

AN ABSTRACT OF THE THESIS OF

Tufan Gökirmak for the Degree of Master of Science in Horticulture presented on June 10, 2005.

Title: Characterization of European Hazelnut (*Corylus avellana* L.) Cultivars Using SSR Markers

Abstract Approved: _____

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Twenty-one pairs of simple sequence repeat (SSR) primers were used to investigate genetic diversity in 270 accessions of European hazelnut (*Corylus avellana*) representing a wide geographic range. A capillary electrophoresis system and ABI Genescan® and Genotyper® software were used to determine the allele size generated from each PCR reaction based on an internal lane standard. A total of 211 alleles were amplified and the number of alleles detected ranged from 5 to 15 per locus with an average of 10.05. The observed heterozygosity (H_o) for individual loci ranged from 0.24 to 0.88, with an average of 0.67 over all loci. The presence of null alleles was detected at three loci (CAC-C010, CaT-C504 and CaT-B508) by comparing the pedigree information of some cultivars. PowerMarker software was used to generate a genetic similarity matrix based on possible pair-wise combinations of accessions using the “proportion of shared alleles”. UPGMA cluster analysis was used to construct a phenogram from the genetic similarity matrix using PowerMarker and MEGA3 software. The phenogram revealed geographically tight clusters and some synonyms among European hazelnut cultivars. Of the 274 accessions in the population, 200 are unique

cultivars, 70 are suspected synonym accessions (different trees), as they are morphologically identical and 4 are duplicate DNA templates from the same tree included as checks. Of the 211 total alleles amplified, 22 were unique, as they were detected only in one cultivar. Nine of the unique alleles were amplified in cultivars that fell outside of the tightly clustered cultivar groups. A subset of 11 loci is recommended for in future hazelnut fingerprinting studies.

A total of 144 seedlings from a controlled cross of OSU 252.146 x OSU 414.062 were scored for 33 SSR markers and 29 of them were successfully integrated into the RAPD marker-based hazelnut linkage map constructed using the two-way pseudo-testcross approach, where they will serve as “anchor loci”. Two loci showed aberrant segregation ratios and two loci remained unlinked. Eleven linkage groups were identified for each parent, corresponding to the haploid chromosomes number of hazelnut ($2n=2x=22$) and spanning a total distance of 668 cM in the susceptible parent and 813 cM in the resistant parent. The order of homologous SSR loci in the two parents was collinear in most cases. Placement of these SSR “anchor loci” on the hazelnut linkage map will make it useful in other populations.

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Characterization of European Hazelnut (*Corylus avellana*) Cultivars Using SSR Markers

by

Tufan Gökirmak

A THESIS

submitted to

Oregon State University

in partial fulfillment of
the requirements for the
degree of

Master of Science

Presented June 10, 2005
Commencement June 2006

Master of Science thesis of Tufan Gökirmak presented on June 10, 2005.

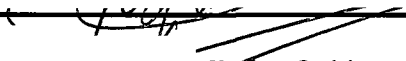
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ACKNOWLEDGEMENTS

My sincere appreciation goes to my major professor, Dr. Shawn A. Mehlenbacher for his financial support, invaluable guidance, assistance and insightful suggestions in experiments and the preparation of this manuscript.

I greatly appreciate the time and helpful suggestions of my outstanding committee members Dr. Nahla V. Bassil, who helped in choosing the SSR markers used in this study and advised me on laboratory procedures and data analysis, my biochemistry minor advisor Dr. Kevin Ahern and my graduate school representative Dr. Robert Duncan. I am also grateful for their support in my academic program in horticulture. In their classes I have gained invaluable knowledge for which I am thankful.

I would also like to thank Dr. Roberto Botta for providing SSR marker sequences and David C. Smith for his support, friendship and helpful suggestions.

I am also thankful to my beloved friends Peter Boches, Cumhuriyet Gelogullari, Barb Gilmore, Omer Gokcumen, Gulden Karakok, Hasan Kesim, Peter Mes, Kerem Ok, Gokay Saldamli and Mona Zubair for their support, help, encouragement and humor.

I would like to dedicate this thesis to my parents Saadet and Ismail Gökirmak and my brother Gökhan Gökirmak in Turkey who always believed in me and provided me with the emotional support when I most needed it.

CONTRIBUTION OF AUTHORS

Dr. Shawn A. Mehlenbacher was the main designer of the experiments. He assisted with data collection and writing of all parts of the thesis and provided the RAPD marker data set used in Chapter 3. Furthermore Dr. Mehlenbacher provided laboratory facilities and funding. Dr. Nahla V. Bassil helped in choosing the SSR markers used in this study and advice on laboratory procedures and data analysis.

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CHAPTER 1

INTRODUCTION

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CHARACTERIZATION OF EUROPEAN HAZELNUT (*Corylus avellana*) CULTIVARS USING SSR MARKERS

History and Biology of Hazelnut

The European hazelnut, *Corylus avellana* L., is grown in many regions of Europe and west Asia and has been used as a food source by humans since prehistoric times. Hazelnut became one of the species in the local flora in parts of Europe in the Boreal period, from 8000 to 5500 B.C. According to ancient Greek literature, hazelnut was brought to Greece from the shores of the Black Sea, the location of present-day Turkey (Lagerstedt, 1975). Based on a study using chloroplast DNA variation and pollen record in *Corylus*, postglacial migration of hazelnut started from southwestern France and spread to the rest of Europe except Italy and the Balkans, where another local expansion had occurred (Palmé and Vendramin, 2002)

Corylus avellana, the species of commerce, is native to Europe and Asia Minor and naturally grows in temperate regions of the Northern Hemisphere from the Atlantic coast of Europe as far north as Norway. The northern boundary includes the British Isles, Scandinavia and northern regions of the Russian Federation. The distribution is bounded in the east by the Ural Mountains. The southern boundary extends from Spain, Morocco and Algeria in the west through Italy, Yugoslavia, Greece, and Turkey to northwestern Iran and Transcaucasia. Although hazelnut is produced in a few regions in the southern hemisphere, it is not native to those regions (Kasapligil, 1972).

Hazelnut-producing regions have mild, moist winters and cool summers. The major production areas are located near large bodies of water at middle latitudes in the

northern hemisphere. Approximately 70% of the world's hazelnut production comes from the Black Sea region of Turkey. Italy follows Turkey with about 20 percent of world production. Spain, France, Georgia, Azerbaijan and the United States account for the remaining 10%. The moderate climate of the Pacific Northwest's coastal valleys is well-suited to hazelnut production. Approximately 99% of the U.S. hazelnut crop is produced in Oregon's Willamette Valley. The Pacific Northwest represents 3 to 5 percent of world hazelnut production (FAO Production Year Book, 2004; Hazelnut Marketing Board, 2004).

The genus name *Corylus* originated from the Greek word korys, which means a helmet or hood. The word hazelnut comes from the Anglo-Saxon word for bonnet, haesel. Hazelnut is a general name used for the nuts of all *Corylus* species. Even though hazelnut is the most commonly used name in world commerce, some growers call these nuts filberts. The name "filbert" probably originated from the German term vollbart, or full beard, descriptive of the long leafy husks of some varieties of hazelnut (Lagerstedt, 1975). The genus *Corylus* is a member of the Betulaceae or Birch family and includes other important forest tree species and ornamentals (Erdogan and Mehlenbacher, 2000). The European hazelnut, *Corylus avellana*, is one of the 25 described species in the genus, all of which produce edible nuts, which are collected from the wild by humans. All *Corylus* species are diploid with $2n = 22$ chromosomes (Kasapligil, 1968; Thompson et al., 1996).

The European hazelnut grows naturally as a bush or a multi-stemmed shrub. In Turkey and southern Europe, hazelnut has been grown in its natural growth habit for

centuries. In the US, however, hazelnuts are usually grown as single-trunk trees for mechanical harvesting purposes. They can reach approx. 13 m, if planted in good soil and managed with proper pruning, fertilization, and pest control practices.

Hazelnut has a unique floral biology, which was reviewed in detail by Germain (1994). It is monoecious, having separate male and female flowers on the same tree, and wind-pollinated (Thompson et al., 1996). The male flowers are borne in catkins, and female inflorescences have no perianth. They appear as a tuft of red stigmatic styles protruding from the apex of compound buds located on shoots or catkin peduncles. The hazelnut tree is self-incompatible, which enforces cross-pollination. Incompatibility is of the sporophytic type, and is under the control of a single locus (the S-locus) with multiple alleles (Mehlenbacher, 1997). If the same allele is expressed in both pollen and pistil, pollen germination is delayed and pollen tubes fail to penetrate the stigmatic surface (Hampson et al., 1993). So far, 25 unique S-alleles have been identified and the hierarchical order among these alleles determines which is expressed in the pollen and thus the direction of the crosses in breeding programs (Pomper et al., 1998; Mehlenbacher, 1997). The dichogamous nature of hazelnut is another factor that promotes cross-pollination. Male flower induction usually occurs a month before female induction. Female flower formation is affected by three main factors: the level of light received by the one-year-old shoots during the previous growing season, the vigor and the origin of these shoots. For an equivalent length, shoots receiving more light bear more inflorescences. The total number of female inflorescences per shoot increases with shoot length irrespective of tree age or variety. On the other hand, the origin of the shoot also

has a significant effect on number of flowers. On shoots originating from glomerules and bearing a nut cluster at the extremity, formation of female flowers is nearly or completely inhibited (Germain, 1994).

Like many other horticultural crops, hazelnut is clonally propagated and highly heterozygous. Controlled crosses (complementary hybridization) and the modified backcross method are used in hazelnut breeding programs (Mehlenbacher, 1995). The modified backcross method involves a series of crosses and is utilized to transfer a desirable single trait from a wild or unadapted source and combine it with other desired qualities. In the modified backcross method, a different “recurrent parent” is used in each backcross generation to avoid inbreeding. The heterozygous nature of the parents results in segregation in the F_1 progeny, allowing linkage map construction (Pomper et al. 1998).

Molecular Markers

Applications of molecular markers

Traditional techniques used for identification of cultivars and clones are based on morphological characters. However these techniques are not always useful due to environmental variation affecting gene expression (Marinoni et al., 2003). Molecular markers offer a direct method of identification of plant material through determination of the differences in the genetic material independent of environmental effects.

Molecular markers can be placed into two main categories: biochemical (e.g. isozymes) and DNA-based markers. Isozymes are different molecular forms of the same enzyme that are specific to a common substrate but differ in electrophoretic mobility.

They may be visualized following gel separation and show codominant inheritance. However, isozymes do not generally show a high level of polymorphism within a population. On the other hand, DNA markers are based on naturally occurring DNA polymorphism (i.e. base pair deletions, substitutions, additions or repeat patterns) throughout the genome (Gupta et al., 1999). They have different applications in plant breeding, scientific research and identification of plants in commerce. Plant breeding applications include marker-assisted selection and confirmation of parent-progeny relationships. Research applications range from taxonomic studies to population genetic analysis and linkage map construction. Molecular markers also have commercial applications such as “fingerprinting” for enforcement of legal protection, quality control in plant production (i.e. trueness to name) and processing and labeling plant-derived foods and other products.

Types of DNA markers

There are several different types of nucleic acid sequence-based markers. They are divided into two main categories: restriction fragment length polymorphism (RFLP) markers and PCR-based molecular markers, such as RAPDs, AFLPs, SSRs, SCARs, etc.

RFLP is one the first molecular markers and has been used in numerous DNA fingerprinting and genetic diversity analyses in species such as rice (Wang and Tanksley, 1989), sorghum (Tao et al., 1993) and wheat (Paull et al., 1998). This technique centers around Southern hybridization of restriction enzyme-digested DNA with genomic or cDNA probes. Polymorphism results from differences in the length of fragments

produced by restriction enzyme digestion. Due to probe sequence homology, such markers are perfectly suitable for phylogenetic analysis between related species, such as within the genus *Musa* (Nwakanma et al., 2003). RFLPs are co-dominant and robust markers, can be easily exchanged between labs, and have high repeatability. However, the technique has some disadvantages that include a requirement for large amounts of high-quality DNA, the use of radioisotopes, probe library construction for previously unexplored species, and difficulties in statistical evaluations and standardization.

PCR based markers

Polymerase chain reaction (PCR)-based markers have some advantages over biochemical and RFLP markers. They are faster than RFLPs, and only a small amount of genomic DNA (5-25 ng) is required. Additionally, exchange of primer sequence information instead of DNA is another advantage of PCR-based markers.

Random amplified polymorphic DNA (RAPD) was the first type of PCR-based marker developed. RAPDs are fragments amplified by PCR using arbitrary, usually 10-12 mer primers (Williams et al., 1990). PCR products are separated by gel electrophoresis and scored for the presence or absence of an amplicon after staining with ethidium bromide (EtBr). RAPD markers are usually dominant and thus they cannot distinguish between homozygotes and heterozygotes. Polymorphism is the result of presence or absence of the priming site in the genomic DNA. RAPD is a fast, easy and inexpensive technique. However, it has some reliability problems. Results are very sensitive to reaction conditions like $MgCl_2$ concentration, primer concentration and annealing

temperature. Even different equipment in different laboratories may give different results. For these reasons, RAPDs are not as reliable as other sequence-specific markers. On the other hand, some of these problems can be overcome by cloning and sequencing the fragments, and converting these into sequence characterized amplified regions (SCAR), which are usually more robust than RAPDs (Paran and Michelmore, 1993). However, the original polymorphism may be lost with the use of longer primers. Several different approaches like PCR optimization, primer redesign and cleaved amplified polymorphic sequences (CAPS) can be used to recover the polymorphism. CAPS may reveal polymorphism lost during SCAR marker development by digesting the PCR product with a “frequent cutter” restriction enzyme that recognizes a 4 bp restriction enzyme site (Moury et al., 2000; Ohmori et al., 1996; Paran and Michelmore, 1993).

Amplified fragment length polymorphism (AFLP) is a PCR-based marker system for DNA fingerprinting developed by Vos et al. (1995). The procedure involves digestion of genomic DNA with two restriction enzymes, a frequent cutter (e.g. *MseI*) and a rare cutter (e.g. *EcoRI*). DNA templates for PCR reactions are generated by ligating oligonucleotide adapters to the restriction fragments. PCR fragments are selectively amplified in two steps using primers that are complementary to the adapter sequence and the restriction enzyme cleavage site and up to four selective nucleotides at the 3' end. Polymorphism is determined by presence or absence of the amplified fragments on high-resolution sequencing gels visualized by silver staining, fluorescent dyes or radioactivity. AFLP enables screening a much larger number of loci per PCR reaction for polymorphism than other available PCR-based techniques and has been demonstrated to

generate a large number of polymorphisms in barley (*Hordeum vulgare* L.) (Becker et al., 1995). Polymorphism produced by AFLPs is generally reproducible. Like RAPDs, AFLPs are also dominant markers. Although they are reliable and a large number of bands is generated by a single PCR, they are expensive, complicated and technologically demanding. Conversion of AFLPs to SCARs reduces their cost and advances their use in marker-assisted selection. However, as mentioned earlier in the conversion of RAPDs to SCARs, the polymorphism may be lost. This problem can be overcome by generating CAPS (Konieczny and Ausubel, 1993).

Microsatellites

Microsatellites or simple sequence repeats (SSRs) are tandemly repeated 1-6 bp sequence motifs found in both eukaryotic and prokaryotic genomes. They are abundant and dispersed throughout the genome and can be found in both coding and non-coding regions. However, they are more abundant in the latter since non-coding DNA can accumulate mutations more easily than coding DNA (Ahmad et al., 2003). Furthermore, they have a high level of length polymorphism relative to other genetic markers (Zane et al., 2002). Although the exact mechanism of microsatellite evolution is not clear, it appears most likely due to the slippage of DNA polymerase during DNA replication or unequal crossing-over between homologous chromosomes during recombination (Schlötterer and Tautz, 1992). In non-coding regions of the genome the most abundant class of microsatellites contains dinucleotide repeats (Li et al., 2002). On the other hand, microsatellites found in coding regions of *Arabidopsis*, especially in the 5' Untranslated

Region (5'UTR) are mainly trinucleotide and hexanucleotide repeats, probably due to negative selection against frameshift mutations in coding regions (Morgante et al., 2002). Simple sequence length polymorphisms generated by the different number of repeat units can be easily detected as size differences obtained from DNA amplification using primers complementary to the flanking regions of the repeat motifs. According to Stallings (1992), Lagercrantz et al. (1993) and Hancock (1999), the most abundant motifs in plants are GA and AT repeats and in animals, GT repeats.

SSRs have many advantages over other marker systems and are extensively used in fingerprinting (Thomas and Scott, 1993), linkage map construction (Bowcock et al., 1994; Hazan et al., 1992), forensic DNA research, and population genetic studies (Jarne and Lagoda, 1996). Valuable characteristics of SSR markers include high polymorphism, co-dominance, sensitivity (even a small quantity of DNA can be amplified by PCR), conservation in related species, reproducibility and ease of data scoring. The exchange of primer sequences instead of probes allows other labs to work with the same loci. The only disadvantages of microsatellite markers are that they must be isolated *de novo* from most species being examined for the first time and considerable investment and technical expertise are required for the initial development (Zane et al., 2002; Jauhar, 1996).

In recent years microsatellites have been successfully used in various genetic applications such as cultivar identification and breeding record verification of apple (Cabe et al., 2005) and pistachio (Ahmad et al., 2003); phylogenetic analysis of almond (Xu et al., 2004) and grape (Fatahi et al., 2003); and evaluation of genetic diversity relationships in fruit crops such as kiwifruit (Zhen et al., 2004), apricot (Romero et al.,

2003) and peach (Aranzana et al., 2002). Microsatellites have also been extensively used for management of fruit germplasm such as olive (Khadari et al., 2003), grape (Martin et al., 2003; Dangl et al., 2001), cherry (Cantini et al., 2001) and peach (Testolin et al., 2000); in different applications such as determination of parentage of clonal crops such as cherry (Struss et al., 2003) and olive (Contento et al., 2002); identification of potential duplicates in collections of apple (Hokanson et al., 2001) and grape (Dangl et al., 2001), and detection of chimeras in grapevines (Franks et al., 2002). Furthermore, microsatellites have also been used in evolutionary studies of cacao (*Theobroma cacao* ssp. *cacao*) (Motamayor et al., 2002) and hop (*Humulus lupulus* L.) (Jakše et al., 2001).

Isolation of SSR markers is an expensive and labor-intensive process. Different approaches have been used to isolate the DNA sequences containing the repeat motifs and their flanking regions. Conventional SSR locus isolation is based on construction of a small insert (< 1000 bp) genomic library and screening thousands of clones using oligonucleotide probes containing the repeat sequences of interest (Rassmann et al., 1991). Standard isolation methods involve fragmentation of genomic DNA with restriction enzymes or sonication. The fragmented DNA is then size-selected in order to obtain small fragments (300-700 bp). Selected fragments are ligated to plasmids and cloned in *Escherichia coli*. The constructed library is then screened by means of Southern hybridization using labeled oligonucleotide probes containing the repeat motifs. Positive clones are selected, sequenced and primers are designed from the regions flanking the repeat motifs. Finally, locus-specific polymerase chain reactions are performed and fragment sizes are determined (Paniego et al., 2002).

In plants, the frequency of positive clones containing dinucleotide repeats in the whole genome is ten times smaller than in the human genome (Powell et al., 1996). In the study of Brown et al. (1996), approximately 0.2% of the library clones of sorghum hybridized with oligonucleotide probes. A second round of hybridization was performed to eliminate false positives, reducing the time and money that would have been wasted on sequencing clones that did not contain microsatellite repeats. Sequencing revealed that 70% of the sequences were useless, because of improper flanking sequences that did not permit primer design, lack of microsatellite repeats in the clones, severely imperfect repeats or a small number of repeats. Furthermore, following oligonucleotide primer synthesis, 65% of the primers failed to produce polymorphic bands in an array of plant genotypes. This low frequency of microsatellite loci in plants generates problems for large-scale isolation of microsatellite loci. Libraries enriched for certain repeat sequences have been constructed to solve this problem.

Different enrichment methods have been developed to increase the efficiency of the microsatellite isolation. They can be categorized according to the biochemical approach used during the enrichment procedure such as enrichment by colony/plaque hybridization, enrichment by primer extension and enrichment by hybridization.

