Identifying the North American Plum Species Phylogenetic Signal Using Nuclear, Mitochondrial, and Chloroplast DNA Markers

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ABSTRACT. *Prunus* phylogeny has been extensively studied using chloroplast DNA (cpDNA) sequences. Chloroplast DNA has a slow rate of evolution, which is beneficial to determine species relationships at a deeper level. The chloroplast-based phylogenies have a limitation due to the transfer of this organelle by interspecific hybridization. This creates difficulties when studying species relationships. Interspecific hybrids in *Prunus* occur naturally and have been reported, which creates a problem when using cpDNA-based phylogenies to determine species relationships. The main goal of this project was to identify nuclear gene regions that could provide an improved phylogenetic signal at the species level in *Prunus*. A total of 11 species in *Prunus* and within section *Prunocerasus* were used. Two peach (*Prunus persica*) haploids were used to test the reliability of the molecular markers developed in this project to amplify single-copy genes. A total of 33 major genes associated with vernalization response, 16 with tree architecture, and 3 with isozymes, were tested. Similarly, 41 simple sequence repeat (SSR) markers, seven cpDNA regions, and the internal transcribed spacer (ITS) region, were used. Multiple gene regions were identified and provided the greatest number of characters, greatest variability, and improved phylogenetic signal at the species level in *Prunus* section *Prunocerasus*. Out of those, *trnH-psbA*, PGI, MAX4, AXR1, LFY, PHYE, and VRN1 are recommended for a phylogenetic analysis with a larger number of taxa. The use of potentially informative characters (PICS) as a measure of how informative a region will be for phylogenetic analyses has been previously reported beneficial in cpDNA regions and it clearly was important in this research. This will allow selecting the region(s), which can be used in phylogenetic studies with higher number of taxa.

Taxonomic conflicts in *Prunus* were reported by Waugh (1901) and Hedrick (1911). Waugh (1901) stated that “plums grow pretty much as they please, and the botanist has to take them as he finds them.” He recognized that new classifications sometimes changed the previously published species groupings and classifications. *Prunus* classifications and discrepancies were well summarized by Bortiri et al. (2001), with Rehder’s (1940) classification being recognized as the most widely used and accepted. Rehder’s (1940) classification divided *Prunus* into five subgenera: *Prunophora* (*Prunus*), *Amygdalus*, *Cerasus*, *Padus*, and *Laurocerasus*. The subgenus *Prunus* was further divided into sections: *Euprunus*, *Prunocerasus* (North American plums), and *Armeniaca*. Recent phylogenetic studies

supported the concept of *Prunus* as a monophyletic group (single genus). However, the genus *Prunus* contained several poorly supported subclades/terminals (subgenera/species) (Bortiri et al., 2001, 2002, 2006; Kaneko et al., 1986; Katayama and Uematsu, 2005; Lee and Wen, 2001; Shaw and Small, 2004, 2005; Wen et al., 2008).

The genus *Prunus* is globally distributed, with ≈200 species. North America is an important center of diversity for plum species adapted to divergent climates and soils. Plums are considered to harbor the greatest diversity of fruit flavor, aroma, texture, color, form, and size among the stone fruits (Hedrick, 1911; Waugh, 1901). Mason’s (1913) and Rehder’s (1940) taxonomic classifications have been used for most of the *Prunus* phylogenetic analyses. Hereafter, the North American plums will be referred to as section *Prunocerasus* (Bortiri et al., 2001; Shaw and Small, 2004).

The phylogeny of the genus *Prunus* was studied by Mowrey and Werner (1990) using isozymes. *Prunus* section *Prunocerasus* was found to be polyphyletic, with a clade composed of *Prunus americana*, *Prunus munsoniana*, *Prunus hortulana*, *Prunus subcordata*, and *Prunus angustifolia*, and with *Prunus maritima* and *Prunus umbellata* in another. Badenes and Parfitt (1995) reported similar results to Mowrey and Werner (1990) using cpDNA sequences. They recovered all conventional

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subgenus classifications based on Rehder's (1940) taxonomic treatment: *P. persica*-*Prunus dulcis*, *Prunus domestica*-*Prunus salicina*, and *Prunus cerasus*-*Prunus fruticosa* monophyletic clades.

Two major groups, the *Amygdalus*-*Prunus* group and the *Cerasus*-*Laurocerasus*-*Padus* group, were recovered by Lee and Wen's (2001) phylogenetic analysis using ITS sequences of ribosomal DNA. These results were not congruent with Rehder's (1940) taxonomic treatment. Bortiri et al. (2001) supported the genus *Prunus* monophyly using ITS and chloroplast *trnL-trnF* spacer DNA sequences. Subgenera *Padus*-*Laurocerasus*-*Cerasus* and subgenera *Prunus*-*Amygdalus*-*Emplectocladus*-*Cerasus* (section *Microcerasus*)-section *Penarmeniaca* formed two major clades, respectively. The plums of northeastern North America were found to be closely related with *Prunus mexicana* as sister to the rest of this clade.

Bortiri et al. (2002) used the nuclear gene sorbitol 6-phosphate dehydrogenase (*s6pdh*) combined with ITS and *trnL-trnF* sequences to improve the lack of definition for deep nodes in the subgenera *Prunus*-*Amygdalus*-*Emplectocladus* clade, as previously reported (Bortiri et al., 2001). Phylogenetic analysis of the combined data supported two major clades: subgenera *Cerasus*-*Laurocerasus*-*Padus* and subgenera *Amygdalus*-*Emplectocladus*-*Prunus*. Section *Microcerasus* (subgenus *Cerasus*) was found nested within subgenus *Prunus*.

Prunus subgenus *Prunus* section *Prunocerasus* was reported to be monophyletic by Shaw and Small (2004) based on the data from seven cpDNA regions: *rpS16*, *rpL16*, *trnL*, *trnG*, *trnL-trnF*, *trnS-trnG*, and *trnH-psbA*. Three clades were strongly supported in section *Prunocerasus* based on Waugh's (1901) classification: "American Clade," "Chickasaw Clade," and "Beach Clade." The American Clade included *P. americana* var. *americana*, *P. americana* var. *lanata*, *P. mexicana*, *Prunus rivularis*, *P. hortulana*, *P. umbellata* var. *injucunda*; the Chickasaw Clade included *P. angustifolia*, *P. munsoniana*, *Prunus gracilis*, *Prunus nigra*, *P. umbellata* var. *umbellata*, *Prunus alleghaniensis* var. *alleghaniensis*, and *P. alleghaniensis* var. *davisii*; and the Beach Clade included *Prunus geniculata*, *P. maritima* var. *maritima*, and *P. maritima* var. *gravesii*.

The majority of phylogenetic research in *Prunus* has been done using cpDNA sequences (Badenes and Parfitt, 1995; Bortiri et al., 2001, 2002, 2006; Kaneko et al., 1986; Katayama and Uematsu, 2005; Shaw and Small, 2004, 2005; Wen et al., 2008). The advantages and disadvantages of using cpDNA for plant phylogenetic analyses have been well summarized by Soltis and Soltis (1998). One of the advantages includes that the chloroplast genome of plants is small. The size of the peach (cv. Hakuhou) chloroplast genome has been estimated to be about 152 kb (Katayama and Uematsu, 2005). The chloroplast genome rate of evolution is considered to be slow in comparison with nuclear genes (Soltis and Soltis, 1998). The latter could be considered an advantage when studying distantly related species and disadvantage when studying closely related species and species at the population level. The maternal inheritance of chloroplasts can be used to track interspecific introgression events, but it could lead to erroneous species relationships (Soltis and Soltis, 1998).

The slow rate of evolution of several cpDNA sequences and their value to infer phylogenetic relationships in closely related species for some angiosperms, including *Prunus*, was revised by Small et al. (1998) and Shaw et al. (2005, 2007). The main objective of the study of Shaw et al. (2007) was to identify

chloroplast regions that would provide the greatest number of characters for low-level molecular phylogenetic studies. Shaw et al. (2007) recommended selecting the top few choices with the greatest variability to be screened in a particular lineage to determine which of those are the most informative for a specific group.

Bortiri et al. (2006) demonstrated the power of including morphological characters for *Prunus* phylogenetic analyses. The combined data provided by ITS sequences, cpDNA regions, and morphological characters for *Prunus* yielded support of some nodes that were previously identified in *Prunus* (Bortiri et al., 2001). Several synapomorphies supported large groups, providing additional resolution for some clades. Similarly, Rohrer et al. (2004) reported that microsatellite markers could provide the genetic variability necessary to resolve the relationships within *Prunus* at the species level.

The main objective of this research was to measure and to identify additional genomic regions that could provide the greatest number of characters, greatest variability, and improved phylogenetic signal at the species level for *Prunus* section *Prunocerasus* relationships.

Materials and Methods

Plant material

A total of 11 species, one accession per taxa, were collected from the wild (excluding *P. persica* haploids) by T.G. Beckman, W.R. Okie, D.J. Chavez, and J.X. Chaparro (Table 1). A total of 13 samples (including two peach haploids) were used for this study. These species represented outgroups and major clades within subgenus *Prunus* section *Prunocerasus*, as reported by Shaw and Small (2004). The American Clade was represented by *P. americana*, *P. hortulana*, and *P. mexicana*; the Chickasaw Clade included *P. angustifolia*, *P. munsoniana*, and *P. umbellata*; and the Beach Clade was represented by *P. geniculata* and *P. maritima*. Outgroups included *Prunus pumila* (subgenus *Prunus* section *Penarmeniaca*); *P. persica* cv. Okinawa, AP05-18ws (haploid peach selection), 02-01c (haploid peach selection) (subgenus *Amygdalus*); and *P. fasciculata* (subgenus *Emplectocladus*). Peach haploids were used for confirmation of sequencing products.

The plant specimens collected were deposited as herbarium vouchers at the University of Florida Herbarium in the Florida Museum of Natural History, Gainesville, FL. Additional leaf material from the collected samples were freeze dried (Free-Zone 2.5 L system; Labconco, KS City, MO) or dried using a mixture of 2.5 kg 28- to 200-mesh silica gel dessicant (catalog no. S157-212; Thermo Fisher Scientific, Waltham, MA) and 500 g 10- to 18-mesh silica gel dessicant (catalog no. S161-500, Tel-Tale™; Thermo Fisher Scientific). Dried sample materials are stored at the Stone Fruit Breeding and Genetics Program at the University of Florida, Gainesville, FL.

DNA isolation

DNA was extracted from leaf tissue using a modified cetyltrimethylammonium bromide (CTAB) method as described by Chavez and Chaparro (2011). Lyophilized leaf tissue (~10 mg) of each sample was added to 2-mL Eppendorf microcentrifuge tubes with three 5-mm stainless-steel beads, 750 µL of CTAB buffer [2% CTAB, 100 mM Tris pH 8.0, 1.4 M NaCl, 0.5 M ethylenediaminetetraacetic acid (EDTA), 1% polyvinylpyrrolidone] previously mixed with mercaptoethanol

Table 1. List of the North American plums (section *Prunocerasus*) and other *Prunus* species collected and used in this project.

Voucher no. ²	Collection no.	Genus	Species	ID ³	Common name	Country	State	Lat.	Long.	Date of collection
FLAS 243688	12	<i>Prunus</i>	<i>americana</i>	PameFL12	American plum	United States	Florida	29°28.965'N	82°14.525'W	13 Apr. 2010
FLAS 243691	15	<i>Prunus</i>	<i>pumila</i>	PbesIL15	Sandcherry	United States	Illinois	41°20.972'N	95°59.167'W	14 Apr. 2010
FLAS 243699	23	<i>Prunus</i>	<i>umbellata</i>	PumbFL23	Hog plum	United States	Florida	30°21.178'N	83°09.957'W	28 Apr. 2010
FLAS 243701	25	<i>Prunus</i>	<i>angustifolia</i>	PangGA25	Chickasaw plum	United States	Georgia	30°43.451'N	84°25.695'W	28 Apr. 2010
FLAS 243760	85	<i>Prunus</i>	<i>mexicana</i>	PmexLA85	Mexican plum	United States	Louisiana			4 June 2010
FLAS 243762	87	<i>Prunus</i>	<i>maritima</i>	PmarNY87	Beach plum	United States	New York	40°51.508'N	73°52.862'W	4 June 2010
FLAS 243763	88	<i>Prunus</i>	<i>munsoniana</i>	PmunTX88	Wild goose plum	United States	Texas			4 June 2010
FLAS 243764	89	<i>Prunus</i>	<i>hortulana</i>	PhorMO89	Hortulan plum	United States	Missouri			4 June 2010
FLAS 243790	115	<i>Prunus</i>	<i>geniculata</i>	PgenFL115	Scrub plum	United States	Florida	27°56.242'N	81°34.564'W	8 July 2010
FLAS 243796	121	<i>Prunus</i>	<i>persica</i> cv. Okinawa	PperJP121	Peach	Japan				8 July 2010
FLAS 243804	131	<i>Prunus</i>	<i>fasciculata</i>	PfasCA131	Desert almond	United States	California	33°5.604'N	116°29.07'W	30 July 2010

²FLAS = University of Florida Herbarium, Gainesville, FL, voucher number.³First letter represents the genus (*Prunus* = P), next three letters represent the species (*americana* = ame, etc.), and the following letters represent the state of origin and collection number (Florida collection 12 = FL12, etc.).

(1 $\mu\text{L}\cdot\text{mL}^{-1}$), and 8 μL of RNase (10 $\text{mg}\cdot\text{mL}^{-1}$). Samples were grounded two/three times at 30 Hz in a tissue lyser (Qiagen, Valencia, CA) for 1.5 min until tissue clumps were not visible. Samples were vortexed and incubated in a 65 °C water bath for 6 min. Then, tubes were vortexed and a volume of 750 μL of chloroform:isoamyl (24:1) was added. Tubes were vortexed, incubated at –20 °C for 6 min, and then centrifuged at 12,000 g_n for 10 min. The aqueous phase was transferred to a new 2-mL centrifuge tube, and 500 μL of cold isopropanol was added. Tubes were gently mixed, incubated at –20 °C for 6 min, and then centrifuged at 16,100 g_n for 10 min. Supernatant was removed, and pellet was washed with 500 μL of cold 70% EtOH (by inverting the tubes carefully). Tubes were incubated at –20 °C for 5 min., and then centrifuged at 16,100 g_n for 5 min. Supernatant was removed, and pellet was washed with 500 μL of cold 90% EtOH (repeating mixing, incubation, and centrifugation, as described before). EtOH was poured off and the pellet was dried at bench top for $\approx$ 30–45 min (room temperature). The pellet DNA was resuspended in 50 μL TE buffer (10 mM Tris-HCl, 0.1 mM EDTA) and 50 μL of DNA grade water. DNA concentration was quantified in a spectrophotometer (UV10; Thermo Fisher Scientific). DNA concentration for all the samples was standardized to 20 $\text{ng}\cdot\mu\text{L}^{-1}$.

Genomic regions

SSR MARKERS. A total of 41 SSR markers distributed across the peach genome ($\approx$ 11.3 cM between markers) were selected from the ‘Texas’ almond (*Prunus dulcis*) $\times$ ‘Earlygold’ peach (T $\times$ E) reference map (Dirlewanger et al., 2004; Jung et al., 2008). Forward primers were modified using a 5' fluorophore label 6-FAM (standard) (6-FAM) or HEX (5HEX) (Eurofins MWG Operon, Huntsville, AL) for multiplex product fragment analysis (Supplemental Table 1).

Polymerase chain reaction (PCR) products were amplified in a 16- μL volume reaction containing 2 μL of 20 $\text{ng}\cdot\mu\text{L}^{-1}$ DNA template, 2.25 μL 10X ThermoPol Reaction Buffer [10 mM KCl, 10 mM $(\text{NH}_4)_2\text{SO}_4$, 20 mM Tris-HCl, 2 mM MgSO_4 , 0.1% Triton X-100, pH 8.8 at 25 °C (New England Biolabs, Ipswich, MA)], 1 μL 2.5 mM dNTPs, 0.2 μL Taq DNA Polymerase (New England Biolabs), 6.55 μL DNA grade water, and 4 μL 5 μM (2 μL forward and 2 μL reverse) primers. PCR parameters were 3 min at 94 °C followed by 40 cycles of 30-s denaturing at 94 °C, 30 s at primer's specific annealing temperature [Ta (°C)] (Supplemental Table 1), and 1 min of elongation at 72 °C, ending with 7 min at 72 °C. PCR products were separated on 3% (m/v) agarose gel. Gels were stained with ethidium bromide and recorded using a digital gel documentation system. Gel images PCR amplification intensities were used to determine PCR dilution ratios for fragment analysis on a sequencer (ABI3730; Applied Biosystems®, Grand Island, NY) at the Interdisciplinary Center for Biotechnology Research, University of Florida, Gainesville, FL. Fragment analysis of chromatographs was visualized using GeneMarker® (version 1.6; SoftGenetics, State College, PA) using 600 LIZ® size standard (Applied Biosystems®).

CHLOROPLAST DNA. Eight cpDNA regions (with product amplification less than 1000 bp) were selected based on their high polymorphism rates or proportion of mutational events for *Prunus*. Primer sequences were obtained from Shaw et al. (2005, 2007) and Morris et al. (2008) (Supplemental Table 2). Chloroplast DNA targets were amplified in a 48- μL volume reaction containing 6 μL of 20 $\text{ng}\cdot\mu\text{L}^{-1}$ DNA template, 6.75 μL

10X ThermoPol Reaction Buffer [10 mM KCl, 10 mM (NH₄)₂SO₄, 20 mM Tris-HCl, 2 mM MgSO₄, 0.1% Triton X-100, pH 8.8 at 25 °C], 3 µL 2.5 mM dNTPs, 0.6 µL Taq DNA Polymerase, 19.65 µL DNA grade water, and 12 µL 5 µM (6 µL forward and 6 µL reverse) primers. A universal cpDNA PCR procedure was used to simplify amplification as reported by Shaw et al. (2007). PCR cycling conditions were 5 min at 80 °C followed by 30 cycles of 1-min denaturing at 95 °C, followed by a ramp of 0.3 °C·s⁻¹ to 65 °C, and 4 min of elongation at 65 °C, ending with a final extension step of 5 min at 65 °C. PCR products were confirmed on 3% (m/v) agarose gel. Gels were stained with ethidium bromide and recorded using a digital gel documentation system. Only cpDNA regions that were easily amplified for all the samples were used for further sequencing (*ndhJ-trnF* and *trnT-trnL* region primers did not amplify products for several species and therefore were not used for further analyses).

INTERNAL TRANSCRIBED SPACER. The use of ITS sequence data has proven of value to define species relationships within the genus *Prunus* (Bortiri et al., 2001, 2002, 2006; Lee and Wen, 2001). This region was amplified using the primers published by Wen and Zimmer (1996): C26A, 5'-GTT TCT TTT CCT CCG CT-3' and Nc18S10, 5'-AGG AGA AGT CGT AAC AAG-3'. PCR products were amplified in a 48-µL volume reaction as previously described for cpDNA amplification. PCR cycling conditions were 3 min at 94 °C followed by 20 cycles of 1-min denaturing at 94 °C, 2 min at 50 °C, and 2 min of elongation at 72 °C. PCR products were separated, stained, and visualized as previously described.

NUCLEAR GENES. Single-copy genes associated with vernalization response (33), two major genes associated with tree architecture, and three genes expressing isozymes were included in this study. Hereafter, gene symbols will be used for these regions throughout the manuscript. The gene description corresponding to each gene region can be found in Supplemental Table 3. GenBank® annotated collection database of DNA sequences was used to find the *Arabidopsis thaliana* gene sequences and accessions corresponding to those genes (Benson et al., 2013). *Arabidopsis* gene sequences were blasted against the annotated peach genome v1.0 using BLASTN option in Phytozome (Goodstein et al., 2012). BLAST results with the highest score and *E* value were used to identify the best peach annotated transcript matching the *Arabidopsis* genes. Gene ancestry for each peach transcript was analyzed in Phytozome to remove possible multiple copy gene targets. Peach gene sequences and their messenger RNA were aligned to identify exon–intron boundaries using MUSCLE, version 3.8 (Edgar, 2004). Specific primers for each region were created in Primer3Plus, version 2.3.5, web-interface (Untergasser et al., 2012) using consecutive exons as annealing sites to amplify across introns (unless otherwise specified). Similarly, an additional 14 candidate genes primer sets associated with axillary meristem formation and tree architecture in peach as reported by Carrillo-Mendoza (2012) were used (Supplemental Table 3).

PCR products were amplified in a 48-µL volume reaction, as previously described for cpDNA and ITS regions amplification. PCR parameters were 3 min at 94 °C followed by 40 cycles of 30-s denaturing at 94 °C, 30 s at primer's specific *T_a* (°C) (Supplemental Table 3), and 1 min of elongation at 72 °C, ending with 7 min at 72 °C. PCR products were separated, stained, and visualized as previously described.

