A Multistate Comparison of Native Octoploid Strawberries from North and South America

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ABSTRACT. An elite group of 38 strawberry accessions representing all subspecies of the beach strawberry [*Fragaria chiloensis* (L.) Miller] and the scarlet strawberry (*F. virginiana* Miller) was planted in a replicated design at five locations across the United States, and evaluated for plant vigor, flowering date, runner density, fruit set, fruit appearance, and foliar disease resistance. Considerable genotype × location interaction was observed for many of these traits. However, a few genotypes were impressive at all locations including PI 551735 (FRA 368) with its unusually large, early fruit, and PIs 612486 (NC 95-19-1), 612493 (Frederick 9), and 612499 (RH 30), which were very vigorous and had unusually good fruit color. Genotypes that were superior at individual locations included PIs 551527 (FRA 110) and 551728 (Pigeon Pt.) in Maryland for their large fruit, and PI 612490 (Scotts Creek) in Oregon which had extremely large fruit, superior color, firmness, and flavor. The PIs 612495 (LH 50-4), 612498 (RH 23), and 612499 (RH 30) performed well as day neutrals at multiple sites.

Most genes in modern North American strawberry cultivars (*Fragaria ×ananassa* Duchesne in Lamarck) come from seven nuclear and 10 cytoplasmic sources, although at least eight native clones have been incorporated into commercial cultivars in the last half century (Hancock and Luby, 1995; Sjulín and Dale, 1987). Because the germplasm base of strawberries remains narrow, additional wild clones should be identified and used in strawberry improvement. To broaden the available wild gene pool, over 20 strawberry germplasm collection trips have been undertaken over the last 2 decades in North and South America (Cameron et al., 1993; Dale et al., 1992; Hancock et al., 1990; Luby et al., 1991). While much of the elite material from these collections has remained in regional breeding programs, the bulk has been deposited in the U.S. Department of Agriculture (USDA), Agricultural Research Service, National Clonal Germplasm Repository (NCGR) at Corvallis, Ore. This collection contains

over 400 cultivars and selections of *F. ×ananassa*, and over 1,000 other strawberry accessions from 29 countries of the world (Hummer, 1996).

To store germplasm for future use, two potentially conflicting goals must be balanced. A large enough collection must be maintained to adequately represent the genes available in the native species, but sample sizes must be kept small enough to be cost-effective. For breeders who want to screen wild germplasm, identification of a core subset is desirable to minimize production and distribution costs and increase evaluation efficiency (Brown, 1988, 1989). Ideally, the core should represent the genetic diversity of a crop species and its wild relatives, with the minimum amount of repetitiveness.

The National Plant Germplasm System (NPGS) recently mandated curators to establish core subsets (Eberhardt, 1994). In forming core subsets, the NPGS recommended 1) assembling and reviewing passport data and other information to be used in establishing nonoverlapping groups, 2) assigning accessions to appropriate groups (and acquiring additional collections from underrepresented or missing groups), 3) choosing accessions for the preliminary core subset from each group, 4) collecting data on

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Table 1. Sample locations of supercore genotypes. The genotypes are denoted by the plant introduction (PI) number of the U.S. National Plant Germplasm System (<http://ars-grin.gov>) and the original collection names.