The first method, colony/plaque hybridization involves further selection by means of hybridization prior to sequencing as in the standard isolation method. This second round of hybridization decreases the cost of sequencing and increases the overall efficiency of microsatellite isolation (Scott et al., 1999).

The second method, enrichment by primer extension, was developed by Ostrander et al. (1992) and Paetkau (1999). This method involves generation of a circular single stranded DNA (ssDNA) library by phagemid or phage vectors. ssDNA clones are used as template for repeat-specific oligonucleotide primers. Circular ssDNA molecules are then converted to circular dsDNA molecules by *in vitro* primer-extension. The two methods differ from each other after this step. In Ostrander's approach, the resulting circular dsDNA molecules are transferred into a specific *E.coli* strain, which favors the replication of clones containing primer-extended products resulting in a highly microsatellite-enriched library. Colonies are then screened for the presence of microsatellite loci using labeled oligonucleotide probes. Finally, positive clones are sequenced and primers are designed from the flanking regions of the repeat motif. It has been shown that an enriched library contains 50-fold more positive clones than an unenriched library (Ostrander et al., 1992). In contrast to this first technique, Paetkau (1999) used 5' biotinylated oligonucleotides and Klenow DNA polymerase in primer extension reactions. The products of these reactions in microsatellite-containing phages are linear primer-extended DNA molecules with a biotin at the 5'-end. Microsatellite-containing clones are selected from the reaction mixtures by streptavidin-coated beads. Finally, recovered single-stranded microsatellite-containing DNA molecules are converted to double-stranded molecules by a second round of primer extension and then used in transformation for secondary library construction.

A third class of enrichment method is based on selective hybridization. This technique can be further subdivided into either streptavidin-coated magnetic bead-

mediated enrichment or nylon membrane-mediated enrichment. Streptavidin-coated beads are paramagnetic beads. They are uniformly coated with a protein called streptavidin, which has a high affinity for biotin. This high affinity provides a fast and reliable way to isolate biotin-labeled target molecules. Genomic DNA fragments containing the desired repeat sequences are selected by biotin-labeled oligonucleotides. These hybrid molecules are then captured by streptavidin-coated magnetic beads. The nylon membrane-mediated enrichment method, in contrast to other enrichment techniques, produces enrichment libraries containing a variety of different microsatellite repeats. Enrichment for a pool of different microsatellite repeats is carried out by hybridization of genomic DNA fragments containing microsatellite repeats to a nylon filter bound with different microsatellite oligonucleotides. These two techniques differ from each other only in the type of selective hybridization. Microsatellite-containing fragments are amplified and sequenced by similar protocols with minor modifications (Karagoyozov et al., 1993; Armour et al., 1994; Kandpal et al., 1994; Kijas et al., 1994; Edwards et al., 1996; Fisher and Backmann, 1998; Hamilton et al., 1999).

In recent years, microsatellites have been identified from expressed sequence tag (EST) databases as an alternative to enrichment. However, this approach is limited to species for which EST databases exist. Indeed, microsatellites from EST databases have been recently developed for certain species such as rice (Cho et al., 2000), grape (Scott et al., 2000), sugarcane (Cordeiro et al., 2001), rye (Hackauf and Wehling, 2002), barley (Thiel et al., 2003) and loblolly pine (Liewlaksaneeyanawin et al., 2004). Sequences obtained from EST databases are good sources of microsatellites. Since EST-derived

microsatellites are in or near transcribed regions of the DNA, they are expected to be more conserved and more transferable than genomic sequences and to have a lower frequency of null alleles. However, Liewlaksaneeyanawin et al. (2004) reported that EST-derived microsatellites have a lower level of polymorphism than those derived from genomic libraries.

PCR fragment detection

There are different methods to determine the sizes of microsatellite-containing PCR products. The most commonly used ones are agarose gel electrophoresis, polyacrylamide gel electrophoresis (PAGE), denaturing PAGE and capillary electrophoresis (CE). Accurate sizing of the fragments with agarose and PAGE gel systems is not easy because of their low resolution power, but denaturing PAGE and capillary electrophoresis can determine fragment size differences as low as a single nucleotide. PCR fragments are visualized in PAGE by silver staining or radioactive labeling. Capillary electrophoresis is the latest and the fastest detection technique. SSR fragments amplified by fluorescently labeled primers can be detected without any post-PCR treatment. Furthermore, different PCR fragments labeled with different fluorescent tags can be multiplexed and then the products can be run in the same lane with an internal size standard (Donini et. al., 1998).

Data analysis and statistical terminology for fingerprinting

Statistical analyses of molecular marker data can be performed with different software packages developed for personal computers. Their easy access, sophisticated and powerful statistical techniques, and user-friendliness make them an attractive alternative to performing calculations on spreadsheets or with self-written programs. Some of the commonly used software packages are MicroSat (Minch et al., 1997), Identity 1.0 (Wagner and Sefc, 1999) and Powermarker 3.23 (Liu and Muse, 2004). These computer programs measure the genetic diversity by calculating the number and the frequency of alleles per locus, the expected heterozygosity (H_e) and observed heterozygosity (H_o), probability of identity (PI), null allele frequency from heterozygote deficiency (r) (Brookfield, 1996; Paetkau et al., 1995; Weir, 1996), polymorphic information content (PIC) and genetic distance (D) among genotypes (Bowcock et al., 1994). Observed heterozygosity (H_o) is the proportion of individuals in a population that is heterozygous at a given number of loci. On the other hand, the expected heterozygosity (H_e) is defined as the proportion of individuals which are prospective heterozygotes based on the allele frequencies and assuming Hardy-Weinberg equilibrium. The expected heterozygosity is calculated by the formula $H_e = 1 - \sum p_i^2$, where p_i is the frequency of i^{th} allele (Nei, 1973). The null allele frequency is calculated according to the formula of Brookfield (1996): $r = (H_e - H_o) / (1 + H_e)$. Probability of identity (PI) is the probability of randomly choosing two individuals in a population that have identical genotypes (Waits et al., 2001). Polymorphic information content (PIC) is defined as the probability that one could identify which homologue of a given parent was transmitted to

a given offspring, the other parent being genotyped as well (Botstein et al., 1980). This value is often used to determine the informativeness of a genetic marker for linkage studies (Guo and Elston, 1999). The PIC value of a locus ranges from 0 (monomorphic) to 1, the latter indicating a highly informative locus. PIC is calculated by the formula

$$PIC = 1 - \sum_i p_i^2 - \sum_{i=1} \sum_{j=i+1} 2p_i^2 p_j^2 \text{ where } p_i \text{ is the frequency of } i^{th} \text{ allele. Genetic distance}$$

among genotypes is calculated as $1 - [\text{proportion of shared alleles}]$ (Bowcock et al., 1994) and a corresponding phenogram can be drawn using the UPGMA (unweighted pair-group method using arithmetic averages) algorithm based on the cluster analysis of the distance data. The proportion of shared alleles method makes no assumption about the populations under study or the frequency of alleles in the population and it does not imply evolutionary divergence. Phenograms are branching phylogenetic diagrams that link entities by estimates of overall similarity. They can be created by different software programs such as TreeView (Page, 1996), PHYLIP CONSENSE (Felsenstein, 1989) and Mega3 (Kumar et al., 2004). Phenograms can be created using one of two different scales, either time or evolutionary divergence. Trees with a time scale are based on some form of physical data, such as a fossil record, that provide dating information. However, more often, the scale used in phylogenetic studies is evolutionary divergence, a measure of change among genotypes. Branches of the phenogram represent the phylogenetic pathway and genetic distance among genotypes and the length of each branch is determined by the scale in horizontal (or vertical) distance.

Linkage Map Construction by the Double Pseudo-testcross Strategy

Mapping and sequencing of plant genomes could provide a better understanding of gene function, gene regulation and expression. Marker-saturated high-density linkage maps have useful applications in both fundamental and applied genetic research. Molecular markers are extensively used in identification and isolation of genes of interest, and linkage analysis is one of the basic and central techniques in genetics. Linkage can define the genetic distances between polymorphic traits which may be expressed as differences in appearance of enzyme activities, restriction fragment lengths or nucleotide sequences at an allelic locus (Mohan et al., 1997). In the past few years linkage maps have been constructed for woody perennial plants like *Citrus* (Sankar and Moore, 2001), *Prunus* (Joobeur et al., 1998), cacao (Pugh et al., 2004), apple (Hemmat et al., 1994; Liebhard et al., 2003), grape (Dalbo et al., 2000, Fischer et al., 2004; Riaz et al., 2004), coniferous forest trees (Scott et al., 1999), and olive (Wu et al., 2004). Among the nut crops, linkage maps have been constructed for European hazelnut (Mehlenbacher et al., 2005), European chestnut (*Castanea sativa* L.) (Casasoli et al., 2001) and macadamia (Peace et al., 2003).

Marker-assisted selection (MAS) appears to have promise in hastening the development of disease-resistant high-quality cultivars of clonally-propagated crops such as hazelnut. Many clonally propagated tree crops have a long juvenile phase. MAS would allow selection at the seedling stage for traits not expressed until reproductive maturity. Furthermore, in the development of resistant cultivars, it would allow identification of resistant seedlings in the absence of the pathogen (Mehlenbacher, 1995). Construction of

a genetic linkage map is a useful step in identifying markers linked to genes controlling traits of interest, and genetic maps can also be used to identify loci that control quantitative traits (Paterson et al., 1991). Similar to other perennial tree crops, the juvenile period of hazelnut ranges from three to six years, with five years being the median, and genotypes exhibit sporophytic self- incompatibility (Mehlenbacher and Smith, 1992; Mehlenbacher, 1997). These problems are overcome by the 'two-way pseudo-testcross strategy'. This method involves linkage analysis of an F_1 population produced by crossing two highly heterozygous (diploid) parent clones. The first linkage map using this method and PCR-based markers was constructed for *Eucalyptus* (Grattapaglia and Sederoff, 1994). Genetic linkage maps can be constructed using software packages such as MapMaker (Lander et al., 1987), JoinMap (Stam, 1993) or GMendel (Holloway and Knapp, 1994). The two important issues in linkage map construction are locus order and distance. The likelihood odds (LOD) score is the test statistic used to test the hypothesis that there is no linkage against the alternative hypothesis that there is linkage. A LOD score of 3.00 is roughly equal to $P=0.001$. So, if $LOD \geq 3.00$, then it is very likely that two loci are linked (Li et al., 2003). Linkage distances with the highest LOD scores are the best estimates of real linkage distances.

Research Objectives

This research project has two main objectives. The first is to fingerprint 274 accessions of European hazelnut (*Corylus avellana*) representing a wide geographical range using 21 of the simple sequence repeat (SSR) markers recently developed by Bassil et al. (2005) and Boccacci et al. (2005) and to create a phenogram that shows the genetic relationships among them. Of the 274, 70 are suspected duplicate accessions, as they are morphologically identical, but were imported from different collections under different names and 4 are duplicate DNA samples extracted at different times from the same trees. Characterization of European hazelnut accessions by means of SSR markers and comparison of the genotype of each cultivar in the collection will provide an ample opportunity to understand the genetic diversity in hazelnut and help in utilization of available genetics resources of *Corylus avellana*. An understanding of genetic diversity in *C. avellana* will provide information useful in managing germplasm collections, choosing parents for controlled crosses and legally protecting new cultivars.

The second objective is to place 33 SSR markers on the preliminary linkage map constructed by Mehlenbacher et al. (2005) based on RAPD markers to generate a high-resolution linkage map using the 'two-way pseudo-testcross' strategy. The mapping population, a total of 144 seedlings, was generated in 1993 from a controlled cross of two heterozygous selections. The maternal parent, OSU 252.146, is susceptible to eastern filbert blight, while the paternal parent, OSU 414.062, is heterozygous resistant. Because of their ease of use, high information content and co-dominant nature, SSR markers are valuable additions to dominant markers and RFLP markers in mapping projects (Dib et

al., 1996). Placement of these SSR markers on the hazelnut linkage map would allow them to serve as “anchor loci”.

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CHAPTER 2

CHARACTERIZATION OF EUROPEAN HAZELNUT (*Corylus avellana*) CULTIVARS USING SSR MARKERS

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Abstract

Twenty-one pairs of simple sequence repeat (SSR) primers were used to investigate genetic diversity in 270 accessions of European hazelnut (*Corylus avellana*) representing a wide geographic range. A capillary electrophoresis system and ABI Genescan® and Genotyper® software were used to determine the allele sizes generated from each PCR reaction based on an internal lane standard. A total of 211 alleles were amplified and the number of alleles detected ranged from 5 to 15 per locus with an average of 10.05. The observed heterozygosity (H_o) for individual loci ranged from 0.24 to 0.88, with an average of 0.67 over all loci. PowerMarker software was used to generate a genetic similarity matrix based on possible pair-wise combinations of accessions using the “proportion of shared alleles”. UPGMA cluster analysis was used to construct a phenogram from the genetic similarity matrix using PowerMarker and MEGA3 software. The phenogram revealed geographically tight clusters and some synonyms among European hazelnut cultivars. Of the 270 cultivars in the population, 200 had unique fingerprints while 70 were duplicates, as suspected based on identical morphology. Of the 211 total alleles amplified, 22 were unique, as they were detected only in one cultivar. Nine of the unique alleles were amplified in cultivars that fell outside of the tightly clustered cultivar groups.

Introduction

The European hazelnut, *Corylus avellana* L., is grown in many regions of Europe and western Asia and has been used as a food source by humans since prehistoric times. *Corylus avellana*, the species of commerce, is native to Europe and Asia Minor and it naturally grows in temperate regions of the Northern Hemisphere from the Atlantic coast of Europe as far north as Norway. The northern boundary includes the British Isles, Scandinavia and northern regions of the Russian Federation. The distribution is bounded in the east by the Ural Mountains. The southern boundary extends from Spain, Morocco and Algeria in the west through Italy, Yugoslavia, Greece, and Turkey to northwestern Iran and Transcaucasia. Although hazelnut is produced in a few regions in the southern hemisphere, it is not native to those regions (Kasapligil, 1972).

Hazelnut-producing regions have mild, moist winters and cool summers. The major production areas are located near large bodies of water at middle latitudes in the northern hemisphere. Approximately 70% of the world's hazelnut production comes from the Black Sea region of Turkey. Italy follows Turkey with about 20% of world production. The United States, Spain, France, Georgia, Azerbaijan and France account for the remaining 10%. The moderate climate of coastal valleys in the Pacific Northwest is well-suited to hazelnut production. Approximately 99% of the U.S. hazelnut crop is produced in Oregon's Willamette Valley. The Pacific Northwest represents 3 to 5 percent of world hazelnut production (FAO Production Year Book, 2004; Hazelnut Marketing Board, 2004).

Hazelnut is a general name used for the nuts of all *Corylus* species. Hazelnut is clonally propagated and a highly heterozygous tree (Mehlenbacher, 1995). It has a unique floral biology, which was reviewed in detail by Germain (1994). It is monoecious, dichogamous and wind-pollinated (Thompson et al., 1996). The male flowers are borne in catkins, and female inflorescences have no perianth. They appear as a tuft of red stigmatic styles protruding from the apex of compound buds located on shoots or catkin peduncles. The hazelnut tree is self-incompatible, which enforces cross-pollination. Incompatibility is of the sporophytic type, and is under the control of a single locus (the S-locus) with multiple alleles (Mehlenbacher, 1997). If the same allele is expressed in both pollen and pistil, pollen germination is delayed and pollen tubes fail to penetrate the stigmatic surface (Hampson et al., 1993).

Traditional techniques used for correct identification of cultivars and clones are based on morphological characters. However, these techniques are not always useful due to environmental variations (Marinoni et al. 2003). Recently, different DNA-based molecular tools were developed that detect polymorphism and offer a reliable system to characterize plant material based on differences in the genetic material independent of environmental effects. Hence, DNA markers have been used in many different commercial and scientific applications such as marker-assisted selection, confirmation of parent-progeny relationships, taxonomic studies, population genetic analysis, linkage map construction, “fingerprinting” for enforcement of legal protection, quality control in plant production (i.e. trueness to name) and processing and labeling of plant-derived foods and other products.

Among the various DNA-based molecular markers, microsatellites have become the marker of choice because of their advantages over other marker systems. Microsatellites or simple sequence repeats (SSRs) are tandemly repeated 1-6 bp sequence motifs found in both eukaryotic and prokaryotic genomes. They are abundant and dispersed throughout the genome and can be found in both coding and non-coding regions. However, they are more abundant in the latter since non-coding DNA can accumulate mutations more easily than coding DNA (Ahmad et al., 2003). Although the exact mechanism of microsatellite evolution is not clear, it appears most likely due to the slippage of DNA polymerase during DNA replication or unequal crossing-over between homologous chromosomes during meiosis (Schlötterer and Tautz, 1992). In non-coding regions of the genome the most abundant class of microsatellites contains dinucleotide repeats (Li et al., 2002). On the other hand, microsatellites found in coding regions of *Arabidopsis*, especially in the 5' Untranslated Region (5'UTR) are mainly trinucleotide and hexanucleotide repeats, probably due to negative selection against frameshift mutations in coding regions (Morgante et al., 2002).

Microsatellite markers have been extensively used in fingerprinting (Thomas et al., 1993), linkage map construction (Bowcock et al., 1994; Hazan et al., 1992), forensic DNA research, and population genetic studies (Jarne and Lagoda, 1996). Valuable characteristics of SSR markers include high polymorphism, co-dominance, sensitivity (even a small quantity of DNA can be amplified by PCR), conservation in related species, reproducibility and ease of data scoring. The exchange of primer sequences instead of probes allows other labs to work with the same loci. The only disadvantages of

microsatellite markers are that they must be isolated *de novo* from most species being examined for the first time and considerable investment and technical expertise are required for their initial development (Zane et al., 2002; Jauhar, 1996).

In recent years microsatellites have been successfully used in various genetic applications such as cultivar identification and breeding record verification of apple (*Malus x domestica*) (Cabe et al., 2005) and pistachio (*Pistacia vera* L.) (Ahmad et al., 2003); phylogenetic analysis of almond (*Prunus dulcis* Mill.) (Xu et al., 2004) and grape (*Vitis vinifera* L.) (Fatahi et al., 2003); and evaluation of genetic diversity relationships in fruit crops such as kiwifruit cultivars (*Actinidia deliciosa* A.Chev.) (Zhen et al., 2004), apricot (*Prunus armeniaca* L.) (Romero et al., 2003) and peach (*Prunus persica* L.) (Aranzana et al., 2002). Microsatellites have also been extensively used for management of fruit germplasm collections in olive (*Olea europaea* L.) (Khadari et al., 2003), grape (Martin et al., 2003; Dangl et al., 2001), cherry (*Prunus avium* L.) (Cantini et al., 2001) and peach (Testolin et al., 2000); in different applications such as determination of parentage of clonal crops such as cherry (Struss et al., 2003) and olive (Contento et al., 2002); identification of potential duplicates in collections of apple (Hokanson et al., 2001) and grape (Dangl et al., 2001), detection of chimeras in grapevines (Franks et al., 2002). Furthermore, microsatellites have also been used in evolutionary studies of cacao (*Theobroma cacao* ssp. *cacao* L.) (Motamayor et al., 2002) and hop (*Humulus lupulus* L.) (Jaksé et al., 2001).

The objective of this study is to use 21 pairs of simple sequence repeat (SSR) primers to investigate genetic diversity in 270 accessions of European hazelnut (*Corylus*

avellana) representing a wide range of geographical regions, and which includes many suspected duplicates. The genotyping or fingerprinting of European hazelnut cultivars provides information important for the management of genetics resources of *Corylus avellana*.

Materials and Methods

Plant material and DNA extraction

Two sets of fresh young leaves for each of 270 accessions of European hazelnut (Table 2.1), representing a wide range of geographical regions, were collected in the spring from the collections of the United States Department of Agriculture-Agriculture Research Service-National Clonal Germplasm Repository (USDA-ARS-NCGR) and Oregon State University in Corvallis, Oregon. DNA was extracted according to Lunde et al. (2000) with minor modifications and RNA was removed by incubation with RNase A (Sigma, St. Louis, MO) at 37 °C for one hour in a shaker, followed by extraction with 25 phenol: 24 chloroform: 1 isoamyl alcohol. The DNA concentrations were determined spectrophotometrically, adjusted to 5 ng/μl and the DNA was stored at -18 °C until used for PCR. A second set of DNA samples was extracted from four trees ('Bard', 'Karidaty', 'Istarski Debeloplodna' and 'Riekchen's Zellernuss') and included as checks.

