Sugarbeet Germplasm Lines Selected from Crosses between Wild Beta vulgaris subsp. maritima from France, Belgium, and Denmark and Cultivated Sugar Beet

L. G. Campbell and K.K. Fugate

USDA-ARS, Red River Valley Agricultural Research Center,
1605 Albrecht Blvd. N., Fargo ND, 58102-2765.
Corresponding author: Larry Campbell
(Larry.Campbell@ars.usda.gov)
DOI: 10.5274/jsbr.5x.x.xx

ABSTRACT

The genetic basis of sugarbeet is very narrow. Moreover, it is recognized that introgression of genetic diversity into elite populations enhances long-term breeding progress. Beta vulgaris subsp. maritima, a wild relative of sugarbeet, is a source for increasing the genetic diversity within cultivated sugarbeet. Being closely related to sugarbeet, fertility problems among hybrid progeny are rare. B. v. subsp. maritima is distributed over a large geographic area and therefore exposed to a wide range of environmental conditions and disease organisms. This report describes eleven sugarbeet germplasm lines; F1044, F1045, F1046, F1047, F1048, F1049, F1050, F1051, F1052, F1053, and F1054; that were selected from crosses between a sugarbeet breeding line and eleven B. v. subsp. maritima accessions originating from France, Belgium, and Denmark. The sucrose concentration of the eleven germplasm lines ranged from 123 g kg-1 to 143 g kg-1 compared to 153 g kg-1 for an adapted hybrid. The 3-year average recoverable sucrose concentration of the lines was 85% of the recoverable sucrose concentration of the adapted hybrid. It is assumed that F1044 – F1054 will be used to introduce genetic diversity into elite breeding populations that have or are segregating for many of the traits desired for commercial production.

Additional Key Words: Beta vulgaris, Beta vulgaris subsp. maritima, crop wild relatives, exotic germplasm, introgression of wild relatives, pre-breeding.

The collection and preservation of exotic germplasm is based upon the premise that exotic germplasm includes useful genes that are not present in the commercial crop (Lewellen, 1992; Hjerdin et al., 1994; Capistrano-Gossmann et al., 2017). The immediate usefulness of exotic germplasm often is restricted to the transfer of a single gene, or very few genes, to introduce a beneficial trait, such as resistance to a disease or pest (Luterbacher et al., 2000; Panella and Lewellen, 2005; Asher et al., 2009), which is not present in elite breeding populations. Furthermore, exotic germplasm is a reservoir of genes for productivity and adaptation (Ober and Luterbacher, 2002); however, allowing for ample genetic recombination, followed by mild selection is essential to the procurement of productive segregates from crosses between exotic germplasm and adapted lines. Because of the time and uncertainties involved with the introduction of genetic diversity into germplasm that is useful to private breeders, the task is generally allocated to public breeders and researchers (Stander, 1993).

The genetic basis of sugarbeet (Beta vulgaris L.) often is assumed to be very narrow, tracing back to selections from a fodder beet population in response to an urgent 1811 decree by Napoleon that beet was to be the replacement for previously available sugar sources (Frese et al., 2001; Francis, 2006). The introduction of monogerm seed, cytoplasmic male sterility, resistance to some threatening diseases, and bolting resistance from single, or only a few, sources has created additional bottlenecks that diminish the genetic diversity within the commercial crop (Fénart, et al., 2008). In spite of its early history and the almost universal use of single sources for some traits essential for production, the crop itself remains the most important genetic resource for the development of improved varieties (Loel, et al., 2014; Panella, et al., 2014), suggesting the genetic basis of sugarbeet may not be as limited as its history suggests (McGrath et al., 1999; Frese, et al., 2001). Early sugarbeet varieties may have benefitted from spontaneous crosses with wild North Atlantic sea-beet (Beta vulgaris subsp. maritima), fodder beet, or chard (Lewellen, 1992; Viard et al., 2002). Hence, although it generally is recognized that the introgression of unique genetic sources into elite populations enhances long-term breeding progress, there is little urgency attached to these endeavors (Hjerdin, et al., 1994; Ober and Luterbacher, 2002).

Among the wild relatives of sugarbeet, B. v. subsp. maritima has long been recognized not only as a readily available source for the introduction of unique disease resistance genes, but also for its potential to increase productivity and adaptation by increasing the genetic diversity within cultivated sugarbeet (Panella and Lewellen, 2007; Biancardi et al., 2012). Being closely related to sugarbeet, crossing or fertility problems among hybrid progeny are rare.

