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Registration of Germplasms

REGISTRATION OF AZ-RON ALFALFA GERMPLASM[1]

(Reg. No. GP114)

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AZ-RON alfalfa (*Medicago sativa* L.) germplasm was developed and tested by personnel of the Arizona Agric. Exp. Stn. and released in November 1978. It was selected for tolerance to frequent herbage removal.

'Moapa' alfalfa was grown in broadcast stands on the Univ. of Arizona Campbell Avenue Farm at Tucson from 1961 to 1964. The planting was harvested 36 times at the early bud stage, when approximately 50% of the stems had prominent flower buds. At the conclusions of this 4-year period the plant population was less than 1% of the original stand density. Sixty of the most vigorous survivors were selected and propagated as parent clones of AZ-Ron.

Synthetic-2 seed of AZ-Ron was used to conduct a forage yield test with 1/15 ha size plots at the Univ. of Arizona, Mesa Exp. Stn. AZ-Ron consistently out-yielded its parent source, Moapa, each year of the test period. Its forage yield was less than the check cultivar 'Mesa-Sirsa' during the 1st and 2nd year. However, AZ-Ron out-yielded Mesa-Sirsa and all other entries during the 3rd and 4th year because of its greater persistence and vigor.

During the "summer slump" period of forage production in southern Arizona (mid-June to mid-September), total available carbohydrate content in the roots of AZ-Ron averaged 16.9% compared to 12.3 and 13.5% for Mesa-Sirsa and Moapa, respectively. This difference represents an average of 24% more energy available in the roots of AZ-Ron than in the two check cultivars. The maintenance of higher carbohydrate levels in alfalfa roots during this critical period of the growing season apparently is essential for stand persistence and vigorous regrowth. Alfalfa producers have maintained stands by prolonging the regrowth period of at least two harvests to the full bloom stage of growth during the summer slump period. AZ-Ron represents a germplasm source which could reduce the need for extending these regrowth periods.

Seed stocks of AZ-Ron will be maintained by the Arizona Agric. Exp. Stn., Tucson, AZ 85721. Fifty grams of seed will be made available upon written request and agreement to make appropriate recognition of its source if the germplasm contributes to the development of a new germplasm source, cultivar, or hybrid. Request seed from M. H. Schonhorst, Dep. of Plant Science, Univ. of Arizona, Tucson, AZ 85721.

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REGISTRATION OF WI-1 AND WI-2 RED CLOVER[1]

(Reg. No. GP 31 and GP 32)

R. R. Smith and D. P. Maxwell[2]

WI-1 and WI-2 red clover (*Trifolium pratense* L.) germplasm lots were developed cooperatively by AR-SEA-USDA and Wisconsin Agric. Exp. Stn. The Syn 2 generation of each line was released as germplasm to scientists in April, 1980. Both germplasm lines provide resistance to northern anthracnose (NA) (causal agent-*Kabatiella caulivora* (Kirchn.) Karak.), rust (R) (causal agent-*Uromyces trifolii* (Hedrow. f. ex DC.) Lev. var. *fallens* Arth.), and powdery mildew (PM) (causal agent-*Erysiphe polygoni* DC. ex St. Amans). Both WI-1 and WI-2 have some resistance to target spot (TS) (causal agent-*Stemphylium sarciniforme* (Cav.) Wiltshire). WI-1 contains 75% plants moderately resistant to TS in contrast to only 15% in WI-2.

Both germplasm lines were developed using phenotypic recurrent selection by successive elimination of 3- to 4-month old susceptible plants under controlled conditions in the greenhouse. After the first cycle of selection approximately 60 to 80 plants were retained each generation and intercrossed using honeybees under controlled isolation in the field. Polycross seed was bulked to continue subsequent selection cycles. Inocula for target spot and northern anthracnose consisted of composites of isolates of the respective pathogens. A single spore isolate was used in the selection for rust resistance.

WI-1 (GP 31) was derived from the cultivars 'Lakeland,' 'Arlington,' 'Dollard,' and 'Kenstar' and four elite breeding lines selected for persistence, at different times, from germplasm developed through sibmating or polycrossing clones adapted to the northcentral region. One hundred forth-four plants (23% from Arlington and 11% from each of the other seven sources) were identified as moderately susceptible to TS and these were intercrossed to provide germplasm for further selection. After the first cycle, four cycles of selection were completed for resistance to TS and NA making a total of five cycles of selection for resistance to TS. One cycle of selection was completed for R resistance. Over 90% of the plants are resistant to NA, 85% to R, and 75% moderately resistant to TS.

