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A MULTIVARIATE ANALYSIS OF A SOUR CHERRY GERMPLASM COLLECTION

By

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A THESIS

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ABSTRACT

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Morphological traits of 16 sour cherry (Prunus cerasus L.) cultivars, and of hybrid and open-pollinated seedlings of germplasm collected in eastern Europe were evaluated with principal component (PC) and cluster analysis. Due to the character loadings of the first three PCs in each analysis, some of the PCs can be interpreted as representing gradations between morphologies characteristic of the two presumed progenitor species, sweet cherry (P. avium L.) and ground cherry (P. fruticosa Pall.). Genetically related cultivars and families tend to cluster, indicating that there is a significant genetic component to the underlying patterns of morphological variation. Families of cold-hardy Russian cultivars generally show a greater morphological resemblence to ground cherry than do families of less cold-hardy cultivars, suggesting that selective forces may also have contributed to the patterns of morphological variation detected.

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INTRODUCTION

Sour cherry (<u>Prunus cerasus</u> L.) has been cultivated in its native habitats of Europe and the Soviet Union for many centuries. In these areas, sour cherry trees are still planted along rural roadways and in home gardens; although, large orchards now account for most of the sour cherry production. The Soviet Union is the world leader in sour cherry production, followed by the United States, West Germany, Yugoslavia, and Hungary.

In the U.S., sour cherries, which have been grown since colonial times, may have been introduced by French settlers. It is only in this century that large commercial plantings have been made, which is attributed to the development of the canning and freezing industries, as well as mechanical harvesters. In the U.S., fresh market demand for sour cherries is very limited, although the fresh fruit are popular in Europe. The primary production sites in the U.S. are along the shores of the Great Lakes in Michigan, New York, and Wisconsin, where spring temperatures are moderated by the large bodies of water.

Nearly the entire U.S. acreage is planted to a single cultivar, Montmorency, that originated in France some 400 years ago (Hedrick, 1915). Although

'Montmorency' is a profitable cultivar for growers, it is not without its shortcomings. These deficiencies include a low percentage of fruit set, susceptibility of the flower buds to spring frosts, much non-bearing wood, and susceptibility to several diseases. Additionally, this monoculture is vulnerable to new strains of disease organisms. New cultivars available to growers could potentially alleviate many of the problems growers encounter with 'Montmorency', thereby increasing grower profits. Other advantages offered by new cultivars would be an ability to extend both the harvest season and the range of environments under which the trees could be profitably grown.

To date, breeding efforts in the U.S. have produced just a few new commercial cultivars, such as Meteor and North Star, which are of primary interest to backyard gardeners. The recently initiated sour cherry breeding program at Michigan State University has cultivar development as the ultimate goal. The initial objectives of this program have been to acquire and characterize a diversity of germplasm from eastern Europe and the Soviet Union, where well established breeding programs have produced several valuable cultivars. Because a lengthy quarantine period is required for clonal material brought into the U.S., the sour cherry germplasm collection at Michigan State University consists primarily of hybrid

and open-pollinated (o.p.) seedlings.

An understanding of morphological variation in sour cherry is critical to cultivar development, future germplasm collection, and eventual setting of priorities for germplasm maintenance. The purpose of the research reported herein was to employ techniques of multivariate analysis to characterize relationships in morphological variability in the sour cherry germplasm collection at Michigan State University.

LITERATURE REVIEW

Geneaology

Sour cherry (<u>Prunus cerasus</u> L.) has 32 chromosomes (2n=4x=32). Working independently, Kobel (1927),

Darlington (1927, 1928), and Okabe (1928) concluded that the species is most likely an allotetraploid, with sweet cherry (<u>Prunus avium L.</u>), (2n=2x=16) as one of the progenitor species. Kobel (1927) suggested ground cherry (<u>P. fruticosa Pallas</u>), (2n=4x=32) or bush cherry (<u>P. frutescens Schneid.</u>) = (<u>P. humilis Bunge.</u>) (Bailey, et al., 1976), as the most likely candidates for the other progenitor species. Darlington (1928) speculated that <u>P. cerasus</u> may have resulted from hybridization between <u>P. avium</u> and <u>P. fruticosa</u> in the Caucasian region.

Since 1936, more detailed cytological studies of meiosis in sour cherry and related hybrids have been conducted (Prywer, 1936; Hruby, 1939, 1950, 1962; Raptopoulos, 1941; Blasse, 1957; Barg, 1958). Only Raptopoulos (1941) contends that sour cherry is an autotetraploid, which he believes may have arisen through spontaneous chromosome doubling of a diploid ancestor of sweet cherry.

Hruby (1939, 1950, 1962) performed the most extensive

cytological investigations by examining numerous pollen mother cells of various specimens of sour cherry, both triploid and tetraploid Duke cherry (sour cherry x sweet cherry, or vice versa), and backcrosses of tetraploid Duke cherry with both sweet cherry and sour cherry. For sour cherry, Hruby found that the mean numbers of univalents, bivalents, trivalents, and quadrivalents were 1.33, 14.75, 0.13, and 0.19 respectively, and for tetraploid Duke cherry, the respective means were 0.27, 3.77, 0.07, and 5.99. Hruby (1950, 1962) reached a similar conclusion regarding the origin of sour cherry as did Kobel (1927) and Prywer (1936) in their own investigations; i.e., that sour cherry is most likely an amphidiploid resulting from hybridization between two related diploid species, followed by spontaneous chromosome doubling. However, Hruby contends that neither sweet cherry nor ground cherry in their present forms were the progenitor species of sour cherry. Rather, Hruby hypothesized that sweet cherry arose through hybridization between two ancient diploid species with similar genomes. Sour cherry, Hruby suggests, may have arisen through hybridization between one of the progenitor species of sweet cherry and a third ancient diploid species (possibly an ancestor of ground cherry), followed by spontaneous chromosome doubling.

Taking a different approach in investigating the origin of sour cherry, Oldén and Nybom (1968) "resynthesized" sour cherry by hybridizing ground cherry with

autotetraploid wild sweet cherry. Morphological comparisons were made between naturally occurring sour cherry, diploid and autotetraploid sweet cherry, and the hybrids. Chemotaxonomic analyses of various phenolic, flavonoid, and anthocyanin compounds contained in the leaves and fruits were performed by means of thin-layer chromatography. The "biochemical distances" between the various species and interspecific hybrids were then calculated. The authors established that the tetraploid hybrids (ground cherry x autotetraploid sweet cherry) and naturally occurring sour cherry are intermediate both morphologically and chemotaxonomically to sweet cherry and ground cherry. These data support the theory that sweet cherry and ground cherry are the progenitors of sour cherry.

Sour cherry is believed to have arisen in the Near East center of origin, which includes Asia Minor, Transcaucasia, Iran, and the highlands of Turkmenistan (Vavilov, 1951), and perhaps as far west as Switzerland and the Adriatic Sea (Hedrick, 1915). In these regions the ranges of the ancestral forms of sweet cherry and ground cherry are thought to have overlapped. Cultivated forms of sour cherry were spread throughout the Roman Empire, extending the western range to England.

Sour cherry grows wild in a diversity of habitats in Scandanavia, across Europe, and into the western Soviet Union. The range is primarily limited by low winter

temperatures in northern latitudes, and by summer heat in southern regions. A great deal of genetic variation is found in eastern Europe and the western regions of the Soviet Union. There, a number of unique landraces have arisen through both natural selection and the regional preferences of peasants, who for several centuries have grown seeds or clones propagated from the best wild germplasm in their localities. Breeders in eastern Europe have gathered many of the best local cultivars from the various landraces, resulting in a diverse collection of elite germplasm.

Most of the work regarding genetic variation in sour cherry has focused on established cultivars, rather than on wild germplasm. Nevertheless, these cultivars exhibit a wide range of genetic diversity for such traits as spring floral bud development (Iezzoni and Hamilton, 1985), growth habit (Stancevic, Janda, and Gavrilovic, 1976), fertility (Redalen, 1984), disease resistance (Enikeev, 1975), cold-hardiness (Kolesnikova, 1975), drought resistance (Khalin, 1977), and ripening date (Gozob, Bodi, and Ivan, 1978). Additionally, Hedrick (1915), Michurin (1949), and others have made qualitative descriptions of morphological traits of various cultivars. French (1943) described and illustrated many taxonomic traits which can aid in the field identification of various sweet cherry and sour cherry cultivars.

Yushev (1975, 1977) focused on the morphological traits of the fruits and leaves of a wide range of cultivars. He examined 119 sour cherry and Duke cherry cultivars in the Soviet Union, after initially dividing the cultivars into two groups: eastern and western European. The eastern European cultivars were subdivided into northern, central, and southern zones of origin. Compared to the fruits of the eastern European cultivars, the fruits of the western cultivars generally had lighter colored juice and larger pits. Of the western European cultivars, 71.4% had long (>50 mm) leaves. Obovate form, large glandules, coarse serrations, and pubescence were typical of the leaves of the western group. The eastern European cultivars, the majority (56.5%) of which had medium sized (30 to 50 mm), typically ovate leaves, exhibited a greater diversity in leaf morphology than the western European group. Considering the traits examined, Yushev concluded that the eastern European cultivars from the southern zone more closely resembled sweet cherry and the western European cultivars than did those eastern European cultivars from the central and northern zones. Yushev suggests that the resemblence of the leaves and fruit of eastern and western European cultivars to those of ground cherry and sweet cherry, respectively, may indicate the relative importance of these two presumed progenitor species in the origins of the eastern and western groups.

Applications of Multivariate Analysis

Although both principal component and cluster analysis are especially useful tools of research in social sciences, these methodologies are also applicable to botanical and plant breeding research. Several books regarding applications of multivariate analysis to botanical research have been published (Blackith and Reyment, 1971; Sneath and Sokal, 1973; Orlaci, 1978). Additionally, Crovello (1970) reviewed numerous publications concerning the analysis of character variation in systematics and ecology.

Brief descriptions of the techniques of principal component (PC) and cluster analysis are as follows. Multivariate observations consisting of sets of quantitative measurements of a number (n) of traits can be represented by the positions they occupy in n-dimensional space (hyperspace). Such a scatter diagram is composed of individual orthogonal axes for each trait on which the standardized values of the traits for each observation are plotted. The relative magnitudes of the Euclidean distances between the points in hyperspace will indicate the similarity between corresponding observations. If some of the traits are linearly correlated (and assuming they are normally distributed), then the cluster of points in hyperspace will resemble an n-dimensional ellipsoidal Through PC analysis, the major axis (PC1) and subsequent orthogonal axes (PC2, PC3, ..., PCn) of this

ellipsoid are found. The first PC (PC1) will account for the maximum variance among all character values that can be attributed to a single axis, i.e., it represents the major axis of the ellipsoid. Each succeeding PC will account for a progressively smaller percentage of the remaining variance. Each PC is defined by a linear combination of the original character scores. combinations are the eigenvectors of the PCs. percentage of the total variance accounted for by each PC is obtained from the eigenvalues. A scatter diagram of the PC scores of the observations on all of the PC axes will retain the same relative distances between observations as the original (untransformed) plot. However, the first two or three PCs often account for a major portion of the variance for most traits. Thus, PC analysis simplifies the original n-dimensional scatter plot by enabling the observations to be plotted on a reduced number of orthogonal axes while minimizing the loss of information. A scatter diagram of the PC scores of the original observations on these few axes provides a visually discernible indication of the similarities among observations (Adams, 1977).

Cluster analysis is sometimes used in conjunction with principal component analysis to provide additional insight into the relationships among observations.

Through this technique, a group of observations is partitioned into homogeneous clusters, based on a measure of

similarity between each observation or group of observations and each other observation or group. The resulting classification is often represented as a dendrogram, that depicts the similarity among observations in a hierarchical fashion. In contrast to PC analysis, cluster analysis does not control all types of correlations between traits (Small, 1979).

The method of PC analysis has been modified to calculate "genetic distance", which is a measure of the geometrical (Euclidean) distance between genotypes represented as points in PC space (Adams and Wiersma, 1978). Adams (1977) applied this method to the study of cultivars of dry bean (Phaseolus vulgaris L.), and found that the "genetic distances" between cultivars, based upon chemical and agronomic traits, were highly inversely correlated to estimates of genetic relationships based upon breeding pedigrees.

Both PC and cluster analysis have been used to relate character variation within a species to area of origin (Morishima, 1969; Rhodes, 1971; Hussaini, Goodman, and Timothy, 1977; Isleib and Wynne, 1983). Martin (1984) performed a PC analysis of morphological and phenological traits of dry bean (Phaseolus vulgaris). He examined the population structure and genetic diversity among 25 inbred lines grown from seeds collected at each of 15 sites in northern Malawi. A combined analysis of the data from the various sites revealed a north-south clinal pattern, which

Martin hypothesized may be a result of environmental adaptation or agricultural practices. Within sites (each with its own landrace), PC analysis provided evidence that genetic variability is being maintained as a result of low levels of natural outcrossing between lines of this normally inbreeding species.

In another study, Murphy, Cox, and Rodgers (1986) used the pairwise coefficients of parentage between 110 red winter wheat (<u>Triticum aestivum L.</u>) cultivars as input in a cluster analysis. The cultivars were found to cluster by class (soft vs hard), and by the geographical origin of the predominant parents within classes.

Carter, Cech, and DeHayes (1983) performed a cluster analysis on leaf traits of black cherry (Prunus serotina Ehrh. subsp. serotina) trees, that are grown for lumber. These trees, that were raised from seed collected throughout the eastern United States, were examined to determine whether patterns of variation in leaf morphology could be interpreted with respect to geographic origin. The primary split of the dendrogram separated trees of southern origin from those from northern and central regions. The authors suggest that gene flow from subspecies hirsuta may account for the morphological differences in the southern specimens.

In addition to uncovering underlying patterns of genetic diversity within a species, PC and cluster

analyses have been used to study species overlap to help explain evolutionary questions (Heiser, Soria, and Burton, 1965; Prance, Rogers, and White, 1969; Bemis, Rhodes, Whitaker, and Carmer, 1970; Small, Jui, and Lefkovitch, 1976). For example, Jensen and Eshbaugh (1976) examined the phenetic relationships between individual oak trees (Quercus) within different populations by means of PC and cluster analysis. The authors concluded that both forms of analysis are useful in identifying specimens of hybrid origin and their putative parental species, particularly in populations with narrow areal distributions and low taxonomic diversity.

Yet another use of multivariate analysis has been to relate ecotypes and species habitats to specific environmental variables (Nevo, Zohary, Brown, and Haber, 1979).

Jensen and Hancock (1982) evaluated three species of strawberry (Fragaria) from several populations collected from a diversity of environments. PC and cluster analyses were used to detect patterns among individual plants, while discriminant analysis was used to examine relationships among populations and communities. Discriminant analysis provided a highly accurate differentiation of populations at the species level. Within each species, discriminant analysis indicated that combinations of morphological traits have evolved which are associated with the various community environments.

MATERIALS AND METHODS

Plant Material

Sixteen cultivars, planted in a completely randomized pattern at the Clarksville Horticultural Experiment
Station, Clarksville, Mich., were evaluated (Table 1).
The trees, propagated on mahaleb rootstock (P. mahaleb L.)
and trained to a modified central leader system, were nine
years old in 1985.