B. v. subsp. maritima is distributed over a large geographic area and therefore exposed to a wide range of environmental conditions and disease organisms (Luterbacher et al., 2000; Frese et al. 2001; Richards et al., 2014). Four lines, y317, y318, y322, and y387, selected from a cross between an annual B.v. subsp. maritima from Greece, PI 546420, and a sugarbeet germplasm line, L53, were characterized by Doney (1995) as unique sources of genetic variability for combining ability and root yield. To ameliorate the relatively low sucrose concentration often associated with populations derived from crosses between sugarbeet and its wild relatives, y318, y322, and y387 were backcrossed to a high-sucrose sugarbeet germplasm line, L19, and after selection released as F1030, F1031, and F1032, respectively (Campbell 2015). Seven additional germplasm lines selected from crosses between wild Beta species and a sugarbeet breeding line from California also will expedite the introduction of genetic diversity into the commercial crop (Campbell, 2009). The average sucrose concentration of nine recently released germplasm lines (F1033 – F1041) selected from populations formed by crossing a USDA-ARS breeding line with B.v. subsp. maritima accessions collected in England, Wales, and the Channel Islands was 92% of the sucrose concentration of an adapted hybrid (Campbell and Fugate, 2017).

This report describes eleven sugarbeet germplasm lines; F1044 (PI 683544), F1045 (PI 686417), F1046 (PI 686418), F1047 (PI 683545), F1048(PI 686419), F1049 (PI 683546), F1050 (PI 683547), F1051 (PI 686420), F1052 (PI 686421), F1053 (PI 686422), and F1054 (PI 683548); that were selected from crosses between a sugarbeet breeding line developed by USDA-ARS in California, R376-43, and eleven B. v. subsp. maritima accessions originating from France, Belgium, and Denmark. The infusion of genes from these and other exotic sources into elite breeding populations may expand the limits of improvement through selection and produce parental lines with enhanced combining ability.

MATERIALS AND METHODS

Population Formation and Line Development

Eleven B. v. subsp. maritima accessions originally collected in August and September of 1989 (Seiler and Doney, 1991) along the coasts of France, Belgium, and Denmark (**Table 1 and Fig. 1**) were crossed with a common breeding line developed by USDA-ARS, Salinas, CA, R376-43. R376-43 is a self-incompatible inbred that can be traced to a broad-based population that included all available virus yellows (casual agents, Beet yellows virus; BYV and Beet western yellows virus; BWYV) resistance sources in the USA and Europe.

Figure 1. Collection locales of the 11 wild Beta vulgaris subsp. maritima populations from France. Belgium, and Denmark (Google Earth®) that were crossed with a cultivated breeding line (R376-43) and subsequently released as F1044, F1045, F1046, F1047, F1048, F1049, F1050, F1051, F1052, F1053, and F1054.

After selection, this population was released as C31 (Lewellen et al., 1978). Resistance to rhizomania (causal agent, Beet necrotic yellow vein virus; BNYVV) was introduced into C31 and the resulting population designated R76. R376-43 is a full-sib family selected for performance and disease resistance from R76. Genetic male-sterile segregates of R376-43 were pollinated with the 11 wild B. v. subsp. maritima accessions. Ten plants from each B.v. subsp. maritima accession were crossed with R376-43. Ten F1 plants from each cross (100 plants) were intercrossed to produce the F2 generation. Equal numbers of seeds from each F2 plant were grown and intercrossed to produce F3 seed. Selection for characteristic sugarbeet plant and root characteristics began in the F3 generation.

Table 1. Accession (PI) number, site information, and location of original collection for the eleven wild *Beta vulgaris* subsp. *maritima* populations from France, Belgium, and Denmark that were crossed with a cultivated sugarbeet breeding line from California (R376-43) and subsequently released as F1044, F1045, F1046, F1047, F1048, F1049, F1950, F1051, F1052, F1053, F1054.

Released germplasm	PI number of wild parent	Site	Locale	Country
F1044	540578	Sandy, above mud and reeds behind yards at port	La Maréchale	France
F1045	540619	Clay with cobbles	Guissény	France
F1046	540638	Silt, under Cyprus trees	L'Île Besnard	France
F1047	540647	Gravel, boat harbor and oyster bed	Portbail	France
F1048	540659	Sandy, estuary of Durdent River	Veulettes sur Mer	France
F1049	540582	Clay and sandy, around oyster beds	Tremblade les Brandes	France
F1050	540593	In gravel at base of sandstone cliff	Esnandes, Charente	France
F1051	540605	Sandy-silt, along top of rock sea wall	St. Brevin les Pins	France
F1052	540579	clay and silt, fodder beet field close by	Talmont St. Hilaire	France
F1053	540689	Clay and sand, along fence	Ostend, W. Flanders	Belgium
F1054	540678	Gravel	Måle Strand, Kerteminde	Denmark

The cross that became F1047 was subjected to six cycles of selection and the cross that became F1045 was subjected to seven selection cycles for morphological plant and root characteristics; the other segregating populations were subjected to eight or nine cycles prior to beginning selection for sucrose concentration. For each cycle, approximately 650 plants of each line were grown in a single block (160 m row-1). Plants that produced seed stalks or had extremely high crowns were rogued throughout the season. During the late summer, all remaining plants were dug and placed on the surface for visual examination. To the extent possible, roots with single crowns, minimal branching, and a dominant tap root were selected for increase. Each cycle, 40 to 60 selected roots of each line were planted in the greenhouse and after random pollination produced seed for the next cycle.