Taxa	PI number	Gender	Other name	Location	Latitude	Longitude
<i>F. chiloensis</i> ssp. <i>pacifica</i>	551445	S ²	RCP 37	California	41°22'N	122°58'W
	551453	P	Westport Light House-8	Washington	46°53'N	124°10'W
	551459	S	BSP-14	Oregon	43°07'N	124°30'W
	551728	H	Pigeon Point; CA 1367	California	37°01'N	122°12'W
	551735	P	Auke Lake; CA1499	Alaska	58°20'N	134°15'W
	612487	P	CFRA 688	British Columbia	50°50'N	127°50'W
	612488	H	CFRA 1267	British Columbia	48°50'N	123°50'W
	612489	P	HMI	Oregon	43°55'N	124°06'W
	612490	P	Scotts Creek; Franklin Point	California	37°01'N	122°12'W
	236579	H	Darrow 72	Chile	32°50'S	72°10'W
<i>F. chiloensis</i> f. <i>chiloensis</i> ssp. <i>chiloensis</i>	551736	H	CA 1541	Peru	14°10'S	72°50'W
	612316	H	2 BRA 1A	Chile	41°50'S	73°55'W
	612318	H	NAH3	Ecuador	1°28'S	78°63'W
	552091	H	Termas de Chillan, TDC	Chile	36°40'S	72°10'W
<i>F. chiloensis</i> f. <i>patagonica</i> ssp. <i>chiloensis</i>	602567	H	2 MAR 1A	Chile	43°47'S	72°27'W
	602568	P	2 PAL 2C	Chile	43°30'S	71°55'W
	602570	H	2 CAR 3B	Chile	46°42'S	72°41'W
	612317	P	2 TAP 4B	Chile	44°38'S	71°42'W
	612491	P	CA 1226	Utah	44°10'N	103°40'W
<i>F. virginiana</i> ssp. <i>glauca</i>	612494	P	LH 5-1; BH 2	South Dakota	33°10'N	103°39'W
	612495	H	LH 50-4	Montana	46°40'N	110°40'W
	612496	P H	N8688; RH 43	Alaska	64°02'N	145°44'W
	612500	P H	RH 45	Alberta	52°13'N	117°10'W
	612501	H	LH 30-4	Montana	46°44'N	114°11'W
	551471	P H	IH 59	California	39°06'N	120°57'W
<i>F. virginiana</i> ssp. <i>platypetala</i>	551527	P H	Cascade	Oregon	44°21'N	121°32'W
	612320	H	JP 95-9-6	Georgia	32°40'N	83°70'W
	612323	P	NC 96-35-2	Alabama	32°43'N	87°59'W
<i>F. virginiana</i> ssp. <i>virginiana</i> (southern)	612324	P	NC 96-48-1	South Carolina	34°40'N	81°14'W
	612325	PH	NC 96-5-3	North Carolina	34°56'N	77°14'W
	612486	P	NC 95-19-1	Mississippi	34°00'N	88°34'W
	612569	P	NC 95-21-1	Mississippi	33°51'N	88°32'W
	612570	PS	JP 95-1	Florida	30°60'N	86°50'W
	612492	P H	Eagle 14	Ontario	42°4'N	81°34'W
	612493	S	Frederick 9	Ontario	49°04'N	81°08'W
<i>F. virginiana</i> ssp. <i>virginiana</i> (northern)	612497	H	Montreal River 10	Ontario	47°14'N	84°39'W
	612498	PH	RH 23; MS 31-19	Minnesota	48°27'N	93°10'W
	612499	PH	RH 30; MS 05-06	Minnesota	47°43'N	90°29'W

²S = staminate flowers, P = pistillate flowers, H = hermaphrodite, and PH = partial hermaphrodite.

phenotypic and genetic traits for accessions in the preliminary core subset and using multivariate analytical methods to construct clusters and dendrograms to elucidate systematic and statistical genetic relationships for further refinement of the core subset, and 5) validation and refinement.

The USDA Small Fruit Germplasm Crop Germplasm Committee initially designated core members of the national strawberry collection in the early 1990s. This core is composed of cultivated and wild species members and is periodically reviewed and revised. To delimit an expanded gene pool for strawberry breeders, we have selected a preliminary supercore of 38 wild octoploid genotypes, that we feel encompass most of the horticulturally desirable traits described in native material from North and South America (Table 1). These selections include genotypes of the scarlet strawberry (*F. virginiana*), and the beach strawberry (*F. chiloensis*), that contain a wide array of useful traits from disease and insect resistance to physiological traits like day neutrality and high fruit number. Emphasis was placed on select-

ing genotypes with several outstanding horticultural traits, but outliers that were remarkable for single traits were also included. Geographic/ taxonomic distances between genotypes were also consulted to include genetically divergent individuals with less impressive horticultural attributes. In addition, habitats of the clones were also considered to incorporate representatives with specific biotic or abiotic adaptations from all representative environmental zones. The supercore clones are fully described in Hancock et al. (2000).

In this paper, we describe the performance of these elite clones across a broad environmental grid encompassing sites in Maryland, Michigan, Minnesota, Oregon, and Pennsylvania during the 1998–99 growing season (Table 1). Data were collected on survival, cold tolerance, disease susceptibility, runner production, flowering and fruiting dates, and fruit size and quality. These data can be used by breeders to select parents from an expanded germplasm base, and should serve as a reference point for future germplasm collections.

