Investigation of the Origin of Aronia mitschurinii using Amplified Fragment Length Polymorphism Analysis

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Abstract. Aronia Medik., commonly known as chokeberry, is a genus of deciduous, multistemmed, rosaceous shrubs native to eastern North America. Three species of chokeberry are commonly accepted, A. arbutifolia (L.) Pers., red chokeberry, A. melanocarpa (Michx.) Elliott, black chokeberry, and A. prunifolia (Marshall) Rehder, or purple chokeberry. In Europe, a fourth species of human origin is recognized as Aronia mitschurinii A.K.Skvortsov & Maitul. In North America this type of Aronia is described as cultivars of A. melanocarpa, including ‘Viking’, ‘Nero’, and ‘Aron’. This species is characterized by near homogeneity of the population, tetraploidy, and a distinct morphology with more robust stems, wider leaf blades, and larger fruits than wild populations of A. melanocarpa. It has been proposed that this genotype originated from Russian pomologist Ivan Michurin’s early 20th century experiments involving Aronia × Sorbus hybridization. In this study we used amplified fragment length polymorphic (AFLP) markers to elucidate the relationships of A. mitschurinii to wild North American Aronia, × Sorbaronia C.K. Schneid, Sorbus L., and six additional genera from subtribe Pyrineae (Rosaceae). Data from seven primer combinations were interpreted by the NTSYSc software package into a similarity matrix using Jaccard’s coefficient. Clustering of AFLP similarity data using the unweighted pair group method with arithmetic mean (UPGMA) identified A. mitschurinii as distinct from wild Aronia, grouping it close to × Sorbaronia fallax C.K. Schneid, and × Sorbaronia ‘Ivan’s Beauty’. Non-metric multidimensional scaling (nMDS) also demonstrated a relationship between A. mitschurinii, × Sorbaronia fallax, a × Sorbaronia × Aronia backcross and compound-leaved Sorbus.

In North America Aronia has been promoted as a native replacement for invasive ornamental species because of its adaptability and multiseason interest provided by spring flowers, summer and fall foliage (Brand, 2010). Commercial fruit cultivation of Aronia in North America has recently increased significantly since fruits have been found to contain exceptionally high levels of antioxidants and polyphenols (Kahkonen et al., 2001; McKay, 2001; Wu et al., 2004; Zheng and Wang, 2003). Furthermore, there is growing evidence that chokeberry consumption can have numerous and varied health benefits (Kokotkiewicz et al., 2010). As a result, there is new interest in conducting research to identify potential avenues for genetic improvement of commercial cultivars of Aronia.

The genus Aronia belongs to the subtribe Pyrineae (formerly subfamily Maloideae) that is rife with taxonomic difficulties (Campbell et al., 2007; Potter et al., 2007). This group includes Sorbus (mountain ash), Malus Mill. (apple), Pyrus L. (pear), Amelanchier Med. (serviceberry), Crataegus L. (hawthorn), and several other woody plants with pomes or apple-like fruits (Campbell et al., 2007). Hybridization between species within genera is common along with polyploidy and apomony (Campbell et al., 2007; Persson-Hovmalm et al., 2004).

Three species of Aronia are commonly accepted: A. arbutifolia, red chokeberry; A. melanocarpa, black chokeberry; and A. prunifolia, purple chokeberry. The third species, A. prunifolia, is generally considered to be a naturally occurring, interspecific hybrid between A. arbutifolia and A. melanocarpa (Brand, 2010; Dirr, 2009; Rehder, 1920). Most sources distinguish the species by either red or black fruit color (Hardin, 1973) plus the degree of pubescence on leaves, stems, and inflorescences (Krussmann, 1986). Aronia arbutifolia possesses denseomentum on the undersides of leaf blades, stems, and inflorescences compared with nearly glabrous A. melanocarpa.