Amplification and allele sizing

Primer pairs for fourteen loci developed in Corvallis (CAC) (Bassil et al., 2005) and for seven loci in Torino (CaT) (Boccacci et al., 2005) (Table 2.2) were chosen for this study. Reverse primers were purchased from Operon Technologies (Qiagen, Valencia, CA). Forward primers fluorescently labeled with FAM and HEX were purchased from Operon Technologies (Qiagen, Valencia, CA) and with NED from Applied Biosystems (Foster City, CA) and PCR reactions were performed in a total

Table 2.1 European Hazelnut accessions characterized using microsatellite markers.

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557207	N04.39	A Pellicola Bianca	Italy	10	11
PI 617226	N05.11	Acorn Hazel	Poland	5	11
PI 557418	N03.67	Alcover	Italy-Piemonte	15	22
—	Reps 72.02	Alli	Estonia	20	?
PI 617190	W15	Amandi	Spain	10	21
PI 557176	N03.62	Apolda	unknown	10	11
PI 557079	N07.46	Arneson's Rootstock	USA-Oregon	?	?
PI 557108	N03.66	Artellet	Spain	14	18
PI 557422	N02.15	Ata Baba Ganja	Azerbaijan (France)	4	4
PI 557195	N05.41	Atlas	Denmark	1	10
PI 557050	N03.34	Aurea	Germany	6	9
PI 557194	N06.71	Aveline d'Angleterre	France or England	5	16
PI 617174	N06.37	Aveline Rouge	France	5	10
PI 557213	N04.37	Avellana Speciale	Italy	1	2
PI 557122	N05.25	B-3	Macedonia	2	25
PI 557125	N06.44	B-4	Macedonia	10	17
PI 304630	N07.17	Badem	Turkey	2	5
PI 557157	N05.67	Bandnuss	England	10	11
PI 557177	N02.60	Barbarella	Italy	5	10
PI 557037	N02.34	Barcelona	Spain-Tarragona	1	2
PI 557156	N05.71	Barcelonner Zellernuss	England	10	17
PI 557241	N02.26	Bard	England	5	11
—	N04.03	Barrettona	Italy-Lazio	2	6
PI 557181	N06.61	Barrettona (not)	Italy	1	2
PI 557158	N05.70	Barr's Zellernuss	England	5	11
PI 557214	N04.48	Bearn	France	5	11
PI 557239	N02.39	Belle di Giubilino #1	Italy (via Spain)	1	10
—	N04.19	Belle di Giubilino #2	Italy-Campania	1	10
PI 557114	N06.13	Bergeri	Belgium	3	25

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557182	N06.62	Bianca	Italy-Campania	2	?
PI 557084	212.053	Blumberger Zellernuss	Germany	4	20
PI 557131	N01.62	Brixley's New	England	1	15
PI 557031	N04.30	Brixnut	USA-Oregon	1	14
PI 557219	N04.27	Bulgaria XI-8	Bulgaria	4	12
PI 557089	N05.45	Burchardt's Zellernuss	Germany	2	7
PI 557077	N04.18	Butler	USA-Oregon	2	3
PI 557094	N04.21	Buttner's Zellernuss	Germany	11	27
PI 617207	N06.09	C. avellana AL55	Albania	3	?
PI 637867	N06.08	C. avellana COR 627	Sweden	9	?
PI 617181	N03.48	C. multiflorum WIR8884	Turkey/Russia	3	11
PI 296204	N02.14	Camponica	Italy-Campania	1	2
PI 557189	N06.70	Carello	Italy	1	2
PI 557033	N03.18	Casina	Spain-Asturias	10	21
PI 557235	N03.31	Ceret	Spain-Tarragona	2	10
PI 617176	N01.47	Cherkesskii II	Southern Russia	4	24
PI 617268	LB3	Clark	OSU : 'Tombul Ghiaghli' x 'Willamette'	3	8
PI 557109	N06.02	Closca Molla	Spain	2	5
PI 557178	N03.19	Comen	Greece	2	9
PI 557223	N02.37	Comun	Portugal	10	?
PI 557184	N06.60	Comun Aleva	Spain	9	23
PI 557185	N03.60	Comune di Sicilia	Italy	1	2
PI 557049	N01.15	Contorta	England	5	10
PI 557424	N06.05	Corabel	France: Barcelona o.p.	1	3
PI 557039	N06.16	Cosford	England	3	11
PI 617172	N07.43	Cozia	Romania	5	15
PI 557024	N04.20	Creswell	USA-Oregon	2	10
PI 557107	N01.21	Culpla	Spain-Tarragona	9	10
PI 557306	N03.42	Cutleaf	England	20	28

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557224	N01.35	Da Viegá	Portugal	10	21
PI 617240	N04.04	Dal Rosso	Italy	5	18
PI 637876	780.067	D'Algers	Netherlands	1	2
PI 557227	N02.35	Daria (104E)	Italy : 'Tonda Gentile delle Langhe' x 'Cosford'	2	3
PI 557040	N05.20	Daviana	England	3	11
PI 637883	LB8.27	Delta	OSU : 'OSU 249.159' x ('Montebello' x 'Gasaway')	1	15
PI 557423	N03.17	Des Anglais	France	5	19
PI 557145	N05.66	Dowton Long #1 COR 314	England	3	14
PI 557190	N07.66	Dowton Long #2 COR 381	England	9	10
PI 557099	N05.29	DuChilly	England	10	14
PI 557161	N03.71	Early Long Zellernuss	Denmark	20	25
PI 557045	N02.30	Ennis	USA-Washington	1	11
PI 637884	LB11.35	Epsilon	OSU : ('Tonda Romana' x 'Tombul Ghiaghli') x 'Zimmerman'	1	4
PI 557236	N03.39	Espinaredo	Spain	10	21
PI 318463	N06.01	Extra Ghiaghli	Greece	4	12
PI 557080	N03.41	Finland COR 18-7	Finland	?	?
PI 557071	N07.48	Fitzgerald	USA-Oregon	?	?
PI 557032	N03.30	Fitzgerald #20	USA-Oregon	2	11
PI 557205	N04.29	Francoli	Spain-Taragona	17	22
PI 617227	N05.10	Frango #2	Poland	5	11
PI 617228	N05.09	Frango #4	Poland	15	25
PI 617229	N5.08	Frango #5	Poland	11	25
PI 557135	N01.63	Freehusker	USA-Oregon	1	11
PI 557097	N07.34	Frizzled Filbert	England	9	10
PI 557238	N01.37	Fructo Albo	France	5	10
PI 557208	N04.45	Fruttogrosso	Italy	10	18
PI 557047	N01.36	Fusco Rubra	Germany	6	19
PI 637882	LB10.11	Gamma	OSU : 'Casina' x ('Riccia di Talanico' x 'Gasaway')	2	10
PI 634202	754.001	Ganja	Azerbaijan (via Georgia)	4	4

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557162	N04.69	Garibaldi	England	5	11
PI 557165	N06.03	Garrofi	Spain	1	6
PI 557042	N02.27	Gasaway	USA-Washington	3	26
PI 557029	N01.22	Gem	USA-Oregon	2	14
PI 557115	N05.17	Ghirara	Italy-Sicily	2	21
PI 270339	N04.71	Gironenc Coldejou	Spain	9	23
PI 270339	N03.25	Gironenc Vermellet	Spain-Taragona	2	17
PI 617230	N05.07	Goc	Poland	6	15
PI 617189	V06	Grande	Spain	1	2
PI 557202	N02.43	Grifoll	Spain-Tarragona	2	22
PI 557148	N04.60	Gubener Barcelloner	Germany	1	23
—	759.016	Gulshishvela (not)	Georgia	4	20
PI 557191	N07.70	Gunslebert	Germany	5	23
PI 557085	N06.51	Gustav's Zellernuss	Germany	15	20
PI 557027	N04.64	Hall's Giant	Germany	5	15
PI 557427	N02.55	Henneman #3	USA-Oregon	6	10
PI 557196	N01.54	Heynick's Zellernuss	Germany	15	20
—	753.001	Hodji (not)	Georgia	14	?
PI 557183	N07.63	Iannusa Racinante	Italy-Sicily	1	8
PI 271105	N01.17	Imp. de Trebizonde #1	Turkey	2	10
PI 211105	N03.49	Imp. de Trebizonde #2	Turkey	2	10
PI 557051	N07.69	Imperatrice Eugenie	France	3	14
PI 557209	N04.23	Istarski Debeloplodna	Croatia	5	10
PI 557210	N04.25	Istarski Okrogloplodna	Slovenia	10	18
PI 557400	N05.27	Istrski Duguljasti	Macedonia	10	17
PI 557034	N01.32	Italian Red	Germany	15	20
PI 557116	N05.31	Jean's	Italy	2	10
PI 557169	N05.64	Jeeve's Samling	England	12	20
PI 557090	N04.62	Kadetten Zellernuss	Germany	20	25

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557240	N06.11	Kalinkara	Turkey	4	21
PI 271105	N03.37	Karidaty	Turkey	2	10
PI 617231	N05.06	Karol	Poland	11	15
PI 617180	V9a	Kerasund Dlinnyi	Russia	8	10
PI 557197	N02.51	Korthaset Zellernuss	Denmark	10	14
PI 557030	N01.34	Kruse	USA-Oregon	1	2
PI 617177	N02.54	Kudryavchik	Russia	4	14
—	755.001	Kudryavchik (not)	Russia	4	14
PI 557170	N05.69	Kunzemuller's Zellernuss	Germany	12	20
PI 557153	N05.68	Lange Landsberger	Germany	15	20
PI 617232	N05.05	Lech	Poland	5	15
PI 617233	N05.04	Lenka #3	Poland	3	5
PI 617234	N05.03	Lenka #4	Poland	11	15
PI 617210	LB1	Lewis	OSU : ('Barcelona' x 'Tombul Ghiaghli') x 'Willamette'	3	8
PI 557147	N04.61	Liegel's Zellernuss	Germany	12	20
PI 617235	N05.02	Little Poland	Poland	3	5
PI 557168	N03.69	Lluenta	Spain-Tarragona	17	22
PI 557186	N06.69	Locale di Piazza Armerina	Italy	1	2
PI 557086	N03.52	Louisen's Zellernuss	Germany	10	25
PI 557091	N04.63	Ludolph's Zellernuss	Germany	5	20
PI 557136	N06.19	Lyons	USA-Oregon	2	14
PI 557137	N07.59	Macrocarpa	Germany	1	2
PI 557174	N06.65	Mansa	Italy	1	2
PI 617236	N05.01	Maria	Poland	11	15
PI 557203	N05.53	Martorella	Spain-Taragona	17	22
—	W21	Mincane	Turkey-Akçakoca	4	10
PI 557215	N04.31	Minnolara	Italy	1	2
PI 557093	N05.62	Mogulnuss	England	5	25
PI 557225	N03.29	Molar	Portugal	2	10

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557028	N01.20	Montebello	Italy-Sicily	1	2
PI 270338	N02.36	Morell	Spain-Tarragona	1	2
PI 339723	N01.59	Mortarella	Italy-Campania	2	17
PI 557152	N04.67	Multiflora	England	3	11
PI 557188	N03.61	Napoletana	Italy-Campania	1	23
PI 557216	N01.14	Napoletanedda	Italy-Campania	2	14
PI 270340	N03.14	Negret	Spain-Tarragona	10	22
—	756.003	Nemsa (not)	Georgia	4	14
PI 271278	N04.26	Neue Riesennuss	Germany	18	25
PI 557138	N07.37	Nixon	USA-Oregon	2	3
PI 557179	N06.67	Nocchiolino Sangrato	Italy-Piemonte	7	17
PI 557180	N06.66	Nocchione	Italy	1	2
PI 557139	N01.65	Noce Lunga	Italy	10	17
PI 557193	N06.63	Nociara	Italy-Sicily	1	3
PI 557038	N01.18	Nonpareil	USA-Oregon	1	3
PI 557259	N04.16	Nooksack	USA-Washington	6	14
PI 557172	N03.63	Nostrale	Italy	1	2
PI 557140	N01.66	Nottingham	England	8	10
PI 637875	780.076	Obrovsky Novy	Slovakia	12	20
PI 557417	N06.64	Ordu	Turkey	4	25
PI 304632	N03.27	Palaz	Turkey	2	4
PI 557187	N06.68	Pallagrossa	Italy-Piemonte	5	25
PI 557119	N02.17	Pauetet	Spain-Tarragona	18	22
PI 557211	N04.33	Payrone	Italy	10	18
PI 557159	N04.70	Pearson's Prolific	England	8	10
PI 271110	N06.20	Pell. Rouge	France	5	10
PI 557048	USDA Shop	Pendula	England	3	9
PI 557164	N04.15	Pere Mas	Spain	9	10
PI 617192	N02.40	Petoka (not)	England	3	11

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557163	N02.25	Pinyolenc #1 COR 339	Spain	2	?
—	212.052	Pinyolenc #1b	Spain	2	?
—	N07.03	Pinyolenc #2	Spain-Tarragona	2	17
—	W10b	Pinyolenc #2b	Spain-Taragona	2	17
PI 617178	V14	Pioneer	Ukraine	2	4
PI 557204	N06.04	Planeta	Spain-Tarragona	1	2
PI 557155	N04.66	Princess Royal	England	11	14
PI 557154	N05.60	Prolific Closehead	England	5	11
PI 557150	N05.63	Prolifique a Coque Serrée	France	3	11
PI 637873	780.072	Pruhovany	Slovakia	3	11
PI 557105	N06.55	Punxenc	Spain	1	10
PI 637909	GH	Purple Aveline	France	5	10
PI 617183	N05.12	Purple Fortrin	USA-Washington	5	10
PI 557128	W16	Quiros	Spain	10	21
PI 557217	N04.35	Racinante clone G	Italy	1	2
PI 557201	N07.57	Ratlada	Spain-Tarragona	10	22
PI 557167	N03.70	Ratoli	Spain-Tarragona	2	10
PI 557098	N05.43	Red Filbert	England	11	14
PI 557098	N05.13	Red Fortrin	USA- Washington	2	6
PI 557129	N01.23	Restiello	Spain-Tarragona	10	22
PI 557055	N05.33	Ribet	Spain-Tarragona	2	16
PI 339725	N03.26	Riccia di Talanico	Italy-Campania	1	2
PI 557199	N04.17	Riekchen's Zellernuss	Germany/Denmark	5	25
PI 637874	780.065	Rimsky	Slovakia	10	25
PI 271280	N07.11	Rode Zeller	Netherlands	6	11
PI 557233	N02.62	Romai		10	18
PI 617173	N05.23	Romavel	Romania	2	?
PI 557171	N05.65	Romische Nuss	unknown	10	18
PI 557112	W09	Ros de la Selva	Spain	2	9

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557113	N07.68	Rosetta	Spain	2	6
PI 557113	N07.29	Rosset de Valls	Spain	14	18
PI 557052	N04.52	Royal	USA-Oregon	1	3
PI 557390	N01.55	Ruby	USA-Oregon : 'Chinese Trazel G-4' x 'Fusco Rubra'	11	19
PI 557044	N02.20	Ryan	USA-Oregon	1	?
PI 557401	N03.65	San Benedetto		4	12
PI 557117	N01.29	San Giovanni	Italy-Campania	2	8
PI 557103	N03.50	Sant Jaume	Spain-Tarragona	1	17
—	N03.21	Sant Joan	Spain	2	25
PI 55 7120	N07.19	Sant Pere	Spain-Tarragona	22	26
PI 557046	N01.16	Segorbe	Spain	9	23
	780.059	Shokoladny	Ukraine	4	11
PI 557175	N03.68	Siciliana	Italy	1	2
PI 557151	N05.61	Sickler's Zellernuss	Germany	5	20
PI 557166	N01.25	Simon	Spain-Tarragona	6	22
PI 304633	N07.47	Sivri Ghiaghli	Turkey-Greece	4	12
—	759.025	Sivri Ocak 5	Turkey	8	10
PI 617175	Reps 57.33	Skorspelka	Russia	4	23
PI 617175	780.063	Syrena	Poland	6	15
PI 617239	780.044	Tapparona di San Colombano Cortemoli	Italy-Liguria	2	24
PI 557149	N02.47	The Shah	England	14	30
PI 637908	Reps 58.32	Tokolyi Cosford	Australia	5	23
PI 557200	N05.19	Tomasina	Spain-Tarragona	17	22
PI 318463	W22	Tombul	Turkey-Akçakoca	4	10
PI 304634	N03.32	Tombul Ghiaghli	Turkey-Greece	4	8
—	759.043	Tombul Ocak 1	Turkey	4	12
PI 296206	N07.62	Tonda Bianca	Italy-Campania	1	23
PI 296207	N01.24	Tonda di Giffoni	Italy-Campania	2	23

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557075	N05.58	Tonda Gentile d. Langhe COR114	Italy-Piemonte	2	7
PI 557025	N02.18	Tonda Romana	Italy-Viterbo	10	20
PI 557118	N02.21	Tonda Rossa	Italy-Campania	8	23
PI 557218	N03.45	Tonnolella	Italy	2	24
PI 557110	N07.23	Trenet	Spain-Tarragona	2	15
PI 557087	N04.65	Truchsess' Zellernuss	Germany	5	25
—	759.007	Tskhenis Dzudzu (not)	Georgia	4	20
PI 557245	N01.68	Turk	USA-Oregon	1	2
PI 557100	N06.58	Ugbrooke	New Zealand	5	9
—	V13	Unknown #3	unknown	4	8
PI 617171	N07.31	Vilcea 22	Romania	2	10
PI 617238	N04.06	Volski Round	Poland	5	11
PI 557144	N07.39	Wanliss Pride	Australia	2	10
—	N07.06	Warsaw Red	Poland	1	6
PI 557160	N04.68	Webb's Prize Cob	England	17	?
PI 557080	N02.50	White Filbert	France	5	10
PI 557101	N04.43	Whiteheart	New Zealand	2	10
PI 557234	N02.71	Willamette	OSU : 'Montebello' x 'Compton'	1	3
PI 557026	N03.22	Woodford	USA-Oregon	1	3
PI 637885	LB11.40	Zeta	OSU : 'OSU 342.019' x 'Zimmerman'	1	1
—	LB 8.40	Zimmerman	USA-Oregon	1	3
PI 323961	N07.60	26.072	Russia-North Caucasus	2	6
PI 557057	N06.18	54.021	Turkey-Giresun	4	5
PI 557060	N06.24	54.039	Turkey-Giresun	8	12
PI 557061	N06.46	54.041	Turkey-Giresun	4	24
PI 557066	N06.22	54.056	Turkey-Giresun	2	5
PI 617266	N05.40	408.040	University of Minnesota	15	20
PI 557421	Reps 46.02	495.049	Southern Russia	22	29

Table 2.1 Continued

Accession #	Location	Cultivar	Origin or Pedigree	S-Alleles	
PI 557421	N06.53	495.072	Southern Russia	6	?
PI 637878	N06.07	556.019	Turkey-Istanbul	8	17
PI 617269	Reps52.35	556.027	Turkey-Istanbul	8	18
—	Reps50.34	622.051	Turkey-Ray Clark	4	25
CCOR 783	LB12.16	681.074	Turkey-Akçakoca	4	12
PI 634203	Reps 63.15	681.078	Russia-Moscow	1	14
CCOR 785	LB12.18	686.124	Turkey-Giresun	10	12
CCOR 792	LB12.25	693.073	Turkey-Giresun	4	10
—	LB12.27	693.117	Turkey-Yomra	4	14
CCOR 799	LB12.32	702.041	Turkey-Yomra	4	8
—	LB12.33	717.087	Turkey-Akçakoca	4	16

Table 2.2 Description of 21 microsatellite loci: the repeat motif, sequence of the fluorescent forward primer (*FAM*, *NED*, *HEX*) and the reverse primer (*R*), the optimum annealing temperature (T_m), dilution cofactor in multiplex, allele size range, and linkage group^e

