Registration of C931, C941, CR11, and CZ25/2
Self-Fertile, Genetic-Male-Sterile Facilitated, Random-Mated, Sugarbeet Germplasm Populations

Sugarbeet (*Beta vulgaris* L.) germplasm populations C931 (Reg. no. GP-252, PI 636340), C941 (Reg. no. GP-253, PI 636341), CR11 (Reg. no. GP-255, PI 636343), and CZ25/2 (Reg. no. GP-254, PI 636342) were developed by the USDA-ARS in cooperation with the Beet Sugar Development Foundation (BSDF) and the California Beet Growers Association. They were released in 2005.

C931, C941, CR11, and CZ25/2 are multigerm (MM), self-fertile (*S'*), genetic male-sterile (*A_ _aa*) facilitated, random-mated populations. These populations were developed in the population improvement program at Salinas. Very succintly, these populations have the following relationships and attributes: C931 = base MM, *S', Aaa, Rz1*, curly-top resistant population similar to C37/C46; C941 = C931 × virus yellows resistant breeding lines; CR11 = C931 × Cercospora leaf spot (caused by *Cercospora beticola* Sacc.) resistant breeding lines; and CZ25/2 = C931 × high sucrose concentration breeding lines.

C931 has been under development for about 35 yr (Lewellen et al., 1978b). In its various developmental phases, it has been used commonly in the breeding and genetics research program at Salinas as a basic breeding population for population improvement and for selecting traits for productivity and disease resistance. C931 has the agronomic characteristics of a moderately broad, open-pollinated (OP, self-sterile) line with disease adaptation to the far western USA. In some breeding, selection, genetic, and germplasm improvement programs, there is a distinct advantage to be able to create easily selfed progeny families with large amounts of seed that can be recombined. C931 can be maintained by bulk increases or like an OP line by harvesting seed from the male-sterile segregates. The combination of self-compatibility (*S'*) and genetic male-sterility allows complete flexibility in the choice of generating progeny and testcross families. The pedigree and development of C931 are complex and have involved both mass or mother root selection and selfed-progeny evaluation and selection. The primary source of germplasm was from C918 (PI 578079) released in 1993. Thus much of the germplasm base comes from C37 (PI 590715) (Lewellen et al., 1985b) and C46 (PI 590757) (Lewellen et al., 1985a). A smaller percentage of the parentage is from C31/6 (PI 590799) (Lewellen et al., 1978a). type sources and wild beet, *Beta vulgaris* subsp. *maritima* L. An estimated 1 to 2% of the germplasm would have come from wild beet through C51 (PI 593694) (Lewellen, 2000b).

From C918, population C931 has the *Rz1* allele that conditions resistance to rhizomania caused by *Beet necrotic yellow vein virus*. C931 is moderately resistant to *Beet curly top virus*, virus yellows (caused by *Beet chlorosis virus* and *Beet yellows virus*), powdery mildew [caused by *Erysiphe polygoni* DC. (syn. *E. betae* Weltzien)], sugarbeet Erwinia (caused by *Erwinia* subsp. *carotovora* betavasculorum Thomson et al.), and bolting. From C918, two cycles of *S*, progeny, recurrent selection, genetic, and germplasm improvement programs, there is a distinct advantage to be able to create easily selfed progeny families with large amounts of seed that can be recombined. Multiple progeny tests were conducted. From C918, two cycles of S1 progeny evaluation and selection, stecklings were produced and released as C931. C931 has been tested as 8931, 9931, 1931, 2931, and 3931. C931 is an adapted population. It could be useful as a direct source of improved parental lines. More likely, it might be most useful, like it has been used in the Salinas program, as a basic breeding population for introgression of useful traits into other populations and breeding lines.

C941 was developed from crosses between Italian populations of C931 and breeding lines C76-2 (Lewellen, 1998) and C69 (PI 599341) (Lewellen, 1998). Selection and improvement program was similar for C931, but greater emphasis was placed on improved resistance to virus yellows based on inoculated progeny tests. Because C941 is about 50% C76–89–5 and C69, its curly top resistance is less than C931, its sucrose concentration and sugar yield combining ability is better. C941 has been developed and tested as C941, 2941, and 3941. Following two cycles of intrapopulation recombination through genetic-male-sterile segregation, population was produced and released as C941.

CR11 was developed from crosses between Italian populations of C931 and CR09 (PI 593695) and CR10 (PI 593693). CR09 and CR10 have moderate resistance to *Cercospora leaf spot* derived from two 1997 Italian accessions named R05 and R06 in the Salinas breeding program. About 12.5% germplasm from these Italian lines and CR10 are 25% modern Italian germplasm. CR11 was produced by the USDA-Rz1 and after 5 cycles of recombination, S1 progenies were generated and evaluated for bolting tendency and resistance to rhizomania and *Cercospora leaf spot*. Stecklings from the selected progenies were bulked and recombined. From the recombinants, seed from individual male-sterile plants was harvested to create half-sib progenies. These lines were evaluated for bolting tendency, sugar concentration, sucrose concentration and yield, and resistance to rhizomania and *Cercospora leaf spot*. About 12% of the families were selected and these lines were recombined to produce population CR311. Plants of CR311 were mass selected for resistance to rhizomania and resynthesized to produce population CR4931. CR11 has been evaluated as CR011, CR4011, and CR311. CR11 should have traits similar to C931 potentially improved for resistance to C. beticola. In tests at Fort Collins, CO, and Shakopee, MN, its reaction was one grade superior to the ‘Monohikari’ check. CR11 expressed better resistance than the level of the check.

CZ25/2 represents additional population improvement. Population CZ25 (PI 599343) released in 2005, CZ25/2 has about 37% of their germplasm from C931 and 25% from C941. The remaining germplasm is from CR09 and CR10.