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Nuclear and Chloroplast Microsatellite Markers to Assess Genetic Diversity and Evolution in Hazelnut Species, Hybrids and Cultivars

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Abstract

The U.S. Department of Agriculture (USDA), Agricultural Research Service (ARS), National Clonal Germplasm Repository (NCGR) in Corvallis, Oregon, preserves more than 800 accessions of hazelnut (*Corylus*) including *C. avellana* cultivars and representatives of 10 other recognized shrub and tree species. Characterization and study of genetic diversity in this collection requires cross-transferable markers such as trinucleotide microsatellite or simple sequence repeat (SSR) markers and universal chloroplast SSR markers. We developed new SSR markers, and evaluated 114 *Corylus* accessions representing 11 species and 44 interspecific hybrids. Eight of 23 SSRs generated easy-to-score alleles in all species and seven were highly polymorphic. For the seven, the average heterozygosity was moderate at 0.49 while allele number, genetic diversity and PIC were high at 11.71, 0.79 and 0.76, respectively. The three most polymorphic SSRs were CaC-C008, CaC-C040 and CaC-C118. Neighbor joining (NJ) clustering and structure analysis agreed with taxonomic analysis and supported inclusion of *C. maxima* in the large polymorphic species *C. avellana*. Analysis also indicated that *C. californica* is a distinct species rather than a botanical variety of *C. cornuta*. Six universal cpSSRs were polymorphic in *Corylus* and generated an average of 3 alleles per locus and 21 chlorotypes. Diversity at these cpSSRs was high and ranged from 0.33 to 0.64, with an average of 0.69. Incongruence in NJ topologies between the nuclear and chloroplast markers could be attributed to chloroplast capture during the ancestral diversification of the genus, or homoplasy. The phylogeographical relationships among the 21 chlorotypes in the 11 *Corylus* species support Asia as a refugium where several hazelnut lineages survived during glaciation and from which they reappeared only later after the dispersal event from Asia through the Mediterranean to Europe, and across the Atlantic to North America.

Keywords: *Corylus*, filbert, simple sequence repeat (SSR) markers, universal chloroplast SSRs.

INTRODUCTION

Hazelnut, *Corylus* L., belongs to the family Betulaceae and subfamily Coryloideae. In addition to *Corylus*, the Coryloideae contains hornbeam (*Carpinus* L.), hophornbeam (*Ostrya* Scopoli), and *Ostryopsis* Decne. (Crane, 1989; Cronquist, 1981). The second subfamily, the Betuloideae, consists of alder (*Alnus* Mill.) and birch (*Betula* L.). The oldest known fossil record attributed to *Corylus* is a fruit involucre from the middle Eocene (~ 45 mya) in the Republic Flora of central Washington (Chen et al. 1999; Pigg et al. 2003). Coryloideae is supported as a monophyletic group (Yoo and Wen 2002, 2007) and shares several distinguishing characters including nutlets without lateral wings, vessels without spiral thickenings, absence of tracheids, and pollen without arci. Hazelnuts, like other members of the birch family, are deciduous, wind-pollinated, monoecious shrubs and trees with toothed, simple, ovate to obovate leaves alternately arranged. Morphological synapomorphies that are characteristic of *Corylus* include large animal-dispersed nuts and filaments that are completely divided longitudinally (Chen et al. 1999). The chromosome number of the genus is $2n = 2x = 22$ (Thompson et al. 1996).

The taxonomy of *Corylus* has been investigated since the mid-nineteenth century, with the number of described species depending on the emphasis placed by the author on certain anatomical and morphological characters (illustrated in Table 1 of Whitcher and Wen 2001). The inclusion of taxa within each section or subgenus of *Corylus* has varied significantly. The division of the genus into two sections, *Acanthochlamys* and *Corylus*, as proposed by de De Candolle (1864) and followed by Schneider (1916), and Li and Cheng (1979), agrees with internal transcribed spacers (ITS) phylogeny (Whitcher and Wen 2001). The tree species *C. ferox* Wall., with its distinctive spiny bur-like involucre, has invariably been placed in section or subgenus *Acanthochlamys* Spach.. Within section *Corylus*, three subclades are traditionally recognized. Subclade *Colurnae* Schneider consists of the tree species *C. colurna* L., *C. jacquemontii* Decne., *C. chinensis* Franch. and *C. fargesii* C. K. Schneider. The latter species was described by Hu (1948). Subclade *Siphonochlamys* contains the bristle-husked

shrubs *C. cornuta* Marshall, *C. californica* Marshall and *C. sieboldiana* Blume. Subclade *Phylloclamys* includes the shrubs with leafy involucre, *C. avellana* L., *C. americana* Marshall and the *C. heterophylla* Fisch. complex. Based on morphological traits (especially the husk or involucre) and molecular ITS and chloroplast *rbcL* phylogenetic analysis, *Acanthochlamys* is sister to the remainder of the genus *Corylus*, and subgenera *Siphonochlamys* and *Phylloclamys* are sister taxa (Erdoğan and Mehlenbacher 2000a; Forest and Bruneau 2000; Forest et al. 2005; Whitcher and Wen 2001).

Corylus contains 11 commonly recognized species disjunctly distributed in the Northern Hemisphere. Of 11 species, two species occur in Europe and Asia Minor (*C. avellana* and *C. colurna*), three in North America (*C. americana* and *C. cornuta* in the east and *C. californica* in the west), and one in the Himalayas (*C. jacquemontii*). The remaining species are endemic to eastern Asia and include the tree hazels *C. chinensis*, *C. fargesii* Schneid. and *C. ferox*, and the shrub hazels *C. heterophylla* and *C. sieboldiana* (Whitcher and Wen 2001). Although these 11 species are commonly recognized, other species designations appear in the literature. *C. maxima* Mill., *C. pontica* Koch., and *C. colchica* Alb. have been described by some authors (Kasapligil, 1972) as distinct species closely related to *C. avellana*. Others consider these three to be variants within the highly polymorphic species *C. avellana*. Their morphological traits show continuous distributions, they are easily crossed with each other and give fully fertile offspring, and their geographic distributions overlap (Mehlenbacher, 1991; Rovira, 1997; Thompson et al. 1996). Within the bristle-husked shrubs (*Siphonochlamys*), *C. californica* is recognized as a distinct species by some authorities, and as a subspecies or botanical variety of *C. cornuta* by others. Within the Asian leafy-husked shrubs, var. *sutchuensis* Franch. and var. *yunnanensis* Franch. are adapted to warmer climates than *C. heterophylla*. They are recognized as botanical varieties of *C. heterophylla* by some authorities, and as the separate species *C. kweichowensis* Hu (Liang, 1988) and *C. yunnanensis* (Franch.) A. Camus, respectively, by others. Further, *C.*

thibetica Batalin is sometimes listed as a variant of *C. ferox* and *C. mandshurica* Maxim and *C. hallaisanensis* Nakai occasionally appear in the literature as synonyms or variants of *C. sieboldiana* while *C. wangii* Hu is considered a form of *C. chinensis*. In this paper, we follow the consensus recognition of six shrub species (*C. avellana*, *C. americana*, *C. heterophylla*, *C. cornuta*, *C. californica*, and *C. sieboldiana*) and five tree species (*C. colurna*, *C. jacquemontii*, *C. chinensis*, *C. fargesii* and *C. ferox*).

The U.S. Department of Agriculture (USDA), Agricultural Research Service (ARS), National Clonal Germplasm Repository (NCGR) in Corvallis, Oregon, preserves more than 800 accessions of hazelnut representing cultivars and representatives of each of the recognized shrub and tree species. Microsatellite or simple sequence repeat (SSR) markers have become valuable molecular tools for fingerprinting accessions, assessment of genetic diversity in collections and linkage mapping due to their abundance, high degree of polymorphism, co-dominance and suitability for automation. In such a diverse collection, markers that are transferable across species are needed. Tri-nucleotide SSRs seem to be better candidates than dinucleotide SSRs for cross-transferability (Kutil and Williams 2001; Morgante et al. 2002; Scotti et al. 2002; Wang et al. 1994; Young et al. 2000). They are often clustered in regulatory genes (Young et al. 2000) and are more likely than dinucleotide SSRs to be found within expressed regions (Morgante et al. 2002; Wang et al. 1994). Trinucleotide repeats were three times more frequent in transcribed than in non-transcribed regions of the *Arabidopsis thaliana* and *Zea mays* genomes (Morgante et al. 2002). They are more likely to be conserved across taxa, but tend to be less polymorphic than dinucleotide SSRs (Kutil and Williams 2001; Rajora et al. 2001; Shepherd et al. 2002). Alleles at trinucleotide SSRs are easier to score due to absence of the characteristic stuttering that plagues most dinucleotide alleles. Trinucleotide and tetranucleotide repeats have become the markers of choice for population, linkage and forensic studies in humans and other animal species (Gastier et al. 1995; Sheffield et al. 1995; Tozaki et al. 2000) and are recommended as universal

markers in plants (Testolin and Cipriani 2010). SSR markers were developed in *C. avellana* (Bassil et al. 2005a, b; Boccacci et al. 2005; Gürcan and Mehlenbacher 2010a, b; Gürcan et al. 2010a) and used for linkage mapping (Mehlenbacher et al. 2006; Gürcan et al. 2010a), to assess genetic relationships among cultivars (Boccacci and Botta 2010; Boccacci et al. 2006, 2008; Ghanbari et al. 2005; Gökirmak et al. 2009, Gürcan et al. 2010b) and to fingerprint cultivars in collections, identify synonyms, and determine parentage (Botta et al. 2005; Gökirmak et al. 2009; Sathuvalli and Mehlenbacher 2011). Cross-species transference of SSRs was demonstrated in *Corylus* (Bassil et al. 2005a; Boccacci et al. 2005) and in the Betulaceae (Gürcan and Mehlenbacher 2010b).

The chloroplast genome has a lower evolutionary rate than the nuclear genome. It is non-recombining and shows a uniparental mode of inheritance, usually maternal in angiosperms and paternal in gymnosperms (Provan et al. 2001). Thus in angiosperms the chloroplast genome can only be disseminated by seeds or cuttings and chloroplast DNA markers provide information on past changes in species distribution that is unaffected by subsequent pollen movements. Despite its conserved gene order and a lack of recombination, the chloroplast genome shows length polymorphism associated with mononucleotide repeats. Non-coding intron and intergenic spacers are particularly variable and contain microsatellite and non-microsatellite polymorphisms even between closely related individuals and taxa in a range of plant groups (Provan et al. 2001). In recent years universal primer pairs have been developed for the analysis of chloroplast SSRs (cpSSRs) in different species (Provan et al. 2001). In several studies, cpSSRs provided insights into intraspecific phylogeographic variability (e.g. Petit et al. 2003) and allowed investigation of origin and domestication in different crop species (e.g. Arroyo-Garcia et al. 2006). Their application to hazelnut is recent and to date has only been applied to *C. avellana* for investigating the post-glacial migration of wild populations in Europe (Palmé and Vendramin 2002) and studying the origin and diffusion of hazelnut cultivars in the Mediterranean basin (Boccacci and Botta 2009).

The aim of this study was to determine cross-transferability of nuclear (n) SSRs isolated from a *C. avellana* library enriched for trinucleotide repeats to 11 species preserved at the NCGR; to identify the nuclear and chloroplast SSR markers most suitable for future studies in *Corylus* species; to fingerprint representative accessions from each species; and to assess diversity, structure and evolution of *Corylus* species.

MATERIALS AND METHODS

Plant material and DNA extraction

The hazelnut accessions evaluated in this study were in the collection at USDA-ARS-NCGR and the Oregon State University's Smith Horticultural Research Farm in Corvallis, OR (Table 1). A total of 158 accessions were evaluated including: 6 *C. avellana* (which include 3 previously assigned to *C. maxima*), 26 *C. americana*, 30 *C. californica*, 9 *C. chinensis*, 13 *C. colurna*, 11 *C. cornuta*, 2 *C. fargesii*, 2 *C. ferox*, 7 *C. heterophylla*, 5 *C. jacquemontii*, 3 *C. sieboldiana* and 44 hybrids. DNA was extracted from actively growing leaves collected from the NCGR field in the spring using a modified PUREGENE® kit (Gentra Systems Inc., MN) protocol. Proteinase K and RNase A treatment were added and the protein precipitation step was repeated twice.

