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REGISTRATIONS OF GERMPLASMS

Registration of N95L11881 and 97L9521 Strong Gluten 1BL.1RS Wheat Germplasm Lines

N95L11881 (Reg. no. GP-745, PI 617064) and 97L9521 (Reg. no. GP-746, PI 617066) hard red winter wheat (*Triticum aestivum* L.) germplasm lines were released by the ARS, USDA, and the Nebraska Agricultural Experiment Station, in June 2002. These lines carry the 1BL.1RS wheat-rye (*Secale cereale* L.) chromosomal translocation inherited from the hard red winter wheat 'Siouxland' (Schmidt et al., 1985), but they possess improved gluten strength relative to this parent. The 1BL.1RS translocation in Siouxland originally was derived from the Russian wheat 'Kavkaz' (PI 367723). While this translocation confers a number of advantageous traits, including resistance to several fungal diseases and improved grain yield and grain yield stability, it has a detrimental effect on the processing quality of hard winter wheat (reviewed by Graybosch, 2001). The most noticeable effect, a lack of dough strength, is overcome in these two germplasm lines.

N95L11881 (Siouxland/2*N86L177) and 97L9521 (Siouxland/4*N86L177) were derived from intermatings and backcrosses between Siouxland and N86L177 (PI 559717). N86L177 is a high protein, strong gluten, non-1RS wheat derived from NapHal/'Lancer'//'Karlik1'/3/NS622/4/'Centurk'/'GK-Tiszataj'//'PlainsmanV. The pedigree of Siouxland is 'Warrior' *5/'Agent' *2//'Kavkaz'. To develop N95L11881, Siouxland was crossed to N86L177 in 1990. In 1991, resultant F_1 plants were backcrossed to N86L177. Single-seed analysis was used to identify BC_1F_1 seed carrying the 1BL.1RS translocation. The brush end of each kernel was removed and the embryo end saved with identity maintained. Seventy-percent ethanol soluble grain storage proteins (prolamins) were extracted, separated by SDS-PAGE, and visualized by silver-staining (Graybosch and Morris, 1990). The presence of 1BL.1RS is inferred in such separations by the presence of secalin proteins (prolamins of rye arising from the *Sec-1* locus on 1RS). Since 1RS arms do not recombine with wheat 1BS arms, the presence of secalins in grain protein extracts provides a consistent marker for this rye chromosome arm. Secalin positive seed were then transplanted to the greenhouse, and self-pollinated until the F_3 generation. Single plant selections were made from F_3 populations, and sown as F_4 single-plant progeny rows at Lincoln, NE, in 1994. After harvest of 1995, secalin proteins were identified in extracts of bulked F_5 seed, via separation of prolamins by high-performance liquid chromatography (HPLC) (Lookhart et al., 1990). HPLC facilitated the identification of homogeneous lines with 1BL.1RS. N95L11881 was identified as one of these homogeneous, homozygous lines. Homogeneity of 1BL.1RS was again confirmed by a third technique, capillary electrophoretic separation of prolamins (Lookhart et al., 1996).

97L9521 was developed in an identical fashion to N95L11881, except two additional cycles of backcrossing to the recurrent parent (N86L177) were conducted. F_1 seed from each backcross was tested for secalins, as described above. BC_4F_1 secalin positive plants were greenhouse grown in 1994. In 1995, BC_4F_2 plants again were greenhouse grown, threshed individually, and screened for homogeneity of secalins from *Sec-1*. Seed from homogeneous individuals was used to seed BC_4F_3 single plant progeny rows at Yuma, AZ, in 1996, and BC_4F_4 lines were grown as single 4-row plots at Lincoln, NE, in 1997. One of these $BC_4F_{2:4}$ plots was selected as 97L9521, on the basis of phenotypic uniformity, homogeneity for secalins, and similarity in field phenotypic appearance to the recurrent parent.