Despite the phenotypic variation among wild North American Aronia species, none have been described as possessing morphology closely resembling the plant material used in Eurasian commercial orchards. This has led to the proposal by Skvortsov and Maitulina (1982) that this phenotype be designated as a fourth species, Aronia mitschurinii. The A. mitschurinii phenotype is most similar to A. melanocarpa in appearance and often the two are distinguished only by a cultivar designation. Both species have black fruits, relatively glossy, glabrous leaves, stems, and flowers, but A. mitschurinii does possess some unique distinctions from A. melanocarpa. Skvortsov and Maitulina (1982) found that A. mitschurinii fruits are 1.5 to 2 times larger than A. melanocarpa and possess distinct morphology. Fruits are dull, globular, and somewhat depressed at the apex in comparison with wild A. melanocarpa fruits, which are shiny and oval or pyriform in shape. A. mitschurinii was also shown to have larger inflorescences, rounder leaf morphology, and a faster growth rate than A. melanocarpa. Skvortsov et al. (1983) also used ploidy as an identifying characteristic because A. mitschurinii is uniformly tetraploid (2n = 68), although Persson-Hovmalm et al. (2004) identified that polyploidy is common in all Aronia species.

Skvortsov et al. (1983) traced A. mitschurinii’s origins back to early 20th century Russia and the research facility of pomologist Ivan Michurin. Michurin focused his research on developing fruit crops suitable for cultivation in Russia. Michurin’s notes describe successful hybridizations among North American Aronia, originally received from Germany, native European Sorbus aucuparia L., and other members of the subtribe Pyrineae, Rosaceae (Michurin, 1948, 1949). The Pyrineae is a group in which wide hybridizations and allopolyploidy have been important factors in speciation (Campbell and Wright, 1996; Dickinson and Campbell, 1991; Nelson-Jones et al., 2002; Phipps et al., 1991; Robertson et al., 2010).

Although literature sources attribute A. mitschurinii to Ivan Michurin’s research, its genetic relationship to wild North American Aronia and other members of the Pyrineae remains unknown. The goal of this study is to determine if A. mitschurinii is a naturally occurring form of Aronia or is the product of intergeneric hybridization as Skvortsov et al. (1983) theorized and to identify potential avenues for breeding. To study the genetics of Aronia and other members of the Pyrinae, allopolyploidy has been important factors in speciation (Campbell and Wright, 1996; Dickinson and Campbell, 1991; Nelson-Jones et al., 2002; Phipps et al., 1991; Robertson et al., 2010).

Materials and Methods

Plant material. Germplasm used in AFLP analysis is listed in Table 1. Fourteen genotypes of Aronia were selected, including nine A. melanocarpa, one A. prunifolia, and two A. arbutifolia. A. melanocarpa accessions were selected to include diploid and tetraploid forms, genotypes from a wide geographic distribution and some with large fruits. Aronia mitschurinii germplasm included the cultivars Nero and Viking. The intergeneric, F₁ hybrid species × Sorbaronia delliipeti (Zabel) C. K. Schneid, (A. melanocarpa × S. aria), × S. alpina (Wild), C. K. Schneid. (A. arbutifolia × S. aria), and × S. fallax (A. melanocarpa × S. aucuparia).
were included as potential intermediate species that may have been involved in development of *A. mitschurinii* and its possible *Sorbus* ancestry. A backcross hybrid between maternal *A. melanocarpa* and ×*S. sorbifolia* (Poir.) C. K. Schneid. (*S. americana* Marshall) was successfully created and designated as ×*S. sorbifolia* BC1. This accession is representative of a possible ×*Sorbaronia* backcross to *Aronia* that may have produced *A. mitschurinii*.

Seven species of *Sorbus* were chosen covering four subgenera. *Sorbus aria* var. *salicifolia* and *S. torminalis* (L.) Crantz. represent subgenera *Aria* and *Torminaria*. *Sorbus aucuparia* and *S. americana* serve as representatives of subgenus *Sorbus*. The East Asian natives *S. alnifolia* (Sieb. & Zucc.) K. Koch and *S. yuana* Spongberg represent Micromeles. *Sorbus latifolia* (Lam.) Pers. is an allopolyploid containing genetic material from *S. aria* and *S. torminalis*. All *Sorbus* taxa were present at the time of this study in the living collections of the Arnold Arboretum of Harvard University, Boston, MA.

