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Evaluation of Wild *Solanum* Species for Resistance to the US-8 Genotype of *Phytophthora infestans* Utilizing a Fine-Screening Technique

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ABSTRACT

Greenhouse assays were carried out to characterize *Solanum* accessions previously reported to be late blight resistant and to identify individuals within the accessions with high levels of resistance to late blight. Foliage of wild *Solanum* species accessions or hybrid cultivated potato x wild species (diploid or tetraploid) from Mexico, Russia, or South America was inoculated with *Phytophthora infestans* (US-8) and was scored for severity of foliar symptoms at 7 and 14 days after inoculation (DAI). Mexican accessions (*S. brachycarpum*, *S. pinnatisectum*, *S. guerreroense*, and *S. fendleri*) were significantly more resistant (1.1% infection at 14 DAI) than either Russian (59.1% infection at 14 DAI) or South American (53.4% infection at 14 DAI) accessions. Moreover, the genotypes within the Mexican accessions tended to be more uniformly resistant whereas genotypes within the Russian and South American accessions tended to segregate for resistance. The more resistant genotypes of Russian and South American accessions (176/546) were retested, and 56 genotypes were identified as having potential for use in potato breeding programs for resistance to late blight. Fifty percent of the selected genotypes were from *S. microdontum* accessions PI498124, PI595510, and PI595511. The potential of these species for incorporation into breeding programs for late blight resistance is discussed.

RESUMEN

Un experimento fue conducido en invernadero para la seleción de genoti.pos entre accesiones de *Solanum* previamente identificados como resistentes al tizón tardÌo de la papa (*Phytophthora infestans*). El foliaje de accesiones de especies silvestres o hibridos entre cultivares de papa y especies silvestres (diploide y tetraploide) de MÈxico, Rusia y America del Sur fue inoculado con el genotipo US-8 de *P. infestans*. El porcentaje del foliage infectado fue evaluado a los 7 y 14 dias despues de la inoculación. Las accesiones de MÈxico (*S. brachycarpum*, *S. pinnatisectum*, *S. guerreroense* y *S. fendleri*) fueron significativamente mas resistentes al tizón tardÌo a los 14 dias depues de la inoculación (1,1%) que las accesiones de Rusia (59,1%) o de America der Sur (53,4%). Tambien, la resistencia al tizón tardÌo fue uniformemente distribuida al nivel de genotipo en las accesiones de MÈxico, pero segregación para resistancia ocurrio en accesiones de Rusia y de America del Sur. Selecciones hechas en las accesiones de Rusia y de America del Sur (176/546) fueron reevaluadas en 1998 y resultarón en 56 genotipos que pueden ser utilizados en un programa de mejoramiento para resistencia al tizón tardÌo de la papa. Un total de 50% de los genotipos seleccionados son *Solanum microdontum* accesiones PI 498124, PI 595510 y PI 595511. Tambien se discuten las posibilidades del uso y las estrategias de mejoramiento para la utilización de estas especies en un programa de resistencia al tizón tardÌo de la papa.

INTRODUCTION

In recent years, late blight (*Phytophthora infestans* Mont. de Bary) has re-emerged as the most important disease of potato

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(*Solanum tuberosum* subsp. *tuberosum* L.) in North America. This disease can rapidly devastate potato foliage in the field and tubers in storage. For several decades, late blight has been effectively controlled in North America through the use of systemic and residual fungicides. The aggressive US-8 genotype of *P. infestans*, the most commonly reported genotype in North America, is resistant to the widely used, systemic fungicide metalaxyl (Deahl *et al.* 1993; Hamm *et al.* 1994). Thus, a durable and economic means of controlling this disease would involve the foliar application of chemical protectants combined with the planting of resistant cultivars. Douches *et al.* (1997) observed that few (20 of 147 lines) North American and European cultivars and breeding lines were resistant to the US-8 genotype of *P. infestans*. Few, if any, of these resistant lines are agronomically competitive with cultivars currently in production in the United States. For long-term breeding progress, it will be necessary to identify and to utilize new and variable sources of late blight resistance for breeding potatoes. These sources may include unadapted cultivars from North America, Europe, and Mexico, somatic hybrids between wild and cultivated potatoes, and wild *Solanum* species.

