, in 1997, and the F_1 plants were grown at the same location in the following summer. The F_2 and F_3 generations were advanced using the single seed descent breeding method (Brim, 1966). The F_2 generation (~3000 plants) was advanced at Clayton, NC, in 1999. Seed were inspected after harvest for seed appearance, and all seed were discarded except those that had yellow or clear hilum and were also free of bleeding hilum and other seed blemishes. The smallest one-third of the seed was also discarded after passing the seed through a series of screens with round holes of progressively smaller diameters. The F_3 generation (~800 plants) was grown at the USDA–ARS Tropical Agriculture Research Station (TARS), Isabela, PR, during the following winter. After harvest, seed with bleeding hilum or other blemishes were discarded. In 2000 approximately 300 individual F_4 plants were grown and harvested at the Sandhills Research Station at Jackson Springs, NC, and evaluated for 100-seed weight. The 32 F_4 plants with the largest 100-seed weight (all above 20 g) and most desirable seed appearance were grown in progeny rows at Clayton, NC, in 2001. One of the progeny rows, N6202, was identified as a promising breeding line and tested subsequently under the experimental designation N01-10974. Seed composition was not monitored during breeding line development.

Breeding Line Evaluation

Yield Trials

In 2002 and 2003, N6202 was evaluated in a total of three replicated trials in NC (data not shown). In 2004, N6202 was submitted to the Maturity Group VI Preliminary tests of the USDA Southern Regional Tests (Paris and Shelton, 2005). Based on the 2004 results, N6202 was advanced to the Maturity group VI Uniform Test and evaluated during 2005 to 2007 (Paris and Shelton, 2006; Gillen and Shelton, 2007, 2008). N6202 was yield tested at 5, 14, 12, and 12 locations in 2004, 2005, 2006, and 2007, respectively, as part of the USDA Southern Regional Tests.

N6202 was yield tested in nine North Carolina environments by the North Carolina Official State Variety Testing Program (OVT) in 2005 through 2007 (Bowman 2005, 2006, 2007). In addition, N6202 was also tested at 14 locations from 2005 through 2007 as part of the Southern Diversity Yield Trial Project sponsored by the USB. Southern Diversity Yield Trials were grown at the Caswell Research Farm near Kinston, NC, and Stoneville, MS (2005 and 2006), the Tidewater Research Station, Plymouth, NC (2007), and all 3 yr at Stuttgart, AR, Athens, GA, and Petersburg, VA.

Plot Technique

Plot technique has been described elsewhere (Carter et al., 2009). Briefly, in the USDA Southern Regional Tests and in the Southern Diversity Yield Trials sponsored by the USB, field plots consisted of four-row plots in most cases. Rows were end-trimmed at maturity, and the two middle rows were harvested for yield determination. Row widths varied among locations from 36 to 102 cm, with the majority planted in 76-cm-wide rows. The length of row harvested varied from 4.6 to 6.5 m. Plant populations were approximately 344,000 ha^{-1}.

In the North Carolina OVT program, individual plots consisted of eight rows that were 7.3 m in length and 19 cm between rows. Neither border rows nor end-trimming was used, and harvested plot area was approximately 11.1 m^2. Plant populations were approximately 430,000 ha^{-1}. Yield estimates were reduced by 10% on all plots as a correction factor in the North Carolina OVT protocol for data analysis because either a lack of end-trimming or an absence of border rows will cause yield inflation in most soybean field trials (Meis et al., 2002; Heatherly and Tyler,1998; Boerma et al., 1976, Burton et al., 1992; Hartwig et al., 1951).

For the USDA breeding program in North Carolina, all plots were three rows 97 cm wide, which were end-trimmed at or near maturity. Harvested plot area was approximately 4.5 m^2. Plant populations were approximately 306,000 ha^{-1}.