Species chosen from the broader Pyrinae included genera used in Michurin’s research such as *Malus* and *Pyrus*. *Malus* taxa included were *M. baccata* (L.) Borkh., *M. domestica* Borkh., *M. hupehensis* (Pamp.) Rehder, and *M. platycarpa* Decne. were included to achieve a potential parentage. *Ame-lanchier* and *Photinia* Lindl. are genera with taxonomic links to *Aronia* but not included in Michurin’s experiments. The East Asian genera *Chaenomeles* Bartl. and *Cydonia* Mill. were selected as outgroups and are not known to hybridize with *Aronia*.

### DNA isolation

DNA was isolated from approximately 0.5 g of newly emerged fresh or frozen leaves (−80 °C) using a modified CTAB procedure (Holm, 1995). Leaf tissue was ground in liquid nitrogen and then transferred to 15 mL conical polypropylene Falcon® tubes (BD Falcon, Franklin Lakes, NJ). Frozen tissue was suspended in 3 mL DNA extraction buffer containing 1 mg·mL−1 RNase and 2.1 μL β-mercaptoethanol. Tubes weremixed vigorously for 1 min and incubated for 1 h in a 60 °C water bath during which time samples were mixed by inversion at 15-min intervals. Samples were then centrifuged for 5 min at 2500 × g and the supernatant was transferred to new 15-mL tubes. Equal volume of 24:1 (v/v) chloroform:isoamyl alcohol was added to the supernatant and shaken for 1 min. Tubes were centrifuged for 10 min at 2500 × g and the aqueous phase was transferred to a new tube. This process was repeated until little to no interphase was visible. DNA was precipitated using 2:1 (v/v) isopropanol at −80 °C until needed for the AFLP procedure. Pellets were dissolved in TEi buffer (pH 8.0) to achieve a concentration of 2 μg·μL−1.

Species chosen from the broader Pyrinae included genera used in Michurin’s research such as *Malus* and *Pyrus*. *Malus* taxa included were *M. baccata* (L.) Borkh., *M. domestica* Borkh., *M. hupehensis* (Pamp.) Rehder, and *M. platycarpa* Rehder. *Pyrus communis* L. and *P. calleryana* Decne. were included to achieve a potential parentage. *Ame- lanchier* and *Photinia* Lindl. are genera with taxonomic links to *Aronia* but not included in Michurin’s experiments. The East Asian genera *Chaenomeles* Bartl. and *Cydonia* Mill. were selected as outgroups and are not known to hybridize with *Aronia*.