The Inter-Regional Potato Introduction Station, NRSP-6, in Sturgeon Bay, WI, is the repository for the *Solanum* species germplasm and valuable enhanced germplasm sources. Numerous *Solanum* species have been previously reported to have some resistance to late blight (Bamberg *et al.* 1994a). However, initial disease evaluations were based on the mean resistance of a species accession and did not take into account genetic variation present among genotypes within the accession. In evaluations for resistance to Colorado potato beetle, Bamberg *et al.* (1996) noted that most accessions reported to be uniform contained small but significant variation for resistance components. Thus, it is necessary to conduct genotype or a fine-screening (Bamberg *et al.* 1996) to identify individuals from *Solanum* species accessions that will be the best candidates for enhancement and breeding.

A greenhouse screen provides a relatively quick means to assess late blight reactions on whole plants and thus, allows for many individuals to be evaluated (Douches *et al.* 1997). Accessions previously reported to be late blight resistant and genotypes within the accessions were characterized for their reaction to late blight under greenhouse conditions.

MATERIALS AND METHODS

Plant Materials

A fine-screening method, as described by Bamberg *et al.* (1996), was applied to examine late blight resistance in the *Solanum* species accessions. A total of 618 genotypes representing 24 accessions including four Mexican species, nine Russian hybrids (*Solanum* species x *S. tuberosum*), and four South American species were obtained from NRSP-6 as true-seed germplasm. From each accession 15-20 plants (genotypes) were grown. Stem cuttings were made and rooted, and rooted cuttings were transplanted to 32-hole seedling trays and grown under 16-h day-length with supplemental lighting from high-pressure sodium lamps in the greenhouse. These plants were tested for susceptibility to late blight 4-5 wk after transplanting in 1997. The most resistant genotypes were selected from each accession for further evaluation, with the exception of the four Mexican accessions, which were uniformly resistant. The selected genotypes were grown from greenhouse tubers and retested for resistance to late blight in 1997 and 1998.

Inoculum

Leaves infected with late blight (*P. infestans*) were collected from potato plants in Montcalm County, MI, in 1995. A pure culture was prepared by a series of transfers from infected tissue to rye agar (Deahl *et al.* 1993). The genotype was determined as US-8/A2 mating type by gel-acetate electrophoretic technique (Goodwin *et al.* 1995). The production of oospores, when grown with an isolate known to be A1 mating type, confirmed the isolate to be the A2 mating type. Cultures were grown on rye agar plates in the dark at 15 C. Sporangia wer harvested from Petri dishes by rinsing the mycelial/sporangial mat in cold (4 C) sterile, distilled water and scraping the mycelial/sporangial mat from the agar surface with a rubber policeman. The mycelial/sporangial suspension was strained through four layers of cheesecloth, and the concentration of sporangia was adjusted to about 1 x 10^6 sporangia ml^{-1}. The suspension was stored at 4 C for 4 h to stimulate zoospore release.

Plants were placed in an inoculation tent (approximately 3 m^3) in which the relative humidity was maintained above 90% by misting the atmosphere for 15 min every hour (6 l of deionized water per 24-h period) with gravity-fed humidifiers (Herrmidifier Series 500). Six mill clear plastic sheets were used to enclose the inoculation tent, and the air temperature within the tent was maintained between 18 and 25 C. Plants were inoculated in the evening, when temperatures were about 18 C, by spraying each tray of plants with 50 ml m^{-2} of inoculum using a hand-held sprayer.

Disease Evaluation

Disease severity was estimated as the percentage of stem and leaf area with symptoms of late blight at 7 and 14 days after inoculation (DAI). Severity values were rated up to 4 wk after inoculation on lines with a low percentage of infection. In the initial screen, each genotype was replicated three to five times. For retesting of selected genotypes, greenhouse tubers were planted in 32-hole seedling trays. Genotypes were replicated five times, and a plant of the cv Atlantic was included in each replication as the susceptible check.