Sequencing

PCR products with multiple bands during electrophoresis were separated, excised, and purified using QIAquick Gel Extraction Kit (Qiagen). Single band products were purified and direct-sequenced by Eurofins MWG Operon following company procedures. Geneious (R6.0.3; Biomatters, Auckland, New Zealand) was used to edit and assemble complementary DNA strands.

Assembled contigs of gene sequence regions were used to create internal primers that would improve sequence coverage, quality, and base-calling accuracy. The list of regions for which internal primers were created can be found in Supplemental Table 4. Two or more polymorphic sites were identified for CUC2, ELF6, FT-TSF, GI-FB, LFY, MAF4, and *s6pdh*. The polymorphisms were confirmed using the internal primers.

Phylogenetic analyses

Genetic variation and cluster analyses for SSR fingerprinting data were performed using Powermarker, version 3.25 (Liu and Muse, 2005) and GenAlEx, version 6.5 (Peakall and Smouse, 2006, 2012). Genetic variation was characterized for each locus by the number of observed alleles (*A*), effective number of alleles (*A_e*), observed heterozygosity (*H_o*), expected heterozygosity (*H_e*), Wright's fixation index [*F* = (*H_e* – *H_o*)/*H_e* = 1 – (*H_o*/*H_e*)], and polymorphism information content (PIC). Nei's genetic distance was calculated and used in neighbor joining (NJ) cluster analysis (Nei and Takezaki, 1983; Saitou and Nei, 1987).

Alignments of DNA sequences were performed using MUSCLE, version 3.8. Manual alignments were made in Geneious R6.0.3 to produce an alignment with the fewest number of changes. Alignments were visually checked for polymorphic sites that resulted in sequence slippage. Polymorphisms (indels and/or substitutions) were manually determined using reference sequences from other species with full sequence coverage (without slippage from forward and reverse sequencing). Alternative sequences or alleles were kept and used in further analyses. A consensus sequence was obtained for each genotype. All genotype sequences per region were realigned using MUSCLE, version 3.8. Haplotypes for each species were calculated based on aligned amplicons using DnaSP, version 5 (Librado and Rozas, 2009).

The number of nucleotide substitutions (Subst) and indels, collectively named potentially informative characters (PICS = Subst + Indels), between the ingroup species (American, Chickasaw, and Beach clades in *Prunus* section *Prunocerasus*), and between ingroup and outgroup species-phased haplotypes, were calculated using DnaSP, version 5. The proportion of observed mutational events or percent variability for each genomic region were calculated as reported by Shaw et al. (2005, 2007) by using the following equation: percent variability = [(Subst + Indels)/*L*] × 100, where *L* = the total aligned sequence length.

Phylogenetic analyses were performed by using the optimal criterion of maximum parsimony (MP) for diploid and phased haplotype sequences. Gaps (indels) were ignored and also considered as an additional binary character matrix, with 0 = absence and 1 = presence of the indel. MP trees were obtained by using PAUP*, version 4.0b10 (Swofford, 2002). A heuristic search for MPTs was conducted by using tree bisection–reconnection branch swapping and 1000 random sequence addition replicates. Bootstrap support (Felsenstein, 1985) was

Fig. 1. Representatives of the North American plums (*Prunus* sp.), subgenus *Prunus* section *Prunocerasus*, and outgroup species: (A) *Prunus americana*, (B) *Prunus umbellata*, (C) *Prunus fasciculata*, (D) *Prunus geniculata*, (E) *Prunus angustifolia*, (F) *Prunus mexicana*, (G) *Prunus hortulana*, (H) *Prunus maritima*, (I) *Prunus munsoniana*, and (J) *Prunus pumila*.

estimated in 1000 replications of heuristic search and simple taxon addition with at least 100,000 rearrangements per replicate. Homoplasy was determined by calculating the consistency index and the retention index.

Model of sequence evolution for each region was determined using the Akaike information criterion [AIC (Akaike, 1974)] and Bayesian information criteria [BIC (Schwarz, 1978)] as implemented in the JModeltest, version 0.1.1 (Posada, 2008). A likelihood ratio test was calculated to choose the best model with the best $-\ln L$ score between the AIC and the BIC criteria. Heuristic searches for maximum likelihood trees (MLTs) were conducted using GARLI 2.0 (Zwickl, 2006) in the CIPRES Science Gateway (Miller et al., 2010). A non-parametric bootstrap was performed using two independent search replicates and 50 bootstrap repetitions. Best MLTs for each bootstrap repetitions and replicates were used to calculate a consensus tree with posterior probability values in Mesquite, version 2.73 (Maddison and Maddison, 2011).

Maximum likelihood analyses of individual and combined sequence data were performed using RAxML, version 7.1.0 (Stamatakis, 2006; Stamatakis et al., 2008). Analyses were calculated under a general-time-reversible model of nucleotide substitution and a gamma model of rate heterogeneity in the CIPRES Science Gateway. A halt bootstrapping, 1000 replicates, was performed. Best MLTs for each bootstrap repetition were used to calculate a consensus tree with posterior probability values in Mesquite, version 2.73.

Network analyses of haplotype and diploid sequence data were performed as described by Oatley et al. (2012). Networks of the phased haplotypes were estimated using TCS, version 1.21 (Clement et al., 2000). TCS analyses were performed treating gaps as missing data and as a fifth character state. Multilocus networks were built using SplitsTree, version 4.11.3 (Huson and Bryant, 2006) based on a distance matrix generated in POAD, version 1.03 (Joly and Bruneau, 2006). Uncorrected p distances from aligned sequences were calculated in PAUP*, version 4.0b10 and were used as input in POAD.

Results

Simple sequence repeats

The 41 SSR markers amplified 471 alleles in the 11 species representing outgroups and the major clades within subgenus *Prunus* section *Prunocerasus* (Fig. 1). An average of nine genotypes (out of 11 samples) were amplified per marker, with A of 10.70, the A_e was 8.10, H_o of 0.58, H_e of 0.84, F of 0.31, and PIC of 0.82 (Table 2). Thirty-four SSR markers successfully worked for all the species. Out

of those, 15 SSR markers amplified a total of 11 genotypes in the 11 samples. The value of A varied from 17 for BPPCT025 to 3 for CPPCT015. BPPCT023, BPPCT025, and BPPCT039 had the highest A_e of 13.44. CPPCT022 had the lowest A_e of 2.35. The value of H_o varied from 1.00 to 0.09 for CPPCT006 and EPDCU3117, respectively. BPPCT025, BPPCT026, and CPDCT025 had the highest H_e of 0.93 compared with the lowest H_e of 0.63 for CPPCT015. Wright's fixation index (F) ranged from 0.87 for CPPCT033 to -0.05 for BPPCT029. Six SSRs, BPPCT025, BPPCT026, BPPCT039, CPDCT025, EPDC3832B, and EPDCU3392, had the highest PIC of 0.92 compared with CPPCT015 of 0.55.

Nei's genetic distance (Nei and Takezaki, 1983) was calculated in combination with NJ (Saitou and Nei, 1987) cluster analysis for 41 SSR markers (Fig. 2A). Subgenus *Prunus* section *Prunocerasus* was monophyletic. Relationships within the North American plum species were not in agreement to those reported by Shaw and Small (2004). The outgroup species clustered together as expected. The Chickasaw Clade (*P. munsoniana* and *P. angustifolia*) was recovered. The American Clade and Beach Clade were not observed.

Cluster analysis using BPPCT025, BPPCT026, BPPCT039, CPDCT025, EPDC3832B, and EPDCU3392, the six SSR markers with the highest PIC values yielded somewhat consistent results (Fig. 2B). Outgroups clustered together, however, *P. mexicana* was found as a sister taxa to the outgroup. The Beach Clade (*P. geniculata* and *P. maritima*) and Chickasaw

Table 2. Summary statistics of 41 simple sequence repeat markers of a subset of 11 *Prunus* species.

Marker	Species amplification ^z	Genotype no.	A ^y	Ae	Ho	He	F	PIC
BPPCT006A	10	10	7	5.56	0.60	0.82	0.27	0.80
BPPCT006B	8	8	8	6.74	0.50	0.85	0.41	0.83
BPPCT008A	10	8	8	5.41	0.50	0.82	0.39	0.79
BPPCT008B	10	8	12	9.52	0.60	0.90	0.33	0.89
BPPCT013	11	10	9	6.54	0.73	0.85	0.14	0.83
BPPCT014	11	11 ^x	14	11.52	0.55	0.91	0.40	0.91
BPPCT016	11	7	7	10.08	0.18	0.76	0.50	0.73
BPPCT017	11	10	13	2.85	0.45	0.90	0.02	0.89
BPPCT023	11	5	4	13.44	0.64	0.65	0.02	0.58
BPPCT025	11	11	17	13.44	0.91	0.93	0.21	0.92
BPPCT026	11	11	16	5.50	0.73	0.93	0.67	0.92
BPPCT027	11	8	9	9.68	0.27	0.82	0.39	0.80
BPPCT028	11	11	12	7.33	0.55	0.90	0.16	0.89
BPPCT029	11	10	10	4.57	0.73	0.86	-0.05	0.85
BPPCT030	11	8	9	7.41	0.82	0.78	0.42	0.76
BPPCT038	10	8	12	12.74	0.50	0.87	0.21	0.85
BPPCT039	11	11	15	13.44	0.73	0.92	0.02	0.92
CPDCT023	10	7	7	8.64	0.20	0.74	0.07	0.71
CPDCT025	11	11	15	7.33	0.91	0.93	0.37	0.92
CPDCT027	11	11	13	10.52	0.82	0.88	0.10	0.87
CPDCT038	11	10	12	6.21	0.55	0.86	0.67	0.85
CPPCT005	11	10	14	2.67	0.82	0.90	0.20	0.90
CPPCT006	10	10	13	10.08	1.00	0.91	0.39	0.90
CPPCT008	11	8	9	11.00	0.27	0.84	0.30	0.82
CPPCT015	2	2	3	9.68	0.50	0.63	0.39	0.55
CPPCT022	11	11	13	2.35	0.55	0.90	0.05	0.89
CPPCT026	11	11	14	8.07	0.64	0.91	0.17	0.90
CPPCT029	11	6	6	12.74	0.27	0.68	0.11	0.64
CPPCT033	11	11	13	3.06	0.55	0.90	0.87	0.89
CPSCT004	11	7	8	8.00	0.55	0.57	-0.03	0.56
CPSCT008	3	3	5	6.21	0.67	0.78	0.24	0.74
CPSCT034	11	10	12	12.10	0.55	0.89	0.31	0.88
EPDC3832A	11	10	12	7.81	0.73	0.88	0.27	0.86
EPDC3832B	11	11	16	4.48	0.82	0.92	0.77	0.92
EPDCU3117	11	5	5	8.64	0.09	0.67	0.59	0.63
EPDCU3392	11	11	15	3.92	0.82	0.92	0.60	0.92
EPPISF002	10	9	10	10.52	0.90	0.88	0.20	0.86
EPPISF032	11	10	10	5.56	0.64	0.84	0.27	0.82
PMS2	11	11	15	6.74	0.64	0.92	0.41	0.91
UDP96-001	11	11	10	5.41	0.64	0.87	0.39	0.86
UDP96-003	11	8	8	9.52	0.18	0.78	0.33	0.76
UDP96-019	11	9	12	6.54	0.36	0.88	0.14	0.87
UDP98-025	11	7	5	11.52	0.30	0.75	0.40	0.70
UDP98-412	11	11	14	10.08	0.73	0.90	0.50	0.90
Average	—	9	10.70	8.10	0.58	0.84	0.31	0.82

^zNumber of species where successful amplification occurred.^yA = number of observed alleles, Ae = effective number of alleles, Ho = observed heterozygosity, He = expected heterozygosity, F = Wright's fixation index [$F = (He - Ho)/He = 1 - (Ho/He)$], PIC = polymorphism information content.^xNumbers in bold represent highest and lowest values for each variable.

Clade (*P. angustifolia* and *P. munsoniana*) were recovered. *Prunus americana* and *P. umbellata* were monophyletic. *Prunus hortulana* was recovered as sister species to all the section *Prunocerasus* Clade.

Chloroplast DNA

Analysis of the seven cpDNA regions indicated that the *ndhJ-trnF* region did not amplify consistently and was removed

for further analyses (Supplemental Table 2). Phased haplotype sequences were generated for the 11 species, for a total of 3584 bp containing 130 PICS and an average polymorphism rate of 3.68% (Table 3). The most informative sites were observed in 3' *trnV-ndhC* and *trnH-psbA* cpDNA regions for section *Prunocerasus* with 7.23% and 3.28% variability, respectively. Similar results were identified among the outgroup species with 3.17% and 1.49% variability, respectively (Fig. 3; Table 3). Both regions yielded good species delimitations within section *Prunocerasus* and outgroup species in MP and ML analyses, similar to those reported by Shaw and Small (2004) (Supplemental Figs. 1 and 4; Supplemental Tables 6 and 7). MP analyses with gaps as an additional character helped identifying additional species relationships in comparison with MP analyses without gaps. Similarly, MP and ML analyses were consistent in all and across the cpDNA regions for sequence data (Supplemental Figs. 1–6).

Phylogenetic analyses of *trnL-trnF*, *trnL* intron and *trnQ-5' rps16* cpDNA regions recovered internal relationships for section *Prunocerasus* (Supplemental Figs. 2 and 3, respectively). Section *Prunocerasus* was found monophyletic in MP and ML analyses with diploid or with haplotype number prefix data. In addition, *P. americana* and *P. mexicana* (American Clade) were found clustered together for all cpDNA regions (except *atpB-rbcL*). *Prunus geniculata* was found near the base of section *Prunocerasus* for *trnL-trnF* and *trnL* intron, *trnQ-5' rps16*, and *trnH-psbA*. Other cpDNA regions were consistent with previous results. Phased haplotype MP analyses found that *P. angustifolia*, *P. umbellata*, and *P. munsoniana* shared the same cpDNA haplotype for *trnL-trnF* and *trnL* introns, *trnQ-5' rps16*, *trnH-psbA*, *ndhF-rpl32*, and *atpB-rbcL*. The results are congruent with the Chickasaw Clade as described by Shaw and Small (2004).

Combined cpDNA regions phylogenetic analyses using MP and ML criteria found section *Prunocerasus* as a monophyletic clade (Fig. 4). *Prunus americana* and *P. mexicana* were found clustered together in all analyses. *Prunus geniculata* was identified as a basal sister species to *P. americana* and *P. mexicana*. Similarly, *P. hortulana*, *P. munsoniana*, *P. maritima*,

Fig. 2. Neighbor-joining cluster analysis based on Nei's genetic distance (Nei and Takezaki, 1983) for 11 *Prunus* species using (A) 41 simple sequence repeat (SSR) markers and (B) six SSR markers with high polymorphism information content values. Cladogram rooted with *Prunus fasciculata* (PfasCA131) at the base. Other species in the cladogram are: *P. americana* (PameFL12), *P. angustifolia* (PangGA25), *P. geniculata* (PgenFL115), *P. hortulana* (PhorMD89), *P. maritima* (PmarNY87), *P. mexicana* (PmexLN85), *P. munsoniana* (PmunTX88), *P. persica* (PperJP121), *P. pumila* (PbesIL15), and *P. umbellata* (PumbFL23).

P. umbellata, and *P. angustifolia* were clustered together. MP and MLTs were consistent across regions. The nonstandardized multilocus combined cpDNA sequence data network (Fig. 5) recovered similar species relationships to those produced by MP and ML analyses. Additional sequence data information and models of sequence evolution are available in Supplemental Tables 6, 7, 8, and 10.

Internal transcribed spacer

A target of 610 bp of alignable haplotype sequence containing 66 PICS and an average variability of 10.82% was obtained (Table 4). The sequence variability of section *Prunocerasus* was 2.30% compared with the outgroup variability of 8.52% (Fig. 3). Section *Prunocerasus* was found monophyletic for both, MP and ML, analyses (Supplemental Fig. 7; Supplemental Tables 6 and 7). When the sequence data were analyzed without the insertion of gaps, *P. munsoniana* and *P. americana* were clustered together in MP. However, these species relationship was lost when the gaps were used as an additional character in MP analyses. Other lower level species relationships among the North American plums were not recovered. The results obtained were consistent across diploid and phased haplotype sequence data analyses. Additional sequence data information and models of sequence evolution are presented in Supplemental Tables 6, 7, 9, and 11.

Nuclear genes

ISOZYMES. Three isozyme genes, *PGI*, *PGDH*, and *s6pdh*, were sequenced in the 11 core species and two peach haploids. Analysis of the 1405 bp of alignable sequence detected 117 PICS with a variability of 8.77% (Table 4). The *PGI* primers used did not amplify the *P. americana* *PGI* sequence. Readable sequences were obtained for all other species. The highest level of polymorphism within section *Prunocerasus* and between the outgroup taxa was obtained for *PGI*, followed by *s6pdh* and *PGDH* (Table 4). The sequence polymorphism rate for *PGI* within section *Prunocerasus* was 7.69% compared with 4.93% and 3.56% for *s6pdh* and *PGDH*, respectively. Similar trends of 4.01%, 3.18%, and 2.94% polymorphism rate, respectively, were observed when the outgroup species (*P. fasciculata*, *P. persica*, and *P. pumila*) were removed (Fig. 3).

Section *Prunocerasus* was recovered as a monophyletic clade with MP and ML analyses using either diploid or haplotype datasets for *PGI* and *PGDH* genes. MP analyses using gaps as an additional source of information for the enzyme sequences did not provide additional resolution of species relationships (Supplemental Figs. 8–10; Supplemental Tables 6 and 7).

Prunus munsoniana and *P. angustifolia* consistently clustered together in all diploid and phased haplotype sequence data analyses with MP and ML for all isozyme genes. Both species integrated into the Chickasaw Clade, as previously described. Other previously known species relationships, such as the

Table 3. Summary statistics of cpDNA (chloroplast DNA) regions sequenced for 11 *Prunus* species.

cpDNA region	<i>3' trnV-ndhC</i>		<i>trnL-trnF^z</i>		<i>trnL intron</i>		<i>trnQ-5' rps16</i>		<i>trnH-psbA</i>		<i>ndhF-rpl32</i>		<i>atpB-rbcL</i>	
Aligned <i>L</i> (bp) ^y	567		472		364		479		335		598		769	
	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst
American ^x	17	19	0	0	0	2	4	3	8	2	1	0	0	0
Beach ^x	13	20	0	0	0	2	3	4	8	1	1	0	0	1
Chickasaw ^x	0	0	0	0	0	0	1	0	5	0	0	0	0	0
<i>Prunocerasus</i> ^x	25	16	0	0	0	3	5	4	9	2	2	0	0	1
PICS ^w	41		0		3		9		11		2		1	
Percent variability ^v	7.23		0.00		0.82		1.88		3.28		0.33		0.13	
Outgroup ^u	9	9	0	3	1	5	5	5	2	3	3	6	3	9
PICS	18		3		6		10		5		9		12	
Percent variability	3.17		0.64		1.65		2.09		1.49		1.51		1.56	
Total PICS	59		3		9		19		16		11		13	
Normalized PICS	3.03		0.15		0.46		0.98		0.82		0.57		0.67	
Percent variability	10.41		0.64		2.47		3.97		4.78		1.84		1.69	

^z*trnL-trnF* and *trnL* introns were sequenced together as they primers amplifying both regions.^yAligned *L* = total aligned sequence length.^xAmerican Clade = *Prunus americana*, *Prunus hortulana*, and *Prunus mexicana*; Beach Clade = *Prunus geniculata* and *Prunus maritima*; Chickasaw Clade = *Prunus angustifolia*, *Prunus munsoniana*, and *Prunus umbellata*; *Prunocerasus* = American Clade + Beach Clade + Chickasaw Clade.^wPotentially informative characters (PICS) = Indels + Subst. Indels = number of insertion/deletion events; subst = substitutions.^v[(Subst + Indels)/*L*] × 100, where *L* = the total aligned sequence length.^uOutgroup = *Prunus fasciculata*, *Prunus persica*, and *Prunus pumila*.

American Clade and Beach Clade, were not recovered. MP and ML analyses of PGI, diploid and phased haplotype sequence data, recovered *P. geniculata* and *P. hortulana* clustered together at the base of the section *Prunocerasus* Clade (Supplemental Fig. 9). ML analysis of PGI haplotypes recovered the Chickasaw Clade (including *P. umbellata*). Analysis of the *s6pdh* sequence data produced a polytomy consisting of *P. americana*, *P. geniculata*, *P. persica*, *P. pumila*, and *P. fasciculata* (Supplemental Fig. 10).

MP and ML haplotype analyses for PGDH revealed that *P. geniculata*, *P. angustifolia*, and *P. munsoniana* shared a common haplotype. In addition, *P. geniculata* was located basal to the section *Prunocerasus* species in a polytomy with *P. persica* and *P. pumila* (PbesIL15) (Supplemental Fig. 8).