SSR Locus	Motif	Primers (5' – 3')	T _m	Dilution	Allele Size Range (nt)	Linkage Gr ^e
CAC-A014a	(CA) ₁₃	<i>FAM</i> -GGTTTGTACAGAAATTCAGACG <i>R</i> -GCGTGTGGTTAATGTTTTCTTT	60°C	1:640	203-251	5S, 5R
CAC-A040	(CA) ₁₃	<i>NED</i> -TGCTCAAGCAAATATTGCAC <i>R</i> -GTTTGGGATCCAATTAACCCTCT	62°C	1:213	234-248	1S, 1R
CAC-B005	(GA) ₂₂	<i>FAM</i> -CAAACCTTATGATAGGCATGCAA <i>R</i> -TGTCACCTTTGGAAGACAAGAGA	62°C	1:320	277-297	7R
CAC-B010	(GA) ₁₆	<i>FAM</i> -AGCTTCCAAATCACACATTACC <i>R</i> -GAAGAGCATCCGTATGATTGAG	62°C	1:320	211-227	3S, 3R
CAC-B028	(AG) ₁₆	<i>NED</i> -ATGGACGAGGAATATTTTCAGC <i>R</i> -CCTGTTTCTCTTTGTTTTTCGAG	55°C	1:213	252-288	5S, 5R
CAC-B029b	(GA) ₁₃	<i>NED</i> -CAATTTACACCTCAGGGAAGAG <i>R</i> -AAGTTCACCCAAGAAATCCAC	58°C	1:160	114-139	1S, 1R
CAC-B105	(GA) ₁₆	<i>HEX</i> -AAAGGAGCAAGCATGTTAGG <i>R</i> -GTTTGTACGGATGATCCACTGAG	62°C	1:320	125-163	10S, 10R
CAC-B111	(GA) ₁₃	<i>FAM</i> -GAAGGAGAAACAAGGGTAGTCA <i>R</i> -AGAAGCGTCGTTCCATAGC	64°C	1:320	170-192	N/A
CAC-C010	(GAA) ^a	<i>NED</i> -GGAGCCACCATGAAATTATACA <i>R</i> -CACTTATTGCGATTGGTTCA	58°C	1:320	272-319	N/A

Table 2.2 Continued

SSR Locus	Motif	Primers (5' – 3')	Tm	Dilution	Allele Size Range (nt)	Linkage Gr ^e
CAC-C028	(GAA) ₁₀	<i>NED</i> -CTACCCCATCGCTTGACAC <i>R</i> -GGAGACTTGTTTGCCACAGA	60°C	1:213	131-147	10R
CAC-C040	(GAA) ₈ (GGA) ₅	<i>FAM</i> -AGCCCCATTAGCCTTCTTAG <i>R</i> -GTTTCCAGATCTGCCTCCATATAAT	62°C	1:320	168-192	4R
CAC-C115	(TAA) ₅ (GAA) ₁₂	<i>FAM</i> -CATTTTCCGCAGATAATACAGG <i>R</i> -GTTTCCAGATCTGCCTCCATATAAT	60°C	1:320	167-225	4S, 4R
CAC-C118	(AAG) ^b	<i>HEX</i> -AGCAACAGAGGTTAGGTGTG <i>R</i> -GCCCCATTAGCCTTCTTA	60°C	1:320	162-185	4R
CAC-C119	(GA) ₇ (GA) ₉	<i>NED</i> -CTCACCTTTACCCCTTCATTTT <i>R</i> -GTTTCCTCATCTTCTGAGAACCATC	62°C	1:213	256-264	8R
CaT-B107	(CT) ₁₄	<i>NED</i> -GTAGGTGCACTTGATGTGCTTTAC <i>R</i> -AACACCATATTGAGTCTTTCAAAGC	58°C	1:160	112-151	10R
CaT-B502	(CT) ^c	<i>FAM</i> -CTCATGACTGCCCATTTCTCG <i>R</i> -AGGCATGCAGGCTTCACAC	62°C	1:400	183-211	10S, 10R
CaT-B504	(CT) ₁₈	<i>HEX</i> -CGCCATCTCCATTTCCCAAC <i>R</i> -CGGAATGGTTTTCTGCTTCAG	60°C	1:400	158-184	7R
CaT-B505	(CT) ₁₇ CC(CT) ₂	<i>NED</i> -AGAGAACGACTTTGTATGACAAAGA <i>R</i> -TTGAACCATTAATAACATCATGTGA	58°C	1:213	106-139	N/A

Table 2.2 Continued

SSR Locus	Motif	Primers (5' – 3')	Tm	Dilution	Allele Size Range (nt)	Linkage Gr ^e
CaT-B507	(GA) ^d	FAM -CTA AGCTCACCAAGAGGAAGTTGAT R -GCTTCTGGGTCTCCTGCTCA	62°C	1:400	176-198	9S, 9R
CaT-B508	(GA) ₁₀	HEX -GGGTCAAGATTTGATAAAGTGGGA R -GCACTCCACTTGTGCGTTTTTC	62°C	1:213	142-167	N/A
CaT-C504	(CTT) ₂ T(CTT) ₈	HEX -GGTCTCCTTCGCTAACATAACCAA R -GTTGCCCTCGAGTTGTAGTA	62°C	1:400	152-173	N/A

^a (GAA)₇GGA(GAA)₂N₂₁(GAA)₂ATT(GAA)₄N₁₅(GAA)₃

^b (AAG)₃(GAA)₃(AAG)₈N₆(AAG)₄

^c GA)₁GC(GA)₂GC(GA)₁₄

^d (CT)₁₆GCTTTTC(CT)₅

^e Chapter 3 (Figure 3.1)

N/A: linkage group not assigned

volume of 10 μ l. The reaction mixture contained 1X Biolase NH_4 reaction buffer, 2 mM MgCl_2 , 200 μ M each of dATP, dCTP, dGTP, and dTTP, 0.3 μ M each of forward and reverse primers, 0.25 units of Biolase DNA polymerase (Biolase Inc., Randolph, MA), and 2.5 ng of template DNA. The PCR program consisted of 35 cycles of a 40 s denaturation step at 94 °C, a 40 s annealing step at the optimum annealing temperature (Table 2.2), and a 40 s extension step at 72 °C. Finally one 30-min extension step at 72 °C was run to maximize non-templated adenosine addition to the 5' ends. PCRs were carried out in Perkin-Elmer model 9700 thermocyclers (PE Applied Biosystems, Foster City, CA). PCR amplification and approximate fragment sizes were confirmed by agarose (3%) gel electrophoresis using 4 μ l of aliquot and 5 μ l of loading dye (15% Ficoll® 400, 0.03% xylene cyanol FF, 0.4% orange G, 10 mM Tris-HCL pH 7.5, and 50 mM EDTA). Gels were stained with ethidium bromide and photographed under UV-light by an imaging system (UVP, Upland, CA). Amplified PCR products were diluted forty times with nanopure water and kept as stock for multiplexing. Stock solutions were further diluted 2 to 16 times (Table 2.2) and 1 μ l of a mix of three to four PCR products (Appendix A) were separated on an ABI 3100 capillary electrophoresis instrument (Applied Biosystems, Foster City, California) at the OSU Central Services Laboratory (CSL), and DNA fragments were sized using GeneScan and Genotyper software.

Data Analysis

The programs *IDENTITY 1.0* (Wagner and Sefc, 1999), *PowerMarker 3.2* (Liu and Muse, 2004) and *Mega3* (Kumar et al., 2004) were used to analyze the data. The number of alleles, allele frequencies, observed heterozygosity (H_o), expected

heterozygosity (H_e), probability of identity (PI) and paternity exclusion probability (PEP) (Paetkau et al., 1995; Weir, 1996) were calculated by *IDENTITY 1.0. PowerMarker 3.2* software was used to estimate the polymorphic information content (PIC). The statistical analysis was carried out twice, both with and without duplicate accessions. The statistical summary (Table 2.4) of 21 SSR loci based on 200 unique accessions is presented in this chapter. A similar table including all 274 accessions is presented in the Appendix B.

Observed heterozygosity (H_o) is the proportion of individuals in a population that is heterozygous at a given locus. On the other hand, the expected heterozygosity (H_e) was defined as the proportion of individuals that are prospective heterozygotes based on the allele frequencies and assuming Hardy-Weinberg equilibrium. The expected heterozygosity was calculated by the formula $H_e = 1 - \sum p_i^2$, where p_i is the frequency of the i^{th} allele (Nei, 1973). The null allele frequency was calculated according to the formula of Brookfield (1996): $r = (H_e - H_o)/(1 + H_e)$. Probability of identity (PI) is the probability of randomly choosing two individuals in a population that have identical genotypes (Waits et al., 2001). Polymorphic information content (PIC) is defined as the probability that one could identify which homologue of a given parent was transmitted to a given offspring, the other parent being genotyped as well (Botstein et al., 1980). This value is often used to determine the informativeness of a genetic marker for linkage studies (Guo and Elston, 1999). The PIC value of a locus ranges from 0 (monomorphic) to 1, the latter indicating a highly informative locus. PIC is calculated by the formula

$$PIC = 1 - \sum_i p_i^2 - \sum_{i=1} \sum_{j=i+1} 2p_i^2 p_j^2 \text{ where } p_i \text{ and } p_j \text{ are the frequencies of the } i^{th} \text{ and } j^{th}$$

alleles. Genetic similarities between genotypes were calculated using the “proportion of

shared alleles” estimator (P_s) of Bowcock et al. (1994) and the genetic distance (D_{ps}) between pairs of cultivars was calculated as $(1-P_s)$. Cluster analysis of the distance data used the UPGMA (unweighted pair-group method using arithmetic averages) method and resulted in a phenogram that depicted the genetic relationships among the accessions (Nei, 1973). An UPGMA tree was constructed from the genetic similarity matrix using *Mega3* (Kumar et al., 2004) and *Power Marker 3.2* software. Clusters on the UPGMA tree were further analyzed by creating a consensus tree produced from 1000 UPGMA trees from mean genetic distance (D_{ps}) and bootstrap values. Finally self-incompatibility alleles (Table 2.1) and phenotypic characters such as nut size, nut shape and husk length (Appendix C) were compared to confirm the results.

Results and Discussion

Genetic diversity

DNA of all genotypes was successfully amplified by all 21 SSR primer pairs and the fragment sizes were determined (Appendix D). All SSR loci were polymorphic. Of the 270 accessions, 200 showed unique fingerprinting. A total of 211 alleles were amplified and the number of alleles per locus ranged from 5 (for loci CAC-C010, CAC-C040, CAC-C119 and CAC-C118) to 15 (for loci CAC-B028, CAC-B105 and CaT-B107) with an average of 10.05 for the 21 loci. The number of alleles per locus varied according to the type of microsatellite repeat. The average number of alleles per locus for dinucleotide SSRs (11.27) was higher than for trinucleotide SSRs (7.00). The allele with the highest frequency (0.845) was 186 bp at locus CAC-C040 (Table 2.3 and Fig 2.1). The low number of alleles at some of the loci cannot be attributed to few genotypes, because a large number of genotypes were used in this study. Twenty-two of 211 alleles were unique, as they were detected only in one cultivar. Three unique alleles were found in 'Ruby' and '495.049', which are the most diverse cultivars in the population, while 'Blumberger' has two unique alleles.

The PIC values ranged from 0.26 to 0.85 with an average of 0.68. The three most polymorphic loci were CaT-B107, CaT-B507 and CAC-B028 with PIC values of 0.85, 0.82 and 0.82 respectively. The three least polymorphic loci were CAC-C040, CAC-C118 and CAC-C119 with PIC values of 0.26, 0.28 and 0.50, respectively (Table 2.3).

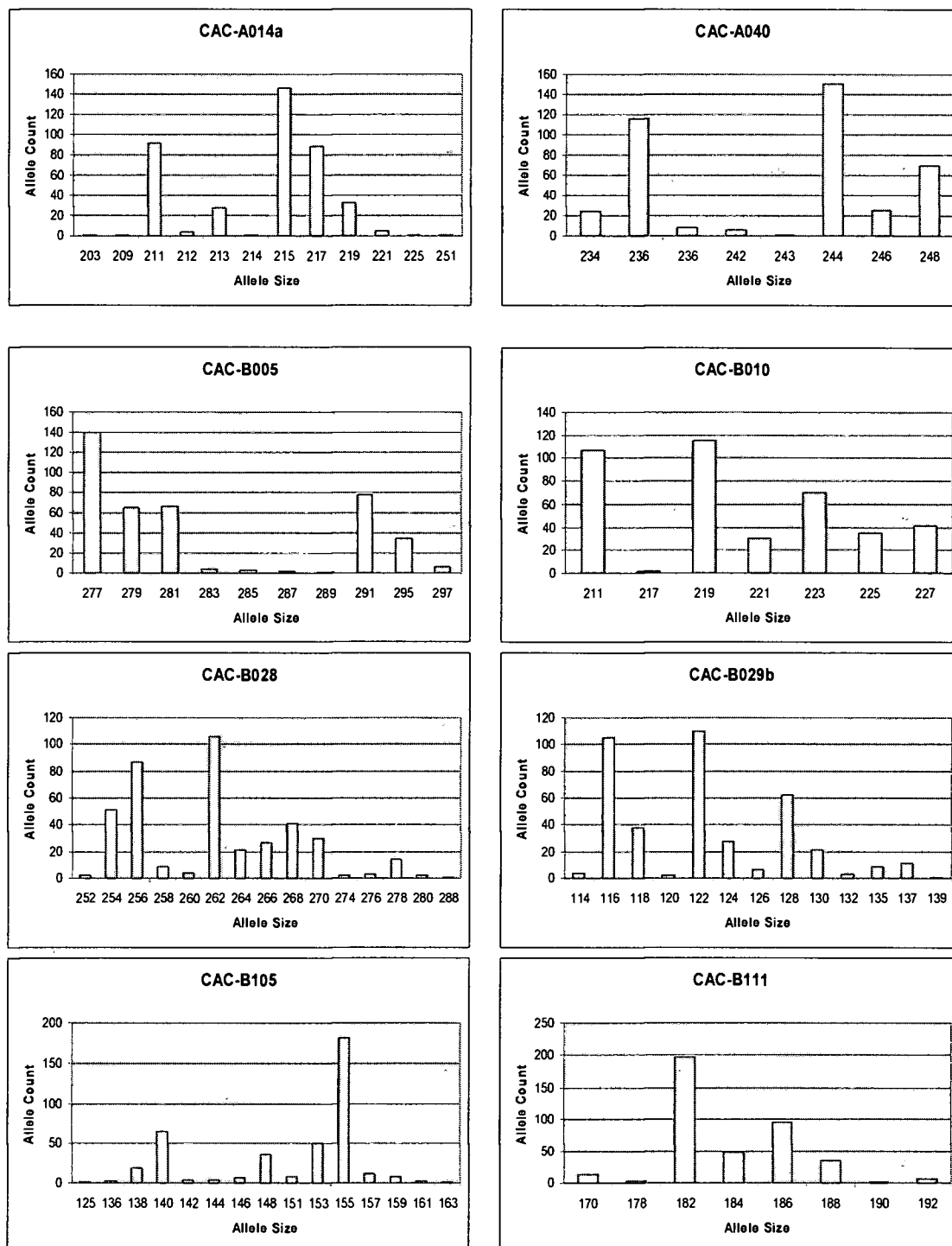


Figure 2.1 Allele frequencies at twenty-one SSR loci in 200 unique European hazelnut cultivars

