were not correlated with aphid number. Seasonal differences in the cultivars are probably important, as evidenced by a significant cultivar-date interaction, but this may be at least partially due to differences in the timing of shoot initiation.

Resistance to aphid colonization might be combined through breeding with resistance to the virus itself, so that cultivars will be protected at 2 levels. This approach shows promise as several cultivars have been screened for BBSSV resistance and at least one ('Bluecrop') appears to be immune to infection (D.C. Ramsdell, personal communication). A similar strategy has apparently worked in the control of other diseases such as mosaic virus on raspberries (1, 4, 5, 6).

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Levels of Inbreeding in Highbush Blueberry Cultivars[1]

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Abstract. **Inbreeding coefficients were calculated for the 63 cultivars of blueberry (*Vaccinium corymbosum* L.) released by public agencies in the United States. A steady increase in coefficients was noted from the period of 1910–1920 (F=0.00) to 1960–1970 (F=0.13). 'Lateblue' and 'Flordablue' had the highest coefficient of 0.25. Most of the genes in the cultivars came from the wild selections 'Brooks', 'Sooy' and 'Rubel'.**

Various naturally outcrossing crop species exhibit inbreeding depression which causes serious genetic, morphological, and physiological abnormalities. Blueberries (*V. corymbosum*) are no exception, as self-pollinations have been shown to produce fewer, smaller seeds than cross pollinations (3, 5, 6, 8), and reductions in vigor and productivity have been observed in highly inbred material (Draper, personal communication). While *V. corymbosum* is tetraploid ($2n = 48$), it is completely diploidized and as such has disomic inheritance. Breeders of tetraploid blueberries have become increasingly concerned about the possibility of inbreeding depression, and to alleviate this problem they have made systematic collections of native blueberry species (2, 7). These collections have also been made to expand the environmental range over which commercial blueberries can be grown.

The purpose of this study was: 1) to calculate the inbreeding coefficients of the various cultivated varieties, 2) to estimate the germplasm content of the cultivars obtained from wild selections, and 3) to determine inbreeding trends over time.

The pedigrees of 63 cultivars released by public agencies were gathered from various sources. Inbreeding coefficients were calculated using the pedigree method of Wright (9):

$$Fx = \Sigma[(1/2)^{n1+n2+1}(1+F_A)],$$

where n_1 is the number of generations from one parent back to the common ancestor and n_2 from the other parent. F_A is the inbreeding coefficient of the common ancestor. The native germplasm composition of each varietal genome was also measured by calculating the maximum percentage of genes in each cultivar which could have originated from wild selections. Cultivars were grouped by the decade in which the hybridizations producing them were made and means were calculated for F (the inbreeding coefficient) and the native germplasm percentage.

The wild germplasm content of current cultivars is diverse. However, 3 native selections ('Brooks', 'Sooy', and 'Rubel') have contributed most of the genes in present day cultivars (Tables 1, 2). The mean contribution of these 3 selections in each decade was: 1910–1920 (66.7%), 1920–1930 (80.4%), 1930–1940 (71.4%), 1940–1950 (67.0%), and 1960–1970 (73.4%).

The inbreeding coefficients of cultivars were observed to range from 0.00 (31 cultivars) to 0.25 ('Lateblue' and 'Flordablue') (Table 3). Further, an increase in inbreeding coefficients over time was observed, although these values have leveled off in the last two decades (Table 4). The cultivars resulting from hybridizations in the period from 1951–1950 had the highest average of 0.1396 and those developed in 1961–1970 were only slightly lower (0.1263).

In many outcrossing species of plants, inbreeding coefficients as high as those in the current blueberry cultivars result in serious inbreeding depression (1, 4). The allotetraploid, heterozygous nature of highbush

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Table 1. Genetic contribution of various "wild" selections to blueberry cultivars based on pedigree analysis.