MP and ML analyses of the combined diploid isozyme data recovered section *Prunocerasus* as a monophyletic group. *Prunus angustifolia* and *P. munsoniana* were clustered together in all analyses (Chickasaw Clade). MP analyses (with and without gaps) did not provide additional resolution of species relationships. However, ML analyses of combined data recovered the Chickasaw Clade as a monophyletic group (*P. umbellata*, *P. angustifolia*, and *P. munsoniana*). The American Clade (*P. americana* and *P. mexicana*) was found clustered to *P. maritima* as a sister species. *Prunus hortulana* and *P. geniculata* were identified as basal to species within section *Prunocerasus* (Supplemental Fig. 63).

The nonstandardized multilocus (phased haplotype) combined isozymes sequence data network (Supplemental Fig. 64) recovered similar species relationships to those produced by MP and ML analyses. The Chickasaw Clade and American Clade were recovered. *Prunus maritima* was identified clustered to *P. umbellata*. *Prunus pumila* was found basal to all North American plums similar to the other outgroup species. Additional sequence data information and models of sequence evolution are available in Supplemental Tables 5, 6, 7, 9, and 11.

TREE ARCHITECTURE. A total of 16 axillary meristem formation and tree architecture genes [AXR1, BRC1, BRC2, CUC1, CUC2, CUC3, LAS, MAX1, MAX2, MAX3, MAX4, PIN, RAX1, RAX2-RAX3, REV, and SPS (Supplemental Table 3)] were sequenced in the 11 core species and 2 peach haploids. CUC1 and MAX1 amplified two targets in all the species studied. Both amplicons were purified, sequenced independently, and identified by A and B suffixes (i.e., CUC1A and CUC1B). *Prunus angustifolia* did not have a product being amplified corresponding to CUC1A (only product amplified for CUC1B).

A total of 6664 bp of sequence containing 426 PICS and having an average polymorphism rate of 6.39% was obtained (Table 4). Two or more indel polymorphisms were detected in the CUC2 amplicon. Additional internal primers were designed to allow the generation of unambiguous sequence data as specified in Supplemental Table 4. Primers designed for all the target sequences yielded product for all species. However, we were not able to completely sequence the BRC2 amplicon from *P. americana*. The highest polymorphisms rate within section *Prunocerasus* and between outgroup were obtained for MAX4, MAX1, CUC2, MAX3, and AXR1 (Table 4). Percent variability within section *Prunocerasus* was 5.02%, 5.53% (3.36% for MAX1A and 2.48% for MAX1B), 3.12%, 2.89%, and 2.28%, respectively (Fig. 3). A similar trend was observed for these genes polymorphism rate when the outgroup species was used for the analyses. MP and ML analyses of diploid and haplotype datasets for AXR1, BRC1 (only for MP), BRC2, CUC2, CUC3, LAS, MAX1 [MAX1A and MAX1B (only for MP)], MAX2, MAX3, MAX4, RAX1, RAX2-RAX3, REV, and SPS recovered section *Prunocerasus* as a monophyletic clade (Supplemental Figs. 11–28; Supplemental Tables 6 and 7). Additional results per gene region can be found in Supplemental Information.

MP and ML analyses of all the tree architecture genes diploid sequences recovered section *Prunocerasus* as a monophyletic group. *Prunus angustifolia* and *P. munsoniana* were

Fig. 3. Sequence variability $[(\text{substitutions} + \text{indels})/L] \times 100$, where L = the total aligned sequence length, comparisons for (A) section *Prunocerasus* vs. outgroup species and (B) exons vs. introns gene regions.

clustered together in all analyses (Chickasaw Clade). Similarly, *P. americana* and *P. mexicana* (American Clade), and *P. maritima* and *P. umbellata*, formed monophyletic clades, respectively. MP analyses (with gaps) yielded two major groups: 1) American Clade (*P. mexicana*, *P. americana*, and *P. hortulana*) and *P. geniculata* and 2) Chickasaw Clade (*P. umbellata*, *P. angustifolia*, and *P. munsoniana*) and *P. maritima*. ML analyses of all sequence data recovered similar species groups to MP analysis with gaps. *Prunus pumila* was identified as a sister species to section *Prunocerasus* (Supplemental Fig. 65).

The nonstandardized multilocus (phased haplotype) combined tree architecture genes sequence data network (Supplemental Fig. 66) recovered similar species relationships to those produced by MP (with gaps) and ML analyses. The Chickasaw Clade and American Clade were recovered. *Prunus maritima* was identified clustered to *P. umbellata* (similar to the isozyme-combined data analyses, Supplemental Fig. 64). Additional sequence data information and models of sequence evolution are presented in Supplemental Tables 5, 6, 7, 9, and 11.

VERNALIZATION. A total of 33 vernalization-related genes [AGL20-SOC1, AGL24, BFT, BRM, CO, CRY1, CRY2, ELF6, FD, FD1, FG, FLC-FLF, FPF1, FRIGIDA, FT-TSF, GI-FB, HOS1, LFY, MAF1-MAF3-AGL31, MAF2, MAF4, MAF5, MFT, PHYA, PHYB-PHYD, PHYE, RGA-RGA1, RGL1-RGL2-RGL3, SPY, TFL1-ATC, TFL2, VRN1, and VRN2 (Supplemental Table 3)] were sequenced in the 11 core

species and 2 peach haploids. MAF2 yielded duplicate products for all species. Duplicate bands were excised and sequenced as described in the Materials and Methods section. Duplicate products were designed using A and B suffixes (i.e., MAF2A and MAF2B).

The AGL20-SOC1 amplicons for *P. americana* and *P. munsoniana* could not be sequenced using the available primers and were removed from the dataset. *Prunus pumila*, *P. americana*, and *P. fasciculata* could not be sequenced for FLC-FLF. FRIGIDA sequences were difficult to assemble. *Prunus umbellata*, *P. angustifolia*, *P. mexicana*, *P. hortulana*, and *P. munsoniana* were not able to be sequenced for FRIGIDA. Similarly, *P. geniculata* and *P. pumila* were not sequenced for MAF2A, and *P. angustifolia* and haploids were not sequenced for MAF2B. The problems with the MAF2 amplicon were due to absence/presence of duplicate amplicon in some species.

A total of 15,646 bp of alignable sequence (1206 PICS, polymorphism rate of 7.71%) was obtained (Table 4). Two or more indels were identified for the ELF6, FT-TSF, GI-FB, LFY, and MAF4 amplicons in one or more species. These amplicons were resequenced for all the samples using specific internal primers as indicated in Supplemental Table 4.

The highest polymorphism rates were observed in MAF4, FLC-FLF, LFY, MAF2A, AGL20-SOC1, ELF6, and AGL24 (Table 4). Percent variability within section *Prunocerasus* was

Fig. 4. Phylogenetic analyses of combined chloroplast DNA sequence data (3584 bp). Majority rule consensus trees using (A) maximum parsimony [75 trees, 126 steps, consistency index (CI) = 0.929, retention index (RI) = 0.890, rescaled consistency index (RC) = 0.827] and (B) maximum parsimony (including gaps) (13 trees, 623 steps, CI = 0.918, RI = 0.809, RC = 0.743) analyses. Bootstrap values greater than 50% are described above the branches. (C) Maximum likelihood tree ($-\ln L = 5414.74$). Branch lengths are described above the branches and posterior probability values below the branches. Trees are rooted with *Prunus fasciculata*. Other species in the cladogram are: *P. americana* (PameFL12), *P. angustifolia* (PangGA25), *P. geniculata* (PgenFL115), *P. hortulana* (PhorMD89), *P. maritima* (PmarNY87), *P. mexicana* (PmexLN85), *P. munsoniana* (PmunTX88), *P. persica* (PperJP121), *P. pumila* (PbesIL15), and *P. umbellata* (PumbFL23).

0.0010

A

0.0010

B

Fig. 5. A nonstandardized multilocus combined chloroplast DNA sequence data network using: (A) gaps as missing characters and (B) gaps as fifth characters. *Prunus* species in the cladogram are: *P. americana* (PameFL12), *P. angustifolia* (PangGA25), *P. fasciculata* (PfasCA131), *P. geniculata* (PgenFL115), *P. hortulana* (PhorMD89), *P. maritima* (PmarNY87), *P. mexicana* (PmexLN85), *P. munsoniana* (PmunTX88), *P. persica* (PperJP121), *P. pumila* (PbesIL15), and *P. umbellata* (PumbFL23).

Table 4. Summary statistics of ITS (internal transcribed spacer) and nuclear gene regions sequenced for 11 *Prunus* species.

Regions	ITS		PGI		PGDH		s6pdh		AXR1		BRC1		BRC2	
Aligned L (bp) ^z	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst
American ^y	6	3	4	4	1	6	9	12	0	0	0	3	0	4
Beach ^y	5	1	6	6	1	14	3	5	0	5	0	2	0	0
Chickasaw ^y	1	4	2	5	2	10	3	4	0	6	0	1	0	0
<i>Prunocerasus</i> ^y	7	7	10	13	2	15	14	17	0	6	0	4	0	6
PICS ^x	14			23	17		31		6		4		6	
Percent variability ^w	2.30			7.69	3.56		4.93		2.28		1.34		2.01	
Outgroup ^y	11	41	3	9	0	14	7	13	0	5	0	2	0	8
PICS	52			12	14		20		5		2		8	
Percent variability	8.52			4.01	2.94		3.18		1.90		0.67		2.68	
Total PICS	66			35	31		51		11		6		14	
Normalized PICS	3.39			1.80	1.59		2.62		0.57		0.31		0.72	
Percent variability	10.82			11.71	6.50		8.11		4.18		2.01		4.70	
Regions	CUC1A ^u		CUC1B		CUC2		CUC3		LAS		MAX1A		MAX1B	
Aligned L (bp)	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst
American	430	2	0	1	1	6	0	5	0	5	3	2	0	2
Beach	1	4	1	3	0	8	2	4	0	4	2	3	1	4
Chickasaw	0	2	0	1	1	9	1	4	0	2	0	4	0	8
<i>Prunocerasus</i>	1	4	1	3	1	17	2	10	0	9	4	7	1	7
PICS	5			4	18		12		9		11		8	
Percent variability	1.16			1.31	3.12		2.37		2.38		3.36		2.48	
Outgroup	1	12	1	12	7	26	15	28	1	13	1	8	0	8
PICS	13			13	33		43		14		9		8	
Percent variability	3.02			4.26	5.72		8.50		3.70		2.75		2.48	
Total PICS	18			17	51		55		23		20		16	
Normalized PICS	0.93			0.87	2.62		2.83		1.18		1.03		0.82	
Percent variability	4.19			5.57	8.84		10.87		6.08		6.12		4.95	
Regions	MAX2		MAX3		MAX4		PIN		RAX1		RAX2-RAX3		REV	
Aligned L (bp)	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst
American	376	2	0	4	1	6	1	1	0	1	0	1	1	5
Beach	0	4	1	6	1	9	0	0	2	2	2	2	0	2
Chickasaw	0	0	0	2	0	6	2	3	1	2	1	1	0	3
<i>Prunocerasus</i>	0	5	1	8	1	11	3	3	2	5	2	2	1	6
PICS	5			9	12		6		7		4		7	
Percent variability	1.33			2.89	5.02		1.75		1.57		0.80		1.85	
Outgroup	1	10	4	20	0	15	2	6	2	15	5	16	5	19
PICS	11			24	15		8		17		21		24	
Percent variability	2.93			7.72	6.28		2.33		3.82		4.17		6.35	
Total PICS	16			33	27		14		24		25		31	
Normalized PICS	0.82			1.70	1.39		0.72		1.23		1.29		1.59	
Percent variability	4.26			10.61	11.30		4.08		5.39		4.97		8.20	

Continued next page

Table 4. Continued.

Regions	SPS	AGL24	AGL20-SOC1	BFT	BRM	CO	CRY1
Aligned <i>L</i> (bp)	363	494	444	458	366	419	500
American	3	2	8	0	8	2	1
Beach	0	5	6	0	1	1	5
Chickasaw	3	3	4	0	3	0	3
<i>Prunocerasus</i>	3	7	16	0	10	1	8
PICS	10	20	23	10	12	9	11
Percent variability	2.75	4.05	5.18	2.18	3.28	2.15	2.20
Outgroup	3	12	8	9	10	5	20
PICS	15	38	23	19	11	25	20
Percent variability	4.13	7.69	5.18	4.15	3.01	5.97	4.00
Total PICS	25	58	46	29	23	34	31
Normalized PICS	1.29	2.98	2.37	1.49	1.18	1.75	1.59
Percent variability	6.89	11.74	10.36	6.33	6.28	8.11	6.20
Regions	CRY2	ELF6	FD	FD1	FG	FLC-FLF	PPF1
Aligned <i>L</i> (bp)	450	593	536	481	394	499	329
American	Indels 2	Subst 3	Indels 0	Subst 3	Indels 3	Subst 6	Indels 8
Beach	0	4	1	0	4	4	8
Chickasaw	2	6	3	0	6	5	6
<i>Prunocerasus</i>	3	8	4	1	8	12	13
PICS	11	24	11	5	13	32	32
Percent variability	2.44	4.05	2.05	1.04	3.30	7.13	0.30
Outgroup	2	26	7	1	26	13	22
PICS	28	42	29	13	18	4	8
Percent variability	6.22	7.08	5.41	2.70	4.57	0.89	2.43
Total PICS	39	66	40	18	31	36	9
Normalized PICS	2.01	3.39	2.06	0.93	1.59	1.85	0.46
Percent variability	8.67	11.13	7.46	3.74	7.87	8.02	2.74
Regions	FRIGIDA	FT-TSF	GI-FB	HOS1	LFY	MAF1-MAF3-AGL31	MAF2A
Aligned <i>L</i> (bp)	630	507	577	198	615	496	268
American	1	0	5	0	6	19	5
Beach	3	9	3	0	6	22	1
Chickasaw	—	—	6	0	3	10	3
<i>Prunocerasus</i>	4	9	13	0	12	29	8
PICS	13	19	22	5	41	18	15
Percent variability	2.06	3.75	3.81	2.53	6.67	3.63	5.60
Outgroup	4	23	7	0	14	14	4
PICS	27	18	28	2	63	19	8
Percent variability	4.29	3.55	4.85	1.01	10.24	3.83	2.99
Total PICS	40	37	50	7	104	37	23
Normalized PICS	2.06	1.90	2.57	0.36	5.35	1.90	1.18
Percent variability	6.35	7.30	8.67	3.54	16.91	7.46	8.58

Continued next page

Table 4. Continued.

Regions	MAF2B		MAF4		MAF5		MFT		PHYA		PHYB-PHYD		PHYE	
Aligned <i>L</i> (bp)	335		474		310		395		493		500		499	
American	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst	Indels	Subst
Beach	1	1	6	5	0	2	0	6	0	0	0	2	1	6
Chickasaw	2	3	5	4	1	0	0	5	0	2	1	2	0	0
<i>Prunocerasus</i>	3	0	20	23	0	0	0	2	0	4	1	6	2	5
PICS	4	3	24	20	1	1	0	12	0	5	2	7	3	12
Percent variability	7		44		2		12		5		9		15	
Outgroup	2.09	4	9.28	33	0.65	24	3.04	16	1.01	7	1.80	16	2	3.01
PICS	9		47		33		19		7		18		17	
Percent variability	2.69		9.92		10.65		4.81		1.42		3.60		3.41	
Total PICS	16		91		35		31		12		27		32	
Normalized PICS	0.82		4.68		1.80		1.59		0.62		1.39		1.65	
Percent variability	4.78		19.20		11.29		7.85		2.43		5.40		6.41	
Regions	RGA-RGA1		RGL1-RGL2-RGL3		SPY		TFL1-ATC		TFL2		VRN1		VRN2	
Aligned <i>L</i> (bp)	454		510		506		457		499		592		418	
American	0	5	0	4	2	2	1	2	1	3	0	0	1	1
Beach	0	4	0	0	0	2	1	3	1	3	0	7	0	4
Chickasaw	0	8	0	0	2	5	0	5	1	6	0	4	1	4
<i>Prunocerasus</i>	0	10	0	4	2	8	2	6	0	10	0	8	2	6
PICS	10		4		10		8		10		8		8	
Percent variability	2.20		0.78		1.98		1.75		2.00		1.35		1.91	
Outgroup	0	6	1	30	3	15	9	9	7	15	0	23	9	19
PICS	6		31		18		18		22		23		28	
Percent variability	1.32		6.08		3.56		3.94		4.41		3.89		6.70	
Total PICS	16		35		28		26		32		31		36	
Normalized PICS	0.82		1.80		1.44		1.34		1.65		1.59		1.85	
Percent variability	3.52		6.86		5.53		5.69		6.41		5.24		8.61	

^zAligned *L* = total aligned sequence length.^yAmerican Clade = *Prunus americana*, *Prunus hortulana*, and *Prunus mexicana*; Beach Clade = *Prunus geniculata* and *Prunus maritima*; Chickasaw Clade = *Prunus angustifolia*, *Prunus munsoniana*, and *Prunus umbellata*; *Prunocerasus* = American Clade + Beach Clade + Chickasaw Clade.^xPotentially informative characters (PICS) = Indels + Subst. Indels = number of insertion/deletion events; subst = substitutions.^w $[(\text{Subst} + \text{Indels})/L] \times 100$, where *L* = the total aligned sequence length.^vOutgroup = *Prunus fasciculata*, *Prunus persica*, and *Prunus pumila*.^uGene symbols followed by letter A and B represent duplicate fragments amplified and independently sequenced using the same primer set. Genes with duplicate fragments were CUC1, MAX1, and MAF2. Gene symbols are described in Supplemental Table 3.

9.28%, 7.13%, 6.67%, 5.60%, 5.18%, 4.05%, and 4.05%, respectively (Fig. 3). Percent variability for the outgroup species did not show a similar trend. Some genes had higher polymorphic rates among outgroup species. Section *Prunocerasus* was monophyletic in MP and ML analyses using diploid and haplotype datasets for all gene regions except FPF1, MAF1-MAF3-AGL31, PHYA, and RGA-RGA1 (Supplemental Figs. 29–62; Supplemental Tables 6 and 7). MP analyses with gaps recovered some of the species relationships within section *Prunocerasus*, the American Clade and Chickasaw Clade, as previously identified using isozymes and tree architecture gene sequences.

AGL20-SOC1, BFT, BRM, CO, FD, FD1, FPF1, HOS1, MAF1-MAF3-AGL31, MAF2B, MAF4, MAF5, MFT, PHYA, PHYB-PHYD, RGA-RGA1, RGL1-RLG2-RLG3, TFL1-ATC, and VRN2, did not identify any novel relationships within section *Prunocerasus*. MP and ML analysis of phased haplotype data for these genes produced more species clusters to those produced using diploid data. *Prunus munsoniana* and *P. angustifolia* were clustered together (in some occasions also with *P. umbellata*). These additional groupings were not consistent across genes (Supplemental Figs. 30–62). Additional results per gene region can be found in Supplemental Information.

MP and ML analyses of combined vernalization-related genes diploid data recovered section *Prunocerasus* as a monophyletic group. *Prunus angustifolia* and *P. munsoniana* were clustered together in all analyses (Chickasaw Clade). Similar relationships were identified for *P. americana* and *P. mexicana*, and *P. maritima* and *P. umbellata*. MP analyses (with gaps) yielded three major groups: 1) Chickasaw Clade (*P. angustifolia* and *P. munsoniana*) and *P. geniculata*; 2) *P. umbellata* and *P. maritima*; and 3) American Clade (*P. mexicana*, *P. americana*, and *P. hortulana*). ML analyses of combined data recovered similar species groups to those produced by MP analysis with gaps. *Prunus pumila* was identified as sister species to section *Prunocerasus* (Supplemental Fig. 67).

The nonstandardized multilocus (phased haplotype) combined tree architecture genes sequence data network (Supplemental Fig. 68) recovered similar species relationships to those produced by MP (with gaps) and ML analyses. *Prunus maritima* was clustered to *P. umbellata* (similar to isozymes and tree architecture genes combined data analyses). Additional sequence data information and models of sequence evolution are available in Supplemental Tables 5, 6, 7, 9, and 11.

MP and ML analyses of the combined diploid sequence data for the nuclear genes (Fig. 6) recovered section *Prunocerasus* as a monophyletic group (similar to combined analyses of isozymes, tree architecture, and vernalization-related genes; Supplemental Figs. 63, 65, and 67, respectively). *Prunus angustifolia* and *P. munsoniana* were clustered together in all analyses (Chickasaw Clade). *Prunus americana* was paired with *P. mexicana*, and *P. maritima* with *P. umbellata*. Similarly, the nonstandardized multilocus sequence data network for the combined nuclear genes recovered similar relationships to those produced by MP and ML (Fig. 7).

Total evidence

The use of cytoplasmic and nuclear markers using the total evidence approach (consensus phylogeny) would allow for the tracking of maternal and paternal lineages present among species. A total of 27,909 bp of alignable sequence (1945

PICS, polymorphism rate of 6.97%) was obtained for cpDNA, ITS, and nuclear genes (Tables 3 and 4). Gene regions were summarized based on their polymorphism rate (percent variability within section *Prunocerasus* and the outgroup species. Sequence information represented both intron(s) and exon(s). As expected, intron(s) had the highest polymorphism rate across the core collection of 11 *Prunus* species (Fig. 3B; Supplemental Table 5).

