Registration of NC06BGTAG12 and NC06BGTAG13 Powdery Mildew–Resistant Wheat Germplasm

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Common winter wheat (*Triticum aestivum* L.) germplasm lines NC06BGTAG12 (Reg. No. GP-813, PI 642416), and NC06BGTAG13 (Reg. no. GP-814, PI 612417), were developed and released by the North Carolina Agricultural Research Service and the USDA-ARS in 2006. These germplasms were released because of their potential to broaden the genetic base of resistance to powdery mildew [caused by *Blumeria graminis* (DC.) E.O. Spear f. sp. *tritici* Em. Marchal] with resistance transferred from the AAGG genome *T. timopheevii* (Zhuk.) Zhuk. subsp. *armeniacum* (Jakubz.) van Slageren. Both germplasms have consistently displayed resistance to the powdery mildew fungus in field evaluations in North Carolina from 1999 through 2005.

In North Carolina, the following genes are effective for resistance to naturally occurring powdery mildew populations: 1a, 3d, 3e, 3 g, 8, 12, 16, 17, 25, 34, and 35 (unpublished data). The following powdery mildew resistance genes are partially or completely defeated: 2a, 3a, 3b, 3c, 3f, 4a, 4b, 5a, 6, 7, and 20.

NC06BGTAG12 is a BC_2F_7–derived line with the pedigree 'Saluda'*3/PI 538457. Saluda (PI 480474) is a soft red winter wheat containing Pm3a (Leath and Heun, 1990) and released by Virginia Polytechnic Institute and State University (Starling et al., 1986). PI 538457 is a winter growth–habit accession collected 19 km east of the city of As-Sulaymaniyah, Iraq (35°38´ N lat., 045°36´ E long., elevation 1050 m). It was deposited in the U.S. National Plant Germplasm System in 1990 by Dr. J. Waines, University of California, Riverside, and was originally collected by Dr. B. L. Johnson, University of California, Riverside, in 1972.

NC06BGTAG13 is a BC_2F_6–derived line with the pedigree 'Saluda'*3/PI 427442. PI 427442 is a winter growth–habit accession collected 1 km northeast of the town of Salahadin in Arbil province, Iraq (36°24´ N lat., 044°12´ E long., elevation 1100 m). It was deposited in the U.S. National Plant Germplasm System in 1978 by Dr. B. L. Johnson, University of California, Riverside, who collected the accession in 1972.

Pentaploid F_1 hybrid (genomes AABGD), BC_1F_1, and BC_2F_1 generations were produced in the 1993–1994 and 1994–1995 greenhouse crossing seasons at North Carolina State University. BC_2F_2 and BC_2F_3 seeds were planted in single 11.1-m^2 plots containing approximately 1700 seeds during the 1996–1997 and 1997–1998 seasons, respectively, at Clayton, NC. Approximately 100 well-filled heads were selected at maturity, threshed in bulk in 1997, and threshed individually in 1998. Field selection using the pedigree breeding method was initiated in the 1998–1999 season at Kinston, NC, with $BC_2F_{3:4}$ lines planted in headrows. Selection during the 1998–1999 and subsequent seasons was primarily for powdery mildew resistance at Feekes growth stages 8 to 10.5, but whenever possible, additional selection for heading date, plant height, and straw strength was conducted with the Saluda phenotype as the benchmark. Natural powdery mildew epidemics occurred annually. NC06BGTAG12 traces to a single $BC_2F_{7:8}$ headrow harvested in 2003. NC06BGTAG13 traces to a single $BC_2F_{6:7}$ headrow harvested in 2002.

NC06BGTAG12 had significantly less powdery mildew than Saluda (mean 0.5 vs. 6.5) over 2 yr of advanced-generation testing in NC during 2003–2004 and 2004–2005. Assessments were based on a 0–9 scale reflecting the extent and position of lesions on the canopy. A score of 0.5 for NC06BGTAG12 indicated lesions were barely detectable in the lower canopy, whereas a score of 6.5 for Saluda indicated lesion coverage of 5% in the middle third of the canopy. NC06BGTAG12 and Saluda were evaluated for agronomic traits at five North Carolina locations in the 2004–2005 season. Mean grain yield and test weight were not significantly different for both lines, but NC06BGTAG12 was significantly different than Saluda in heading date (112 vs. 113 d) and plant height (84 vs. 79 cm). NC06BGTAG12 was one

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Table 1. Powdery mildew reactions of NC06BGTAG12, NC06BGTAG13 and five check lines to eight isolates of *Blumaria graminis* f. sp. *tritici*.

