Journal American Pomological Society 54(3):148-152 2000

Sweet Cherry Pollination: Recommendation Based on Compatibility Groups and Bloom Time

CHEOL CHOI, KENNETH LIVERMORE AND ROBERT L. ANDERSEN[1]

Abstract

Results of controlled pollination tests, PCR based S allele typing analysis and examining bloom times on sweet cherry (*Prunus avium* L) at the NYSAES, were compiled. In sweet cherry, at least 20 pollen incompatibility groups were detected from currently used and newly developed cultivars and bloom times were classified into 5 groups. Based on long-term field observation and lab results, a comprehensive sweet cherry pollination chart was developed.

Introduction

One of the most important events in sweet cherry cultivation is good pollination and fertilization for abundant fruit set. The successful completion of a sequence of reproductive events depends on adequate supplies of viable, compatible pollen; an effective transfer of pollen when stigmas are receptive; proper growth of pollen tubes and entering the ovule during the period when embryo sacs have matured and ovules are viable; and successful double fertilization followed by growth and development of the embryo and endosperm (16). After fertilization, other physiological factors play a contributing role.

As with other self-incompatible fruit tree species of the Rosaceae, sweet cherry exhibits the homomorphic and monofactorial gametophytic self-incompatibility system, which controlled by the S-locus with multiple alleles (6, 14). With this system, self or cross incompatibility exists when the specific S allele that carried by a pollen grain is the same as one of the two specific S alleles carried by the somatic tissue of the receptor pistil. Thus, sweet cherry requires accurate pollination group knowledge to assure fruit set in commercial orchards. Also, sweet cherry S allele genotype classification and pollen incompatibility group information are critical to breeding programs as well as genetic studies. For effective cross-pollination, at least 2-3 cross-compatible varieties which have synchronous bloom times should be planted in an orchard and bees provided as pollinators.

The sweet cherry pollination compatibility problem in commercial orchards was first realized and studied in the state of Oregon in about 1914 (7). Pollen incompatibility studies in sweet cherry were pioneered and developed at the John Innes Institute (5, 6). Subsequently six specific S alleles responsible for pollen incompatibility were identified (3). The identification of six specific S alleles theoretically gives 15 different incompatibility groups. However, only ten incompatibility groups and their specific S allele were reported (10). Additionally three groups whose S alleles were unknown at that time, plus group 'O,' were reported to exist but their specific S alleles were not identified (10, 14). Recently, three more S-alleles (S_z, S_y *and* S_x) were newly identified and these extended to a total of nine the S-alleles currently reported (4). This increases to 36 the number of pollen incompatibility groups which theoretically exist in sweet cherry.

In order to achieve abundant fruit set, bloom time of cross compatible cultivars must be reliably synchronous so that pollen is available as soon as flowers begin to open on the receptor cultivars (16). Compatible and viable pollen should be transferred to the stigma during the effective pollination period in order to achieve

[1]Corresponding author, Department of Horticultural Sciences, Cornell University, New York State Agricultural Experimental Station, Geneva, NY& 14456, USA. E-mail: rla2@nysaes.cornell.edu.

fruit set. This effective pollination period represents the period of ovule longevity minus the period required for pollen tubes to grow down the style and effect fertilization (16). In sweet cherry, this effective pollination period may be as short as 1-2 days or as long as 1 week depending on cultivars, environmental factors and the season (8, 12, 17).

Both pollen compatibility and bloom time information should be considered when establishing a new orchard or replacing existing cultivars since many sweet cherry cultivars are self-incompatible. The present paper is a survey of compatibility in sweet cherry cultivars, which are important for commercial or breeding material, based on controlled pollination tests and/or S-allele genotyping by PCR analysis and bloom time records from the New York State Agriculture Experiment Station (NYSAES) in Geneva, NY.

Methods and Materials

Our data for pollen incompatibility information were compiled mostly from Choi (4), Tehrani and Brown (14) and Knight (10). These were supplemented with the unpublished results of PCR based S-allele typing analysis and controlled pollination crosses made in the sweet cherry breeding program at the NYSAES in Geneva, NY. The PCR based S-allele typing was carried out under conditions based on the method of Tao et al. (13). Field confirmations of S-genotypes accomplished through controlled pollination test crosses were made between cultivars/selections with unknown or possibly mis-classified cultivars/selections and a series of testers with previously reported, known S-alleles. Pollen preparation, test crosses and determination were made by using the standard method used in many sweet cherry breeding programs as described in Way (18).