Cross-species amplification

GAA-enriched library 'C' construction and primer design were previously described (Bassil et al. 2005a; Gürcan et al. 2010). Twenty-three primer pairs were designed from 22 SSR-containing sequences and were tested for amplification in each of the accessions. Amplification success was indicated by the presence of a PCR product after ethidium bromide staining of 3% agarose gels. All 11 *Corylus* species were represented by the accessions. The 15 unique SSR primer pairs (Suppl Table 1,

Suppl Table 2) that generated a product in all of the species representatives were investigated further, with sizing by capillary electrophoresis.

Microsatellite marker analysis

Fluorescently-labeled forward primers for the 15 SSRs were used for PCR amplification (Suppl Table 2). PCR reactions were carried out separately for each primer pair and up to three PCR products (one per SSR primer set) were multiplexed and separated using an ABI 3100 capillary electrophoresis instrument (Applied Biosystems, Foster City, Calif.) at the Core Labs of the Center for Genome Research and Biocomputing at Oregon State University. PCR reactions were carried out in 10 μ L volumes using forward primers fluorescently labeled with 6-FAM, 5-HEX, or NED and unlabeled reverse primers (Operon Biotechnologies, Huntsville, AL). The PCR reactions were diluted with water by a factor ranging from 1:80 (FAM-labeled amplicons) and 1:160 (HEX-labeled products) to 1:320 (NED-labeled amplicons) and 0.5 μ L was injected into the instrument. GeneScan version 2.1 (Applied Biosystems) was used for automated data collection and Genotyper version 2.0 (Applied Biosystems) was used for estimation of allele sizes.

PCR reactions were performed in a 10 μ L volume containing 1x reaction buffer, 2 mM MgCl₂, 0.2 mM dNTPs, 0.3 μ M of each primer, 0.25 units of Biolase *Taq* DNA polymerase (Bioline USA Inc., Randolph, MA), and 2.5 ng genomic DNA. The PCR protocol consisted of one cycle of initial denaturation at 94 °C for 3 min, followed by 35 cycles of denaturation at 93 °C for 40 s, annealing at optimum T_a (Suppl. Table 1) for 40 s, and extension at 72 °C for 40 s. A final extension cycle at 72 °C for 30 min followed. DNA was amplified in an Eppendorf Gradient thermocycler (Brinkmann Instruments, Inc., Westbury, NY) or an MJ Research Tetrad thermocycler (MJ Research Inc., Watertown, MA). The success of the PCR reaction was verified by 2% agarose gel electrophoresis prior to capillary electrophoresis.

Diversity and clustering

Of the 23 primer pairs that were tested, eight (CaC-C001a, CaC-C010, CaC-C020, CaC-C023, CaC-C035, CaC-C103, CaC-C115 and CaT-C502) were either difficult to amplify or failed to amplify in one or more *Corylus* species and were not pursued further (Supplementary Table 1). Of the 15 primer pairs that generated a product in all of the species, CaC-C114 generated up to four PCR products, indicating its presence in more than one location in the hazelnut genome. Data for CaC-C114 were not included for analysis or clustering. PowerMarker (Version 3.25) (Liu and Muse 2005) was used to calculate genetic diversity parameters for the 11 species at the remaining 14 SSRs (Table 2). These diversity measures consisted of: number of alleles (A); observed heterozygosity (H_o) or the number of heterozygous individuals in that population; gene diversity, often referred to as expected heterozygosity (H_e) and defined as the probability that two randomly chosen alleles from the population are different; and polymorphism information content (PIC) (Botstein et al. 1980). Species-specific or unique alleles (A_u) observed in only one species were also noted (Table 2).

Eight of the 14 SSRs characterized in each species were easy to score in all species and generated allele sizes expected on the basis of repeat motif (Supplementary Table 1). Genetic distance matrices were computed with PowerMarker using data for these eight SSRs by the proportion of shared alleles distance (D_{sa}):

$$D_{sa} = \frac{1}{m} \sum_{j=1}^m \sum_{i=1}^{a_j} \min(p_{ij}, q_{ij})$$

where p_{ij} and q_{ij} are the frequencies of the i th allele at the j th locus, m is the number of loci examined, and a_j is the number of alleles at the j th locus. Neighbor joining (NJ) cluster analysis was used to group accessions using the eight SSRs (Fig. 2).

Structure analysis

The software program Structure 2.3.3 (Prichard et al. 2000) was used to infer population structure and assign individuals to populations based on the SSR genotypes. Structure uses a Bayesian approach to model-based clustering. Multiple runs were performed by setting the number of populations, k , from 5 to 12. The burn-in length was set to 200,000 with runs of 100,000 steps and each run was replicated three times.

Chloroplast haplotype determination and data analysis

A total of ten cpSSR loci were analyzed: ccmp1, ccmp2, ccmp3, ccmp4, ccmp5, ccmp6, ccmp7, ccmp8, ccmp9, and ccmp10. The primer pairs were designed by Weising and Gardner (1999) for *Nicotiana tabacum* L. and loci were initially tested in 40 accessions representing 11 *Corylus* species. Then, polymorphic cpSSR were used to determine the chloroplast haplotype in a total of 158 accessions of which 114 represented *Corylus* species and 44 were interspecific hybrids. PCR amplification was carried out using a reaction mixture (15 μ l) consisting of 40 ng DNA template, 0.5 μ M of each primer, 200 μ M dNTPs, 2 mM MgCl₂, 1.5 μ l 10x NH₄ buffer [160 mM (NH₄)₂SO₄, 670 mM Tris-HCl (pH 8.8 at 25°C), 0.1% Tween-20], and 0.5 U BioTaq DNA polymerase (Bioline, London, UK). A thermocycler (MJ Research Inc., Watertown, MA) was used with the following temperature profile: 3 min of denaturation at 95°C, then 28 cycles of 30 sec of denaturation at 95°C, 45 sec of annealing at 54°C, and 90 sec of extension at 72°C; 10 min at 72°C as final extension step. Amplified fragments were loaded on a capillary sequencer ABI-PRISM 3130 Genetic Analyzer (Applied Biosystems, Foster City, Calif., USA). Results of the run were processed with Genemapper v. 4.0 software and allele sizes were estimated using a GeneScan-500 LIZ size standard (Applied Biosystems).

In order to characterize the allelic diversity and informativeness of polymorphic cpSSRs in *Corylus* species, the number of alleles (A) and the gene diversity (H_e) were calculated for 114 *Corylus*

accessions (excluding hybrids) and 37 additional *C. avellana* cultivars characterized by Boccacci and Botta (2009) using the aforesaid methods (PCR amplification and SSR analysis). A was directly estimated, while H_e was calculated as:

$$H_e = 1 - \sum p_i^2$$

where p_i is the frequency of the i^{th} allele (Nei 1987).

Genetic distances (1000 bootstraps) between 151 *Corylus* accessions were computed as:

$$D = [1 - (\text{proportion of shared alleles})]$$

using the program Microsat (Minch, 1997). A NJ tree was constructed using Mega v. 5 software (Tamura et al. 2011), including an individual of *Carpinus betulus* L. as outgroup taxon. To reconstruct a chloroplast DNA genealogy, a reduced median (RM) network was built based on the length multi-state of microsatellites. This maximum-parsimony analysis was performed using the Network software (Bandelt et al. 1999), selecting the reduced median algorithm and the maximum parsimony (MP) option in order to clean the unnecessary median vectors and links.

RESULTS

SSR amplification and polymorphism

SSRs developed from a GAA-enriched library contained GA/CT, GAA/CTT, AGG/TCC, and GTAA motifs (Supplementary Table 1). Only CaC-C001b and CaC-C119 contained dinucleotide motifs while CaC-C001a contained the hepta-nucleotide motif CACAGAG. Amplification and polymorphism at the 23 SSRs was assessed first after 3% agarose gel electrophoresis (Supplementary Table 1). Polymorphism in *C. fargesii* was not evaluated since a single accession (Table 1) was available from this species at that time. Amplification rate across species was high and ranged from 74% to 100 %. All 23 primer pairs amplified in *C. avellana* as well as *C. americana*. In fact, CaC-C103 only amplified in these two species and failed to amplify in any of the accessions in the other

nine species. Of the SSRs that amplified for all the species, the polymorphism rate ranged from 41% in *C. jacquemontii* to 90% in *C. heterophylla*. The results (Supplementary Table 1) indicate that a variety of options are available for researchers interested in using SSRs for *Corylus* diversity assessments, even in those that are disjunctly distributed (Fig. 1).

Of the 15 primer pairs that were evaluated by capillary electrophoresis in the 158 accessions, six proved less reliable for inclusion in the analyses. CaC-114 generated one or two PCR products ranging in size from 260 to 279 bp in *C. avellana*, the bristle-husked species *C. californica*, *C. cornuta* and *C. sieboldiana*, and the tree hazels *C. fargesii* and *C. chinensis*, where it can be used for genetic studies. However, it generated up to four PCR products in the remaining species, indicating a possible presence in two locations of the genome. Of the two dinucleotide-containing SSRs identified in this library, CaC-C001b was highly diverse as estimated from A , H_o , H_e and PIC in each of the species while CaC-C119 was less polymorphic in hazelnut species (A , 2 - 4; PIC , 0.22 - 0.63) and amplified a single product in *C. californica*, *C. jacquemontii* and most of the *C. cornuta* accessions (Table 2). CaC-C001b also generated a large number (9) of species-specific alleles (Table 2). Four of the trinucleotide containing SSRs (CaC-C108, CaC-C112, CaT-C501 and CaT-C504) generated many alleles that differed by 1 or 2 bp, possibly indicating sequence differences other than in repeat number. The resulting alleles were also difficult to score and were thus excluded in cluster or structure analyses. The abovementioned 6 SSRs were excluded from further analysis.

Among the remaining 8 SSRs that generated easy-to-score alleles in all species, CaC-C036 contained a tetra-nucleotide motif and amplified the same allele (163) in all species except in *C. californica* and *C. jacquemontii* where it generated a 155 bp long fragment. In the other 7 SSRs, the average heterozygosity was moderate at 0.49 while allele number, genetic diversity and PIC were high at 11.71, 0.79 and 0.76, respectively. A single allele, 128, was in common between *C. cornuta* and *C. fargesii* accessions at CaC-C028 which generated another single unique allele, 138, in *C. ferox*. CaC-

C028 was polymorphic in the remaining species. The three most polymorphic tri-nucleotide SSRs based on largest number of alleles (A) and a relatively high number of unique alleles (A_u) as compared to the other SSRs were CaC-C008, CaC-C040 and CaC-C118 (Table 2). The largest number of alleles ($A = 21$) was observed at CaC-C008; this included five species-specific alleles. At CaC-C040, A was 15 and A_u was 4 (Table 2). At CaC-C118, A was 4 and A_u was 2 (Table 2).

Nuclear microsatellite-based clustering

NJ cluster analysis based on the shared allele distance (D) is depicted in Figure 2. The hazelnut accessions were grouped into six groups: a 'Species' group that contained eight of the species but not *C. americana*, *C. avellana* or *C. fargesii*; two small hybrid groups (Hyb1 and Hyb2); two *C. americana* groups (Americana-Winkler and Americana-Rush) and a *C. avellana* group.

Species cluster

In the 'Species' group, accessions of the tree species *C. colurna*, *C. jacquemontii* and *C. chinensis* were grouped together, as were accessions of the bristle-husked species *C. sieboldiana*, *C. cornuta* and *C. californica*. Five of the seven *C. heterophylla* accessions formed a *C. heterophylla* group, which also included one *C. heterophylla* x *C. avellana* hybrid (Estrella #1). *C. heterophylla* CCOR124 was in a mixed subgroup in the Americana group and the sole *C. heterophylla* var. *thunbergii* accession (CCOR64) was sister to the *C. colurna* group. The two *C. ferox* accessions grouped together and were sister to the *C. cornuta* complex. Three groups of *C. colurna* x *C. avellana* accessions were also found in this large group: Newberg (CCOR168) grouped with *C. colurna* accession CCOR450 in the tree species group; five *C. colurna* x *C. avellana* hybrids, mostly from Gellatly's work in British Columbia, grouped together and with the *C. heterophylla* x *C. avellana* hybrid Estrella #2 and *C. x colurnoides* CCOR9; and a third group was composed of two hybrid accessions Filcorn and Chinoka.