Subsequently, each of the eleven populations was subjected to between two and six additional selection cycles based upon the sucrose concentration of individual roots relative to other roots within a single cell of a 10-cell grid. Individual cells of the grid were 10 m long and two rows wide with a row-spacing of 56 cm. Plants on the ends of the rows were not sampled. Moderate-size roots were chosen for the individual sucrose measurements. Samples for analysis were obtained by collecting the tissue removed diagonally from the taproot with a 3.2 cm wood bit (~ 10 cm long) attached to an electric drill. Sampled roots remained viable and were used as mother roots to produce seed for additional selection cycles. Forty plants were selected from each population and each selection cycle. Selected roots from the final cycle provided seed for replicated field trials.

EXPERIMENTAL PROCEDURES AND ANALYSIS

The experimental design for the 2014, 2015, and 2017 field evaluations was a randomized complete block with four replicates. Individual experimental units were two-row by 10-m plots with rows 56 cm apart. Trials were planted near Fargo, ND during the first two weeks of May and harvested during the last two weeks of September. Roots were harvested by removing the leaves with a mechanical flail defoliator, followed by raising the roots in the soil with a two-row lifter, and finally removing the roots from the soil by hand. Root yield was the fresh weight of all roots from a single plot at harvest expressed as Mg ha-1. Sucrose concentration, and the sodium, potassium, and amino-nitrogen concentrations that were used to calculate recoverable sucrose per ton (Dutton and Huijbregts, 2006) were based upon the brei of a composite random sample of 10—12 roots from each plot. Three adapted check hybrids, ACH-817 (Crystal Beet Seed, Moorhead, MN), ACH-R761 (Crystal Beet Seed), and Triton (Seedex, Fargo, ND), were included for comparisons. Also included in the yield trials were a line selected for relative high sugar by USDA-ARS, Fargo, ND (Campbell,

1990), F1010 (PI 535818), and a line developed by USDA-ARS, Salinas, CA, C81-22 (PI 634216), that is closely related to R376-43.

The SAS GLM procedure (ver. 9.4, SAS Institute, Inc., Cary, NC) was used for the analysis of variance. Years were assumed to be random effects and genotypes fixed effects (McIntosh, 1983). Fisher's Protected LSD was used to determine when differences among means were significant ($P \leq 0.05$).

The brei from each field-plot sample or individual root was mixed and a portion quickly frozen for later analysis. Sucrose was determined polarimetrically (Autopol 880, Rudolph Research Analytical, Flanders, NJ) using aluminum sulfate-clarified brei samples (McGinnis, 1982). The aluminum sulfate-clarified filtrate used to determine sucrose concentration also was used to measure sodium, potassium, and amino-nitrogen, concentrations for determining the sugar-loss-to-molasses used to calculate recoverable sucrose concentration, an estimate of the sucrose that will be extracted during normal factory operations. Sodium and potassium concentrations were determined by flame-photometry (Corning 410C, Cole-Parmer Instrument Co., Chicago, IL). Amino-nitrogen concentration was determined with a spectrophotometer (Spectronic-21D, Milton Roy Co., Ivyland, PA) using the copper method and a wavelength of 610 nm (International Commission for Uniform Methods of Sugar Analysis, 2007).

F1044 – F1054 were included in specialized disease nurseries to obtain an initial assessment of disease development when exposed to Cercosproa beticola (Cercospora leaf spot), Fusarium spp. (Fusarium root rot), Aphanomyces cochlioides (Aphanomyces root rot), Beet necrotic yellow vein virus (BNYVV; rhizomania) and Beet curly top virus (curly top). The Cercospora leaf spot nurseries were in southern MN (Betaseed, Inc, Shakopee, MN) in 2015-2016. Aphanomyces root rot and Fusarium root rot were evaluated in nurseries near Shakopee, and Sabin, MN (Betaseed, Inc.), respectively in 2015 and 2016. The rhizomania and curly top evaluations were conducted by USDA-ARS, Kimberly, ID in 2015 and 2016. These nurseries were located and managed with the objective of providing a reliable indication of the response to a single disease organism with minimal interference from other diseases. Each nursery included entries from other breeding programs and representative resistant and susceptible cultivars selected by the nursery managers. Sugarbeet root aphid (Pemphigus sp.) damage was assessed by Betaseed, Inc. in a greenhouse assay in 2015. The root aphid trials were not randomized, so statistical analysis was not appropriate (Panella et al., 2008). However, comparisons between lines and with checks provide insight into the relative performance of lines when challenged by sugarbeet root aphid.