Total evidence (combined diploid sequence data for cpDNA, ITS, and nuclear genes) MP (with gaps) analyses yielded two major groups: 1) American Clade (*P. mexicana*, *P. americana*, and *P. hortulana*) and *P. geniculata* and 2) Chickasaw Clade (*P. angustifolia*, *P. munsoniana*, and *P. umbellata*) and *P. maritima*. ML analyses of combined data recovered similar species groups to those recovered using MP analysis with gaps. *Prunus pumila* was identified as sister species to section *Prunocerasus* (Fig. 8).

The nonstandardized multilocus (phased haplotype) sequence data network for the combined tree architecture genes sequence data (Fig. 9) recovered similar species relationships to those produced by MP (with gaps) and ML analyses. *Prunus maritima* was clustered to *P. umbellata* (similar to isozymes, tree architecture, and vernalization-related genes combined data analyses). Additional sequence data information and models of sequence evolution are available in Supplemental Tables 5–11.

Discussion

The current discussion will be focused in the use of SSR, cpDNA, ITS, and nuclear genes for the phylogenetic analyses of a core collection of North American plum species to differentiate species relationships. Although, our results included more specific details of the analyses for each one of the gene regions, the discussion is focused on the applicability of these regions to determine species relationships.

Chloroplast DNA has been extensively used for phylogenetic studies in *Prunus* (Badenes and Parfitt, 1995; Bortiri et al., 2001, 2002, 2006; Kaneko et al., 1986; Katayama and Uematsu, 2005; Shaw and Small, 2004, 2005; Wen et al., 2008). However, evidence for hybridization among *Prunus* species may not be detected if the analysis is based solely on cpDNA information. Human disturbance, relocation of species, and other factors could increase contact between previously isolated species and facilitate their hybridization.

The existence of hybrids of native plum species with other *Prunus* species has been reported by Wight (1915) based on morphological traits. Wight (1915) reported that *P. americana* hybridized with *P. angustifolia*, *Prunus besseyi* (i.e., *P. pumila*), *P. hortulana*, *P. munsoniana*, and *P. simonnii*. Similarly, *P. angustifolia* hybridized freely with *P. americana*, *Prunus triflora*, *P. besseyi*, *P. munsoniana*, *P. cerasifera*, and *P. orthosepala*.

Shaw et al. (2005, 2007) identified chloroplast regions that provided the greatest number of characters for low-level molecular phylogenetic studies. From those, seven regions (out of eight) were sequenced for our core collection of 11 species. Our polymorphism rate estimates were different to those reported by Shaw et al. (2005, 2007) results. They used *P. hortulana*, *P. nigra*, and *Prunus virginiana* L. to determine the number of PICS. *Prunus hortulana* and *P. nigra* belong to subgenus *Prunus* section *Prunocerasus* and *P. virginiana* to subgenus *Cerasus*.

Fig. 6. Phylogenetic analyses of combined nuclear genes diploid sequence data (23,429 bp). Majority rule consensus trees using (A) maximum parsimony [2 trees, 1400 steps, consistency index (CI) = 0.913, retention index (RI) = 0.920, rescaled consistency index (RC) = 0.840] and (B) maximum parsimony (including gaps) (1 tree, 2535 steps, CI = 0.879, RI = 0.881, RC = 0.775) analyses. Bootstrap values greater than 50% are described above the branches. (C) Maximum likelihood tree (-lnL = 41,509.34). Branch lengths are described above the branches and posterior probability values below the branches. Trees are rooted with *Prunus fasciculata*. (PfasCA131). Other species in the cladogram are: *P. americana* (PameFL12), *P. angustifolia* (PangGA25), *P. geniculata* (PgenFL115), *P. hortulana* (PhorMD89), *P. maritima* (PmarNY87), *P. mexicana* (PmexLN85), *P. munsoniana* (PmunTX88), *P. persica* (PperJP121), *0201c_hap*, *AP0518ws_hap*, *P. pumila* (PbesIL15), and *P. umbellata* (PumbFL23).

Fig. 7. A nonstandardized multilocus combined nuclear genes sequence data network using (A) gaps as missing characters and (B) gaps as fifth characters. *Prunus* species in the cladogram are: *P. americana* (PameFL12), *P. angustifolia* (PangGA25), *P. fasciculata* (PfasCA131), *P. geniculata* (PgenFL115), *P. hortulana* (PhorMD89), *P. maritima* (PmarNY87), *P. mexicana* (PmexLN85), *P. munsoniana* (PmunTX88), *P. persica* (PperJP121, 0201c_hap, AP0518ws_hap), *P. pumila* (PbesIL15), and *P. umbellata* (PumbFL23).

Fig. 8. Phylogenetic analyses of combined nuclear + chloroplast DNA + internal transcribed spacer diploid sequence data (27,623 bp). Majority rule consensus trees using (A) maximum parsimony [1 tree, 1,594 steps, consistency index (CI) = 0.908, retention index (RI) = 0.910, rescaled consistency index (RC) = 0.827] and (B) maximum parsimony (including gaps) (2 trees, 2,732 steps, CI = 0.878, RI = 0.875, RC = 0.768) analyses. Bootstrap values greater than 50% are described above the branches. (C) Maximum likelihood tree (-lnL = 48,496.34). Branch lengths described above the branches and posterior probability values below the branches. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are: *P. americana* (PameFL12), *P. angustifolia* (PangGA25), *P. geniculata* (PgenFL115), *P. hortulana* (PhorMD89), *P. maritima* (PmarNY87), *P. mexicana* (PmexLN85), *P. munsoniana* (PmunTX88), *P. persica* (PperJP121), 0201c_hap, AP0518ws_hap, *P. pumila* (PbesIL15), and *P. umbellata* (PumbFL23).

Fig. 9. A nonstandardized multilocus combined nuclear + chloroplast DNA + internal transcribed spacer sequence data network using (A) gaps as missing characters and (B) gaps as fifth characters. *Prunus* species in the cladogram are: *P. americana* (PameFL12), *P. angustifolia* (PangGA25), *P. fasciculata* (PfasCA131), *P. geniculata* (PgenFL115), *P. hortulana* (PhorMD89), *P. maritima* (PmarNY87), *P. mexicana* (PmexLN85), *P. munsoniana* (PmunTX88), *P. persica* (PperJP121, 0201c_hap, AP0518ws_hap), *P. pumila* (PbesIL15), and *P. umbellata* (PumbFL23).

The regions with the highest PICS proved to be beneficial for the recovery of the phylogenetic relationships within section *Prunocerasus* (based on Shaw and Small, 2004).

Our analyses showed that the highest polymorphism rate (indels and substitutions) were mostly found at the outgroup level (Tables 3 and 4; Fig. 3). The limited number of species within section *Prunocerasus* and the broad comparison of levels across the genus *Prunus* was probably the reason for the higher polymorphism rates reported by Shaw et al. (2005, 2007). The highest frequency of informative sites in our study was observed in 3'*trnV-ndhC* and *trnH-psbA* cpDNA regions (Fig. 3). Similar results were reported by Shaw et al. (2005, 2007).

It is important to recognize that although PICS are a good measure of how informative a region could be for a phylogenetic analysis, it did not represent the final phylogenetic relationships obtained from that region. Both methods were combined to select regions that could be used across species levels to identify phylogenetic patterns.

The presence of common alleles between the different species could be evidence for interspecific hybridization and gene flow between species. The use of cytoplasmic and nuclear markers would allow for the tracking of maternal and paternal lineages present in a more diverse phylogenetic study (Chavez, 2013).

Rohrer et al. (2004) analyzed the values of SSRs to resolve the relationships within *Prunus* at the species level. He concluded that the resolution of species relationships within section *Prunocerasus* required the use of regions more variable than ITS and less variable than SSRs. In our study, the outgroup species clustered together using 41 and six (highest PIC values) SSRs (Fig. 2). Cluster analyses using information from the 41 SSRs supported *P. angustifolia* and *P. munsoniana* as sister species to *P. mexicana* and *P. geniculata*. Similarly, *P. americana*, *P. maritima*, and *P. umbellata* clustered together. No previously reported relationships (such as the American Clade, Beach Clade, and Chickasaw Clade) were obtained.

Analysis of the species with the six SSR primers with the highest PIC values identified *P. mexicana* as sister species to all the outgroup species. The Beach Clade (*P. geniculata* and *P. maritima*) and Chickasaw Clade (*P. angustifolia* and *P. munsoniana*) were recovered. *Prunus americana* and *P. umbellata* were monophyletic, and *P. hortulana* was found basal to all the section *Prunocerasus* Clade (Fig. 2).

The SSR data indicated a high level of heterozygosity as described by Rohrer et al. (2004). The use of SSRs distributed across the genome was expected to provide a sample of different levels of polymorphisms. However, it was observed that the use of six SSR markers (with the highest PIC values) yielded more consistent results than the analyses with 41 SSR markers, in comparison with known phylogenetic relationships in section *Prunocerasus* (Shaw and Small, 2004).

The observed level of heterozygosity for all genotypes was high compared with University of Florida's peach germplasm, 0.58 and 0.41, respectively (Chavez et al., 2014). Wild *Prunus* species typically express gametophytic self-incompatibility, making them highly heterozygous. Our results were concordant with these expectations.

ITS results were consistent with the remarks of Rohrer et al. (2004). He was not able to define the species relationships within section *Prunocerasus* using this region. In our study, ITS sequence data were an important baseline for comparison with other regions (nuclear and cpDNA). A polymorphism rate of

10.82% was obtained for ITS (Table 4). This rate was intermediate between nuclear (high) and cpDNA (low) regions. The results obtained from the ITS phylogenetic results were consistent with our cpDNA results (Supplemental Fig. 7).

Three different groups of nuclear genes were used in this study: 1) isozymes, 2) tree architecture genes, and 3) vernalization-related genes. The isozyme genes were used due to their expected neutrality to selection and adaptation. The highest PICS values within section *Prunocerasus* and between outgroup were obtained for PGI, followed by *s6pdh* and PGDH (Table 4; Fig. 3). Section *Prunocerasus* was recovered as a monophyletic clade for all analyses (Supplemental Figs. 8–10; Supplemental Tables 6 and 7). These regions were more variable than cpDNA and less variable than ITS within section *Prunocerasus* (Fig. 3). Similar results were also obtained for tree architecture and vernalization-related genes (Supplemental Figs. 11–62; Supplemental Tables 6 and 7).

The tree architecture and vernalization-related genes were used due to their importance in plant development and expected selection and adaptation pressure. The highest PICS values within section *Prunocerasus* and between outgroup for tree architecture genes were obtained for MAX4, MAX1, CUC2, MAX3, and AXR1 (Table 4). Section *Prunocerasus* was recovered as a monophyletic clade with MP and ML analyses using diploid and haplotype datasets (Supplemental Figs. 11–28; Supplemental Tables 6 and 7). MP analyses with gaps did provide additional support (bootstrap) for some clades when using different genes. Similarly, the highest amount of PICS within section *Prunocerasus* and between outgroup for vernalization-related genes were observed in MAF4, FLC-FLF, LFY, MAF2A, AGL20-SOC1, ELF6, and AGL24 (Table 4). Section *Prunocerasus* was monophyletic in MP and ML analyses using diploid and haplotype datasets for all gene regions except FPF1, MAF1-MAF3-AGL31, PHYA, and RGA-RGA1 (Supplemental Figs. 29–62; Supplemental Tables 6 and 7). MP analyses with gaps recovered additional species grouping within section *Prunocerasus*.

MP and ML phased haplotype and the nonstandardized multilocus analyses yielded similar results as using diploid sequence data. This consistency across analyses and different gene regions supported the presence of a phylogenetic signal. It was observed that regions with the highest polymorphism rates within section *Prunocerasus* allowed identification of additional species relationships (clades), as compared with known clades in section *Prunocerasus* (Shaw and Small, 2004). These regions constituted good candidates for future phylogenetic relationships in *Prunus*.

MP and ML analyses of isozymes, tree architecture, and vernalization-related genes found two major groups, similar to those described by Waugh's (1901) classification of section *Prunocerasus*. The American Clade and Chickasaw Clade were identified in our analyses. Our results support section *Prunocerasus* as a monophyletic group using individual and combined analyses as previously reported by Bortiri et al. (2001) and Shaw and Small (2004). However, there was no evidence for *P. maritima* and *P. geniculata* being sister species (Beach Clade) as reported by Shaw and Small (2004). In the majority of the analyses, *P. maritima* was supported as a member of the Chickasaw Clade (in specific sister species to *P. umbellata*). Similarly, *P. geniculata* was identified as a member species of the American Clade (Supplemental Figs. 63–68; Figs. 6 and 7).

Our analyses provided similar results to those reported by Mowrey and Werner (1990). They identified a clade formed by *P. maritima* and *P. umbellata* within section *Prunocerasus* based on isozyme data. In another study, Rohrer et al. (2008) used LEAFY and *s6pdh* sequences to examine the North American plums phylogeny. They reported that *P. geniculata* was clustered with *P. texana*. In addition, *P. umbellata*, *P. maritima*, *P. alleghaniensis*, and *P. gracilis* formed a paraphyletic group using LEAFY.

The use of different sequence regions, in a core collection of section *Prunocerasus* and outgroup species, constituted an important study to identify genome regions with the highest level (number) of PICS and the most valuable phylogenetic signal based on previously known clades within section *Prunocerasus* (Shaw and Small, 2004). Out of the 52 nuclear genes (3 isozyme, 16 tree architecture, and 33 vernalization-related genes), 7 cpDNA regions, and ITS sequences, *trnH-psbA*, PGI, MAX4, AXR1, LFY, PHYE, and VRN1, are recommended and chosen to be used for a phylogenetic analysis with a larger number of taxa. Regions with high polymorphism rates and strong phylogenetic signal as compared with known phylogenetic relationships within section *Prunocerasus* were *trnH-psbA*, PGI, MAX4, AXR1, and LFY. PHYE and VRN1 were regions with low polymorphism rates. However, they presented a strong phylogenetic signal (polymorphism within these regions were highly informative).

Conclusions

The identification and use of additional genomic regions that provided the greatest number of characters, greatest variability, and improved the phylogenetic signal at the low level in *Prunus* section *Prunocerasus* relationships was achieved. The PICS content was highly variable across regions, with nuclear genes being the highest, followed by ITS, and cpDNA regions. The species relationships within section *Prunocerasus* and outgroup species were recovered for the majority of regions in comparison with known clades as reported by Shaw and Small (2004). Our study yielded a set of candidate regions that could be used for future phylogenetic relationships in *Prunus*.

It is important to identify PICS as a good measure of how informative a region will be for phylogenetic analysis, but always complemented with the phylogenetic analysis by itself. A preliminary study should always include several species that fall in different levels of the genus of study. Both methods should be combined to select regions that will provide the most value.

These sequences could be used to create hybridization probes for microarray chips to study the presence or absence of certain polymorphic sites associated with vernalization response, and plant architecture and branching genes.

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Supplemental Information

TREE ARCHITECTURE. AXR1 recovered the American Clade relationships in diploid sequence analyses using maximum parsimony (MP) and maximum likelihood (ML). In haploid sequence analyses, two major groups were identified: 1) *Prunus maritima*, *Prunus umbellata*, and *Prunus angustifolia*, which shared the same haplotype sequence and 2) *Prunus angustifolia* (additional haplotype), *Prunus geniculata*, *Prunus munsoniana*, *Prunus mexicana*, *Prunus americana*, and *Prunus hortulana*. Both groups represented the Chickasaw Clade and the American Clade. *P. geniculata* and *P. angustifolia* haplotypes contained haplotypes in each clade (Supplemental Fig. 11). AXR1 recovered the American Clade and the Chickasaw Clade within section *Prunocerasus* and constituted a good candidate for further studies in genus *Prunus*.

BRC1, BRC2, and CUC1 (CUC1A and CUC1B) sequence data provided limited information for elucidating species relationships within section *Prunocerasus*. MP analyses recovered section *Prunocerasus* as a monophyletic group [except for CUC1 (Supplemental Figs. 12–15)]. The polymorphism rate of these genes was similar to some of the cpDNA regions. These regions could be candidates for analyses at the subgenus/genus level in *Prunus*.

Analysis of CUC2 recovered section *Prunocerasus* as monophyletic group in MP and ML analyses using diploid and phased haplotype sequence data. *Prunus americana*, *P. maritima*, and *P. mexicana* clustered together in both analyses (Supplemental Fig. 16). Similarly, CUC3 phylogenetic analyses differentiated section *Prunocerasus* from the outgroup species for MP and ML analyses. Only the ML analyses of the diploid sequence data yielded monophyletic clades that supported the Beach Clade (with *P. umbellata* joined to this clade), the American Clade, and the Chickasaw Clade within section *Prunocerasus*. Haplotype sequence analyses recovered species haplotypes in different clades (Supplemental Fig. 17).

LAS analyses yielded a monophyletic clade for section *Prunocerasus*. The diploid MP analyses did not identify additional relationships. Diploid ML and phased haplotype MP–ML analyses presented *P. americana* and *P. mexicana* clustered together. Similarly, *P. angustifolia*, *P. umbellata*, and *P. munsoniana* (from the Chickasaw Clade) were clustered together (Supplemental Fig. 18).

Analysis of diploid and haplotype sequence for MAX1 [MAX1A and MAX1B (only for MP)] also identified section *Prunocerasus* as a monophyletic group, but it did not provide any additional resolution to species relationships within section *Prunocerasus* (Supplemental Figs. 19 and 20). Similarly, MAX2, MAX3, PIN, and RAX1 did not recover any species relationships within section *Prunocerasus* (Supplemental Figs. 21, 22, 24, and 25).

MAX4 identified section *Prunocerasus* as a monophyletic clade. Two major groups were recovered within section *Prunocerasus* in all analyses: 1) American Clade species and *P. geniculata* and 2) Chickasaw Clade species, *Prunus pumila* and *P. maritima* (Supplemental Fig. 23). This was the region with the highest percent variability. MP and ML recovered several species clusters within section *Prunocerasus*. MAX4 is a good candidate for a whole phylogenetic analysis to identify additional species clades in section *Prunocerasus*.

RAX2–RAX3 recovered Chickasaw Clade relationships in diploid sequence analyses using MP (with gaps) and ML.

Prunus maritima, *P. umbellata*, and *P. angustifolia* shared the same haplotype sequence and were clustered together (Supplemental Fig. 26). The phylogenetic relationships identified with RAX2–RAX3 were somewhat similar to those recovered with AXR1. No additional species groupings were obtained.

REV differentiated section *Prunocerasus* from the outgroup species in MP and ML analyses. The American Clade species, *P. americana* and *P. mexicana*, were clustered together in MP analyses. Additional species relationships within section *Prunocerasus* were recovered when using phased haplotype sequences (Supplemental Fig. 27).

VERNALIZATION. MP clustered the Chickasaw Clade species and *P. geniculata* together using the AGL24 diploid and phased haplotype data. ML analyses did not yield similar results. *Prunus maritima* was located near the base of section *Prunocerasus*. Haplotype MP phylogenetic analysis recovered the American Clade and the Chickasaw Clade (Supplemental Fig. 29). The use of gaps in this analysis did not provide additional information. This region had some difficulties during sequencing due to high polymorphisms. Additional internal primers could be created to improve sequence quality and coverage.

CRY1 identified section *Prunocerasus* as a monophyletic group in MP analyses with diploid and phased haplotype sequence data. *Prunus munsoniana* and *P. angustifolia* were clustered together (Chickasaw Clade). This clade was sister to the other species within section *Prunocerasus*. *Prunus maritima* and *P. umbellata* were identified in a cluster. No additional species relationships were observed (Supplemental Fig. 34).

CRY2, ELF6, and FG diploid data analyses generated somewhat similar results than CRY1 (Supplemental Figs. 35–37). *Prunus munsoniana* and *P. angustifolia* were clustered together (Chickasaw Clade). However, different species relationships were identified when using haplotype sequence data for each region. ELF6 MP analyses (with gaps) for diploid and haplotype data yielded more species clusters than their counterpart. FG phased haplotype MP and ML analyses recovered the Americana Clade and Chickasaw Clade relationships. No additional clusters were identified across these genes.

FLC–FLF recovered section *Prunocerasus* as a monophyletic clade. Additional species relationships within this section were not consistent, with MP (with and without gaps) and ML analyses producing different results (Supplemental Fig. 40). This region did not improve species phylogenetic relationships within section *Prunocerasus*, although this region had high polymorphism rate in comparison with other gene regions. Furthermore, *P. americana*, *P. fasciculata*, and *P. pumila* were not able to be sequenced with the primers designed (multiple fragments).

FRIGIDA phylogenetic analyses were not representative of the core collection species relationships as the *P. umbellata*, *P. angustifolia*, *P. mexicana*, *P. hortulana*, and *P. munsoniana* amplicons were not able to be sequenced. FRIGIDA MP and ML analyses of diploid and phased haplotype sequence data did recover section *Prunocerasus* as a monophyletic clade (Supplemental Fig. 42).