Materials and Methods

Trials were conducted at Excelsior, Minn.; Beltsville, Md.; Benton Harbor, Mich.; Corvallis, Ore.; and Rock Springs, Pa. During the course of the experiment, considerable environmental variation was observed across the sites (Hancock et al., 2000). Maryland and Oregon had the warmest winters, with temperatures only occasionally falling below freezing, while in Minnesota, Michigan, and Pennsylvania temperatures below 0 °C were not uncommon. Minnesota had the coldest winter (lows below –30 °C), followed by Michigan (–20 °C), and then Pennsylvania (–16 °C). Summer temperatures commonly exceeded 30 °C in Maryland, while in Oregon, they were rarely above 25 °C. Highs in Minnesota, Michigan, and Pennsylvania generally fell between these extremes. The number of frost-free days exceeded 200 in Maryland and Oregon, but was below 180 at the other locations. Rainfall also varied greatly across sites with Oregon being by far the wettest; however, at all locations plantings were irrigated if rainfall was below 2 to 3 cm a week.

Plants were propagated in a greenhouse at Michigan State University, East Lansing, in late Winter 1998, by rooting runners in a 1 peat : 1 perlite (by volume) medium as they emerged from mother plants. Most of the medium was removed from the plants and they were shipped in plastic bags by overnight mail to each of the cooperators on 29 Apr. 1998. Plants were set into the individual fields within 7 to 10 d. The experimental design was a randomized complete block with four replications at each location except Pennsylvania, where two replications were utilized. At each location but Pennsylvania, each plot was established with two plants spaced at 30 cm within the row and allowed to form a 60 × 30-cm mat. In Pennsylvania, each plot was established with four plants at 45 cm and allowed to form a 30 × 180-cm mat. The plants received no fertilization or pest control sprays, although they were provided with 3 to 4 cm of water a week through overhead sprinklers. Weeds were controlled by periodic hoeing.

During the bloom period at each site, plant vigor was rated on a 1 to 9 scale (least vigorous to most vigorous) and an estimation was made of the percentage of each plot that was filled with runner plants. The percentage of plants that appeared to have been killed by winter cold was also estimated in Michigan. At weekly intervals at each site, each plot was rated as to whether it was in flower or fruit. A genotype was considered day neutral if it flowered in the spring and again in the summer when day lengths exceeded 13 h. Genotypes that fruited in spring and fall, but not in summer were considered short day types. In addition, the gender of the majority of flowers within each plot was determined at midbloom, along with the average number of flowers per inflorescence. After fruiting, the plots were rated for prevalence of leaf diseases on a 1 to 9 scale (least to most). The most common diseases at all sites were leaf scorch [*Diplocarpon earlianum* (Ellis & Everh.) F.A. Wolf] and leaf spot [*Mycosphaerella fragariae* (Tul.) Lindau], but no effort was made to distinguish between them.

When ≈30% of the fruit were ripe in each plot, the average percentage of flowers developing into fruit and the percentage of achenes that matured per fruit was estimated by 10% increments. The weight of 10 randomly sampled fruit per plot was determined along with their firmness and flavor on a 1 to 9 scale (poor to excellent). Skin and flesh color was also rated on a 1 to 9 scale (white to deep red), and the percentage of the skin and flesh that was colored was estimated by 10% intervals.

Model variance components were estimated using SAS proce-

dures (SAS Inst., Inc., 1990). Among the individuals that survived at all sites, variance was partitioned into location, taxon, genotype, location × taxon interaction, location × genotype interaction, and error. Because there was considerable location specific mortality, variance patterns were also evaluated at each location individually, so that locally successful genotypes could be identified. Individual location values and genotype performances can be found at <http://www.berrygenetics.org>.

Results

All the traits, except flavor, varied significantly ($P < 0.05$) across location, taxa, and genotype. However, only percentage bed fill, foliar disease incidence, 50% bloom date, and number of flowering cycles showed significant interactions between genotypes and locations (Table 2). Among the genotypes that survived at all locations, bed fill was lowest in Oregon and highest in Maryland. Plants bloomed earliest in Oregon and latest in Minnesota. The mean number of flowering cycles was highest in Pennsylvania and lowest in Michigan. The lowest incidence of foliar disease was observed in Oregon and Michigan, while the highest was observed in Maryland.

Average percentage bed fill was over 50% greater in *F. virginiana* than *F. chiloensis* (Table 2). In general, *F. virginiana* ssp. *glauc*a had more densely filled beds and higher vigor than *F. virginiana* ssp. *virginiana* and *F. virginiana* ssp. *platypetala*. North American *F. chiloensis* ssp. *pacifica* were more vigorous than the South American *F. chiloensis*, particularly cultivated *F. chiloensis* ssp. *chiloensis* f. *patagonica*. Most clones of *F. chiloensis* had greater vigor in Oregon than the other four sites (<http://www.berrygenetics.org>).