Pollen was collected in Spring 1983 from the following locations in eastern Europe: Fruit Research Institute, Cacak, Yugoslavia; Fruit Growing Research Institute, Plovdiv, Bulgaria; Research Institute for Pomology, Pitesti, Romania; Enterprise in Extension in Fruit Growing and Ornamentals, Budapest, Hungary; and Research Institute of Pomology, Skierniewice, Poland. The pollen was brought back to Michigan and used in crosses with the sour cherry cultivars English Morello, Rheinische Schattenmorelle, Wolynska, and Montmorency, generating four half-sib families (Tables 2, 3, 4, and 5). Openpollinated (o.p.) seeds were collected in Hungary and Romania in 1984 (Table 6). The resulting seedlings were planted in a completely randomized pattern, also at the Clarksville Station, and were two years old when evaluated.

Table 1. Number of clones evaluated, with names and abbreviations of 16 sour cherry cultivars.

| Cultivar | Abbreviation | Number clones evaluated |
|----------------------------|--------------|-------------------------------|
| Bartozek | Bt | 3 |
| Coronation | Cn | 2 |
| English Morello | EM | 3 |
| Fruchtbare von Michurin | FM | 2 |
| George Glass | GG | 1 |
| Griotte du Pays | GP | 1 |
| Montearly | Me | 4 |
| Meteor | Mr | 3 |
| Montmorency | Mt | 4 |
| Nefris | Nf | 1 |
| North Star | NS | 2 |
| Ostheim | Os | 4 |
| Suda Hardy | sн | 2 |
| Ukrainische Griotte | UG | 2 |
| Vladimirskaya | V1 | 2 |
| Wolynska | Wl | 4 |

Table 2. Number of progenies evaluated in the 'English Morello' half-sib family, with names and abbreviations of the paternal parents.

| Paternal parent | Abbreviation | Number progenies evaluated |
|--------------------|--------------|----------------------------------|
| Érdi Bötermö | EB | 35 |
| English Morello | EM | 28 |
| Galaxy | Gl | 11 |
| M 71 | Н1 | 8 |
| M 172 | Н2 | 7 |
| Hungarian Meteor | нм | 71 |
| Karessova | Kr | 15 |
| Meteor Korai | MK | 6 |
| Meteor | Mr | 43 |
| Nefris | Nf | 5 |
| North Star | NS | 26 |
| Oblacinska | Ob | 33 |
| Н 18/21 | R1 | 5 |
| Rexelle | Rx | 8 |
| Šumadinka | Su | 49 |

Table 3. Number of progenies evaluated in the 'Rheinische Schattenmorelle' half-sib family, with names and abbreviations of the paternal parents.

| Paternal parent | Abbreviation | Number progenies evaluated |
|-----------------|--------------|----------------------------------|
| Crisana 1/8 | Cr | 18 |
| Érdi Bötermö | EB | 32 |
| M 112 | нз | 56 |
| Mocanesti 16 | Мо | 16 |
| Šumadinka | Su | 7 |

Table 4. Number of progenies evaluated in the 'Wolynska' half-sib family, with names and abbreviations of the paternal parents.

| Paternal parent | Abbreviation | Number progenies evaluated |
|-----------------|--------------|----------------------------------|
| M 172 | Н2 | 13 |
| Kelleris 16 | Kl | 13 |
| Oblacinska | Ob | 16 |
| Šumadinka | Su | 46 |
| Umbra | Um | 6 |

Table 5. Number of progenies evaluated in the 'Montmorency' half-sib family, with names and abbreviations of the paternal parents.

| Paternal parent | Abbreviation | Number progenies evaluated |
|------------------------|--------------|----------------------------------|
| Amnestic Visin | AV | 8 |
| M 63 | H4 | 18 |
| Meteor Korai | MK | 15 |
| Nefris | Nf | 9 |
| H 18/21 | R1 | 22 |
| Н 17/39 | R2 | 7 |
| Tschatschakov Rubin | TR | 6 |

Table 6. Number of progenies evaluated in the open-pollinated families, with names and abbreviations of the maternal parents.

| Maternal parent | Abbreviation | Number progenies evaluated |
|-------------------------------|--------------|----------------------------------|
| Csengödi Csokras | s CC | 23 |
| Cigány Meggy | CM | 30 |
| D076 | DO | 10 |
| Dobraya | Db | 15 |
| Érdi Jubileum | EJ | 17 |
| Kántorjánosi | Kn | 8 |
| Korai Pipacs Meggy (M 152) | KP | 25 |
| Lyubskaya | Lb | 30 |
| Montmorency | Mt | 30 |
| Nefris | Nf | 30 |
| Pitic de Iasi | PI | 23 |
| Pándy 114 | Pn | 26 |
| Rheinische Schattenmorelle | RS | 5 |
| Stark Montmoreno | cy sm | 30 |
| Wolynska | Wl | 30 |

Table 7 lists the known pedigrees and putative origins of the cultivars and of the parents of the seedlings that were examined in this study.

Characters Measured

Representative samples of flowers, fruits, and leaves were collected from the nine year old cultivars for evaluation and analysis in 1985. Because of their juvenile state, only leaf samples were collected from the seedlings. Quantitative measurements were made of various traits of the collected samples to enable numerical analysis of the data.

The average value for each trait (averaged over both samples and replicates) is termed the "family (or cultivar) mean". The term "half-sib family" refers to all full-sib families with a common (maternal) parent. The terms "character" and "trait" are used interchangeably. Examples of traits are leaf length, and vein angle. A "character value" refers to an actual quantitative measurement, or an average of such measurements. Examples of character values are a leaf length of 80 millimeters, and a vein angle with a family mean of 59 degrees. A "character state" indicates a qualitative distinction in character values. Examples of character states are long (vs short) leaves, and wide (vs narrow) vein angles.

In 1985, the cultivars and the 'English Morello', 'Rheinische Schattenmorelle', and 'Wolynska' half-sib

Table 7. Pedigrees of cultivars and of parents of seedlings evaluated in the sour cherry germplasm collection.

| Cultivar | Pedigree | Comments | References ¹ |
|----------------------------|-------------------------------------|--|-------------------------|
| Amnestic Visin | unknown | Romanian cultivar | 7 |
| Bartozek | unknown | | |
| Cigány Meggy | | Hungarian landrace | 7, 14 |
| Coronation | o.p. seedling of Shubianka (sic) | Canadian cultivar. Shubinka is an old Russian cultivar | 3, 8 |
| Crisana 1/8 | | Romanian clonal selection of the Crisana landrace | 2, 7, 12 |
| Csengödi Csokras | unknown | Hungarian cultivar | 7 |
| D076 | | Hungarian clonal selection of the Pándy landrace (see Pándy) | 7 |
| Dobraya | Vladimirskaya x Lyubskaya | Russian cultivar | 8 |
| English Morello | unknown | an old cultivar, presumably German | 6 |
| Érdi Bötermö Pa | ándy 38 x Nagy Angol | Hungarian cultivar | 1, 13, 14 |
| Érdi Jubileum | Pándy 38 x Eugenia | Hungarian cultivar. Eugenia is presumably a Duke. | 1, 2, 13 |
| Fruchtbare von Michurin | uncertain | presumably Russian, probably the same as Plodorodnaya Michurina (see Pitic de Iasi) | 2, 10 |
| Galaxy (HTO 405) | unknown (see Montmorency) | an irradiated clone of Montmorency | 7 |
| George Glass | unknown | presumably from norther Germany, possibly a Duke x sour cherry | n 6 |

Table 7 (cont'd.).

| Cultivar | Pedigree | Comments | References ¹ |
|-------------------------------------|---|--|-------------------------|
| Griotte du Pays | unknown | | |
| Н 17/39 | Vladimirskaya x Polevka | Romanian hybrid. Polevka is an o.p. progeny of Ideal. Ideal is ground cherry (Stepnaya Dikaya) x P. pennsylvanica. | 2, 4, 10, 11 |
| Н 18/21 | English Timpurii x Visin Tufa | Romanian hybrid. English Timpurii is presumably a Duke | 4, 12 |
| Hungarian Meteor | unknown | Hungarian cultivar | 7 |
| Kántorjánosi | | Hungarian clonal selection of the Pándy landrace (see Pándy) | 7 |
| Karessova | | clonal selection of the Pándy landrace, poller obtained from Bulgaria | า |
| Kelleris 16 (Morellen- feuer) | (Ostheim x Früheste der Mark) o.p. (paternal parent is possibly Reine Hortense) | Danish cultivar. Früheste der Mark is a sweet cherry. Reine Hortense is a Duke. (see Ostheim) | 3, 6, 12 |
| Korai Pipacs Meggy (M 152) | Pándy x Császár | Hungarian cultivar. | 1 |
| Lyubskaya | unknown | old Russian cultivar | 8 |
| M 63 | Pándy x Nagy Gobet | Hungarian hybrid. Nagy Gobet is also called Gros Gobet. | 2, 7 |
| M 71 | unknown | Hungarian | 7 |
| M 112 | unknown | Hungarian | 7 |
| M 172 | unknown | Hungarian | 7 |

Table 7 (cont'd.).

| Cultivar | Pedigree | Comments | References ¹ |
|---------------|---|---|-------------------------|
| Meteor | Montmorency x a Russia seedling tracing back two or more generations to Vladimirskaya and Shubianka (sic) | USA cultivar | 3 |
| Meteor Korai | Pándy 29 x Nagy Angol | Hungarian cultivar | 1, 13 |
| Mocanesti 16 | | Romanian clonal selection of the Mocanesti landrace | 2, 7, 12 |
| Montmorency | unknown (possibly a progeny of Cerise Hâtive or Cerise Commune) | old French cultivar | 6 |
| Montearly | unknown | USA cultivar | 3 |
| Nefris | unknown | presumably Polish | 7, 12, 14 |
| North Star | English Morello x Serbian Pie No.1 | USA cultivar. Serbian Pie No.1 is from seed obtained in Yugoslavia | 3 |
| Oblacinska | ******** | Carpathian landrace, mostly in Yugoslavia | 7, 12, 14 |
| Ostheim | unknown | old Spanish cultivar | 6, 8, 10 |
| Pándy 114 | | Hungarian clonal selection of the Pándy landrace. Pándy is the Hungarian name for Crisana | 2, 7, 12 |
| Pitic de Iasi | o.p. seedling of Plodorodnaya Michurina | Moldavian cultivar. Plodorodnaya Michurina is ground cherry x sour cherry (Stepnaya Samarskaya x Michurina Karlikovaya) | · |
| Rexelle | unknown | Danish cultivar | 14 |

Table 7 (cont'd.).

| Cultivar | Pedigree | Comments I | References |
|-------------------------------|---|--|-----------------|
| Rheinische Schattermorelle | unknown | an old cultivar, presumably German or Dutch, sometimes equated to English Morello, Lyubsky, or Lyubskaya | 8, 9, 12, 14 |
| Stark Montmorency | unknown (see Montmorency) | a USA clonal selection of Montmorency | 6 |
| Suda Hardy | unknown (possibly a progeny of English Morello) | USA cultivar | 6 |
| Šumadinka | maternal parent is Fanal | Yugoslavian cultivar. Fanal (syn. Heimann's Conserve) is very similar to Nefris | 7 |
| Tschatschakov Rubin | 'Hungarian' x Schattenmorelle | (syn. Yugoslavian Cacak), pollen obtained from Bulgaria | 14 |
| Ukrainische Griotte | unknown | presumably Russian | 15 |
| Umbra | unknown | | |
| Vladimirskaya | | old Russian landrace | 6, 8 |
| Wolynska | unknown | Polish cultivar | 5, 7 |

¹Numerical code for references:

Apostol, J. (pers. commun. to A. Iezzoni)
 Bordeianu, et al., 1965
 Brooks and Olmo, 1972
 Cociu and Gozob, 1985
 Dzieciol, et al., 1983
 Hedrick, 1915
 Iezzoni, A. (pers. commun.)
 Kramer, 1985
 Michurin, 1949
 Michurin, 1955
 Parnia, et al., 1985
 Vasilov, et al., 1982
 Yushev, 1975

families were evaluated. In 1986, the 'Montmorency' half-sib family and the o.p. families were evaluated. Seventeen seedlings evaluated in 1985 were randomly selected for re-evaluation in 1986. An analysis of variance indicated significant variation between years for most traits, so data between years were not combined.

Thirteen flower and fruit characters and seven leaf characters were measured for the 16 cultivars (Table 8). The seedlings, which had not yet flowered, were only evaluated for vegetative characters (Table 8). Samples were collected row by row to randomize the error introduced by sampling over time.

Flower and fruit traits of the cultivars were evaluated as follows. Ten mature fruit were randomly collected from each tree. Five of these cherries (which had their pedicels removed) were oven dried, and weighed. The remaining five fruit were measured for the following traits: pedicel length, measured from the "skirt" to the abcission zone; fruit and pit length and width, measured at their largest dimensions; pit weight, measured after oven drying; and flesh color, which was visually rated on a qualitative scale of 0 to 9, with 0=clear and 9=dark red. Fruit dry weight without pits was calculated by subtracting the mean dry weight of the five pit samples from the mean dry weight of the fruits. The length:width ratios of both fruits and pits were calculated. The pit:fruit dry

Table 8. Character codes and units for characters and character ratios employed in numerical analyses.

| Code | Character | Cultivars | Seedlings |
|--------------|-------------------------------|-----------|-----------|
| Flowe | er and Fruit Characters | | |
| F1 | Stigma length (mm) | x | |
| F2 | Pedicel length (mm) | x | |
| F3 | Fruit length (mm) | x | |
| F4 | Fruit width (mm) | x | |
| F5 | Fruit length/width | x | |
| F6 | Fruit dry weight w/o pit (g) | x | |
| F7 | Fruit flesh color | x | |
| | (0=light, to 9=dark red) | | |
| F8 | Pit length (mm) | x | |
| F9 | Pit width (mm) | x | |
| F10 | Pit length/width | x | |
| F11 | | x | |
| F12 | | x | |
| F13 | Pit/fruit dry weight | × | |
| <u>Veget</u> | ative Characters | | |
| V1 | Internode length (mm) | | × |
| V2 | Petiole length (mm) | x | x |
| V3 | Petiole width (mm) | | x |
| V4 | Petiole width/length | | x |
| V5 | Petiole glands | | x |
| V6 | Leaf length (mm) | x | x |
| V7 | Leaf width (mm) | x | x |
| V8 | Leaf thickness (mm) | | x |
| V9 | Leaf width/length | x | x |
| V10 | , , | x | x |
| V11 | | | x |
| V12 | | x | x |
| V13 | Serrations per centimeter | x | x |
| V14 | Pubescence (0=max. of three | | x |
| | trichomes, to 4=many trichome | es) | |

weight ratios were calculated using the means of the dry pit weights and dry fruit weights (with pit weight subtracted out). Both the pit:fruit length and weight ratios were also included in the analysis.