Hybrid groups

The first hybrid group (Hyb1) contained the only *C. ×vilmorinii* accession (CCOR14) which grouped with a *C. americana* accession from Missouri (CCOR228). These two accessions were adjacent to the *C. colurna* x *C. avellana* hybrids Moturk-B from Michigan and Eastoka from British Columbia. The second hybrid group (Hyb 2) was formed by the *C. americana* x *C. avellana* hybrids CCOR638 and NY 200.

Americana groups

Two large groups contained the majority of the *C. americana* accessions. The first group included ‘Winkler’, and the second included ‘Rush’. The Americana-Winkler group contained the largest number of *C. americana* accessions and was divided into three subgroups. The first two subgroups consisted of *C. americana* accessions from West Virginia, North Dakota, Kentucky, Wisconsin, Michigan, Iowa, Maryland, Massachusetts and Minnesota. The third subgroup included *C. americana* accessions CCOR675 from Illinois and CCOR686 from Pennsylvania, and *C. heterophylla* CCOR124 from China. Also in this subgroup were *C. americana* x *C. avellana* hybrid Rutter G227S, *C. colurna* LB01.26 from Serbia and a *C. colurna* x *C. avellana* hybrid Freeoka from British Columbia. The second subgroup contained the two *C. fargesii* accessions which grouped together, in addition to a *C. colurna* accession (97093) from Serbia and a group of *C. americana* accessions from Iowa (‘Winkler’ and CCOR684), Pennsylvania, Missouri, New Jersey and Minnesota.

The Americana-Rush group contained the early selections of *C. americana* x *C. avellana* hybrids of early breeders John F. Jones (Lancaster, Pennsylvania), Clarence A. Reed (Washington, DC), George L. Slate (Geneva, New York), and Carl Weschcke (St. Paul, Minnesota). This group was subdivided into two subgroups. The first one contained the three ‘Weschcke’ hybrids (TP1, TP2 and

TP3), Slate's New York selections NY F-45, NY 110, NY 104, and NY F-20, and two *C. americana* accessions, CCOR685 from Wisconsin and CCOR694 from Minnesota. The second subgroup contained Jones hybrid 'Buchanan' which grouped with its parent 'Rush', the hybrid selections of Reed ('Reed' and 'Potomac'), Yoder #5, *C. americana* accession CCOR386 from Missouri, the Slate selections NY 616 and NY 1464, and Medium Long whose origin is unknown but was maintained and described by Slate.

Avellana group

The Avellana group contained a single *C. americana* x *C. avellana* hybrid accession Rutter G081S and three subgroups. Subgroup 1 contained the 3 *C. maxima* and 3 *C. avellana* accessions in this study in addition to the *C. colurna* x *C. avellana* hybrid Chinese Trazel J-1 from Oregon. Subgroup 2 was close to Subgroup 1 and contained three *C. colurna* x *C. avellana* hybrids: 'Dundee' and USOR 13-71 from Oregon, and Turkish Trazel Gellatly #15 from British Columbia. Subgroup 3 contained the remaining *C. colurna* x *C. avellana* hybrids from British Columbia (Chinese Trazels Gellatly #6 and #11, and 'Faroka'), and three selections of Cecil Farris (Grand Traverse, 88BS and Lisa) which are descended from Faroka.

Structure analysis

We evaluated population structure and differentiation in the 109 *Corylus* accessions and 44 hybrid accessions (153 in total) with a Bayesian Markov Chain Monte Carlo approach implemented in Structure 2.1 (Pritchard et al. 2000). This approach is well-suited for outcrossing taxa like hazelnuts and minimizes deviations from Hardy–Weinberg equilibrium within an inferred population. The analyses using Structure with the species only dataset produced a clear 'plateau' in the estimated log probability of data $\ln Pr(X/K)$ between $k = 9$ (-1756.43 on average) and $k = 10$ (-1741.23 on average) and increased after $k = 11$ (-1766.13 on average). Therefore we chose $k = 9$ (Fig. 3) based on the ad hoc ln

Pr(X|K) method (Pritchard et al. 2000) which recommends picking the smallest value of K that captures the major structure of the data. However, when the hybrid accessions were included in the dataset, log probability of data Pr(X/K) did not reach a plateau at $k = 11$ and thus we elected to describe population differentiation in the data from only species. However, it is interesting to note that in the Structure analysis of the full data set, unlike the species only data set, *C. colurna* x *C. avellana* hybrids formed a distinct group at $k = 9$, before *C. ferox* accessions which were differentiated at $k = 10$. In the species only data set, at $k = 2$, the hazelnut accessions split into two groups, the *C. cornuta* complex + *C. ferox* group and the remaining *Corylus* species. At $k = 3$, *C. americana* accessions separated from the species group. At $k = 4$, *C. avellana* accessions formed a distinct group. At $k = 5$, *C. californica* accessions differentiated into a distinct group. At $k = 6$, *C. Jacquemontii* accessions formed a distinct group while at $k = 7$, *C. chinensis* formed a distinct cluster. At $k = 8$, *C. colurna* accessions and *C. heterophylla* accessions were clearly differentiated. Finally, at $k = 9$, the two *C. ferox* accessions were differentiated into single cluster. The *C. fargesii* accessions had the highest average ancestry coefficient (defined as the inferred proportion of membership in the hazelnut gene pool) from the *C. americana* population (0.56) followed by that from *C. chinensis* population (0.39) (Fig. 3). *C. sieboldiana* accessions had an average ancestry coefficient of 0.35 and 0.34 from *C. ferox* and *C. cornuta*, respectively. As K increased, accessions from these two species, *C. fargesii* and *C. sieboldiana* never differentiated into their respective species populations.

In each of the species groups differentiated by Structure, the highest ancestry coefficient for each accession was from that population except for some accessions of *C. americana* and *C. colurna* and one accession of *C. heterophylla*. *C. americana* accessions CCOR180, CCOR685, CCOR694 (4, 17 and 21, respectively in Fig. 3) had the highest average ancestry coefficient from *C. avellana*. These results agree with those obtained from NJ cluster analysis where these three *C. americana* accessions, along with 'Rush' (7 in Fig. 3) whose highest ancestry coefficient was from the *C. colurna* gene pool

(0.567) followed by *C. avellana* (0.226), were found in the Americana-Rush cluster (Fig. 2). CCOR228 (6 in Fig. 3) also had the highest ancestry coefficient from *C. avellana* (0.8) and was not found in the major *C. americana* only clusters of the NJ dendrogram. Instead, it grouped with *C. avellana* hybrid accessions in the Hyb 1 cluster. The highest ancestry coefficient in CCOR679 (12 in Fig. 3), the only accession from West Virginia, was from *C. chinensis* (0.675) indicating its diversity from the included *C. americana* gene pool. One (*C. colurna* 97098, 47 in Fig. 3) out of the three *C. colurna* accessions [97100, CCOR452 = 49 and 53, respectively in Fig. 3) that had the highest ancestry coefficient from the *C. chinensis* pool grouped with *C. chinensis* accession in the NJ cluster dendrogram (Fig. 2). Both of the *C. colurna* accessions that had the second highest ancestry coefficient from the *C. americana* pool (97093 and LB1_26, 42, and 50, respectively, in Fig. 3) grouped with *C. americana* accessions in the Americana cluster (Fig. 2), as did the sole *C. heterophylla* accession (CCOR124, 96 in Fig. 3) that had the highest ancestry coefficient from the *C. americana* population.

Chloroplast haplotype determination

Preliminary analysis of 40 *Corylus* accessions at 10 cpSSRs identified polymorphism in six loci. Locus ccmp10 showed four size variants. Three variants were found at loci ccmp2, ccmp3, ccmp4, and ccmp5 while two variants were observed at locus ccmp6. The allele variations differed by increments of 1 bp due to variation in the number of A or T residues within mononucleotide repeats. Ccmp2, ccmp3, ccmp4, and ccmp10 loci were previously found to be polymorphic in 26 European natural hazelnut populations (Palmé and Vendramin, 2002) and 75 *C. avellana* cultivars (Boccacci and Botta, 2009), but ccmp5 and ccmp6 revealed polymorphism only in this work and in other species. This set of 6 cpSSR loci was then used to assess genetic variability in the *Corylus* complex. Of the remaining four loci, ccmp1 (129 bp) and ccmp7 (153 bp) were monomorphic, ccmp8 showed a very low PCR amplification level and ccmp9 gave no amplification products. Since the chloroplast genome

is inherited maternally in hazelnut, results were used to verify which *Corylus* species (known or hypothesized) was the female parent of each hybrid or to identify possible mistakes (Table 1).

The allelic diversity and informativeness of polymorphic chloroplast microsatellites was determined using the number of alleles (A) and the diversity values (H_e) in 114 *Corylus* accessions and 37 cultivars of *C. avellana* analyzed by Boccacci and Botta (2009) but not in the hybrids. *Corylus avellana* is economically the most important species of the genus and is the source of the most important cultivars. This species is very polymorphic based on morphology (Mehlenbacher, 1991) and genetic studies (Boccacci and Botta 2010; Gökirmak et al. 2009). Four chlorotypes were observed by Boccacci and Botta (2009) in a study of 75 *C. avellana* genotypes. Thus a representative set of hazelnut cultivars from Spain, Italy, Turkey, and Iran (Table 1) were included in this study in order to better evaluate the polymorphism of cpSSR and to investigate relationships among the *Corylus* species. Eighteen chlorotypes were observed in the 114 *Corylus* accessions and 44 hybrids (Table 1) using 6 polymorphic cpSSR loci (ccmp2, ccmp3, ccmp4, ccmp5, ccmp6, and ccmp10). The number of alleles per locus ranged from 2 to 4, with an average of 3. Diversity values ranged from 0.33 to 0.64, with an average of 0.69 (Table 3). This average value is higher than those reported in rice (Ishii and McCouch, 2000) and wheat (Ishii et al. 2001).

After including 37 previously analyzed *C. avellana* cultivars (Boccacci and Botta 2009), the number of detected chlorotypes increased to 21 (Table 3) and most *Corylus* species showed a unique most frequent haplotype (Table 1). Chlorotypes A, B, C, and D were reported in *C. avellana* by Boccacci and Botta (2009). Of these, chlorotype A was the most frequent and present in all geographical groups. All accessions of *C. colurna* showed chlorotype E with the exception of one individual (CCOR451) that had chlorotype F. A single chlorotype was found in *C. ferox* (H), *C. californica* (P), *C. Jacquemontii* (G), and *C. sieboldiana* (N). All but one accession of *C. cornuta* had chlorotype Q. Chlorotype N was observed both in *C. heterophylla* and *C. sieboldiana*, but one

individual of *C. heterophylla* showed chlorotype O. Three chlorotypes were observed in *C. chinensis* (I, J, and K) and two in *C. fargesii* (L and M). The most frequent chlorotype (Q) in *C. americana* was also most frequent in *C. cornuta*. However, the *C. americana* accession CCOR679 from West Virginia had a *C. avellana* chlorotype (B). Furthermore, four additional chlorotypes were specific to *C. americana*: S (mostly in Iowa accessions), T, U (only in two Michigan accessions), and V (Table 1).

The phylogenetic relationships among *Corylus* species using cpSSRs were examined in a NJ phylogram (Fig. 4) and a RM network diagram (Fig. 5). In the phylogram, 151 *Corylus* accessions were placed in five main clusters (Fig 4). The accessions of *C. colurna* were placed in the first cluster with two *C. avellana* cultivars (Tonda Bianca and Tonda Rossa) from southern Italy. The accessions of *C. chinensis* were placed separately in two subgroups in the second cluster with the *C. heterophylla* and *C. sieboldiana* accessions. The third group included almost all of the *C. avellana* cultivars and the two *C. fargesii* samples. The fourth group consisted of the North American species and the fifth cluster included all accessions of *C. ferox* and *C. jacquemontii* placed in two main clades.

In the reduced median network (Fig. 5), the 21 chlorotypes found in 11 *Corylus* species were placed in three main groups. The first group included the haplotypes observed in *C. heterophylla* and *C. sieboldiana* (N and O) and *C. chinensis* (I, J, and K) from eastern Asia and *C. colurna* (E and F). Moreover, chlorotype E was related to the rare chlorotype D observed in two *C. avellana* cultivars (Tonda Bianca and Tonda Rossa). The second cluster included the chlorotypes reported in *C. avellana* (A, B, and C) that were related to the chlorotypes obtained in *C. fargesii*. Chlorotypes H (*C. ferox*) and G (*C. jacquemontii*) were placed in an intermediate position between the second and the third group. The third group comprised the 6 haplotypes observed in the North American species (*C. californica*, *C. cornuta*, and *C. americana*) (Fig. 5).