Among individual genotypes, the *F. virginiana* ssp. *virginiana* clones, PI 612495, PI 612569, PI 612325, and PI 612499 of *F. virginiana* ssp. *glauc*a, produced the most densely filled plots and had some of the highest vigor ratings of all genotypes. The PI 551735 had the highest percentage bed fill and vigor of all the *F. chiloensis* clones.

Fragaria virginiana generally survived the winter better than *F. chiloensis* in Michigan (Fig. 1). Clones of northern *F. virginiana* ssp. *virginiana* had the highest survivorship, followed by *F. virginiana* ssp. *platypetala*, *F. virginiana* ssp. *glauc*a and southern *F. virginiana* ssp. *virginiana*. Cultivated *F. chiloensis* ssp. *chiloensis* f. *chiloensis* from South America was the most subject to winter injury of all the subspecies. The hardest genotypes of *F. virginiana* were PI 612495 and 612500 (*F. virginiana* ssp. *glauc*a), PI 551527 (*F. virginiana* ssp. *platypetala*), and PIs 612492, 612498, and 612499 (northern *F. virginiana* ssp. *virginiana*). The hardest *F. chiloensis* were the subspecies *F. chiloensis* ssp. *pacifica* PIs 612488 and 551735.

There was a significant genotype × location interaction for foliar disease incidence, but several genotypes were impressive at multiple sites and had low average levels of disease (Table 2, <http://www.berrygenetics.org>). The PIs 551471 and 551527 of *F. virginiana* ssp. *platypetala* had very low mean disease incidence and were among the most resistant genotypes in all states but Michigan. *Fragaria chiloensis* PI 612489 also had very low disease incidence and did well everywhere except Minnesota.

In general, the fruit of *F. chiloensis* ssp. *pacifica* were much larger than those of northern and southern *F. virginiana*, and were more poorly colored and slightly less firm (Table 3). The northern genotypes of *F. virginiana* ssp. *virginiana* were smaller, but better colored than the southern ones. Day-neutral genotypes

were found in northern *F. virginiana*, but not in southern *F. virginiana* or *F. chiloensis* ssp. *pacifica*.

Among the most impressive genotypes that survived and fruited across all sites were the *F. chiloensis* ssp. *pacifica* PI 551735 with its cold hardiness and unusually large, early fruit (although it was in general poorly colored), and the *F. virginiana* ssp. *virginiana* PIs 612493, 612499, and 612486 which had unusually deep red color. There were no significant genotype $\times$ location interactions for these traits.

The genotype $\times$ location interaction for number of fruiting cycles was significant, but several genotypes averaged more than one flowering cycle across sites, most notably, PIs 612492, 612493, 612495, 612498, and 612499 (Table 3 and Fig. 2). The PI 612495 fruited in August in only Michigan, Pennsylvania, and Maryland, while 612498 had a midseason crop in Oregon, Minnesota, and Pennsylvania, and 612499 exhibited multiple cropping in Michigan, Minnesota, and Pennsylvania. The PIs 612495, 612493, 612498, and 612499 flowered and fruited more

Table 2. Location, taxa, and genotype means for percentage bed fill, plant vigor, and disease resistance in strawberry genotypes from the supercore collection.

