REGISTRATION OF 15 INTERSPECIFIC SUNFLOWER GERMPLASM LINES DERIVED FROM WILD ANNUAL SPECIES

Fifteen interspecific sunflower (Helianthus spp.) germplasm lines derived from wild annual species crossed with cultivated sunflower (*H. annuus* L.), ANO-1509-1 (Reg. no. GP-135; PI 539894), ANO-1509-2 (Reg. no. GP-136; PI 539893), ARG-420 (Reg. no. GP-137; PI 539890), PAR-1084 (Reg. no. GP-138; PI 539901), PAR-1671-1 (Reg. no. GP-139; PI 539903), PAR-1671-2 (Reg. no. GP-140; PI 539902), PET-PET-1741-1 (Reg. no. GP-141; PI 539882), PET-PET-1741-2 (Reg. no. GP-142; PI 539881), BOL-774 (Reg. no. GP-143; PI 539892), DEB-SIL-367-1 (Reg. no. GP-144; PI 539909), DEB-SIL-367-2 (Reg. no. GP-145; PI 539908), DEB-CUC-1810 (Reg. no. GP-146; PI 539911), NEG-1255 (Reg. no. GP-147; PI 539904), PRA-HIR-437 (Reg. no. GP-148; PI 539983), and PRA-PRA-1142 (Reg. no. GP-149; PI 539910), were developed by the USDA-ARS, Fargo, ND, in cooperation with North Dakota Agricultural Experiment Station, Fargo, ND, and released in October 1989. These lines are potential sources of genes for insect, disease, and agronomic characteristics (drought and salt tolerance) and also provide genetic diversity for cultivated sunflower (1,2).

The potential value of interspecific germplasms derived from *H. anomalus* Blake, and *H. argophyllus* Raf. may be for water stress tolerance required for survival in habitats where the wild species naturally occur (1,3,4). Lines derived from *H. paradoxus* Heiser are potential sources of salt tolerance because *H. paradoxus* grows under very saline conditions (5).

Interspecific sunflower germplasm lines ANO-1509-1 and ANO-1509-2 originated from hand pollination of cmsHA 89, released by the USDA-ARS and the Texas Agricultural Experiment Station in 1971, with bulked pollen from 12 plants of wild diploid *H. anomalus* accession 1509 (Table 1). Nine F₁ plants were used for backcrossing. BC₁, F₁ plants were pollinated with RHA 265, a single-headed restorer line released by the USDA-ARS and the Texas Agricultural Experiment Station in 1971. ANO-1509-1 and ANO-1509-2 are F₂, bulks of 40 and 38 selfed plants, respectively. ANO-1509-2 has the same parentage and breeding history as ANO-1509-1, except that it was selected for its shorter plant height, and most plants were single-headed, with a few plants having axial branching (Table 2).

ARG-420 originated from bulked pollen from 10 plants of wild diploid *H. argophyllus* accession 420 (Table 1). Fourteen F₁ plants were used for backcrossing. ARG-420 is an F₁, bulk of 35 selfed plants.

PAR-1084 originated from bulked pollen from 10 plants of wild diploid *H. paradoxus* accession 1084 (Table 1). Eight F₁ plants were used in backcrossing. PAR-1084 is an F₁, bulk of 50 selfed plants.

PAR-1671-1 and PAR-1671-2 originated from bulked pollen from 15 plants of wild annual diploid *H. paradoxus* accession 1671 (Table 1). Fourteen F₁ plants were used in backcrossing. Germplasm lines PAR-1671-1 and PAR-1671-2 are F₂, bulks of 38 and 29 selfed plants, respectively.

PET-PET-1741-1 originated from bulked pollen from 25 plants of wild annual diploid of *H. petiolaris* ssp. petiolaris Nutt. accession 1741 (Table 1). Twenty F₁ plants were used in backcrossing. PET-PET-1741-1 is an F₂, bulk of 44 selfed plants. Plants in this germplasm were selected for their multiple-branching characteristic (Table 2). The germplasm had mostly fertile plants, with an occasional male sterile plant.