DISCUSSION

The high cross-amplification of hazelnut microsatellite markers in this study (74-100%) agrees with previous reports in *Corylus* (Bassil et al. 2005a; Boccacci et al. 2005; Gürcan and Mehlenbacher 2010a). Based on seven trinucleotide SSRs, the average heterozygosity was moderate at 0.49 while allele number, genetic diversity and PIC were high (means 11.71, 0.79 and 0.76, respectively). The diversity parameters were higher than those previously observed for 6 tri-nucleotide SSRs evaluated in 28 accessions that included seven *Corylus* species (Bassil et al. 2005a). The higher values were expected, as this study included a larger number of species representatives. In fact, for five of the SSRs in common between the two studies (CaC-C003, CaC-C005, CaC-C028, CaC-C111 and CaC-C118) (Bassil et al. 2005a), all of the diversity parameters were higher in this study (Table 2). Based on diversity parameters, trinucleotide motifs have been reported as less informative than the dinucleotide types (Bassil et al. 2005a; Liewlaksaneeyanawin et al. 2004; Stigel et al. 2008) and are typically associated with a low level of variability. When compared in hazelnut (Bassil et al. 2005a), the number of alleles as well as heterozygosity were lower for trinucleotide SSRs. The moderate heterozygosity and high number of alleles of the seven best trinucleotide SSRs chosen for this study is mostly biased as we chose the best performing trinucleotide SSRs.

The amplification and polymorphism rates were not correlated to the distance of each species from *C. avellana* but were definitely limited by the number of accessions representing each species. For example, a lower rate of amplification (78%) in *C. ferox* and the lowest rate of polymorphism (41%) in *C. sieboldiana* are likely the result of the use of few accessions of these species (2 and 3, respectively). Additional importations of east Asian *Corylus* would benefit future studies. Furthermore, reported polymorphism could also be lower than if assessed by capillary electrophoresis since polymorphism in all species was initially assessed with the relatively lower resolution 3% agarose gel electrophoresis technique. In fact, using capillary electrophoresis, CaC-C028 and CaC-C003 were

polymorphic in *C. avellana* and *C. jacquemontii*, respectively, while four SSRs (CaC-C005, Cac-C112, CaC-C119 and CaC-C501) were polymorphic in *C. colurna* (Supplementary Table 1).

Despite the small number of nuclear SSRs used in this study (8), nuclear SSR-based clustering mostly agreed with previous taxonomic classification in hazelnut (Erdoğan and Mehlenbacher 2000a; Forest and Bruneau 2000; Forest et al. 2005; Whitcher and Wen 2001). The bristle-husked shrub species of subclade *Siphonochlamys* (*C. californica*, *C. cornuta* and *C. sieboldiana*) grouped together in the Species clade; as did the *Colurnae* subclade tree species *C. jacquemontii* (all 5 accessions), most of the *C. colurna* (8 of 13 accessions) and *C. chinensis* (all 9 accessions). However, the two accessions of *C. fargesii* grouped together but were placed in the Americana-Winkler clade. Accessions of other species formed distinct and separate groups: *C. ferox* (n=2) and *C. heterophylla* (5 of 7). Accessions of *C. avellana* (n=3) and *C. maxima* (n=3), grouped together in the dendrogram, supporting their placement in one large, polymorphic species designated *C. avellana*. The sample sizes for each species in this study are small. Still, this study agrees with previous results and does not support *C. maxima* as a separate taxon. However, our data clearly indicates that *C. californica* is a separate species rather than a botanical variety of *C. cornuta* (Erdoğan and Mehlenbacher 2000a).

The leafy-husked shrub species of the subclade *Phyllochlamys* did not group together, most likely due to the large number of hybrid accessions between *C. americana* and *C. avellana*, or that contained *C. avellana*, included in this study. This is illustrated by clade Americana-Rush where ‘Rush’, the *C. americana* selection used in early efforts to breed hazelnuts adapted to the eastern U.S., grouped with its hybrid offspring ‘Buchanan’, ‘Reed’, ‘Potomac’, and several of the New York selections of Slate. The diversity among accessions of *C. colurna*, *C. americana*, *Americana* × *Avellana* hybrids, and *Colurna* × *Avellana* hybrids is striking, as illustrated by their presence in multiple clades in the dendrogram (Fig. 2). These results with *C. americana* and *C. americana* × *C. avellana* hybrids agrees with previous findings (Sathuvalli and Mehlenbacher 2011). Hybrids between

C. colurna and *C. avellana* were found in the Species, Hybrid1, Americana-Winkler and Avellana clades. Hybrids between *C. americana* and *C. avellana* were found in all except the Species clade. *C. americana* accessions were found in the many groups of the Americana-Winkler clade and in the Hybrid1 and Americana-Rush clades. Such diversity in *C. americana* and its hybrids is very useful in the breeding of new hazelnut cultivars adapted to the eastern U.S.

Structure, a Bayesian clustering approach that probabilistically assigns individuals to populations based on genotype, differentiated all species into groups except for *C. fargesii* (n=2) and *C. sieboldiana* (n=3). These two species never differentiated into individual populations, which is not surprising given the small number of accessions available for these two species. Assignment of some individuals from *C. americana* and *C. colurna* to multiple populations (Fig. 3) agreed with their placement in the distance-based NJ dendrogram (Fig. 2) and further supports the high diversity of accessions in these species.

The NJ phylogenetic trees produced from nuclear and chloroplast SSR loci did not give congruent topologies (Fig. 2 and 4, respectively). The phylogeny obtained with nSSR markers corresponded fairly well with those based on morphological characteristics or ITS sequences (Erdoğan and Mehlenbacher 2000a; Whitcher and Wen 2001) and on nontranscribed spacer of the 5S rRNA genes (Whitcher and Wen 2001). The classification based on cpSSR markers is not in agreement with the results of taxonomic classification, but was very similar to that of Erdoğan and Mehlenbacher (2000a) who compared chloroplast *matK* gene sequences. The cpSSR-based tree separated American, European, and Asian species, in spite of morphological similarity of some of the species across continents.

The incongruence between nuclear and chloroplast phylogenetic topologies is typically explained by either lineage sorting or hybridization (Wendel and Doyle 1998). Lineage sorting assumes that there was notable ancestral polymorphism that was rapidly fixed, so that little remains

detectable today. The discrepancy in the two topologies could also result from ancient hybridization and subsequent chloroplast capture, so that chloroplast topologies do not accurately reflect organismal relationships. The cpSSR results suggested possible hybridizations among some *Corylus* species that shared the same chlorotype profile: chlorotype N was observed in almost all *C. heterophylla* accessions and in all *C. sieboldiana* individuals; and 12 *C. americana* accessions shared chlorotype Q with *C. cornuta*. Sharing of chlorotypes between two potentially hybridizing species only in areas where they are sympatric would lend support to the local hybridization hypothesis. As reported in Figure 1, each pair of species considered are found in the same geographical area: *C. heterophylla* and *C. sieboldiana* are from eastern Asia, and *C. americana* and *C. cornuta* from eastern North America. Controlled hybridizations among eight *Corylus* species showed that crosses between *C. heterophylla* and *C. sieboldiana*, and *C. americana* and *C. cornuta* are very difficult (Erdoğan and Mehlenbacher 2000b). This contrasted with our cpSSR results. However, chloroplast capture might not be recent and could have occurred during the ancestral diversification of the genus (Whitcher and Wen 2001). Alternatively the same cpSSR profile observed in these pairs of species could be a consequence of homoplasy (occurrence of alleles identical in state but not identical by descent). For *C. maxima* and *C. avellana*, cpSSR data agree with nSSR results, and indicate that *C. maxima* is not a separate taxon.

The RM network based on cpSSR polymorphism enabled the identification of three main chlorotype lineages (Fig. 5). General distribution of plastid lineages was not fully congruent with present-day taxonomy, but was very similar to the topology of the cpSSR-based NJ tree (Fig. 4). The clear geographical distribution of lineages supported an early differentiation among *Corylus* species from Asia, Europe, and North America with a few exceptions. *C. fargesii* (chlorotypes L and M) and *C. jacquemontii* (chlorotype G) did not cluster with other Asian species, while two *C. avellana* accessions (chlorotype D) were closely related to *C. colurna* (chlorotype E) in the Asian lineage. Divergence between the Himalayan *C. jacquemontii* and the other Asian species, particularly the tree

species of the subsection *Colurnae*, was probably due to the rise of the Himalaya mountains (Whitcher and Wen 2001). *C. fargesii* from China, called the paperbark tree hazel, is morphologically distinct from the other tree species in that its bark exfoliates like a paper birch (*Betula papyrifera* Marsh.) (Erdoğan and Mehlenbacher 2000a). The PCR-RFLP and SSR data from cpDNA obtained by Palmé and Vendramin (2002) suggested that hybridization could have occurred between *C. colurna* and several wild *C. avellana* individuals. The close relationship between *C. colurna* and two *C. avellana* accessions ('Tonda Bianca' and 'Tonda Rossa') supports this hypothesis. Nevertheless, *C. colurna* is found from the Balkans to Asia Minor while 'Tonda Bianca' and 'Tonda Rossa' are only located in southern Italy. This might seem to argue against hybridization, but chloroplast capture might not have taken place directly and transfer could have occurred via wild and cultivated forms of *C. avellana*, during migrations in the Mediterranean Basin (Bocacci and Botta 2009).

The phylogeographical relationships among the 21 chlorotypes found in 11 *Corylus* species support several biogeographic observations reported in the literature (Chen et al. 1999; Whitcher and Wen 2001). Asia may have served as a refugium where several hazelnut lineages survived during the glaciations and from which they reappeared only later after the dispersal event from Asia through the Mediterranean to Europe, and across the Atlantic to North America (Whitcher and Wen 2001). The high number of cpSSR haplotypes observed among the Asian species supports this hypothesis, already demonstrated on the basis of morphological, fossil and molecular data (Chen et al. 1999; Whitcher and Wen 2001). In the RM network, the intermediate position of Asian chlorotypes I, J, and K (*C. chinensis*), and N and O (*C. heterophylla* and *C. sieboldiana*) between the European chlorotypes A, B, and C (*C. avellana*), which were associated with the Chinese chlorotypes L and M (*C. fargesii*), also support the migration hypothesis from Asia to the Mediterranean Basin and Europe from local common ancestors (Whitcher and Wen 2001). Moreover, the position of chlorotype Q in the American group, observed both in *C. cornuta* and in several accessions of *C. americana*, supports the hypothesis that

long distance migration to North America may have occurred during the late Tertiary both from Asia via the Bering land bridge (*C. cornuta* and *C. californica*) and from Europe via the Atlantic (*C. americana*) (Whitcher and Wen 2001).

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Table 1 List of *Corylus* accessions used in this study. Their Plant Introduction (PI) Number, Local inventory number (prefix CCOR for Corvallis *Corylus*) taxon, origin and chlorotype are listed. O.P. indicates open pollinated. The number listed for each accession corresponds to the numbers in Fig. 3.

Table 2 Diversity parameters of 12 single-locus hazelnut loci in each of the 11 species evaluated in this study. Allele number (A), observed heterozygosity (H_o), expected heterozygosity (H_e), and polymorphism information index (PIC) were calculated for each species with PowerMarker. Overall A , H_o , H_e and PIC were calculated only for the eight SSRs that amplified in all species and were used for cluster and structure analysis.

Table 3 Chlorotypes genotyped and allelic diversity at 6 cpSSR loci in 114 *Corylus* species individuals and 37 additional *C. avellana* accessions

Fig. 1. Geographical distribution of *Corylus* species

Fig. 2. NJ cluster analysis of hazelnut accessions using the proportion of shared allele distance based on 8 trinucleotide-containing SSRs (except for CAC-C036 which contains a tetranucleotide repeat).

Fig. 3. Assignment of 109 *Corylus* accessions to 9 populations by Structure version 2.3.3. Each individual bar represents an accession (see Table 1 for accession information) Numbers 1–26=*C. americana*, 27–32=*C. avellana*, 33–41=*C. chinensis*, 42–54=*C. colurna*, 55–65=*C. cornuta*, 66–90=*C. californica*, 91–92=*C. fargesii*, 93–94=*C. ferox*, 95–101=*C. heterophylla*, 102–106=*C.*

jacquemontii, 107-109=*C. sieboldiana*. The *Y-axis* displays the estimated membership of each individual in a particular cluster or population.