Grain yield (five Nebraska locations) and quality (three Nebraska locations) characteristics of N95L11881 and 97L9521 were tested in 1997 and 1998 (Table 1). Grain yield of N95L11881 was significantly ($p = 0.05$) greater than both parental lines, while that of 97L9521 did not differ significantly from either Siouxland or N86L177. Bake mix time, flour protein content, and Mixograph tolerance of 97L9521 were all significantly higher than Siouxland and did not differ significantly from N86L177. N95L11881 was significantly higher than Siouxland in flour protein content, bake mix time, Mixograph mix time, and Mixograph tolerance. Bake mix times, an indicator of gluten strength, of both lines exceeded that of Siouxland by at least two minutes and did not differ from that of N86L177. Mixograph tolerance of N95L11881 was intermediate between that of its two parents. The development and performance of these lines demonstrates that the dough weakening effect of 1BL.1RS may be overcome by introgression of the chromosome into suitable genetic backgrounds.

Both N95L11881 and 97L9521 are susceptible to prevalent races of leaf rust (caused by *Puccinia triticina* Eriks.) but are resistant to current North American races of stem rust (caused by *Puccinia graminis* Pers.: Pers.). Both carry the stem rust resistance gene *Sr31*, found on the Kavkaz 1BL.1RS chromosome (Schmidt et al., 1985). In addition, N95L11881 carries *Sr24*, and is postulated to also carry *Lr24* and *Lr26*. Plant heights and lodging resistance of N95L11881 are similar to Siouxland. 97L9521 is nearly identical to its recurrent parent N86L177 in both plant height and lodging resistance.

Due to its greater yield potential, N95L11881 was entered in the 1999 and 2000 USDA-ARS Western Plains Regional Performance Nursery (WPRPN). In eight locations in 1999, average grain yield of N95L11881 was 3554 kg ha^{-1}. In the same tested environments, the check cultivars Trego (PI 612576), Arapahoe (PI 518591), and Prowers (PI 605389) averaged 3555, 3633, and 3418 kg ha^{-1} respectively (LSD 0.05 = 356 kg ha^{-1}). In seven locations in 2000, average yields for N95L11881, Trego, Arapahoe, and Prowers were 2360, 2911, 2497, and 2126 kg ha^{-1}, respectively (LSD = 323 kg ha^{-1}). In the 1999 WPRPN, N95L11881 displayed a mean volume weight of 77.6 kg hL^{-1}, a mean plant height of 87 cm and averaged 144 d after 1 January to heading. Respective means for Trego, Arapahoe, and Prowers were volume weights of 79.5, 75.4, and 79.6 kg hL^{-1}, plant heights of 77, 84, and 88 cm, and days to heading of 144, 145, and 145. In the 2000 WPRPN, respective means of N95L11881, Trego, Arapahoe, and Prowers were volume weights, 71.9, 75.8, 74.6, and 71.9 kg hL^{-1}; plant heights of 66, 59, 63, and 68 cm; days to heading of 135, 134, 134, and 133. Quality characteristics from composite samples over locations in each year (Table 2) of N965L11881 were similar or superior to these three non-1RS check cultivars.

Seed of N95L11881 and 97L9521 has been deposited in the USDA National Small Grains Collection, Aberdeen, ID. Small quantities of seed may be obtained from R. Graybosch, USDA-ARS, University of Nebraska, Lincoln, NE 68583. It is requested that the source of this material be acknowledged in future usage by wheat breeding and genetics programs.

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Table 1. Mean grain yield and quality attributes of 1BL.1RS germplasm lines relative to parents.

	Grain yield	Flour protein	Loaf volume	Bake mix time	Mixograph mix time	Mixograph tolerance
	kg ha^{-1}	g kg^{-1}	mL	min		0–7
N95L11881	3049	141	868	7.6	5.6	3.3
97L9521	2740	138	902	6.7	4.4	3.7
Siouxland	2734	127	913	4.8	3.8	2.4
N86L177	2614	132	926	7.3	5.3	4.5
LSD (0.05)	285	5	38	0.9	0.9	0.9

Table 2. Quality characteristics of N95L9511 relative to check cultivars in the 1999 and 2000 WPRPN.

