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# Registration of Common Bacterial Blight Resistant Pinto Bean Germplasm Line ABCP-8

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line Roazon, having the diagnostic DNA marker locus, Xgwm682 (Helguera et al., 2003). It was free of leaf rust (caused by *Puccinia triticina* Eriks.) and stripe rust (caused by *Puccinia striiformis* Westend.) in tests where Patterson scored as 10 S (10 = percentage flag leaf infected, S = susceptible reaction type) for leaf rust and 70 S for stripe rust. Powdery mildew (caused by *Blumeria graminis* DC. f. sp. *tritici* Em. Marchal) develops more slowly on P961341 than on susceptible wheat lines; P961341 is typically scored at 2 to 4 (0–9, 0 = no lesions to 9 = severe disease) compared to scores of 6 to 8 for cultivar Patterson in the same tests in Indiana. P961341 is resistant to *Soilborne mosaic virus*, scored as 0 to 1 (0 = no yellow mottling, 9 = severe mottling and plant stunting) compared to cultivar Roane, with a score of 4, and cultivar 'Coker 9375', score of 8, in a severely infested plot area at Urbana, IL. Flowering date of P961341 in Indiana is similar to that of cultivar Patterson. P961341 has yellow anthers, with awnlets typically 3 to 5 mm long.

P961341 is intended to provide a source of resistance to BYDV and CYDV for wheat breeding and genetic research. Small quantities of seed are available on written request to the corresponding author. Appropriate recognition of source should be given when this germplasm contributes to research or development of a new breeding line or cultivar.

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### References

- Crasta, O.R., M.G. Francki, D.B. Bucholtz, H.C. Sharma, J. Zhang, R.-C. Wang, H.W. Ohm, and J.M. Anderson. 2000. Identification and characterization of wheat-wheatgrass translocation lines and localization of barley yellow dwarf virus resistance. *Genome* 43: 698–706.
- Helguera, M., I.A. Khan, J. Kolmer, D. Lijavetzky, L. Zhong-qi, and J. Dubcovsky. 2003. PCR assays for the *Lr37-Yr17-Sr38* cluster of rust resistance genes and their use to develop isogenic hard red spring wheat lines. *Crop Sci.* 43:1839–1847.
- Sharma, H.C., H.W. Ohm, and K.L. Perry. 1997. Registration of barley yellow dwarf virus resistant wheat germplasm line P29. *Crop Sci.* 37:1032–1033.
- Sharma, H., M. Francki, O. Crasta, G. Gyulai, D. Bucholtz, H. Ohm, J. Anderson, K. Perry, and F. Patterson. 1999. Cytological and molecular characterization of wheat lines with *Thinopyrum intermedium* chromosome additions, substitutions and translocations resistant to barley yellow dwarf virus. *Cytologia* (Tokyo) 64:93–100.

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### Registration of Common Bacterial Blight Resistant Pinto Bean Germplasm Line ABCP-8

Pinto bean (*Phaseolus vulgaris* L.) germplasm line ABCP-8 (Reg. no. GP-237, PI 635118) was developed by the University of Nebraska Agricultural Research Division in cooperation with USDA-ARS and released in 2004. This line was bred specifically for enhanced resistance to common bacterial blight [caused by *Xanthomonas campestris* pv. *phaseoli* (Smith) Dye]. Pinto and other dry bean market classes (dark red kidney, great northern, navy, etc.) grown in the U.S.A. east of the continental divide are often attacked by common bacterial blight, a seed-transmitted disease that causes up to 40% yield

loss in susceptible cultivars as well as reduction of seed quality through discoloration of infected seed. Development of cultivars with genetic resistance combined from different sources is the most cost effective method to control common bacterial blight.

ABCP-8 is the first pinto bean to combine the XAN 159 and great northern Montana No. 5 (Miklas et al., 2003) sources of common bacterial blight resistance. Combined resistance was confirmed by the presence of previously developed SCAR markers SU91 (Pedraza et al., 1997) and SAP6 (Miklas et al., 2003) tightly linked with quantitative trait loci (QTL) from XAN 159 and Montana No. 5, respectively. In addition to common bacterial blight resistance, ABCP-8 possesses the *Ur-3* gene for resistance to rust [caused by *Uromyces appendiculatus* (Pers.:Pers.) Unger] as indicated by resistance to rust Races 41, 53, and 108, and the *bc-1<sup>2</sup>* gene for resistance to *Bean common mosaic virus* (BCMV) and *Bean common mosaic necrosis virus* (BCMNV) Pathogroups 1, 2, 3, and 5 and partial resistance to NL-3 strain of Pathogroup 6 of BCMNV.