The bloom time was estimated based on records of full bloom dates since 1991 and cultivar descriptions prepared by Cornell Sweet Cherry Breeding Program (CSCBP). These full bloom times were rated using a 1 to 5 scale with 1 being the earliest bloom time and 5 the latest.

Results and Discussion

The results of our investigations with regard to the pollen incompatibility of cherry cultivars are presented in Table 1. Three novel S-alleles, S_x, S_y and S_z were added to the six previously known S-alleles in sweet cherry. So the number of pollen incompatibility groups increases from 15 to 36 along with increasing the number of S-alleles from 6 to 9. A total of 20 of the 36 possible pollen incompatibility groups were verified in this investigation. S-genotypes of some cultivars have

Table 1. S-genotypes and pollen-incompatibility groups of sweet cherry cultivars/selections as tested by controlled pollination and PCR based S-allele genotyping analyses.

S-genotypes	Cultivars/selections
S1S2	Early Rivers, Summit
S1S3	Regina*, Van, Venus, Windsor
S1S4	Hudson, NY 1725*, Rainier, Republican, Sylvia*, Viscount
S1S5*	RN4R7T160**
S1S6*	Noble, NY 518, NY 8182
S2S3	Knights Bigarreau*, Vega*, Velvet, Victor, Viva, Vogue
S2S4*	Royalton, Sam, Schmidt, Vic
S2S6*	RN004R1T102**, RN004R1T117**
S3S4	Bing, Büttners Späte Röte Knorpelkirsche*, Emperor Francis, Kristin, Napoleon, Somerset, Turkey Heart B*, Ulster*
S3S5*	Burlat, Chelan, Moreau
S3S6	Gold, Governor Wood, Hartland
S4S5	RN004R7T163**
S4S6	RN004R2T175**
S5S6*	Early Lyons
S2Sz*	Cryalls Seedling, Guigne d'Annonay
S3Sy*	Schneiders
S4Sy*	NY 9801
S1Sx*	Noir de Guben, Seneca, Valera
S3Sx*	Hedelfingen, Nadino
S4Sx*	NY 1625

*S-genotypes have been newly assigned or changed from previously classified as in Tehrani and Brown (1992) or Knight (1969).

**Seedling identification number: RN004 (Orchard identification) R7 (Row) T156-176 (Tree).

Bloom Time	Early		Early Mid					Mid										Late Mid							Late	
	Somerset	Viscount	Kristin	Viva	Chelan	Burlat	Republican	Royalton	Summit	Rainier	Napoleon	Valera	Ulster	Bing	Emperor Francis	Hartland	Schmidt	Van	Hedelfingen	Regina	Lambert	Windsor	Vogue	Sam	Gold	Hudson
Somerset	X		X								X		X	X	X				Δ	Δ	X	Δ	Δ	Δ	Δ	Δ
Viscount		X					X			X									Δ	Δ	Δ	Δ	Δ	Δ	Δ	X
Kristin	X		X								X		X	X	X				Δ	Δ	X	Δ	Δ	Δ	Δ	Δ
Viva				X															Δ	Δ	Δ	Δ	X	Δ	Δ	Δ
Chelan					X	X													Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ
Burlat					X	X													Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ
Republican		X					X			X									Δ	Δ	Δ	Δ	Δ	Δ	Δ	X
Royalton								X									X		Δ	Δ	Δ	Δ	Δ	X	Δ	Δ
Summit									X										Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ
Rainier		X					X			X									Δ	Δ	Δ	Δ	Δ	Δ	Δ	X
Napoleon	X		X								X		X	X	X						X					
Valera												X														
Ulster	X		X								X		X	X	X						X					
Bing	X		X								X		X	X	X						X					
Emperor Francis	X		X								X		X	X	X						X					
Hartland																X									X	
Schmidt								X									X							X		
Van																		X		X		X				
Hedelfingen	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ								X							
Regina	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ							X		X		X				
Lambert	X	Δ	X	Δ	Δ	Δ	Δ	Δ	Δ	Δ	X		X	X	X						X					
Windsor	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ							X		X		X				
Vogue	Δ	Δ	Δ	X	Δ	Δ	Δ	Δ	Δ	Δ	Δ												X			
Sam	Δ	Δ	Δ	Δ	Δ	Δ	Δ	X	Δ	Δ	Δ						X							X		
Gold	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ	Δ					X									X	
Hudson	Δ	X	Δ	Δ	Δ	Δ	X	Δ	Δ	X	Δ															X

□ All Compatible
X Incompatible
Δ Compatible but Different Bloom Sequence

Figure 1. Sweet cherry pollination and bloom time chart in NYSAES.

been corrected from those previously reported as in Tehrani and Brown (14) and Knight (10). Additionally, some relatively recently introduced cultivars were identified as to their S-genotypes and self-incompatibility groups.