Statistical Analysis

In the initial screening, data were analyzed by ANOVA to compare late blight resistance among the three different sources of plant materials (Mexico, Russia, and South America). Source means were compared at P = 0.05 using least-square means (LSmeans) due to variable numbers of replications for genotypes. In the retest of selected Russian and South American genotypes at 7 DAI (1998) genotypes were considered replications to compare accessions. These data were analyzed by ANOVA and accession means compared at P = 0.05 level of significance by the Tukey's multiple range comparison test.

RESULTS

Mexican accessions were more resistant to late blight than the Russian and South American accessions (Table 1). Mean disease severity values were highly variable between and within Russian and South American accessions ranging from 27.2% to 90.5% and 8.3% to 97% for Russian and South American accessions, respectively. Within accessions of both sources, mean foliar disease severity values ranged from 0% to 99%. Two Russian accessions (PI 595517 and PI 595518) were slightly more resistant (27%) than others, and in seven out of nine accessions, genotypes with foliar infection less than 5% were identified. Among South American accessions, five had mean severity rating less than 11%, and some genotypes within the accessions had foliar infection less than 5%. Russian accessions did not differ

TABLE 1—*Severity of foliar symptoms of late blight in* Solanum *species and/or hybrids from different sources in 1997.*

Accession number	Pedigree	Genotypes tested (#)	Disease Severity 7DAI[a]	Disease Severity 14 DAI
Mexican Species				
PI 225661	*S. brachycarpum* Correll	18	0	1
PI 161727	*S. pinnatisectum* Dunal	18	0	0
PI 275236	*S. guerreroense* Correll	18	0	2
PI 275180	*S. fendleri* Gray	18	0	1
Russian Hybrids				
PI 595516	((*S. megistacrolobum* Bitter x Gatchinski) x Umbra) x Fausta	21	30.4	90.5
PI 595517	(S. *verrucosum* Schldl. x MPI 50.140/5) x MPI 50.140/5	21	5.8	27.2
PI 595518	(S. *microdontum* Bitter x Atzimba) x Earlaine	21	9.6	27.5
PI 595519	(S. *polytrichon* Rydb. x Anoka) x Runo	21	21.1	44.9
PI 595520	((S. *microdontum* Bitter x MPI 50.140/5) x Boone) x Desiree	21	14.6	52.0
PI 595521	*S. berthaultii* Hawkes x *S. andigena* Hawkes	21	29.8	87.8
PI 595522	*S. vernei* Bitter & Wittm. x MPI 50.140/5	20	35.4	82.9
PI 595523	(*S. gourlayi* Hawkes x Hannibal) x Hannibal	20	13.0	66.6
PI 595524	*S. berthaultii* Hawkes x Taiga	21	21.0	54.2
South American Species				
PI 498104	*S. berthaultii* Hawkes	4	20.3	29.2
PI 595509	*S. microdontum* Bitter	7	31.3	31.3
PI 595510	*S. microdontum* Bitter	11	6.9	14.7
PI 595511	*S. microdontum* Bitter	16	4.5	10.5
PI 458358	*S. microdontum* Bitter	4	23.1	23.1
PI 473170	*S. microdontum* Bitter	13	34.5	34.5
PI 498124	*S. microdontum* Bitter	19	7.0	9.3
PI 458367	*S. okadae* Hawkes & Hjert.	7	27.6	44.6
PI 498404	*S. okadae* Hawkes & Hjert.	5	53.3	97.0
PI 595512	*S. sucrense* Hawkes	10	6.6	24.8

[a]DAI = days after inoculation. Each accession replicated 3-5 times.