FT–TSF analyses supported section *Prunocerasus* as a monophyletic clade. MP analyses clustered *P. angustifolia*, *P. munsoniana*, and *P. geniculata* in one clade. Similarly, *P. maritima* and *P. umbellata* were identified as sister species in other clade. MP analyses using gaps (as additional characters)

improved support for some clades. The American Clade was recovered. Analyses with phased haplotype sequence data yielded similar results. No major clades representing the American Clade and Chickasaw Clades within section *Prunocerasus* were found (Supplemental Fig. 43).

GI-FB analyses supported section *Prunocerasus* monophyly. Two major groups were obtained in MP (with gaps) and ML analyses using diploid and haplotype sequence data: 1) American Clade (*P. americana*, *P. mexicana*, and *P. hortulana*) and 2) Chickasaw Clade and Beach Clade species. Haplotype analyses did not show any additional groupings (Supplemental Fig. 44).

LFY identified section *Prunocerasus* as a monophyletic clade. Two major groups were recovered within section *Prunocerasus* for all analyses: 1) American Clade species and *P. geniculata* and 2) Chickasaw Clade species and *P. maritima* (Supplemental Fig. 46). This region had a high polymorphism rate and recovered several species relationships within section *Prunocerasus* as described above. LFY is a good candidate for a whole phylogenetic analysis within section *Prunocerasus*. Similar results were observed for MAF2A (Supplemental Fig. 48). MP analyses including gaps increased support for each clade. Diploid and phased haplotype results were similar.

PHYE analyses produced similar results that LFY and MAF2A phylogenetic results. One group represented Chickasaw Clade and Beach Clade species. The other group

represented American Clade species. No additional support was obtained by using gaps in MP. Haplotype sequence data produced similar results to those produced by diploid data (Supplemental Fig. 55).

SPY-MP analyses with diploid and phased haplotype sequence data recovered *P. americana* and *P. mexicana* clustered together (American Clade). Similarly, *P. angustifolia* and *P. munsoniana* were found as sister species (Chickasaw Clade). ML analyses did not support any species relationships (Supplemental Fig. 58). Similarly, *P. angustifolia* and *P. munsoniana* were supported as sister species using TFL2 diploid and phased haplotype sequence data (Supplemental Fig. 60).

VRN1 supported section *Prunocerasus* monophyly. Two major groups were recovered within section *Prunocerasus* for all analyses: 1) American Clade species, *P. umbellata* and *P. maritima* and 2) Chickasaw Clade species. *Prunus maritima* was observed in a polytomy with the Chickasaw Clade (Supplemental Fig. 65). Results from diploid and haplotype sequence data were similar. No additional species clusters were identified using haplotype sequence data. VRN1 had a small polymorphism rate of 1.35% within section *Prunocerasus*. However, VRN1 is a good candidate for a whole phylogenetic analysis within section *Prunocerasus*, because its few amount of potentially informative characters represented a good phylogenetic signal.

Supplemental Fig. 1. Majority rule consensus trees for 3'trnV-ndhC chloroplast DNA region diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and sequence data (with haplotype number prefix) using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 2. Majority rule consensus trees for *trnL-trnF* and *trnL* intron chloroplast DNA regions diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and sequence data (haplotypes) using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 3. Majority rule consensus trees for *trnQ*-5' *rps16* chloroplast DNA region diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and sequence data (with haplotype number prefix) using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 4. Majority rule consensus trees for *trnH-psbA* chloroplast DNA region sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and sequence data (with haplotype number prefix) using (D) maximum parsimony (including gaps) and (E) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 5. Majority rule consensus trees for *ndhF-rpL32* chloroplast DNA region diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and sequence data (with haplotype number prefix) using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 6. Majority rule consensus trees for *atpB-rbcL* chloroplast DNA region diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and sequence data (with haplotype number prefix) using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 7. Majority rule consensus trees for internal transcribed spacer diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 8. Majority rule consensus trees for PGDH diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 9. Majority rule consensus trees for PGI diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 10. Majority rule consensus trees for S6PDH diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 11. Majority rule consensus trees for AXR1 diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and haplotypic sequence data using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 12. Majority rule consensus trees for BRC1 diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and haplotypic sequence data using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 13. Majority rule consensus trees for BRC2 diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and haplotypic sequence data using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 14. Majority rule consensus trees for CUC1A diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 15. Majority rule consensus trees for CUC1B diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 16. Majority rule consensus trees for CUC2 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 17. Majority rule consensus trees for CUC3 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 18. Majority rule consensus trees for LAS diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 19. Majority rule consensus trees for MAX1A diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 20. Majority rule consensus trees for MAX1B diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 21. Majority rule consensus trees for MAX2 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 22. Majority rule consensus trees for MAX3 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 23. Majority rule consensus trees for MAX4 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), 0201c_hap, AP0518ws_hap, *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 24. Majority rule consensus trees for PIN diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 25. Majority rule consensus trees for RAX1 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, O201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 26. Majority rule consensus trees for RAX2-RAX3 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 27. Majority rule consensus trees for REV diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 28. Majority rule consensus trees for SPS diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 29. Majority rule consensus trees for AGL24 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 30. Majority rule consensus trees for AGL20-SOC1 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 31. Majority rule consensus trees for BFT diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 32. Majority rule consensus trees for BRM diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 33. Majority rule consensus trees for CO diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 34. Majority rule consensus trees for CRY1 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 35. Majority rule consensus trees for CRY2 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 37. Majority rule consensus trees for FD diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 38. Majority rule consensus trees for FD1 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 39. Majority rule consensus trees for FG diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 40. Majority rule consensus trees for FLC-FLF diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 41. Majority rule consensus trees for FPF1 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 42. Majority rule consensus trees for FRIGIDA diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 43. Majority rule consensus trees for FT-TSF diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 45. Majority rule consensus trees for HOS1 diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and haplotypic sequence data using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 46. Majority rule consensus trees for LFY diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 47. Majority rule consensus trees for MAF1-MAF3-AGL31 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 48. Majority rule consensus trees for MAF2A diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 49. Majority rule consensus trees for MAF2B diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 50. Majority rule consensus trees for MAF4 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), 0201c_hap, AP0518ws_hap, *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 51. Majority rule consensus trees for MAF5 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 52. Majority rule consensus trees for MFT diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, O201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 53. Majority rule consensus trees for PHYA diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and haplotypic sequence data using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 54. Majority rule consensus trees for PHYB-PHYD diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, O201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 55. Majority rule consensus trees for PHYE diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 56. Majority rule consensus trees for RGA-RGA1 diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and haplotypic sequence data using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 57. Majority rule consensus trees for RGL1-RGL2-RGL3 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 58. Majority rule consensus trees for SPY diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 59. Majority rule consensus trees for TFL1-ATC diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 60. Majority rule consensus trees for TFL2 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 61. Majority rule consensus trees for VRN1 diploid sequence data using (A) maximum parsimony and (B) maximum likelihood; and haplotypic sequence data using (C) maximum parsimony and (D) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 62. Majority rule consensus trees for VRN2 diploid sequence data using (A) maximum parsimony, (B) maximum parsimony (including gaps), and (C) maximum likelihood; and haplotypic sequence data using (D) maximum parsimony, (E) maximum parsimony (including gaps), and (F) maximum likelihood. Bootstrap values greater than 50% are described above the branches for maximum parsimony tree. Posterior probability values are described above the branches for maximum likelihood tree. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 63. Phylogenetic analyses of combined isozymes diploid sequence data (1399 bp). Majority rule consensus trees using (A) maximum parsimony [38 trees, 82 steps, consistency index (CI) = 0.902, retention index (RI) = 0.922, rescaled consistency index (RC) = 0.832] and (B) maximum parsimony (including gaps) (4 trees, 127 steps, CI = 0.874, RI = 0.890, RC = 0.778) analyses. Bootstrap values greater than 50% are described above the branches. (C) Maximum likelihood tree ($-\ln L = 2464.46$). Branch lengths described above the branches and posterior probability values below the branches. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121), 0201c_hap, AP0518ws_hap, *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 64. A nonstandardized multilocus combined isozymes genes sequence data network using (A) gaps as missing characters and (B) gaps as fifth characters. *Prunus* species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus fasciculata* (PfasCA131), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 65. Phylogenetic analyses of combined tree architecture genes diploid sequence data (6659 bp). Majority rule consensus trees using (A) maximum parsimony [10 trees, 363 steps, consistency index (CI) = 0.917, retention index (RI) = 0.927, rescaled consistency index (RC) = 0.850] and (B) maximum parsimony (including gaps) (2 trees, 560 steps, CI = 0.914, RI = 0.920, RC = 0.842) analyses. Bootstrap values greater than 50% are described above the branches. (C) Maximum likelihood tree ($-\ln L = 11,668.52$). Branch lengths described above the branches and posterior probability values below the branches. Trees are rooted with *Prunus fasciculata* (*PfasCA131*). Other species in the cladogram are *Prunus americana* (*PameFL12*), *Prunus angustifolia* (*PangGA25*), *Prunus geniculata* (*PgenFL115*), *Prunus hortulana* (*PhorMD89*), *Prunus maritima* (*PmarNY87*), *Prunus mexicana* (*PmexLN85*), *Prunus munsoniana* (*PmunTX88*), *Prunus persica* (*PperJP121*, *0201c_hap*, *AP0518ws_hap*), *Prunus pumila* (*PbesIL15*), and *Prunus umbellata* (*PumbFL23*).

Supplemental Fig. 66. A nonstandardized multilocus combined tree architecture genes sequence data network using (A) gaps as missing characters and (B) gaps as fifth characters. *Prunus* species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus fasciculata* (PfasCA131), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 67. Phylogenetic analyses of combined vernalization-related genes diploid sequence data (15,371 bp). Majority rule consensus trees using (A) maximum parsimony [2 trees, 943 steps, consistency index (CI) = 0.924, retention index (RI) = 0.929, rescaled consistency index (RC) = 0.859] and (B) maximum parsimony (including gaps) (2 trees, 1876 steps, CI = 0.875, RI = 0.876, RC = 0.766) analyses. Bootstrap values greater than 50% are described above the branches. (C) Maximum likelihood tree (–lnL = 27,249.04). Branch lengths described above the branches and posterior probability values below the branches. Trees are rooted with *Prunus fasciculata* (PfasCA131). Other species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Fig. 68. A nonstandardized multilocus combined vernalization-related genes sequence data network using (A) gaps as missing characters and (B) gaps as fifth characters. *Prunus* species in the cladogram are *Prunus americana* (PameFL12), *Prunus angustifolia* (PangGA25), *Prunus fasciculata* (PfasCA131), *Prunus geniculata* (PgenFL115), *Prunus hortulana* (PhorMD89), *Prunus maritima* (PmarNY87), *Prunus mexicana* (PmexLN85), *Prunus munsoniana* (PmunTX88), *Prunus persica* (PperJP121, 0201c_hap, AP0518ws_hap), *Prunus pumila* (PbesIL15), and *Prunus umbellata* (PumbFL23).

Supplemental Table 1. Simple sequence repeat markers selected from the ‘Texas’ almond (*Prunus dulcis*) × ‘Earlygold’ peach (T × E) reference map.

Chromosome	Position	Marker	Fluorophore	Ta (°C) ^z	Forward sequence	Reverse sequence
1	9	CPSCT008	HEX	62	TGGATCCAATCCAAGAGTCTG	GCAGCAAGTTGTTCTTGGTTC
1	25.8	CPDCT038	HEX	62	ATCACAGGTGAAGGCTGTGG	CAGATTCATTGGCCCATCTT
1	33.9	CPPCT026	HEX	55	AGACGCAGCACCCAACTAC	CATTACATCACCGCCAACAA
1	47.3	BPPCT027	HEX	57	GGACGGACAGAAATGAAGGT	CCTTAACCCACGCAACTCC
1	55.2	BPPCT016	HEX	57	GATTGAGAGATTGGGCTGC	GAGGATTCTCATGATTTGTGC
1	65.1	CPPCT029	HEX	55	CCAAATTCCAAATCTCCTAACA	TGATCAACTTTGAGATTGTGAA
1	77.4	BPPCT028	HEX	57	TCAAGTTAGCTGAGGATCGC	GAGCTTGCCATGAGAAGACC
2	9.6	UDP98-025	FAM	57	GGGAGGTACTATGCCATGAAG	CGCAGACATGTAGTAGGACCTC
2	25	BPPCT013	HEX	57	ACCCACAAATCAAGCATATCC	AGCTTCAGCCACCAAGC
2	38	BPPCT030	HEX	57	AATTGTACTTGCCAATGCTATGA	CTGCCTTCTGCTCACACC
2	48.6	CPSCT034	HEX	62	AGGTGGACAATAGCCGTGAT	TTTCCAGACCCTGAGAAAGC
3	18	BPPCT039	FAM	57	ATTACGTACCCTAAAGCTTCTGC	GATGTCATGAAGATTGGAGAGG
3	36.4	CPDCT025	HEX	62	GACCTCATCAGCATCACCAA	TTCCCTAACGTCCCTGACAC
3	46.4	CPDCT027	HEX	62	TGAGGAGAGCACTGGAGGAG	CAACCGATCCCTCTAGACCA
4	10.4	CPPCT005	FAM	52	CATGAACTCTACTCTCCA	TGGTATGGACTCACCAAC
4	28.3	UDP96-003	FAM	57	TTGCTCAAAAGTGTCGTTGC	ACACGTAGTGCAACACTGGC
4	34.1	EPDC3832	FAM	57	CTTTTGAAGGCCAATACCA	ATCACTGCTTCGCCTTCATT
4	45.4	BPPCT023	HEX	57	TGCAGCTCATTACCTTTTGC	AGATGTGCTCGTAGTTCGGAC
4	52.7	EPPISF032	HEX	57	TCCCCACAGATAATTTTCAGC	GTCGAGGAGAGAGGGCTTTT
5	5.2	BPPCT026	FAM	57	ATACCTTTGCCACTTGCG	TGAGTTGGAAGAAAACGTAACA
5	20.1	BPPCT017	HEX	57	TTAAGAGTTTGTGATGGGAACC	AAGCATAATTTAGCATAACCAAGC
5	32.9	BPPCT038	FAM	57	TATATTGTTGGCTTCTTGCATG	GAGCTTGCCATGAGAAGACC
5	44	BPPCT014	HEX	57	TTGTCTGCCTCTCATCTTAACC	CATCGCAGAGAACTGAGAGC
6	8.7	CPPCT008	FAM	59	GAGCTCTCACGCATTAGTTT	TTTGACTGCATAACAAAACG
6	17.5	UDP96-001	HEX	57	AGTTTGATTTTCTGATGCATCC	TGCCATAAGGACCGGTATGT
6	30.1	BPPCT008	FAM	57	ATGGTGTGTATGGACATGATGA	CCTCAACCTAAGACACCTTCACT
6	35.8	CPPCT015	FAM	50	TGGAGTGCCAATACTATTTA	CATATGCATGGTTATGGT
6	41	EPPISF002	FAM	56	CGACGTGTGACCAAAGGAC	GCAACTCCATCCACATTTCTC
6	56.4	BPPCT025	FAM	57	TCCTGCGTAGAAGAAGGTAGC	CGACATAAAGTCCAAATGGC
6	72	UDP98-412	HEX	57	AGGGAAAAGTTTCTGCTGCAC	GCTGAAGACGACGATGATGA
7	9.5	CPSCT004	FAM	62	GCTCTGAAGCTCTGCATTGA	TTTGAAATGGCTATGGAGTACG
7	18.6	CPPCT022	FAM	50	CAATTAGCTAGAGAGAATTATTG	GACAAGAAGCAAGTAGTTTG
7	29.6	BPPCT029	FAM	57	GGACGGACAGAAATGAAGGT	CCTTAACCCACGCAACTCC
7	38.9	CPPCT033	HEX	50	TCAGCAAAGTAAACAAACC	TTGCAATCTGGTTGATGTT
7	47.8	PMS2	FAM	55	CACTGTCTCCCAGGTTAAACT	CCTGAGCTTTTGACACATGC
7	64.7	EPDCU3392	HEX	57	CTTTTCATGGGTTCCCTCACC	ATCAACCAGTTCACGCACAA
8	14.1	BPPCT006	HEX	57	GCTTGTGGCATGGAAGC	CCCTGTTTCTCATAGAACTCACAT
8	20.8	UDP96-019	HEX	57	TTGGTCATGAGCTAAGAAAACA	TAGTGGCACAGAGCAACACC
8	24.8	CPPCT006	HEX	59	AATTAAGTCCAACAGCTCCA	ATGGTTGCTTAATTCAATGG
8	42.6	CPDCT023	FAM	62	GTGGCAAATGTTGGCAAAG	AACACAAAGCAGCACCAGA
8	54.7	EPDCU3117	FAM	57	CAGAGGGAACAGTGTGAGCA	TGTTGTTGTGACCCCTGAAA

^zTa = annealing temperature.

Supplemental Table 2. Primer sequences of chloroplast DNA as described by Shaw et al. (2005, 2007) and Morris et al. (2008).

Region	Primer name and sequence (5'-3')
<i>3'trnV-ndhC</i>	trnV ^(UAC) _{x2} : GTC TAC GGT TCG ART CCG TA ndhC: TAT TAT TAG AAA TGY CCA RAA AAT ATC ATA TTC
<i>ndhJ-trnF</i>	ndhJ: ATG CCY GAA AGT TGG ATA GG TabE: GGT TCA AGT CCC TCT ATC CC (Taberlet et al., 1991)
<i>trnL-trnF</i> and <i>trnL</i> intron	5'trnL ^(UAA) -F: CGA AAT CGG TAG ACG CTA CG trnF ^(GAA) : ATT TGA ACT GGT GAC ACG AG (Taberlet et al., 1991)
<i>trnT-trnL</i>	trnT ^(UGU) -F: CAT TAC AAA TGC GAT GCT CT 5'trnL ^(UAA) -R: TCT ACC GAT TTC GCC ATA TC (Taberlet et al., 1991)
<i>trnQ-5'rps16</i>	trnQ ^(UUG) : GCG TGG CCA AGY GGT AAG GC rpS16x1: GTT GCT TTY TAC CAC ATC GTT T
<i>trnH-psbA</i>	trnH ^(GUG) : CGC GCA TGG TGG ATT CAC AAT CC (Tate and Simpson, 2003) psbA: GTT ATG CAT GAA CGT AAT GCT C (Sang et al., 1997)
<i>ndhF-rpl32</i>	rpL32-R: CCA ATA TCC CTT YYT TTT CCA A ndhF: GAA AGG TAT KAT CCA YGM ATA TT
<i>atpB-rbcL</i>	atpB-1: ACATCKARTACKGGACCAATAA (Chiang et al., 1998) rbcL-1: AACACCAGCTTTTRAATCCAA

Supplemental Table 3. Primers for candidate genes associated with flowering time response, branching, plant architecture, and isozymes in peach.