Fig. 4. A NJ tree showing phylogenetic relationships among *Corylus* accessions revealed by 6 cpSSR

Fig. 5. Reduced median network representing relations of 21 chlorotypes in the *Corylus* complex. Legend: A, B, C, and D - *C. avellana*; E and F - *C. colurna*; G - *C. jacquemontii*; H - *C. ferox*; I, J, and K - *C. chinensis*; L and M - *C. fargesii*; N and O - *C. heterophylla* and *C. sieboldiana*; P - *C. californica*; Q – *C. cornuta* and *C. americana*; R, S, T, and U – *C. americana*

Supplementary Table 1. Amplification and polymorphism of twenty-three SSRs developed from a trinucleotide-enriched library (GAA) of hazelnut. Also listed are the SSR motif, primer sequences, expected size, optimum annealing temperature linkage group location, and citation where available.

Table 1

No.	Accession number	Local Inv. (CCOR)	Taxon	Name	Origin	Chlorotype	Name in dendrogram
1	PI 557018	61.001	<i>C. americana</i>	C. amer. 61.001	Missouri	Q	C. amer. CCOR61
2	PI 557019	99.001	<i>C. americana</i>	Winkler	Iowa	R	C. amer. Winkler
3	PI 557020	117.001	<i>C. americana</i>	C. amer. 117.001	Minnesota	Q	C. amer. CCOR117
4	PI 495606	180.002	<i>C. americana</i>	C. amer. 180.002	Iowa	Q	C. amer. CCOR180.002
5	PI 557021	225.001	<i>C. americana</i>	C. amer. 225.001	Iowa	Q	C. amer. CCOR225
6	PI 617169	228.001	<i>C. americana</i>	C. amer. 228.001	Missouri	Q	C. amer. CCOR228
7	PI 557022	386.001	<i>C. americana</i>	Rush	Pennsylvania	Q	C. amer. Rush
8	PI 617242	675.001	<i>C. americana</i>	C. amer. 675.001	Illinois	R	C. amer. CCOR675
9	PI 617243	676.001	<i>C. americana</i>	C. amer. 676.001	Wisconsin	Q	C. amer. CCOR676
10	PI 617244	677.001	<i>C. americana</i>	C. amer. 677.001	North Dakota	Q	C. amer. CCOR677
11	PI 617245	678.001	<i>C. americana</i>	C. amer. 678.001	Pennsylvania	S	C. amer. CCOR678
12	PI 617246	679.001	<i>C. americana</i>	C. amer. 679.001	West Virginia	B	C. amer. CCOR679
13	PI 617248	681.001	<i>C. americana</i>	C. amer. 681.001	Kentucky	Q	C. amer. CCOR681
14	PI 617249	682.001	<i>C. americana</i>	C. amer. 682.001	Michigan	T	C. amer. CCOR682
15	PI 617250	683.001	<i>C. americana</i>	C. amer. 683.001	Iowa	R	C. amer. CCOR683
16	PI 617251	684.001	<i>C. americana</i>	C. amer. 684.001	Iowa	R	C. amer. CCOR684
17	PI 617252	685.001	<i>C. americana</i>	C. amer. 685.001	Wisconsin	U	C. amer. CCOR685
18	PI 617253	686.001	<i>C. americana</i>	C. amer. 686.001	Pennsylvania	U	C. amer. CCOR686
19	PI 617254	687.001	<i>C. americana</i>	C. amer. 687.001	Maryland	S	C. amer. CCOR687
20	PI 617260	693.001	<i>C. americana</i>	C. amer. 693.001	New Jersey	Q	C. amer. CCOR693
21	PI 617261	694.001	<i>C. americana</i>	C. amer. 694.001	Minnesota	R	C. amer. CCOR694
22	PI 617262	695.001	<i>C. americana</i>	C. amer. 695.001	Minnesota	Q	C. amer. CCOR695

23	PI 617263	696.001	<i>C. americana</i>	C. amer. 696.001	Michigan	T	C. amer. CCOR696
24	PI 617272	709.001	<i>C. americana</i>	C. amer. 709.001	Wisconsin	U	C. amer. CCOR709
25	PI 617275	712.001	<i>C. americana</i>	C. amer. 712.001	Massachusetts	Q	C. amer. CCOR712
26	PI 617278	715.001	<i>C. americana</i>	C. amer. 715.001	Michigan	U	C. amer. CCOR715
27	PI 270340	8.001	<i>C. avellana</i>	Negret	Spain	A	C. av. Negret
28	PI 557037	36.001	<i>C. avellana</i>	Barcelona	Spain	A	C. av. Barcelona
29	PI 557167	344.001	<i>C. avellana</i>	Ratoli	Spain	A	C. av. Ratoli
30	PI 271110	38.001	<i>C. maxima</i>	Pellicule Rouge	France	A	C. max. Pellicule Rouge
31	PI 557400	272.001	<i>C. maxima</i>	Istarski duguljasti	Croatia	A	C. max. Istarski duguljasti
32	PI 557401	357.001	<i>C. maxima</i>	di San Benedetto	Italy	A	C. max. San Benedetto
33			<i>C. chinensis</i>	OSU 567.011	China	I	C. chi. CCOR567.011
34			<i>C. chinensis</i>	OSU 567.018	China	I	C. chi. CCOR567.018
35			<i>C. chinensis</i>	OSU 529.001	China	K	C. chi. OSU 529.001
36			<i>C. chinensis</i>	OSU 529.017	China	K	C. chi. OSU 529.017
37			<i>C. chinensis</i>	OSU Lagerstedt East	China via Australia	J	C. chi. OSU Lag. East
38			<i>C. chinensis</i>	OSU Lagerstedt West	China via Australia	J	C. chi. OSU Lag. West
39			<i>C. chinensis</i>	OSU W03	China via Australia	J	C. chi. OSU W3
40			<i>C. chinensis</i>	OSU W05	China via Australia	J	C. chi. OSU W5
41	PI 617204	591.001	<i>C. chinensis</i>	OSU 91502	China	I	C. chi. CCOR591.001
42			<i>C. colurna</i>	C. colurna 97093	Serbia	E	C. col. 97093
43			<i>C. colurna</i>	C. colurna 97094	Serbia	E	C. col. 97094
44			<i>C. colurna</i>	C. colurna 97095	Serbia	E	C. col. 97095
45			<i>C. colurna</i>	C. colurna 97096	Serbia	E	C. col. 97096
46			<i>C. colurna</i>	C. colurna 97097	Serbia	E	C. col. 97097
47			<i>C. colurna</i>	C. colurna 97098	Serbia	E	C. col. 97098
48			<i>C. colurna</i>	C. colurna 97099	Serbia	E	C. col. 97099
49			<i>C. colurna</i>	C. colurna 97100	Serbia	E	C. col. 97100

50			<i>C. colurna</i>	C. colurna LB1.26	Serbia	E	C. col. LB1_26
51			<i>C. colurna</i>	OSU Pole Barn	France	E	C. col. Pole Barn
52	PI 557253	450.001	<i>C. colurna</i>	C. colurna N451	Warsaw, Poland	F	C. col. CCOR450
53	PI 557255	452.001	<i>C. colurna</i>	C. colurna N504	Slepcany, Czech Rep.	E	C. col. CCOR452
54	PI 557256	453.001	<i>C. colurna</i>	C. colurna 550	Geisenheim, Germany	E	C. col. CCOR453
55	PI 557269	109.001	<i>C. cornuta</i>	C. cornuta Minnesota	Maine	Q	C. cor. CCOR109
56	PI 637894	814.001	<i>C. cornuta</i>	C. cornuta CC2.50 Minnesota	New York	Q	C. cor. CCOR814
57	PI 637895	815.001	<i>C. cornuta</i>	C. cornuta CC3.01 New York	Minnesota	Q	C. cor. CCOR815
58	PI 637896	816.001	<i>C. cornuta</i>	C. cornuta CC3.47 Wisconsin	New York	Q	C. cor. CCOR816
59	PI 637897	817.001	<i>C. cornuta</i>	C. cornuta CC3.58	Wisconsin	Q	C. cor. CCOR817
60	PI 637898	818.001	<i>C. cornuta</i>	C. cornuta CC3.113 Quebec	Quebec	Q	C. cor. CCOR818
61	PI 637899	819.001	<i>C. cornuta</i>	C. cornuta CC4.46 North Dakota	North Dakota	Q	C. cor. CCOR819
62	PI 637900	820.001	<i>C. cornuta</i>	C. cornuta CC4.53 Manitoba	Manitoba	Q	C. cor. CCOR820
63	PI 637901	821.001	<i>C. cornuta</i>	C. cornuta OSU 373.032 British Columbia	British Columbia	Q	C. cor. CCOR821
64	PI 637886	801.001	<i>C. cornuta</i>	C. cornuta 661.081 Manitoba	Minnesota	Q	C. cor. CCOR801
65	PI 637887	802.001	<i>C. cornuta</i>	C. cornuta 662.006 Saskatch	Manitoba	Q	C. cor. CCOR802
66	PI 557280	233.001	<i>C. californica</i>	C. californica 61-4 Lewis, WA	Oregon	P	C. cal. CCOR233
67	PI 557281	234.001	<i>C. californica</i>	C. californica 27-5 Hood River	Oregon	P	C. cal. CCOR234
68	PI 557282	235.001	<i>C. californica</i>	C. californica 49-2 Clatsop	Oregon	P	C. cal. CCOR235
69	PI 557283	236.001	<i>C. californica</i>	C. californica 58-5 Columbia	Oregon	P	C. cal. CCOR236
70	PI 557284	237.001	<i>C. californica</i>	C. californica 52-5 Multnomah	Oregon	P	C. cal. CCOR237
71	PI 557285	238.001	<i>C. californica</i>	C. californica 51-3 Multnomah	Oregon	P	C. cal. CCOR238

72	PI 557286	239.001	<i>C. californica</i>	C. californica 59-1 Douglas	Oregon	P	C. cal. CCOR239
73	PI 557287	240.001	<i>C. californica</i>	C. californica 23-6 Wash. Co.	Oregon	P	C. cal. CCOR240
	PI 557288	241.001	<i>C. californica</i>	C. californica 21-5 Lincoln	Oregon	P	C. cal. CCOR241
74	PI 557290	243.001	<i>C. californica</i>	C. californica 10-6 Benton	Oregon	P	C. cal. CCOR243
75	PI 557291	244.001	<i>C. californica</i>	C. californica 45-6 Lane	Oregon	P	C. cal. CCOR244
76	PI 557293	428.001	<i>C. californica</i>	C. californica 13-3 Oregon	Oregon	P	C. cal. CCOR428
77	PI 557294	429.001	<i>C. californica</i>	C. californica 3-6 Oregon	Oregon	P	C. cal. CCOR429
78	PI 557295	430.001	<i>C. californica</i>	C. californica 25-5 Oregon	Oregon	P	C. cal. CCOR430
79	PI 557297	432.001	<i>C. californica</i>	C. californica 20-6 Oregon	Oregon	P	C. cal. CCOR432
	PI 557298	433.001	<i>C. californica</i>	C. californica 41-2 Oregon	Oregon	P	C. cal. CCOR433
80	PI 557299	434.001	<i>C. californica</i>	C. californica 53-4 Oregon	Oregon	P	C. cal. CCOR434
81	PI 557300	435.001	<i>C. californica</i>	C. californica 13-5 Oregon	Oregon	P	C. cal. CCOR435
82	PI 557273	470.001	<i>C. californica</i>	C. californica #8	Oregon	P	C. cal. CCOR470
83	PI 557274	497.001	<i>C. californica</i>	C. californica # 8/D	Oregon	P	C. cal. CCOR497
	PI 557275	498.001	<i>C. californica</i>	C. californica # 2/S	Oregon	P	C. cal. CCOR498
	PI 557276	503.001	<i>C. californica</i>	C. californica #3	Oregon	P	C. cal. CCOR503
84	PI 557277	504.001	<i>C. californica</i>	C. californica #15	Oregon	P	C. cal. CCOR504
	PI 557278	506.001	<i>C. californica</i>	C. californica #16	Oregon	P	C. cal. CCOR506
85	PI 617197	583.001	<i>C. californica</i>	C. californica 4-6	Oregon	P	C. cal. CCOR583
86	PI 617198	584.001	<i>C. californica</i>	C. californica 13-3	Oregon	P	C. cal. CCOR584
87	PI 617199	585.001	<i>C. californica</i>	C. californica 25-3	Oregon	P	C. cal. CCOR585
88	PI 617200	586.001	<i>C. californica</i>	C. californica 53-6	Oregon	P	C. cal. CCOR586
89	PI 617201	588.001	<i>C. californica</i>	C. californica 66-5	Oregon	P	C. cal. CCOR588
90	PI 617202	589.001	<i>C. californica</i>	C. californica 19-4	Oregon	P	C. cal. CCOR589
91	OSU	Mehlenb	<i>C. fargesii</i>	C. fargesii 1*	China	L	C. fargesii 1
92		Mehlenb	<i>C. fargesii</i>	Paperbark C-3 Farris		M	C. fargesii C-3
93	PI 557302	185.001	<i>C. ferox</i>	C. ferox 185.001	China	H	C. ferox CCOR185