Vegetative traits of the cultivars and seedlings were evaluated following terminal bud set in July. Internode length was measured in the mid-shoot portion of five randomly selected shoots of the current year's growth. Five random leaf samples per tree, also collected from the midshoot portion of the current year's growth, were evaluated for all other traits. Leaf samples were placed in plastic bags, packed in ice, and evaluated in the laboratory. Leaf blade length was measured from the apex to the point of attachment to the petiole, while the distance from this point to the abcission zone was recorded as the petiole length. Leaf blade and petiole widths were measured at their mid-lengths. Leaf blade thickness was measured with a micrometer in an area relatively free of secondary veins. Both the number of petiole glands and swollen glands on the basal leaf edge (near the point of petiole attachment) were counted with the aid of a dissecting microscope. Two types of swollen leaf glands are common. One type is usually green and often has a depression in the center, while the other type is typically smaller and darker, resembling those glands found at the tip of each serration. Although both types of gland were counted,

only the first type was used in the analysis since the second type had a very high variance, even between clones of the same cultivar. Vein angles were measured between the midvein and the secondary vein closest to the leaf blade mid-length, on a line near the point of intersection of the two veins and tangent to the secondary vein (which is often curved). The number of serrations per centimeter on the leaf edge near the mid-length of the leaf blade was counted. Pubescence on the abaxial (lower) leaf surface between the secondary veins was subjectively rated (with the aid of a dissecting microscope) on a qualitative scale of 0 to 4, with 0=a maximum of three trichomes per leaf, and 4=very pubescent. The width: length ratios of both the leaves and petioles, as well as the petiole:leaf length ratio, were calculated.

Data Analysis

Principal component analysis was performed using the PRINCOMP procedure of the SAS statistical package (SAS Institute, 1985a). Family means were used to create a correlation matrix from which standardized principal component scores were extracted. Scatter plots of the first three PCs were created with SAS/GRAPH (SAS Institute, 1985b). To determine which of the first three PCs accounted for the greatest amount of variation for each trait, the eigenvectors (Tables 10, 13, and 15) of the three PCs were compared for each trait, and the trait

being considered was ascribed to the PC having the eigenvector with the largest absolute value.

Cluster analysis was performed using version 1C of the Clustan statistical package (Wishart, 1975). Separate analyses were performed on the cultivars, on each of the half-sib families, and on the set of o.p. families.

After standardizing the data means, a dissimilarity matrix of distance coefficients was created using squared Euclidean distance as the dissimilarity criterion. A fusion hierarchy was then produced using 'Ward's mimimum variance method' to optimize the error sum of squares (Ward, 1963). Dendrograms were plotted with the Plink procedure of Clustan (Wishart, 1975).

Analysis of variance followed a General Linear Models procedure capable of analyzing unbalanced designs (SAS Institute, 1985a).

Pearson's correlation coefficients were calculated between each pair of traits for the cultivars and for each of the o.p. families. The means of all samples from all replicates (clones) were used to compute the cultivar correlations, while the sample means of each replicate (progeny) were used for the o.p. families. All correlations were tested for significance at the 95% level.

Examples of the computer programs used in data analysis are presented in Appendix B.

RESULTS

A measure of the morphological similarities among cultivars or families can be inferred from the spatial proximity of the PC1, PC2, and PC3 values that characterize each cultivar or family mean in PC1-PC2-PC3 space. The values of the PC coordinates were generated by the PRINCOMP procedure of the SAS statistical package. Such a mapping of the data is given in Figures 1, 3, and 7. A computer generated cluster analysis provides another means of showing the degree of morphological similarity among observations. Dendrograms illustrating such cluster analyses are given in Figures 2, 4, 5, 6, 8, and 9. Appendix A lists the average character values obtained for each cultivar, and for each full-sib and open-pollinated family. Tables A2 and A3 also list the ranges in character values (averaged over samples) among trees within each seedling family.

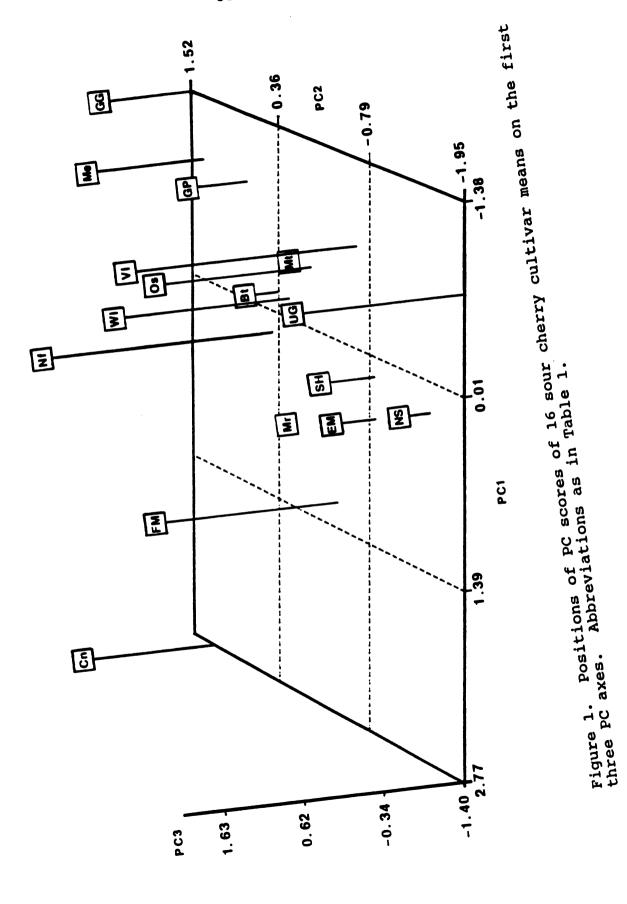
Cultivar Analysis

The first three PCs of the cultivar data account for 71% of the total variance among cultivar means; i.e., for 30%, 21%, and 20% of the variance, respectively (Table 9).

Table 9. Eigenvalues of the first seven PC axes from PC analysis of 16 sour cherry cultivars, with proportion of total variance accounted for by each axis.

| Principal Component | Eigenvalue | Proportion of variance | Cumulative variance | |
|------------------------|------------|------------------------|------------------------|--|
| 1 | 5.940 | 0.297 | 0.297 | |
| 2 | 4.267 | 0.213 | 0.510 | |
| 3 | 3.948 | 0.197 | 0.708 | |
| 4 | 2.295 | 0.115 | 0.822 | |
| 5 | 1.236 | 0.062 | 0.884 | |
| 6 | 0.691 | 0.035 | 0.919 | |
| 7 | 0.551 | 0.028 | 0.946 | |

Coronation (Cn), a cultivar with a Russian maternal parent, is an outlier (Figure 1). The other Russian cultivars, Fruchtbare von Michurin (FM), Ukrainische Griotte (UG), and Vladimirskaya (Vl), are morphologically diverse; i.e., situated at or near the extremes of both PC1 and PC2. 'George Glass' (GG), which may have a sweet cherry grandparent, groups with 'Griotte du Pays' (GP) and 'Montearly' (Me), both of unknown origin. 'Montearly's' distance from 'Montmorency' (Mt) was not unexpected, since they are not believed to be clonal variants of the same cultivar. 'North Star' (NS) groups with its maternal parent, 'English Morello', (EM) and with 'Suda Hardy' (SH), which Hedrick (1915) believed may also be a progeny of 'English Morello'. 'Meteor' (Mr), a hybrid between 'Montmorency' (Mt) and a Russian seedling, is situated with its maternal parent on both PC2 and PC3. The two Polish cultivars Wolynska (Wl) and Nefris (Nf) are



similar, as are 'Montmorency' (Mt) and 'Bartozek' (Bt).

Proceeding from negative to positive values of PC1, the cultivar means generally show an increase in the lengths and length: width ratios of both fruits and pits, as well as in fruit dry weight, while leaf length, width, and the width: length ratio tend to decrease 1. From negative to positive values of PC2, the trend is toward increasing stigma and petiole lengths, fruit width, and the petiole: leaf length ratio, while flesh color and the number of serrations per centimeter generally decrease. From negative to positive values of PC3, pit width and weight, pedicel length, and the pit: fruit length and weight ratios tend to increase, while vein angle tends to decrease.

The cluster analysis of the 16 cultivars illustrates relationships similar to those indicated by the PC analysis (Figure 2). However, the cluster analysis does suggest that 'Fruchtbare von Michurin' (FM) is more similar to the other Russian cultivars than the PC analysis indicates. Also, 'Meteor' (Mr) clusters with 'Montmorency' (Mt), its maternal parent.

There are numerous statistically significant correlations between the traits of the 16 cultivars (Table 11).

¹Summarized from the eigenvectors of the first three PCs (Table 10).

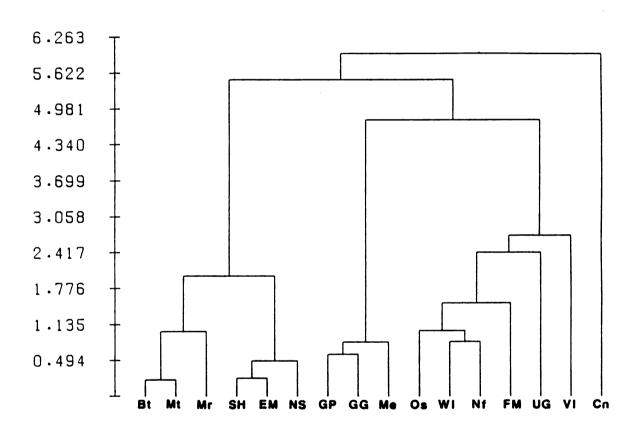


Figure 2. Dendrogram representing cluster analysis of 16 sour cherry cultivars. Abbreviations as in Table 1.

Table 10. Eigenvectors of the first seven PC axes from PC analysis of 16 sour cherry cultivars.

| Char- | Eigenvectors | | | | | | | | | | | |
|---------------|--------------|-------|-------|-------|-------|-------|-------|--|--|--|--|--|
| acter Code | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | | | | | |
| F1 | -0.21 | 0.31 | 0.17 | -0.10 | -0.11 | 0.23 | 0.42 | | | | | |
| F2 | 0.14 | -0.14 | 0.23 | -0.25 | 0.46 | -0.46 | -0.02 | | | | | |
| F3 | 0.36 | 0.20 | -0.01 | 0.15 | 0.03 | 0.14 | -0.03 | | | | | |
| F4 | 0.09 | 0.43 | -0.02 | 0.12 | -0.11 | 0.19 | -0.06 | | | | | |
| F5 | 0.39 | 0.05 | 0.00 | 0.11 | 0.10 | 0.05 | 0.01 | | | | | |
| F6 | 0.26 | 0.20 | 0.13 | 0.25 | -0.26 | -0.35 | -0.04 | | | | | |
| F7 | 0.10 | -0.28 | 0.26 | 0.02 | -0.27 | 0.16 | 0.54 | | | | | |
| F8 | 0.37 | 0.15 | 0.12 | 0.10 | 0.03 | 0.04 | -0.02 | | | | | |
| F9 | -0.01 | 0.21 | 0.42 | 0.03 | -0.11 | -0.18 | 0.15 | | | | | |
| F10 | 0.36 | -0.02 | -0.15 | 0.12 | 0.13 | 0.26 | -0.07 | | | | | |
| F11 | 0.10 | 0.14 | 0.44 | 0.06 | 0.10 | 0.11 | -0.05 | | | | | |
| F12 | 0.17 | -0.21 | 0.33 | 0.03 | 0.15 | 0.01 | -0.23 | | | | | |
| F13 | -0.13 | -0.08 | 0.34 | -0.22 | 0.34 | 0.46 | -0.06 | | | | | |
| V2 | -0.15 | 0.38 | -0.10 | 0.02 | 0.37 | -0.03 | 0.15 | | | | | |
| V6 | -0.27 | 0.11 | 0.26 | 0.27 | 0.11 | -0.19 | -0.02 | | | | | |
| V 7 | -0.27 | 0.02 | 0.19 | 0.41 | 0.07 | -0.03 | -0.14 | | | | | |
| V9 | -0.22 | -0.10 | -0.00 | 0.45 | 0.04 | 0.30 | -0.32 | | | | | |
| V10 | -0.00 | 0.36 | -0.22 | -0.09 | 0.37 | 0.01 | 0.13 | | | | | |
| V12 | -0.08 | -0.16 | -0.19 | 0.47 | 0.24 | -0.21 | 0.38 | | | | | |
| V13 | 0.17 | -0.27 | -0.05 | 0.24 | 0.28 | 0.16 | 0.36 | | | | | |
| | | | | | | | | | | | | |

¹See Table 8 for a description of character codes.

Table 11. Pearson correlation coefficients between traits for 16 sour cherry cultivars.

| | | | | (| Charac | ter O | ode ¹ | | | | | |
|-----|----------|-----|------|-------|------------|-----------|------------------|------|-------------|-------|----------|------|
| | F2 | F3 | F4 | F5 | F6 | F7 | F8 | F9 | F10 | F11 | F12 | F13 |
| F1 | 30 | 19 | .44 | 44 | 06 | 14 | 19 | .58* | 56* | .34 | 31 | .34 |
| F2 | j | .06 | 34 | .26 | .06 | .27 | .26 | .22 | .10 | .42 | .57* | .43 |
| F3 | | | .61* | .93** | .77** | 03 | .95** | .14 | .82** | .34 | .19 | 37 |
| F4 | | | | .27 | .54* | 46 | .48 | .37 | .20 | .29 | 39 | 28 |
| F5 | | | | | .68** | .19 | .93** | .01 | .90** | .29 | .41 | 31 |
| F6 | | | | | | .13 | .79** | .46 | .42 | .51* | .20 | 44 |
| F7 | | | | | | | .17 | .21 | .07 | .33 | .60* | .28 |
| F8 | | | | | | | | .33 | .74** | .51* | .43 | 20 |
| F9 | | | | | | | | | 36 | .81** | .29 | .38 |
| F10 | | | | | | | | | | 02 | .26 | 38 |
| F11 | | | | | | | | | | | .51* | .54* |
| F12 | | | | | | | | | | | | .42 |

Table 11 (cont'd.).

| | Character Code ¹ | | | | | | | | | | |
|-----|-----------------------------|-------------|-----------|---------------|------|------------|-----|--|--|--|--|
| | V2 | V6 | V7 | V 9 | V10 | V12 | V13 | | | | |
| F1 | 1 .60* | .56* | 1 36 | I - 02 | 1 34 | 1- 321 | 60* | | | | |
| F2 | | • | • | • | 1 | 22 | • | | | | |
| | | 40 | • | • | • | 15 | | | | | |
| F4 | I | I | Ι | - | .55* | : : | | | | | |
| F5 | | 53 * | • | • | • | 06 | • | | | | |
| | • | 05 | • | • | • | 12 | • | | | | |
| F7 | 70 * * | • | • | • | • | | • | | | | |
| | · | • | 38 | • | • | 24 | | | | | |
| | 1.14 | • | • | • | • | | • | | | | |
| | 23 | • | • | • | • | | • | | | | |
| | .00 | • | • | • | • | | | | | | |
| | .00 55* | • | • | • | • | : : | | | | | |
| | • | • | • | • | • | 1 0 | • | | | | |
| | 02 | • | • | • | • | | • | | | | |
| | | • | • | • | • | | • | | | | |
| | | • | • | • | • | | • | | | | |
| | | • | • | • | • | | • | | | | |
| V9 | • | • | • | • | 21 | | | | | | |
| | ļ | | • | • | • | | • | | | | |
| V12 | | | | | | | .45 | | | | |

¹ See Table 8 for a description of character codes.

* r values significantly different from zero at the 0.05 level.