TABLE 2. *Comparison among Solanum sources for resistance to late blight.*

Resistance Sources	Accessions tested (#)	Genotypes tested (#)	Mean disease severity (%)*	Least square means	Source comparison	Significance of comparison
Mexico	4	72	1.1	2.4	Mexico:Russia	0.001
Russia	9	187	59.1	51.8	Russia:South America	0.849
South America	4	334	53.4	49.7	South America:Mexico	0.001

*Evaluated 14 days after inoculation.

significantly in resistance to late blight from South American accessions, but they were significantly less resistant (P = 0.05) than the Mexican accessions (Table 2).

Genotypes with high and intermediate levels of resistance to late blight were selected from most accessions for retesting in 1998. No selections were made in the Mexican accessions because most genotypes had high levels of resistance to late blight. A total of 58% and 29% of the genotypes from the Russian and South American accessions, respectively, were selected for retesting. Using genotypes as replications for accessions, accessions, years, and the interaction accession x year for disease severity was significant (P < 0.01) (Table 3). In the retest, only four accessions were significantly more resistant than those that were identified as resistant in the initial test. Among the four Russian hybrids that had low mean late blight infection in the initial test, PI 595509 and PI 595517 grouped with the most susceptible accessions in the retest. The four most resistant accessions were South American species of which three accessions were of *S. microdontum* and one of *S. sucrense* species (Table 3).

Because of the high range of variability for late blight reaction found within all accessions (Table 3), genotypes with good levels of resistance could be identified within both the Russian hybrids and South American species (Table 4). Considering the

TABLE 3—*Severity of foliar symptoms of late blight in* Solanum *species and/or hybrids from different sources in 1998.*

Accession number	Pedigree	Genotypes tested (#)	Disease Severity 7 DAI[a]	Disease Severity 14 DAI
Russian Hybrids				
PI 595516	((*S. megistacrolobum* Bitter x Gatchinski) x Umbra) x Fausta	4	17.5	—[b]
PI 595517	(S. *verrucosum* Schldl. x MPI 50.140/5) x MPI 50.140/5	11	21.3	—
PI 595518	(S. *microdontum* Bitter x Atzimba) x Earlaine	7	21.5	—
PI 595519	(S. *polytrichon* Rydb. x Anoka) x Runo	6	9.8	—
PI 595520	((S. *microdontum* Bitter x MPI 50.140/5) x Boone) x Desiree	5	29.0	—
PI 595521	*S. berthaultii* Hawkes x *S. andigena* Hawkes	5	28.1	—
PI 595522	*S. vernei* Bitter & Wittm. x MPI 50.140/5	5	20.3	—
PI 595523	(*S. gourlayi* Hawkes x Hannibal) x Hannibal	6	12.5	—
PI 595524	*S. berthaultii* Hawkes x Taiga	6	38.9	—
South American Species				
PI 595507	*S. berthaultii* Hawkes	25	16.7	29.9
PI 498104	*S. berthaultii* Hawkes	4	20.3	29.2
PI 595509	*S. microdontum* Bitter	7	31.3	31.3
PI 595510	*S. microdontum* Bitter	11	7.1	14.7
PI 595511	*S. microdontum* Bitter	16	3.5	10.5
PI 458358	*S. microdontum* Bitter	4	23.1	23.1
PI 473170	*S. microdontum* Bitter	13	34.5	34.5
PI 498124	*S. microdontum* Bitter	19	7.0	9.3
PI 458367	*S. okadae* Hawkes & Hjert.	7	27.6	44.6
PI 498404	*S. okadae* Hawkes & Hjert.	5	42.7	97.0
PI 595512	*S. sucrense* Hawkes	10	6.6	24.8

[a] DAI = days after inoculation. Each accession replicated 3-5 times.
[b] Plants died before evaluation date.