94	OSU	Mehlenb	<i>C. ferox</i>	C. ferox WS		H	C. ferox WS
95	PI 557309	67.001	<i>C. heterophylla</i>	C. heterophylla Korea-10	Korea	N	C. het. CCOR67
96	PI 557310	124.001	<i>C. heterophylla</i>	C. heterophylla Jilin	China	N	C. het. CCOR124
97	PI 557311	146.001	<i>C. heterophylla</i>	C. heterophylla 'Nanking'		N	C. het. CCOR146
98	PI 557311	147.001	<i>C. heterophylla</i>	C. heterophylla 'Nanking'		N	C. het. CCOR147
99	PI 557315	351.001	<i>C. heterophylla</i>	C. heterophylla seedling A		N	C. het. CCOR351
100	PI 557328	64.001	<i>C. heterophylla</i> var. <i>thunbergii</i>	C. heterophylla var. <i>thunbergii</i> Korea-66	Korea	O	C. het. thunbergii CCOR64
101	PI 557330	286.001	<i>C. heterophylla</i> var. <i>yunnanensis</i>	C. heterophylla var. <i>yunnanensis</i> China	China	N	C. het. yun. CCOR286
102	OSU	Mehlenb	<i>C. jacquemontii</i>	OSU 397.027	Pakistan	G	C. jacqu. OSU397.027
103	OSU	Mehlenb	<i>C. jacquemontii</i>	OSU 397.050	Pakistan	G	C. jacqu. OSU397.050
104	OSU	Mehlenb	<i>C. jacquemontii</i>	OSU 397.024	Pakistan	G	C. jacqu. OSU397.024
105	PI 557268	311.001	<i>C. jacquemontii</i>	C. jacquemontii 880430 Pakistan	Pakistan	G	C. jacqu. CCOR311
106	PI 617206	593.001	<i>C. jacquemontii</i>	C. jacquemontii OSU 88501	India	G	C. jacqu. CCOR593
107	PI 557404	348.001	<i>C. sieboldiana</i>	C. sieboldiana	Korea	N	C. sieb. CCOR348
108	PI 557409	347.001	<i>C. sieboldiana</i> var. <i>brevirostris</i>	C. sieboldiana var. <i>brevirostris</i> seedling	Korea	N	C. sieb. brevisrostris CCOR347
109	PI 557415	349.001	<i>C. sieboldiana</i> var. <i>mandshurica</i>	C. sieboldiana var. <i>mandshurica</i>	Korea	N	C. sieb. mand. CCOR349
	PI 557337	100.001	<i>Corylus</i> hybrid (Ame - Ave)	C. americana hybrid NY 104	New York	Q	C. amer. hybrid NY 104
	PI 557338	101.001	<i>Corylus</i> hybrid (Ame - Ave)	C. americana hybrid NY 110	New York	Q	C. amer. hybrid NY 110
	PI 557339	102.001	<i>Corylus</i> hybrid (Ame - Ave)	C. americana hybrid NY F- 45	New York	Q	C. amer. hybrid NY F-45
	PI 557340	103.001	<i>Corylus</i> hybrid (Ame - Ave)	C. americana hybrid NY 200	New York	P	C. amer. hybrid NY 200
	PI 557341	104.001	<i>Corylus</i> hybrid (Ame - Ave)	C. americana hybrid NY 616	New York	Q	C. amer. hybrid NY 616
	PI 557379	189.001	<i>Corylus</i> hybrid (Ame - Ave)	C. americana hybrid NY F- 20	New York	Q	C. amer. hybrid NY F-20
	PI 557383	194.001	<i>Corylus</i> hybrid	C. americana hybrid NY	New York	Q	C. amer. hybrid NY 1464

			(Ame - Ave)	1464			
	PI 557391	377.001	<i>Corylus</i> hybrid (Ame - Ave)	Potomac	Maryland	Q	Potomac
	PI 557334	378.001	<i>Corylus</i> hybrid (Ame - Ave)	Buchanan	Pennsylvania	Q	Buchanan
	PI 557392	383.001	<i>Corylus</i> hybrid (Ame - Ave)	Reed	Maryland	Q	Reed
	PI 617214	638.001	<i>Corylus</i> hybrid (Ame - Ave)	<i>Corylus americana</i> hybrid	Oregon	Q	C. amer. hybrid CCOR638
	OSU	G081S	<i>Corylus</i> hybrid (Ame - Ave)	Rutter G081S	Minnesota	R	Rutter G081S
	OSU	G227S	<i>Corylus</i> hybrid (Ame - Ave)	Rutter G227S	Minnesota	Q	Rutter G227S
	OSU		<i>Corylus</i> hybrid (Ame - Ave)	Weschcke TP2	Wisconsin	Q	Weschcke TP2
	PI 617187	561.001	<i>Corylus</i> hybrid (Ame - Ave)	Weschcke TP3	Wisconsin	Q	Weschcke TP3
	PI 641155	853.001	<i>Corylus</i> hybrid (Ame - Ave)	Yoder 5	Ohio	Q	Yoder 5
	OSU		<i>Corylus</i> hybrid (Ame - Ave)	Weschcke TP1	Wisconsin	Q	Weschcke TP1
	PI 557331	33.001	<i>Corylus</i> hybrid (Col - Ave)	Morrisoka	British Columbia	E	Morrisoka
	PI 557332	53.001	<i>Corylus</i> hybrid (Col - Ave)	Filcorn	Oregon	A	Filcorn
	PI 557333	57.001	<i>Corylus</i> hybrid (Col - Ave)	Laroka	British Columbia	E	Laroka
	PI 557349	137.001	<i>Corylus</i> hybrid (Col - Ave)	Moturk-D	Michigan	E	Moturk-D
	PI 557261	138.001	<i>Corylus</i> hybrid (Col - Ave)	Chinese Trazel Gellatly No. 6	British Columbia	E	Chinese Trazel Gellatly No. 6
	PI 557357	148.001	<i>Corylus</i> hybrid (Col - Ave)	Eastoka	British Columbia	E	Eastoka
	PI 557359	150.001	<i>Corylus</i> hybrid (Col - Ave)	Moturk-B	Michigan	E	Moturk-B
	PI 557362	154.001	<i>Corylus</i> hybrid (Col - Ave)	Freeoka	British Columbia	E	Freeoka
	PI 557369	165.001	<i>Corylus</i> hybrid	Dundee	Oregon	E	Dundee

			(Col - Ave)				
	PI 557372	168.001	<i>Corylus</i> hybrid (Col - Ave)	Newburg	Oregon	E	Newburg
	PI 557263	170.001	<i>Corylus</i> hybrid (Col - Ave)	Chinese Trazel J-1	Oregon	E	Chinese Trazel J-1
	PI 557374	171.001	<i>Corylus</i> hybrid (Col - Ave)	USOR 13-71	Oregon	E	USOR 13-71
	PI 557264	173.001	<i>Corylus</i> hybrid (Col - Ave)	Chinese Trazel Gellatly No. 11	British Columbia	E	Chinese Trazel Gellatly No. 11
	PI 557387	199.001	<i>Corylus</i> hybrid (Col - Ave)	Chinoka	British Columbia	B	Chinoka
	PI 557389	201.001	<i>Corylus</i> hybrid (Col - Ave)	Erioka	British Columbia	B	Erioka
	PI 557390	202.001	<i>Corylus</i> hybrid (Col - Ave)	Ruby	Oregon	B	Ruby
	PI 557393	405.002	<i>Corylus</i> hybrid (Col - Ave)	Faroka	British Columbia	E	Faroka
	PI 557394	406.001	<i>Corylus</i> hybrid (Col - Ave)	Karloka	British Columbia	E	Karloka
	PI 557396	408.001	<i>Corylus</i> hybrid (Col - Ave)	Turktrazel Gellatly No. 15	British Columbia	E	Turktrazel Gellatly No. 15
	PI 617185	559.001	<i>Corylus</i> hybrid (Col - Ave)	Grand Traverse	Michigan	E	Grand Traverse
	PI 617191	574.001	<i>Corylus</i> hybrid (Col - Ave)	Farris 88 BS	Michigan	E	Farris 88 BS
	OSU		<i>Corylus</i> hybrid (Col - Ave)	Lisa	Michigan	E	Lisa
	PI 557429	9.001	<i>Corylus</i> x <i>colurnoides</i> C. K. Schneider (Col x Ave)	C. x colurnoides L-1		E	C. x colurnoides L-1
	PI 557350	139.001	<i>Corylus</i> hybrid (Het Sut - Ave)	Estrella No.1	Michigan	N	Estrella No.1
	PI 557351	140.001	<i>Corylus</i> hybrid (Het Sut - Ave)	Estrella No.2	Michigan	N	Estrella No.2
	PI 557430	14.001	<i>Corylus</i> x <i>vilmorinii</i> Rehder (Chi x Ave)	C. x vilmorinii Arnold Arboretum	Massachusetts	B	C. x vilmorinii CCOR14

	PI 617265	701.001	<i>Corylus hybrid</i> (or <i>avellana</i> ?)	18-32 EFB-resistant	New York	A	Medium Long
			<i>C. avellana</i> L.	Culplà	Spain	A	C. av_Culplà
			<i>C. avellana</i> L.	Gironell	Spain	A	C. av_Gironell
			<i>C. avellana</i> L.	Grifoll	Spain	A	C. av_Grifoll
			<i>C. avellana</i> L.	Morell	Spain	A	C. av_Morell
			<i>C. avellana</i> L.	Pauetet	Spain	A	C. av_Pauetet
			<i>C. avellana</i> L.	Ribet	Spain	A	C. av_Ribet
			<i>C. avellana</i> L.	Trenet	Spain	A	C. av_Trenet
			<i>C. avellana</i> L.	Camponica	Italy	A	C. av_Camponica
			<i>C. avellana</i> L.	Mortarella	Italy	A	C. av_Mortarella
			<i>C. avellana</i> L.	Nocchione	Italy	A	C. av_Nocchione
			<i>C. avellana</i> L.	Riccia di Talanico	Italy	A	C. av_Riccia di Talanico
			<i>C. avellana</i> L.	San Giovanni	Italy	A	C. av_San Giovanni
			<i>C. avellana</i> L.	Tonda bianca	Italy	D	C. av_T.Bianca
			<i>C. avellana</i> L.	Tonda di Giffoni	Italy	A	C. av_T.Giffoni
			<i>C. avellana</i> L.	Tonda Gentile Langhe	Italy	A	C. av_T.G.Langhe
			<i>C. avellana</i> L.	Tonda Gentile Romana	Italy	A	C. av_T.G.Romana
			<i>C. avellana</i> L.	Tonda rossa	Italy	D	C. av_T.Rossa
			<i>C. avellana</i> L.	Badem	Turkey	A	C. av_Badem
			<i>C. avellana</i> L.	Extra Ghiagli	Turkey	A	C. av_Extra Ghiagli
			<i>C. avellana</i> L.	Imperiale di Trebisonda	Turkey	B	C. av_I.Trebizonde
			<i>C. avellana</i> L.	Incekara	Turkey	B	C. av_Incekara
			<i>C. avellana</i> L.	Kalinkara	Turkey	B	C. av_Kalinkara
			<i>C. avellana</i> L.	Palaz	Turkey	B	C. av_Palaz
			<i>C. avellana</i> L.	Sivri	Turkey	A	C. av_Sivri
			<i>C. avellana</i> L.	Sivri Ghiagli	Turkey	B	C. av_Sivri Ghiagli
			<i>C. avellana</i> L.	Tombul	Turkey	A	C. av_Tombul

			<i>C. avellana</i> L.	Tombul Ghiaghi	Turkey	B	C. av_Tombul Ghiagli
			<i>C. avellana</i> L.	Asle Gharebag	Iran	C	C. av_Asle Gharebag
			<i>C. avellana</i> L.	Dobooseh	Iran	A	C. av_Dobooseh
			<i>C. avellana</i> L.	Jorow Gharebag	Iran	C	C. av_Jorow Gharebag
			<i>C. avellana</i> L.	Mish-pestan	Iran	C	C. av_Mish-pestan
			<i>C. avellana</i> L.	Nakhoni Rood	Iran	C	C. av_Nakhoni Rood
			<i>C. avellana</i> L.	Pashmineh	Iran	C	C. av_Pashmineh
			<i>C. avellana</i> L.	Rasmi	Iran	C	C. av_Rasmi
			<i>C. avellana</i> L.	Shastak-2	Iran	C	C. av_Shastak-2
			<i>C. avellana</i> L.	Shirvani	Iran	C	C. av_Shirvani
			<i>C. avellana</i> L.	Tabari Rood	Iran	B	C. av_Tabari Rood

*indicates single accession of *C. fargesii* included in assessing amplification an polymorphism of the 15 SSRs described in Supplementary Table 1.