** r values significantly different from zero at the 0.01 level.

The correlations of most interest are those between vegetative and fruit characters. For example, fruit flesh color is negatively correlated with petiole length (r=-0.70), and the pit length:width ratio is negatively correlated with leaf length (r=-0.63).

1985 Seedling Analysis

In a similar analysis of the 1985 seedling data, the first three PCs of the full-sib family means for the 'English Morello', 'Rheinische Schattenmorelle', and 'Wolynska' half-sib families account for 71% of the total variance; i.e., for 43%, 18%, and 10% of the variance, respectively (Table 12). The families with maternal

Table 12. Eigenvalues of the first seven PC axes from PC analysis of the 'English Morello', 'Rheinische Schattenmorelle', and 'Wolynska' half-sib families, with proportion of total variance accounted for by each axis.

| Principal Component | Eigenvalue | Proportion of variance | Cumulative variance | | |
|------------------------|------------|------------------------|---------------------|--|--|
| 1 | 5.967 | 0.426 | 0.426 | | |
| 2 | 2.526 | 0.180 | 0.607 | | |
| 3 | 1.428 | 0.102 | 0.709 | | |
| 4 | 1.175 | 0.084 | 0.793 | | |
| 5 | 1.001 | 0.072 | 0.864 | | |
| 6 | 0.574 | 0.041 | 0.905 | | |
| 7 | 0.435 | 0.031 | 0.936 | | |

parent 'Rheinische Schattenmorelle' group together, with 'Rheinische Schattenmorelle' x Crisana 1/8 (Cr) as the most distant (Figure 3). Three of the families with maternal parent 'Wolynska' are in close proximity, although the families with paternal parents 'Umbra' (Um) and Oblacinska (Ob) are dissimilar. Families with maternal parent 'English Morello' are morphologically diverse; i.e., located at the extremes of each of the first three PCs. The families of self-pollinated 'English Morello' (EM), 'North Star' (NS) backcrossed to 'English Morello', and 'Wolynska' x Oblacinska (Ob) are proximate and separate from the other families. The 'English Morello' families with paternal parents 'Sumadinka' (Su) and 'Nefris' (Nf) are closely situated. The two families with paternal parent 'Érdi Bötermö' (EB) are also closely situated to one another. Located near the center of the figure are the families with paternal parents Crisana 1/8 (Cr) (Crisana is the Romanian name for Pándy), 'Karessova' (Kr) (also a clonal selection of Pándy), and 'Meteor Korai' (MK) (a progeny of Pándy).

Proceeding from negative to positive values of PC1, the family means generally increase in leaf and petiole lengths and widths, the number of petiole glands, and vein angle¹. From negative to positive values of PC2,

¹Summarized from the eigenvectors of the first three PCs (Table 13).

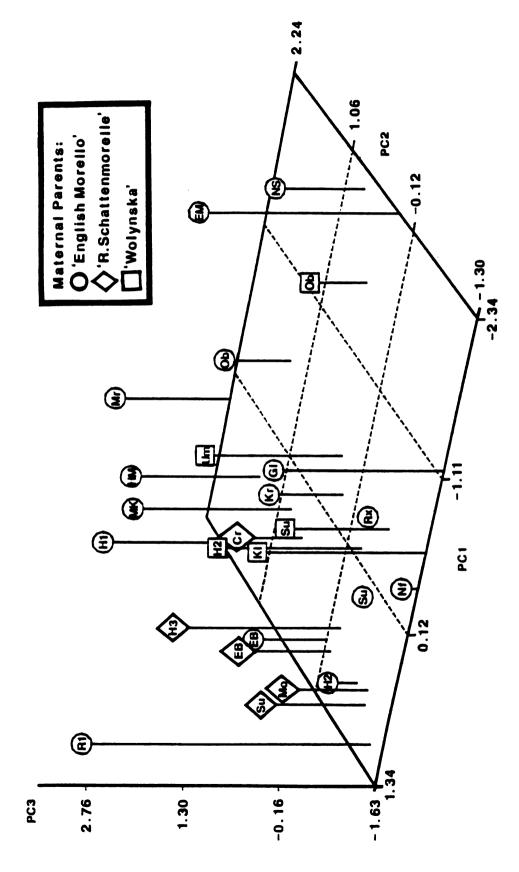


Figure 3. Positions of PC scores of family means on the first three PC axes for the 'English Morello', 'Rheinische Schattenmorelle', and 'Wolynska' half-sib Abbreviations as in Tables 2, 3, and 4 indicate paternal parents. families.

internode length and the petiole width:length ratio generally increase, while the petiole:leaf length ratio tends to decrease. Movement from negative to positive values of PC3 is characterized by an increase in the leaf width:length ratio and the amount of pubescence, while the number of serrations per centimeter and swollen glands on the basal leaf edge generally decrease.

Table 13. Eigenvectors of the first seven PC axes from PC analysis of the 'English Morello', 'Rheinische Schattenmorelle', and 'Wolynska' half-sib families.

| Char- | Eigenvectors | | | | | | | | | | |
|---------------|--------------|-------|-------|-------|-------|-------|-------|--|--|--|--|
| acter Code | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | | | | |
| V1 | 0.09 | 0.44 | 0.14 | -0.33 | -0.07 | 0.44 | -0.11 | | | | |
| V2 | 0.36 | -0.24 | 0.22 | -0.04 | -0.04 | 0.05 | -0.14 | | | | |
| V3 | 0.38 | 0.12 | 0.07 | -0.08 | -0.16 | -0.05 | -0.24 | | | | |
| V4 | -0.10 | 0.56 | -0.20 | 0.03 | -0.09 | -0.15 | -0.11 | | | | |
| V5 | 0.35 | -0.09 | -0.24 | -0.02 | 0.12 | -0.15 | -0.12 | | | | |
| V6 | 0.38 | 0.07 | 0.21 | -0.07 | 0.07 | -0.04 | -0.30 | | | | |
| V7 | 0.36 | 0.13 | 0.30 | 0.09 | -0.05 | -0.05 | -0.11 | | | | |
| V8 | 0.32 | 0.01 | -0.33 | -0.28 | 0.05 | -0.03 | 0.40 | | | | |
| V9 | 0.07 | 0.25 | 0.40 | 0.53 | -0.38 | -0.04 | 0.43 | | | | |
| V10 | 0.16 | -0.52 | 0.12 | -0.02 | -0.21 | 0.15 | 0.21 | | | | |
| V11 | 0.28 | 0.08 | -0.33 | 0.26 | -0.02 | -0.55 | 0.06 | | | | |
| V12 | 0.28 | 0.15 | -0.32 | -0.10 | -0.18 | 0.38 | 0.43 | | | | |
| V13 | 0.12 | -0.04 | -0.33 | 0.65 | 0.22 | 0.53 | -0.27 | | | | |
| V14 | 0.12 | 0.14 | 0.30 | 0.04 | 0.82 | -0.01 | 0.36 | | | | |

¹See Table 8 for a description of character codes.

In the cluster analysis of the 'English Morello' half-sib family (Figure 4), the clustering of the families with paternal parents 'Sumadinka' (Su), 'Karessova' (Kr), and Oblacinska (Ob), and with paternal parents 'Nefris' (Nf), 'Rexelle' (Rx), and 'Galaxy' (Gl) was unexpected, since the families within these two groups are not closely situated on the PC figure.

Cluster analyses of the half-sib families with maternal parents 'Rheinische Schattenmorelle' (Figure 5) and 'Wolynska' (Figure 6) generally suggest that the phenotypic relationships among full-sib families are similar to those indicated by the PC analysis. However, the dendrogram of the 'Rheinische Schattenmorelle' half-sib family suggests that the family with Mocanesti 16 (Mo) is more similar to the family with Crisana 1/8 (Cr) than to the family with 'Šumadinka' (Su). Additionally, the dendrogram of the 'Wolynska' half-sib family indicates a greater morphological similarity between the families with paternal parents 'Šumadinka' (Su) and 'Umbra' (Um) than is indicated by the PC analysis.

1986 Seedling Analysis

In a combined analysis of the full-sib families with maternal parent 'Montmorency' and of the 15 o.p. families, the first three PCs account for 71% of the total variance among the family means; i.e., for 37%, 21%, and 13% of the variance, respectively (Table 14).

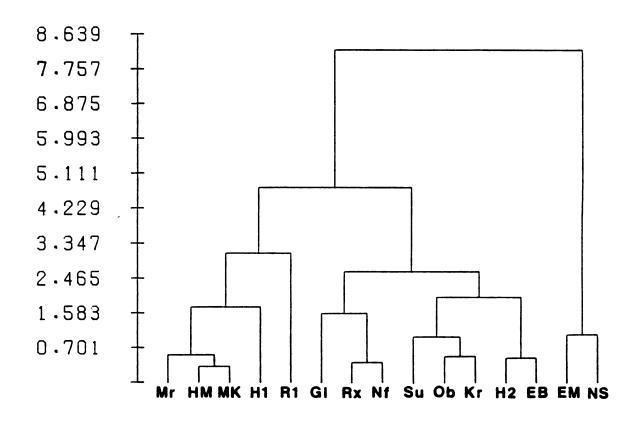


Figure 4. Dendrogram representing cluster analysis of the 'English Morello' half-sib family. Abbreviations as in Table 2 indicate paternal parents.

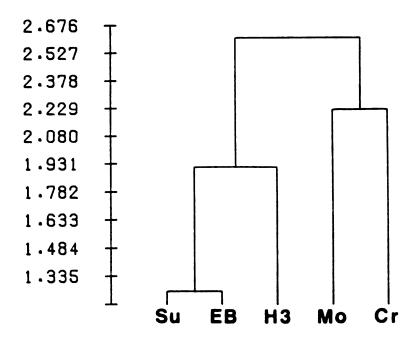


Figure 5. Dendrogram representing cluster analysis of the 'Rheinische Schattenmorelle' half-sib family. Abbreviations as in Table 3 indicate paternal parents.

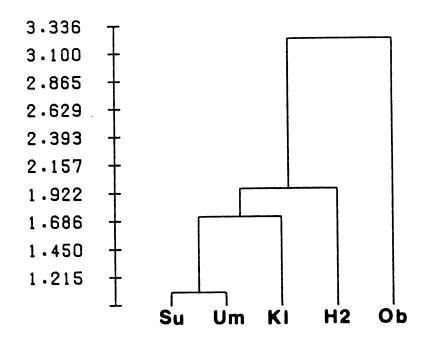


Figure 6. Dendrogram representing cluster analysis of the 'Wolynska' half-sib family. Abbreviations as in Table 4 indicate paternal parents.

Table 14. Eigenvalues of the first seven PC axes from PC analysis of the open-pollinated and 'Montmorency' half-sib families, with proportion of total variance accounted for by each axis.

| Principal Component | Eigenvalue | Proportion of variance | Cumulative variance | |
|------------------------|------------|------------------------|---------------------|--|
| 1 | 5.239 | 0.374 | 0.374 | |
| 2 | 2.897 | 0.207 | 0.581 | |
| 3 | 1.766 | 0.126 | 0.707 | |
| 4 | 1.169 | 0.083 | 0.791 | |
| 5 | 0.804 | 0.057 | 0.848 | |
| 6 | 0.749 | 0.054 | 0.902 | |
| 7 | 0.507 | 0.036 | 0.938 | |

The 'Montmorency' half-sib family groups together, although the family with paternal parent H 18/21 (R1) (a hybrid between a Duke and a sour cherry) is an outlier (Figure 7). The o.p. families with maternal parents 'Montmorency' (Mt) and 'Stark Montmorency' (SM) are in fairly close proximity to one another and to the o.p. family with maternal parent 'Meteor Korai' (MK). The three o.p. families with cold-hardy maternal parents 'Pitic de Iasi' (PI), 'Lyubskaya' (Lb), and 'Rheinische Schattenmorelle' (RS) are closely situated and separate from the central grouping. The three o.p. families with maternal parents 'Dobraya' (Db), 'Wolynska' (W1), and D076 (D0) form a compact group situated near the assemblage of cold-hardy types. The o.p. 'Cigány Meggy' (CM) family is an outlier. The closely situated families of 'Montmorency' x H 18/21 (R1) and o.p. 'Csengödi Csokras' (CC) are also outliers, situated farthest from the

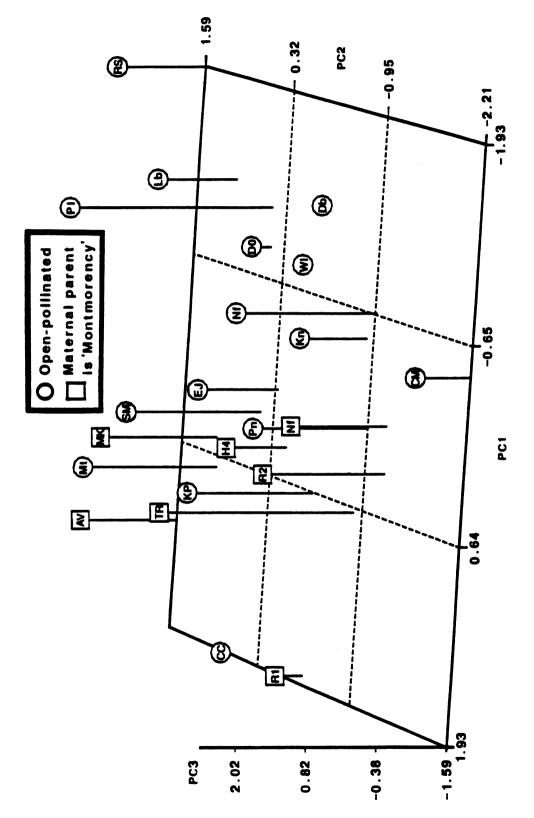


Figure 7. Positions of PC scores of family means on the first three PC axes for the 'Montmorency' half-sib family and open-pollinated families. Abbreviations as in Tables 5 and 6 indicate paternal parents of the 'Montmorency' families, and maternal parents of the open-pollinated families.

assemblage of families with cold-hardy maternal parents. As in the PC figure of the 1985 seedling data (Figure 3), families related to Pándy are located near the center of the plot: Pándy 114 (Pn), D076 (D0), and 'Kántorjánosi' (Kn) are clonal selections of the Pándy landrace, while M 63 (H4), 'Érdi Jubileum' (EJ), 'Meteor Korai' (MK), and 'Korai Pipacs Meggy' (KP) are progenies of Pándy.

The character loadings of the first three PCs are generally similar to those of the 1985 seedling analysis. Proceeding from negative to positive values of PC1, the lengths and widths of the leaves and petioles, as well as the leaf width:length ratio and vein angle, generally increase, while the number of serrations per centimeter tends to decrease¹. Proceeding from negative to positive values of PC2, leaf thickness, the petiole width:length ratio, and the number of swollen glands on the basal leaf edge generally increase, while the petiole:leaf length ratio tends to decrease. Proceeding from negative to positive values of PC3 is characterized by an increase in the number of petiole glands and a decrease in both internode length and pubescence.

Cluster analyses of the 'Montmorency' half-sib family (Figure 8) and the o.p. families (Figure 9) revealed relationships similar to the PC analysis.

¹Summarized from the eigenvectors of the first three PCs (Table 15).