RESULTS

F1044, F1045, F1046, F1047, F1048, F1049, F1050, F1051, F1052, F1053, and F1054 are multigerm diploid biennial lines that produce roots with white skin and flesh (Fig. 2 and 3). All eleven lines have tapered roots with a relatively shallow grove, minimal branching, and non-protruding crowns. F1048, F1049, and F1054 can generally be considered as having broad-elliptical roots somewhat similar to ACH-817 and the remaining eight germplasm lines as having narrow-triangular roots. No bolters were observed and plants with multiple crowns were infrequent in the trials that were the basis of the data for Table 2. The hypocotyls of F1044, F1046, F1047, F1049, F1050, F1051, and F1054 are red. The hypocotyls of F1045, F1052, and F1053 are predominately red (> 95%) with the remainder being green. The ratio of red to green hypocotyls for F1048 is approximately 3 red to 1 green.

Table 2. Sucrose concentration, recoverable sucrose concentration, and root yield of F1044, F1045, F1046, F1047, F1048, F1049, F1050, F1051, F1052, F1053, F1054, C81-22, F1010, and three adapted check hybrids (Triton, ACH-817, and ACH-R716), Fargo, ND, 2014, 2015, and 2017.

Germplasm / *check*	Year						**Mean**	
	2014		2015		2017			
	Sucrose, g kg^{-1}							
F1044	122	c-f[†]	131	b-f	158	d	**137**	**D-F**
F1045	122	c-e	136	ab	164	cd	**141**	**B-D**
F1046	112	fg	122	f	162	cd	**132**	**F**
F1047	115	e-g	133	b-d	161	cd	**136**	**D-F**
F1048	111	g	108	g	150	e	**123**	**G**
F1049	114	e-g	129	b-f	165	cd	**136**	**D-F**
F1050	118	c-g	135	a-c	162	cd	**138**	**B-E**
F1051	127	a-d	127	c-f	174	ab	**143**	**BC**
F1052	116	e-g	126	d-f	163	cd	**135**	**EF**
F1053	117	d-g	122	f	160	cd	**133**	**EF**
F1054	133	ab	132	b-e	164	cd	**143**	**BC**
C81-22	122	c-f	127	c-f	164	cd	**138**	**C-F**
F1010	123	b-e	130	b-f	179	a	**144**	**B**
Triton	128	a-c	129	b-f	167	bc	**141**	**B-D**
ACH-817	134	a	144	a	180	a	**153**	**A**
ACH-R761	118	c-g	123	ef	166	c	**136**	**D-F**
Mean	**121**	**C**	**128**	**B**	**165**	**A**	**138**	

Table 2 Continued...

				Recoverable sucrose, g kg^{-1}				
F1044	94	c-f	97	b-d	132	de	**108**	**DE**
F1045	96	c-f	104	a-c	145	cd	**114**	**B-D**
F1046	85	f	85	d	140	cd	**103**	**E**
F1047	92	c-f	100	bc	140	cd	**111**	**B-D**
F1048	87	ef	69	d	124	e	**93**	**F**
F1049	92	c-f	99	bc	144	c	**112**	**B-D**
F1050	91	d-f	107	ab	141	cd	**113**	**B-D**
F1051	102	1-d	93	cd	157	ab	**117**	**B**
F1052	88	ef	96	b-d	143	cd	**109**	**C-E**
F1053	92	c-f	92	cd	139	cd	**108**	**DE**
F1054	111	a	96	b-d	138	cd	**115**	**BC**
C81-22	100	a-d	99	bc	146	bc	**115**	**BC**
F1010	98	b-e	94	b-d	160	a	**118**	**B**
Triton	104	a-c	101	bc	148	bc	**118**	**B**
ACH-817	110	ab	115	a	161	a	**129**	**A**
ACH-R761	93	c-f	95	b-d	148	bc	**112**	**B-D**
Mean	**96**	**B**	**97**	**B**	**144**	**A**	**112**	
				Root yield Mg ha^{-1}				
F1044	28.3	fg	38.9	ef	34.5	ef	**33.9**	**GH**
F1045	33.1	ef	44.3	de	37.2	de	**38.2**	**FG**
F1046	29.2	fg	35.9	fg	26.8	gh	**30.6**	**H**
F1047	37.0	c-e	48.2	cd	42.8	b-d	**42.7**	**C-E**
F1048	41.1	b-d	45.7	cd	28.6	f-h	**38.4**	**EF**
F1049	33.0	ef	44.4	de	32.9	e-g	**36.8**	**FG**
F1050	43.5	bc	45.6	cd	42.8	b-d	**43.9**	**CD**
F1051	30.8	ef	13.9	h	31.5	e-g	**25.4**	**I**
F1052	35.0	d-f	44.4	de	32.2	e-g	**37.2**	**FG**
F1053	23.6	g	33.8	fg	21.2	h	**26.2**	**I**
F1054	23.5	g	30.4	g	23.5	h	**25.8**	**I**
C81-22	35.4	d-f	47.6	cd	37.9	c-e	**40.3**	**D-F**
F1010	31.3	ef	44.2	de	38.8	b-e	**38.1**	**FG**
Triton	47.3	b	56.7	b	45.7	b	**49.9**	**B**
ACH-817	43.2	bc	51.1	bc	45.3	bc	**46.6**	**BC**
ACH-R761	58.6	a	66.2	a	55.8	a	**60.2**	**A**
Mean	**35.9**	**B**	**43.2**	**A**	**36.1**	**B**	**38.4**	