Table 2.

Marker	<i>C. americana</i>					<i>C. avellana</i>					<i>C. californica</i>				
	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u
CaC-C001b	0.75	0.81	0.72	8	127	0.74	0.17	0.70	5	-	0.22	0.24	0.21	4	95, 112
CaC-C003	0.39	0.35	0.36	4	-	0.40	0.17	0.36	3	-	0.69	0.72	0.64	5	-
CaC-C005	0.30	0.31	0.28	4	115, 121	0	0	0	1	-	0.68	0.76	0.61	4	-
CaC-C008	0.72	0.38	0.69	7	236	0.71	1	0.65	4	-	0.81	0.80	0.79	8	189
CaC-C028	0.75	0.35	0.71	8	-	0.64	1	0.57	4	-	0.40	0.32	0.37	5	-
CaC-C036	0	0	0	1	-	0	0	0	1	-	0	0	0	1	-
CaC-C040	0.58	0.69	0.49	3	-	0.50	0.33	0.45	3	-	0.50	1	0.38	2	-
CaC-C108	0.15	0.12	0.14	5	178	0.44	0	0.35	2	-	0.11	0.12	0.11	2	-
CaC-C111	0.61	0.62	0.53	3	-	0.44	0.33	0.35	2	-	0	0	0	1	-
CaC-C112	0.59	0.15	0.51	4	256, 276	0	0	0	1	-	0.63	0.44	0.59	4	266
CaC-C118	0.64	0.69	0.58	5	-	0.28	0.33	0.24	2	-	0.53	0.40	0.49	7	-
CaC-C119	0.41	0.35	0.39	4	-	0.42	0.50	0.39	4	-	0	0	0	1	-
CaT-C501	0.79	0.50	0.76	10	188	0.72	0.83	0.68	5	212, 213	0.80	0.72	0.78	10	183, 191, 192
CaT-C504	0.81	0.62	0.78	8	-	0.61	0	0.54	3	-	0.34	0.32	0.32	4	-
Mean	0.53	0.42	0.50	5.29		0.42	0.33	0.38	2.86		0.41	0.42	0.38	4.14	

Species	<i>C. chinensis</i>					<i>C. colurna</i>					<i>C. cornuta</i>				
	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u
CaC-C001b	0.45	0.44	0.42	4	107	0.78	0.85	0.74	8	101	0.79	0.73	0.76	6	118, 122
CaC-C003	0.55	0.44	0.49	3	-	0.46	0.00	0.40	3	-	0.67	0.64	0.63	5	-
CaC-C005	0.44	0.22	0.41	4	94	0.07	0.08	0.07	2	-	0.46	0.36	0.36	2	-
CaC-C008	0.84	0.78	0.82	8	-	0.60	0.62	0.54	3	-	0.64	0.64	0.58	6	187
CaC-C028	0.69	0.67	0.63	4	-	0.67	0.38	0.62	5	-	0	0	0	1	-
CaC-C036	0	0	0	1	-	0	0	0	1	-	0	0	0	1	-
CaC-C040	0.38	0.44	0.35	4	-	0.71	0.54	0.65	5	170	0.60	0.45	0.57	6	206

CaC-C108	0	0	0	1	-	0.51	0.46	0.45	3	-	0.62	0.64	0.54	3	-
CaC-C111	0.54	0.78	0.47	3	206	0	0	0	1	-	0.17	0.18	0.15	2	-
CaC-C112	0	0	0	1	-	0.07	0.08	0.07	2	-	0.09	0.09	0.08	2	-
CaC-C118	0.59	0.56	0.57	6	-	0.73	0.54	0.68	5	165	0.68	0.45	0.64	6	200
CaC-C119	0.64	0.67	0.58	4	-	0.21	0.23	0.20	3	-	0.09	0.09	0.08	2	-
CaT-C501	0.71	0.33	0.66	5	206	0.47	0	0.36	2	-	0.79	0.91	0.75	6	-
CaT-C504	0.73	0.67	0.69	6	156, 162, 175	0.82	0.92	0.79	7	-	0.71	0.73	0.67	5	147
Mean	0.47	0.43	0.44	3.86		0.44	0.34	0.40	3.57		0.45	0.42	0.42	3.79	

Species	<i>C. fargesii</i>					<i>C. ferox</i>					<i>C. heterophylla</i>				
	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u
CaC-C001b	0.5	0	0.38	2	-	0.50	0	0.38	2	98	0.76	0.71	0.73	7	-
CaC-C003	0	0	0	1	-	0.38	0.50	0.30	2	-	0.52	0.43	0.46	3	-
CaC-C005	0	0	0	1	-	1	1	0.38	2	-	0.52	0.57	0.46	3	118, 124
CaC-C008	0	0	0	1	-	0.63	1	0.55	3	-	0.78	0.86	0.74	6	230, 245
CaC-C028	0	0	0	1	-	0	0	0	1	138	0.65	0.43	0.60	5	-
CaC-C036	0	0	0	1	-	0	0	0	1	-	0	0	0	1	-
CaC-C040	0.38	0.50	0.30	2	-	0.63	1	0.55	3	218	0.53	0.57	0.48	4	-
CaC-C108	0	0	0	1	-	0	0	0	1	-	0.54	0.57	0.50	4	-
CaC-C111	0	0	0	1	-	0	0	0	1	-	0.64	1	0.57	3	-
CaC-C112	0	0	0	1	-	0.38	0.50	0.30	2	259, 280	0	0	0	1	-
CaC-C118	0.38	0.5	0.30	2	-	0.63	1	0.55	3	-	0.46	0.43	0.43	4	-
CaC-C119	0.5	1	0.38	2	-	0.63	0.50	0.55	3	-	0.69	0.57	0.63	4	-
CaT-C501	0.38	0.50	0.30	2	211	0.50	0	0.38	2	-	0.74	0.71	0.72	7	221, 224, 225
CaT-C504	0	0	0	1	-	0	0	0	1	-	0.55	0.57	0.52	5	-
Mean	0.15	0.18	0.12	1.36		0.34	0.39	0.28	1.93		0.53	0.53	0.49	4.07	

Species	<i>C. jacquemontii</i>	<i>C. sieboldiana</i>	Overall
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Marker	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u	H_e	H_o	PIC	A	A_u
CaC-C001b	0.50	0.60	0.38	2	-	0.67	0.67	0.59	3	106					-
CaC-C003	0	0	0	2	100, 103	0.50	0.33	0.38	2	-	0.78	0.39	0.74	8	-
CaC-C005	0	0	0	1	-	0.28	0.33	0.24	2	103	0.68	0.34	0.66	12	-
CaC-C008	0.50	0.60	0.38	2	-	0.78	1	0.74	5	-	0.92	0.66	0.91	21	-
CaC-C028	0.48	0.40	0.36	2	-	0.50	0.33	0.45	3	-	0.80	0.44	0.78	9	-
CaC-C036	0	0	0	1	-	0	0	0	1	-					-
CaC-C040	0.54	0.80	0.47	3	173	0.28	0.33	0.24	2	-	0.83	0.65	0.80	14	-
CaC-C108	0.48	0.40	0.36	2	-	0	0	0	1	182					-
CaC-C111	0	0	0	1	-	0.44	0.67	0.35	2	-	0.68	0.38	0.64	6	-
CaC-C112	0	0	0	1	-	0.44	0	0.35	2	-					-
CaC-C118	0.42	0.60	0.33	2	-	0.50	0.67	0.45	3	-	0.82	0.54	0.80	12	-
CaC-C119	0	0	0	1	-	0.28	0.33	0.24	2	-					-
CaT-C501	0.34	0.40	0.31	3	187	0.72	1	0.67	4	-					-
CaT-C504	0.62	0.20	0.55	3	177	0.72	1	0.67	4	-					-
Mean	0.31	0.29	0.25	1.86		0.44	0.48	0.38	2.57		0.79	0.49	0.76	11.7	

Table 3

Chlorotype	ccmp2	ccmp3	ccmp4	ccmp5	ccmp6	ccmp10	N. individuals*
A	212	118	116	107	98	107	26
B	212	117	116	107	98	107	8
C	213	117	116	107	98	107	8
D	214	118	115	107	98	106	2
E	214	117	115	107	98	106	12
F	213	117	115	106	98	106	1
G	212	117	116	106	98	109	5
H	212	117	116	106	98	107	2
I	213	117	116	108	98	106	3
J	213	117	116	106	98	106	4
K	213	117	117	108	98	106	2
L	213	118	116	107	98	107	1
M	213	118	116	108	98	107	1
N	213	117	116	107	98	106	9
O	212	117	115	108	98	106	1
P	213	116	116	106	99	108	30
Q	212	116	116	106	99	108	23
R	212	116	115	106	99	109	5
S	212	116	115	106	99	108	2
T	212	116	115	107	99	108	2
U	213	116	115	106	99	108	4
Number of alleles	3	3	3	3	2	4	
Gene diversity	0.576	0.636	0.330	0.542	0.493	0.688	

*N. individuals did not include any of the hybrids

Fig. 1

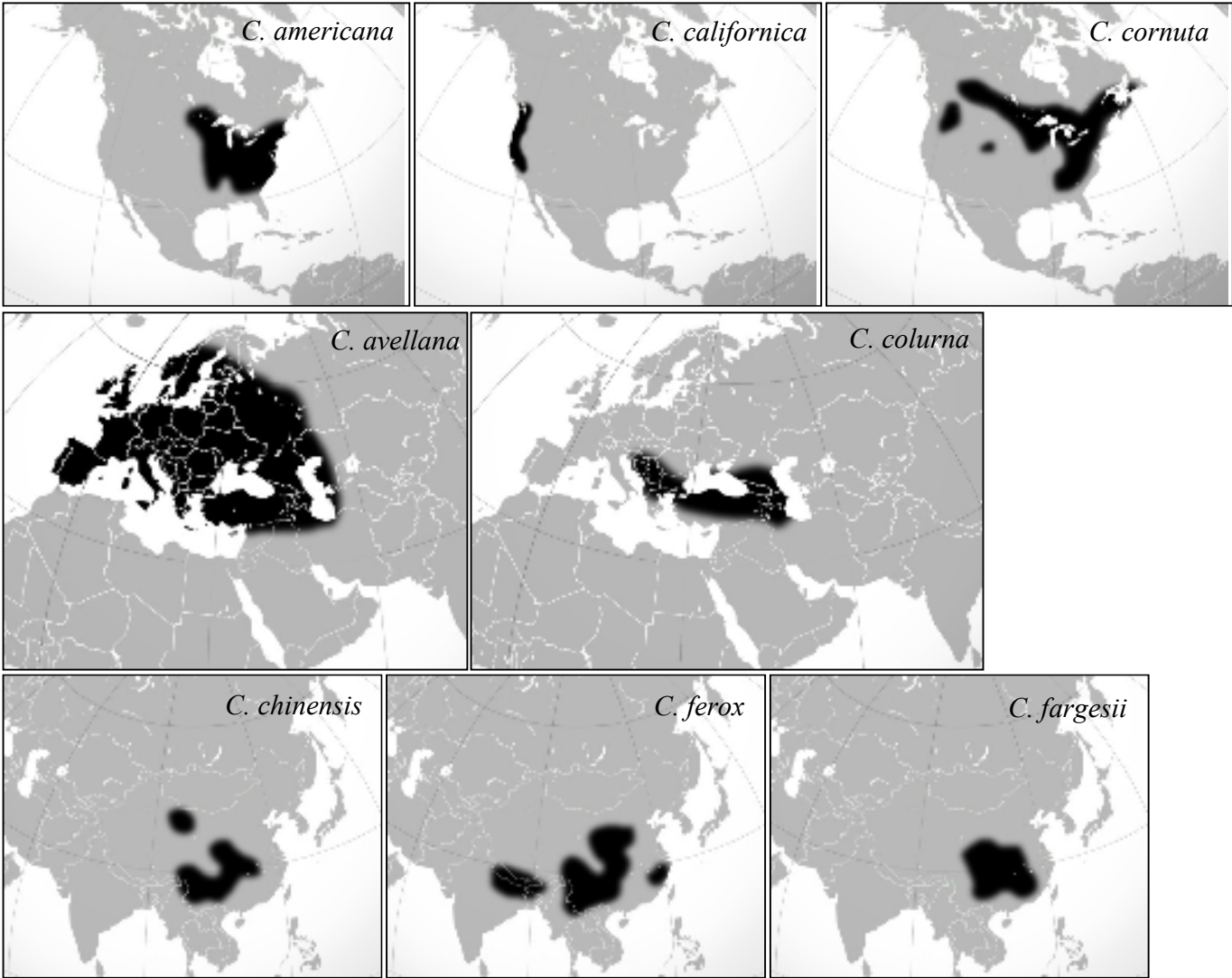




Fig. 2.