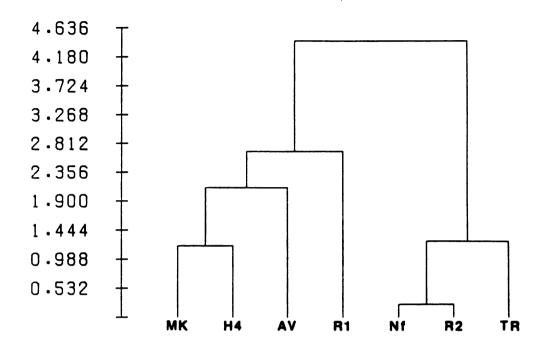


Figure 8. Dendrogram representing cluster analysis of the 'Montmorency' half-sib family. Abbreviations as in Table 5 indicate paternal parents.

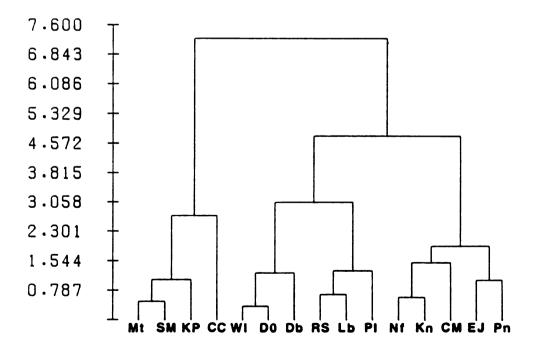


Figure 9. Dendrogram representing cluster analysis of the open-pollinated families. Abbreviations as in Table 6 indicate maternal parents.

Table 15. Eigenvectors of the first seven PC axes from PC analysis of the open-pollinated and 'Montmorency' half-sib families.

| Char- acter | Eigenvectors | | | | | | | | | | | |
|----------------|--------------|-------|-------|-------|-------|-------|-------|--|--|--|--|--|
| Code | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | | | | | |
| V1 | 0.14 | 0.15 | -0.40 | 0.37 | 0.46 | -0.52 | 0.06 | | | | | |
| V2 | 0.39 | -0.22 | -0.07 | -0.04 | 0.16 | 0.06 | 0.15 | | | | | |
| V3 | 0.37 | 0.25 | 0.12 | 0.15 | 0.10 | -0.13 | 0.08 | | | | | |
| V4 | -0.17 | 0.49 | 0.14 | 0.15 | -0.06 | -0.10 | -0.06 | | | | | |
| V5 | 0.13 | -0.23 | 0.57 | 0.27 | 0.21 | 0.02 | 0.06 | | | | | |
| V6 | 0.37 | 0.16 | -0.07 | 0.17 | -0.05 | 0.23 | -0.26 | | | | | |
| V7 | 0.40 | 0.17 | -0.06 | -0.06 | -0.01 | 0.28 | -0.17 | | | | | |
| V8 | 0.13 | 0.37 | 0.24 | -0.16 | -0.32 | -0.23 | 0.68 | | | | | |
| V9 | 0.32 | 0.15 | -0.01 | -0.39 | 0.03 | 0.28 | 0.03 | | | | | |
| V10 | 0.20 | -0.46 | -0.02 | -0.22 | 0.23 | -0.11 | 0.36 | | | | | |
| V11 | -0.16 | 0.33 | -0.07 | 0.08 | 0.54 | 0.51 | 0.32 | | | | | |
| V12 | 0.22 | -0.16 | 0.13 | 0.63 | -0.33 | 0.16 | 0.10 | | | | | |
| V13 | -0.32 | -0.09 | 0.30 | 0.15 | 0.22 | 0.25 | 0.13 | | | | | |
| V14 | -0.12 | -0.12 | -0.55 | 0.24 | -0.31 | 0.28 | 0.38 | | | | | |

¹See Table 8 for a description of character codes.

Table 16 lists the number of o.p. families having a significant correlation for each pair of traits, along with the sign (positive or negative) of the correlation. As with the cultivar data, many of the correlations were predictable. A few notable exceptions include the positive correlations found in several families between petiole length and the number of petiole glands, between internode length and leaf width, and between petiole width and leaf thickness. In most cases, when a statistically significant correlation was found between a pair of traits in more than one family, the correlations had the same sign. However, in a few cases opposing signs were found. The o.p. family with 'Dobraya' shows a negative correlation between pubescence and leaf length (r=-0.61), while the o.p. family with 'Csengödi Csokras' shows a negative correlation between the number of petiole glands and both leaf length (r=-0.45), and leaf width (r=-0.52). Only positive correlations were found between these traits among the other o.p. families.

Table 16. Sign and number for the 15 open-pollinated families in which there were significant Pearson correlation coefficients between traits.

| | | Character Code ² | | | | | | | | | | | |
|------------|-------------|-----------------------------|------------|---------------|------|------|-----------|-----------|------------|-----|-------------|-----------|-------------|
| | ٧ı | V2 | V3 | V4 | V5 | V6 | V7 | V8 | V 9 | V10 | V11 | V12 | V 13 |
| V1 | | | | | | | | | | | | | |
| V2 | j +3 | i | i | i | i | i | i | i | i | i | j | i | i |
| V3 | • | • | • | • | • | • | i | • | • | • | • | • | • |
| V4 | j+2-1 | -14 | i+3 | i | i | i | i | i | i | i | i | - | i |
| V 5 | i | + 8 | j+3 | i –4 | j | i | | | | i | i | | i |
| V6 | j+3 | +13 | +14 | j - 2 | +3-1 | | | | | i | | j i | - |
| V 7 | +8 | +10 | +14 | +1 - 3 | +3-1 | +14 | i | | | i | i | | i |
| V8 | i | +1 | +11 | +1-1 | +3 | +4 | +4 | | | i | i | ii | |
| V9 | +3 | | | | | | | | | | | | |
| V10 | +1-2 | +12 | j+1 | -14 | +6 | +1-1 | +1-1 | +1 | +2 | | i | - | |
| V11 | +1-1 | +1-2 | +2-1 | +3-1 | +1 | +1 | +2 | | +2-1 | -2 | i | | |
| V12 | +2 | +1 | +1 | +2 | +2-1 | +3 | +3 | -1 | -1 | -2 | +1-2 | ii | |
| V13 | -2 | | | | | | | | | | | | |
| | i | | | | | | | | | | | | |

 $^{^{1}}_{2}$ r values significantly different from zero at the 0.05 level. See Table 8 for a description of character codes.

Legend: +2-1, for example, means two families had positive correlations and one family had a negative correlation.

Blank spaces indicate that no significant correlations were found.

DISCUSSION

Morphology

A major point of interest in this study has been to relate the character variation of leaves and fruit observed in the sour cherry germplasm collection to the character states which typify the putative progenitors; i.e., ground cherry and sweet cherry.

Ground cherry and sweet cherry are morphologically distinct (Hedrick, 1915; Rehder, 1958; Oldén and Nybom, 1968; Kolesnikova, 1975; Bailey, et al., 1976). Ground cherry, considered the most winter hardy of the cherry species (Kolesnikova, 1975), reaches a height of about one meter, with a spreading form. The leaves (Figure 10) are generally short (20 to 50 mm), thick, glabrous, finely serrated (Figure 11), and have somewhat narrower vein angles than leaves of sweet cherry (Figure 12). The basal leaf edge typically has two to four swollen glands (Figure 13). The petioles are short (5 to 12 mm) and without glands. The fruits are usually small (about 10 mm across), with small pits (Figure 14), and 15- to 25-mm pedicels. In contrast, sweet cherry trees are tall (to 18 m), with a pyramidal form. The leaves (Figure 10) are generally long (60 to 150 mm), thin, variably pubescent beneath, coarsely serrated (Figure 11), with wider vein

Figure 10. Leaf samples of <u>P. avium</u>, <u>P. cerasus</u>, and <u>P. fruticosa</u>.

Figure 11. Serrations on edges of leaves of <u>P. avium</u>, <u>P. fruticosa</u>, and <u>P. cerasus</u>. Abbreviations as in Table 6 indicate maternal parents of open-pollinated <u>P. cerasus</u> specimens, except Mc='Montmorency'.

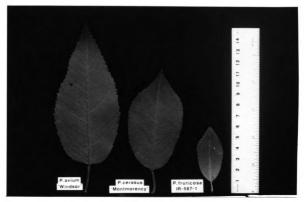


Figure 10.

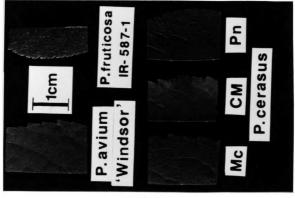


Figure 11.

Figure 12. Leaf veination of P. avium and P. fruticosa.

Figure 13. Swollen glands on leaves and petioles of P. avium, P. cerasus, and P. fruticosa. Abbreviations as in Table 6 indicate maternal parents of open-pollinated P. cerasus specimens.

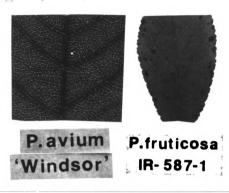


Figure 12.

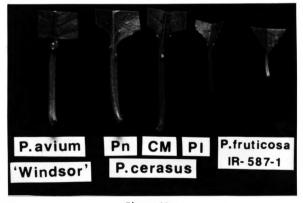


Figure 13.

angles than leaves of ground cherry (Figure 12). The petioles are relatively long, and frequently have two or more swollen glands. Swollen glands are usually lacking on the basal leaf edge (Figure 13). The wild fruits are generally small, although cultivated fruits can be large (about 25 mm across), with larger pits than those of ground cherry (Figure 14), and 20- to 50-mm pedicels.

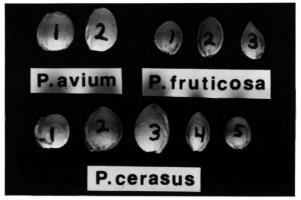


Figure 14. Pits of P. avium, P. fruticosa, and P. cerasus. (P. avium: 1='Schmidt', 2='Napoleon'; P. fruticosa: 1=IR 883-1, 2=IR 587-1, 3=IR 323-2; P. cerasus: 1='English Morello' x 'Hungarian Meteor', 2='Montmorency', 3='North Star', 4='Montmorency' o.p., 5='Rheinische Schattenmorelle' o.p.).

Soviet investigators have divided cultivated sour cherry into two ecotypes based on morphological differences and winter hardiness: western European and middle-

Russian (Kolesnikova, 1975). The western European group, in which Kolesnikova (1975) and Yushev (1975, 1977) include examples of Duke cherry (hybrids between sour cherry and sweet cherry), is characterized by lower winter hardiness than the middle-Russian group. The western European cultivars generally have larger leaves and fruit than the middle-Russian types, the fruit having better eating quality and nearly colorless juice. The middle-Russian group, comprised of eastern European cultivars, is adapted to harsh winter conditions under which only those individuals which have a high degree of winter hardiness can survive. Additionally, human selection pressure has probably contributed to the differences between the two groups (Kolesnikova, 1975). In southern and western Europe, clear- or pink-juiced cultivars are preferred, while in eastern and northern Europe and the Soviet Union, red-juiced selections are preferred.

Character Variation

For all of the morphological traits of the sour cherry trees that were examined, there is a gradation in the character values. These values generally encompass a wide range, intermediate to the character values that typify the present-day forms of the two presumed progenitor species. For instance, the range in the mean leaf length of the progenies in the largest full-sib seedling family (71 progenies) is 42 to 114 mm (Table A2).

These values are intermediate and approximate to the typical leaf lengths of ground cherry and sweet cherry, respectively. However, for certain specimens, character values were measured which may exceed the character value range demarcated by ground cherry and sweet cherry. For example, a sample mean of 20 leaf serrations per centimeter was calculated for one of the 'English Morello' x M 71 progenies. However, a survey of the ground cherry specimens in our collection indicated a value near 10 serrations per centimeter may be more characteristic of the species.

It is of particular interest that character states associated with sweet cherry and ground cherry generally fall at opposite ends of some of the PCs. Therefore, the values of these PCs may be interpreted as representing gradations between ground cherry- and sweet cherry-like morphology. For example, movement from negative to positive values of PC1 in Figure 7 tends to result in increasingly sweet cherry-like characteristics; i.e., longer, wider, more coarsely serrated leaves with longer petioles and wider vein angles.

A similar gradation of ground cherry- vs sweet cherry-like traits occurs in each figure, with the progression toward increasingly sweet cherry-like traits toward negative for PC1 and positive for PC2 in Figure 1, toward positive for both PC1 and PC3 in Figure 3, and

toward positive for PC1 and negative for PC2 in Figure 7. The gradation in morphological resemblance to the two presumed progenitor species is most evident along PC2 in Figure 1, and along PC1 in Figure 7. In both cases, for all of the traits measured for which a distinction between ground cherry- and sweet cherry-like morphology was made, the direction of the progression along the PC axes toward increasingly ground cherry- or sweet cherry-like morphology is the same. Traits having eigenvectors with an absolute value less than 0.15 were not considered on the corresponding PCs because of their minimal loading. This value was chosen because it is relatively small; also, there tends to be a gap near this value in the magnitude of the eigenvectors for the majority of the PCs. PC2 in Figure 3, and PC3 in both Figures 1 and 7 have combinations of sweet cherry and ground cherry character states, so no directionality was ascribed to these axes.

It should be kept in mind that the ascription of particular traits to individual PC axes (which facilitates the interpretation of the figures) is a simplification; only a portion of the variance of each trait is accounted for by any individual PC. Also, the progressive increase or decrease of the cultivar or family means of each trait along a given PC represents a general trend that may not precisely follow a monotonic progression.

In general, the sign and magnitude of the statistically significant correlation coefficients between traits are consistent across the cultivar and seedling data. signs and magnitudes of some of the r values (correlation coefficients), that were shown to be significant across the large majority of families, were expected. Examples of large, positive r values include those between leaf length and leaf width, and between pit length and pit weight. However, a number of less predictable correlations were also found. Within the cultivar data (Table 10), significant correlations were found between petiole length and fruit flesh color (r=-0.70), and between leaf length and the pit length: width ratio (r= -0.63). The pit ratio has economic importance, since long, narrow pits chip during mechanical pitting. Correlations between vegetative and fruit characters are of particular interest, since they could be an aid in indirect selection for fruit traits at the seedling stage. Since the correlations listed in Table 11 are based on a small number (16) of cultivars, it would be desirable to sample a much larger population to improve the reliability of such correlations before these values are used as selection tools or criteria. Since the statistical significance of a correlation with a trait rated on a subjective scale is questionable, a truly objective method of rating fruit flesh color and pubescence is needed.

The location of the o.p. families of the cold-hardy cultivars Pitic de Iasi, Lyubskaya, and Rheinische Schattenmorelle near the "ground cherry" ends of the first two PCs in Figure 7 may indicate a positive correlation between ground cherry-like leaf morphology (Figure 15) and cold-hardiness.



Figure 15. A typical leaf from each open-pollinated sour cherry family. Abbreviations as in Table 6 indicate maternal parents, except Mc='Montmorency'.