[†]Differences among genotypes within a year followed by the same lower case letter are not significant, based upon Fischer's protected $LSD_{0.05}$; Differences among main-effect means followed by the same upper case letter are not significant ($P \leq 0.05$).

Figure 2. Roots of F1044, F1045, F1046, F1047, F1048 and F1049, Fargo ND, 2017.

ROOT YIELD AND QUALITY

Among the 11 germplasm lines, F1051 and F1054 had the highest 3-year average sucrose concentration (Table 2). The 143 g kg-1 concentration of these two lines was 10 g kg-1 less than the 153 g kg-1 of ACH-817, the adapted hybrid with the highest sucrose concentration, and 2 – 7 g kg-1 more than the sucrose concentration of the other two adapted hybrids; Triton and ACH-R716. F1054 ranked between first and fourth in each of the three years and F1051 ranked first in 2017, second in 2014 and was near average in 2015. Two other lines, F1045 and F1050, had relative high average sucrose concentrations and average or above sucrose concentration in each of the three years. F1048 had the lowest average sucrose concentration, 20 g kg-1 less than F1051 and F1054, and also had the lowest sucrose concentration in each of the three years. F1046 and F1053 also had relatively low average sucrose concentrations.

Figure 3. Roots of F1050, F1051, F1052, F1053, F1054, and an adapted cultivar, ACH-817, Fargo, ND, 2017.

ACH-817 had the highest average recoverable sucrose concentration with 129 g kg-1. Triton and ACH-R761 had recoverable sucrose concentrations of 118 and 112 g kg-1, respectively. The 3-year average recoverable sucrose concentration for F1044 to F1054 was 109 g kg-1, ranging from 93 g kg-1 for F1048 to 117 g kg-1 for F1051. The germplasm lines with relatively high sucrose concentrations, F1045, F1050, F1051, and F1054, also had relatively high recoverable sucrose concentrations and the germplasm lines with relatively low sucrose concentrations, F1046, F1048, and F1053, had relatively low recoverable sucrose concentrations.

Root yields of F1044 – F1054 ranged from 13.9 Mg ha-1 for F1051 to 48.2 Mg ha-1 for F1047, both in 2015 (Table 2). The yearly average root yields of the eleven germplasm lines ranged from 65 to 67% of the average yield of the three adapted hybrids and from 84% of the two lines included for comparison (C81-22 and F1010) in 2015 and 2017 to 98% of the two lines in 2014. Three-year average root yields of the 11 germplasm lines ranged from 25.4 Mg ha-1 for F1051 to 43.9 Mg ha-1 for

F1050. F1050 was included among the lines with relatively high yield in all three years. The low average root yield of F1051 was the result of an extremely low yield in 2015 and below average yields in 2014 and 2017. F1047 was the germplasm line with the second highest average root yield, the line with the highest yield in 2015 and 2017, and the third highest yield in 2014. The three-year average root yield of F1044 – F1054 was 74% of the low-yielding adapted hybrid (ACH-817), 57% of the high-yielding adapted hybrid (ACH-R761) and 88% of the of the average of a line related to the female parent of the source populations (C81-22) and an unrelated line (F1010) developed by USDA-ARS, Fargo, ND.