### Table 1. Germplasm information for material used in amplified fragment length polymorphism analysis.

<table>
<thead>
<tr>
<th>Species</th>
<th>Accession</th>
<th>Germplasm source</th>
<th>Germplasm origin</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Amelanchier arborea</em></td>
<td>None</td>
<td>Blue Ridge Hills Reservation, Milton, MA</td>
<td>Massachusetts</td>
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<td><em>Aronia arbutifolia</em></td>
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<td>Spring Meadow Nursery, Grand Haven, MI</td>
<td>Unknown</td>
</tr>
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<td><em>Aronia arbutifolia</em></td>
<td>P17580096</td>
<td>USDA, Ames, IA</td>
<td>Virginia</td>
</tr>
<tr>
<td><em>Aronia melanocarpa</em></td>
<td>AMES27010</td>
<td>USDA, Ames, IA</td>
<td>Michigan</td>
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<tr>
<td><em>Aronia melanocarpa</em></td>
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<td>USDA, Ames, IA</td>
<td>Michigan</td>
</tr>
<tr>
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<td>USDA, Ames, IA</td>
<td>Tennessee</td>
</tr>
<tr>
<td><em>Aronia melanocarpa</em></td>
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<td>USDA, Ames, IA</td>
<td>Wisconsin</td>
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<td><em>Aronia melanocarpa</em></td>
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<td>University of Connecticut, Storrs, CT</td>
<td>Connecticut</td>
</tr>
<tr>
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<td>University of Connecticut, Storrs, CT</td>
<td>Maine</td>
</tr>
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<td>University of Connecticut, Storrs, CT</td>
<td>Maine</td>
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<td><em>Aronia melanocarpa</em></td>
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<tr>
<td><em>Aronia mitschurinii</em></td>
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<td>University of Connecticut, Storrs, CT</td>
<td>Cultivated origin</td>
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<td>University of Connecticut, Storrs, CT</td>
<td>Maine</td>
</tr>
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<td>829-84-A</td>
<td>Arnold Arboretum, Boston, MA</td>
<td>France</td>
</tr>
<tr>
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<td>1843-80-A</td>
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<td>China</td>
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<tr>
<td><em>Malus domestica</em></td>
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<td>Wright Orchard, Willington, CT</td>
<td>Cultivation</td>
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<td>Cultivation</td>
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<tr>
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<td>North Carolina</td>
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<td>Arnold Arboretum, Boston, MA</td>
<td>China</td>
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<tr>
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<td>Unknown</td>
</tr>
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<td><em>Pyrus calleryana</em></td>
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</tr>
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<td><em>Pyrus communis</em></td>
<td>‘Bartlet’</td>
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<td>England</td>
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<td>England</td>
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<tr>
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<td>222-27-A</td>
<td>Arnold Arboretum, Boston, MA</td>
<td>Scotland</td>
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<td>260-27-A</td>
<td>Arnold Arboretum, Boston, MA</td>
<td>Scotland</td>
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<tr>
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<td>180-57-A</td>
<td>Arnold Arboretum, Boston, MA</td>
<td>England</td>
</tr>
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<td><em>Sorbus latifolia</em></td>
<td>18462-B</td>
<td>Arnold Arboretum, Boston, MA</td>
<td>France</td>
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<td><em>Sorbus terminalis</em></td>
<td>183-2002-C</td>
<td>USDA, Ames, IA</td>
<td>Unknown</td>
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<tr>
<td><em>Sorbus yuana</em></td>
<td>1539-80-C</td>
<td>Arnold Arboretum, Boston, MA</td>
<td>China</td>
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<tr>
<td>×<em>Sorbaronia alpina</em></td>
<td>994-84-A</td>
<td>Arnold Arboretum, Boston, MA</td>
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<tr>
<td>×<em>Sorbaronia dippelii</em> 1</td>
<td>759-78</td>
<td>Arnold Arboretum, Boston, MA</td>
<td>Germany</td>
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<tr>
<td>×<em>Sorbaronia dippelii</em> 2</td>
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<td>UC007 × <em>S. aria</em> 222-27-A</td>
<td>Connecticut</td>
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<td>×<em>Sorbaronia fallax</em></td>
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<td>University of Connecticut, Storrs, CT</td>
<td>Massachusetts</td>
</tr>
<tr>
<td>×<em>Sorbaronia fallax</em></td>
<td>‘Ivan’s Beauty’</td>
<td>University of Connecticut, Storrs, CT</td>
<td>Cultivation</td>
</tr>
<tr>
<td>×<em>Sorbaronia sorbifolia</em> BC1</td>
<td>UC120</td>
<td>UC007 ×<em>S. sorbifolia</em> 1239-85-A</td>
<td>Connecticut</td>
</tr>
</tbody>
</table>