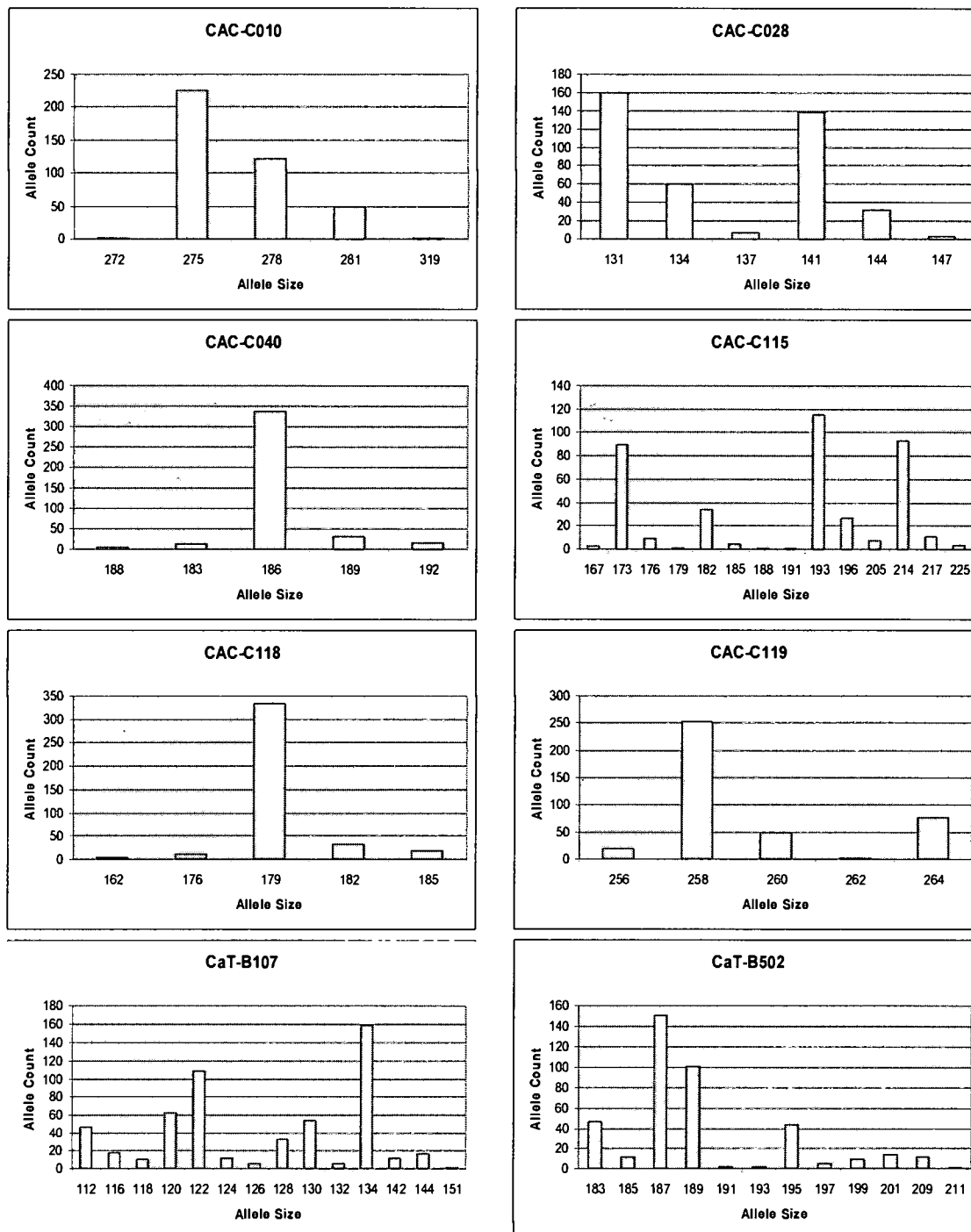


Figure 2.1 Continued

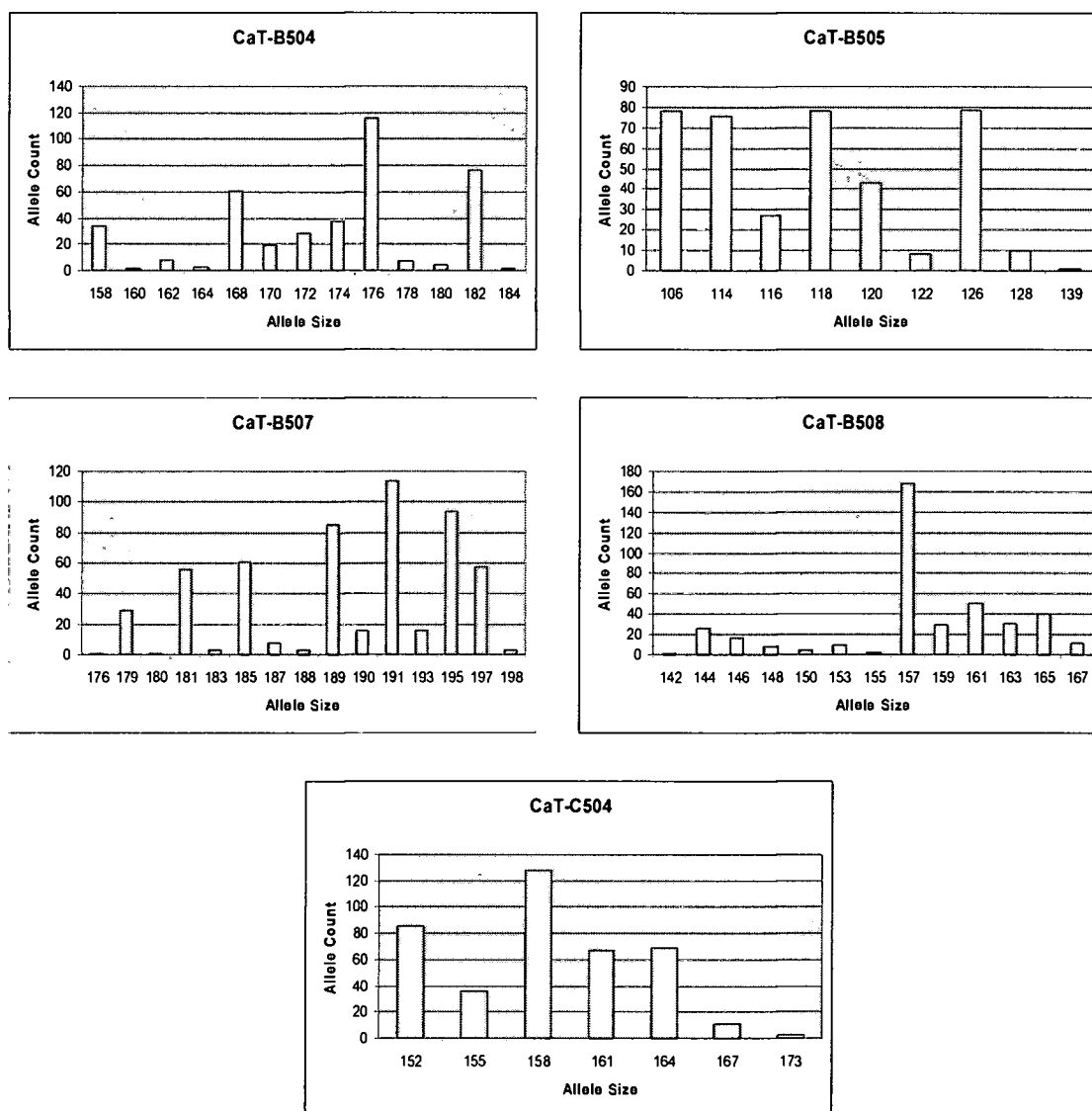


Figure 2.1 Continued

The observed heterozygosity (H_o) for individual loci ranged from 0.24 to 0.88, with an average of 0.67 over all loci. Expected heterozygosity (H_e) ranged from 0.28 to 0.87 and averaged 0.71 (Table 2.3). The total paternity exclusion probability (PEP) was 0.9999 ranging from 0.15 to 0.73 for individual loci with a mean value of 0.52.

Although all of the 5670 PCRs carried out for genotyping 270 European hazelnut cultivars with 21 microsatellites gave PCR products, 15 of the 21 SSR markers showed a positive estimated frequency of null alleles (r). CAC-C10 had the highest positive r value of 0.214, which indicates a likely occurrence of null alleles. The probability of identity (PI) index ranged from 0.06 for CaT-B107 to 0.56 for CAC-C040 and the total probability of identity was calculated as 1.8×10^{-17} .

Hazelnut diversity and cultivar pedigrees

A second set of DNA samples was extracted from four trees ‘Bard’, ‘Karidaty’, ‘Istarski Debeloplodna’ and ‘Riekchen’s Zellernuss’) and included as checks. In all cases these duplicates gave identical SSR allele sizes. They were not included in the statistical analyses. The phenogram constructed from an UPGMA cluster analysis of genetic distances showed that there is a large amount of diversity among European hazelnut accessions (Fig. 2.2). The phenogram revealed some tight and mixed geographical groupings. Each major group in the phenogram is condensed and discussed below separately.

Table 2.3 Allele numbers (n), expected heterozygosity (H_e), observed heterozygosity (H_o), polymorphic information content (PIC), probability of identity (PI), parental exclusion probability (PEP) and frequency of null alleles (r) of 21 SSR loci studied in 200 unique European hazelnut cultivars.

SSR Locus	n	H_e	H_o	PIC	PI	PEP	r
CAC-A014a	12	0.75	0.69	0.72	0.17	0.54	0.036
CAC-A040	8	0.74	0.77	0.69	0.19	0.51	-0.020
CAC-B005	10	0.78	0.82	0.75	0.14	0.57	-0.024
CAC-B010	7	0.79	0.80	0.76	0.13	0.59	-0.002
CAC-B028	15	0.84	0.70	0.82	0.08	0.69	0.076
CAC-B029b	13	0.81	0.76	0.79	0.11	0.64	0.026
CAC-B105	15	0.74	0.70	0.71	0.14	0.55	0.019
CAC-B111	8	0.67	0.59	0.63	0.23	0.44	0.050
CAC-C010	5	0.57	0.24	0.50	0.40	0.30	0.214
CAC-C028	6	0.69	0.74	0.64	0.26	0.44	-0.031
CAC-C040	5	0.28	0.27	0.26	0.56	0.15	0.006
CAC-C115	14	0.80	0.80	0.77	0.12	0.61	0.003
CAC-C118	5	0.30	0.28	0.28	0.53	0.16	0.010
CAC-C119	5	0.54	0.46	0.50	0.34	0.32	0.055
CaT-C504	7	0.78	0.59	0.75	0.14	0.58	0.109
CaT-B107	15	0.87	0.86	0.85	0.06	0.73	0.002
CaT-B508	13	0.78	0.69	0.76	0.10	0.61	0.049
CaT-B502	12	0.76	0.74	0.73	0.15	0.56	0.013
CaT-B504	13	0.83	0.84	0.81	0.08	0.67	-0.007
CaT-B505	9	0.83	0.88	0.81	0.10	0.66	-0.026
CaT-B507	14	0.84	0.80	0.82	0.07	0.70	0.025
Total	211	14.99	14.02	14.35	4.1	11.02	
Average	10.05	0.71	0.67	0.68			

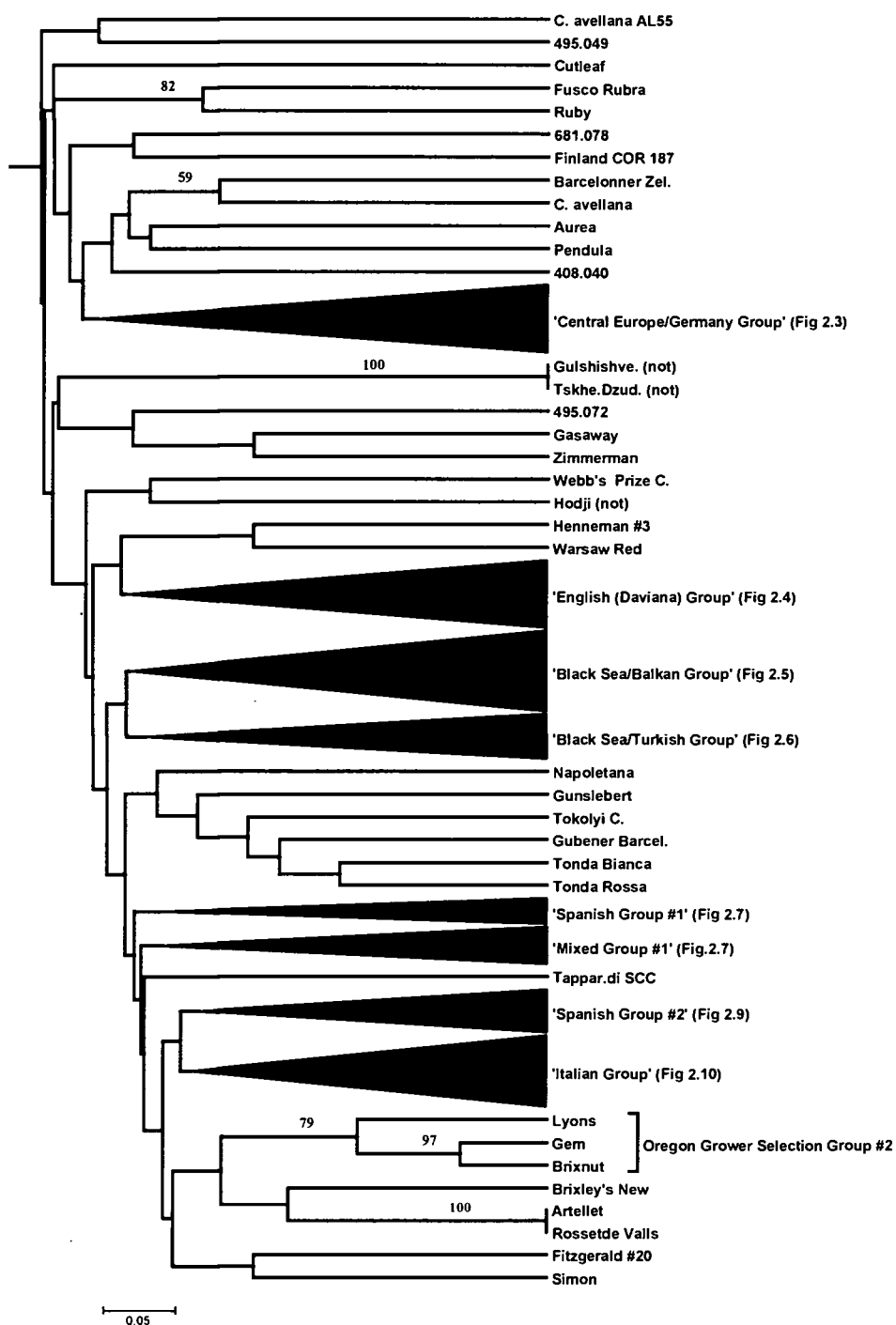


Figure 2.2 Phenogram of 270 cultivars based on cluster analysis (UPGMA) of genetic dissimilarity

Group 1: ‘Central Europe/Germany Group’

The first group has one Polish cluster, one English group of synonyms and one big German cluster, (Fig 2.3). The Polish cluster includes two synonyms, ‘Maria’ and ‘Lenka #4’. They have identical incompatibility alleles S_{11} and S_{15} and very similar large and long nuts in intermediate length husks. They clustered with five other Polish cultivars, ‘Acorn Hazelnut’, ‘Lenka #3’, ‘Frango #2’, ‘Volski Round’ and ‘Frango #5’, forming a geographically distinct Polish cluster. All cultivars in the Polish cluster have medium to large nuts and adjacent cultivars share at least one incompatibility allele. SSR profiles and S-alleles of these cultivars suggested that they might be seedlings of ‘Cosford’ (Table 2.4).

The English group of synonyms has three cultivars: ‘Bard’, ‘Barr’s Zellernuss’ and ‘Bearn’. All three cultivars have identical SSR profiles and incompatibility alleles (S_5 and S_{11}). They also show similar phenotypic traits such as long nuts of small to medium size in short husks.

The German cluster includes many cultivars from Germany and nearby central European countries and has four synonym groups. The first group of synonyms consists of four cultivars: ‘Obrovsky Novy’ from Slovakia, ‘Liegel’s Zellernuss’ from Germany, ‘Kunzenmuller Zellernuss’ from Germany and ‘Jeeve’s Samling’ from Germany. According to Goeschke (1887), ‘Jeeve’s Samling’ was received from England, but the exact origin is not known. All four cultivars have identical incompatibility alleles (S_{12} , S_{20}) and produce medium size, long and compressed nuts in short husks.

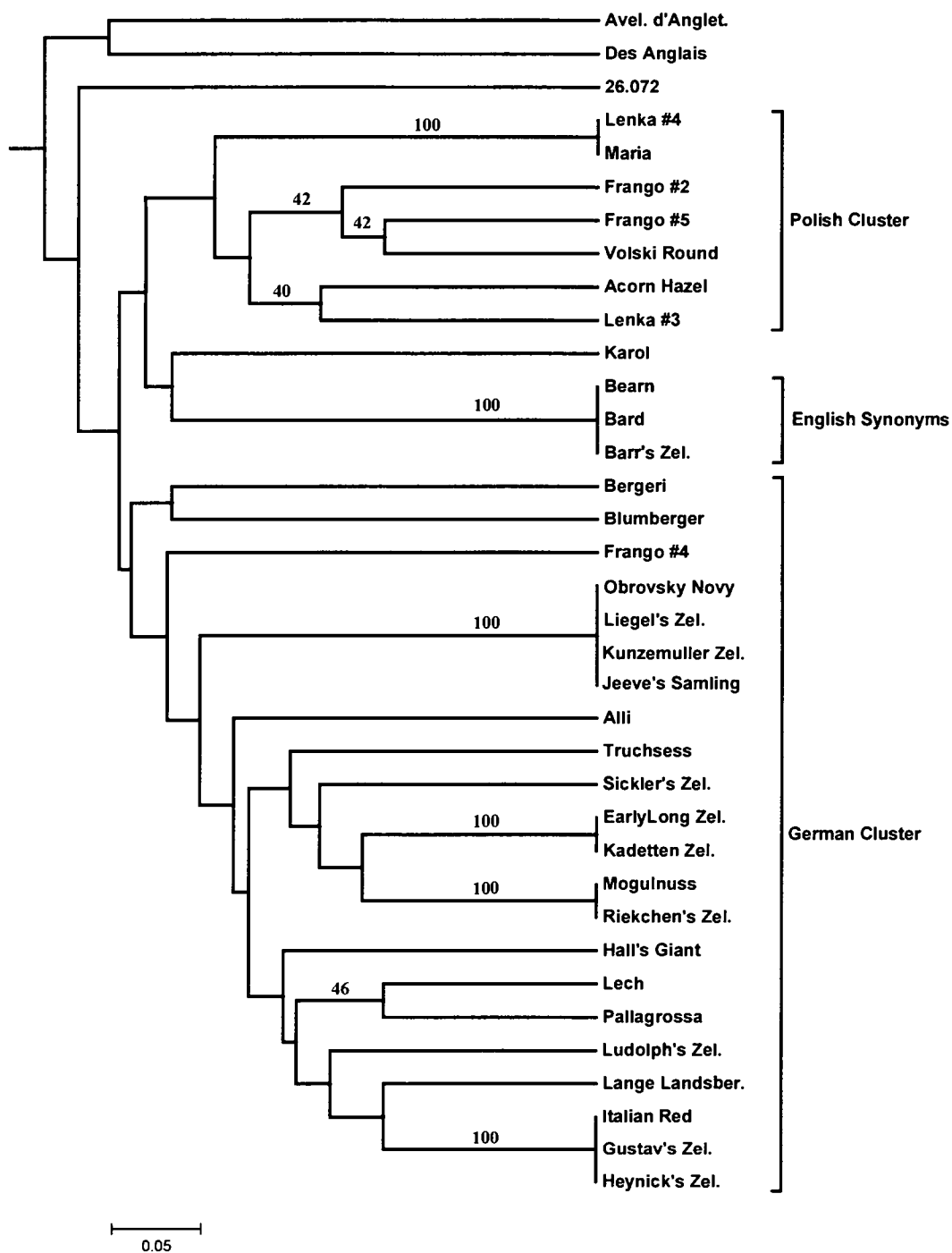


Figure 2.3 Phenogram of 'Central Europe/Germany Group' (36 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

The second group of synonyms is a pair: 'Kadetten Zellernuss' from Germany and 'Early Long Zellernuss' from Denmark. Their incompatibility alleles are S_{20} and S_{25} and they have medium to large size and long nuts in short husks.

The third group of synonyms is 'Mogulnuss' from England and 'Riekchen's Zellernuss' from Landsberg-Germany. They have identical incompatibility alleles, S_5 and S_{25} . 'Riekchen's Zellernuss' has medium size long nuts in intermediate length husks and 'Mogulnuss' has large size long nuts in intermediate length husks. This slight difference may be a phenotypical measurement error or crop load might be responsible for the difference in sizes of nuts. However, 21 SSR loci detected no difference. The second and third group of synonyms clustered with two German cultivars 'Sickler's Zellernuss' from and unknown origin and 'Truchsess' from Landsberg.

The second and third groups of synonyms clustered close to each other. All four cultivars have common S-allele S_{25} , providing a further indication that they are genetically related.

The fourth and the last group of synonyms consists of three cultivars from Germany ['Italian Red' (Crane et al., 1937), 'Heynick's Zellernuss' and 'Gustav's Zellernuss' from Landsberg-Germany]. All three have identical S-alleles (S_{15} and S_{20}). Although there are slight differences between phenotypic characteristics of the nuts of these cultivars, they all have medium to large and long nuts in short husks. These synonyms clustered with a 'Lange Landsberger' from Landsberg-Germany and Ludolph's Zellernuss' from an unknown origin in Germany (Goeschke, 1887).

‘Bergeri’ from an unknown origin in Germany and ‘Blumberger’ from Blumberg-Germany (Goeschke, 1887) clustered together and they are the most genetically diverse cultivars in German Cluster.

Group 2: ‘English (Daviana) Group’

The second group has three geographically tight clusters and four different synonym groups (Fig 2.4). The first and the most divergent cluster of this group is of four redleaf cultivars, ‘Rote Zellernuss’ from the Netherlands, ‘Red Fortrin’ from USA-Washington, ‘Syrena’ from Poland and ‘Goc’ from Poland. The two Polish cultivars clustered together and they have the same incompatibility alleles (S₆ S₁₅). ‘Rote Zellernuss’ clustered with ‘Red Fortrin’. According to the SSR profiles and S-alleles, ‘Red Fortrin’ might have resulted from a cross of ‘Barcelona’ x ‘Rote Zellernuss’ (Table 2.4)

The first synonym group includes four cultivars. ‘*C. multiflorum*’ from Turkey or Russia, ‘Cosford’ from England, ‘Prolifique a Coque Serrée’ from France, ‘Petoka (not)’ and ‘Multiflora’ from England. They have identical incompatibility alleles (S₃ and S₁₁) and produce similar large and long nuts in short husks. ‘Little Poland’ from Poland, ‘Pruhovany’ from Slovakia and ‘Daviana’ from Calcot Garden near Reading-England (Goeschke, 1887), of which the two latter are closely related to each other, clustered with ‘Cosford’. Of the scored 21 SSR loci, they differ from each other only at locus CAC-C115, at which ‘Daviana’ carries two alleles (173/193), while ‘Pruhovany’ has a single allele (193/193). Additionally, the S-alleles of ‘Daviana’ and ‘Pruhovany’ are identical (S₃ and S₁₁) and both have large and long nuts in short husks. ‘Little Poland’ has

incompatibility alleles S_3 and S_5 and it also has large and long nuts in short husks. SSR locus profiles, S-alleles and phenotypic traits of the cultivars in this cluster suggest that they have a common origin.