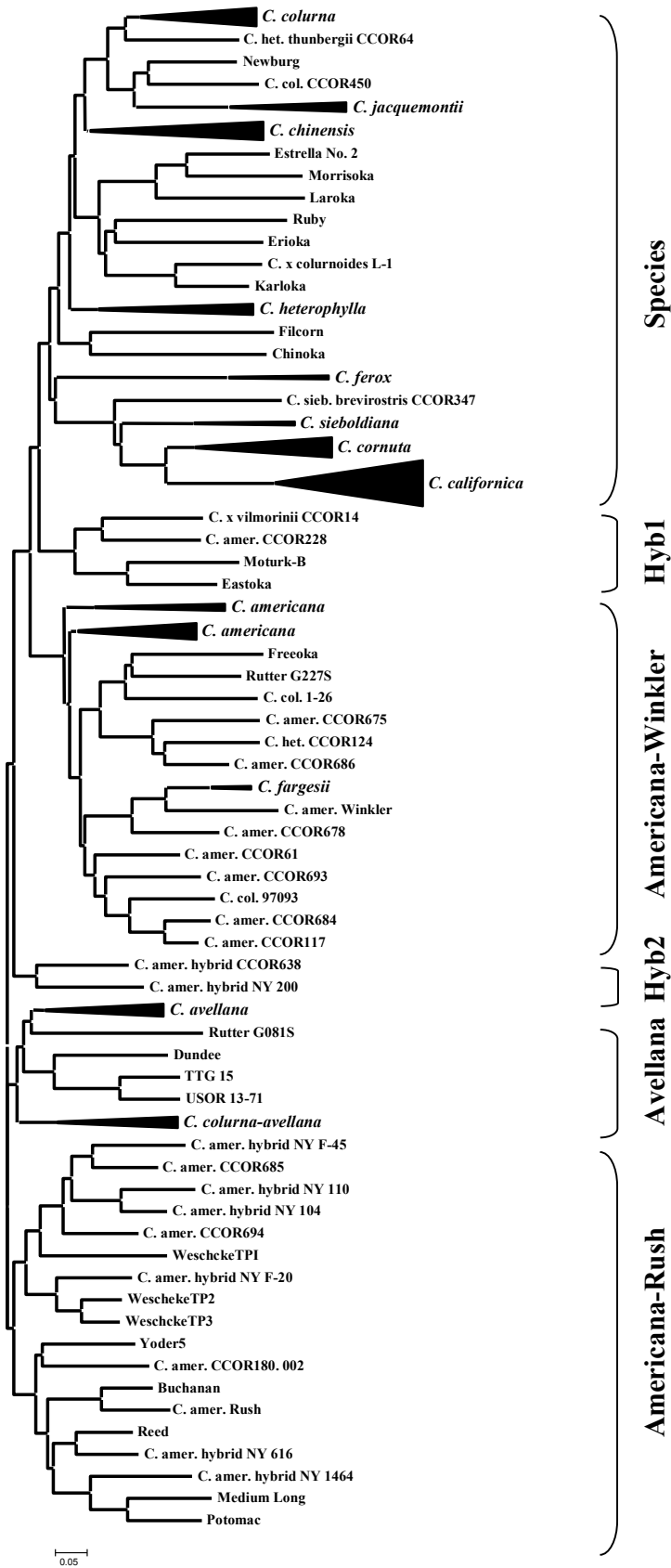


Fig. 3.

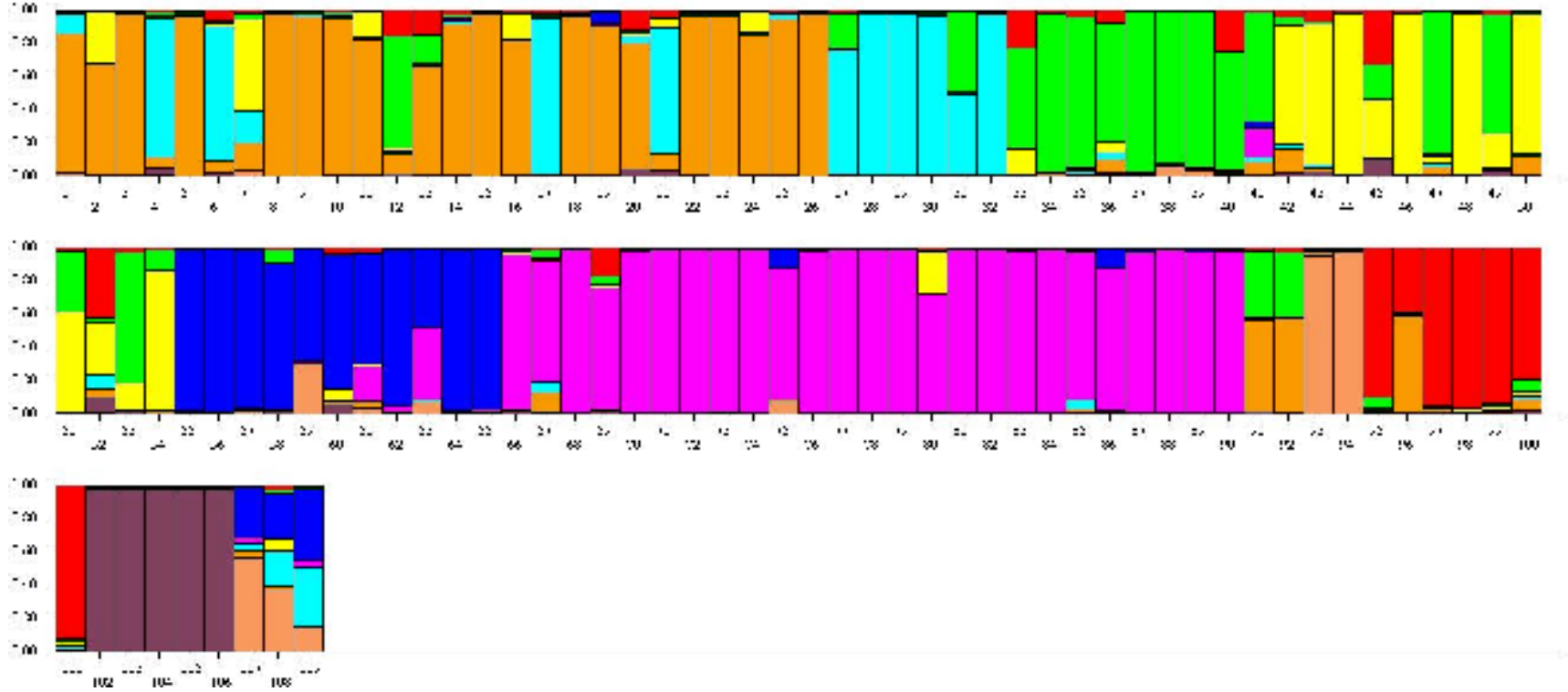


Fig. 4.

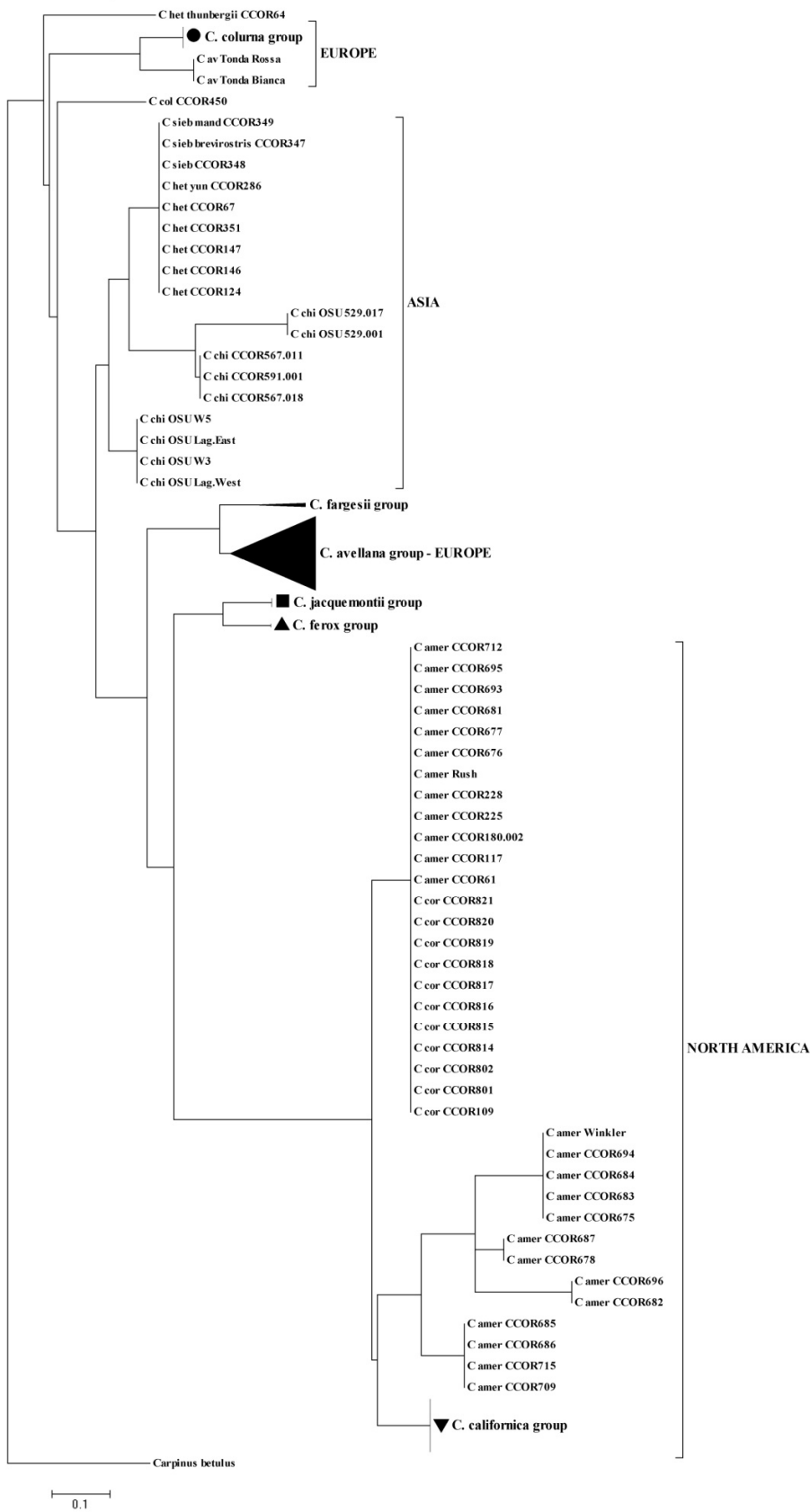


Fig. 5.