* ×*Sorbaronia alpina* is a cross between *Sorbus aria* and *Aronia arbutifolia*.
* ×*Sorbaronia dippelii* is a cross between *Sorbus aria* and *Aronia melanocarpa*.
* ×*Sorbaronia fallax* is a cross between *Sorbus aucuparia* and *Aronia melanocarpa*.
* ×*Sorbaronia sorbifolia* is a cross between *Sorbus americana* and *Aronia melanocarpa*.
* ×*Sorbaronia sorbifolia* 1239-85-A is in the living collections of the Arnold Arboretum, Boston, MA. Accession was collected as a feral hybrid in Nova Scotia, Canada.
Amplified fragment length polymorphism procedure. The AFLP steps including restriction digestion, adaptor ligation, and preselective and selective amplification reactions were carried out as outlined in the AFLP plant mapping protocol (Anonymous, 2007). Restriction-ligation enzymes were purchased from New England Biolabs (Ipswich, MA). Adaptor sequences, AFLP preselective primers, and polymerase chain reaction (PCR) amplification core mix were purchased from Applied Biosystems (Foster City, CA). Preselective primers had one selective nucleotide (Eco RI-A + Mse I-C). Seven primer combinations were chosen for selective amplification (Eco RI-ACT + Mse I-CAC, Eco RI-ACT + Mse I-CTA, Eco RI-ACT + Mse I-CAT, Eco RI-AGG + Mse I-CTG, Eco RI-AGG + Mse I-CTC, Eco RI-AGG + Mse I-CAC). Fluorescently labeled Eco RI and unlabeled Mse I primers were purchased from Applied Biosystems. The DNA fragments from selective PCR were visualized by capillary electrophoresis on an ABI3730xl analyzer (Applied Biosystems) using GeneScan™ 500 LIZ® size standard. To ensure reproducibility, DNA for all individuals was isolated in duplicate and final AFLP fragment products were compared.

Amplified fragment length polymorphism data analysis. Fragments between 60 and 500 bp long generated by each primer pair were scored using GeneMarker™ Version 1.95 software (SoftGenetics, State College, PA). Peaks were first binary scored (1 for peak present and 0 for peak absent) using automatic settings followed by visual inspection and manual adjustment of each peak to ensure accurate scoring. Similarity matrices were constructed using the SIMQUAL function in NTSYSpc 2.21 software (Exeter Software, Setauket, NY) (Rohlf, 2005). Phenograms were constructed in NTSYSpc using an UPGMA cluster analysis. Bootstrapping was performed using PAUP*4.0 (Swofford, 2002) and Nei-Li genetic distances (Nei and Li, 1979) with 2000 replicates. Cophenetic correlation coefficients were calculated to test the goodness of fit using a two-way Mantel test in the MXCOMP module of NTSYSpc. The DCENTER and EIGEN functions were used to perform the original principal coordinates analysis, which served as inputs for the nMDS using MDSCALE (Kruskal, 1964a, 1964b). To test the goodness of fit between the original distances and fitted values, the Stress1 coefficient was used.

Results

Amplified fragment length polymorphism analysis. The seven primer combinations produced 769 useable markers, 761 of which were polymorphic. Aronia samples UC007 and PI578096 produced non-reproducible profiles for primer combinations Eco RI-ACT + Mse I-CTA and Eco RI-AGG + Mse I-CTC, respectively, and were treated as missing data (0.7% of the entire data set). Aronia mitschurinii cultivars Viking and Nero produced identical AFLP marker profiles. Of the 761 markers that were polymorphic across all included taxa, 36 were polymorphic between A. mitschurinii and the aggregate of wild North American Aronia accessions. Within that group of 36 markers, 32 were monomorphic with one or
more ×Sorbaronia species, the most of any genera tested. ×Sorbaronia ‘Ivan’s Beauty’ shared 29 markers with A. mitschurinii, ×S. fallax shared 28, and ×S. sorbifolia BC1 shared nine. Among hybrids between Aronia sp. and S. aria (×S. alpina and ×S. dippelii), seven of the 36 markers were monomorphic with A. mitschurinii. Sorbus also shared a large number (24) of the 36 markers that were polymorphic between A. mitschurinii and wild Aronia accessions. Of the four Sorbus subgenera, Sorbus had 24 monomorphic bands with A. mitschurinii, Torminaria had eight, and Aria and Micromeles each shared six markers. S. aucuparia (subgenus Sorbus) shared 22 markers with A. mitschurinii and S. americana shared 21. Malus (12 markers), Amelanchier (nine markers), Photinia (nine markers), Pyrus (nine markers), Chaeonomeles (six markers), and Cydonia (four markers) had relatively small numbers of monomorphic markers from the group of 36 A. mitschurinii markers that were polymorphic with wild Aronia accessions.

