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## Registration of Seven Forage Sorghum Genetic Stocks Near-Isogenic for the Brown Midrib Genes *bmr-6* and *bmr-12*

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### Registration of Seven Forage Sorghum Genetic Stocks Near-Isogenic for the Brown Midrib Genes *bmr-6* and *bmr-12*

Seven forage sorghum [*Sorghum bicolor* (L.) Moench] genetic stocks, N592 to N598, (Reg. no. GS-121–GS-127, PI639702–PI639708) 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 January 2005.

The genetic stocks were developed by crossing the recurrent parents Atlas, Kansas Collier, Rox Orange, and Early Hegari-Sart to brown midrib sources N121 (*bmr-6*) and F220 (*bmr-12*, donated to our project by the late Robert Kalton), followed by a minimum of four cycles of selfing and backcrossing. Crossing was facilitated by the use of the nuclear male-sterility gene *ms<sub>3</sub>*. Following the last 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 loci in the male-fertile condition (*Ms<sub>3</sub> Ms<sub>3</sub>*). The brown midrib near-isolines were then selected for similarity to the wild-type phenotype and for male fertility. The genetic stocks closely resemble the recurrent parent with descriptive information shown in Table 1.

Release of these genetic stocks makes brown midrib genes known to downregulate two specific enzymes important in lignin synthesis, cinnamyl alcohol dehydrogenase (*bmr-6*) and O-methyltransferase (*bmr-12*), available in diverse near-isogenic forage sorghum backgrounds allowing direct comparison of gene effects across these broad backgrounds. They have immediate application for basic research involving lignin synthesis and also may be utilized as germplasm for development of improved brown midrib forage sorghum lines and hybrids. Because of the presence of a high-tannin testa layer in seed of

all but one of these lines, direct increase and use of these genetic stocks as cultivars is strongly discouraged.

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 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 number	Genetic stock	Recurrent parent	Brown midrib gene	Days to anthesis	Height	Plant color	Seed color	Endosperm	Testa	Awns	Culms	A <sub>1</sub> Fertility restoration reaction‡
				d	cm							
PI639702	N592	Rox Orange	wild type	71	232	purple	brown	normal	yes	no	juicy	-
PI639703	N593	Rox Orange	<i>bmr-6</i>	70	205	purple	brown	normal	yes	no	juicy	B
		Rox Orange	<i>bmr-12</i>	74	230	purple	brown	normal	yes	no	juicy	B
PI639704	N594	Kansas Collier	wild type	76	236	purple	brown	normal	yes	no	juicy	-
PI639705	N595	Kansas Collier	<i>bmr-6</i>	77	214	purple	brown	normal	yes	no	juicy	B
		Kansas Collier	<i>bmr-12</i>	77	228	purple	brown	normal	yes	no	juicy	B
PI639706	N596	Early Hegari-Sart	wild type	71	153	purple	white	normal	yes	no	juicy	-
PI639707	N597	Early Hegari-Sart	<i>bmr-6</i>	74	139	purple	white	normal	yes	no	juicy	R
		Early Hegari-Sart	<i>bmr-12</i>	78	156	purple	white	normal	yes	no	juicy	R
PI639708	N598	Atlas	wild type	80	238	purple	white	normal	no	no	juicy	-
		Atlas	<i>bmr-6</i>	77	216	purple	white	normal	no	no	juicy	B
	SE§			2	12							

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

‡ B = did not restore fertility in A<sub>1</sub> cytoplasmic male-sterile lines under greenhouse conditions; R = restore fertility A<sub>1</sub> cytoplasmic male-sterile lines under greenhouse conditions.

§ SE = Standard error.