Traits Evaluated

Agronomic traits evaluated in the yield trials included maturity, lodging, plant height, seed quality, 100-seed weight, and disease reactions. In the USDA Southern Regional Tests, seed protein and seed oil content were analyzed using near-infrared spectroscopy (American Association of Cereal Chemists, 1999). The near-infrared analyses were performed at the National Center for Agricultural Utilization Research, USDA–ARS, Peoria, IL. Samples for analyses of carbohydrates and phytate were taken from large increase and purification plots at Sandhills Research Station in NC in 2006 and 2007, "in-house" yield tests at Plymouth, NC, in 2006 and 2007, and lastly in yield tests at Athens, GA, Petersburg, VA, and Kinston, NC, that were part of the Southern Diversity Yield Trial Project in 2007. Seed carbohydrates were evaluated using the protocol described by Carter et al. (2009). Phytate was extracted from 100 mg of dried, ground seeds in 2 mL of 0.5 M HCl. The samples were centrifuged at 4100 × *g* and the supernatant solution was moved to a microcentrifuge tube, carefully avoiding the pellet and the oil layers. The samples were centrifuged at 9000 × *g* and filtered through a 0.22-μm filter (milipore). The filtrate was collected in a high performance liquid chromatography autosampler vial. Phytate was analyzed as described by Kwanyuen and Burton (2005).

Statistical Analysis

Seed yield and other agronomic traits were evaluated in the field with a randomized complete block experimental design. For yield, replication number within an individual test was two in 2004 and three thereafter for USDA Southern Regional Tests, five for the North Carolina OVT Program, three for the Southern Diversity Yield Trial Project, and three or four for the USDA breeding program in North Carolina, depending on year and location. For the USDA regional trials, agronomic data other than yield were usually taken on only one replication within individual trials. For the other trials, data were collected on each replication.

Analysis of variance was conducted using SAS (SAS Institute, 2007). Year, location, and replication were considered random effects and genotypes fixed. Entries changed extensively from year to year in all regional, state, and local yield trials. Thus, to assess the performance of N6202 over years and locations within these testing programs, we identified those entries (e.g., control cultivars and promising new breeding lines) that were common over all location-year combinations in yield trials and performed an analysis of variance on this subset of the original data. Genotypic means from each individual test were used in the analysis, and each location-year combination was considered as an environment. The LSD was constructed from the genotype × environment error term and used only when the overall *F*-test for genotypic effects was significant ($P < 0.05$).

The analysis over years described here is commonly used in breeding programs and reported in registration manuscripts. However, Piepho and Mohring (2006) have pointed out the dangers in pooling test data across years when the test population is truncated annually on the basis of yield results, as is the case with most breeding trials. This concern has been addressed in a previous soybean registration (Carter et al., 2009).

Seed Purification and Increase

Seed purification of N6202 began in 2004 and continued through 2008. Plants and seed from 2003 ($F_{4:6}$) test plots were rogued to remove visible contamination and then planted in an increase block consisting of six rows of 30.4 m length and 96.5 cm row spacing at Jackson Springs, NC. The increase block was rogued at flowering and maturity to eliminate off-type plants. Outside rows served as borders and were not harvested for seed increase. Before harvest of the increase block, the plot combine was cleaned with a gasoline-powered leaf blower to eliminate extraneous seed. In addition, the first 3 kg of seed harvested from the increase were discarded in an effort to further reduce the possibility of contamination from hidden seed within the combine. This practice was followed each year as part of the standard protocol for increase of promising lines in the breeding program.

Plant Characteristics

Agronomic and Botanical Description

N6202 has purple flowers, gray pubescence, a tan pod wall, and determinate growth habit. The seed has a clear or yellow hilum and yellow seed coat color. N6202 matured 5 d earlier than 'NC-Roy' (Burton et al., 2005) in the USDA Southern Regional Tests (Table 2) and 3 d earlier than NC-Roy in USB Southern Diversity Trials (Table 3). Thus, N6202 is mid–Maturity Group VI in maturity. The germplasm was named so that the first digit in the name, *6*, refers to Group

VI maturity and the second digit, *2*, refers to large seed size. Lodging scores and height were similar in N6202 and NC-Roy for all tests.

Yield Performance

Over 43 environments of the USDA Regional Tests, N6202 yielded 92% of the highest-yielding control cultivar NC-Roy (3254 kg ha^{-1}) and 96 and 99% of controls 'Boggs RR' and 'Dillon', respectively (Boerma et al., 2000; Shipe et al., 1997) (Table 2). Boggs RR is a backcross-derived cultivar that has the patented Roundup Ready trait and is virtually identical to 'Boggs' for yield and all other agronomic traits in the absence of Roundup herbicide (Monsanto, St. Louis, MO). N6202 yielded 90% of NC-Roy in the North Carolina OVT (9 environments) (Table 4) and 93% of NC-Roy in the Southern Diversity Yield Trials (13 environments), a project sponsored by the USB (Table 3).