Several Oregon Grower Selections clustered with 'Daviana' and 'Cosford' and placed in two adjacent clusters. These selections believed to have resulted from a cross of 'Barcelona' and 'Daviana'. 'Barcelona' has incompatibility alleles S_1 and S_2 and 'Daviana' has incompatibility alleles S_3 and S_{11} . However, SSR loci profiles suggested that some of the cultivars were selected from crosses made by 'Daviana' and some by 'Cosford' as pollenizer. 'Woodford', 'Fitzgerald', 'Nonpareil', 'Ryan' and 'Ennis' have one allele from 'Barcelona' and one allele from 'Daviana'. 'Daviana' was suggested as the pollen parent of these cultivars by the presence of null alleles at locus CaT-B508 and CAC-B028. The scored genotypes of 'Barcelona' and 'Daviana' at CaT-B508 are 157/157 and 161/161 respectively. The expected genotypes of seedlings from this cross would be 157/161. However, 157/157 was scored in these four cultivars at this locus (Table 2.4). This can be explained by the presence of a null allele in 'Daviana' at locus CaT-B508. The expected null allele frequency of locus CaT-B508 is 0.047. On the other hand, the scored genotypes of 'Barcelona' and 'Daviana' at CAC-B508 are 254/262 and 270/270 respectively. The expected genotypes of seedlings from this cross would be 254/270 and 262/270. However, 254/254 was scored in 'Ryan' and 'Ennis' at this locus (Table 2.4). This can be explained by the presence of a null allele in 'Daviana' at locus CAC-B028. The expected null allele frequency of this locus is 0.076. These two loci have a moderately high frequency of null allele. On the other hand, according to the scored

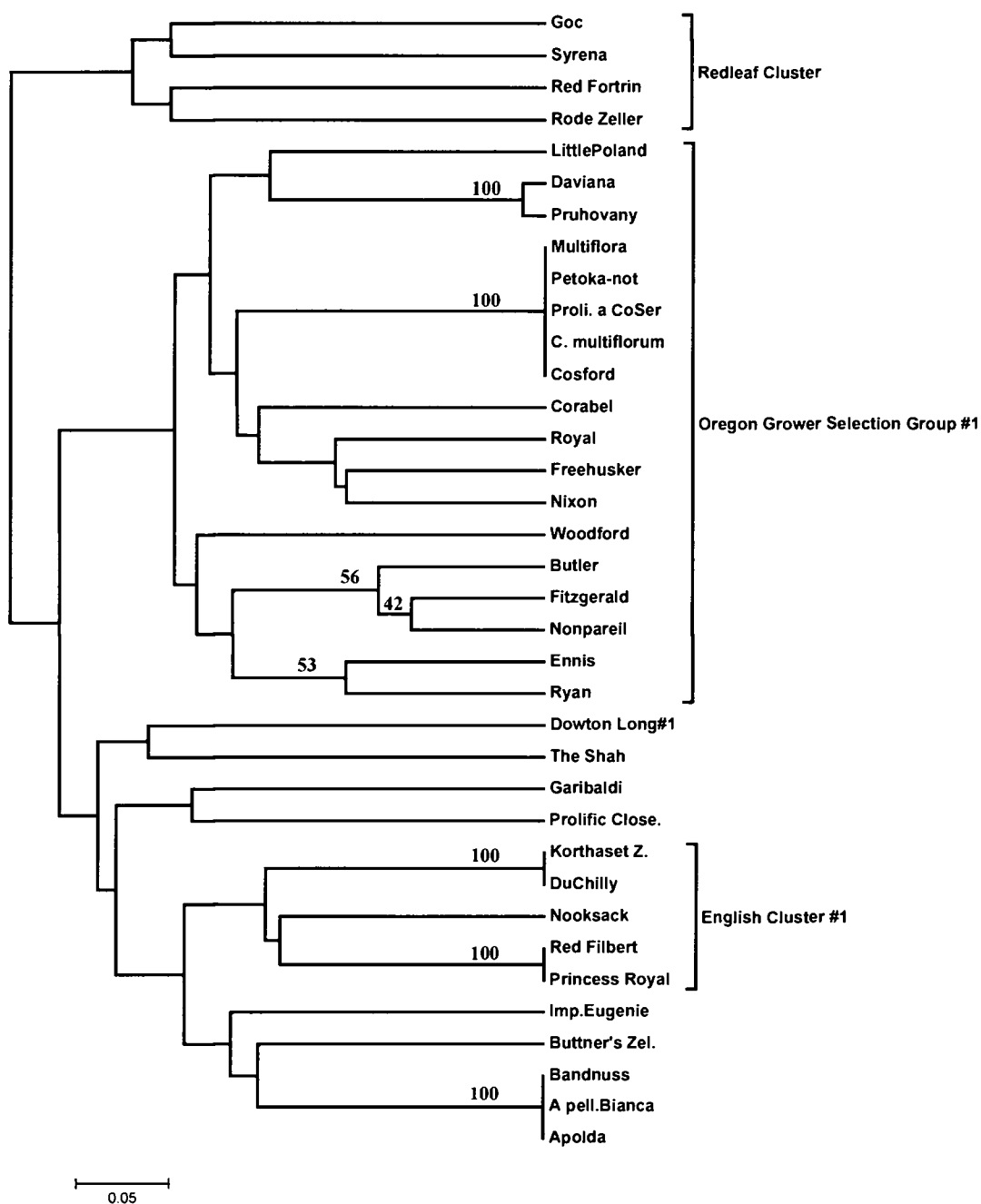


Figure 2.4 Phenogram of 'English (Daviana) Group' (36 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

genotypes, 'Freehusker', 'Corabel', 'Nixon' and 'Royal' might have resulted from a cross of 'Barcelona' x 'Cosford'. 'Cosford' was confirmed as the pollen parent of these cultivars by the presence of unique alleles: "211" at locus CAC-A014a, "148" at CAC-B105 and "148" at CaT-B508. Furthermore, 'Cosford' also has incompatibility alleles S_3 and S_{11} . The exact pollen parent of 'Butler' could not be determined by the 21 SSR loci, as either 'Daviana' or 'Cosford' could be the pollen parent of this cultivar. However, according to the phenogram (Figure 2.3), they clustered with 'Daviana' seedlings and might be the seedlings of 'Daviana'. SSR loci profiles of 'Daviana' and 'Cosford' suggested that they might be sister seedlings (Fig.2.4).

English Cluster #1 has two groups of synonyms. The first pair of synonyms is 'Korthaset Zellernuss' from Denmark and 'Du Chilly'(syn.'Kentish Cob') from England. They have incompatibility alleles S_{10} and S_{14} and both produce medium size very long nuts in long tubular husks. The second synonyms of the English Cluster #2 are 'Red Filbert' from England and 'Princess Royal' from Calcot Garden near Reading-England (Goeschke, 1887), both of which have incompatibility alleles S_{11} and S_{14} . Morphologically, these two cultivars are very similar. Both have medium size and very long nuts in short husks. The phenotypic traits and SSR-profiles suggest that these cultivars might be identical. This result should be further confirmed by identifying the second S-allele of 'Red Filbert'. Two other English cultivars, 'Dowton Long #1' and 'The Shah', and 'Nooksack' from USA-Washington were placed in English Cluster #2. 'Nooksack' originated in Nooksack, Washington and was introduced in 1928 (Brooks and Olmo, 1997). It might be a chance seedling of 'DuChilly'. Indeed, the genotype of

‘Nooksack’ at 21 SSR loci indicates that it could be a seedling of ‘Du Chilly’. Beside that, some phenotypic traits such as tree habit and large nut size are also similar to ‘Du Chilly’. ‘Downton Long #1’ is the first of two cultivars with the same name. The second one clustered with other English cultivars in Group 2, which was mentioned earlier. According to the SSR profiles of these two trees, although they have the same name, they are genetically different. However, their clustering indicates both originated in England.

The sixth group of synonyms consists of three cultivars: ‘Bandnuss’ from England, ‘A Pellicola Bianca’ from Italy and ‘Apolda’ from Italy. They have identical S-alleles S₁₀ and S₁₁. They are also identical morphologically. All three have large and long nuts in short husks. Two other cultivars, ‘Buttner’s Zellernuss’ from Germany and ‘Imperatrice Eugenie’ from France clustered with these synonyms.

Group 3: ‘Black Sea/Balkan Group’

The third group on the phenogram included diverse cultivars primarily from Black Sea countries and the Balkan Peninsula (Fig 2.5). Five groups of synonyms and five tight geographical clusters were detected. The first synonym group consists of ‘White Filbert’ from France, ‘Purple Fortrin’ from USA-Washington, ‘Purple Aveline’ from France, ‘Pellicule Rouge’ from France, ‘Istarski Debeloplodna’ from Croatia, ‘Fructo Albo’ from France, ‘Barbarella’ from Italy and ‘Aveline Rouge’ from France. The identical SSR profiles of these cultivars are supported by phenotypes and S-alleles. They have small long nuts, long tubular husks and incompatibility alleles S₅ and S₁₀. ‘Purple Fortrin’, ‘Purple Aveline’, ‘Pellicule Rouge’, ‘Barbarella’ and ‘Aveline Rouge’, have red-purple pellicle (skin covering the kernel). This unusual pellicle color might have

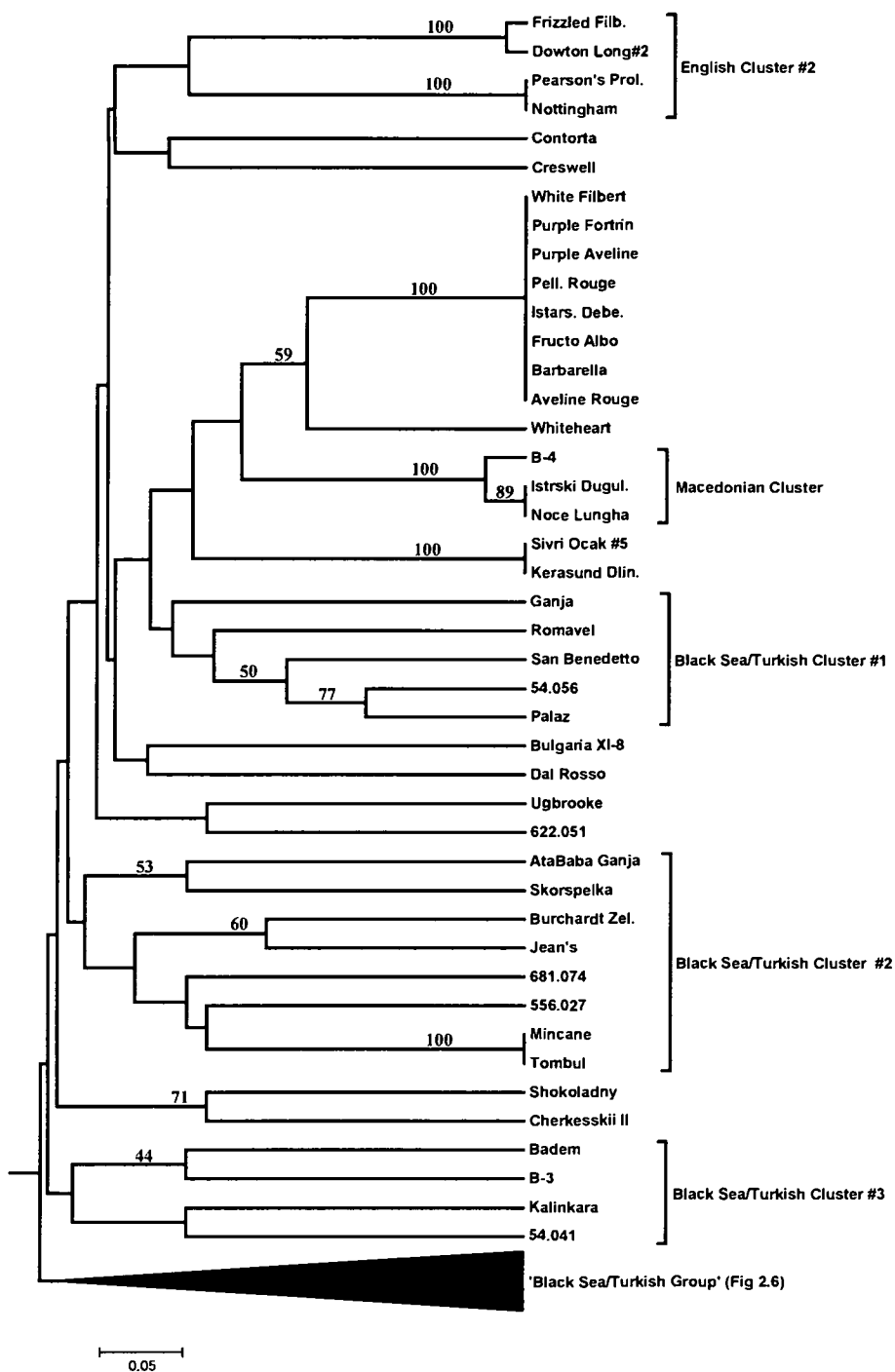


Figure 2.5 Phenogram of 'Black Sea/Balkan Group' (44 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

arisen by mutation. However they have the same SSR alleles as ‘Fructo Albo’ and ‘Istarski Debeloplodna’ which have brown pellicles. ‘Whiteheart’, a cultivar from New Zealand clustered with these accessions and has incompatibility alleles S_2 and S_{10} . The SSR profiles and S-alleles suggest that ‘Whiteheart’ is a seedling of ‘White Filbert’.

The second group of synonyms was ‘Noce Lungha’ from Italy and ‘Istarski Duguljasti’ from Croatia. They clustered with Macedonian cultivar ‘B-4’. According to the SSR loci profile, ‘B-4’ is closely related to ‘Noce Lungha’ and ‘Istarski Duguljasti’. It differs only at two loci. At CAC-A014a ‘B-4’ carries two alleles (211/215), while ‘Noce Lungha’ and ‘Istarski Duguljasti’ carry two alleles (211/217) and at the locus CaT-B507 ‘B-4’ carries 122/134, while ‘Noce Lungha’ and ‘Istarski Duguljasti’ carry 134/134. Moreover, ‘B-4’ is phenotypically similar to ‘Noce Lungha’ and ‘Istarski Duguljasti’ with long large nuts and a long tubular husk. This cluster with a Croatian, a Macedonian and an Italian cultivar was geographically distinct from other cultivars in the group. Probably the synonymous cultivars ‘Noce Lungha’ and ‘Istarski Duguljasti’ had been transferred across the Adriatic Sea and different names used for the same cultivar.

The third group of synonyms was ‘Sivri Ocak #5’ from Turkey and ‘Kerasund Dlinnyi’ from the Russian Federation. Both have medium-sized long pointed nuts, very long husks and the same S-alleles (S_8 S_{10}). ‘Kerasund Dlinnyi’ was probably carried from Turkey to Russia. The first word “Kerasund” is similar to “Giresun” the major hazelnut producing province of Turkey, and “Dlinnyi” means “long” in Russian.

The fourth group of synonyms was two cultivars from England, ‘Pearson’s Prolific’ and ‘Nottingham’, which clustered with two other English cultivars, ‘Frizzled

Filbert' and 'Downton Long #2'. Both 'Pearson's Prolific' and 'Nottingham' have incompatibility alleles S_8 and S_{10} and are morphologically identical. Both are vigorous trees with small and very long nuts and intermediate length husks. SSR profiles show that 'Frizzled Filbert' and 'Downton Long #2' are closely related to each other. They only differ from each other at locus CaT-B508, where 'Frizzled Filbert' has alleles 153/161, while 'Downton Long #2' has alleles 153/163. The difference in these two cultivars might be due to a mutation at this locus. Otherwise, they are phenotypically similar with small long nuts and long husks, and they have the same S-alleles (S_9 S_{10}).

In this group, three Black Sea/Turkish clusters were revealed. The first cluster consists of 'Ganja' from Azerbaijan, 'Romavel' from Romania, 'San Benedetto' from Italy-Torino, 'Palaz' from Turkey, and '54.056' from Turkey. Morphologically, they are similar, having with medium to small and slightly oblate to round nuts and long husks. 'San Bendetto' was received from Italy-Torino as a selection of *Corylus maxima*. However it seems that this cultivar did not originate in Italy. The second Black Sea/Turkish cluster includes 'Skorspelka' from the Russian Federation, 'Ata Baba Ganja' from Bordeaux, 'Jean's' of unknown origin, 'Burchardt's Zellernuss' from Germany, '681.074' from Turkey, '556.027' from Turkey, 'Tombul' from Turkey-Akçakoca, and 'Mincane' from Turkey-Akçakoca. 'Tombul' and 'Mincane' were received as scions from an orchard in Turkey-Akçakoca. They have identical SSR profiles and both have incompatibility alleles S_4 and S_{10} . Synonymy based on DNA profiles was also confirmed phenotypically.

The last Black Sea/Turkish cluster, which consists of ‘Badem’ from Turkey, ‘B-3’ from Macedonia, ‘Kalinkara’ from Turkey and ‘54.041’ from Turkey, is distinct from other clusters in the group. They are phenotypically similar in that they have small to medium-sized and slightly long or long nuts.

Group 4: ‘Black Sea/Turkish Group’

This group includes 25 cultivars that were divided into two different distinct Black Sea/Turkish clusters (Fig 2.6). In the first cluster two groups of synonyms were revealed. The first synonym group includes ‘Vilcea 22’ from Romania, a selected sport of ‘Imperial de Trebizonde’ (Turcu and Botu, 1997), ‘Wanliss Pride’ from Australia, two trees of the ‘Imperial de Trebizonde’, and ‘Karidaty’ from Turkey. All six cultivars have identical phenotypes (large, round nuts and intermediate husk length) and incompatibility alleles S_2 and S_{10} . In the second synonym group, ‘Nemsa (not)’ and ‘Kudryavchik (not)’ brought from Georgia and, which are not true-to-name, appeared to be genetically identical. Moreover, both trees have incompatibility alleles S_4 and S_{14} . Both trees produce large round nuts and have long husks and are otherwise phenotypically identical. Although not true-to-name, the true identity of this accession remains unknown.

In the second cluster, two different synonyms were detected. According to SSR loci profiles, ‘Tombul Ocak 1’ from Turkey and ‘Extra Ghiaghli’ from Greece are identical. They both have small and pointed nuts and very long husks and S-alleles 4 and 12. The second pair of synonyms in this cluster is ‘Tombul Ghiaghli’ from Greece and ‘Unknown #3’, a tree whose label was lost at planting time. According to the SSR loci profiles and S-alleles (4, 8), ‘Unknown #3’ and ‘Tombul Ghiaghli’ are synonyms.

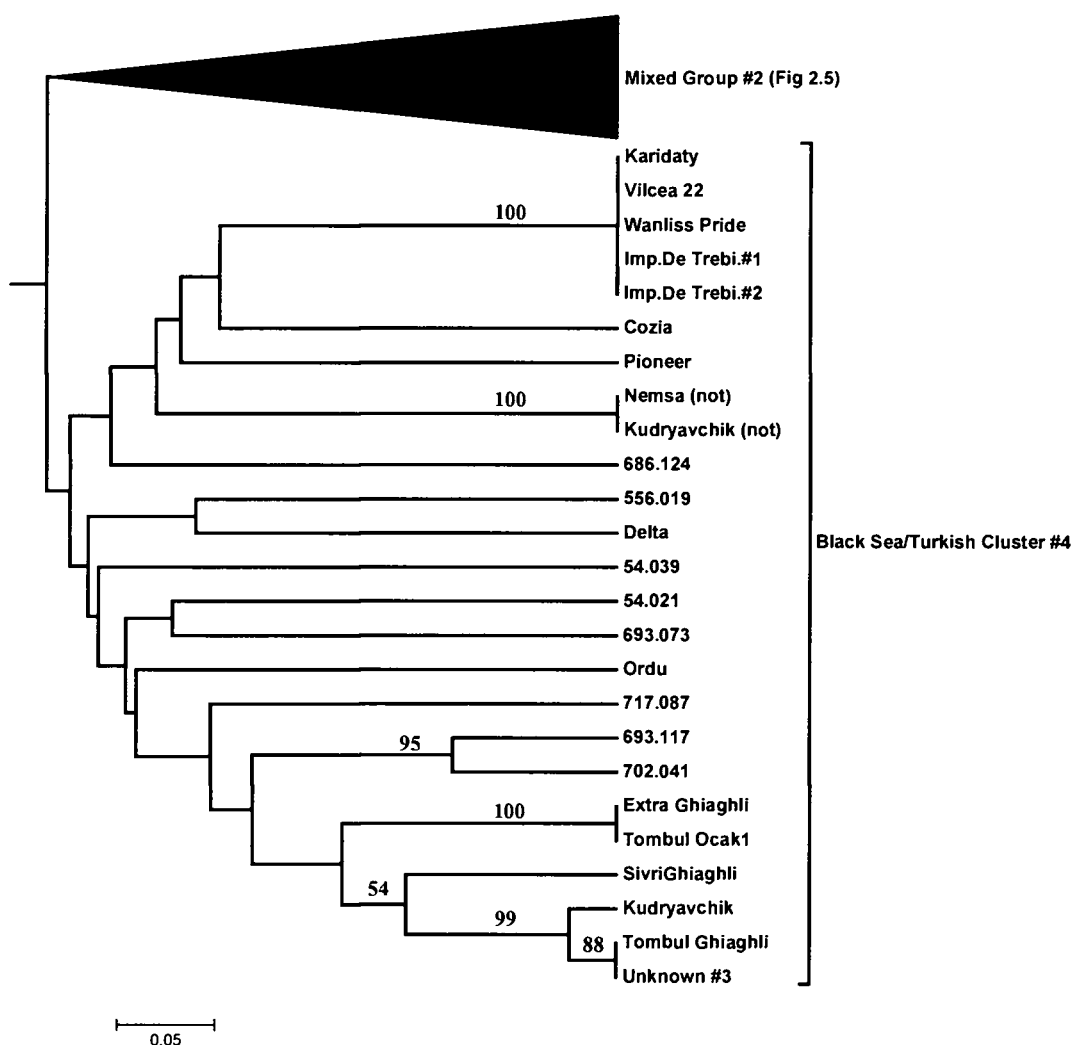


Figure 2.6 Phenogram of ‘Black Sea/Turkish Group’ (25 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

‘Ordu’, imported as scions from Italy-Torino and selected seedlings of Turkish origin (‘686.124’, ‘556.019’, ‘54.039’, ‘693.073’, ‘54.021’, ‘717.087’ ‘693.117’, ‘702.041’ and ‘693.117’) clustered together. Although the two Russian cultivars, ‘Kudryavchik’ and ‘Kudryavchik (not)’ have the same name, they have different SSR

profiles and the morphology of the nuts is also different. ‘Kudryavchik’ has small round nuts, but ‘Kudryavchik (not)’ produces large round nuts. The leaf samples of ‘Kudryavchik’ were collected from National Clonal Germplasm Repository (NCGR) Corvallis, OR hazelnut collection and ‘Kudryavchik (not)’ was from the OSU hazelnut collection and propagated from scions received from the Republic of Georgia. The true ‘Kudryavchik’ appears to be closely related to ‘Tombul Ghiaghli’. The genetic profile of ‘Kudryavchik’ differed from ‘Tombul Ghiaghli’ at locus CAC-C119, at which ‘Kudryavchik’ carries two alleles (258/260), while ‘Tombul Ghiaghli’ carries a single allele (260/260). Additionally, the S-alleles of ‘Kudryavchik’ are S₄ and S₁₄, while they are S₄ and S₈ for ‘Tombul Ghiaghli’. So, the difference at the S-locus indicates that they are similar but different accessions.