Cultivar	Genetic contribution							
	Brooks	Chatsworth	Crabbe 4	Grover	Sooy	Rubel	Russell	Other[z]
Angola	25.0	12.5	25.0		6.3	25.0	6.3	
Atlantic	25.0			25.0	25.0	25.0		
Avonblue	16.4	1.6		3.1	14.0	20.3	0.8	HAR(6.3),UNK(25.0), VAS(6.3),VDA(6.3)
Berkeley	25.0			12.5	25.0	37.5		
Bluechip	25.0	6.3	12.5	6.3	12.5	31.3	6.3	
Bluecrop	25.0			12.5	18.8	37.5	6.3	
Bluehaven	18.8			6.3	18.7	18.7		MLI(25.0),UNK(12.5)
Bluejay	25.0			6.3	25.0	18.8		TAY(25.0)
Blueray	25.0			12.5	18.8	37.5	6.3	
Bluetta	18.5			9.3	18.8	28.2		NSL(25.0)
Burlington	25.0				25.0	50.0		
Cabot	50.0	50.0						
Catawba	50.0						50.0	
Collins	31.3	12.5			12.5	37.5	6.3	
Concord	50.0					50.0		
Coville	25.0			12.5	25.0	37.5		
Croatan	25.0	12.5	25.0		6.3	25.0	6.3	
Darrow	25.0			6.3	21.9	31.3	3.1	HAR(12.5)
Dixi	25.0			12.5	25.0	37.5		
Earliblue	31.3	12.5			12.5	37.5	6.3	
Elizabeth	25.0	12.5		12.5	12.5	37.5		
Elliot	25.0			9.4	25.0	40.6		
Flordablue	1.6				1.6	4.7	1.6	VDA(25.0),VAS(12.5), UNK(50.0),CAR(3.1)
Greenfield	50.0						50.0	
Herbert	25.0			12.5	25.0	37.5		
Harrison	25.0	6.3	12.5	6.3	12.5	31.3	6.3	
Ivanhoe	18.8	25.0			12.5	37.5	6.3	
Jersey				50.0		50.0		
June		25.0				50.0	25.0	
Katherine	50.0					50.0		
Lateblue	25.0			12.5	25.0	37.5		
Meader	28.1	6.3		6.3	15.6	37.5	6.3	
Morrow	12.5	6.3	12.5		3.3	12.5	3.1	ADA(50.0)
Murphy	25.0	12.5	25.0		6.3	25.0	6.3	
Northland	18.8			6.3	18.8	18.8		MLI(25.0),UNK(12.5)
Patriot	21.9	6.3		3.1	12.5	28.1	3.1	MLI(25.0)
Pemberton	25.0				25.0	50.0		
Pioneer	50.0				50.0			
Rancocas	25.0					50.0	25.0	
Redskin	50.0						50.0	
Scammell	25.0	25.0				50.0		
Sharpblue	6.6	2.3		0.8	3.9	9.4	1.2	HIL(6.3),UNK(25.0), VDA(31.3),VAS(12.5)
Spartan	28.1	6.3		6.3	15.6	37.5	6.3	
Stanley	25.0				25.0	50.0		
Wareham						50.0		HAR(50.0)
Weymouth	37.5	25.0				25.0	12.5	
Wolcott	25.0	12.5	25.0		6.3	25.0	6.3	
Cu-5	25.0				12.5	50.0	12.5	
GM-37	25.0			25.0	25.0	25.0		
GS-149	25.0			25.0	25.0	25.0		
394-Y	50.0						50.0	
F-72	25.0				25.0	25.0		HAR(25.0)
US 11-93	25.0			12.5	18.8	37.5	6.3	

[z]Adams (ADA), Carter (CAR), Harding (HAR), Hildebrand (HIL), Michigan lowbush 1 (MLI), North Sedgwick lowbush (NSL), Taylor (TAY), Unknown (UNK), *Vaccinium ashei* (VAS), and *V. darrowi* (VDA).

Table 2. Mean percentage of wild blueberry selections found in cultivars resulting from hybridizations in different decades.

Wild selection	Mean percentage in decade					
	1911–20	1921–30	1931–40	1941–50	1951–60	1961–70
Adams	0.0	0.0	0.0	5.0	0.0	0.0
Brooks	33.3	26.8	25.0	21.8	25.8	12.4
Chatsworth	8.3	3.6	6.3	2.5	4.7	2.5
Carter	0.0	0.0	2.5	1.3	0.0	0.8
Crabbe 4	0.0	0.0	10.0	1.3	0.0	3.1
Grover	4.2	7.1	5.0	6.9	5.5	2.6
Harding	4.2	0.0	0.0	1.3	0.0	1.6
Hildebrand	0.0	0.0	0.0	0.0	0.0	1.6
Mich. lowbush I	0.0	0.0	0.0	5.0	6.3	0.0
North Sedgwick	0.0	0.0	0.0	5.0	0.0	0.0
Sooy	8.3	21.4	13.8	16.3	17.2	8.0
Rubel	25.0	32.1	32.5	28.9	30.5	16.4
Taylor	0.0	0.0	0.0	0.0	6.3	0.0
Russell	16.7	8.9	5.0	1.9	3.9	2.5
V. ashei[z]	0.0	0.0	0.0	0.0	0.0	7.8
V. darrowi[z]	0.0	0.0	0.0	0.0	0.0	15.6
Unknown	0.0	0.0	0.0	2.5	0.0	25.0