ABCP-8 pinto is a BC<sub>3</sub>F<sub>3,5</sub> line obtained from five backcrosses ('Chase'\*5/XAN 159) between the donor parent XAN 159 and recurrent parent Chase pinto. Seeds of XAN 159 are medium (25 g 100 seed<sup>-1</sup>) with a flat cylindrical shape and a gray-speckled fine-dotting seed coat pattern. XAN 159 was developed for resistance to common bacterial blight at the Centro Internacional Agricultura Tropical (CIAT) by selection from the interspecific cross 'UI 114' pinto/PI 319441//PI 319443 (*P. acutifolius* A. Gray)/'Masterpiece' made by Thomas and Waines (1984). XAN 159 was estimated to have up to five QTL for resistance to common bacterial blight (Eskridge and Coyne, 1996). It is susceptible to rust and BCMV. Chase was derived from a cross between a great northern breeding line, GN-WM-84-17, and a pinto breeding line, P-WM-84-45, from the University of Nebraska dry bean breeding program. Chase is resistant to rust (*Ur-3* gene) and moderately resistant to bacterial brown spot (caused by *Pseudomonas syringae* pv. *syringae* van Hall) and common bacterial blight, and expresses moderate avoidance to white mold [caused by *Sclerotinia sclerotiorum* (Lib.) de Bary] due to a porous canopy, but is susceptible to BCMV (Coyne et al., 1994).

The first cross was made in the spring 1997. Only BC<sub>n</sub>F<sub>1</sub> plants resistant to common bacterial blight isolates DR-7 and EK-11 as determined by multiple-needle leaf inoculation tests in the greenhouse (Andrus, 1948) were used for successive backcrossing. In addition to common bacterial blight resistance, selection for desirable pinto seed characteristics began after BC<sub>3</sub>. Single plant selections were made from inbred BC<sub>5</sub> lines expressing the highest common bacterial blight resistance. Field evaluation of selected BC<sub>5</sub>F<sub>3,5</sub> lines were conducted at the West Central Research and Extension Center (North Platte) and Panhandle Research and Extension Center (Scottsbluff) in Nebraska in 2001, 2002, and 2003 and at the Washington State University Experiment Station in Othello, WA, in 2002. In addition to phenotypic selection for common bacterial blight resistance, marker-assisted selection for the SU91 and SAP6 markers was conducted in the BC<sub>1</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>1</sub>.

The seed size (30 g 100 seed<sup>-1</sup>) for ABCP-8 across locations was less than Chase (33 g 100 seed<sup>-1</sup>). The yield for ABCP-8 was 117, 148, and 129% of the yield of Chase in Nebraska (2001 and 2003) and Washington (2002), respectively. ABCP-8 matured 4 d later than Chase in Washington. The line exhibits an indeterminate semi-prostrate growth habit similar to Chase. ABCP-8 exhibited greater resistance to common bacterial blight (6% infection in field and greenhouse tests) than the

recurrent parent Chase (33% field and 46% greenhouse) and susceptible check 'Othello' pinto (59% field and 100% greenhouse), and similar resistance to the donor parent XAN 159 (8% in field and 5% in greenhouse). Disease scores were recorded as percentage diseased plants (leaves and pods) in the field under natural infection and percentage common bacterial blight symptoms visible within the inoculated leaf area of greenhouse grown plants.

The ABCP-8 breeding line will be useful for improving resistance to common bacterial blight in the pinto bean market class. Limited quantity of seed is available from P.N. Miklas (pmiklas@pars.ars.usda.gov). We ask that appropriate recognition of source be given when this germplasm contributes to the development of a new cultivar.

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### References

- Andrus, C.F. 1948. A method of testing beans for resistance to bacterial blights. *Phytopathology* 38:757-759.
- Coyne, D.P., D.S. Nuland, D.T. Lindgren, and J.R. Steadman. 1994. 'Chase' pinto dry bean. *HortScience* 29:44-45.
- Esckridge, K.M., and D.P. Coyne. 1996. Estimating and testing hypotheses about the number of genes using inbred-backcross data. *J. Hered.* 87:410-412.
- Miklas, P.N., D.P. Coyne, K.F. Grafton, N. Mutlu, J. Reiser, D. Lindgren, and S.P. Singh. 2003. A major QTL for common bacterial blight resistance derives from the common bean great northern landrace cultivar Montana No. 5. *Euphytica* 131:137-146.
- Pedraza, F., G. Gallego, S. Beebe, and J. Tohme. 1997. Marcadores SCAR y RAPD parala resistencia a la bacteriosis comun (CBB). p.130-134. In S.P. Singh and O. Voysest (ed.) Taller de mejoramiento de frijol para el Siglo XXI: Bases para una estrategia para America Latina. CIAT, Cali, Colombia.
- Thomas, C.V., and J.G. Wainnes. 1984. Fertile backcross and allotetraploid plants from crosses between tepary beans and common beans. *J. Hered.* 75:93-98.