Line	Flour protein	Loaf volume	Bake mix time	Mixograph mix time	Mixograph tolerance
	g kg^{-1}	mL	min		0–5
			1999		
N95L11881	107	805	5.5	5.8	4
Arapahoe	105	795	5.6	5	3
Trego	102	860	4.1	4.4	4
Prowers	106	825	6.8	4.8	4
Std. dev.	6	39	1	0.8	1
			2000		
N95L11881	143	970	5.1	4.6	5
Arapahoe	138	865	4.9	3.8	3
Trego	128	900	3.3	2.9	2
Prowers	141	940	6.5	5.3	5
Std. dev.	6	48	0.9	0.9	1

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Registration of Nineteen Waxy Spring Wheats

Nineteen spring waxy (amylose-free) wheat (*Triticum aestivum* L.) germplasm lines (Reg. no. GP-748 to GP-766, PI 619354–619357, 619359–619363, 619365–619369, 619371–619375) were developed and released by the ARS, USDA, and the Nebraska Agricultural Experiment Station in cooperation with the Agricultural Experiment Stations of North Dakota and Idaho in September 2002. Waxy wheats carry three nonfunctional (null) alleles (*Wx-A1b*, *Wx-B1b*, and *Wx-D1b*) at the genetic loci encoding the enzyme granule-bound starch synthase (GBSS, EC 2.4.1.21) (Nakamura et al., 1995). GBSS also is known as the "waxy" protein. Waxy wheats produce endosperm starch that is nearly devoid of amylose. Such starch confers unique functional properties to derived wheat flour. Suggested uses for waxy wheats include the production of modified food starches, a blending agent to create flours with optimal amylose concentration for the production of a variety of sheeted and baked food products, and as an animal feed (reviewed by Graybosch, 1998). Waxy wheats also are useful as donors of the *Wx* null alleles, which may be used to develop partial waxy or reduced-amylose wheats. The presence of one or two such alleles can result in wheat flours with superior performance in certain food applications including white salted noodles (Epstein et al., 2002). Few waxy wheats have been publicly available to date, and those released (Morris and Konzak, 2001) are ill-adapted to North American spring wheat production zones. The release of this set of 19 waxy lines greatly expands the number of available genetic backgrounds carrying the waxy trait in wheat. Pedigrees and Plant Introduction (PI) numbers of the lines are listed in Table 1.

Lines were developed from matings between Asian and North American sources of the *Wx* null alleles. After the last cross in each pedigree, the brush end of F_2 plants was stained with a dilute solution of I_2KI and the germ end was saved for planting. Under these staining conditions, waxy seed were identified by their red-brown color, as opposed to the dark purple-black color typical of wild-type or partial waxy lines (Nakamura et al., 1995). F_2 plants were grown, without vernalization, in greenhouses in the fall of 1998, and maintained and harvested individually. Only true spring growth habit types (e.g., those that flowered and set seed under nonvernalizing conditions) were harvested. F_2–derived F_3 single-plant progeny rows were grown at Aberdeen, ID, USA in the spring of 1999. At harvest the 19 $F_{2:4}$ waxy lines were selected from these progeny rows, on the basis of uniformity of phenotype under field conditions and uniformity of the waxy trait.

Grain yields of the 19 waxy lines, based on replicated tests in three locations (Fargo, ND and Aberdeen, ID, 2000; Mead, NE, 2001), are given in Table 2. Grain yields ranged from a high of 3606 kg/ha in PI 619362 to a low of 2076 kg/ha in PI 619360. In the same testing environments, the spring wheat cultivars 'Express' (PI 573003), 'Westbred 926' and 'Klasic' (PI 486139) averaged 3441, 3703, and 2799 kg/ha, respectively. On the basis of assessment by a Perten Single Kernel Hardness Characterization System, mean hardness scores (Table 2) identified three soft endosperm textured wheats, while the remaining 16 waxy wheats were classified as hard wheats. Fifteen of the lines breed true for red grain color, while four are heterogeneous for red and white grain (Table 2).

Table 2 also lists postulated resistance genes to foliar diseases. On the basis of reactions to current races of leaf rust

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