Gene symbol	Gene description	Expected size (bp)	Ta (°C)	Forward sequence		Reverse sequence		Reference
AGL20-SOC1	AGAMOUS-like 20/SUPPRESSOR OF OVEREXPRESSION of CONSTANS 1	569	55	ATGCAGACAACCATAGAACG		CTATTGAAAAATGCAGCACA		This study
AGL24 AXR1	AGAMOUS-like 24 AUXIN RESISTANT 1	653	55	GGATGAGCTGCTGAAGTTAG		TTTTTCTCCAGTGCCATAAT		This study Carrillo-Mendoza (2012)
		419	59	AGCAAGGACAGACAGCCCTA		CTTGCCCTTAACAGCATCGT		
BFT	BROTHER of FLOWERING LOCUS T and TERMINAL FLOWER 1	570	55	GAGCCATTGACTCTTTGGTAG		GCAACCCTATTCTTTGTCT		This study
BRC1	BRANCHED 1	342	57	CACAAGCACACCCCTTACT		CCTGAATGAGCAACCACTCA		Carrillo-Mendoza (2012)
BRC2	BRANCHED 2	692	57	TCAAGCGGGAATAAGGACAG		GCTCCACTGGGAATTGTTGT		Carrillo-Mendoza (2012)
BRM	BRAHMA	704	55	AATCAACAGGAAAGTGAAGA		GTTTCCAGTCCGTAAACATTG		This study
CO	CONSTANS	567	55	AAGGCTGCCTACAGTTACAA		ACAAAGGGAATGAAACACTG		This study
CRY1	Cryptochrome 1	523	55	CACCAAGAGGTCCACTGA		CTGAATCTGTCCCACTGTT		This study
CRY2	Cryptochrome 2	554	55	ATTGAAGCCATTGGAGCTA		GTGACATGTGCCTTCAACTA		This study
CUC1	CUP-SHAPED COTYLEDON 1	364	57	CTTGACAGCAGCTTCACTGG		AGCTCTGCCACGGTAGAAAA		Carrillo-Mendoza (2012)
CUC2	CUP-SHAPED COTYLEDON 2	741	57	GTTTTCTACCGTGGCAGAGC		TTGCTCATTCGGGCTCTTCT		Carrillo-Mendoza (2012)
CUC3	CUP-SHAPED COTYLEDON 3	751	57	GAGTGAGCTGAGTGGGGAAG		TGGCCCTGTTGGTCTTAAAC		Carrillo-Mendoza (2012)
ELF6	EARLY FLOWERING 6	850	55	AATTCACCTGAGGTTGTTG		CTACTTCAAGCCAGTGTGGT		This study
FD	FERREDOXIN	701	55	CTGTTCTCAGCTTGACCAAT		ATCGATGAAGATTGTGCTTT		This study
FD1	FERREDOXIN 1	518	55	GTAACCAATATGGCAGCTC		CAGCAGCTATCAAAACATGA		This study
FPF1	FLOWERING PROMOTING FACTOR 1	335	55	CCAAAGCACTAGCTACTACCA		GATGTTGGGGTTTTTAAATGA		This study
FG	FLOWERING LOCUS C/FLOWERING LOCUS F	505	55	TCCAAGGTCTTCTACCTCAA		CCCATCCATAATTCTACCAA		This study
FLC-FLF	FLOWERING LOCUS C/FLOWERING LOCUS F	540	55	AAATTGGAAGAGGCAAGATT		TTCTAGGGCCACTTTACTCA		This study
FRIGIDA	FRIGIDA	751	55	AATACCAATGGTTTCACGTC		TTAACTGCATCAAAATTGTGCG		This study
FT-TSF	FLOWERING LOCUS T/TWIN SISTER of FLOWERING LOCUS T	558	55	CAAGGTCTGTTTCTCTCAGG		TTGAACTCGAAACCTCAACT		This study
GI-FB	GIGANTEA	692	55	AAGTTAATTGCAGCTCCTGA		CTGGTTGATTCTCCACATCT		This study

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Gene symbol	Gene description	Expected size (bp)	Ta (°C)	Forward sequence	Reverse sequence	Reference
HOS1	HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 1	568	55	CGCCTTATATCCAAGAAAGTG	ATGAATCCAGAACATCAAGC	This study
LAS	LATERAL SUPPRESSOR	402	57	ATGCGCCAAATGCTCAATTAC	AAAGTCGAGGATGTGGATGG	Carrillo-Mendoza (2012)
LFY	LEAFY	795	55	GTGATTTCTTGATCCAGGTC	ATCTTGGGGCTTGTGATGTA	This study
MAF1-MAF3-AGL31	MADS AFFECTING FLOWERING 1/ MADS AFFECTING FLOWERING 3/ AGAMOUS-like 31	594	55	AGATGGGAGAGGAAAAGATT	CTGCAGCATGTACTAGAGGA	This study
MAF2	MADS AFFECTING FLOWERING 2	545	55	GATCGAAAACACAAACAACC	ACCCATTAAAAGCACATACA	This study
MAF4	MADS AFFECTING FLOWERING 4	568	55	TGTGACATTGACATTGCTCT	ATCATCGTCAACATGCATAA	This study
MAF5	MADS AFFECTING FLOWERING 5	354	55	GCTTCAGATCAAGAGGATTG	ATTAACATAGCGTGCCAGAA	This study
MAX1	MORE AXILLARY BRANCHES 1	331	57	TTACGAGCATCTCCTTGCTG	TTGCAACTAATGGGGAAACC	Carrillo-Mendoza (2012)
MAX2	MORE AXILLARY BRANCHES 2	441	57	AAAACTTGATGCTGCTGCT	TCCGAATCTCCTCCAGATTG	Carrillo-Mendoza (2012)
MAX3	MORE AXILLARY BRANCHES 3	387	57	TTGCTTCCTCGGTCTCCTAA	GAGGTAGCGTCTTGCTTTGG	Carrillo-Mendoza (2012)
MAX4	MORE AXILLARY BRANCHES 4	341	57	CGGTCATTGCAGATTGTGT	CAACCCTCTTCCCATGTTCGT	Carrillo-Mendoza (2012)
MFT	MOTHER OF FLOWERING LOCUS T	529	55	AACATGTCCGTCTACTTTGG	TTTACCTCTAACAGGGGCTTG	This study
PGDH	PHOSPHOGLYCERATE DEHYDROGENASE	614	55	ATCTCACTGCATATGCCTCT	GCTATTTCAATGGCTACACC	This study
PGI	PHOSPHOGLUCOSE ISOMERASE 1	528	55	CACCTGAAAACCTTTGGAGAAG	CCAAGATCCACTTTCGAATAC	This study
PHYA	PHYTOCHROME A	520	55	TAAAGCAATTGGAAACCAATT	GATTCCACTCAGAACACCCAG	This study
PHYB-PHYD	PHYTOCHROME B/ PHYTOCHROME D	600	55	ACTTCTTTCCGGCGCTTA	TGTGTTCCAAATCATCAAAA	This study
PHYE	PHYTOCHROME E	573	55	TGAAATTGTTTGTGAGGACT	GCCCTGCTAAAAGGAGTATTT	This study
PIN	PIN-FORMED	447	57	ATTTCAGCTTTGGCAACAGG	GCCAAAGTCCTGCATCAGATAG	Carrillo-Mendoza (2012)
RAX1	REGULATOR OF AXILLARY MERISTEMS 1	666	55	CTTAACCTACCTGAGGCCAAA	TGATGAGAGGAAGAAAGGAAA	This study

Continued next page

Supplemental Table 3. Continued.

Gene symbol	Gene description	Expected size (bp)	Ta (°C)	Forward sequence	Reverse sequence	Reference
RAX2-RAX3	REGULATOR OF AXILLARY MERISTEMS 2/ REGULATOR OF AXILLARY MERISTEMS 3	638	55	AAGACAGGATCATCTGCAAC	GCTCCAAAGCACTAGAGAAA	This study
REV	REVOLUTA	480	57	CGCCAGTATGTTGGAAGTGT	CCAAGGAATCAGGTCTCAGC	Carrillo-Mendoza (2012)
RGA-RGA1	REPRESSOR OF GIBERELIN/ REPRESSOR OF GIBERELIN 1	478	55	CCACTCATTCTCCGATATGT	CATTGCTTAACCCACAGACA	This study
RGL1-RGL2-RGL3	RGA-like 1/RGA-like 2/ RGA-like 3	542	55	CAGTCCACTACAAACCCATCT	AGCTTCAGCAAAAGTAAGTGG	This study
sôpdh	SORBITOL 6-PHOSPHATE DEHYDROGENASE	800	57	AGAATAAGGTGTTGGACATAGACG	AGAGTGGTCTGGATTTCCTT ATCTA	Bortiri et al. (2002)
SPS	SUPERSHOOT	485	57	ACTCAAAAGACGCCAGTGGTC	GCCCTTGGGGGATGAAAGTAAT	Carrillo-Mendoza (2012)
SPY	SPINDLY	633	55	ATTTGACAGTTTCACGGAAG	CAGTCCCCTCTTGAGTATTGC	This study
TFL1-ATC	TERMINAL FLOWER 1/CENTRORADIALIS	562	55	TGGTCATGAGCTATTTCCTT	TTAGACTCAAGGAGAGCATC	This study
TLF2	TERMINAL FLOWER 2	587	55	TGAGCTCCAGTATCTCATCA	AGAGGGAAAATGGAAGAAAAAC	This study
VRN1	REDUCED VERNALIZATION	621	55	TTCAATTTAATGTAAACAGAGCTT	CCTGGCTTAATTTTGCTCTA	This study
VRN2	RESPONSE 1 REDUCED VERNALIZATION RESPONSE 2	770	55	TTCAACTATAGGGACTACAACA	ACATTGCATCAAGCAAAAAG	This study

Ta = annealing temperature.

Supplemental Table 4. Internal primers used to improve sequence coverage, quality, and base-calling accuracy of gene regions associated with axillary meristem formation, vernalization response, and isozyme expression.

Gene symbol	Ta (°C)	Sequence
CUC2int-F	55	GAACCTTTAGTGATCTCATGCTA
CUC3int-R	55	CAAGCTGAAGAAGTACCACT
RAX2-RAX3int-F	55	TCAATGTTTGTCTCTCACA
PGIint-F	55	TCAAATTAGCAGAGGTGGG
PGIint-R	55	CAGAGAACTTTTGGATCTTG
PGDHint-F	55	CAAAGGTGTTCAATGATGAA
PGDHint-R	55	GTGTGAGAGTGACATTCTCA
sp6dhint-F	55	CAACTACGAGCTCTTCTGA
AGL20-SOC1int-F	55	TGACCAAAATATGCAGGTGA
AGL20-SOC1int-R	55	CTCTCCAACGTGTGCTCAAT
BRMint-F	55	CTGGCCTCTTAATTTGTC
COint-F	55	CTTTGCTTAATGCTAGCTCA
COint-R	55	CTGAAGATACTCCAAGAATATT
ELF6int-F	55	CAATTCCTTTGTGAACAT
ELF6int-R	55	TCAATAAGGCATTGGCAGAG
FDint-R	55	GTTCTTGCTGCCTTTTGAG
FRIGIDAint-R	55	CTATGTTTCGCCATGTTGGT
FT-TSFint-F	55	ATTAAGTGCATACGTACGGG
FT-TSFint-R	55	AATACACACCAATGCAAATA
GI-FBint-F	55	ATGTTAGGTCGTTGATGCAT
GI-FBint-R	55	TTAGACCTGAAGAACCACTG
HOS1int-F	55	GACGTCCAACGCCTTTATTC
HOS1int-R	55	CATTAGATATGCCAGCCAAT
LFYint-F	55	ACCAAGGTACGGAGTTTACC
LFYint-R	55	TGGAATCACTATATATTCTAACAA
LFYint2-F	55	ATATAGTGATTCCAATAATGATG
MAF2Aint-R	55	TCTCAACTCAACTGAGTACCAT
MAF4int-F	55	TGATCATGTGTGGGAACCTT
MAF4int-R	55	AAGAAGTTCCACACATGAT
TFL2int-F	55	AGAGGGAAATGGAAGAAAAC

F = forward sequence; R = reverse sequence; Ta = annealing temperature.

Supplemental Table 5. Continued.

Region ID	Exon(s)			Intron(s)			Total			Variability (%)	
	L (bp)	Subst	Indels ^z	Variability (%) ^y	L (bp)	Subst	Indels	Variability (%)	L (bp)	Subst	Indels
PIN	165	1	1	1.21	178	8	4	6.74	343	9	5
VRN1	424	16	0	3.77	168	19	0	11.31	592	35	0
VRN2	—	—	—	—	418	25	11	8.61	418	25	11
RAX1	47	1	0	2.13	398	22	4	6.53	445	23	4
RAX2-RAX3	215	6	0	2.79	288	14	7	7.29	503	20	7
RGA-RGA1	454	15	0	3.30	—	—	—	—	454	15	0
REV	105	10	0	9.52	273	20	6	9.52	378	30	6
RGL1-RGL2-RGL3	510	36	1	7.25	—	—	—	—	510	36	1
s6pdh	339	7	0	2.06	290	26	18	15.17	629	33	18
SPS	215	7	0	3.26	148	14	5	12.84	363	21	5
SPY	100	3	0	3.00	406	20	5	6.16	506	23	5
TFL1-ATC	92	2	0	2.17	365	14	11	6.85	457	16	11
TFL2	77	2	0	2.60	422	25	7	7.58	499	27	7
Total	9,072	330	28	4	14,451	1,094	412	11	23,203	1,424	440

L = total aligned sequence length; subst = substitutions.

^zIndels = number of insertion/deletion events.^yVariability % = [(Subst + Indels)/L] × 100.

Supplemental Table 6. Summary results of the phylogenetic analyses for diploid sequence data for 11 *Prunus* species.

Gene ID	Maximum parsimony						Maximum parsimony (including gaps)						Maximum likelihood				
	L (bp) ^z	Informative Trees			L (bp)	Informative Trees			L (bp)	Informative Trees			L (bp)	Informative			
		no.	no.	Length		CI	RI	RC		no.	no.	Length		CI	RI	RC	no.
AGL20-SOC1	443	13	27	28	1.000	1.000	1.000	464	21	11	62	0.790	0.740	0.585	443	13	-772.842
AGL24	493	24	1	42	0.976	0.984	0.960	584	56	1	134	0.985	0.989	0.974	493	24	-936.960
AXR1	263	8	24	10	1.000	1.000	1.000	—	—	—	—	—	—	—	263	8	-406.360
BRM	221	4	10	10	1.000	1.000	1.000	240	4	10	29	1.000	1.000	1.000	221	4	-332.595
BRC1	299	1	2	4	1.000	1.000	1.000	—	—	—	—	—	—	—	299	1	-480.679
BRC2	298	5	1	12	1.000	1.000	1.000	—	—	—	—	—	—	—	298	5	-470.726
BFT	458	9	3	20	1.000	1.000	1.000	477	25	3	39	1.000	1.000	1.000	458	9	-817.102
CO	416	13	1	20	1.000	1.000	1.000	420	16	3	25	0.960	0.974	0.935	416	13	-713.811
CRY1	500	12	5	28	0.964	0.960	0.926	549	40	5	77	0.987	0.981	0.969	500	12	-881.916
CRY2	450	15	6	30	1.000	1.000	1.000	485	24	3	66	0.985	0.982	0.968	450	15	-759.729
CUC1A	430	2	6	11	1.000	1.000	1.000	431	2	6	12	1.000	1.000	1.000	430	2	-644.941
CUC1B	305	2	26	10	1.000	1.000	1.000	306	2	26	11	1.000	1.000	1.000	305	2	-460.375
CUC2	577	20	36	50	0.920	0.922	0.848	630	47	6	104	0.952	0.965	0.919	577	20	-1,076.250
CUC3	503	23	11	38	1.000	1.000	1.000	561	67	11	96	1.000	1.000	1.000	503	23	-909.547
ELF6	585	26	4	53	0.868	0.894	0.776	627	45	6	112	0.786	0.789	0.620	585	26	-1,054.082
FD	536	16	16	37	0.973	0.980	0.953	551	19	16	53	0.962	0.966	0.929	536	16	-924.255
FD1	481	5	3	12	1.000	1.000	1.000	520	5	3	51	1.000	1.000	1.000	481	5	-730.555
FG	394	16	3	32	0.969	0.974	0.943	418	40	542	70	0.786	0.885	0.696	394	16	-754.585
FLC-FLF	459	14	64	23	1.000	1.000	1.000	535	82	1	106	0.943	0.965	0.910	459	14	-762.478
FT-TSF	503	14	75	18	1.000	1.000	1.000	561	54	3	82	0.927	0.950	0.880	503	14	-756.323
FPI1	329	1	1	5	1.000	1.000	1.000	336	5	1	12	1.000	1.000	1.000	329	1	-470.312
FRIGIDA	522	11	12	32	1.000	1.000	1.000	579	41	1	104	0.856	0.810	0.693	522	11	-907.176
GI-FB	573	16	12	31	0.968	0.976	0.945	644	45	3	106	0.953	0.965	0.920	573	16	-954.621
HOS1	198	5	1	7	1.000	1.000	1.000	—	—	—	—	—	—	—	198	5	-312.347
LAS	378	8	52	18	1.000	1.000	1.000	381	11	52	21	1.000	1.000	1.000	378	8	-648.781
LFY	611	48	1	106	0.858	0.873	0.749	670	80	2	175	0.857	0.866	0.743	611	48	-1,465.959
MAF1-MAF3-AGL31	494	15	6	30	0.933	0.470	0.884	524	36	8	64	0.906	0.929	0.842	494	15	-846.279
MAF2A	265	6	36	15	0.933	0.944	0.881	283	17	5	31	0.839	0.884	0.741	265	6	-462.861
MAF2B	335	8	3	18	1.000	1.000	1.000	400	23	22	88	0.943	0.821	0.775	335	8	-533.146
MAF4	471	20	155	58	0.948	0.933	0.885	572	35	24	164	0.951	0.895	0.851	471	20	-962.605
MAF5	310	16	1	23	1.000	1.000	1.000	361	44	1	74	1.000	1.000	1.000	310	16	-555.134
MAX1A	327	7	1	14	1.000	1.000	1.000	341	10	2	29	0.966	0.966	0.932	327	7	-523.030
MAX1B	323	4	1	16	1.000	1.000	1.000	324	4	1	17	1.000	1.000	1.000	323	4	-540.059
MAX2	376	10	3	11	1.000	1.000	1.000	382	16	3	17	1.000	1.000	1.000	376	10	-579.672
MAX3	311	13	24	30	0.967	0.971	0.938	335	27	24	59	0.898	0.895	0.804	311	13	-595.726
MAX4	238	14	2	25	1.000	1.000	1.000	240	15	2	27	1.000	1.000	1.000	238	14	-455.622
MFT	394	10	4	24	1.000	1.000	1.000	398	12	4	28	1.000	1.000	1.000	394	10	-671.169
PGI	297	13	6	24	0.958	0.969	0.928	309	19	9	37	0.946	0.955	0.903	297	13	-583.154
PGDH	477	14	44	22	1.000	1.000	1.000	478	14	44	23	1.000	1.000	1.000	477	14	-784.529
PHYA	493	1	6	10	1.000	1.000	1.000	—	—	—	—	—	—	—	493	1	-750.176
PHYB-PHYD	500	16	18	28	0.964	0.974	0.940	546	48	18	74	0.986	0.993	0.979	500	16	-825.974

Continued next page

Gene ID	Maximum parsimony						Maximum parsimony (including gaps)						Maximum likelihood				
	Informative Trees			Trees			Informative			Trees			Informative				
	<i>L</i> (bp) ^z	no.	Length	CI	RI	RC	<i>L</i> (bp)	no.	Length	CI	RI	RC	<i>L</i> (bp)	no.	lnL		
PHYE	499	14	6	26	1.000	1.000	1.000	517	29	6	44	1.000	1.000	1.000	499	14	-835.046
PIN	343	4	10	7	1.000	1.000	1.000	349	5	10	13	1.000	1.000	1.000	343	4	-546.355
VRN1	592	14	1	26	1.000	1.000	1.000	—	—	—	—	—	—	—	592	14	-973.535
VRN2	418	7	14	18	1.000	1.000	1.000	465	9	14	65	1.000	1.000	1.000	418	7	-654.134
RAX1	445	15	4	23	1.000	1.000	1.000	450	17	4	28	1.000	1.000	1.000	445	15	-734.114
RAX2-RAX3	503	5	2	18	1.000	1.000	1.000	547	9	8	64	0.969	0.913	0.885	503	5	-810.005
RGA-RGA1	454	2	29	10	1.000	1.000	1.000	—	—	—	—	—	—	—	454	2	-720.811
REV	377	15	10	27	1.000	1.000	1.000	386	19	10	36	1.000	1.000	1.000	377	15	-710.356
RGL1-RGL2-RGL3	510	17	1	32	1.000	1.000	1.000	513	17	1	35	1.000	1.000	1.000	510	17	-929.111
isopdh	625	15	12	33	0.879	0.897	0.789	649	28	1	61	0.869	0.886	0.770	625	15	-1,051.341
SPS	363	8	11	14	1.000	1.000	1.000	370	13	3	21	1.000	1.000	1.000	363	8	-583.152
SPY	506	8	1	20	1.000	1.000	1.000	524	25	1	38	1.000	1.000	1.000	506	8	-838.247
TFL1-ATC	457	8	212	15	0.867	0.882	0.765	495	37	20	53	0.962	0.982	0.945	457	8	-717.034
TFL2	499	7	6	24	0.917	0.900	0.825	511	9	8	38	0.921	0.870	0.801	499	7	-785.199
3'trnV-ndhC	567	29	1,082	67	0.896	0.821	0.735	906	96	75	437	0.913	0.775	0.708	567	29	-998.774
trnL-trnF and trnL intron	836	3	1	12	1.000	1.000	1.000	—	—	—	—	—	—	—	836	3	-1,167.722
trnQ-5' rps16	479	8	10	17	0.882	0.889	0.784	509	19	3	50	0.900	0.848	0.764	479	8	-724.826
trnH-psbA	335	4	2,925	10	1.000	1.000	1.000	384	17	675	61	0.967	0.955	0.923	335	4	-446.838
ndhF-rpl32	598	1	1	7	1.000	1.000	1.000	625	7	1	34	1.000	1.000	1.000	598	1	-780.124
atpB-rbcL	769	3	1	13	1.000	1.000	1.000	779	3	1	23	1.000	1.000	1.000	769	3	-1,085.826
ITS	610	7	2	54	0.981	0.889	0.872	646	16	2	94	0.947	0.783	0.741	610	7	-1,099.593

^zLn = total aligned sequence length; Inf = parsimony informative sites; CI = consistency index; RI = retention index; RC = rescaled consistency index.

^zL = total aligned sequence length; Inf = parsimony informative sites; CI = consistency index; RI = retention index; RC = rescaled consistency index.