Line	Isolate†							
	1	2	3	4	5	6	7	8
NC06BGTAG12	L‡	L	H	L	L	L	I	L
NC06BGTAG13	L	L	H	L	L	L	L	L
Saluda	H	H	H	H	L	L	L	L
Chancellor	H	H	H	H	H	H	H	H
NC99BGTAG11	L	L	L	L	L	L	L	L
KS96WGRC37	I	H	I	I	H	I	I	I
CI 12632 (Pm6)	L	L	H	H	H	L	L	H

†The virulence/avirulence combinations for the *B.g.tritici* isolates are
#1: Pm 3a,3c,3f,4a,7/1a,2,3b,4b,5,6,8,17,25
#2: Pm 3a,3b,3c,3f,4a,5,7/1a,2,4b,6,8,17,25
#3: Pm 1a,2,3a,3c,3f,5,6,7,25/3b,4a,4b,8,17
#4: Pm 2,3a,3b,3c,3f,5,6,7/1a,4a,4b,8,17,25
#5: Pm 1a,2,3f,5,6,7/3a,3b,3c,4a,4b,8,17,25
#6: Pm 3b,3c,4a,4b,5,7,8,17,25/1a,2,3a,3f,6
#7: Pm 3b,3c,3f,4a,4b,5,7,8,17,25/1a,2,3a,6
#8: Pm 2,3c,6,7,8/1a,3a,3b,3f,4a,4b,5,17,25.

‡Reaction types are L = low (avirulence), I = intermediate, and H = high (virulence).

Table 2. Leaf rust infection types of germplasm lines NC06BGTAG12 and NC06BGTATG13 to six races of *Puccinia triticina*.

Line	Race					
	MBRJ†	MCRK	TLGF	THBJ	BBBD	PNMQ
NC06BGTAG12	0;‡	0;	0;3$^+$	;	;	3$^+$
NC06BGTAG13	0;	0;	0;3$^+$	;	;	3$^+$
Thatcher	3$^+$	3$^+$	3$^+$	3$^+$	3$^+$	3$^+$
Thatcher *Lr18* RL6009	;2$^-$	3$^+$	3$^+$	;2$^-$	2$^+$	2$^+$3
Saluda	3$^+$	3$^+$	3$^+$	2$^+$3$^+$	22$^-$	2$^+$
KS96WGRC36 *Lr50*	0;	0;	;3$^+$	;3$^+$	;3$^-$	;2

†Lr gene avirulence/virulence combinations
MBRJ 2a, 2c, 9, 16, 24, 26, 17, B, 18/1, 3, 3ka, 11, 30, 10, 14a, 18
MCRK 2a, 2c, 9, 16, 24, 17, B/1, 3, 26, 3ka, 11, 30, 10, 14a, 18
TLGF 16, 24, 26, 3ka, 17, 30, B, 10/1, 2a, 2c, 3, 9, 11, 14a, 18
THBJ 9, 24, 3ka, 11, 17, 30, B, 18/1, 2a, 2c, 3, 16, 26, 10, 14a
BBBD 1, 2a, 2c, 3, 9, 16, 24, 26, 3ka, 11, 17, 30, B, 10, 18/14a
PNMQ 2a, 16, 26, 11, 17, B, 10,/1, 2c, 3, 9, 24, 3ka, 30, 14a, 18

‡The infection types were classified using a 0 to 4 scale (Long and Kolmer 1989): 0 = immunity, no hypersensitive flecks or uredinia, 0; = faint hypersensitive flecks, ; = distinct hypersensitive flecks, 1 = small uredinia surrounded by distinct necrosis, 2 = small uredinia surrounded by distinct chlorosis, 3 = moderate size uredinia without chlorosis, 4 = very large uredinia lacking chlorosis. Designations of "+" or "−" indicate larger-than-normal uredinia and smaller uredinia, respectively. Infection types from 0 to 2$^+$ were considered as low-infection types, and infection types 3$^+$ to 4, were considered as high.

of the few entries to exhibit lodging at any location. Milling- and baking-quality evaluations were conducted at the USDA-ARS Soft Wheat Quality Laboratory, Wooster, OH, in 2004. NC06BGTAG12 had lower flour yield (69.8 vs. 71.7%), lower softness equivalent (36.5 vs. 59.2%), and lower sucrose retention (86.4 vs. 88.6%) compared with Saluda. NC06BGTAG12 had a higher grain protein percentage (10.5 vs. 8.7%) but a lower lactic acid retention value (88.6 vs. 108.6), than Saluda. It would be advisable to cross NC06BGTAG12 with an excellent milling- and baking-quality parent when developing breeding populations due to its low flour yield and softness equivalent values.