Genetic similarity matrix and cluster analysis. Cophenetic correlation values for Jaccard’s and Dice similarity coefficients were compared with Jaccard’s producing the highest value (0.93). Pairwise similarities ranged from 0.149 to 0.876 for non-identical taxa with a mean of 0.322. Pairwise cophenetic correlation coefficients observed for A. mitschurinii were highest among ×S. ‘Ivan’s Beauty’ (0.675), ×S. fallax (0.612), and ×S. sorbifolia BC1 (0.608). Intergeneric hybrids involving S. aria, including ×S. alpina and ×S. dippelii, had lower cophenetic correlation coefficients with A. mitschurinii (0.471 and 0.502, respectively).

A. mitschurinii also had relatively high similarity values with S. aucuparia (0.459) and S. americana (0.411), which were significantly higher than for other Sorbus including S. aria (0.236), S. yuana (0.256), and S. torminalis (0.245). In comparing A. mitschurinii with other Aronia species, mean similarity values for A. melanocarpa (0.535) and A. prunifolia (0.537) were higher than for A. arbutifolia (0.461). Among Aronia accessions tested, A. melanocarpa UC010 was observed to have the highest coefficient at 0.597.

The phenogram (Fig. 1) resolved five groups with greater than 50% bootstrap support. Cydonia clustered with Chaeonomeles forming an outgroup (#1). Amelanchier formed a group (#2), Photinia formed a group (#3), and Malus/Pyrus formed a group (#4). The fifth large cluster consisted of Sorbus, ×Sorbaronia, and Aronia and was supported with 65% bootstrap support. Within this cluster, a branch consisting of ×S. fallax, ×S. ‘Ivan’s Beauty’, and A. mitschurinii was resolved between Sorbus and Aronia with a bootstrap support of 66%. Within the large Sorbus, ×Sorbaronia, and Aronia group, A. mitschurinii was more closely aligned with S. aucuparia and S. americana than the Asian Sorbus species, simple-leaved European Sorbus, or ×Sorbaronia species derived from these Sorbus.

Non-metric multidimensional scaling (nMDS) was applied to the group of Aronia, ×Sorbaronia, and Sorbus from Table 1. The nMDS ordination was run on up to five dimensions with the fifth (0.05) considered an excellent fit of the data based on Kruskal (1964a, 1964b). Additional simulations produced insignificant changes in stress values. Because more than two dimensions were chosen, a principal components analysis was performed on the nMDS ordination to line up trends of variation in the configuration space with the coordinate axes. The first three dimensions explained 85.2% of the observed variation; however, for ease of viewing, this analysis focused on two dimensions, explaining 71.5% of the observed variation.

In Figure 2, accessions of wild North American Aronia species formed a well-defined cluster (A) and the genus Sorbus formed two distinct groups. The European simple-leaved species S. aria and S. latifolia grouped with the East Asian simple-leaved species S. alnifolia, S. torminalis, and S. yuana to form a cluster (E). The North American compound-leaved S. americana grouped with the European compound-leaved species, S. aucuparia, to form the second Sorbus cluster (D). Two individuals of ×Sorbaronia dippelii (A. melanocarpa × S. aria) formed a cluster (F) with ×Sorbaronia alpina (A. arbutifolia × S. aria), which fell halfway between the Aronia cluster (A) and the simple-leaved Sorbus cluster (E) as would be expected given the parentage of the two ×Sorbaronia taxa. ×Sorbaronia fallax (A. melanocarpa × S. aucuparia) and ×Sorbaronia ‘Ivan’s Beauty’ (reported to be a triploid ×S. fallax plant) formed cluster (C), halfway between the compound-leaved Sorbus cluster (D) and the Aronia cluster (A), as would be expected based on parentage. Aronia mitschurinii ‘Viking’ and ‘Nero’ clustered together with
× *Sorbaronia sorbifolia* BC1 (B). Cluster B fell halfway between the *Aronia* group (A) and the × *Sorbaronia fallax* group (C). Because × *S. sorbifolia* BC1 was produced by backcrossing *A. melanocarpa* to × *S. sorbifolia* (*A. melanocarpa × S. americana*), it is likely that *A. mitschurinii* ‘Viking’ and ‘Nero’ are also products of an *A. melanocarpa* backcross to a × *Sorbaronia*.