Supplemental Table 7. Summary results of the phylogenetic analyses for phased haplotype sequence data for 11 *Prunus* species.

Gene ID	Maximum parsimony						Maximum parsimony (including gaps)						Maximum likelihood				
	Informative			Trees			L (bp)	no.	no.	Length	CI	RI	RC	L (bp)	no.	no.	
	L (bp) ^z	no.	no.														
AGL20-SOC1	444	29	229	36	0.889	0.972	0.864	469	54	871	93	0.613	0.877	0.537	444	29	852.61
AGL24	494	48	8	64	0.922	0.971	0.895	590	107	15	167	0.928	0.975	0.904	494	48	-1,067.87
AXR1	263	8	1	11	1.000	1.000	1.000	—	—	—	—	—	—	—	263	8	-441.17
BRM	366	15	1	22	0.955	0.963	0.919	386	35	8	45	0.911	0.918	0.837	366	15	-662.89
BRC1	299	3	1	6	1.000	1.000	1.000	—	—	—	—	—	—	—	299	3	-440.99
BRC2	298	9	1	15	1.000	1.000	1.000	—	—	—	—	—	—	—	298	9	-516.30
BFT	458	14	1	25	1.000	1.000	1.000	478	32	8	48	0.938	0.980	0.919	458	14	-803.13
CO	419	23	3	30	1.000	1.000	1.000	427	31	48	42	0.905	0.957	0.865	419	23	-777.69
CRY1	500	19	6	35	0.971	0.972	0.944	549	47	6	84	0.988	0.989	0.977	500	19	-913.50
CRY2	450	31	6	39	0.949	0.975	0.925	485	66	7	79	0.911	0.955	0.870	450	31	-865.10
CUC1A	430	12	2,494	22	0.773	0.844	0.652	431	13	2,494	23	0.783	0.848	0.664	430	12	-732.94
CUC1B	305	5	3	17	0.941	0.889	0.837	306	5	3	18	0.944	0.889	0.840	305	5	-534.29
CUC2	577	35	4	53	0.925	0.957	0.885	630	62	54	112	0.911	0.953	0.868	577	35	-1,123.05
CUC3	505	31	1	49	1.000	1.000	1.000	566	82	28	112	0.973	0.985	0.959	505	31	-995.94
ELF6	593	50	3	55	0.927	0.979	0.908	643	98	312	149	0.678	0.897	0.608	593	50	-1,177.99
FD	536	31	2	41	0.976	0.992	0.968	564	52	4	73	0.932	0.969	0.903	536	31	-1,023.21
FD1	481	10	1	20	1.000	1.000	1.000	520	12	1	59	1.000	1.000	1.000	481	10	-817.46
FG	394	17	3	38	0.974	0.978	0.952	418	41	4,684	76	0.803	0.891	0.715	394	17	-732.76
FLC-FLF	448	25	48	27	0.926	0.979	0.906	547	118	1,796	162	0.765	0.936	0.716	448	25	-805.14
FT-TSF	507	18	150	20	1.000	1.000	1.000	573	79	1	102	0.843	0.951	0.802	507	18	-783.89
FPI1	329	1	1	6	1.000	1.000	1.000	336	5	1	13	1.000	1.000	1.000	329	1	-511.56
FRIGIDA	630	36	2	40	0.950	0.971	0.922	681	87	3	99	0.899	0.945	0.850	630	36	-1,116.61
GI-FB	577	39	48	45	0.956	0.984	0.940	662	119	80	153	0.837	0.953	0.798	577	39	-1,076.97
HOS1	198	6	3	9	0.889	0.929	0.825	—	—	—	—	—	—	—	198	6	-366.16
LAS	378	15	1	25	1.000	1.000	1.000	381	18	1	28	1.000	1.000	1.000	378	15	-666.32
LFY	615	101	318	149	0.732	0.914	0.669	693	179	352	249	0.751	0.924	0.694	615	101	-1,681.58
MAF1-MAF3-AGL31	496	27	1	43	0.860	0.906	0.780	531	59	7	87	0.828	0.882	0.730	496	27	-997.52
MAF2A	268	13	3	17	0.941	0.972	0.915	283	23	15	41	0.756	0.863	0.653	268	13	-465.01
MAF2B	335	9	1	19	1.000	1.000	1.000	393	24	3	82	0.939	0.839	0.788	335	9	-584.64
MAF4	474	69	48	95	0.758	0.907	0.687	584	178	148,731	244	0.746	0.898	0.670	474	69	-1,228.68
MAF5	310	26	1	29	1.000	1.000	1.000	361	71	1	80	1.000	1.000	1.000	310	26	-554.88
MAX1A	327	11	1	18	1.000	1.000	1.000	342	15	3	34	0.971	0.977	0.949	327	11	-579.13
MAX1B	323	10	1	20	1.000	1.000	1.000	324	11	1	21	0.857	0.850	0.729	323	10	-567.47
MAX2	376	10	1	16	1.000	1.000	1.000	382	16	1	22	1.000	1.000	1.000	376	10	-583.46
MAX3	311	22	24	40	0.925	0.963	0.890	335	45	24	64	0.953	0.979	0.933	311	22	-648.98
MAX4	239	22	1	34	0.941	0.962	0.906	242	24	1	37	0.946	0.966	0.914	239	22	-588.05
MFT	395	17	1	31	1.000	1.000	1.000	398	18	1	35	0.971	0.979	0.951	395	17	-728.50
PGI	299	19	18	25	1.000	1.000	1.000	317	36	12	49	0.878	0.952	0.835	299	19	-562.10
PGDH	477	25	12	35	0.886	0.952	0.843	478	26	68	40	0.800	0.909	0.727	477	25	-899.96
PHYA	493	3	3	12	1.000	1.000	1.000	—	—	—	—	—	—	—	493	3	-746.53
PHYB-PHYD	500	22	12	35	0.943	0.962	0.907	545	63	44	86	0.907	0.952	0.864	500	22	-841.73

Continued next page

Gene ID	Maximum parsimony						Maximum parsimony (including gaps)						Maximum likelihood	
	Informative			Trees			Informative			Trees			Informative	
	<i>L</i> (bp) ^z	no.	no.	Length	CI	RI	<i>L</i> (bp)	no.	no.	Length	CI	RI	<i>L</i> (bp)	no.
PHYE	499	16	1	31	1.000	1.000	514	31	1	46	1.000	1.000	499	16
PIN	343	8	3	10	1.000	1.000	348	13	4	19	0.789	0.857	343	8
VRN1	592	25	1	36	0.972	0.984	0.956	—	—	—	—	—	592	25
VRN2	418	20	1	27	1.000	1.000	481	45	1	91	0.989	0.986	418	20
RAX1	445	18	304	28	0.929	0.957	0.888	23	96	36	0.861	0.915	445	18
RAX2-RAX3	503	18	1	21	0.952	0.980	0.933	548	63	20	0.915	0.966	503	18
RGA-RGA1	454	12	1	17	0.941	0.957	0.900	—	—	—	—	—	454	12
REV	378	20	1	32	0.969	0.982	0.951	388	30	2	0.953	0.972	378	20
RGL1-RGL2-RGL3	510	22	1	39	1.000	1.000	513	22	1	42	1.000	1.000	510	22
sopdh	629	30	12	42	0.810	0.925	0.748	658	48	19,962	0.700	0.861	629	30
SPS	363	11	1	22	1.000	1.000	370	16	4	31	0.935	0.957	363	11
SPY	506	15	1	27	0.963	0.964	0.929	524	33	1	0.957	0.976	506	15
TFL1-ATC	457	14	82	21	0.857	0.949	0.814	496	53	180	0.877	0.974	457	14
TFL2	499	24	21	32	0.875	0.956	0.836	513	33	33,824	0.764	0.897	499	24
3'trnV-ndhC	567	29	1,082	67	0.896	0.821	0.735	906	96	75	0.913	0.775	567	29
trnL-trnF and trnL intron	836	3	1	12	1.000	1.000	1.000	—	—	—	—	—	836	3
trnQ-5' rps16	479	15	16	17	0.882	0.961	0.848	508	43	72	0.815	0.910	479	15
trnH-psbA	335	4	2,925	10	1.000	1.000	1.000	385	18	42,147	0.968	0.963	335	4
ndhF-rpl32	598	1	1	7	1.000	1.000	1.000	625	7	1	1.000	1.000	598	1
atpB-rbcL	769	3	1	13	1.000	1.000	1.000	779	3	1	1.000	1.000	769	3
ITS	611	33	2	49	0.959	0.958	0.919	653	70	9	0.817	0.847	611	33

^z*L* = total aligned sequence length; Inf = parsimony informative sites; CI = consistency index; RI = retention index; RC = rescaled consistency index.

Supplemental Table 8. Models of sequence evolution of chloroplast DNA (cpDNA) sequence data using JModelTest for 11 *Prunus* species.

cpDNA Region	3'trnV-ndhC			trnL-trnF and trnL intron			trnQ-5'rps16			trnH-psbA			ndhF-rpl32			atpB-rbcL		
Criterion	AIC ^z	BIC	F81+G	AIC	BIC	F81	AIC	BIC	F81	AIC	BIC	F81	AIC	BIC	F81	AIC	TPM1uf	BIC
Model	TVM+G	000000	000000	010010	000000	000000	000000	000000	000000	010020	010020	000000	000000	000000	000000	012210	1092.93	10010
Partition	998.83	1003.29	1193.21	1193.21	1195.26	1195.26	721.90	724.05	724.05	463.63	463.63	791.38	791.38	791.38	791.38	1089.65	1092.93	10010
-lnL	28	24	24	24	23	23	24	23	23	25	25	23	23	23	23	25	24	24
freqA	0.42	0.42	0.36	0.36	0.36	0.36	0.32	0.32	0.32	0.44	0.44	0.36	0.36	0.36	0.36	0.34	0.34	0.34
freqC	0.06	0.06	0.16	0.16	0.16	0.16	0.13	0.13	0.13	0.13	0.13	0.12	0.12	0.12	0.12	0.15	0.15	0.15
freqG	0.11	0.11	0.15	0.15	0.15	0.15	0.12	0.12	0.12	0.08	0.08	0.11	0.11	0.11	0.11	0.14	0.14	0.14
freqT	0.41	0.42	0.33	0.33	0.33	0.33	0.43	0.43	0.43	0.35	0.34	0.40	0.40	0.40	0.40	0.37	0.37	0.37
R(a) [AC]	0.30									1.00	1.00					1.00		
R(b) [AG]	0.32									1.86	1.86					1.51		
R(c) [AT]	0.51									1.00	1.00					0.00		
R(d) [CG]	0.00									1.00	1.00					0.00		
R(e) [CT]	0.32									0.11	0.11					1.51		
R(f) [GT]	1.00									1.00	1.00					1.00		
gamma shape		0.015					0.017											
pinv(I)																		
alpha(G)																		
pinv(IG)																		
alpha(IG)																		
Free parameters	8	4	4	4	3	3	4	3	3	5	5	3	3	3	3	5	4	4
Likelihood ratio	8.92		4.10	4.10			4.31			-	-	-	-	-	-	6.55		
test (LRT)																		
P-value	0.06		0.04	0.04			0.04			-	-	-	-	-	-	0.01		

^zAkaike information criterion (AIC; Akaike, 1974) and Bayesian information criteria (BIC; Schwarz, 1978).

Supplemental Table 9. Models of sequence evolution of diploid internal transcribed spacer (ITS) and candidate gene regions sequence data using JModelTest for 11 *Prunus* species.

Region	ITS				PGDH				PGI				s6pdh				AXR1				BRC1				BRC2			
Criterion	AIC ^z	BIC	TPM1uf	AIC	BIC	F81	000000	AIC	HKY	BIC	HKY	AIC	TPM1uf+G	BIC	TPM1uf+G	AIC	TIM1	012230	010010	000000	AIC	JC	BIC	JC	AIC	TPM3uf	F81	000000
Model	012230	012210	012032	012032	012210	012032	000000	010010	010010	010010	010010	010010	012210	012210	012210	012230	012230	010010	000000	000000	000000	000000	000000	000000	012012	000000	000000	
Partition	1143.87	1144.91	800.94	806.57	554.32	554.32	806.57	554.32	554.32	554.32	554.32	554.32	1067.34	1067.34	1067.34	420.73	431.00	445.69	445.69	445.69	445.69	445.69	445.69	476.01	480.33	480.33		
-lnL	26	25	30	27	26	26	27	26	26	26	26	26	26	26	26	30	25	24	24	24	24	24	24	29	27	27		
K	0.19	0.19	0.19	0.28	0.27	0.27	0.28	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.35	0.35	0.35		
freqA	0.31	0.31	0.31	0.18	0.18	0.18	0.19	0.18	0.18	0.18	0.18	0.18	0.21	0.21	0.21	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.15	0.15	0.14		
freqC	0.31	0.31	0.31	0.20	0.20	0.20	0.20	0.18	0.18	0.18	0.18	0.18	0.20	0.20	0.20	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.27	0.27	0.27		
freqG	0.19	0.18	0.18	0.34	0.34	0.34	0.34	0.37	0.37	0.37	0.37	0.37	0.32	0.32	0.32	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.23	0.23	0.24			
freqT	1.00	1.00	1.00	3.34	3.34	3.34	3.34	3.34	3.34	3.34	3.34	3.34	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.00	0.00	0.00		
R(a) [AC]	2.72	2.16	2.16	1.43	1.43	1.43	1.43	1.43	1.43	1.43	1.43	1.43	2.45	2.45	2.45	1.49	1.49	1.49	1.49	1.49	1.49	1.49	1.77	1.77	1.77	1.77		
R(b) [AG]	0.40	0.40	0.40	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.18	0.18	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.00	1.00		
R(c) [AT]	0.40	0.40	0.40	3.34	3.34	3.34	3.34	3.34	3.34	3.34	3.34	3.34	0.18	0.18	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		
R(d) [CG]	1.60	2.16	2.16	6.23	6.23	6.23	6.23	6.23	6.23	6.23	6.23	6.23	2.45	2.45	2.45	6.01	6.01	6.01	6.01	6.01	6.01	6.01	6.01	1.77	1.77	1.77		
R(e) [CT]	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
R(f) [GT]																												
gamma shape																												
pinv(l)																												
alpha(G)																												
pinv(lG)																												
alpha(lG)																												
Free parameters	6	5	6	3	4	4	3	4	4	4	4	4	6	6	6	6	6	1	0	0	0	0	5	5	3	3		
Likelihood ratio test (LRT)	2.08		11.26													20.55							8.66					
P-value	0.15		0.0008													0.001							0.01					

Region	CUC1A				CUC1B				CUC2				CUC3				LAS				MAX1A				MAX1B				
Criterion	AIC ^z	BIC	TPM1uf	AIC	BIC	JC	000000	AIC	TIM2+G	BIC	TPM2uf+G	AIC	TIM1	BIC	F81	000000	AIC	TIM1	012230	010010	010010	AIC	HKY	BIC	HKY	AIC	HKY	JC	000000
Model	012210	000000	012210	012210	000000	000000	000000	010232	010232	010232	010212	010010	012230	010010	010010	000000	010010	012230	012230	010010	010010	010010	010010	010010	010010	010010	010010	010010	000000
Partition	670.90	675.76	483.54	493.47	483.54	493.47	493.47	1086.88	1086.88	1086.88	1088.04	901.80	903.84	903.84	903.84	903.84	622.74	622.74	622.74	625.70	534.79	534.79	534.79	534.79	552.48	562.59	562.59		
-lnL	24	22	29	24	29	24	24	31	31	31	30	28	27	27	27	27	30	30	30	28	28	28	28	28	28	24	24		
K			0.28		0.28		0.28		0.28	0.28	0.28	0.28	0.31	0.31	0.31	0.31	0.24	0.24	0.24	0.23	0.26	0.26	0.26	0.26	0.28	0.28	0.28		
freqA			0.18		0.18		0.18		0.19	0.19	0.19	0.19	0.21	0.21	0.21	0.21	0.37	0.37	0.37	0.38	0.19	0.19	0.19	0.19	0.19	0.19	0.19		
freqC			0.24		0.24		0.24		0.17	0.17	0.17	0.17	0.14	0.14	0.14	0.14	0.16	0.16	0.16	0.15	0.20	0.20	0.20	0.21	0.21	0.21	0.21		
freqG			0.30		0.30		0.30		0.36	0.36	0.36	0.36	0.34	0.34	0.34	0.34	0.23	0.23	0.23	0.24	0.36	0.36	0.36	0.32	0.32	0.32	0.32		
freqT			1.00		1.00		1.00		0.38	0.38	0.38	0.38					1.00												
R(a) [AC]	490.29		629.03		629.03		629.03		3.92	3.92	3.92	3.92					3.40												
R(b) [AG]	278.81		401.92		401.92		401.92		0.38	0.38	0.38	0.38					4.38												
R(c) [AT]	278.81		401.92		401.92		401.92		1.00	1.00	1.00	1.00					4.38												
R(d) [CG]	490.29		629.03		629.03		629.03		2.17	2.17	2.17	2.17					17.22												
R(e) [CT]	1.00		1.00		1.00		1.00		1.00	1.00	1.00	1.00					1.00												
R(f) [GT]									0.02	0.02	0.06	0.06																	
gamma shape																													
pinv(l)																													
alpha(G)																													
pinv(lG)																													
alpha(lG)																													
Free parameters	2	0	5	0	5	0	0	7	7	7	6	4	3	4	4	4	6	6	6	4	4	4	4	4	4	0	0		
Likelihood ratio test (LRT)	9.71		19.86		19.86		19.86		2.32	2.32	2.32	2.32	4.09	4.09	4.09	4.09	5.92							20.23					
P-value	0.008		0.001		0.001		0.001		0.13	0.13	0.13	0.13	0.04	0.04	0.04	0.04	0.05							0.0005					

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Supplemental Table 9. Continued.

Region		MAX2		MAX3		MAX4		PIN		RAX1		RAX2-RAX3		REV	
Criterion	AIC ^z	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	REV
Model	TPM1uf	F81	TPM3uf	TPM3uf	TrN	TrN	TPM1uf	JC	HKY	HKY	TPM3uf	F81	HKY+G	JC	
Partition	012210	000000	012012	012012	010020	010020	012210	000000	010010	010010	012012	000000	010010	000000	
-lnL	574.49	579.74	598.92	598.92	462.86	462.86	518.29	526.33	736.74	736.74	796.63	802.36	685.16	696.10	
K	29	27	29	29	29	29	29	24	28	28	29	27	29	24	
freqA	0.24	0.24	0.30	0.30	0.30	0.30	0.27	0.27	0.33	0.33	0.30	0.30	0.25	0.25	
freqC	0.15	0.15	0.18	0.18	0.13	0.13	0.23	0.23	0.17	0.17	0.23	0.23	0.23	0.23	
freqG	0.34	0.34	0.18	0.18	0.19	0.19	0.20	0.20	0.15	0.15	0.14	0.15	0.21	0.21	
freqT	0.28	0.28	0.34	0.34	0.38	0.38	0.31	0.31	0.34	0.34	0.32	0.32	0.32	0.32	
R(a) [AC]	1.00		3.87	3.87	1.00	1.00	1.00	1.00			13.26				
R(b) [AG]	487.95		6.48	6.48	4.84	4.84	2.32	2.32			10.39				
R(c) [AT]	900.49		1.00	1.00	1.00	1.00	0.00	0.00			1.00				
R(d) [CG]			3.87	3.87	1.00	1.00	0.00	0.00			13.26				
R(e) [CT]	487.95		6.48	6.48	2.04	2.04	2.32	2.32			10.39				
R(f) [GT]	1.00		1.00	1.00	1.00	1.00	1.00	1.00			1.00				
gamma shape															0.73
pinv(I)															
alpha(G)															
pinv(IG)															
alpha(IG)															
Free parameters	5	3	5	5	5	5	5	0	4	4	5	3	5	5	0
Likelihood ratio test (LRT)	10.50		-	-	-	-	16.09		-	-	11.48		21.87		
P-value	0.005		-	-	-	-	0.007		-	-	0.003		0.0006		