Differences among years were significant for root yield, sucrose concentration, and recoverable sucrose concentration. Average root yields for 2014 and 2017 were almost equal (Table 2). However, the average sucrose concentration in 2014 was 44 g kg-1 less than the 165 g kg-1 observed in 2017. Significant variety X year interactions for all three variables indicated that the relative performance of the germplasm lines may be dependent upon environmental conditions. With only three year's data, determining the environmental conditions which might favor one line over another is not feasible.

DISEASE AND ROOT APHID RESISTANCE

In all comparisons, the Cercospora leaf spot (CLS) rating for the resistant check was significantly lower (more resistant) than the CLS ratings of all 11 germplasm lines (Table 3). With three exceptions, the final (last) ratings for F1047, F1050, and F1053 in 2015, the CLS ratings of the germplasm lines were significantly ($P \leq 0.05$) lower than the susceptible check. Five germplasm lines, F1044, F1045, F1046, F1048, and F1049, had final and average CLS ratings lower ($P \leq 0.05$) than the moderate check in both years. There is no indication that utilizing any of the 11 germplasm lines to introduce genetic diversity into an elite population would contribute root aphid resistance to the population **(Table 3)**.

Table 3. Last (final) and mean Cercospora leaf spot (CLS) ratings for F1044-F1054, a CLS susceptible check, a moderately susceptible check and a resistant check, 2015 and 2016, and root aphid ratings 2015.

	Cercospora leaf spot				Root aphid
	2015		2016		
Germplasm	Last	Mean(6)[†]	Last	Mean (5)	2015
	Disease rating, 1 - 9[‡]				Rating, 0 - 4
Lines					
F1044	5.0	2.8	5.8	4.0	3.9
F1045	5.0	3.1	5.0	3.6	3.8
F1046	6.7	4.0	6.0	4.1	3.5
F1047	7.8	4.5	7.3	5.2	3.6
F1048	6.7	3.5	5.7	4.0	3.5
F1049	3.8	2.7	4.8	3.9	3.5
F1050	8.0	4.5	6.2	4.3	3.7
F1051	6.2	3.8	6.7	4.6	3.7
F1052	7.3	4.0	5.7	3.9	3.8
F1053	7.5	4.0	6.7	4.3	3.5
F1054	7.2	3.7	6.7	4.1	3.8
Checks					
Resistant	1.7	1.3	1.0	1.2	1.1
Moderate Susc.	8.7	4.7	8.0	5.1	- - -
Susceptible	9.0	6.8	9.0	7.8	3.7
$LSD_{0.05}$	1.5	0.7	1.3	0.8	- - -

[†]Number in parenthesis indicates the number of observation dates included in the mean. The last reading is almost always the highest (most severe Cercospora leaf spot ratings) recorded for the season.

[‡]Higher ratings are indicative of increased severity.

With one exception, F1053, all 11 germplasm lines had lower Aphanomyces ratings (less severe symptoms) than the susceptible check in 2016 (Table 4). In 2015 all the germplasm lines had lower ratings than the susceptible check ($P \leq 0.05$). F1047 and F1053 were the only lines with ratings higher than the moderate check in 2016 ($P \leq 0.05$). F1049 and F1052 had relatively low Aphanomyces ratings in both 2015 and 2016.

All 11 germplasm lines had lower Fusarium root rot ratings than the moderately susceptible check and differences between the resistant check and the germplasm lines were not significant in 2015 (Table 4). In 2016, the difference between the resistant check and the moderately susceptible check was not significant. All 11 germplasm lines had lower Fusarium ratings than the moderately susceptible check; however, the difference between F1047 and F1048 and the moderately susceptible check was not significant. Two germplasm lines, F1049 and F1050, had lower Fusarium rating than the resistant check in 2016 ($P \leq 0.05$).

None of the 11 germplasm lines had curly top ratings that were equal to or lower than the ratings for the resistant check in 2015 or 2016 (Table 4). Only two germplasm lines, F1048 and F1052, had curly top ratings lower than the susceptible check in both years ($P \leq 0.05$). With the exception of the relative high indices for F1051 and F1052, differences between the rhizomania indices for the germplasm lines and the rhizomania susceptible (rzrz) check were not significant ($P \leq 0.05$) in 2015 (Table 4). In 2016, none of the germplasm lines had rhizomania indices lower than the Rz1Rz1 or the Rz1Rz1+Rz2Rz2 checks. However, differences between the rhizomania indices for four of the germplasm lines, F1045, F1046, F1047, and F1050, and the Rz2Rz2 check were not significant in 2016 ($P \leq 0.05$).

Table 4. Aphanomyces and Fusarium root rot, curly top, and rhizomania ratings for F1044 – F1054 and corresponding resistant, moderately susceptible and susceptible checks, 2015 and 2016.