The results of the cluster analyses generally suggest morphological relationships among cultivars and families similar to those indicated by PC analysis. However, a discrepency was found between a few of the interfamily (full-sib) relationships, as indicated by the PC and cluster

analyses. In the cluster analysis of the 'English Morello' half-sib family (Figure 4), (as well as in a combined analysis of the 'English Morello', 'Rheinische Schattenmorelle', and 'Wolynska' half-sib families), the families with paternal parents 'Karessova' (Kr), Oblacinska (Ob), and 'Šumadinka' (Su) cluster together, as do the families with paternal parents 'Nefris' (Nf), 'Rexelle' (Rx), and 'Galaxy' (G1). However, the PC analysis of the 1985 seedling data (Figure 3) indicates that the families with paternal parents 'Nefris', 'Rexelle', and 'Sumadinka' are morphologically similar, while those families with paternal parents 'Galaxy', 'Karessova', and Oblacinska are dissimilar. The morphological patterns indicated by the PC analysis seem to reflect the origins and known genetic relationships among the paternal parents of these families more accurately than does the cluster analysis of the same data. disparity in the results of the two types of analysis may be a result of the variance unaccounted for by the first three PC axes.

The interpretation of the PC analyses of the seedling data is complicated by the fact that the genetic effects of the maternal parents of the half-sib families are confounded with those of the paternal parents. To simplify the interpretation of the seedling analyses, it was assumed that each full-sib family received a random sampling of the maternal alleles, so that the maternal

contribution to the morphological variation among full-sib families could be considered constant. However, it is recognized that such effects as dominance and heterosis will result in an arrangement of the seedlings in PC1-PC2-PC3 space with respect to the paternal parents that will differ from the spatial arrangement that would be obtained if the PC values of the paternal cultivars themselves were plotted (all else being equal). It is likely that the positions on the PC figures of the families with relatively few individuals are less accurate than the positions of the larger families, due to error resulting from the restricted genetic sampling of the parental cultivars.

A similarly complicated situation occurs in the analysis of the o.p. seedling data, since the pollinators may not have been random. Thus, it is possible that a single cultivar may be the paternal parent of an o.p. family. It is quite probable that the progenies in some o.p. families are grown from seed obtained through self-pollination of the maternal parent. It is well established that sour cherry cultivars vary widely in their degree of self-compatibility, from highly self-fertile to completely self-sterile (Kolesnikova, 1975; Redalen, 1984).

An additional concern results from the confusion in the literature as to the names and origins of a number of the cultivars and seedling parents examined in this study. Thus, an interpretation of the analyses with respect to geographic origins is somewhat tenuous. Furthermore, there is speculation in the literature that certain cultivars are interspecific hybrids (eg. George Glass), while other cultivars may be unrecognized as such (eg. Coronation).

The tendency of the three PC analyses to differentiate the sour cherry germplasm with respect to its morphological resemblence to ground cherry and sweet cherry may have been enhanced by the inclusion in each analysis of interspecific hybrids (both known and suspected) between sour cherry and either of its presumed progenitor species. Such hybrids and their progenies tend to be outliers on the PC figures. The gradation in the morphological resemblence of the "sour cherry" germplasm to ground cherry and sweet cherry, as indicated by some of the PCs, may have been less clearly defined had these hybrids been excluded from the analyses. It is noted that the gradation in the morphological resemblence of the full-sib families to the presumed progenitor species is not as well defined in the PC analysis of the seedlings evaluated in 1985 as it is in both the cultivar and 1986 seedling analyses. The 1985 seedling analysis included a smaller proportion of families with (known) interspecific hybrid parents, which may have effectively diminished the influence of such hybrids on the loading of the traits on the PCs.

In the analysis of the seedlings evaluated in 1985 (Figure 3), the families of self-pollinated 'English Morello', and 'North Star' backcrossed to 'English Morello', are outliers. One possible explanation is inbreeding depression. However, inbreeding depression is expected to be less severe in tetraploids (such as sour cherry) than in diploids, particularly if there is tetrasomic inheritance. An alternate hypothesis is that 'English Morello' has ground cherry in its recent ancestry, and its self-pollinated progenies are segregating for unequal genetic contributions by sweet cherry and ground cherry.

Genetic Implications

Since the germplasm examined in the present study does not represent a random sampling of the wild sour cherry gene pool, and since a narrow range of traits was examined, the data are inadequate to substantiate the view that there are two distinct ecotypes.

Hybridization between sweet and ground cherry may have occurred many times, and gene flow between sour cherry and its putative progenitor species may be a significant evolutionary factor. The tetraploid Duke cherry, presumed to arise through pollination of sour cherry by an unreduced gamete of sweet cherry (Hruby, 1950), occurs naturally. Unreduced pollen occurs in a number of sweet cherry cultivars (Galletta, 1959; Iezzoni

and Hancock, 1984). Interspecific hybrids between sour cherry and ground cherry have been reported growing wild in regions where these species coexist (Kárpáti, 1944).

Evidence accumulated through historical (Hedrick, 1915), anatomical (Yushev, 1970), cytogenetic (Hruby, 1962; Hancock and Iezzoni, 1988), and taxonomic (Yushev, 1975, 1977) investigations, including the present study, suggests that cultivated "sour cherry" may represent an intergradation between ground cherry and sweet cherry. Since the ancestries of most (if not all) "sour cherry" cultivars are unknown, the extent to which ground cherry and sweet cherry may have participated in the origins of the various "sour cherry" cultivars is conjectural. Possibly, cultivated "sour cherry" represents all degrees of hybridization between sour cherry and its two progenitor species; i.e., primary hybrids of sour cherry with sweet cherry or ground cherry, secondary hybrids (backcrosses) of primary hybrids with one of the three species, tertiary hybrids, and so on. Such hybrids may have been selected from the wild, or arisen under cultivation. The pedigrees of many of the new "sour cherry" cultivars being introduced by European breeders (including some of the parental cultivars included in this study) include cultivars of Duke cherry, and to a lesser extent, ground cherry.

All of the cultivars and many of the o.p. families evaluated in the present investigation were previously

surveyed for their malate dehydrogenase (MDH) isozyme banding patterns (Hancock and Iezzoni, 1988). Although Cigány Meggy, a Hungarian landrace, has the MDH banding pattern associated with sour cherry, two out of 34 o.p. progenies of Cigány Meggy segregated for a unique MDH pattern not found for any of the other <u>Prunus</u> specimens evaluated. The o.p. Cigány Meggy family is an outlier, located at the "sweet cherry" end of PC2 (Figure 7). On PC1, however, this family is intermediate.

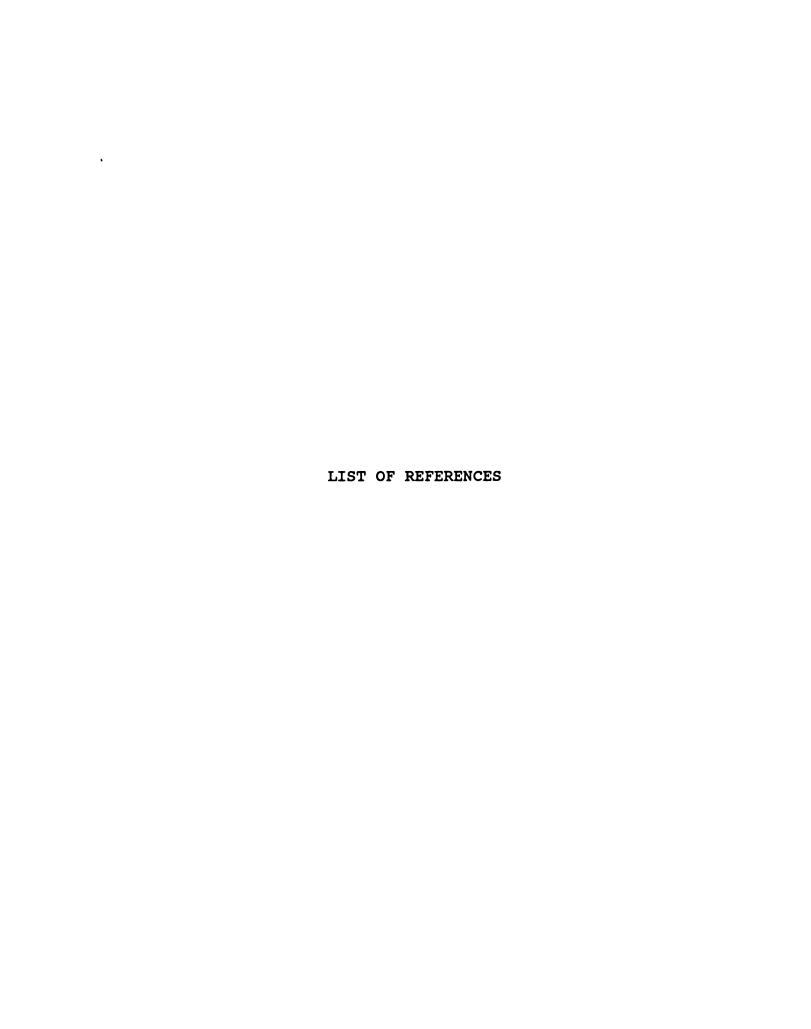
All but one of the 16 cultivars (Table 1) have the MDH banding pattern associated with sour cherry. The exception, 'Coronation', has the MDH pattern associated with ground cherry (A. Hancock, personal communication). This cultivar (Cn) is an outlier, located at the "ground cherry" end of PCl in Figure 1. 'Coronation' is an o.p. progeny of the cold-hardy Russian cultivar Shubinka, which Kolesnikova (1975) classifies as sour cherry. Morphologically, 'Coronation' resembles ground cherry, although the fruit are relatively large. Also, the leaf and canopy size of 'Coronation' are larger than those of the ground cherry specimens in our collection.

Located near the "ground cherry" ends of the first two PCs in Figure 7 is a separate cluster of o.p. families of the cold-hardy cultivars Pitic de Iasi (PI), Lyubskaya (Lb), and Rheinische Schattenmorelle (RS). Although 'Pitic de Iasi' has the MDH banding pattern

typical of sour cherry, four out of 22 o.p. progenies of 'Pitic de Iasi' segregated for the MDH pattern associated with ground cherry (Hancock and Iezzoni, 1988). 'Pitic de Iasi' is an o.p. seedling of the very cold-hardy, late-blooming, self-fertile Russian cultivar Plodorodnaya Michurina, an interspecific hybrid between ground cherry and sour cherry (Michurin, 1955). 'Pitic de Iasi' is a self-fertile, highly productive cultivar grown in the Moldavia region of Romania, where winter temperatures frequently reach -32°C. Both 'Coronation' and 'Pitic de Iasi' appear to combine the fruit quality of sour cherry with the cold-hardiness of ground cherry.

Temperature is probably the most significant environmental variable in delimiting the natural habitat of sour cherry (Kolesnikova, 1975), which includes the region extending from the Mediterranean coast to northern Europe, Scandanavia, and the western Soviet Union (Hedrick, 1915; Oldén and Nybom, 1968; Kolesnikova, 1975). In regions of the Soviet Union where middle-Russian type sour cherry cultivars are grown, winter temperatures can reach -35°C with little yield reduction. In such a harsh environment, natural selection will presumably be for those alleles contributed by ground cherry that impart cold-hardiness. The milder climates of southern and western Europe result in decreased selection pressure toward extreme cold-hardiness. In this environment, alleles contributed by

sweet cherry that impart vigor may have an adaptive advantage. Human selection may also have resulted in an increase in the frequencies of alleles within cultivated sour cherry that impart desirable fruit traits generally associated with sweet cherry, such as large size and high sugar content.



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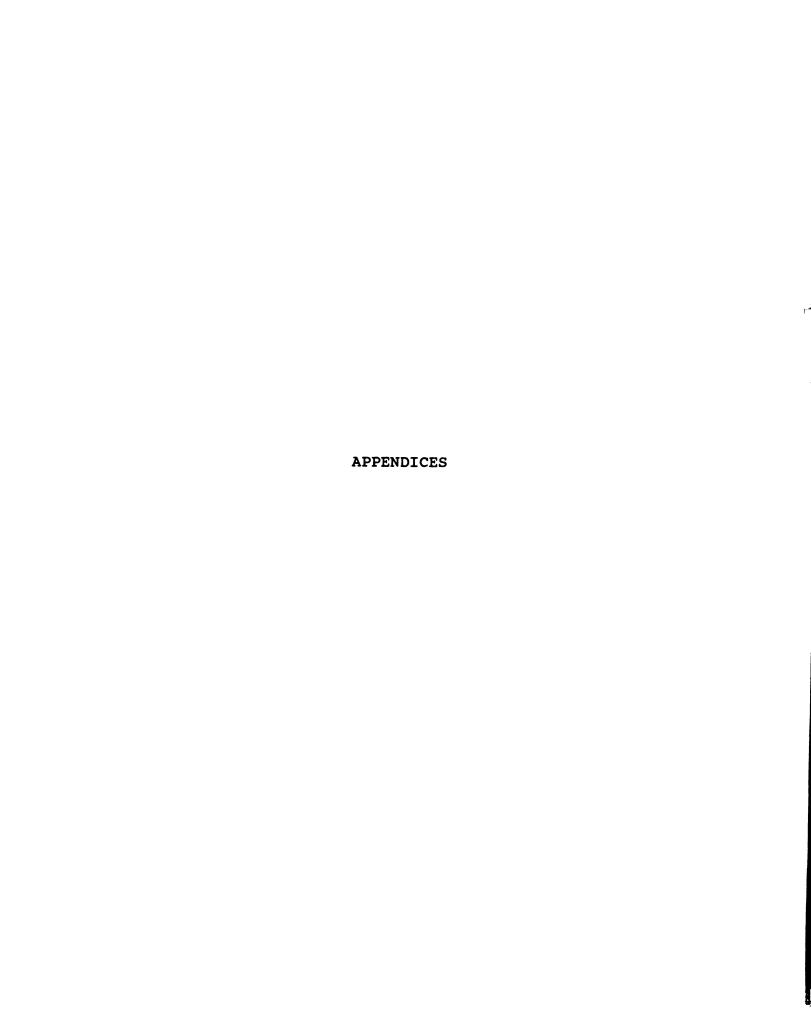
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APPENDIX A

Means and Ranges of Morphological Traits

APPENDIX A: Means and Ranges of Morphological Traits.