Five new S-genotype combinations: S_1S_5, S_1S_6, S_2S_6, S_4S_6, and S_5S_6, which were possible combinations of 6 S-alleles but had not previously been identified (14), were identified from CSCBP seedling selections and/or cultivars as in Table 1. The new S-genotype combinations of S_1S_5, S_2S_6, and S_4S_6 were identified from our seedling populations that were purposely made to create these groups. The S-genotype combinations of S_1S_6, and S_5S_6, were cultivars which were previously classified as belonging to pollen incompatibility groups 'XII' and 'X,' respectively (14).

The S-genotype of 'Noble,' which was previously classified as Group 'XII' also with unknown S-genotype, and two NY selections, 'NY 518' and 'NY 8182' were determined as S_1S_6. Similarly, the S-genotype of S_5S_6, was identified in 'Early Lyons' by PCR based S-allele typing analysis, This cultivar was previously classified as Group 'X' with unknown S-genotype (14).

The S-genotypes of Group 'V' (S_3S_5), 'VII' (S_4S_5), 'VIII' (S_2S_5), 'XIII' (S_2S_4) were assigned from previous works by Knight (10) and Tehrani and Brown (14). However, results shown here dispute the previously reported S-genotype of the cultivars that were listed as belonging to these groups. All cultivars previously reported as Group V (S_3S_5), which included 'Turkey Heart,' 'Late Black Bigarreau' and 'Turkey Heart B' as well as 'NY 1625' (10) should be reconsidered as to their S-genotypes. 'Turkey Heart' and 'Late Black Bigarreau' were considered to be S_4SY where SY was interpreted to be S_5 through S-RNase zymogram analysis (1, 2). Further, 'Turkey Heart B' and 'NY1625' were suggested by our preliminary results to be S_3S_4 and S_4S_x, respectively (4). The actual S-genotype of S_3S_5, was identified in 'Burlat' and 'Moreau' which were previously wrongly reported as Group 'VII' (S_4S_5).

The Group 'VIII' (S_2S_5) included the cultivars, 'Peggy Rivers,' 'Schmidt' and 'Büttners Späte Röte Knorpelkirsche' (10). However, 'Peggy Rivers' was suggested to be S_2S_4 (2) and confirmed to be S_2S_4 (1, 13). Also, the S-genotype of 'Schmidt' as well as 'Royalton,' 'Sam' and 'Vic' were suggested to all be S_2S_4 (4). Further, 'Büttners Späte Röte Knorpelkirsche' is S_3S_4 and may not belong to Group 'VIII' (4). This result with 'Büttners Späte Röte Knorpelkirsche' was also supported by current results of controlled pollination tests which showed compatibility with 'Schmidt' and incompatibility with several cultivars that carry S_3S_4. Furthermore, Way (18) concluded that 'Büttners Späte Röte Knorpelkirsche' and ' Emperor Francis' possibly are the same clone based on the fruit and tree characteristics, which appeared to be indistinguishable in the clones he evaluated th Geneva, NY.

'Vic' and 'Ulster' were first assigned to the Group XIII (S_2S_4) (10). However, Way (18) concluded that 'Vic' should have been assigned to Group 'O.' A controlled pollination test and PCR based S-allele genotyping analysis confirmed 'Ulster' to be S_3S_4 and 'Vic' to be S_2S_4 (4). Further supporting data comes from the parentage of 'Ulster,' which reportedly is a result of the cross 'Schmidt' (S_3S_4) X 'Lambert' (S_3S_4) (Brooks and Olmo, 1997). If 'Schmidt' is S_2S_5, 'Ulster' could not be S_3S_4; but if 'Schmidt' is S_2S_4, as we report, then 'Ulster' could have received S_4 from 'Schmidt.'

Cultivars previously known as 'Universal donor cultivars': 'Hedelfingen,' 'Nadino,' 'Noir de Guben,' 'Seneca,' and 'Valera' (10, 11, 15), were shown by our 1/2 diallele controlled pollination test to consist of two sub-divided groups: i) 'Hedelfinger' and 'Nadino' and ii) 'Noir de Guben,' 'Seneca' and 'Valera.' The S-genotypes of 'Hedelfinger' and 'Nadino' are suggested to be S_3S_x; Noir de Guben,' 'Seneca' and 'Valera' are suggested to be S_1S_x by DNA analysis (unpublished).

Twenty-six sweet cherry cultivars are arranged vertically and horizontally in the same order as by bloom time (Figure 1). Cross compatibility is presented based on our controlled pollination and PCR based S-allele genotyping analyses.