TABLE 4—*Severity of foliar symptoms of late blight of selected genotypes in each* Solanum *accession.*

	Disease Severity				
Genotype	1997		1998		
ID number	7 DAI[a]	14 DAI	7 DAI	14 DAI	Pedigree
PI 595516-10	20.0	94.4	5.0	C[b]	((*S. megistacrolobum* Bitter x Gatchinski) x Umbra) x Fausta
PI 595516-18	15.0	76.0	2.3	C	((*S. megistacrolobum* Bitter x Gatchinski) x Umbra) x Fausta
PI 595517-1	4.0	12.5	1.3	C	(S. *verrucosum* Schldl. x MPI 50.140/5) x MPI 50.140/5
PI 595517-17	4.5	6.3	16.0	C	(S. *verrucosum* Schldl. x MPI 50.140/5) x MPI 50.140/5
PI 595518-1	20.0	65.0	10.8	C	(S. *microdontum* Bitter x Atzimba) x Earlaine
PI 595518-9	2.0	5.2	7.5	C	(S. *microdontum* Bitter x Atzimba) x Earlaine
PI 595519-2	1.3	1.3	3.3	C	(S. *polytrichon* Rydb. x Anoka) x Runo
PI 595519-6	1.0	2.0	8.3	C	(S. *polytrichon* Rydb. x Anoka) x Runo
PI 595520-9	1.0	6.3	1.3	C	((S. *microdontum* Bitter x MPI 50.140/5) x Boone) x Desiree
PI 595521-5	33.8	92.0	24.0	C	*S. berthaultii* Hawkes x *S. andigena* Hawkes
PI 595521-12	2.4	64.0	7.5	C	*S. berthaultii* Hawkes x *S. andigena* Hawkes
PI 595522-2	18.6	57.0	20.0	C	*S. vernei* Bitter & Wittm. x MPI 50.140/5
PI 595522-19	0.8	3.6	1.0	C	*S. vernei* Bitter & Wittm. x MPI 50.140/5
PI 595523-8	2.0	30.3	5.4	C	(*S. gourlayi* Hawkes x Hannibal) x Hannibal
PI 595523-20	0.5	20.0	4.6	C	(*S. gourlayi* Hawkes x Hannibal) x Hannibal
PI 595523-21	8.3	52.5	5.0	C	(*S. gourlayi* Hawkes x Hannibal) x Hannibal
PI 595524-20	7.3	30.0	8.0	C	*S. berthaultii* Hawkes x Taiga
South American Species					
PI 498104-3	5.5	30.0	3.5	20.0	*S. berthaultii* Hawkes
PI 498104-15	11.5	87.5	11.2	40.8	*S. berthaultii* Hawkes
PI 498104-19	4.0	7.5	14.5	17.5	*S. berthaultii* Hawkes
PI 595507-3	C[b]	C	0.3	3.7	*S. berthaultii* Hawkes
PI 595507-8	C	C	2.8	2.8	*S. berthaultii* Hawkes
PI 595507-12	C	C	4.0	4.4	*S. berthaultii* Hawkes
PI 595507-13	C	C	3.6	6.4	*S. berthaultii* Hawkes
PI 595507-16	C	C	3.6	3.6	*S. berthaultii* Hawkes
PI 595507-20	C	C	1.0	C	*S. berthaultii* Hawkes
PI 458358-8	5.0	51.0	2.0	6.7	*S. microdontum* Bitter
PI 473170-17	4.0	95.0	8.0	8.0	*S. microdontum* Bitter
PI 473170-33	33.7	52.5	6.0	6.0	*S. microdontum* Bitter
PI 498124-1	1.0	2.8	2.2	2.6	*S. microdontum* Bitter
PI 498124-5	1.8	7.0	2.4	3.8	*S. microdontum* Bitter
PI 498124-6	0.2	7.0	3.4	4.4	*S. microdontum* Bitter
PI 498124-7	1.2	4.6	0.6	4.6	*S. microdontum* Bitter
PI 498124-12	0.0	1.0	2.0	0.2	*S. microdontum* Bitter
PI 498124-17	0.6	2.0	2.4	3.6	*S. microdontum* Bitter
PI 498124-20	0.2	1.8	1.2	2.4	*S. microdontum* Bitter
PI 498124-21	0.8	2.8	0.8	0.8	*S. microdontum* Bitter
PI 498124-25	0.0	1.3	1.3	3.4	*S. microdontum* Bitter
PI 595509-12	1.0	1.0	9.0	9.0	*S. microdontum* Bitter
PI 595510-10	2.0	2.0	0.8	C	*S. microdontum* Bitter
PI 595510-14	0.7	1.7	4.4	22.0	*S. microdontum* Bitter
PI 595510-16	0.7	0.0	6.5	5.6	*S. microdontum* Bitter
PI 595510-19	1.0	1.0	2.6	2.6	*S. microdontum* Bitter
PI 595510-22	0.3	0.7	4.0	6.0	*S. microdontum* Bitter
PI 595511-2	2.5	2.5	0.2	1.2	*S. microdontum* Bitter
PI 595511-3	1.0	1.0	0.6	0.6	*S. microdontum* Bitter
PI 595511-5	2.0	2.0	0.2	0.7	*S. microdontum* Bitter
PI 595511-13	0.5	0.5	3.8	3.8	*S. microdontum* Bitter
PI 595511-14	0.5	0.5	0.0	0.2	*S. microdontum* Bitter
PI 595511-18	1.0	1.0	2.2	2.2	*S. microdontum* Bitter
PI 595511-22	1.7	1.7	0.2	1.2	*S. microdontum* Bitter
PI 595511-23	2.0	2.0	0.0	0.8	*S. microdontum* Bitter
PI 595511-25	0.3	0.3	0.6	0.6	*S. microdontum* Bitter
PI 595512-16	1.0	5.0	6.6	7.6	*S. sucrense* Hawkes
PI 595512-17	1.0	2.0	2.8	2.8	*S. sucrense* Hawkes
PI 595512-19	10.0	10.0	0.8	8.2	*S. sucrense* Hawkes