Table Al. Means of the flower, fruit, and vegetative characters measured on 16 sour cherry cultivars.

| | Character Code ² | | | | | | | | | | | | | |
|---------------|-----------------------------|----|----|----|------|------|----|------|-----|------|-----|-----|-----|--|
| Cultī ivar | F1 | F2 | F3 | F4 | F5 | F6 | F7 | F8 | F9 | F10 | F11 | F12 | F13 | |
| Bt | 11 | 32 | 17 | 19 | .90 | .70 | 2 | 9.4 | 7.9 | 1.19 | .17 | .55 | .31 | |
| Cn | 10 | 35 | 23 | 21 | 1.12 | 1.08 | 7 | 13.5 | 9.1 | 1.47 | .25 | .58 | .26 | |
| EM | 9 | 29 | 18 | 19 | .93 | .67 | 6 | 9.7 | 7.6 | 1.28 | .18 | .55 | .37 | |
| FM | 9 | 43 | 19 | 20 | .96 | .81 | 3 | 11.2 | 8.9 | 1.25 | .24 | .60 | .44 | |
| GG | 12 | 29 | 15 | 20 | .77 | .79 | 0 | 8.1 | 8.9 | .90 | .21 | .52 | .36 | |
| GP | 11 | 26 | 16 | 20 | .81 | . 69 | 0 | 8.9 | 8.1 | 1.08 | .17 | .55 | .33 | |
| Me | 13 | 23 | 18 | 21 | .84 | .71 | 4 | 9.7 | 9.1 | 1.04 | .20 | .55 | .40 | |
| Mr | 9 | 25 | 20 | 20 | .99 | .78 | 2 | 10.4 | 7.4 | 1.47 | .17 | .57 | .29 | |
| Mt | 10 | 30 | 17 | 19 | .88 | .60 | 0 | 9.1 | 7.9 | 1.15 | .15 | .54 | .34 | |
| Nf | 12 | 29 | 19 | 20 | .92 | .92 | 7 | 10.7 | 9.1 | 1.18 | .30 | .58 | .49 | |
| NS | 9 | 30 | 16 | 19 | .87 | .70 | 8 | 8.9 | 7.6 | 1.16 | .14 | .56 | .26 | |
| Os | 12 | 28 | 16 | 19 | .84 | .72 | 7 | 9.1 | 8.9 | 1.05 | .20 | .56 | .38 | |
| SH | 9 | 30 | 17 | 19 | .89 | .72 | 5 | 9.4 | 7.9 | 1.19 | .17 | .55 | .32 | |
| UG | 10 | 36 | 14 | 17 | .82 | .56 | 9 | 8.1 | 8.1 | 1.00 | .19 | .60 | .51 | |
| V1 | 10 | 32 | 16 | 19 | .87 | .93 | 7 | 9.7 | 9.4 | 1.01 | .25 | .59 | .36 | |
| Wl | 11 | 42 | 17 | 19 | .89 | .78 | 6 | 9,7 | 8.6 | 1.12 | .25 | .57 | .48 | |

| 0.1±_ | Character Code | | | | | | | | | | | | |
|---------------|----------------|----|------------|-----|-----|-----|-----|--|--|--|--|--|--|
| Cultī ivar | V2 | V6 | V 7 | V9 | V10 | V12 | V13 | | | | | | |
| Bt | 28 | 70 | 39 | .56 | .40 | 52 | 8 | | | | | | |
| Cn | 20 | 53 | 24 | .46 | .37 | 41 | 7 | | | | | | |
| EM | 17 | 58 | 35 | .60 | .29 | 49 | 9 | | | | | | |
| FM | 17 | 68 | 34 | .51 | .27 | 41 | 9 | | | | | | |
| GG | 30 | 76 | 42 | .57 | .40 | 41 | 6 | | | | | | |
| GP | 24 | 73 | 42 | .58 | .33 | 44 | 5 | | | | | | |
| Me | 30 | 78 | 46 | .60 | .39 | 49 | 7 | | | | | | |
| Mr | 24 | 66 | 40 | .60 | .36 | 53 | 8 | | | | | | |
| Mt | 29 | 69 | 38 | .55 | .42 | 55 | 8 | | | | | | |
| Nf | 21 | 77 | 46 | .60 | .28 | 44 | 8 | | | | | | |
| NS | 14 | 61 | 34 | .56 | .23 | 56 | 9 | | | | | | |
| Os | 18 | 77 | 40 | .50 | .23 | 43 | 7 | | | | | | |
| SH | 15 | 62 | 38 | .60 | .25 | 49 | 8 | | | | | | |
| UG | 15 | 64 | 37 | .57 | .24 | 44 | 7 | | | | | | |
| V1 | 19 | 93 | 62 | .67 | .21 | 58 | 8 | | | | | | |
| Wl | 27 | 76 | 41 | .54 | .36 | 49 | 7 | | | | | | |

See Table 1 for a description of cultivar abbreviations. See Table 8 for a description of character codes.

Table A2. Full-sib family means and ranges of morphological characters measured on the 'English Morello', 'Rheinisihe Schattermorelle', and 'Wolynska' half-sib families.

| | | | | | Cha | arac | ter O | ode ³ | | | | | |
|----------------------------|-------------------------|-------------------|-------------------|-------------------|-----------------|----------------|-------------------|-------------------|-------------------|-------------------|----------------|-----|-------------------|
| Cross ² | V1 V2 | V3 | V4 | V5 | V6 | V 7 | V8 | V9 | V10 | V11 | V12 | V13 | V14 |
| EMXEB Mean Min. Max. | 19 14 10 8 34 22 | 1.5 | .16 .09 .23 | 1.7 0.0 4.6 | 75 49 94 | 45 28 58 | .29 .23 .35 | .61 .52 .92 | .19 .13 .31 | 2.5 0.8 4.8 | 59 53 67 | | 1.1 0.0 3.6 |
| EMXEM Mean Min. Max. | 17 9 10 5 25 16 | 1.1 | .12 | 0.3 0.0 0.6 | 56 37 78 | 36 26 47 | .21 .16 .28 | .65 .52 .77 | .17 .11 .23 | 1.4 0.0 3.0 | 54 39 66 | 7 | 1.0 0.0 2.0 |
| EMxGl Mean Min. Max. | 17 13 10 8 23 19 | 1.3 | .11 | 0.3 0.0 2.0 | 67 43 96 | 37 24 47 | .25 .21 .29 | .56 .46 .66 | .19 .14 .22 | 1.4 0.6 2.4 | 56 50 67 | 6 | 1.2 0.0 2.2 |
| EMMHI Mean Min. Max. | 21 14 15 7 33 19 | 2.2 1.6 2.8 | .17 .13 .23 | 1.5 0.0 4.0 | 84 57 118 | 37 | .29 .24 .32 | .61 .53 .70 | .16 .12 .21 | 2.0 1.2 2.4 | 64 56 69 | 8 | 2.0 0.8 3.2 |
| EMMH2 Mean Min. Max. | 11 10 | 2.1 1.9 2.3 | .16 .11 .20 | 1.6 0.2 3.2 | 78 68 87 | 45 38 54 | .29 .26 .31 | .57 .51 .69 | .18 .14 .27 | 2.5 1.4 3.4 | 62 58 68 | 8 | 1.2 0.6 2.6 |
| EMXHM Mean Min. Max. | 20 13 10 7 37 20 | | .11 | 1.2 0.0 4.0 | 80 42 114 | 49 27 65 | .27 .19 .33 | .62 .46 .79 | .10 | 2.2 0.2 4.4 | 62 49 75 | 7 | 1.2 0.0 3.8 |
| EMxKr Mean Min. Max. | 16 12 9 8 22 16 | 1.9 1.3 2.4 | .17 .13 .21 | 1.2 0.0 2.2 | 73 44 88 | 43 24 55 | .25 .20 .29 | .60 .55 .67 | .12 | 2.2 0.8 3.8 | 61 53 67 | 10 | 1.4 0.2 2.6 |
| EMXMK Mean Min. Max. | 18 13 9 6 28 19 | 2.2 1.5 2.7 | .18 .12 .25 | 1.0 0.0 2.6 | 82 48 108 | 50 32 67 | .26 .24 .28 | .61 .53 .68 | .17 .12 .24 | 2.1 1.2 3.2 | 60 57 66 | 8 | 1.4 0.2 3.4 |
| EMxMr Mean Min. Max. | 19 12 11 7 26 15 | 2.2 1.5 2.9 | .13 | 1.2 0.0 3.2 | 77 50 105 | 50 27 66 | .27 .23 .31 | .64 .51 .83 | .15 .11 .22 | 2.3 0.8 4.8 | 62 50 73 | 7 | 1.1 0.0 3.4 |
| EMXNf Mean Min. Max. | 16 12 10 10 25 15 | 1.8 1.5 2.1 | .13 | 1.4 0.4 2.4 | 66 49 79 | 38 30 46 | .27 .22 .36 | .59 .54 .62 | .19 .15 .24 | 1.6 0.4 2.2 | 64 59 67 | 10 | 0.8 0.4 1.0 |
| EMXNS Mean Min. Max. | 19 9 13 4 25 15 | 1.5 1.0 2.0 | .17 .10 .30 | 0.0 | 61 41 83 | 34 20 46 | .23 .16 .31 | .57 .36 .70 | .15 .09 .23 | 1.4 0.0 5.2 | 57 35 67 | 8 | 1.0 0.0 2.6 |
| EMxOb Mean Min. Max. | 18 11 14 5 28 17 | 1.4 | .18 .11 .33 | 0.7 0.0 1.8 | 68 43 93 | 30 | .26 .20 .33 | .62 .54 .72 | .10 | 2.5 0.4 4.0 | 59 48 71 | 9 | 1.4 0.0 3.6 |
| EMXR1 Mean Min. Max. | 16 17 12 11 23 19 | 2.1 1.8 2.3 | .13 .11 .19 | 0.0 | 86 69 102 | 55 45 67 | .26 .21 .29 | .64 .59 .66 | .20 .13 .25 | 1.0 | 60 54 67 | 9 | 1.7 1.2 2.0 |
| EMxRx Mean Min. Max. | 11 9 | 1.9 1.6 2.2 | .16 .13 .21 | 0.0 | 67 52 89 | 40 29 55 | .28 .24 .31 | .59 .56 .63 | .18 .14 .20 | 0.6 | 61 57 68 | 7 | 0.8 0.0 1.8 |
| EMxSu Mean Min. Max. | 15 12 7 5 26 19 | 1.8 1.4 2.6 | .16 .11 .27 | 1.6 0.0 5.6 | 73 40 117 | 30 | .27 .21 .34 | .59 .52 .73 | .17 .11 .24 | 2.7 1.2 4.2 | 59 47 69 | 8 | 1.4 0.0 2.2 |

Table A2 (cont'd.).

| | | Character Code ³ | | | | | | | | | | | | | |
|--------------------|--------------|-----------------------------|----|------------|------------|-----|-----------|-----------------|------------|------------|-----|------------|-----|---------|------------|
| Cross ² | | V1 | V2 | V 3 | V4 | V5 | V6 | V 7 | V8 | V9 | V10 | V11 | V12 | V13 | V14 |
| RSxCr 1 | | | | | .17 | | | | | | | | 62 | | 1.0 |
| | Min. Max. | | | | .13 | | | | | | | 1.4 4.2 | | 8 15 | |
| RSXEB ! | | | | | .16 | | | | | .60 | | | | | 1.0 |
| | Min. Max. | | | | .11 | | | | .23 .30 | | | 5.6 | | 7 16 | 2.6 |
| RSxH3 | | | | | .15 | | | | | .62 | | | | | 1.4 |
| | Min. Max. | | | 2.8 | .09 .22 | | 42 118 | | .20 .31 | | | 0.2 4.4 | | 7 16 | 4.0 |
| RSxMo 1 | | | | | .14 | | | | | .60 | | | | | 1.2 |
| | Min. Max. | | | 2.5 | .11 .20 | | | | | | | 4.6 | | 9 14 | 2.4 |
| RSxSu 1 | Mean Min. | | | | .15 | | | | | .59 .56 | | | | | |
| _ | Max. | | | 2.2 | | 4.8 | | 50 | .29 | | | | 64 | | 2.4 |
| WlxH2 I | Mean | 19 | 13 | 2.0 | .16 | 1.4 | 75 | 43 | .27 | .57 | .18 | 1.8 | 58 | 10 | 1.3 |
| | Min. Max. | | | 1.4 2.4 | | | 61 92 | 33 49 | | .50 .62 | | | | | 0.0 4.0 |
| WlxKl I | | | | 1.7 | | | | 41 | | | | | | | 1.1 |
| | Min. Max. | | | | .10 .17 | | | 33 57 | | | | | | | 0.2 2.2 |
| WlxOb ! | | | | | | | | | | | | | | | |
| | | | | | | | | | .19 .33 | | | | | | |
| WlxSu ! | | | | | | | | | .26 .19 | | | | | | 1.4 |
| | | | | | | | | | .33 | | | | | | 3.0 |
| WlxUm 1 | | | | | | | | | .27 .22 | | | | | | 1.5 |
| | | | | | | | | | .29 | | | | | | |

 $^{^1}_2$ Range values are of progeny means (averaged over samples). 3_3 See Tables 2, 3, and 4 for descriptions of cultivar abbreviations. See Table 8 for a description of character codes.

Table A3. Full-sib family means and ranges of morphological characters measured on the 'Montmorency' half-sib family.

| Pate | Paternal Character Code ³ | | | | | | | | | | | | | | |
|------|--------------------------------------|----|----|-----|-----|-----|-----|----|-----|------|-----|-----|-----|-----|-----|
| | | | | | | | | | | | | | | | |
| Pare | ent ² | V1 | V2 | V3 | V4 | V5 | V6 | V7 | V8 | V9 | V10 | V11 | V12 | V13 | V14 |
| AV | Mean | 19 | 14 | 2.1 | .16 | 0.2 | 89 | 60 | .27 | .69 | .16 | 1.2 | 58 | 7 | 0.8 |
| | Min. | | | | | | | | .24 | | | | | | - |
| | Max. | 28 | 23 | 2.6 | .19 | 1.2 | 113 | 77 | .32 | .79 | .23 | 2.2 | 62 | 9 | 1.8 |
| H4 | Mean | | 14 | 1.9 | | | | | .24 | | | | | | |
| | Min. | | | 1.4 | | | 58 | | | .49 | | | | | |
| | Max. | 30 | 22 | 2.6 | .19 | 2.8 | 114 | 69 | .31 | .76 | .24 | 3.0 | 67 | 13 | 2.6 |
| MK | Mean | 21 | 13 | 2.1 | .17 | 1.0 | 82 | 52 | .26 | . 64 | .15 | 1.4 | 63 | 8 | 1.3 |
| | Min. | 15 | 7 | 1.7 | .11 | 0.0 | 67 | 40 | .20 | .54 | .10 | 0.6 | 54 | 5 | 0.0 |
| | Max. | 24 | 18 | 2.7 | .24 | 3.4 | 102 | 65 | .33 | .75 | .20 | 2.2 | 71 | 12 | 2.4 |
| Nf | Mean | 20 | 14 | 1.8 | .13 | 0.9 | 76 | 46 | .24 | .60 | .19 | 0.9 | 60 | 9 | 1.2 |
| | | | | | | | | | .22 | | | | | | |
| | Max. | 26 | 18 | 2.1 | .16 | 2.2 | 86 | 53 | .27 | .70 | .25 | 2.0 | 64 | 14 | 2.2 |
| R1 | Mean | 23 | 17 | 2.2 | .13 | 0.8 | 91 | 59 | .25 | .66 | .19 | 1.1 | 62 | 8 | 1.5 |
| | Min. | 13 | 9 | 1.5 | .09 | 0.0 | 59 | 41 | .19 | .47 | .13 | 0.0 | 57 | 6 | 0.4 |
| | Max. | 32 | 28 | 2.7 | .21 | 3.6 | 119 | 74 | .30 | .79 | .28 | 2.4 | 67 | 13 | 2.8 |
| R2 | Mean | 19 | 14 | 1.8 | .13 | 0.9 | 77 | 48 | .24 | .62 | .19 | 0.7 | 60 | 8 | 1.0 |
| | Min. | 16 | 9 | 1.3 | .11 | 0.0 | 63 | 41 | .19 | .57 | .13 | 0.2 | 56 | 7 | 0.0 |
| | Max. | 23 | 20 | 2.2 | .16 | 2.0 | 88 | 62 | .29 | .70 | .22 | 1.6 | 66 | 10 | 2.2 |
| TR | Mean | 20 | 14 | 2.0 | .14 | 1.7 | 84 | 52 | .24 | .61 | .18 | 0.8 | 62 | 11 | 0.9 |
| | Min. | | | 1.6 | | | | | .20 | | | | | | |
| | Max. | 28 | 17 | 2.4 | .15 | 3.0 | 109 | 69 | .27 | .66 | .20 | 2.0 | 67 | 13 | 2.0 |

¹ Range values are of progeny means (averaged over samples).
2 See Table 5 for a description of cultivar abbreviations.
3 See Table 8 for a description of character codes.