Region		SPS		AGL24		AGL20-SOC1		BFT		BRM		CO		CRY1	
Criterion	AIC ^z	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	CRY1
Model	TrNef	JC	TPM3uf	TPM3uf	F81	F81	TPM3uf	HKY	F81	F81	TPM3uf	F81	TrN	HKY	
Partition	010020	000000	012012	012012	000000	000000	012012	010010	000000	000000	012012	000000	010020	010010	
-lnL	598.18	602.68	919.44	919.44	793.33	793.33	754.18	755.39	349.82	349.82	672.79	675.91	834.37	835.51	
K	26	24	29	29	23	23	29	28	27	27	29	27	29	28	
freqA			0.32	0.32	0.28	0.28	0.30	0.30	0.23	0.23	0.26	0.26	0.22	0.22	
freqC			0.17	0.17	0.18	0.18	0.18	0.18	0.15	0.15	0.19	0.19	0.15	0.15	
freqG			0.19	0.19	0.20	0.20	0.18	0.18	0.16	0.16	0.15	0.15	0.20	0.20	
freqT			0.33	0.33	0.34	0.34	0.34	0.34	0.45	0.45	0.40	0.39	0.43	0.43	
R(a) [AC]	1.00		0.33	0.33			3.70				4.22		1.00		
R(b) [AG]	1.54		3.78	3.78			9.88				2.88		3.90		
R(c) [AT]	1.00		1.00	1.00			3.70				4.22		1.00		
R(d) [CG]	1.00		0.33	0.33			9.88				2.88		1.00		
R(e) [CT]	5.91		3.78	3.78			1.00				1.00		1.75		
R(f) [GT]	1.00		1.00	1.00							1.00		1.00		
gamma shape															
pinv(I)															
alpha(G)															
pinv(IG)															
alpha(IG)															
Free parameters	2	0	5	5	3	3	5	4	3	3	5	3	5	5	4
Likelihood ratio test (LRT)	9.00		-	-	-	-	2.43		-	-	6.25		2.29		
P-value	0.01		-	-	-	-	0.12		-	-	0.04		0.13		

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Region		CRY2		ELF6		FD		FD1		FG		FLC-FLF		FPF1	
Criterion	AIC ^z	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC
Model	TPM2uf	F81	TrN+G	TrN+G	TPM1uf+G	F81	TPM3uf	K80	TPM2uf	HKY	F81+G	F81	TPM3	JC	
Partition	010212	000000	010020	010020	012210	000000	012012	010010	010212	010010	000000	000000	012012	000000	
-lnL	783.52	788.42	1123.01	1123.01	969.91	975.19	743.21	750.84	737.69	738.73	746.41	748.07	487.81	489.89	
K	29	27	30	30	30	27	29	25	29	28	22	21	26	24	
freqA	0.28	0.27	0.30	0.30	0.27	0.27	0.19	0.19	0.26	0.26	0.26	0.26	0.26	0.26	
freqC	0.18	0.18	0.18	0.18	0.19	0.20	0.25	0.25	0.19	0.19	0.19	0.23	0.23	0.23	
freqG	0.17	0.17	0.16	0.16	0.19	0.20	0.28	0.28	0.22	0.22	0.22	0.13	0.13	0.13	
freqT	0.38	0.38	0.36	0.36	0.34	0.34	0.28	0.28	0.33	0.33	0.33	0.38	0.38	0.38	
R(a) [AC]	0.29		1.00	1.00	1.00		0.001		0.45				494.00		
R(b) [AG]	1.23		2.73	2.73	1.41		1.99		1.89				656.79		
R(c) [AT]	0.29		1.00	1.00	0.45		1.00		0.45				1.00		
R(d) [CG]	1.00		1.00	1.00	0.45		0.001		1.00				494.00		
R(e) [CT]	1.23		5.88	5.88	1.41		1.99		1.89				656.79		
R(f) [GT]	1.00		1.00	1.00	1.00		1.00		1.00				1.00		
gamma shape			1.00	1.00	0.12						0.01				
pinv(l)															
alpha(G)															
pinv(lG)															
alpha(lG)															
Free parameters	5	3	6	6	6	3	5	1	5	4	4	3	2	0	
Likelihood ratio test (LRT)	9.79		-	-	10.55		15.25		2.08		3.33		4.17		
P-value	0.007		-	-	0.01		0.004		0.15		0.07		0.12		

Region		FRIGIDA		FT-TSF		GI-FB		HOS1		LFY		MAF1-MAF3-AGL31		MAF2A	
Criterion	AIC ^z	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC	BIC	AIC
Model	TPM3uf	HKY	TPM3uf	F81	TPM3uf	F81	TPM3uf	HKY+G	HKY+G	HKY+G	TPM3uf+G	TPM3uf	F81+G	F81	
Partition	012012	010010	012012	000000	012012	000000	012012	010010	010010	010010	012012	012012	000000	000000	
-lnL	888.68	890.74	787.17	790.60	952.97	957.07	309.35	309.35	1448.28	1448.28	867.65	870.21	438.59	440.61	
K	19	18	27	25	29	27	27	27	29	29	30	29	24	23	
freqA	0.27	0.27	0.24	0.24	0.25	0.25	0.27	0.27	0.32	0.32	0.29	0.29	0.21	0.21	
freqC	0.16	0.16	0.25	0.26	0.18	0.18	0.14	0.14	0.13	0.13	0.21	0.21	0.18	0.18	
freqG	0.17	0.17	0.14	0.14	0.16	0.16	0.20	0.20	0.20	0.20	0.17	0.17	0.16	0.16	
freqT	0.40	0.40	0.37	0.36	0.41	0.41	0.39	0.39	0.35	0.35	0.33	0.33	0.46	0.46	
R(a) [AC]	0.18		5.29		3.08										
R(b) [AG]	2.21		5.29		3.23										
R(c) [AT]	1.00		1.00		1.00										
R(d) [CG]	0.18		5.29		3.08										
R(e) [CT]	2.21		5.29		3.23										
R(f) [GT]	1.00		1.00		1.00										
gamma shape															
pinv(l)									0.329	0.329	0.011		0.015		
alpha(G)															
pinv(lG)															
alpha(lG)															
Free parameters	5	4	5	3	5	3	3	3	5	5	6	5	4	3	
Likelihood ratio test (LRT)	4.11		6.87		8.20		-	-	-	-	5.13		4.04		
P-value	0.04		0.03		0.02		-	-	-	-	0.02		0.04		

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Supplemental Table 9. Continued.

Region		MAF2B			MAF4			MAF5			MFT			PHYA			PHYB-PHYD			PHYE			
Criterion	AIC ^z	BIC	F81	000000	AIC	TPM2uf	BIC	HKY	010010	AIC	TPM1uf	BIC	F81	000000	AIC	TrN+G	BIC	TrN	010020	AIC	TPM3uf	BIC	HKY
Model	TIM2	010232	536.00	539.81	935.31	010212	935.31	937.25	010010	010212	935.25	532.52	534.91	699.02	701.87	738.31	743.35	820.51	821.78	843.32	845.60	010010	010010
Partition	-lnL	22	19	22	19	22	19	22	19	22	19	22	19	22	19	22	19	22	19	22	19	22	19
Free parameters	6	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Likelihood ratio test (LRT)	7.63																						
P-value	0.05																						
gamma shape																							
pinv(I)																							
alpha(G)																							
pinv(IG)																							
alpha(IG)																							
Free parameters	6	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Likelihood ratio test (LRT)	7.63																						
P-value	0.05																						
gamma shape																							
pinv(I)																							
alpha(G)																							
pinv(IG)																							
alpha(IG)																							
Free parameters	6	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Likelihood ratio test (LRT)	15.98																						
P-value	0.01																						

Region		RGA-RGA1			RGL1-RGL2-RGL3			SPY			TFL1-ATC			TFL2			VRN1			VRN2				
Criterion	AIC ^z	BIC	JC	000000	AIC	TPM2+G	K80	010010	AIC	TVM	012314	000000	AIC	TPM2uf+I	BIC	TPM2uf	HKY+G	BIC	HKY	010010	AIC	TPM1uf	BIC	HKY
Model	TIM2	010232	698.85	706.84	908.84	010212	908.84	911.10	821.93	828.25	814.55	700.83	814.55	816.35	816.35	816.35	816.35	816.35	816.35	816.35	816.35	816.35	816.35	816.35
Partition	-lnL	30	24	24	27	27	25	25	31	27	27	29	29	29	29	29	29	29	29	29	29	29	29	29
Free parameters	6	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Likelihood ratio test (LRT)	7.63																							
P-value	0.05																							
gamma shape																								
pinv(I)																								
alpha(G)																								
pinv(IG)																								
alpha(IG)																								
Free parameters	6	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Likelihood ratio test (LRT)	15.98																							
P-value	0.01																							

^zAkaike information criterion (AIC; Akaike, 1974) and Bayesian information criteria (BIC; Schwarz, 1978).

Supplemental Table 10. Models of sequence evolution of chloroplast DNA (cpDNA) sequence data (classified by haplotypes) using JModelTest for 11 *Prunus* species.

Region	3'tmV-ndhC			tmL-tmF and tmL intron			tmQ-5' rps16			tmH-psbA			ndhF-rpl32			atpB-rbcL		
Criterion	AIC ^z	BIC		AIC	BIC		AIC	BIC		AIC	BIC		AIC	BIC		AIC	BIC	
Model	TVM+G	F81+G	HKY	F81+G	F81	F81+G	F81	F81	TrN	F81	F81	F81	F81	F81	F81	TPM1uf	HKY	
Partition	012314	000000	010010	000000	000000	000000	000000	000000	010020	000000	000000	000000	000000	000000	000000	012210	010010	
-lnL	998.85	1003.29	1193.21	1195.26	1195.26	721.90	724.05	724.05	463.62	465.72	465.72	791.38	791.38	791.38	1089.65	1092.93		
K	28	24	24	23	23	46	45	45	35	33	33	23	23	23	25	24		
freqA	0.42	0.42	0.36	0.36	0.36	0.32	0.32	0.32	0.44	0.45	0.45	0.36	0.36	0.36	0.34	0.34		
freqC	0.06	0.06	0.16	0.16	0.16	0.13	0.13	0.13	0.13	0.13	0.13	0.12	0.12	0.12	0.15	0.15		
freqG	0.11	0.11	0.15	0.15	0.15	0.12	0.12	0.12	0.08	0.08	0.08	0.11	0.11	0.11	0.14	0.14		
freqT	0.41	0.42	0.33	0.33	0.33	0.43	0.43	0.43	0.35	0.34	0.34	0.40	0.40	0.40	0.37	0.37		
R(a) [AC]	0.30								1.00						1.00			
R(b) [AG]	0.32								1.86						1.51			
R(c) [AT]	0.51								1.00						0.00			
R(d) [CG]	0.005								1.00						0.00			
R(e) [CT]	0.32								0.11						1.51			
R(f) [GT]	1.00								1.00						1.00			
gamma shape						0.02												
pinv(I)																		
alpha(G)																		
pinv(IG)																		
alpha(IG)																		
Free parameters	8	4	4	3	3	4	3	3	5	3	3	3	3	3	5	4		
Likelihood ratio test (LRT)	8.89		4.10			4.31			4.20			-			6.55			
P-value	0.06		0.04			0.04			0.12			-			0.01			

^zAkaike information criterion (AIC; Akaike, 1974) and Bayesian information criteria (BIC; Schwarz, 1978).

Supplemental Table 11. Models of sequence evolution of phased haplotype internal transcribed spacer (ITS) and candidate gene regions sequence data using JModelTest for 11 *Prunus* species.

Region	ITS			PGDH			PGI			s6pdh			AXR1			BRC1			BRC2		
	AIC ^z	BIC	HKY+G	AIC	TIM3+G	F81+G	BIC	HKY	TPM1uf	AIC	HKY+G	HKY+G	BIC	TIM1ef	TIM1ef	AIC	JC	HKY	AIC	HKY	F81
Model	TPM1uf+G	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010	010010
Partition	-lnL	1135.44	1137.35	895.18	902.98	568.67	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76	569.76
K	44	43	43	57	54	43	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
freqA	0.19	0.20	0.29	0.29	0.28	0.28	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27
freqC	0.31	0.31	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18
freqG	0.31	0.31	0.20	0.20	0.20	0.20	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18
freqT	0.19	0.19	0.34	0.34	0.34	0.34	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37
R(a) [AC]	1.00		3.13	3.13	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
R(b) [AG]	2.43		1.98	1.98	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18
R(c) [AT]	0.35		3.13	3.13	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37	0.37
R(d) [CG]	0.35		6.79	6.79	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18	2.18
R(e) [CT]	1.00		0.12	0.12	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
R(f) [GT]	0.18		0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
gamma shape																					
pinv(l)																					
alpha(G)																					
pinv(lG)																					
alpha(lG)																					
Free parameters	6	5	7	15.60	4	5	4	5	5	4	5	5	5	5	5	4	0	0	4	4	3
Likelihood ratio test (LRT)	3.83			0.001		569.76		569.76											2.06		
P-value	0.05					0.14		0.14											0.15		

Region	CUC1A			CUC1B			CUC2			CUC3			LAS			MAX1A			MAX1B		
	AIC ^z	BIC	TPM2+G	AIC	TPM1uf	TPM1uf	BIC	F81	F81+G	AIC	HKY	HKY	BIC	TVM+G	TVM+G	AIC	HKY	TPM2uf+G	AIC	HKY	TPM2uf+G
Model	TIM2ef+G	010232	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212	010212
Partition	-lnL	739.45	742.28	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25	536.25
K	51	49	49	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
freqA				0.28	0.18	0.18	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24
freqC				0.18	0.24	0.24	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18
freqG				0.24	0.30	0.30	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24	0.24
freqT				0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30
R(a) [AC]	296.59	248.70		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
R(b) [AG]	477.79	704.68		5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77
R(c) [AT]	296.59	248.70		2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53
R(d) [CG]	1.00	1.00		2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53	2.53
R(e) [CT]	1252.17	704.68		5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77
R(f) [GT]	1.00	1.00		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
gamma shape	0.05	0.02																			
pinv(l)	0.50																				
alpha(G)																					
pinv(lG)																					
alpha(lG)																					
Free parameters	5	3	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5	5
Likelihood ratio test (LRT)	5.66			-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P-value	0.06																				

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Supplemental Table 11. Continued.

Region		CRY2		ELF6		FD		FDI		FG		FLC-FLF		FPF1	
Criterion	AIC ^z	BIC	AIC	HKY+G	BIC	AIC	TPM1uf	AIC	TrN	BIC	HKY	AIC	HKY	AIC	BIC
Model	TPM3	K80	TPM3uf	HKY	F81	TPM1uf	F81	TPM2uf	K80	TPM2uf	HKY	TPM2uf	HKY	TPM3	JC
Partition	012012	010010	010010	010010	000000	012210	000000	010212	010010	010010	010010	010010	010010	012012	000000
-lnL	1476.11	1478.05	1170.56	1172.17	1006.54	1009.15	803.56	810.82	780.92	782.73	769.82	771.44	495.07	497.78	
K	52	51	73	72	47	45	41	37	39	38	62	61	28	26	
freqA			0.30	0.30	0.27	0.27	0.19	0.26	0.26	0.26	0.25	0.25			
freqC			0.17	0.17	0.19	0.19	0.24	0.19	0.19	0.19	0.23	0.24			
freqG			0.16	0.16	0.20	0.20	0.28	0.22	0.22	0.22	0.12	0.12			
freqT			0.36	0.36	0.34	0.34	0.28	0.33	0.33	0.33	0.39	0.40			
R(a) [AC]	0.56				1.00		1.00	0.37					353.19		
R(b) [AG]	1.60				1.20		3.65	1.89					577.61		
R(c) [AT]	1.00				0.48		1.00	0.37					1.00		
R(d) [CG]	0.56				0.48		1.00	1.00					353.19		
R(e) [CT]	1.60				1.20		8.14	1.89					577.61		
R(f) [GT]	1.00				1.00		1.00	1.00					1.00		
gamma shape															
pinv(l)															
alpha(G)															
pinv(lG)															
alpha(lG)															
Free parameters	2	1	5	4	5	3	5	1	5	4	4	3			
Likelihood ratio test (LRT)	3.88		3.22		5.21		14.52		3.61		3.23				
P-value	0.05		0.07		0.07		0.006		0.06		0.07				

Region		FRIGIDA		FT-TSF		GI-FB		HOS1		LFY		MAF1-MAF3-AGL31		MAF2A	
Criterion	AIC ^z	BIC	AIC	TPM3uf	F81	BIC	HKY	AIC	F81	BIC	HKY+G	AIC	TPM2uf+G	AIC	BIC
Model	TPM3uf	TPM3uf	TPM3uf	TPM3uf	F81	TPM3uf+G	HKY	TPM3uf	F81	TPM3uf	HKY+G	TPM2uf+G	TPM2uf+G	TIM1+G	F81
Partition	012012	012012	012012	000000	000000	012012	010010	000000	000000	010010	010010	010212	010212	012230	000000
-lnL	1092.00	1092.00	807.88	812.06	1074.71	1071.66	1074.71	324.16	324.16	1757.52	1757.52	975.20	976.40	456.56	461.43
K	31	31	49	47	68	70	68	33	33	79	79	42	41	35	31
freqA	0.29	0.29	0.23	0.23	0.25	0.25	0.25	0.27	0.27	0.33	0.33	0.29	0.29	0.21	0.21
freqC	0.16	0.16	0.25	0.25	0.18	0.18	0.18	0.14	0.14	0.14	0.14	0.20	0.20	0.18	0.18
freqG	0.17	0.17	0.14	0.14	0.16	0.16	0.16	0.20	0.20	0.19	0.19	0.17	0.17	0.15	0.16
freqT	0.39	0.39	0.37	0.36	0.41	0.41	0.41	0.39	0.39	0.34	0.34	0.33	0.33	0.46	0.46
R(a) [AC]	0.13	0.13	6.08		2.35							0.46	0.46	1.00	
R(b) [AG]	1.73	1.73	5.89		3.29							1.97	1.97	1.67	
R(c) [AT]	1.00	1.00	1.00		1.00							0.46	0.46	0.33	
R(d) [CG]	0.13	0.13	6.08		2.35							1.00	1.00	0.33	
R(e) [CT]	1.73	1.73	5.89		3.29							1.97	1.97	0.33	
R(f) [GT]	1.00	1.00	1.00		1.00							1.00	1.00	1.00	
gamma shape												0.02	0.02	0.16	
pinv(l)															
alpha(G)															
pinv(lG)															
alpha(lG)															
Free parameters	5	5	5	3	6	4	4	3	3	5	5	6	5	7	3
Likelihood ratio test (LRT)	-	-	8.37		6.09			-	-	-	-	2.39		9.75	
P-value	-	-	0.02		0.05			-	-	-	-	0.12		0.04	

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Region	MAF2B			MAF4			MAF5			MFT			PHYA			PHYB-PHYD			PHYE		
	AIC ^z	BIC	F81	AIC	TrN+G	BIC	HKY+G	AIC	TPM3uf	BIC	F81	AIC	TPM2uf+G	BIC	F81	AIC	TrN+G	BIC	TrN	AIC	HKY
Criterion	TIM2	010232	547.23	551.12	1243.79	1245.46	572.91	575.79	748.08	012345	766.73	753.31	010212	000000	759.70	877.01	878.87	886.48	886.48	886.48	886.48
Model	010232	547.23	551.12	1243.79	1245.46	572.91	575.79	748.08	012345	766.73	753.31	010212	000000	759.70	877.01	878.87	886.48	886.48	886.48	886.48	886.48
Partition	-lnL	24	21	84	83	35	33	47	38	37	38	37	37	38	33	44	43	34	34	34	34
Free parameters	freqA	0.22	0.22	0.28	0.28	0.28	0.28	0.28	0.20	0.20	0.20	0.27	0.27	0.27	0.27	0.27	0.32	0.32	0.32	0.24	0.24
Likelihood ratio test (LRT)	freqC	0.17	0.18	0.15	0.14	0.14	0.15	0.15	0.24	0.24	0.24	0.18	0.18	0.18	0.18	0.15	0.15	0.15	0.21	0.21	0.21
P-value	freqG	0.18	0.17	0.14	0.14	0.14	0.15	0.15	0.21	0.21	0.21	0.22	0.22	0.22	0.22	0.17	0.17	0.17	0.17	0.17	0.17
	freqT	0.43	0.43	0.43	0.42	0.42	0.40	0.39	0.35	0.35	0.35	0.33	0.33	0.33	0.33	0.36	0.36	0.36	0.37	0.37	0.37
	R(a) [AC]	3.37	3.37	1.00	1.00	1.00	2.16	2.16	0.42	0.42	0.42	0.19	0.19	0.19	0.19	1.00	1.00	1.00	1.00	1.00	1.00
	R(b) [AG]	1.35	1.35	4.14	4.14	4.14	2.84	2.84	0.49	0.49	0.49	1.64	1.64	1.64	1.64	7.10	7.10	7.10	6.37	6.37	6.37
	R(c) [AT]	3.37	3.37	1.00	1.00	1.00	1.00	1.00	1.51	1.51	1.51	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	R(d) [CG]	1.00	1.00	1.00	1.00	1.00	2.16	2.16	1.49	1.49	1.49	1.64	1.64	1.64	1.64	1.34	1.34	1.34	1.43	1.43	1.43
	R(e) [CT]	6.32	6.32	2.24	2.24	2.24	2.84	2.84	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
	R(f) [GT]	1.00	1.00	1.00	1.00	1.00	1.00	1.00	100.00	100.00	100.00	0.01	0.01	0.01	0.01	0.14	0.14	0.14	0.14	0.14	0.14
	gamma shape																				
	pinv(l)																				
	alpha(G)																				
	pinv(lG)																				
	alpha(lG)																				
Free parameters																					
Likelihood ratio test (LRT)																					
P-value																					

^zAkaike information criterion (AIC; Akaike, 1974) and Bayesian information criteria (BIC; Schwarz, 1978).