Source	Bed fill (%)	Vigor ^z	Foliar disease incidence ^y
Location			
Maryland	65.1	---	7.4
Michigan	42.0	5.5	3.6
Minnesota	40.2	4.7	5.3
Oregon	17.4	5.9	3.2
Pennsylvania	51.1	6.0	6.5
Taxa			
<i>F. chiloensis</i> ssp. <i>pacifica</i>	36.2	6.1	4.6
<i>F. chiloensis</i> ssp. <i>chiloensis</i> f. <i>chiloensis</i>	25.5	4.3	4.7
<i>F. chiloensis</i> ssp. <i>chiloensis</i> f. <i>patagonica</i>	5.1	2.2	---
<i>F. virginiana</i> ssp. <i>glauc</i>	65.3	6.6	5.7
<i>F. virginiana</i> ssp. <i>platypetala</i>	33.1	3.6	3.8
<i>F. virginiana</i> ssp. <i>virginiana</i> (North)	50.6	5.8	5.1
<i>F. virginiana</i> ssp. <i>virginiana</i> (South)	48.3	6.6	5.9
Genotype			
PI 236579	32.7	3.9	4.4
PI 551471	30.9	2.7	4.1
PI 551527	35.2	4.6	5.3
PI 551735	45.2	8.4	4.9
PI 551736	35.9	4.6	3.9
PI 612318	7.7	0.2	6.3
PI 612320	31.0	7.8	6.1
PI 612323	42.5	4.2	5.3
PI 612324	45.2	7.1	6.4
PI 612325	63.0	6.9	6.0
PI 612486	49.3	7.8	3.5
PI 612487	39.6	5.4	4.7
PI 612489	34.1	4.5	4.2
PI 612490	25.9	2.8	4.1
PI 612492	59.6	7.4	5.0
PI 612493	50.3	5.2	5.4
PI 612495	62.3	6.6	5.7
PI 612497	37.8	4.4	4.7
PI 612498	47.2	5.1	5.5
PI 612499	58.3	6.9	5.0
PI 612569	60.8	7.8	5.9
PI 612570	46.6	5.3	5.7
Significance (<i>P</i>)			
Replication	0.297	0.948	0.001
Location (L)	0.001	0.101	0.001
Taxa (T)	0.010	0.171	0.019
Genotype (G)	0.018	0.004	0.000
L $\times$ T	0.070	0.089	0.000
L $\times$ G	0.045	0.166	0.000

^z1 = lowest vigor, 9 = highest vigor.

^y1 = least infection, 9 = most infection.

Fig. 1. Mean percentage winter kill in strawberry genotypes (A) and species (B) of the supercore collection grown in Michigan. Vertical lines represent SE. Species codes are as follows: 1 = *F. chiloensis* ssp. *chiloensis* f. *chiloensis*, 2 = *F. chiloensis* ssp. *chiloensis* f. *patagonica*, 3 = *F. chiloensis* ssp. *pacifica*, 4 = *F. virginiana* ssp. *glauca*, 5 = *F. virginiana* ssp. *platypetala*, 6 = *F. virginiana* ssp. *virginiana* (northern), 7 = *F. virginiana* ssp. *virginiana* (southern).

than two times in Pennsylvania, but the last flowering period occurred in the short days of late September to October (data not presented).

Representatives of all subspecies survived

in Maryland, allowing for complete subspecies comparisons on at least this site (Table 4). Southern *F. virginiana* ssp. *virginiana* had the highest fruit set and best flavor. Northern *F. virginiana* ssp. *virginiana* had the deepest red flesh color and were the earliest and longest blooming. *Fragaria virginiana* ssp. *platypetala* produced the largest fruit with the most evenly colored skin. *Fragaria chiloensis* ssp. *chiloensis* f. *patagonica* had the firmest fruit and were the last to begin blooming. Day neutrals were found in *F. virginiana* ssp. *glauca*, *F. virginiana* ssp. *platypetala*, and northern *F. virginiana* ssp. *virginiana*. No day neutrals were observed in southern *F. virginiana* ssp. *virginiana*, or any of the *F. chiloensis* genotypes, although a few of the *F. chiloensis* clones flowered during the short days of fall (PIs 551735 and 602570).

Among the most impressive genotypes that survived and fruited in Maryland, but not all other sites were PIs 551527 and 551728, which had very large fruit and excellent flavor. PI 551527 also had unusually dark color. Both these clones survived at all five locations, but produced little fruit at any of them but Maryland. PI 551728 was a particularly impressive clone in Maryland, with among the deepest skin color of any clone and large fruit size. This clone performed poorly at all other sites but Oregon, where it had

among the largest fruit, and exceptional skin and flesh color, firmness and flavor (<http://www.berrygenetics.org>).

Discussion

As was observed previously by Darrow (1966), *F. chiloensis* and *F. virginiana* displayed many complementary traits. *Fragaria chiloensis* had larger fruit and greater foliar disease resistance, while *F. virginiana* was more vigorous and produced higher numbers of better-colored fruit. Among the individual taxa, the largest fruit sizes were observed in the cultivated land races of *F. chiloensis* from South America, although the native clones of North American, *F. chiloensis* ssp. *pacifica*, were much more vigorous. *Fragaria virginiana* ssp. *platypetala* had by far the largest fruit of any *F. virginiana* subspecies, rivaling the native clones of *F. chiloensis*. Day neutrals were found among northern *F. virginiana* ssp. *virginiana* and *F. virginiana* ssp. *glauca* accessions. Northern *F. virginiana* ssp. *virginiana* flowered the earliest and longest of any taxa, and had the most deeply colored fruit.