	Aphanomyces		Fusarium		Curly top		Rhizomania	
Germplasm	2015	2016	2015	2016	2015	2016	2015	2016
			Disease rating, 0 - 9[†]				Disease index, 0 - 100	
Lines								
F1044	2.2	3.9	2.3	3.3	7.2	6.2	34	35
F1045	4.7	5.9	2.0	3.0	7.4	6.2	30	29
F1046	4.8	6.5	2.0	3.3	6.6	6.1	31	25
F1047	4.8	7.1	3.0	4.5	6.9	7.6	39	30
F1048	3.3	2.5	2.2	4.5	5.6	6.0	36	35
F1049	1.8	2.3	2.8	2.2	7.0	5.7	43	34
F1050	3.7	3.6	2.3	2.2	7.0	6.0	29	30
F1051	3.8	5.8	2.0	2.7	7.2	6.0	56	44
F1052	1.8	1.6	2.0	3.0	6.7	5.1	56	46
F1053	4.7	7.3	1.8	2.8	7.4	7.1	35	40
F1054	4.7	6.5	2.0	3.5	7.2	7.3	34	32
Checks								
Resistant	1.0	4.1	2.7	4.0	3.8	2.5	- - -	- - -
Moderate Susc.	4.2	5.8	5.0	5.3	- - -	- - -	- - -	- - -
Susceptible	6.3	8.5	7.8	8.7	7.7	6.6	- - -	- - -
Rz_1Rz_1 + Rz_2Rz_2[‡]	- - -	- - -	- - -	- - -	- - -	- - -	10	22
Rz_2Rz_2	- - -	- - -	- - -	- - -	- - -	- - -	15	24
Rz_1Rz_1	- - -	- - -	- - -	- - -	- - -	- - -	15	18
rzrz (susc.)	- - -	- - -	- - -	- - -	- - -	- - -	36	46
$LSD_{0.05}$	1.2	1.2	0.7	1.3	0.9	0.6	10	6

[†] Higher ratings or indices are indicative of increased severity; Aphanomyces ratings and rhizomania indices are based upon root symptoms, Fusarium and curly top ratings on foliar observations.

[‡]Resistance to rhizomania conferred by both Rz_1 and Rz_2, either Rz_1 or Rz_2, or neither Rz_1 or Rz_2 (rzrz = susceptible).

ACKNOWLEDGEMENTS

The technical support of Joe Thompson and Nyle Jonason is gratefully acknowledged. Pat O'Boyle, Margaret Rekoske, and Carl Strausbaugh, with assistance from their respective support staffs, managed the disease evaluation nurseries. The use of trade, firm, or corporate names is for the information and convenience of the reader. Such use does not constitute an endorsement or approval by the Agricultural Research Service of any product or service to the exclusion of others that may be suitable. USDA is an equal opportunity provider and employer.

LITERATURE CITED

Asher, M.J.C., M.K. Grimmert, and E.S. Mutasa-Goettgens. 2009. Selection and characterization of resistance to Polymyxa betae, vector of Beet necrotic yellow vein virus, derived from wild sea beet. Plant Pathology 58: 250-260.

Biancardi, E., L.W. Panella, and R.T. Lewellen. 2012. Beta maritima, the origin of beets. Springer, New York. 239 p.

Campbell, L.G. 1990. Registration of F1010 sugarbeet germplasm. Crop Sci. 30: 429-430.

Campbell, L.G. 2009. Registration of seven sugarbeet germplasms selected from crosses between cultivated sugarbeet and wild Beta species. J. Plant Reg. 4:149-154.

Campbell, L.G. 2015. F1030, F1031, and F1032 sugarbeet germplasm selected from crosses between L19 and three cultivated/wild germplasms. J. Plant Reg. 9: 382-387.

Campbell, L.G., and K.K. Fugate. 2017. Sugarbeet germplasm lines selected from crosses between cultivated sugarbeet and wild Beta vulgaris subsp. maritima from the United Kingdom. J. Sugar Beet Res. 54: 20-34.

Capisttrano-Gossmann, G.G., D. Ries, D. Holtgräwe, A. Minoche, T. Kraft, S.L.M. Frerichmann, T.R. Soerensen, J.C. Dohm, J. Gonzáles, et al. 2017. Crop wild relative populations of Beta vulgaris allow direct mapping of agronomically important genes. Nature Commun. 8:15708. doi: 10.1038/ncomms15708

Doney, D.L. 1995. Registration of four sugarbeet germplasms: y317, y318, y322, and y387. Crop Sci. 35: 947.

Dutton, J., and T. Huijbregts. 2006. Root quality and processing. p.

409-422. In: A.P. Draycott, editor, Sugar Beet. Blackwell, Oxford, UK.