WI-2 (GP 32) was derived from Lakeland (10%) and six elite breeding lines (15% each) selected for persistence and to a lesser extent for resistance to NA from material similar to that described for WI-1 above. Four cycles of selection for resistance were completed for NA and R and one cycle for TS. Over 95% of the plants are resistant to NA, 90% to R, and 15% moderately resistant to TS.

At Madison, Wis. in a 2 year forage trial, forage yields of WI-1 and WI-2 were 101 and 97% of Arlington, respectively. Spring and fall flowering for both populations are comparable to Arlington. Both populations have over 75% plants resistant to PM.

Seed stocks of WI-1 Syn 2 and WI-2 Syn 2 are maintained by AR-SEA-USDA, Dep. of Agronomy, Univ. of Wisconsin, Madison, WI 53706. An 8-g seed sample of each population will be supplied to each applicant upon written request and agreement to make appropriate recognition of the source if the germplasm contributes to a new cultivar.

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[2] Research geneticist, AR-SEA-USDA and professor of plant pathology, University of Wisconsin, Madison, WI 53706, respectively.

REGISTRATION OF AMERICAN PIMA COTTON GERMPLASM[1]

(Reg. No. GP159 and GP160)

Carl V. Feaster and E. L. Turcotte[2]

Two breeding lines of American Pima cotton (*Gossypium barbadense* L.), 79-103 (GP 159) and 79-106 (GP 160), were developed and released by AR-SEA-USDA and the Arizona Agric. Exp. Stn. in 1980. These lines are early maturing and short statured and may be suitable for use in combination with G.

hirsutum L. cultivars for interspecific hybrid cotton production.

79-103, an F_5 selection from the cross of experimental strains 6503-33-3-1 and 6612-62-5, and 79-106, an F_5 selection from the cross of experimental strains 6503-33-3-1 and 6614-91-11, are approximately 2 weeks earlier maturing than 'Pima S-5,' the current commercial American Pima cultivar. 79-103 has short statured plants, averaging 50 to 75% of the height of Pima S-5. 79-106 is taller with its plant height averaging 65 to 95% of the height of Pima S-5. The greatest deviations in height for these lines from Pima S-5 are in environments where Pima S-5 grows tallest. A high degree of height stability is exhibited by 79-103 and 79-106. The height stability in the *G. barbadense* parent may reduce the excessive vegetative growth that has been a persistent problem in *G. hirsutum* × *G. barbadense* hybrids.

The lint yield from 79-103 and 79-106 averaged 4 and 9% higher than for Pima S-5, respectively, in two tests at Phoenix (low elevation) and two tests at Safford (high elevation). Their fiber properties are equal or superior to those for Pima S-5.

Seed (25 g) of these breeding lines may be obtained from AR-SEA-USDA, Univ. of Arizona Cotton Res. Ctr., 4207 E. Broadway, Phoenix, AZ 85040.

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[2] Research agronomist and research geneticist, AR-SEA-USDA, Phoenix, AZ 85040.

REGISTRATION OF SUNFLOWER GERMPLASM COMPOSITE CROSSES CMG-1, CMG-2, AND CMG-3[1]

(Reg. Nos. GP2 to GP4)

Ernest D. P. Whelan and W. Dedio[2]

GERMPLASMS CMG-1, CMG-2, and CMG-3 are open-pollinated composites of partial interspecific substitutions of the nucleus of cultivated sunflower (*Helianthus annuus* L.) cv. 'Saturn' into the cytoplasms of the annual species *H. petiolaris* Nutt., and the two perennial species *H. giganteus* L. and *H. maximiliani* Schrad. (2, 3). This is the first successful hybridization of the latter two species with *H. annuus*, and subsequent attempts to repeat the cross have been unsuccessful. The three germplasms are potential new sources of both cytoplasmic male sterility and fertility restoration. The average 1,000-seed weights of the original species were 6.7, 1.7, and 1.9 g, respectively, and oil contents were 32.5, 27.4, and 29.4%. Values for the recurrent pollen parent Saturn were 60 g and 44.4%, respectively (1).