Acknowledgments

We acknowledge Jay Freer for his assistance on pollination test crosses and aid during all aspects of the research.

Literature Cited

1. Boskovic, R., K. Russell and K. R. Tobutt. 1997. Inheritance of stylar ribonucleases in cherry progenies, and reassignment of incompatibility alleles to two incompatibility groups. Euphytica 95:221-228.
2. Boskovic, R. and K. R. Tobutt. 1996. Correlation of stylar ribonuclease zymograms with incompatibility alleles in sweet cherry. Euphytica 90:254-260.
3. Brown, A. G. 1955. Incompatibility. John Innes Inst. Annu. Rpt. for 1954. pp. 7-8.

4. Choi, C. 1999. On the genetics of self-incompatibility in sweet cherry: Identification of S-genotypes; genetical and physiological effects on self-fertility and breakdown of self-incompatibility. Ph.D Thesis. Cornell University.
5. Crane, M. B. and A. G. Brown. 1937. Incompatibility and sterility in the sweet cherry, *Prunus avium* L. J. Pomol. Hort. Sci. 15:86-116.
6. Crane, M. B. and W. J. C. Lawrence. 1929. Genetical and cytological aspects of incompatibility and sterility in cultivated fruits. J. Pomol. Hort. Sci. 7:276-301.
7. Gardener, V. R. 1946. The cherry and its culture. New York, Orange Judd Publishing Company, Inc.
8. Guerrero-Prieto, V. M., M. D. Vasilakakis and P. B. Lombard. 1989. Factors controlling fruit set of 'Napoleon' sweet cherry in western Oregon. HortScience 29:913-914.
10. Knight, R. L. 1969. Abstract Bibliography of Fruit breeding and Genetics to 1965, *Prunus*. Commonwealth Agricultural Bureaus. pp. 540-544.
11. Schmidt, H. and E. D. Timmann. 1997. On the genetics of incompatibility in sweet cherries 1. Identification of S alleles in self-incompatible cultivars. Gartenbauwissenschaft 62: 102-105.
12. Stosser, R. and S. F. Anvari. 1983. Pollen tube growth and fruit set as influenced by senescence of stigma, style and ovules. Acta Horticulturae 139:13-22.
13. Tao, R., H. Yamane, A. Sugiura, H. Murayama, H. Sassa and H. Mori. 1999. Molecular typing of S-alleles through identification, characterization and cDNA cloning for S-RNases in sweet cherry. J. Amer. Soc. Hort. Sci. 124:224-233.
14. Tehrani, G. and S. K. Brown. 1992. Pollen-incompatibility and self-fertility in sweet cherry. Plant Breeding Reviews 9:367-388.
15. Tehrani, G. and W. Lay. 1991. Verification through pollen incompatibility studies of pedigrees of sweet cherry cultivars from Vineland. HortScience 26:190-191.
16. Thompson, M. 1996. Flowering, pollination and fruit set, pp. 223-241. In: A. D. Webster and N. E. Looney (eds.). Cherries: Crop physiology, production and uses. Cab International, UK.
17. Toyama, T. 1980. The pollen receptivity period and its relation to fruit setting in stone fruits. Fruit Varieties Journal 34:2-4.
18. Way, R. D. 1968. Pollen incompatibility groups of sweet cherry clones. Proc. Am. Soc. Hort. Sci. 92:119-123.

Grape Root Development

Recovery of gas exchange of half dried grapevines occurred without any further change in soil water content of the dried half of the root system, and coincided with the point at which there was no further decrease in soil water content. For half dried plants, there was a relative increase in root development in moist soil layers, both in the wet container as a whole or in the lower part of the dry container. Recovery of gas exchange of half dried plants occurred at the time when there were no more roots dried in the dry container. Authors propose for half-dried plants, the part of the root system in dry soil can survive because water moves from wet roots to dry roots. From Dry et al. 2000. Vitis 39(1):9-12.

Grape–Conventional vs Minimal Pruning

Minimal pruned (MP) vines showed higher shoot numbers, reduced leaf and shoot size, higher cluster number, smaller berries, fewer berries/cluster than hand pruned (HP) vines. MP vines had 4-6 fold higher CO_2 fixation than HP vines from 3 weeks after bud break until bloom. Pn recovered in the HP vines concurrently with the transition to a faster shoot growth although Pn was still 13% higher in MP vines. Berry sugar was not lower in MP compared to HP despite a 70% yield increase. From Poni et al. 2000. Vitis 39(1):13-18.