Seed Traits

Protein and Oil Content

Average seed protein concentration was significantly higher ($p < 0.05$) for N6202 (457 g kg^{-1}) than for all three check cultivars in the USDA Southern Regional Tests; Dillon (420 g kg^{--}), NC-Roy (424 g kg^{-1}), and Boggs RR (431 g kg^{-1}) (zero moisture basis) (Table 2). In these USDA Southern Regional Tests, seed oil concentration of N6202 (181 g kg^{-1}) was significantly lower than NC-Roy (187 g kg^{-1}), Dillon (198 g kg^{-1}), and Boggs RR (198 g kg^{-1}). In seven other southeastern trials, seed protein of N6202 was significantly higher than NC-Roy (456 vs. 426 g kg^{-1}), and seed oil was similar (184 vs. 187 g kg^{-1}) (Table 5).

100-Seed Weight

N6202 exhibited large seed in USDA regional trials, with an average 100-seed weight of 21.4 g, which was significantly greater ($p < 0.05$) than that of Dillon, NC-Roy, and Boggs RR (15.2, 13.4, and 12.4 g, respectively) (Table 2). In eight environments in the USB Southern Diversity Tests, its 100-seed seed weight (20.2 g) was significantly more ($p < 0.05$) than the control cultivars NC-Roy (13.2 g) and Dillon (15.1 g) (Table 3).

Sugar and Phytate Content

Seed carbohydrate composition was analyzed for N6202 and control cultivar NC-Roy over seven southeastern U.S. environments (Table 5) and for the parents of N6202 and grandparent Young over two environments in 2007 (Tables 6). Sucrose levels were significantly higher ($p > 0.05$) in N6202 than in the parental lines tested (Table 6). However, no consistent difference was observed between NC-Roy and N6202 in the trials. Levels of glucose and fructose were lower than the other sugars but not statistically different between the lines evaluated except that glucose levels were significantly higher ($p = 0.05$) in N6201 than in N6202. N6202 inherited the lower levels of stachyose observed in N95-7390 and Young instead of the higher levels measured in N6201 (Table 6). N6202 had higher levels of raffinose than observed in any of the parents tested but comparable to NC-Roy. Raffinose and stachyose are

Table 2. Means of agronomic traits of N6202 soybean in the USDA Regional Tests over 2004 (5 environments), 2005 (14 environments), 2006 (12 environments), and 2007 (12 environments) with three replications within each environment at most locations.

Genotype	Seed yield	Seed protein†	Seed oil	Maturity	Lodging‡	Height	Seed quality§	100-seed weight
	kg ha^{-1}	——— g kg^{-1} ———		1 Oct. = 1	1–5	cm	1–5	g
Dillon	3118	420	198	11	1.7	84	1.9	15.2
Boggs RR	3012	431	198	16	2.3	84	1.8	12.4
NC-Roy	3254	424	187	19	2.2	85	2.1	13.4
N6202	2993	457	181	14	2.1	85	2.1	21.4
$LSD_{0.05}$	159	8	4	1.9	0.3	2.7	0.3	0.5
Environments, no.	43	22	22	37	39	43	31	37

†Expressed on a zero moisture basis.

‡A score of 1 indicates no lodging; 5 indicates a prostrate plant.

§Seed quality is rated on a 1–5 scale, where 1 is very good and 5 is very poor.

Table 3. Means of agronomic traits of N6202 soybean in the Southern Collaborative Soybean Diversity Yield Trials 2005–2007. Three replications were used in most environments. This project was sponsored by the United Soybean Board.

Cultivar	Seed yield	Maturity	Lodging†	Height	Seed quality‡	100-seed weight
	kg ha^{-1}	1 Oct. = 1	1–5	cm	1–5	g
N6202	2822	13	2.2	81	1.8	20.2
NC-Roy	3027	16	2.4	85	1.6	13.2
Dillon	2984	11	1.8	78	2.1	15.1
$LSD_{0.05}$	184	4	0.3	6.7	0.4	2.6
Environments, no.	13	11	13	14	4	8

†A score of 1 indicates no lodging; 5 indicates a prostrate plant.

‡Seed quality is rated on a 1–5 scale where 1 is very good and 5 is very poor.

Table 4. Means of agronomic traits of N6202 soybean in North Carolina State University Official Variety Trials 2005–2007 (nine environments with five replications per test).