Table A4. Means and ranges $^{\! 1}$ of morphological characters measured on the open-pollinated families.

| Mater | mal | | | · <u>-</u> | | | Cha | arac | ter O | ode ³ | | | · · · · · · · · · · · · · · · · · · · | | |
|-------|----------------------|----------------|----------------|-------------------|-------------------|-------------------|-----------------|----------------|-------------------|-------------------|-------------------|-------------------|---------------------------------------|--------------|-------------------|
| Paren | | V1 | V2 | V3 | V4 | V5 | | V 7 | V8 | | V10 | V11 | V12 | V13 | V14 |
| œ | Mean Min. Max. | 23 14 31 | 12 | 2.1 1.3 2.6 | .13 .10 .16 | 0.2 0.0 1.8 | 98 61 119 | 64 40 78 | .25 .21 .29 | .66 .57 .75 | .17 .13 .25 | 1.6 0.4 2.0 | 60 56 69 | 5 | 1.1 0.0 3.6 |
| CM | Mean Min. Max. | 18 5 32 | 15 6 25 | 1.6 1.2 2.1 | .07 | 0.9 0.0 2.8 | 52 | 44 29 64 | .22 .18 .29 | .61 .48 .77 | .21 .11 .29 | 1.4 0.4 3.8 | 46 | 6 | 1.6 0.0 3.2 |
| DO | Mean Min. Max. | 22 13 35 | 10 | 1.8 1.4 2.2 | .16 .11 .20 | 0.1 0.0 0.4 | 79 59 93 | 45 37 58 | .24 .22 .29 | .57 .50 .70 | | 1.5 0.2 2.2 | 61 51 66 | | 1.6 0.8 2.2 |
| Db | Mean Min. Max. | 24 13 34 | 7 | 1.7 1.3 2.3 | .15 .11 .22 | 0.1 0.0 1.4 | 71 57 103 | 40 27 59 | .22 .19 .27 | .57 .47 .68 | .12 | 1.2 0.4 2.0 | 44 | 9 7 14 | 1.2 0.4 2.0 |
| EJ | Mean Min. Max. | 19 14 22 | | 1.9 1.4 2.2 | .16 .11 .25 | 0.5 0.0 3.0 | 59 | 52 40 63 | .24 .21 .28 | .63 .54 .72 | .15 .08 .21 | 0.8 0.0 1.8 | 52 | 6 | 1.2 0.4 2.0 |
| Kn | Mean Min. Max. | 20 14 24 | 13 9 16 | 1.7 1.5 1.9 | | 0.3 0.0 1.4 | 73 61 92 | 43 36 52 | .26 .21 .28 | .59 .56 .66 | | 0.8 0.2 1.2 | 56 | | 1.5 0.6 2.2 |
| KP | Mean Min. Max. | 21 15 29 | 14 10 19 | 1.9 1.6 2.6 | .14 .10 .19 | 1.1 0.0 2.6 | 76 61 107 | | .25 .21 .30 | .67 .57 .77 | .19 .15 .26 | 1.2 0.2 3.2 | 49 | 9 6 12 | 0.9 0.0 1.6 |
| Ιb | Mean Min. Max. | 20 14 36 | 7 | 1.8 1.3 2.3 | .17 .11 .25 | 0.3 0.0 2.0 | | 46 28 58 | .24 .18 .30 | .62 .53 .78 | | 1.9 0.6 3.8 | 47 | | 1.3 0.4 2.6 |
| Mt | Mean Min. Max. | 23 12 41 | 14 7 22 | 2.2 1.6 2.8 | .17 .09 .25 | 1.1 0.0 3.6 | 83 56 102 | 49 36 67 | .27 .22 .35 | .60 .51 .69 | | 1.2 0.0 2.6 | 49 | | 0.8 0.0 1.8 |
| Nf | Mean Min. Max. | 19 12 26 | 13 8 17 | 1.7 1.3 2.7 | .13 .09 .17 | 0.8 0.0 2.0 | 73 54 98 | 42 30 65 | .25 .21 .33 | .58 .42 .78 | .18 .13 .25 | 1.0 0.0 2.4 | | 5 | 0.9 0.2 2.4 |
| PI | Mean Min. Max. | 19 11 26 | 7 | 1.7 1.4 2.3 | .11 | 1.2 0.0 3.8 | 76 57 101 | 44 31 57 | .25 .17 .31 | .58 .46 .68 | .11 | 2.0 0.2 3.4 | 59 51 66 | 8 | 0.7 0.0 1.8 |
| Pn | Mean Min. Max. | 12 | 8 | 1.8 1.6 2.5 | .08 | 1.1 0.0 2.4 | 85 60 107 | 32 | .23 .17 .28 | .58 .50 .71 | .11 | 1.0 0.0 3.8 | 63 47 74 | 6 | 1.2 0.0 2.0 |
| RS | Mean Min. Max. | 19 15 22 | 8 | 1.7 1.4 2.0 | .14 | 0.2 0.0 0.8 | 72 58 92 | | .26 .23 .28 | .58 .52 .68 | .14 .13 .16 | | 54 47 58 | 9 | 1.4 0.2 1.8 |
| SM | Mean Min. Max. | 13 | 8 | 2.1 1.2 3.0 | .11 | 0.9 0.0 4.0 | 79 53 115 | 31 | .25 .17 .31 | .61 .51 .70 | .17 .13 .24 | 0.0 | 60 51 70 | 9 5 15 | 0.8 0.0 3.0 |
| Wl | Mean Min. Max. | 13 | 7 | 1.7 1.1 2.3 | .15 .09 .22 | 0.0 | 76 52 90 | 31 | .24 .18 .30 | | .16 .11 .24 | | 59 49 66 | 6 | 1.7 0.0 3.0 |

 $^{^{1}}_{2}$ Range values are of progeny means (averaged over samples). See table 6 for a description of cultivar abbreviations. See table 8 for a description of character codes.

APPENDIX B

Computer Programs

APPENDIX B: Computer Programs

Table B1. SAS program for computing means and ranges.

```
Command ===>
                                         Program Editor
00001 CMS FILEDEF RAWDATA DISK FILENAME FILETYPE A;
00002 DATA CHERRY;
00003
        INFILE RAWDATA;
00004
          INPUT FEMALE 1-2 MALE 4-5 REP 7-8 SAMPLE 16
          INTRNODE 18-19 PETLNGTH 21-22 PETWIDTH
00005
00006
          24-26 .3 LEAFLNG 28-30 LEAFWDTH 32-33
00007
          LEAFTHIK 35-36 .3 VEINANGL 38-39 SERRPRCM
          41-42 PETGLNDS 44 LEAFHAIR 46 SWGLONLF 48;
80000
00009
      PETWIDTH=PETWIDTH*25.4;
00010 LEAFTHIK=LEAFTHIK*25.4;
00011
        LFRATIO=LEAFWDTH/LEAFLNG;
00012
        PETRATIO=PETWIDTH/PETLNGTH;
00013
        PTLFRATO=PETLNGTH/LEAFLNG;
00014 PROC SORT;
        BY MALE REP;
00015
00016 PROC MEANS NOPRINT;
00017
       BY MALE REP;
00018
          VAR INTRNODE PETLNGTH PETWIDTH LEAFLING
00019
          LEAFWOTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
          LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO;
00020
00021
        OUTPUT OUT=DATAMNS
00022
          MEAN=INTRNODE PETLNGTH PETWIDTH LEAFLNG
00023
          LEAFWOTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
00024
          LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO;
00025 PROC SUMMARY DATA=DATAMNS;
          VAR INTRNODE PETLNGTH PETWIDTH LEAFLING
00026
00027
          LEAFWDTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
00028
          LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO;
        BY MALE:
00029
00030
          OUTPUT OUT=MEANS MEAN= ;
00031 PROC PRINT DATA=MEANS;
00032 PROC SUMMARY DATA=DATAMNS;
00033
          VAR INTRNODE PETLIGTH PETWIDTH LEAFLING
00034
          LEAFWDTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
          LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO;
00035
00036
        BY MALE;
          OUTPUT OUT=RANGES RANGE= ;
00037
00038 PROC PRINT DATA=RANGES;
00039 RUN;
```

Table B2. SAS program for computing Pearson correlation coefficients.

Command ===> Program Editor 00001 CMS FILEDEF RAWDATA DISK FILENAME FILETYPE A; 00002 DATA CHERRY; 00003 INFILE RAWDATA; 00004 INPUT FEMALE 1-2 MALE 4-5 REP 7-8 SAMPLE 16 00005 INTRNODE 18-19 PETLNGTH 21-22 PETWIDTH 00006 24-26 .3 LEAFLNG 28-30 LEAFWDTH 32-33 00007 LEAFTHIK 35-36 .3 VEINANGL 38-39 SERRPRCM 41-42 PETGLNDS 44 LEAFHAIR 46 SWGLONLF 48; 80000 00009 PETWIDTH=PETWIDTH*25.4; 00010 LEAFTHIK=LEAFTHIK*25.4; 00011 LFRATIO=LEAFWDTH/LEAFLNG; PETRATIO=PETWIDTH/PETLNGTH; 00012 00013 PTLFRATO=PETLNGTH/LEAFLNG; 00015 PROC SORT; 00016 BY MALE REP; 00017 PROC MEANS NOPRINT; 00018 BY REP; 00019 VAR INTRNODE PETLINGTH PETWIDTH LEAFLING 00020 LEAFWDTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO; 00021 00023 OUTPUT OUT=DATAMNS 00024 MEAN=INTRNODE PETLNGTH PETWIDTH LEAFLNG LEAFWOTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS 00025 00026 LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO; 00028 PROC CORR RANK; VAR INTRNODE PETLIGTH PETWIDTH LEAFLING 00029 00030 LEAFWDTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS 00031 LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO; 00040 RUN;

Table B3. SAS program for analysis of variance.

```
Command ===>
                                         Program Editor
00001 CMS FILEDEF RAWDATA DISK FILENAME FILETYPE A;
00002 DATA CHERRY:
        INFILE RAWDATA;
00003
00004
          INPUT FEMALE 1-2 MALE 4-5 REP 7-8 SAMPLE 16
00005
          INTRNODE 18-19 PETLNGTH 21-22 PETWIDTH
          24-26 .3 LEAFLNG 28-30 LEAFWDTH 32-33
00006
00007
          LEAFTHIK 35-36 .3 VEINANGL 38-39 SERRPRCM
          41-42 PETGLNDS 44 LEAFHAIR 46 SWGLONLF 48;
80000
        PETWIDTH=PETWIDTH*25.4;
00009
00010
      LEAFTHIK=LEAFTHIK*25.4;
00011
        LFRATIO=LEAFWDTH/LEAFLNG;
        PETRATIO=PETWIDTH/PETLNGTH;
00012
00013
        PTLFRATO=PETLNGTH/LEAFLNG;
00014
        IF FEMALE=1;
00015 PROC GLM;
        CLASSES MALE REP SAMPLE;
00016
00017
          MODEL INTRNODE PETLIGTH PETWIDTH LEAFLING
          LEAFWOTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
00018
00019
          LEAFHAIR SWGLONLF LFRATIO PETRATIO
          PTLFRATO = MALE REP(MALE);
00020
        MANOVA H=MALE E=REP(MALE) / PRINTH PRINTE
00021
00022
       HTYPE=1 ETYPE=1;
00023 RUN;
```

Table B4. SAS program for principal component analysis.

```
Program Editor
Command ===>
00001 CMS FILEDEF RAWDATA DISK FILENAME FILETYPE A:
00002 DATA CHERRY;
00003
        INFILE RAWDATA;
          INPUT FEMALE 1-2 MALE 4-5 REP 7-8 SAMPLE 16
00004
          INTRNODE 18-19 PETLNGTH 21-22 PETWIDTH
00005
          24-26 .3 LEAFLNG 28-30 LEAFWDTH 32-33
00006
          LEAFTHIK 35-36 .3 VEINANGL 38-39 SERRPRCM
00007
          41-42 PETGLNDS 44 LEAFHAIR 46 SWGLONLF 48;
80000
00009
        PETWIDTH=PETWIDTH*25.4;
        LEAFTHIK=LEAFTHIK*25.4;
00010
00011
        LFRATIO=LEAFWDTH/LEAFLNG;
00012
        PETRATIO=PETWIDTH/PETLNGTH;
00013
        PTLFRATO=PETLNGTH/LEAFLNG;
00014
        ID=MALE;
00015 PROC SORT:
        BY MALE;
00016
00017 PROC MEANS NOPRINT;
00018
        BY MALE:
          VAR INTRNODE PETLNGTH PETWIDTH LEAFLING
00019
          LEAFWOTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
00020
00021
          LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO
00022
          ID;
        OUTPUT OUT=DATAMNS
00023
          MEAN=INTRNODE PETLNGTH PETWIDTH LEAFLING
00024
          LEAFWDTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
00025
00026
          LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO
          ID;
00027
00028 PROC PRINCOMP STANDARD DATA=DATAMNS OUT=PCA;
        VAR INTRNODE PETLNGTH PETWIDTH LEAFLING
00029
        LEAFWOTH LEAFTHIK VEINANGL SERRPRCM PETGLNDS
00030
        LEAFHAIR SWGLONLF LFRATIO PETRATIO PTLFRATO;
00031
00032 PROC BROWSE;
        LIST 1, #MEANS PRIN1 PRIN2 PRIN3;
00033
00034 PROC PLOT;
        PLOT PRIN2*PRIN1=ID / HREF=0 VREF=0;
00035
00036 PROC PLOT:
00037
        PLOT PRIN3*PRIN1=ID / HREF=0 VREF=0;
00038 PROC PLOT;
        PLOT PRIN3*PRIN2=ID / HREF=0 VREF=0;
00039
00040 RUN;
```

Table B5. Clustan program for cluster analysis.

```
01=IEZZONI, PNXXXXXXX, RG2, CM150000.
02=HAL, L*UNSUP, CLUSTAN.
03=*EOS
04=FILE
05=
               S 10E
06=
         16
      (2F4.2,F4.3,2F4.2,F3.3,2F4.2,3F3.2,F2.2,F3.2,3F4.4)
08=167 124 177 744 414 26 583 099 13 14 20 3 24 559 149 168
09=168 127 168 678 413 26 586 097 07 11 20 6 26 611 136 190
10=185 133 199 753 430 27 579 095 14 13 18 2 20 573 155 178
11=166 090 150 567 330 26 581 101 06 16 19 4 24 586 178 161
12=170 116 179 711 433 27 577 101 10 15 21 6 27 611 161 164
13=CORREL
14 = 15
15=HIERARCHY
16=6 2 4
17=PLINK
18=
           6.7 4.3 0.15
19=DENDROGRAM OF THE 'WOLYNSKA' HALF-SIB FAMILY.
20=RESULT
21=XX
22=STOP
```

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