[a] DAI = days after inoculation

[b] Genotype evaluated only in 1998 or many plants died before evaluation in 1998.

accession and year interaction (Table 4), the two most resistant genotypes from each accession in both years were selected to identify a broad genetic base with late blight resistance. A greater number of selections were made in accessions with a high level of disease resistance (Table 3). Selections were also made in the accession PI 595507 of *S. berthaultii* (evaluated only in 1998) because the mean foliar infection was similar to the other *S. berthaultii* accession (PI 498104) (Table 3). No selections were made in the two accessions of *S. okadae* because of high disease severity values. A total of 56 genotypes, representing nine Russian hybrids and three South American species, was selected based on low disease severity values in both years (Table 4). Among the Russian hybrids, a total of 17 genotypes (9%) were selected as late-blight-resistant germplasm. A total of 39 genotypes (11%) were selected among South American species of which 28, 9, and 3 were *S. microdontum*, *S. berthaultii*, and *S. sucrense* species, respectively. *S. microdontum* (PI 498124, PI 595510. and PI 595511) also had the strongest late blight resistance based on either genotype reaction (Table 4) or accession mean (Table 3).

DISCUSSION

A central component for management of late blight of potatoes is resistant cultivars. Initial efforts to develop late-blight-resistant cultivars emphasized specific resistance conferred by major resistance genes (R genes) (Ross 1986). Although this type of resistance was very effective, it was not durable. Thus current breeding efforts target general resistance (non-R gene). One of the difficulties in breeding for general (non-specific) resistance is that it is difficult to maintain the level of resistance during crossing and backcrossing (Black 1970). In such cases, the mean resistance of the progenies is usually less than the parental mean. For this reason, it is necessary to use a broad genetic base for late blight resistance to cross with adapted germplasm. The offspring of these crosses can be combined to pyramid multiple resistance genes in a single cultivar. This strategy is currently being used in our breeding program to combine late blight resistance with tuber quality and early maturity at the tetraploid level (Douches, unpublished data).