Cultivar	Seed yield	Lodging†
	kg ha^{-1}	1–5
N6202	2553	1.3
NC-Roy	2829	1.6
$LSD_{0.05}$	267	1.0

†A score of 1 indicates no lodging; 5 indicates a prostrate plant.

antinutritional sugars formed when one or two galactose molecules, respectively, are linked to sucrose (Hawton et al., 1996; Hata et al., 1991). Monogastric animals lack the α-galactosidase needed to digest the raffinose family of oligosaccharides.

Phytate levels of N6202 were significantly higher (p = 0.05) than NC-Roy but similar in levels to its parents and grandparent (Tables 5 and 6). Phytate is an inositol derivative that causes nutritional and environmental problems when present in high amounts in soybean (Erdman, 1979). Inositol levels did not reflect the genotypic differences observed in phytate (Tables 5 and 6).

Seed Quality

The seed quality rating for N6202 (a score of 2.1) was similar to that for NC-Roy (2.1), Dillon (1.9), and Boggs RR (1.8) in USDA Southern Regional Tests (Table 2). Seed quality was rated on a 1 to 5 scale, where 1 indicates good and 5 very poor quality. Seed quality of N6202 was similar to the checks in the Southern Collaborative Soybean diversity tests (Table 3).

Disease Resistance and Shattering

N6202 is resistant to soybean mosaic virus but susceptible to root knot (*Meloidogyne incognita* and *M. arenaria*) species of nematode as well as races 2, 3, and 14 of soybean cyst (*Heterodera glycines* Ichinohe) nematode (Paris and Shelton, 2006; Gillen and Shelton, 2007, 2008). N6202 was rated resistant to stem canker (caused by *Diaporthe phaseolorum* var. *caulivora)* in 2 yr of testing using the toothpick inoculation method (Gillen and Shelton, 2007, 2008; Keeling, 1982). N6202 is prone to moderate levels of bleeding hilum in some environments (especially when planted late) and, thus, is not sufficiently resistant for most commercial soyfoods production. N6202 is resistant to shattering even when harvest is delayed extensively in North Carolina.

Availability

N6202 will be available for research purposes and for use as parental stock in development and commercialization of new cultivars. It is requested that appropriate recognition be made if this germplasm contributes to the development of a new breeding line or cultivar. Seed of N6202 is available from the corresponding author.

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Table 5. Seed carbohydrate, phytate, protein, and oil composition of N6202 and standard control cultivar NC-Roy over seven southeastern environments (2004–2007).

Cultivar	Sucrose†	Inositol	Glucose	Fructose	Raffinose	Stachyose	Total carbohydrate	Phytate	Protein	Oil
	mg kg^{-1}							mg g^{-1}	g kg^{-1}	
NC-Roy	45,709	1559	394	131	9,179	31,631	88,847	11.2	426	187
N6202	43,765	1932	407	124	10,262	30,521	87,278	13.1	456	184
$LSD_{0.05}$	5,063	484	130	70	1,650	2,766	6,365	1.6	10	5
Environments, no.	4	4	4	4	4	4	4	4	7	7

†All seed composition traits expressed on a zero moisture basis.

Table 6. Seed carbohydrate, phytate, protein, and oil composition of N6202, its parents, adapted grandparent, and standard control cultivar NC-Roy over two environments (Kinston and Jackson Springs), North Carolina, in 2007.

Genotype†	Sucrose‡	Inositol	Glucose	Fructose	Raffinose	Stachyose	Total carbohydrate§	Total phytate	Protein	Oil
	mg kg^{-1}							mg g^{-1}	g kg^{-1}	
N6201	36,079	1253	343	118	7105	33,163	78,296	14.6	427	202
N95–7390	37,888	1772	352	101	7790	29,175	77,295	14.7	441	218
Young	35,344	1333	318	93	7103	29,872	74,336	14.3	422	211
NC-Roy	40,347	1572	336	100	8947	29,144	80,732	11.7	417	203
N6202	43,484	1507	307	74	9157	29,863	84,624	14.0	445	201
$LSD_{0.05}$	5,593	714	108	43	1024	2,820	7,749	1.5	13	13

†N6202 is derived from the cross of N6201 × N95-7390. Young is a parent of both N6201 and N95-7390. Nakasennari is a parent of N6201. Fukuyataka is a parent of N95-7390.

‡All seed composition traits expressed on a zero moisture basis.

§Total carbohydrate concentration is slight larger than sum of listed components because of the presence of other minor carbohydrates.

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