**Discussion**

We found AFLP to be very useful in resolving closely related members of the Pyrrineae subtribe of the Rosaceae. Genera and species were clearly identified with high levels of certainty. In addition, subgenera of *Sorbus* were easily differentiated. AFLP also reliably identified and confirmed intergeneric hybrids between *Sorbus* and *Aronia* as well as backcrosses.

Our genetic analysis could not differentiate between the two common large-fruit commercial cultivars, Viking and Nero. Persson-Hovmalm et al. (2004) was also unable to distinguish between ‘Viking’ and ‘Nero’ using random amplified polymorphic DNA (RAPD) markers. Using both RAPDs and intersimple sequence repeats, Smolik et al. (2011) found that among European black chokeberry cultivars, only ‘Hugin’ differed significantly from several very similar cultivars, including ‘Viking’ and ‘Nero’. It is likely that the majority, if not all, of the commonly grown, large-fruit black chokeberry cultivars are apomictic seedlings derived from an initial progenitor.

Results of this study demonstrate the use of the AFLP technique for identifying hybridity in closely related species. Generic × *Sorbaronia* were resolved, as expected, between *Aronia* and their respective *Sorbus* ancestors. The clustering of *A. mitschurinii* with a known (× *Aronia × Sorbus*) × *Aronia* hybrid provides strong evidence that it has hybrid origins and is not a unique strain of wild hybrid. As suggested by Michurin (1948, 1949) does not mention crossing *Aronia* with *S. americana* or receiving any wild × *Sorbaronia* hybrids from North America. This historic documentation and the relative ease with which *S. aucuparia* hybridizes with *Aronia* leads us to believe that *S. aucuparia* is the source of *Sorbus* genetic material observed in *A. mitschurinii*. Furthermore, we believe *A. mitschurinii* is the product of × *S. fallax* backcrossed to a black-fruited *Aronia* species.

The belief that Michurin received a large-fruited form of *A. melanocarpa* that subsequently was rebranded as *A. mitschurinii* is not supported by our data. The large-fruited accessions UC031 and P6603106 produced lower cophenic correlation coefficients with *A. mitschurinii* than did *Aronia* accessions with average-sized fruits. It does seem likely that the *Aronia* parent was either *A. prunifolia* or a dark-fruited form of *A. prunifolia* as indicated by Michurin’s notes specifying a “black-fruited” *Aronia* (Skvortsov et al., 1983). Our data support this, showing higher pairwise similarities between *A. mitschurinii* and dark-fruited *A. melanocarpa* and *A. prunifolia* than between *A. arbutifolia*. Although we present *A. mitschurinii* as an intergeneric hybrid, we do not propose nomenclatural changes to express *Sorbus* genetics. The large-fruited forms of *Aronia*, such as ‘Viking’ and ‘Nero’, are largely *Aronia* with lesser amounts of a *Sorbus* genome included; therefore, we supported Skvortsov and Maitulina’s (1982) treatment of these plants as *Aronia* × *A. K. Skvortsov & Maitul.*

Understanding the intergeneric hybrid composition of commercial *A. mitschurinii* as well as the genetic uniformity of all *A. mitschurinii* cultivars is useful in developing strategies to breed improved forms of *Aronia*. Persson-Hovmalm et al. (2004) identified wild North American *Aronia* as one potential source of novel genetic material to expand *A. mitschurinii*’s limited genetic base. Based on our study, intergeneric hybridization of *Aro-ania* with *Sorbus* is another approach that will likely yield novel and improved *Aronia* for the nutraceutical fruit industry.

**Literature Cited**


X. Sorbaronia sorbifolia BC1. (B). Cluster B fell halfway between the Aronia group (A) and the Sorbaronia fallax group (C). Because × S. sorbifolia BC1 was produced by backcrossing A. melanocarpa to × S. sorbifolia (A. melanocarpa × S. americana), it is likely that A. mitschurinii ‘Viking’ and ‘Nero’ are also products of an A. melanocarpa backcross to a × Sorbaronia.
