selection of ND8955 was initiated in 1994 from 500 random F₀ plants and grown as individual rows in 1995. Eighty-three plant rows were selected based on uniformity for spike type, plant height, and resistance to natural leaf rust infections (caused by *Puccinia graminis*). In 1996, 75 of these selections were bulk harvested and designated ND8955-A. Both ND8955 and ND8955-A were tested at six North Dakota locations in 1997 and no significant differences were observed in their yield or other agronomically significant traits such as heading date or reaction to other diseases. The 1996 harvest of ND8955-A produced the Breeder seed used to initiate increase seed of Ransom.

Ransom is mid-maturity, similar to ‘Roughrider.’ The plant height of Ransom averaged 79 cm, compared with 74 cm for ‘Arapahoe’ and 84 cm for Seward. Ransom spikes are mid-dense, fusiform, awned, and white at maturity. Glumes are medium length and width with rounded shoulders and acuminate beak. Seeds are ovate, with rounded cheeks and medium brush.

In 39 North Dakota trials from 1991 through 1997, the grain yield of Ransom averaged 3422 kg ha⁻¹ which was 1% greater than Seward, 2% greater than Arapahoe, 3% greater than ‘Elkhorn,’ and 10% greater than Roughrider. Ransom was tested in the Northern Regional Performance Nursery from 1992 to 1994 (24 site-years across Minnesota, Montana, North Dakota, and South Dakota) and had an average grain yield of 3650 kg ha⁻¹, 4% greater than Elkhorn and 10% greater than Roughrider. Winterhardiness is similar to Seward, greater than Arapahoe, but less than Elkhorn and Roughrider. Straw strength is similar to Elkhorn and Roughrider and weaker than Seward.

Ransom has shown resistance to stem rust (caused by *Puccinia graminis* Pers. Pers. f. sp. triticis Eriks. & E. Hem.) races Pgt-QCCJ and -TPMK after inoculation of greenhouse-grown seedlings at moderate temperature (21°C), but susceptibility to these same races at high temperature (27–29°C). Field-grown adult plants have consistently shown resistance to the prevalent races of stem rust. Ransom is moderately resistant to prevalent races of leaf rust, but is more resistant than Roughrider or Seward. Ransom is susceptible to tan spot (caused by *Pyrenophora tritici-repentis* (Drechs.) Drechs.).

The grain quality of Ransom has been tested by the Department of Cereal Science and Food Technology at North Dakota State University since 1992. Ransom has a relatively low grain volume weight of 746 kg m⁻³, which is less than Roughrider (764 kg m⁻³) and Seward (755 kg m⁻³). The grain protein content of Ransom (127 g kg⁻¹) is intermediate between Roughrider (136 g kg⁻¹) and Seward (121 g kg⁻¹). Flour extraction and mixograph water absorption are intermediate between Roughrider and Seward. Dough mixing properties and bread baking performance of Ransom are acceptable, similar to Arapahoe.

Cultivar protection of Ransom under the U.S. Plant Variety Protection Act is pending. Breeder and Foundation seed is maintained by the Seedstocks Project, Agric. Exp. Stn., North Dakota State Univ., Fargo, ND 58105-5051. U.S. Plant Variety Protection of Ransom wheat has been applied for (PVP certificate no. 9900250).

**J.A. Anderson,* G.W. Johnson, D.J. Cox, W. Moore, J.D. Miller, J.B. Rasmussen, and L.J. Francl (1)**

**References and Notes**

1. J.A. Anderson, Dep. of Agronomy and Plant Genetics, 411 Borrbaugh Hall, Univ. of Minnesota, St. Paul, MN 55105; G.W. Johnson, Dep. of Plant Sciences, North Dakota State Univ., Fargo, ND 58105; D.J. Cox, ECHO, 17430 Durrance Rd., North Fort Myers, FL 33917; W. Moore, ConAgra Grain Processing Co., 1521 N. 15th St., Omaha, NE 68110; J.D. Miller, USDA-ARS, Northern Crop Science Laboratory, Box 5677, State Univ. Station, Fargo, ND 58105; J.B. Rasmussen and L.J. Francl, Dep. of Plant Pathology, North Dakota State Univ., Fargo, ND 58105. Accepted 30 Sept. 2000. * Corresponding author (ander319@tc.umn.edu).


**REGISTRATION OF GERMPLASM**

**Registration of Six Isogenic T1BL.1RS Chromosome Translocation and Six Chromosome 1B Durum Germplasms**

The International Maize and Wheat Improvement Center announces the release of six pairs of durum (*Triticum turgidum* L. var. durum Desf) germplasms differing for the T1BL.1RS chromosome translocation. The chromosome T1BL.1RS translocation was transferred to six chromosome 1B durum wheat cultivars ‘Laru,’ ‘Croc 1,’ ‘Dvergand 2,’ ‘Pardo,’ ‘Gutros,’ and ‘Bia.’ For each cultivar, we are registering one 1RS (3). Since this chromosome has substituted 1B in the six durum cultivars ‘Laru,’ ‘Croc 1,’ ‘Dvergand 2,’ ‘Pardo,’ ‘Gutros,’ and ‘Bia.’ For each cultivar, we are registering one 1RS (3). Since this chromosome has substituted 1B in the six durum germplasms differing for the T1BL.1RS chromosome.

The 1B derived lines of each cultivar are anticipated to yield the first backcross (BC) derivative. Two heterozygous BC plants with 28 chromosomes (1B, T1BL.1RS) were identified by Glucose-phospho-isomerase (GPI) electrophoresis and Giemsa C-banding. (2) All BC₁F₁ heterozygotes were backcrossed to their respective durums until the BC₇ generation and then self-pollinated. From the selfed progeny, plants homozygous for chromosomes 1B and T1BL.1RS were identified biochemically and cytologically.

The germplasms were developed by the Wide Cross program of the International Maize and Wheat Improvement Center (CIMMYT) in Mexico. All T1BL.1RS wheat germplasms possess disease resistance genes Lr26, Sr31, Yr9, and *Pm8* located on the rye (*Secale cereale*) chromosome arm 1RS (3). Since this chromosome has substituted 1B in the six durums, the above four genes are anticipated to be present.

The 1B derived lines of each cultivar are anticipated to differ from their parental stock for the recombination events occurring on the 1B chromosome arm of the T1BL.1RS translocation and on the other 26 chromosomes during the backcross procedure (4) since a different durum cultivar was involved in the production of each 1B, T1BL.1RS F₁ heterozygote. There are two earlier reports of durum germplasms with T1BL.1RS translocation (1,4). The six durum germplasms being registered here enhance existing diversity, and shall further elucidate the contribution of the T1BL.1RS chromosome.