Germplasm CMG-1 (GP2) is an open-pollinated composite of 43 BC_2 lines from two interspecific F_1 hybrids from the cross *Helianthus petiolaris* Accession 1479 by the open-pollinated sunflower (*H. annuus*) cv. Saturn (3). It is a potential new source of cytoplasmic male sterility (cms). In advanced backcross generations, cms plants with indehiscent anthers and white pollen were obtained. Such plants had normal seed set, but the pollen failed to germinate in in vivo tests and, when used to pollinate a standard cms line CM 400, no seed was produced. Pollen shed was partially or completely restored in F_1 progenies of crosses with the French restorer source Bb2a1, the U.S. restorer RHA 280, and Accession 1356, but not in crosses with RHA 273, RHA 296, Accession 1338, nor wild *H. annuus* Accession 1357. All restorer sources partially or completely restored another cms line, CM 338. The genetics of fertility restoration is complex and involves at least two different dominant genes (4). Parental lines in the composite were highly variable for all plant characteristics including branching, maturity, 1,000-seed weight, and oil content. The 1,000-seed weight of 45 BC_3 lines ranged from 27 to 84 g, and of 68 BC_4 lines from 32 to 137 g. Oil content for the same material ranged from 35.5 to 51.1% for BC_3, and 30.9 to 44.5% for BC_4. Trisomic ($2n + 1$) plants were found in BC_1 and BC_2, but not in subsequent generations (3).

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Germplasm CMG-2 (GP3) is an open-pollinated composite of 15 lines from three interspecific F_1 hybrids from the three-way cross *H. giganteus*/wild *H. annuus* Accession 1357//2* Saturn. This germplasm is a potential source of male sterility, believed to be cytoplasmic. Male sterile plants were obtained in advanced backcross generations and remained sterile with further backcrossing, suggesting cytoplasmic male sterility. Pollen fertility was similar to that described for CMG-1. Crosses of four *H. giganteus*/wild *H. annuus*//4* Saturn lines with the three restorer sources Bb2a1, RHA 273, and RHA 280 gave F_1 plants with complete or partial restoration of pollen shed with Bb2a1 only, but not with either RHA 273 or RHA 280 (E. D. P. W., unpublished data). Parental lines in the composite were extremely variable for all plant and seed characteristics, and expressed marked hybrid vigor. The 1,000-seed weight and oil content for 328 *H. giganteus*/wild *H. annuus*//3* Saturn plants varied from 29 to 121 g, and 27.9 to 50.1%, respectively.

Germplasm CMG-3 (GP4) is an open-pollinated composite of eight lines from two interspecific F_1 hybrids from the three-way cross *H. maximiliani*/wild *H. annuus* Accession 1357//2* Saturn. Advanced backcross generations segregated for plants with highly modified and almost vestigial anthers that contained little or no pollen. Trisomic ($2n + 1$) plants with normal pollen shed also occurred (5). Parental lines in the composite were less variable and not as vigorous or branched as those in CMG-2. The 1,000-seed weight for 51 *H. giganteus*/wild *H. annuus*//3* Saturn and 162//4* Saturn plants ranged from 38 to 126 g, and 41 to 138 g, respectively. Oil contents of the same materials were 30.8 to 50.6%, and 25.7 to 47.9%, respectively.

Limited samples of the three germplasm composites can be obtained from Dr. Roland Loiselle, Plant Gene Resources of Canada, Agriculture Canada, Research Branch, Ottawa, Ontario, Canada K1A 0C6.

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REGISTRATION OF 16 LINES OF CLUB WHEAT GERMPLASM[1]

(Reg. No. GP 140 to GP 155)

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THE isolines of winter wheat (*Triticum aestivum* L. em. Thell.) listed in Table 1 were selected from the backcross population 'Omar'// 'Suwon 92'/6*Omar. This backcross series was started in 1959 with the primary objective of transferring the two semidwarf genes of Suwon 92 (CI 12666), both singly and in combination, to Omar (CI 13072). Suwon 92 has both the Sd_1 and Sd_2 genes for semidwarf stature (1, 4). The accepted symbols for these two genes have been redesignated as Rht_1 and Rht_2, respectively (5). A secondary objective was to transfer a gene for stripe rust (caused by *Puccinia striiformis* West.) resistance from Suwon 92 to these genetic stocks. Omar is a winter-type, mid-season to late, mid-tall, white-stemmed cultivar

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