Fénart, S., J-F Amaud, I. DeCauwer, and J. Cuguen. 2008. Nuclear and cytoplasmic genetic diversity in weed beet and sugar beet accessions compared to wild relatives: new insights into the genetic relationships within the Beta vulgaris complex species. Theor. Appl. Genet. 116: 1063-1077.

Francis. 2006. Development of sugar beet. p. 9-29. In: A.P. Draycott, editor, Sugar Beet. Blackwell, Oxford, UK.

Frese, L., B. Desprez, and D. Ziegler. 2001. Potential of genetic resources and breeding strategies for base-broadening in Beta. p. 295-309. In: H.D. Cooper, C. Spillane, and T. Hodgkin, editors, Broadening the genetic base of crop production, CABI Publishing, Oxon, UK.

Hjerdin, A., T. Säll, N.O. Nilsson, C.H. Bornman, and C. Halldén. 1994. Genetic variation among wild and cultivated beets of the section Beta as revealed by RFLP analysis. J. Sugar Beet Res. 31: 59-67.

International Commission on Uniform Methods of Sugar Analysis. 2007. Method GS6-5, Determination of α-amino nitrogen by the copper method ('Blue number'). Verlag Dr. Albert Bartens, KG, Berlin.

Lewellen, R.T. 1992. Use of plant introductions to improve populations and hybrids of sugarbeet. p. 117-136. In: H.L. Shands and L.E. Weisner, editors, Use of Plant Introductions in Cultivar Development, Part 2. CSSA Spec. Publ. 20, CSSA, Madison, WI.

Lewellen, R.T., J.S. McFarlane, and J.O. Skoyen. 1978. Registration of 11 germplasm lines of sugarbeet. Crop Sci. 18: 1100-1101.

Loel, J., C. Kenter, B. Märländer, and C. Hoffmann. 2014. Assessment of breeding progress in sugar beet by testing old and new varieties under greenhouse and field conditions. Europ. J. Agron. 52: 146-156.

Luterbacher, M.C., J.M. Smith, M.J.C. Asher, and L. Frese. 2000. Disease resistance in collections of Beta species. J. Sugar Beet Res. 37: 39-47.

McGinnis, R.A. 1982. Analysis of sucrose content. p. 67-76. In: R.A. McGinnis, editor, Beet Sugar Technology, 3rd ed. Beet Sugar Development Foundation, Denver, CO.

McGrath, J.M., C.A. Derrico, and Y.Yu. 1999. Genetic diversity in selected historical US sugarbeet germplasm and Beta vulgaris ssp. maritima. Theor. Appl. Genet. 98: 968-976.

McIntosh, M.S. 1983. Analysis of combined experiments. Agron. J. 75:153-155.

Ober, E.S., and M.C. Luterbacher. 2002. Genotypic variation for drought tolerance in Beta vulgaris. Annals of Botany 89: 917-924.

Panella, L., S.R. Kaffka, R.T. Lewellen, J.M. McGrath, M.S. Metzger, and C.A. Strausbaugh. 2014. Sugarbeet. p. 357-395. In: S. Smith, B. Diers, J. Specht, and B. Carver, editors, Yield Gains in Major U.S. Field Crops. CSSA Special Pub. 33. CSSA, Madison, WI.

Panella, L., and R.T. Lewellen. 2005. Plant introduction and genetic diversity. p. 34-38. In: E. Biancardi, L.G. Campbell, G.N. Skaracis, and M. De Biaggi, editors, Genetics and Breeding of Sugar Beet. Science Publishers, Enfield, NH.

Panella, L., and R.T. Lewellen. 2007. Broadening the genetic base of sugar beet: introgression from wild relatives. Euphytica 154: 383-400.

Panella, L., R.T. Lewellen, and L.E. Hanson. 2008. Breeding for multiple disease resistance in sugarbeet: Registration of FC220 and FC221. J. Plant. Reg. 2: 146-155.

Richards, C.M., P.A. Reeves, A.L. Fenwick, and L. Panella. 2014. Genetic structure and gene flow in Beta vulgaris subspecies along the Atlantic coast of France. Genetic Resources and Crop Evolution 61:651-662.

Seiler, G.J., and D.L. Doney. 1991. Collection of wild sugarbeet species (Beta spp.) from Europe. J. Sugar Beet Res. 28: 88.

Stander, J.R. 1993. Pre-breeding from the perspective of the private breeder. J. Sugar Beet Res. 30: 197-207.

Viard, F., J. Bernard, and B. Desplanque. 2002. Crop-weed interactions in the Beta vulgaris complex at a local scale. Theor. Appl. Genet. 104: 688-697.