[z]Selection not named.

Table 3. Inbreeding coefficients of highbush blueberry cultivars released by public agencies.

Cultivar	Origin	Decade of hybridization	F
Adams	USDA	WHS[z]	0.0000
Angola	USDA/NC AES	1930	0.0547
Atlantic	USDA	1920	0.0000
Avonblue[y]	FL AES	1960	0.0381
Berkeley	USDA/NJ AES	1930	0.1250
Bluechip	USDA/NC AES	1960	0.1211
Bluecrop	USDA/NJ AES	1930	0.1094
Bluehaven[y]	MI AES	1940	0.0469
Bluejay	MI AES	1950	0.0937
Blueray	USDA/NJ AES	1930	0.1094
Bluetta	USDA/NJ AES	1940	0.0000
Brooks	USDA	WHS	0.0000
Burlington	USDA	1920	0.0000
Cabot	USDA	1910	0.0000
Carter	USDA	WHS	0.0000
Catawba	USDA	1910	0.0000
Chatsworth	USDA	WHS	0.0000
Collins	USDA/NJ AES	1930	0.1094
Concord	USDA	1910	0.0000
Coville	USDA/NJ AES	1920	0.1250
Croatan	USDA/NC AES	1930	0.0547
Darrow	USDA/NJ AES	1940	0.1328
Dixi	USDA	1920	0.1250
Dunfee	USDA	WHS	0.0000
Earliblue	USDA/NJ AES	1940	0.1094
Elizabeth	NJ BC[w]	1940	0.0948
Elliot	USDA	1940	0.1875
Flordablue	FLAES	1960	0.2500
Greenfield	USDA	1910	0.0000
Grover	USDA	WHS	0.0000
Harding	USDA	WHS	0.0000
Herbert	USDA/NJ AES	1930	0.1250
Harrison	USDA/NC AES	1940	0.1250
Ivanhoe	USDA	1930	0.0781
Jersey	USDA	1910	0.0000
June	USDA	1910	0.0000
Katherine	USDA	1910	0.0000
Keweenaw	MI AES	1920	0.0000
Lateblue	USDA/NJ AES	1940	0.2500
Meader	NH AES	1950	0.1816
Morrow	USDA/NC AES	1940	0.0000
Murphy	USDA/NC AES	1930	0.0547
Northland	MI AES	1940	0.0469
Patriot	USDA/ME AES	1950	0.1016
Pemberton	USDA	1920	0.0000
Pioneer	USDA	1910	0.0000
Rancocas	USDA	1910	0.0000
Redskin	USDA	1910	0.0000
Rubel	USDA	WHS	0.0000
Russell	USDA	WLS	0.0000
Sam	USDA	WHS	0.0000
Scammell	USDA	1910	0.0000
Sharpblue	FL AES	1960	0.0967
Sooy	USDA	WHS	0.0000
Spartan	USDA	1950	0.1816
Stanley	USDA	1920	0.0000
Taylor	MI AES	WHS	0.0000
Wareham	USDA	1910	0.0000
Weymouth	USDA	1920	0.0625
Wolcott	USDA/NC AES	1930	0.0547

[z]Wild highbush selection.
[y]Unknown parent — F value estimated.
[x]Wild lowbush selection.
[w]New Jersey Blueberry Council.

Table 4. Mean inbreeding coefficients of blueberry cultivars resulting from hybridizations in different decades.