Group 5: Spanish Group #1

This group consists of two Italian cultivars, one Portuguese cultivar and 11 Spanish cultivars (Fig. 2.7). The Spanish cultivars ‘Tomasina’, ‘Francoli’, ‘Martorella’, ‘Pauetet’, ‘Restiello’ and ‘Negret’ clustered closely together. ‘Restiello’ and ‘Negret’ have identical SSR profiles and S-alleles (S₁₀, S₂₂). Both have small, slightly long nuts and short husks. ‘Tomasina’ and ‘Francoli’ have incompatibility alleles S₁₇ and S₂₂ and ‘Pauetet’ has incompatibility alleles S₁₈ and S₂₂. Comparison of SSR profiles of these cultivars and ‘Negret’ suggests that ‘Tomasina’ and ‘Pauetet’ could be seedlings of ‘Negret’. However, the SSR profile of ‘Francoli’ is not consistent with the SSR profile of ‘Negret’ at four loci (Table 2.4). The second major cluster in this group includes cultivars from Italy (‘Nocchiolino Sangrato’ and ‘Tonda Gentile delle Langhe’) and Spain (‘Morell’,

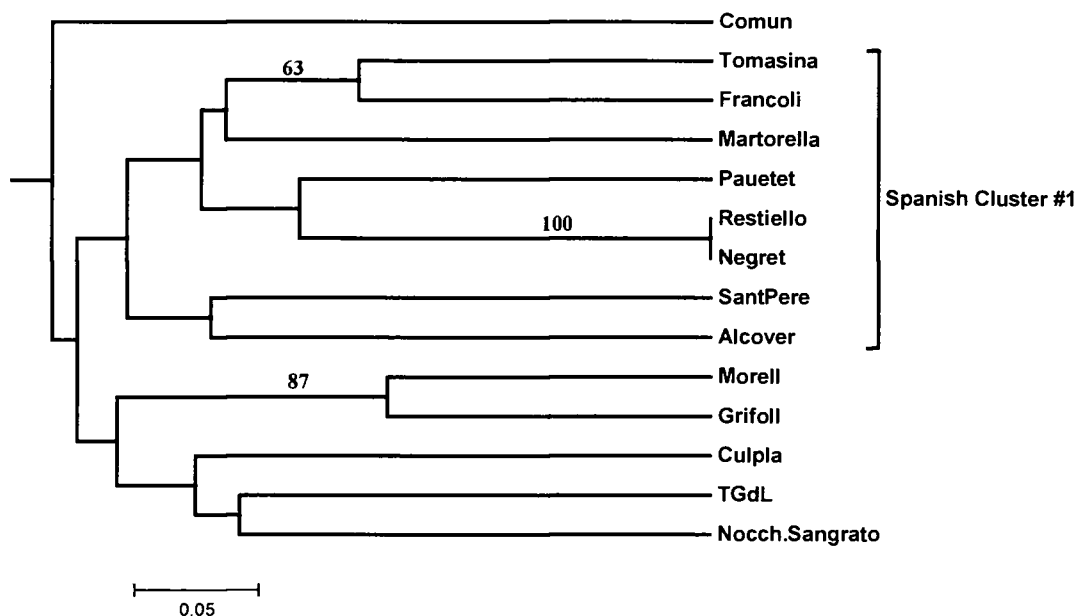


Figure 2.7 Phenogram of 'Spanish Group #1' (14 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

'Grifoll' and 'Culpla'). These cultivars appear genetically related to each other, possibly due to exchange between Italy and Spain decades or centuries ago. The most divergent cultivars in this group is 'Comun' from Portugal, which clustered loosely with other cultivars in the group.

Group 6: 'Mixed Group #1'

The sixth group on the phenogram has diverse cultivars from Italy, Spain, Germany, Slovakia and four pollenizers ('Delta', 'Epsilon', 'Gamma' and 'Zeta') released by the Oregon Agricultural Experiment Station (Fig 2.8). Four groups of synonyms were detected.

The first synonym group consists of ‘Fruttogrosso’ from Italy, ‘Istarski okrogloplodna’ from Slovenia, ‘Römische Nuss’ from Italy, ‘Payrone’ from Italy and ‘Romai’, which might be from Italy. The identical SSR profiles of these cultivars are consistent with their phenotypes and S-alleles. They have large round nuts with short husks and incompatibility alleles S₁₀ and S₁₈. Although the name ‘Römische Nuss’ indicates a Roman origin, its true origin is unknown but is included in English, French, and Italian collections.

The second synonym group includes three cultivars from Spain: ‘Segorbe’, ‘Comun Aleva’ and ‘Gironenc Colldejou’. These three synonyms have identical S-alleles (S₉ and S₂₃) and the same phenotype. All three cultivars have small and slightly long nuts and intermediate husk length.

The third group of synonyms is the pair ‘Louisen’s Zellernuss’ from Germany and ‘Rimsky’ from Slovakia. They clustered with Italian and Spanish cultivars as mentioned earlier. They have identical S-alleles (S₁₀ and S₂₅) and produce very large round nuts with short husks. The last synonyms in this group are four Spanish cultivars (‘Quiros’, ‘Espinaredo’, ‘Casina’ and ‘Amandi’). SSR profiles are consistent with the identical S-alleles (S₁₀, S₂₁) and phenotypes of the cultivars. All four cultivars have small, slightly long nuts and intermediate husk length. ‘Gamma’, a pollenizer released by the Oregon Agricultural Experiment Station, clustered together with ‘Casina’ and its synonyms. ‘Gamma’ resulted from a cross of ‘Casina’ x VR 6-28. VR 6-28 was selected from a cross of ‘Riccia di Talanico’ x ‘Gasaway’ (Mehlenbacher and Smith, 2004). The

genotype of ‘Casina’ and expected genotype of VR 6-28 (‘Riccia di Talanico’ x ‘Gasaway’) were consistent with that observed for ‘Gamma’ (Table 2.4).

‘Epsilon’, one of four pollenizers released by the Oregon Agricultural Experiment Station, clustered together with its grandparent, Italian cultivar ‘Tonda Romana’.

‘Epsilon’ resulted from a cross of OSU 350.089 x ‘Zimmerman’. OSU 350.089 was selected from the cross ‘Tonda Romana’ x ‘Tombul Ghiaghli’ (Mehlenbacher and Smith, 2004). The genotype of ‘Zimmerman’ and the expected genotype of OSU 350.089 based

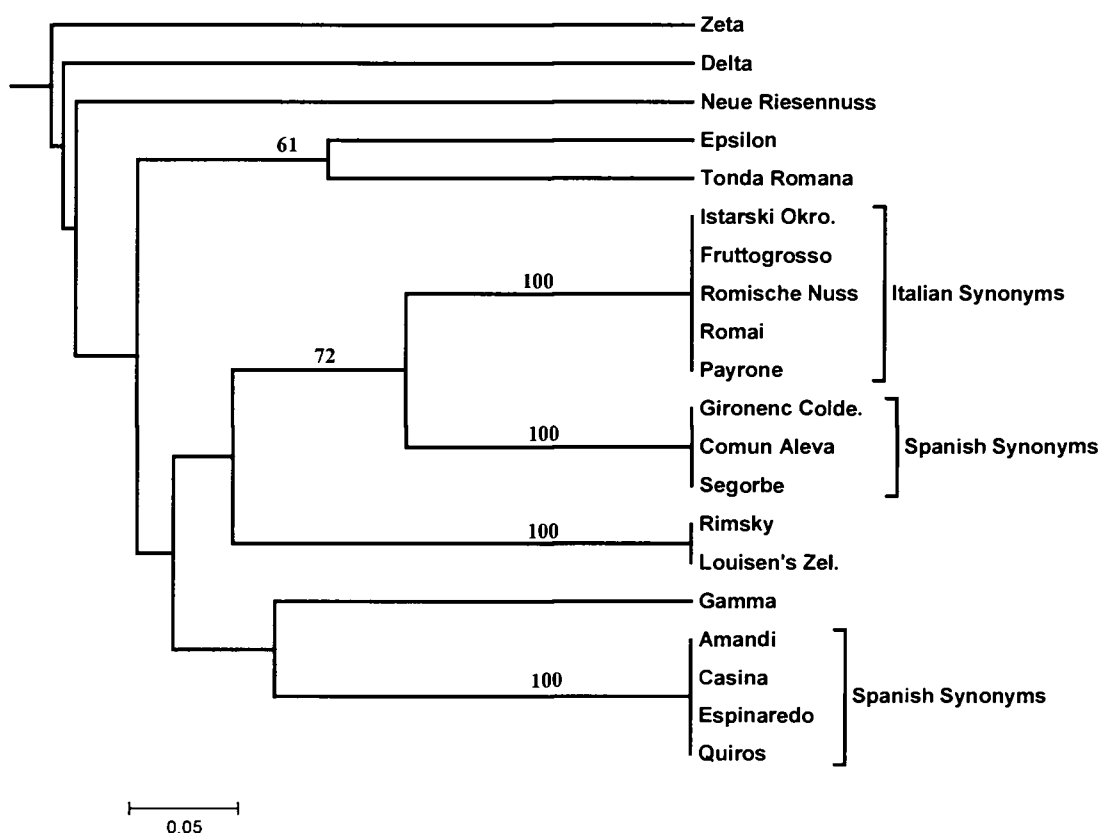


Figure 2.8 Phenogram of ‘Mixed Group #1’ (21 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

on its parents ‘Tonda Romana’ and ‘Tombul Ghiaghli’ showed that the pedigree information of ‘Epsilon’ was correct except at locus CAC-C010 (Table 2.4). According to Mendelian segregation, the genotype of ‘Epsilon’ at locus CAC-C010 should be 275/278 or 278/281, but the scored genotype was 275/275. This result can be explained by the presence of null alleles in ‘Tombul Ghiaghli’ and/or ‘Tonda Romana’ and ‘Zimmerman’ at this locus. The expected null allele frequency of locus CAC-C010 is 0.222, a very high frequency. The other pollenizers, ‘Delta’ and ‘Zeta’ clustered outside of the group as the two most diverse accessions. ‘Zeta’ resulted from a cross of OSU 342.019 x ‘Zimmerman’. OSU 342.019 was a selected seedling of the cross of ‘Casina’ x OSU 43.091 (Mehlenbacher and Smith, 2004). According to the SSR profiles, ‘Zimmerman’ is indeed one of parents of ‘Zeta’ (Table 2.4).

Group 7: ‘Spanish Group #2’

This group includes 23 cultivars: 18 from Spain and 2 from Portugal (Figure 2.9) and three cultivars from outside the Iberian Peninsula, ‘Barrettona’ and ‘Daria’ from Italy and ‘Comen’ of an unknown origin and. ‘Comen’ was received from Italy. Manzo and Tamponi (1982) suggested that it might have originated in Greece. However, SSR profiles indicate that it has a Spanish origin, because it clustered with the three Spanish cultivars ‘Sant Joan’, ‘Lluenta’ and ‘Gironenc Vermellet’.

Four groups of synonyms were identified. According to the phenogram, the Spanish cultivar ‘Molar’ and the Portuguese cultivar ‘Cerret’ are synonyms. However, the S-alleles and phenotypic traits of these two cultivars are different. ‘Molar’ has medium

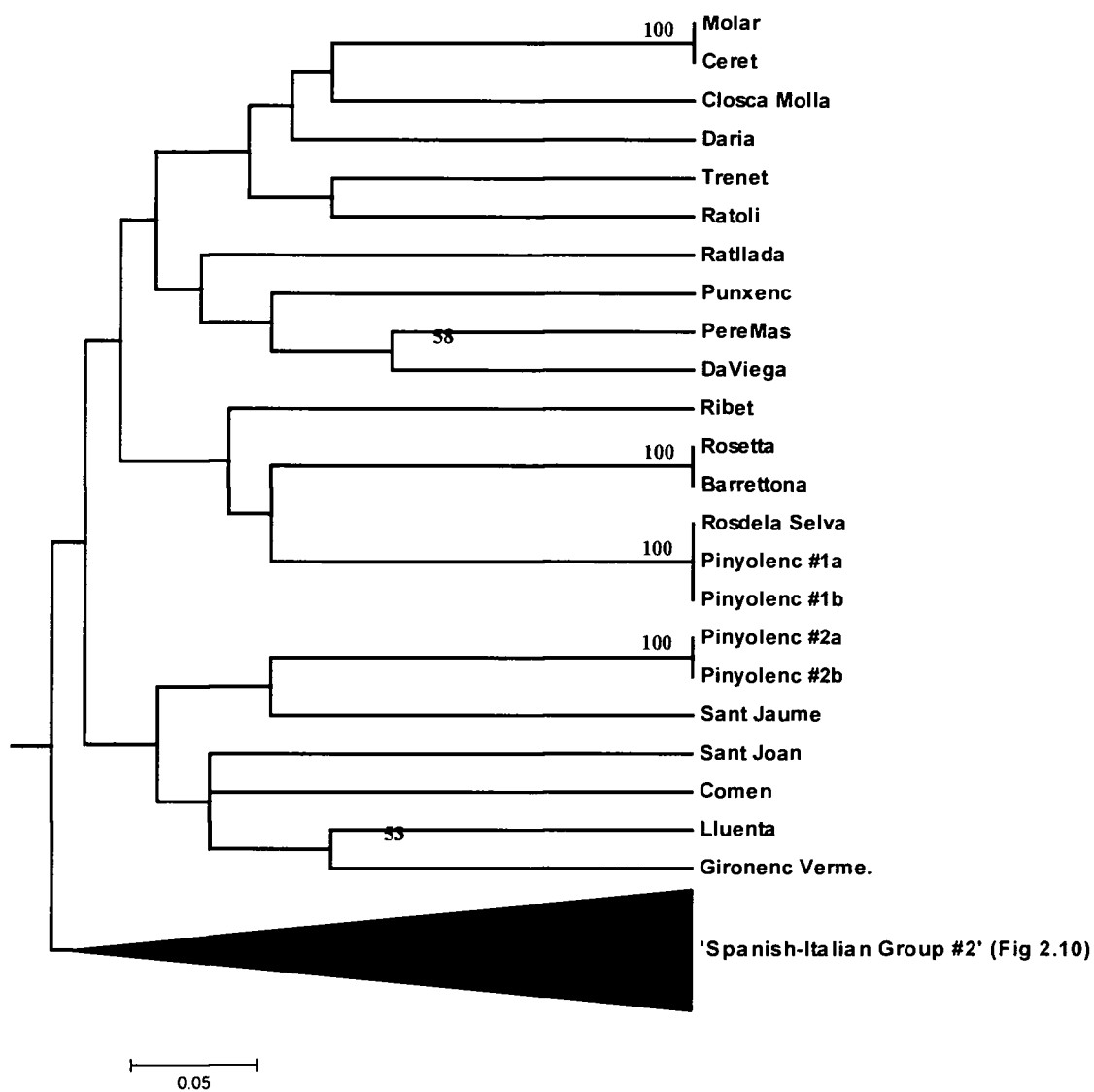


Figure 2.9 Phenogram of 'Spanish Group #2' (23 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

size, round nuts with intermediate length husk and incompatibility alleles S_2 and S_{10} .

‘Ceret’ has small, round nuts with long husks and incompatibility alleles S_1 and S_2 .

Italian cultivar ‘Daria’ resulted from a cross of ‘Tonda Gentile delle Langhe’ (TGdL) from Italy and ‘Cosford’ from England. The genotypes of ‘Daria’ and its parents are consistent with the pedigree information at all SSR loci except at CAC-C010. ‘TGdL’ and ‘Cosford’ carry single alleles, (275/275) and (278/278) respectively at CAC-C010. The expected genotype of ‘Daria’ at this locus was 275/278. However, it was scored as 278/278 (Table 2.4). This result can be explained by the presence of a null allele at CAC-C010 in ‘TGdL’. Indeed, CAC-C010 has a high positive expected null allele frequency (0.214). The Spanish cultivar ‘Rossetta’ and the Italian cultivar ‘Barrettona’ have identical SSR profiles and S-alleles (S_2 and S_6). Both have large round nuts with intermediate length husks. Probably ‘Barrettona’ has a Spanish origin, because it clustered with other Spanish cultivars and no Italian cultivar was placed in this cluster. ‘Barrettona’ was imported as scions from an orchard near Lago di Vico in Italy. ‘Pinyolenc #1a’ and ‘Pinyolenc #1b’ are two trees of the same genotype and have identical SSR loci profiles. Both have medium size round nuts with intermediate husk length. Their incompatibility alleles are S_2 and an unknown S-allele, or they may be homozygous $S_2 S_2$. ‘Ros de la Selva’, another cultivar from Spain, has an identical SSR profile and is morphologically indistinguishable from ‘Pinyolenc #1a’ and ‘Pinyolenc #1b’ based on nut size and shape and husk length. It has incompatibility alleles S_2 and S_9 . So, this suggests that the unknown S-allele of ‘Pinyolenc #1a’ and ‘Pinyolenc #1b’ is S_9 .

‘Pinyolenc #2a’ and ‘Pinyolenc #2b’ have identical SSR profiles, S-alleles (S_2 and S_{17}), and morphological characters. Both trees have small and slightly long nuts with intermediate length husks. Although ‘Pinyolenc #1’ and ‘Pinyolenc #2’ have the same name, they were shown to be different cultivars. They were placed in two different clusters in the ‘Spanish Group #2’.

The second Portuguese cultivar, ‘Da Viega’ is genetically related to the Spanish cultivar ‘Pere Mas’ and clustered with two other Spanish cultivars, ‘Ratlada’ and ‘Punxenc’.