PET-PET-1741-2 originated from pollination of nuclear male sterile (nms) P21 VR1, a plant selection from ‘Pere-dovik’ carrying a recessive gene for nuclear male sterility released by the USDA-ARS and the Texas Agricultural Experiment Station in 1970, with bulked pollen from 20 plants of the wild diploid *H. petiolaris* ssp. petiolaris accession 1741 (Table 1). Seventeen F₁ plants were used in backcrossing. The germplasm line is an F₂, bulk of 48 selfed plants. Plants were mostly single-headed, with some with upper axially branching (Table 2).

BOL-774 originated from bulked pollen from eight plants of wild diploid *H. bolanderi* A. Gray accession 774 (Table 1). Nine F₁, plants were used in backcrossing. BOL-774 is an F₂, bulk of 34 sibbed plants. Taxonomically, *H. bolanderi* has been variously treated. Olivieri and Jain recognized two distinct species, *H. exilis* Gray and *H. bolanderi* (6). Helianthus bolanderi accessions 774 and 164 were considered as Olivieri and Jain’s *H. exilis*. Schilling and Heiser consider *H. exilis* synonymous with *H. bolanderi* (7). The line was segregating for male sterile and male fertile plants.

DEB-SIL-367-1 originated from bulked pollen from 20 plants of wild diploid *H. debilis* ssp. silvestris Heiser accession 367 (Table 1). Twelve F₁, plants were used in backcrossing. DEB-SIL-367-1 is an F₂, bulk of 39 selfed plants. Plants of the germplasm were selected for their multiple-branching characteristic (Table 2).

DEB-SIL-367-2 had the same parentage and breeding history as DEB-SIL-367-1, but was selected for the single-headed plant type (Table 2). DEB-SIL-367-2 is an F₂, bulk of 32 selfed plants. The germplasm generally had fertile plants, with an occasional male sterile or partially fertile plant.

DEB-CUC-1810 originated from bulked pollen from 22 plants of wild diploid *H. debilis* ssp. cumanferifolius (T. & G.) Heiser accession 1810 (Table 1). Seven F₁, plants were used in backcrossing. This germplasm line is an F₂, bulk of 28 sibbed plants. Plants were generally single-headed (Table 2).

NEG-1255 originated from bulked pollen from 16 plants of wild diploid *H. neglectus* Heiser accession 1255 (Table 1). Ten F₁ plants were used in backcrossing. NEG-1255 is an F₂, bulk of 28 sibbed plants. Plants were generally single-headed, with an occasional axillary branch (Table 2).

PRA-HIR-437 originated from bulked pollen from 22 plants of wild diploid *H. praecox* ssp. hirtus Heiser accession 437 (Table 1). Eight F₁ plants were used in backcrossing. PRA-HIR-437 is an F₂, bulk of 33 sibbed plants. Plants of the germplasm were mostly single-headed (Table 2). Plant stems remained green well past physiological maturity.

PRA-PRA-1142 originated from bulked pollen from 19 plants of wild diploid *H. praecox* ssp. praecox Engl. & Gray accession 1142 (Table 1). Eight F₁ plants were used in backcrossing. PRA-PRA-1142 is an F₂, bulk of 31 selfed plants. All germplasm lines based on cmsHA 89 have fertility restoration genes. The lines have not been tested for fertility restoration of other cytoplasms. Germplasm lines based on nms P21 were fully fertile because of the recessiveness of nms genes. It is not known whether the wild species (male parents) used in PRA-PRA-1142, NEG-1255, and DEB-CUC-1810 germplasm lines carry fertility restoration genes. We do know that PET-PET-1741-1 restores fertility to the cmsHA 89 cytoplasm. It is highly probable that *H. praecox* ssp. praecox, *H. neglectus*, and *H. debilis* ssp. cumanferifolius contain restoration genes for cmsHA 89 cytoplasm because of the generally high frequency of restorer genes in the wild species, especially the annual species.

These germplasms will allow sunflower breeders to incor-