Significant genotype $\times$ location interactions were observed for percentage bed fill, foliar disease incidence, 50% bloom date, and number of flowering cycles, but not for fruit weight, skin color, flesh color, or firmness. This suggests that a single site can be used to rank fruit characteristics of wild germplasm, but multiple sites are necessary to predict their broad physiological adaptations and disease resistances. The most efficient germplasm evaluation strategy might be to evaluate clones first at a single location for fruit quality, and then send the best performing clones to multiple locations to evaluate their overall adaptations.

Several factors probably contributed to overall vigor and survival, including tolerance to extreme temperatures and pathogen resistance. Heat tolerance was not evaluated at any site but could have played a role in differential performance in Maryland.

Table 3. Location, taxa, and genotype means across five locations for 9 flowering and fruiting traits in strawberry genotypes from the supercore collection.

Source	Bloom date ^z (%)	Flowering cycle ^y	Fruit wt (g)	Skin color ^x	Skin colored ^w (%)	Flesh color ^x	Flesh colored ^v (%)	Firmness ^u	Flavor ^d
Location									
Maryland	142	1.5	2.2	7.3	63	4.9	48	4.4	6.3
Michigan	138	1.0	2.1	7.2	75	6.1	41	3.8	4.9
Minnesota	151	1.2	1.7	7.0	70	4.8	46	5.7	6.6
Oregon	137	1.2	1.4	5.1	80	2.9	35	5.2	6.6
Pennsylvania	146	1.9	2.2	5.9	86	4.7	43	6.2	4.4
Taxa									
<i>F. chiloensis</i> ssp. <i>pacifica</i>	138	1.0	3.3	5.3	73	4.1	41	4.6	6.1
<i>F. virginiana</i>									
ssp. <i>virginiana</i> (north)	148	1.7	0.9	7.1	72	5.5	52	5.4	5.7
<i>F. virginiana</i>									
ssp. <i>virginiana</i> (south)	143	1.0	1.6	7.1	79	4.4	35	5.2	5.5
Genotype									
PI 551735	139	1.0	4.8	4.6	67	3.8	41	4.5	6.0
PI 612323	138	1.0	1.7	5.4	77	3.0	28	4.8	5.3
PI 612324	140	1.0	1.6	---	81	5.0	29	4.3	5.1
PI 612486	152	1.0	1.6	7.0	85	6.3	52	6.0	6.8
PI 612487	138	1.0	1.8	6.1	78	4.4	41	4.8	6.3
PI 612492	142	1.3	1.3	6.5	70	4.9	57	5.3	5.7
PI 612493	152	1.4	0.6	7.5	71	5.4	50	5.4	4.9
PI 612494	144	1.3	---	---	---	---	---	---	---
PI 612498	155	1.5	0.9	6.7	76	5.9	50	5.0	6.0
PI 612499	143	1.6	0.7	7.5	73	5.8	51	5.9	6.1
PI 612569	141	1.1	1.5	5.0	73	2.8	27	4.7	4.8
PI 612570	143	1.0	1.5	7.2	80	5.0	40	6.1	5.6
Significance (<i>P</i>)									
Replication	0.949	0.782	0.491	0.374	0.235	0.450	0.657	0.849	0.029
Location (L)	0.480	0.005	0.224	0.376	0.000	0.000	0.413	0.199	0.017
Taxa (T)	0.500	0.950	0.000	0.472	0.133	0.291	0.039	0.731	0.682
Genotype (G)	0.221	0.307	0.512	0.107	0.148	0.011	0.113	0.135	0.223
L × T	0.023	0.015	0.141	0.369	0.272	0.219	0.150	0.005	0.119
L × G	0.001	0.016	0.840	0.474	0.626	0.143	0.230	0.228	0.055

^zDays after 1 Jan. when 50% of the flowers were open.

^yNumber of times plants flowered.

^x1–9 scale (white to deep red).

^w% of surface colored.

^v% of flesh colored.

^u1–9 scale (soft to firm).

^d1–9 scale (poor to excellent).

Winter cold was shown to be important in Michigan, and probably played an important role in Minnesota where conditions were even harsher. In Oregon, soil pathogens appeared to play a predominant role in plant death, as external symptoms of verticillium wilt (*Verticillium albo-atrum* Reinke and Berth) were observed in many of the clones (data not presented). Black root rot may also have contributed to mortality at many of the sites, as *Pythium* sp. and *Rhizoctonia* sp. are commonly associated with losses of vigor in the northern United States and Canada. In a companion study, we have found some of the most vigorous clones to also be resistant to the common soil pathogens in Michigan and to root knot (*Meloidogyne hapla* Chitwood) and root lesion nematodes [*Pratylenchus penetrans* (Cobb) Filipjev and Schuurmans Stekhoven] based on artificial inoculation studies in greenhouses in Oregon (Pinkerton and Finn, personal communication).