NC06BGTAG13 had significantly less powdery mildew than Saluda (mean 0.3 vs. 6.7) over 3 yr of advanced-generation testing at Kinston, NC, during 2002–2003, 2003–2004, and 2004–2005. Assessments were based on the same 0–9 scale described above. NC06BGTAG13 headed 6 d earlier and was taller than Saluda. Milling- and baking-quality evaluations were conducted at the USDA-ARS Soft Wheat Quality Laboratory, Wooster, OH, in 2004. NC06BGTAG13 had lower flour yield (67.9 vs. 71.7%), lower softness equivalent (46.6 vs. 59.2%), and lower sucrose retention (87.4 vs. 88.6%) compared with Saluda. NC06BGTAG13 had a higher grain protein percentage (10.3 vs. 8.7%) but a lower lactic acid retention value (102.6 vs. 108.6), than Saluda. It would be advisable to cross NC06BGTAG13 to an excellent milling- and baking-quality parent when developing breeding populations due to its low flour yield and softness equivalent values.

Laboratory evaluations for resistance to powdery mildew were conducted using a detached-leaf technique (Leath and Heun, 1990), which was replicated four times. Eight isolates of *B. graminis* f. sp. *tritici* were used to differentiate powdery mildew interactions among the lines NC06BGTAG12, NC06BGTAG13, Saluda, the susceptible check 'Chancellor'(CI*tr* 12333). and three other *T. timopheevii*–derived sources of resistance, NC99BGTAG11 (PI 615588), KS96WGRC37 (PI 604222), and CI*tr* 12632 (a source of *Pm6*) (Table 1). The reaction types of NC06BGTAG12 and NC06BGTAG13 were distinctly different from Saluda, NC99BGTAG11, KS96WGRC37, and CI 12632. Both germplasm lines had susceptible reactions to isolate #3, and resistant reactions to all other isolates except #7, which consistently produced intermediate reactions on NC06BGTAG12 and resistant reactions on NC06BGTAG13. The donor accession for NC99BGTAG11 (Murphy et al., 2002) and the donor accession for NC06BGTAG13 were collected at the same location in Iraq. The differential response to isolate #3 between NC99BGTAG11 and NC06BGTAG13 was key to our decision to release the latter germplasm line. We did not compare the two germplasms to *Pm27*, the other documented mildew-resistance gene derived from *T. timopheevii* (Jarve et al., 2000).

NC06BGTAG12 and NC06BGTAG13 were tested for resistance to leaf rust, caused by *Puccinia triticina* Eriks., in seedling tests with the races listed in Table 2. Also included were the leaf rust–susceptible spring wheat 'Thatcher' (CI*tr* 10003); the Thatcher near-isogenic line RL6009 with *Lr18*, which was originally derived from *T. timpoheevii*; KS96WGRC36 (PI 604221), a hard red winter wheat germplasm with *Lr50*, which was also derived from *T. timopheevii*; and Saluda. Both NC06BGTAG12 and NC06BGTAG13 had very low infection types to races MBRJ, MCRK, THBJ, and BBBD. Both germplasm lines had a 0;3$^+$ infection type (faint hypersensitive flecks with large pustules) to race TLGF and had high infection type of 3$^+$ to race PNMQ. Both germplasm lines had lower infection types to races MBRJ, MCRK, THBJ, and TLGF, compared with the background parent Saluda. Both germplasm lines differed from RL6009 and KS96WGRC36

for infection types to at least one leaf rust race, which indicated that these lines may carry gene(s) for leaf rust resistance derived from *T. timopheevii* that have not yet been characterized.

Small quantities of seed (2 g) of the germplasm lines are available from the corresponding author on written request. Appropriate recognition of source should be given if this germplasm contributes to research or development of new cultivars.

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