

Registration of Twelve Grain Sorghum Genetic Stocks Near-isogenic for the Brown Midrib Genes *bmr-6* and *bmr-12*

Twelve grain sorghum [*Sorghum bicolor* (L.) Moench] genetic stocks, N599 to N610, (Reg. no. GS-128–GS-139, PI 639709–PI 639720) near-isogenic to their wild-type counterparts for the brown midrib genes *bmr-6* and *bmr-12* were developed jointly by the USDA-ARS, and the Agricultural Research Division, Institute of Agriculture and Natural Resources, University of Nebraska, and were released in May 2005.

The genetic stocks were developed by crossing the recurrent parents Wheatland, Redlan, RTx430, BTx623, BTx630, and BTx631 to the brown midrib sources N121 (*bmr-6*) and F220 or F324 (*bmr-12*, donated to our project by the late Robert Kalton). Crossing was facilitated by the use of the nuclear male-sterility gene *ms₃* with three to four cycles of backcrossing and selfing to recover the recurrent parent phenotype. Following the final backcross, the lines were selfed and advanced head-to-row for four generations to fix the brown midrib genes in the homozygous recessive condition (*bmr-6 bmr-6* or *bmr-12 bmr-12*) and the male-sterility genes in the male-fertile condition (*Ms₃ Ms₃*). The brown midrib near-isolines were selected for similarity to the wild-type phenotype and for male fertility. The near-isolines were crossed to A₁ cytoplasmic male-sterile lines to evaluate fertility restoration. Lines that maintained sterility (B-lines) were converted to cytoplasmic male-sterile A-lines by crossing them to their A-line wild-type counterparts and recovering the brown midrib lines in A₁ cytoplasm after a minimum of four additional backcross generations. The genetic stocks resemble the recurrent parent with descriptive information shown in Table 1.

Release of these genetic stocks makes brown midrib genes known to reduce activity of two specific enzymes important in lignin synthesis, cinnamyl alcohol dehydrogenase (*bmr-6*) and O-methyltransferase (*bmr-12*), available in diverse near-isogenic grain sorghum backgrounds. This will allow direct comparison of

gene effects across these backgrounds. They have immediate application for basic research involving lignin synthesis and also may be utilized as germplasm for development of improved brown midrib lines and hybrids.

Since genetic drift may have occurred within the recurrent parent inbred lines during multiple generations of maintenance at Lincoln, NE, seed of the recurrent parents used by this project will be distributed with the genetic stocks to maximize similarity of nuclear genes in each set of lines in the various backgrounds.

Seed of these genetic stocks will be maintained and distributed by the USDA-ARS, Wheat, Sorghum, and Forage Research Unit, Department of Agronomy, University of Nebraska, Lincoln, NE 68583-0937, and will be provided without cost to each applicant on written request. Genetic material of this release will be deposited in the U.S. National Plant Germplasm System where it will be available for research purposes, including development and commercialization of new varieties or cultivars. It is requested that appropriate recognition be made if this germplasm contributes to the development of a new breeding line, variety, or cultivar.

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Table 1. Genetic stock designations, recurrent parent, brown midrib gene, and descriptive characteristics of sorghum brown midrib near-isolines averaged over four environments.†

PI	Genetic stock	Recurrent parent	Brown midrib gene	Brown midrib source	Days to anthesis‡	Height‡	Fertility reaction§	Plant color	Caryopsis color	Endosperm	Testa	Awns	Culm
					days	cm							
PI639709	A/BN599	Wheatland	wild type	N121	68b	101a	B	purple	red	normal	no	no	juicy
PI639710	A/BN600	Wheatland	<i>bmr-6</i>	F220	70a	88b	A/B	purple	red	normal	no	no	juicy
		Redlan	<i>bmr-12</i>		71a	101a	A/B	purple	red	normal	no	no	juicy
PI639711	A/BN601	Redlan	wild type	N121	72c	123b	B	purple	red	normal	no	no	juicy
PI639712	A/BN602	Redlan	<i>bmr-6</i>	F324	73b	119c	A/B	purple	red	normal	no	no	juicy
		BTx623	<i>bmr-12</i>		75a	135a	A/B	purple	red	normal	no	no	juicy
PI639713	A/BN603	BTx623	wild type	N121	69b	130a	B	purple	white	normal	no	no	juicy
PI639714	A/BN604	BTx623	<i>bmr-6</i>	F220	66c	116c	A/B	purple	white	normal	no	no	juicy
		BTx630	<i>bmr-12</i>		73a	119b	A/B	purple	white	normal	no	no	juicy
PI639715	A/BN605	BTx630	wild type	N121	73b	130a	B	tan	white	mixed¶	no	no	juicy
PI639716	A/BN606	BTx630	<i>bmr-6</i>	F220	77a	110c	A/B	tan	white	normal	no	no	juicy
		BTx631	<i>bmr-12</i>		77a	125b	A/B	tan	white	normal	no	no	juicy
PI639717	A/BN607	BTx631	wild type	N121	74b	129a	B	tan	white	normal	no	no	juicy
PI639718	A/BN608	BTx631	<i>bmr-6</i>	F220	73c	121c	A/B	tan	white	normal	no	no	juicy
		RTx430	<i>bmr-12</i>		79a	125b	A/B	tan	white	normal	no	no	juicy
PI639719	N609	RTx430	wild type	N121	73c	125b	R	purple	yellow	normal	no	no	juicy
PI639720	N610	RTx430	<i>bmr-6</i>	F220	74b	121c	R	purple	yellow	normal	no	no	juicy
	SE#		<i>bmr-12</i>		77a	137a	R	purple	yellow	normal	no	no	juicy
					3	4							

† Environments were Ithaca and Lincoln, NE in 2002 and 2003.

‡ Means within recurrent parent set followed by different letters differ at $P = 0.05$ using an F -protected LSD.

§ Fertility reaction to A₁ cytoplasmic male-sterile cytoplasm: A/B = male-sterile/maintainer pair, R = fertility restorer.

¶ The BTx630 recurrent parent seed source used was discovered to be segregating for wild-type and waxy phenotype.

SE, standard error.