Decade of hybridizations	No. of cultivars	Mean inbreeding coefficient (F)	SD
<1911	3	0.0000	0.0000
1911–1920	19	0.0000	0.0000
1921–1930	9	0.0347	0.0551
1931–1940	10	0.0875	0.0300
1941–1950	10	0.0993	0.0800
1951–1960	4	0.1396	0.0486
1961–1970	4	0.1263	0.0632

blueberries has apparently allowed this outcrossed species to be substantially inbred without serious difficulties. However, the reduced size and viability of selfed seeds (3, 5, 6, 8) indicates that there is a limit to the amount of inbreeding *V. corymbosum* can tolerate. Accurate measurements need to be made to determine where this point is so that future breeding programs will not be stalled due to inbreeding depression.

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Identification of Seedless Table Grape Cultivars and a Bud Sport with Berry Isozymes[1]

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Additional index words. Vitis vinifera, starch gel electrophoresis, enzymes

Abstract. **Isozyme banding patterns from ripe berry extracts made it possible to distinguish between 3 cultivars of table grape (*Vitis vinifera* L. cvs. Perlette, Thompson Seedless and Superior Seedless) and an earlier ripening bud sport of 'Superior Seedless'. Catechol oxidase provided the most useful data as it was possible to distinguish between all 4 samples. Differences in banding patterns were noted in acid phosphatase, esterase, alcohol dehydrogenase, indophenol oxidase and leucine aminopeptidase. No differences were observed in the banding patterns for catalase, glutamate-oxalacetate transaminase, peroxidase, malic enzyme or malate dehydrogenase.**

Electrophoresis is a useful tool for studying genetic variation and has been used successfully to study the genetic variation in a number of organisms (1, 2, 5, 6, 7, 10, 12). Enzyme extraction and preparation is simple (3, 4) and the method can be used to rapidly determine an organism's genotype, independent of judgment based on phenotypic information (2). Polyacrylamide and starch gel electrophoresis have been used to determine differences between cultivars and species of peach (1), pear (6), and grape (3, 12). Recently, enzyme electrophoresis has been used to distinguish between apomictic nucellar and zygotic *Citrus* seedlings (10) and to serve as genetic markers for avocado (11).

The objective of this research was to determine if starch gel electrophoresis could provide sufficient information to distinguish between the 3 main cultivars of white seedless table grapes and an earlier ripening bud sport of one of the cultivars.

'Superior Seedless' and its earlier ripening bud sport were collected at harvest in Indio, California and shipped to Tucson. Two other seedless cultivars ('Thompson Seedless' and 'Perlette') were harvested from the University of Arizona's Campbell Avenue Farm Tucson.

Whole berries (ca. 30 g, fresh weight) which had been cut into eighths were homogenized for 2 min in 50 ml buffer (0.35M phosphate with 0.01M cysteine, pH 7.2) in a Waring blender equipped with a 30 to 200 ml Eberbach chamber at 0°C in an ice bath. The homogenate was filtered through 4 layers of cheesecloth and centrifuged for 10 min at 10,000 × g. The supernatant was discarded and the pellet rinsed with distilled water at 0°. The pellet was rehomogenized in 5 ml extraction buffer (0.01M phosphate, 0.01M cysteine, pH 7.0, with 2% polyethylene-glycol 5,000) with a glass rod and centrifuged for 20 min at 20,000 × g. The supernatant was absorbed into 6 × 8 mm paper wicks (Watman No. 30).

Horizontal slab starch gels were prepared using the system described by Scandalios (7). The gel buffer consisted of 9 parts Buffer A (0.05M tris and 0.0076M citric acid) and 1 part Buffer B (0.038M lithium hydroxide and 0.19M boric acid). Gel buffer (200 ml) was boiled and rapidly mixed with 35 g starch (Connaught Starch Hydrolyzed) previously suspended in 75 ml gel buffer. The hot viscous starch suspension was evacuated and poured into the gel form (16 × 18 × 0.8 cm), covered with a glass plate, and cooled to 20°C.

The paper wicks were inserted into a vertical cut in the gel 5 cm from the cathodal end, across the 18 cm width. Up to 20 samples could be assayed simultaneously. The electrode reservoirs were filled with 150 ml Buffer B, and thin sponges soaked in Buffer B were used as bridges to the gel. The gel was covered with plastic wrap and a glass plate and placed in a cold room (4 ± 1°C) for the electrophoretic run. After 10 min of equilibrium, 300 volts (at 65 mA) were applied for 10 min (Buchler Instruments power supply

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