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### Registration of MD 52ne High Fiber Quality Cotton Germplasm and Recurrent Parent MD 90ne

Cotton (*Gossypium hirsutum* L.) germplasm MD 52ne (Reg. no. GP-787, PI 634930) and its recurrent parent MD 90ne (Reg. no. GP-788, PI 634931) were developed by the USDA-ARS, Stoneville, MS, and released in August 2003. The two germplasms were each produced by using the backcross breeding method and using MD 65-11ne in both cases

as the donor parent. Both MD 52ne and MD 90ne possess high fiber bundle strength combined with the nectariless trait ( $2_{ne1, ne2}$ ) and semi-smooth leaf ( $2t_3$ ) and offer breeders and cotton physiologists opportunities to manipulate and study a fiber property deemed essential by modern yarn manufacturing technologies.

The first backcross program produced MD 90ne. It is a BC<sub>4</sub> line in about F<sub>8</sub> that was produced by using 'Deltapine Acala 90'<sup>1</sup> as the recurrent parent and germplasm line MD 65-11ne as the donor parent. MD 65-11ne has not been officially released, but has been used in studies of canopy physiology (Wells et al., 1986) and lint trash content (Novick et al., 1991) and in breeding programs (Meredith, 1993). Deltapine Acala 90 was a widely grown cultivar until about 2001, first produced in 1981, and a major cultivar since 1982 (USDA-AMS, 1982-2003). It possesses high yield potential, good fiber bundle strength by stelometer measurement, and the semi-smooth leaf trait. The semi-smooth leaf trait results in less trash in ginned lint (Novick et al., 1991; Williford et al., 1987) and results in lower populations of the cotton aphid (*Aphis gossypii* Glover) compared with hirsute cottons (Weathersbee et al., 1994). The nectariless trait's yield, yield components, and fiber quality are similar to those of near isogenic nectaried cultivars unless tarnished plant bugs [*Lygus lineolaris* (Palisot de Beauvois)] are present in large numbers (Meredith, 1975). In those cases, cultivars possessing the nectariless trait produce similar yield components and fiber quality and result in significantly higher yields.

MD 65-11ne was produced by five backcrosses to Deltapine 16ne as the recurrent parent and FTA 263-20 as the donor parent (GP 154, Culp and Harrel, 1980). In each segregating generation, selection was practiced for high bundle strength. 'Deltapine 16'<sup>1</sup> was a popular commercial cultivar in the 1960s and 1970s and is half the parentage of Deltapine Acala 90 (Calhoun et al., 1997). The high bundle strength of MD 65-11ne descends from FTA 263-20. It has a complex parentage involving Sea Island (*G. barbadense* L.) and Triple Hybrid [*G. arboretum* L. × *G. thurberi* Todaro] × *G. hirsutum*] germplasm.

The second backcross program produced MD 52ne by using MD 90ne as the recurrent parent in five backcrosses and MD 65-11ne was the donor parent. Selection in each backcross was for high bundle strength. MD 52ne has about 10% higher bundle strength, 22% less short fibers, and 7% longer mean fiber length than its near-isoline recurrent parent MD 90ne (Meredith, 2005). The unique aspect of MD 52ne is that the inheritance of improved fiber quality appears to be controlled by a small number of genes. A genetic study conducted with BC<sub>6</sub> F<sub>2.3</sub> progenies estimated bundle strength was controlled by 1.23 (± 0.16) genes (Meredith, 2005). The small number of genes conferring high fiber strength implies small segregating populations are needed to recover high fiber strength. However, as found in many fiber quality studies, yield and lint percentage are negatively correlated with high fiber strength.

MD 90ne is included in the release to provide a near-isogenic check for those wishing to study physiological-genetic associations. Small quantities of seed (100 seed) of these germplasm lines may be obtained from the corresponding author for research purposes. Recognition of the source of the germplasm is expected if it is used in the development of a new cultivar or in genetic-physiological host plant resistance studies.

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<sup>1</sup> Mention of trade names or commercial products in this release are solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U. S. Department of Agriculture.