The relationship between environment and the expression of

Fig. 2. Mean number of flowering cycles of day-neutral genotypes in the strawberry supercore collection at five locations. Vertical lines represent SE.

Table 4. Taxa and genotype means for 12 vegetative, flowering and fruiting characteristics in strawberry genotypes from the supercore collection, evaluated at Beltsville, Md.

Source	First bloom ^z (d)	Last bloom ^y (d)	Flowering cycle ^v	Fruit wt (g)	Fruit set ^u	Skin color ^t	Skin colored ^x (%)	Flesh color ^t	Flesh colored ^w (%)	Firmness ^s	Flavor ^r	Leaf diseases ^q
Taxa												
<i>F. chiloensis</i> ssp. <i>pacifica</i>	119	146	1.2	3.2	51.2	5.2	54.1	3.0	26.7	4.1	5.7	6.7
<i>F. chiloensis</i> ssp. <i>chiloensis</i>												
<i>f. chiloensis</i>	123	153	1.0	2.4	55.7	5.4	59.0	2.8	28.0	4.6	6.1	6.7
<i>F. chiloensis</i> ssp. <i>chiloensis</i>												
<i>f. patagonica</i>	123	140	1.2	2.1	44.1	6.5	65.5	2.8	29.2	6.4	4.2	6.0
<i>F. virginiana</i> ssp. <i>glauca</i>	115	177	1.9	0.9	45.5	5.8	49.7	4.5	43.4	4.4	6.6	7.6
<i>F. virginiana</i>												
ssp. <i>platypetala</i>	115	153	1.7	3.8	24.6	5.8	77.5	5.4	39.8	4.7	5.3	6.4
<i>F. virginiana</i>												
ssp. <i>virginiana</i> (north)	113	206	1.8	1.1	30.4	6.0	62.1	5.8	54.4	4.8	6.1	7.7
<i>F. virginiana</i>												
ssp. <i>virginiana</i> (south)	116	146	1.0	1.8	73.9	6.4	66.7	4.0	39.3	5.2	6.8	8.1
Genotype												
PI 236579	111	147	1.0	2.0	38.3	5.9	59.1	2.4	29.9	3.3	5.5	6.4
PI 551445	126	146	1.0	2.5	12.9	4.9	43.4	2.1	24.7	5.9	4.1	6.7
PI 551453	127	147	1.0	1.7	46.0	4.1	45.0	1.3	0.0	4.9	6.3	6.1
PI 551471	110	168	1.3	1.6	12.6	5.6	68.2	3.7	35.4	3.1	3.0	5.6
PI 551527	120	138	2.0	6.0	36.6	8.6	86.7	7.0	44.1	6.3	7.7	7.3
PI 551728	122	145	1.0	6.3	14.6	4.6	51.8	1.3	3.6	4.0	6.7	7.2
PI 551735	111	153	2.8	5.6	52.2	5.5	52.5	5.5	50.8	4.1	6.5	7.9
PI 551736	111	165	1.0	2.9	56.3	5.3	56.5	1.6	29.1	4.5	7.6	6.4
PI 602568	120	152	1.0	2.1	44.4	6.5	72.1	2.8	28.7	5.4	4.6	6.1
PI 602570	125	129	2.0	3.0	42.4	6.6	35.9	2.5	32.3	7.3	4.2	6.8
PI 612316	129	156	1.0	2.5	37.7	6.9	71.1	5.1	47.3	5.7	5.6	6.7
PI 612317	125	140	1.0	1.1	45.4	4.0	88.4	3.1	26.6	6.6	3.8	5.1
PI 612318	141	146	1.0	2.1	90.4	1.5	49.2	2.1	5.7	5.1	5.8	7.6
PI 612320	111	143	1.0	2.3	86.8	6.3	65.1	2.5	29.0	6.4	6.1	7.8
PI 612323	111	141	1.0	2.1	84.7	6.1	67.2	3.0	35.0	4.6	6.0	8.3
PI 612324	111	145	1.0	1.9	83.0	6.5	68.9	3.6	42.5	4.0	6.7	7.8
PI 612325	111	142	1.0	0.6	30.6	4.6	70.9	4.3	38.8	5.2	8.0	8.4
PI 612486	130	161	1.0	2.2	77.8	8.1	83.4	6.8	65.7	6.1	7.6	8.6
PI 612487	111	141	1.0	2.6	75.1	5.6	65.2	4.8	51.7	2.5	5.8	6.4
PI 612488	116	141	1.0	2.4	90.0	5.0	54.7	4.9	48.7	3.4	5.8	6.8
PI 612489	111	152	1.0	1.0	53.2	5.8	63.7	3.1	34.1	4.6	5.0	6.4
PI 612490	125	147	1.0	3.6	65.9	6.8	56.3	1.0	0.0	3.6	5.4	6.3
PI 612492	111	187	1.8	0.6	13.0	5.8	64.3	5.8	57.2	4.6	5.5	8.5
PI 612493	111	271	1.0	1.1	11.9	5.9	57.8	4.1	44.3	5.3	5.9	8.6
PI 612494												
PI 612495	116	191	1.5	1.2	32.0	5.5	52.3	4.9	47.2	4.8	6.0	8.4
PI 612497	111	147	2.0	2.4	44.9	6.0	60.6	7.0	70.8	4.6	6.0	7.1
PI 612498	111	272	1.0	0.6	36.4	5.1	70.9	5.5	41.2	4.2	6.5	6.2
PI 612499	119	152	2.0	0.8	45.7	5.8	56.8	6.5	58.2	5.3	6.5	7.9
PI 612500	120	198	1.5	1.0	14.6	4.3	36.3	3.3	30.6	5.0	7.5	6.9
PI 612569	118	141	1.0	1.8	84.3	5.5	51.5	2.8	24.5	4.5	6.0	8.5
PI 612570	120	147	1.0	1.7	70.2	7.1	60.0	5.1	39.3	5.5	7.1	7.6
Significance (P)												
Replication	0.217	0.441	0.606	0.884	0.495	0.974	0.350	0.061	0.812	0.020	0.410	0.052
Taxa	0.482	0.018	0.004	0.033	0.057	0.019	0.075	0.072	0.148	0.152	0.041	0.001
Genotype	0.000	0.000	0.000	0.000	0.000	0.000	0.289	0.000	0.000	0.000	0.000	0.000