Wild *Solanum* species have been a useful source of variation for many traits including resistance to various diseases. Accessions from several species, of both Mexican and South American origin, have been noted as possessing resistance to late blight (Huaman 1987; Colon and Budding 1988; Bamberg *et al.* 1994a). Bamberg *et al.* (1994a), however, noted that resistance might be segregating within accessions of each wild species. The results of our study indicate that, indeed, resistance to late blight is variable both between and within accessions. This was evident in Russian accessions where a wide range in disease severity was noted between and within accessions. Also, the Russian accessions did not have the same level of late blight resistance as South American species; these hybrids, however, may be a source of other important agronomic characteristics since they were already crossed with *S. tuberosum*. Based on these results, a genotype or a fine-screen is necessary to identify parental lines with the best resistance to late blight to include in a breeding program.

A number of U.S. and European potato cultivars and breeding lines have some resistance to late blight (Douches *et al.* 1997). In this study, several wild *Solanum* species and species hybrids were identified that were more resistant than the susceptible check varieties. This resistance was identified in 2x, 4x, and 6x germplasm. In addition, Colon *et al.* (1995) evaluated eight South American *Solanum* species and found genetic diversity between species for both type and relative importance of the components conferring partial resistance to late blight. Therefore, it might be possible to combine different components of late blight resistance from wild species with other sources found in cultivated potato. In many cases, this may be done by simple crosses resulting in populations with high levels of general resistance to late blight. *Solanum* species accessions *S. fendleri*, *S. guerroense*, *S. pinnatisectum*, and *S. brachycarpum* from Mexico had the highest levels of resistance to late blight, but are difficult to cross with cultivated *S. tuberosum* due to a combination of ploidy level and endosperm balance number (EBN) incompatibility. Consequently, more elaborate introgression techniques will be necessary for utilizing late blight resistance in the Mexican germplasm. Several methods have been used for inter-EBN hybrid production including embryo rescue and double pollination (Singsit and Hanneman 1991) somatic fusion (Helgeson *et al.* 1998) and bridging crosses (Bamberg *et al.* 1994b; Hanneman 1999). Although highly successful in some cases, these techniques are difficult and/or time consuming, and the resulting hybrids require multiple backcrosses to cultivated potato to approach commercial tuber quality. The South American and Russian accessions were, on average, not as resistant as the Mexican species, but there were individual genotypes in these accessions that were moderately to highly resistant. Also, no significant differences were found between Russian and South American accessions. This can be explained, in part, by the fact that the Russian hybrids are breeding accessions that used mostly South American sources of late blight resistance. Although the Russian hybrids were not consistently and highly resistant, they had been crossed to *S. tuberosum* and might be expected to produce tubers with better quality than wild species. In addition, the South American species with high levels of resistance are much more closely related to *S. tuberosum* and hence it would be easier to introgress into commercial potato cultivars than would be the Mexican species. In the short term, the Russian and South American materials may be more useful for developing late-blight-resistant cultivars than the Mexican species. Also, among South American species, two selections from *S. microdontum* (PI 473170) with intermediate late blight resistance set a high number of tubers with good appearance per plant in the greenhouse, indicating that genotypes can have other important characteristics besides late blight resistance that can be explored in the breeding program. These findings make the South American accessions *S. microdontum*, *S. sucrense*, and *S. berthaultii* good wild species candidates from which to develop mapping populations to identify quantitative trait locus (QTL) for late blight resistance.

We currently have a set of genotypes with resistance to the US-8 genotype of *P. infestans* that constitute a broad genetic base of *Solanum* germplasm (Table 4). This germplasm has been used to incorporate late blight resistance into breeding lines. Using a broad genetic base we have the potential to combine alternative sources of late blight resistance and thereby develop more durable host plant resistance. However, we have only tested this germplasm against one isolate of the predominant genotype of *P. infestans* in the United States (US-8). We plan to evaluate this germplasm against other genotypes of *P. infestans* as well as for resistance to tuber blight. In addition, some of this resistant germplasm has been crossed to susceptible *Solanum tuberosum* at the 2x level to establish mapping populations from which we can identify QTLs for late blight resistance. These QTLs will be useful in a marker-assisted selection program to introgress genes conferring resistance to late blight from different wild species to cultivated potato.

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