^zDate first flower appeared after 1 Jan.

^yDate last flower appeared after 1 Jan.

^xPercentage of surface colored.

^wPercentage of flesh colored.

^vNumber of times plants flowered.

^uPercentage of achenes fully developed per fruit.

^t1–9 scale (white to deep red).

^s1–9 scale (soft to firm).

^r1–9 scale (poor to excellent).

^q1–9 scale (least to most).

day neutrality proved complex, as has been noted elsewhere (Barritt et al., 1982; Hancock et al., 2000; Nicholl and Galletta, 1987). By far, the highest expression of day neutrality was observed in Maryland and Pennsylvania, where midsummer temperatures were quite different, with Maryland being the hottest site, and Pennsylvania one of the cooler sites. In previous work, we found Ontario, Canada, which is relatively cool in summer, to display a higher proportion of day neutrality than hotter Michigan and Minnesota (Hancock et al., 2001). To select breeding parents most effectively, it appears necessary to identify regionally adapted genotypes, rather than relying on the Wasatch source of day neutrality that has been incorporated into the California cultivars (Bringhurst and Voth, 1979).

In conclusion, we have selected a supercore that clearly encompasses a broad range of useful genetic variability. We were able to identify several wild genotypes of *F. chiloensis* and *F. virginiana* that have breeding potential regionally and across the northern half of North America. Numerous clones of *F. chiloensis* have been incorporated previously into North American breeding populations (Sjulin and Dale, 1987), but *F. virginiana* has only rarely been exploited (Bringhurst and Voth, 1978; Powers, 1945). Our work identifies several clones of *F. virginiana* that deserve greater attention including PIs 612496, 612493, 612495, 612497, 612498, and 612499. We also discovered that *F. virginiana* ssp. *platypetala* has a number of desirable traits including large fruit, good color, winter hardiness, and disease resistance. This taxon should be collected further and evaluated.

We feel our work sets a baseline for future germplasm evaluation. As new material is collected and selected at individual sites, these elite selections should be compared with our supercore at several regional locations representing the climatic conditions of the strawberry production regions. With this information, breeders will be able to select potential wild parents more effectively, and a well characterized supercore of native germplasm can be constructed periodically for those interested in working with a genetically diverse set of horticulturally relevant germplasm.

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