Group 8: ‘Italian Group’

This group includes cultivars mainly from Italy and a few from Spain and the OSU hazelnut breeding program (Fig. 2.10). The most divergent cultivar was ‘Tonnolella’ from Italy. Four groups of synonyms were revealed in this group. The first synonyms are ‘Macrocarpa’ from Germany, ‘Kruse’ from USA-Oregon and ‘Turk’ from USA-Oregon. All three have incompatibility alleles S_1 and S_2 . Additionally, they have large round nuts with intermediate length husks. According to the SSR loci profiles, Oregon cultivars ‘Turk’ and ‘Kruse’ are related to ‘Barcelona’, the leading cultivar in Oregon. ‘Turk’ and ‘Kruse’ share a common allele with ‘Barcelona’ at 17 out of 21 SSR loci. These synonyms clustered with the Oregon rootstock selection ‘Arneson’s Rootstock’ and five Italian cultivars (‘Riccia di Talanico’, ‘San Giovanni’, ‘Tonda di Giffoni’ and ‘Camponica’).

The second group of synonyms includes ‘D’Algers’ from the Netherlands, ‘Barcelona’ from Spain and ‘Grande’ from Spain-Asturias. They have identical incompatibility alleles (S_1 and S_2) and large round nuts with intermediate length husks. Although according to the NCGR-Corvallis *Corylus* Catalog, ‘D’Algers’ was imported from the Netherlands, it might have originated in Spain. Another Spanish cultivar ‘Planeta’ also clustered closely with these synonyms. The third synonym group has three accessions, ‘Atlas’ from Denmark and two trees of ‘Belle di Giubilino’ from Italy. Their incompatibility alleles are S_1 and S_{10} and they have large round nuts with short husks. ‘Atlas’ might have originated in Italy and been carried to the collection in Denmark.

The last group of synonyms consists of 11 cultivars from Italy-Sicily. They are ‘Racinante clone G’, ‘Nostrale’, ‘Montebello’, ‘Minnolora’, ‘Barettona (not)’, ‘Avellana Speciale’, ‘Siciliana’, ‘Mansa’, ‘Locale di Piazza Armerina’, ‘Comune di Sicilia’ and ‘Carello’. They all have medium size, round-oblate nuts with short husks. Furthermore, they have identical S-alleles (S_1 and S_2). ‘Nocchione’ from central Italy clustered closely with the Sicilian synonyms. It has the same S-alleles, and produces morphologically similar nuts. They only differ from each other at locus CaT-C504, where ‘Nocchione’ has two alleles (153/164), while the Sicilian synonyms have two alleles (158/167).

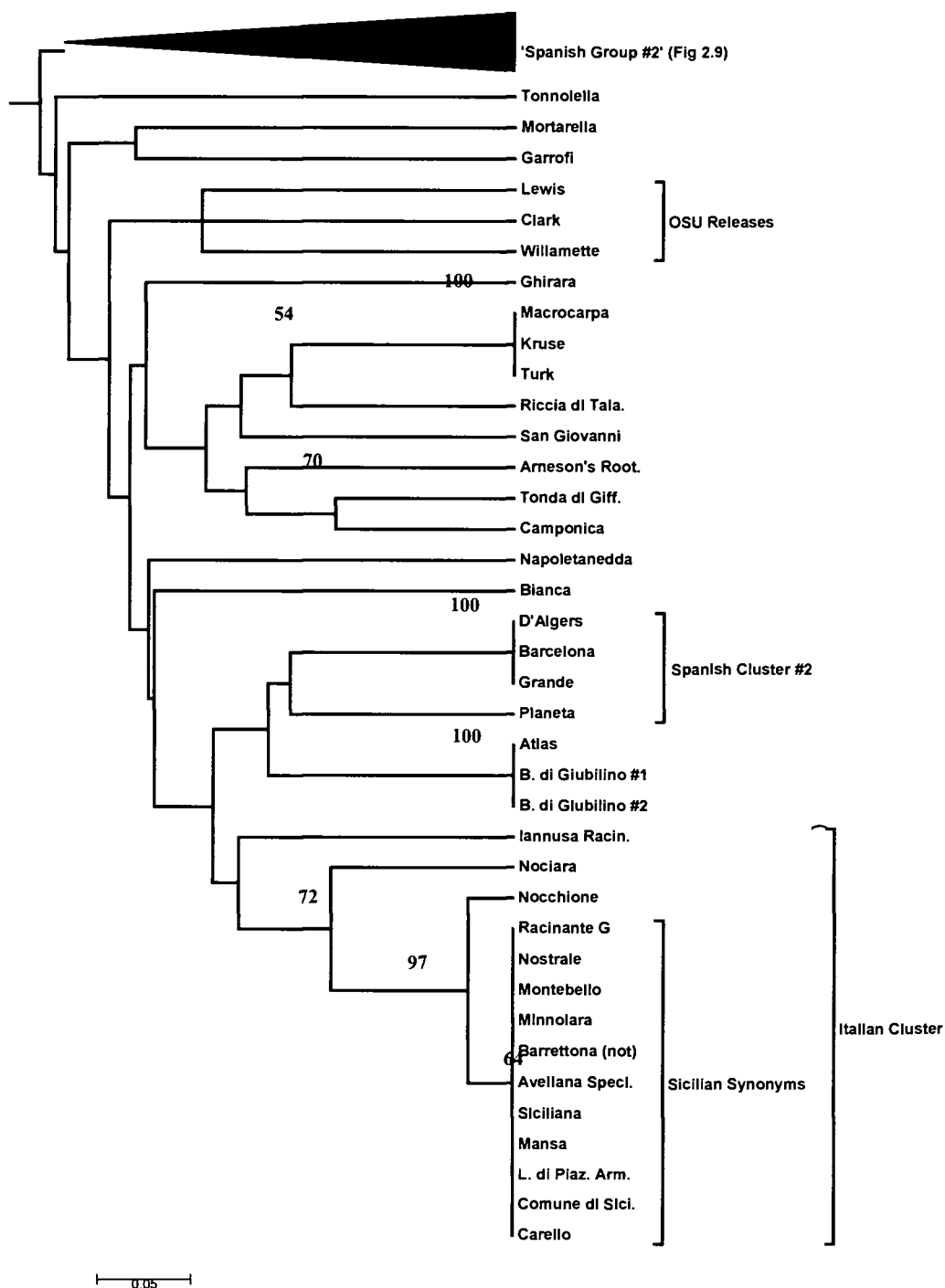


Figure 2.10 Phenogram of 'Italian Group' (38 cultivars) based on cluster analysis (UPGMA) of genetic dissimilarity

‘Nocchione’ might have diverged from this group by mutation at this locus. Two other Italian cultivars, ‘Nociara’ and ‘Iannusa Racinante’, were also placed in the Sicilian Cluster.

The Oregon State University releases ‘Willamette’ (Mehlenbacher et al., 1991), ‘Clark’ (Mehlenbacher et al., 2001) and ‘Lewis’ (Mehlenbacher et al., 2000) clustered together and they are denoted on the phenogram under the group of ‘OSU Releases’ (Fig. 2.10). These cultivars were released for the kernel market. ‘Clark’ and ‘Lewis’ have quantitative resistance to eastern filbert blight caused by *Anisogramma anomala* (Peck) E. Müller and are seedlings of ‘Willamette’.

According to the pedigree of ‘Willamette’, it resulted from a cross of ‘Montebello’ from Italy and ‘Compton’, a selection of O.C. Compton of Corvallis, Ore. (Mehlenbacher et al., 1991). ‘Compton’ was not included this study. However, the SSR profiles of ‘Willamette’ and ‘Montebello’ show that ‘Montebello’ could be one of the parents of ‘Willamette’ (Table 2.4).

‘Clark’ was selected from a progeny of 231 seedlings from a cross of ‘Tombul Ghiaghli’ and ‘Willamette’ (Mehlenbacher et al., 2001). Genotypes of ‘Clark’ and both parents are consistent with the pedigree information at all SSR loci except at CAC-C010. ‘Tombul Ghiaghli’ and ‘Willamette’ carry single alleles, (281/281) and (278/278) respectively at CAC-C010. The expected genotype of ‘Clark’ at this locus was 278/281. However, it was scored as 278/278 (Table 2.4). This result can be explained by the presence of a null allele at CAC-C010 in ‘Tombul Ghiaghli’. Indeed, the CAC-C010 locus has a high positive expected null allele frequency (0.214).

‘Lewis’ was selected from a progeny of 428 seedlings resulting from a cross of OSU 17.028 x ‘Willamette’. OSU 17.028 resulted from a cross of ‘Barcelona’ x ‘Tombul Ghiaghli’ (Mehlenbacher et al., 2000). The genotypes of ‘Lewis’, ‘Willamette’ and the expected genotype of OSU 17.028 (‘Barcelona’ x ‘Tombul Ghiaghli’) showed that the pedigree information of ‘Lewis’ was confirmed except at locus CaT-C504. According to Mendelian segregation, the genotype of ‘Lewis’ at locus CaT-C504 should be 155/167, 158/167 or 161/167. However, the scored genotype was 155/155 (Table 2.4). This can be explained by the presence of a null allele in ‘Willamette’ at this locus. The expected null allele frequency of locus CaT-C504 is 0.109. This locus has a moderately high frequency of null alleles and so the presence of a null allele might be expected.

Outer Groups on UPGMA Phenogram

The outer groups of the phenogram (Fig. 2.2) include the most genetically diverse cultivars of this study. They did not cluster in tight geographic clusters but rather sit on the outside of the major groups discussed. The first outermost cluster includes two cultivars: ‘*C. avellana* AL55’ from Albania and ‘495.049’ from Southern Russia.

The second outlying group includes ‘Cutleaf’ from England and two red leaf cultivars, ‘Fusco Rubra’ from Germany and ‘Ruby’, which resulted from a cross of ‘Chinese Trazel G-4’ x ‘Fusco Rubra’ (Lagerstedt, 1990). The SSR loci data were consistent with the pedigree of ‘Ruby’ (Table 2.4).

The third outlying cluster includes two cultivars, ‘681.078’ from Russia and ‘COR 187’ from Finland. The final outlying cluster consists of ‘Aurea’ from Germany,

‘*C. avellana* COR 627’ from Sweden, ‘Barcelonner Zellernuss’ from England, ‘408.040’ received from the University of Minnesota and ‘Pendula’ from England.

Besides these four outlying clusters, five inner divergent clusters were revealed. The first inner cluster includes 5 cultivars: ‘Zimmerman’ from USA-Oregon, ‘Gasaway’ from USA-Washington, ‘495.072’ from Southern Russia, ‘Tskhenis Dzudzu (not)’ from Georgia and ‘Gulshishvela (not)’ from Georgia. According to the SSR-profiles, ‘Zimmerman’ might be a seedling of ‘Barcelona’ X ‘Gasaway’. This suggestion is supported by the incompatibility alleles of ‘Barcelona’ (S1, S2), ‘Gasaway’ (S3, S26) and ‘Zimmerman’ (S1, S3). Beside that ‘Zimmerman’, like ‘Gasaway’ has qualitative resistance to eastern filbert blight. Tskhenis Dzudzu (not)’ and ‘Gulshishvela (not)’ have complete resistance to EFB. Although they are synonyms, their true identity remains unknown.

The second inner cluster consists of ‘Hodji (not)’ from Georgia and ‘Webb’s Prize Cob’ from England. The third inner pair includes ‘Warsaw Red’ from Poland and ‘Henneman#3’ from USA-Oregon.

In the fourth inner cluster no tight geographical clustering was revealed. Cultivars from different geographical regions grouped together: ‘Napoletana’ from Italy, ‘Gunslebert’ from Germany, ‘Tokolyi Cosford’ from Australia, ‘Gubener Barcelloner’ from Germany, ‘Tonda Bianca’ from Italy and ‘Tonda Rossa’ from Italy. Although hazelnut is produced in a few regions in the southern hemisphere, it’s not native to those regions. ‘Tokolyi Cosford’ is closely related to the German cultivar ‘Gubener Barcelloner’, and Italian cultivar ‘Tonda Rossa’, and all three cultivars have S₂₃ as a

common incompatibility allele. So, 'Tokolyi Cosford' might have German and/or Italian parents.

The last inner group includes Oregon Grower Selection Group # 2 ('Brixnut', 'Gem' and 'Lyons'), 'Brixley's New' and a pair of synonyms: 'Rosset de Valls' and 'Artellet' from Spain. The Oregon Grower Selection Group #2 cultivars are suggested to be selected seedlings of 'Barcelona' and 'Du Chilly', a less important cultivar occasionally used as pollenizer in Oregon. 'Barcelona' has incompatibility alleles S_1 and S_2 , while 'Du Chilly' has S_{10} and S_{14} . All cultivars in Oregon Grower Selection cluster #2 have one incompatibility allele from 'Barcelona' and one allele from 'Du Chilly'. The asserted paternities of these cultivars are consistent with alleles at 21 SSR loci (Table 2.4). The synonyms 'Rosset de Valls' and 'Artellet' have incompatibility alleles S_{14} and S_{18} and produce phenotypically similar medium size, round and compressed nuts in short husks. Furthermore, 'Brixley's New', 'Simon' from Spain and 'Fitzgerald #20' from USA-Oregon placed in this group. 'Tapparona di San Colombano Cortemoli' from Italy clustered loosely with the last inner group, 'Spanish Group #2' and 'Italian Group' (Figure 2.2)

Table 2.4 SSR profiles of some hazelnut accessions at 21 loci

Cultivars	CAC-A014a	CAC-A040	CAC-B005	CAC-B010	CAC-B028	CAC-B29b	CAC-B105	CAC-B111	CAC-C10	CAC-C28	CAC-C040
Cosford	211/217	236/236	277/281	211/211	266/270	116/128	148/153	182/182	278/278	131/141	186/186
Frango #2	211/215	236/246	277/277	211/221	266/266	116/128	140/148	182/188	275/278	141/141	186/186
Volski Round	211/215	236/244	277/277	211/221	256/266	116/116	148/148	182/188	275/278	134/141	186/186
Frango #5	211/215	236/244	277/281	211/221	256/266	116/116	140/148	182/184	275/278	141/141	186/186
Lenka #3	217/217	236/246	277/281	211/221	270/270	128/128	140/153	182/186	278/278	141/141	186/186
Acorn Hazel	217/217	236/246	281/281	211/221	270/270	116/116	140/148	182/188	278/278	141/141	186/186
Barcelona	215/219	234/248	291/295	211/223	254/262	122/128	153/155	182/182	275/278	131/141	186/186
Cosford	211/217	236/236	277/281	211/211	266/270	116/128	148/153	182/182	278/278	131/141	186/186
Daviana	217/217	236/248	277/281	211/211	270/270	116/116	153/155	182/186	278/278	131/131	186/186
Freehusker	211/219	236/248	277/291	211/211	254/266	116/122	148/153	182/182	278/278	131/141	186/186
Ryan	217/219	234/236	277/291	211/223	254/254	116/122	153/155	182/182	275/275	131/141	186/186
Corabel	211/215	234/236	277/295	211/223	262/266	128/128	148/153	182/182	275/278	131/141	186/186
Nixon	215/217	236/248	277/291	211/211	262/270	116/128	148/153	182/182	278/278	131/141	186/186
Woodford	217/219	248/248	281/291	211/211	254/270	116/122	153/153	182/182	278/278	131/131	186/186
Royal	217/219	236/248	277/291	211/211	254/270	116/122	153/153	182/182	278/278	131/144	186/186
Ennis	217/219	234/248	277/295	211/223	254/254	116/128	153/155	182/182	278/278	131/141	186/186
Fitzgerald	217/219	234/236	277/295	211/223	254/270	116/128	155/155	182/186	278/278	131/131	186/186
Nonpareil	217/219	234/248	277/295	211/211	254/270	116/128	153/155	182/186	278/278	131/131	186/186
Butler	217/219	234/248	277/295	211/211	254/270	116/128	153/153	182/182	278/278	131/131	186/186
Barcelona	215/219	234/248	291/295	211/223	254/262	122/128	153/155	182/182	275/278	131/141	186/186
DuChilly	213/217	244/244	281/281	211/223	254/268	124/137	140/155	186/186	278/281	131/144	186/186
Lyons	215/217	234/244	281/291	223/223	262/268	122/137	153/155	182/186	278/281	131/131	186/186
Gem	213/215	234/244	281/291	223/223	254/262	128/137	140/153	182/186	275/278	131/144	186/186
Brixnut	213/219	234/244	281/291	223/223	254/254	128/137	140/153	182/186	275/278	131/144	186/186
Barcelona	215/219	234/248	291/295	211/223	254/262	122/128	153/155	182/182	275/278	131/141	186/186
Rode Zeller	211/217	236/244	277/281	211/219	264/266	116/128	153/155	182/184	275/278	131/141	186/189
Red Fortrin	215/217	234/244	281/295	211/211	262/264	128/128	153/155	182/182	275/275	141/141	186/189

Table 2.4 Continued

Cultivars	CAC-C115	CAC-C118	CAC-C119	CaT-B107	CaT-B502	CaT-B504	CaT-B505	CaT-B507	CaT-B508	CaT-C504
Cosford	193/214	179/179	256/258	134/144	187/195	172/176	106/116	189/195	148/161	152/164
Frango #2	193/214	179/179	256/264	130/144	187/187	172/174	106/118	189/195	148/165	152/152
Volski Round	193/214	179/179	256/264	130/134	187/201	172/174	116/118	189/189	144/161	152/164
Frango #5	193/214	179/179	258/264	130/134	187/187	172/176	116/118	190/195	144/161	152/152
Lenka #3	193/214	179/179	258/264	122/134	187/187	174/176	106/118	190/195	161/161	152/164
Acorn Hazel	214/214	179/179	256/264	130/134	187/187	176/176	116/118	189/189	144/161	152/164
Barcelona	173/193	179/179	258/258	112/134	187/189	158/182	106/120	181/191	157/157	155/158
Cosford	193/214	179/179	256/258	134/144	187/195	172/176	106/116	189/195	148/161	152/164
Daviana	173/193	179/179	258/258	134/134	189/195	172/176	106/116	185/195	161/161	152/164
Freehusker	173/193	179/179	256/258	112/134	187/189	172/182	116/120	181/195	157/161	152/158
Ryan	173/193	179/179	258/258	134/134	187/195	172/182	116/120	191/195	157/161	152/158
Corabel	193/193	179/179	258/258	112/134	187/189	158/172	106/120	181/195	157/161	152/158
Nixon	193/193	179/179	258/258	134/134	187/189	172/182	106/116	181/195	157/161	152/158
Woodford	193/193	179/179	258/258	134/134	189/195	176/182	106/106	185/191	157/157	158/164
Royal	193/193	179/179	258/258	112/134	189/195	172/182	106/116	181/189	148/157	152/158
Ennis	173/193	179/179	258/258	134/134	187/195	158/172	116/120	185/191	157/157	152/155
Fitzgerald	173/193	179/179	258/258	112/134	189/189	158/172	106/120	181/195	157/157	152/155
Nonpareil	173/193	179/179	258/258	134/134	189/189	158/172	106/106	181/185	157/157	152/155
Butler	193/193	179/179	258/258	112/134	189/189	158/172	106/114	181/195	157/161	152/155
Barcelona	173/193	179/179	258/258	112/134	187/189	158/182	106/120	181/191	157/157	155/158
DuChilly	173/193	179/179	258/264	122/130	189/195	176/176	106/114	185/189	157/165	164/164
Lyons	193/193	179/179	258/264	122/134	189/189	176/182	114/120	181/185	157/157	158/164
Gem	173/193	179/179	258/264	112/130	189/195	176/182	114/120	181/185	157/157	158/164
Brixnut	173/193	179/179	258/258	112/122	189/195	176/182	114/120	181/185	157/157	158/164
Barcelona	173/193	179/179	258/258	112/134	187/189	158/182	106/120	181/191	157/157	155/158
Rode Zeller	193/214	179/182	256/264	130/134	187/195	168/176	106/126	189/197	148/157	158/164
Red Fortrin	173/214	179/182	258/264	134/134	187/187	158/176	106/106	189/191	157/157	158/164

Table 2.4 Continued

<i>Cultivars</i>	<i>CAC-A014a</i>	<i>CAC-A040</i>	<i>CAC-B005</i>	<i>CAC-B010</i>	<i>CAC-B028</i>	<i>CAC-B29b</i>	<i>CAC-B105</i>	<i>CAC-B111</i>	<i>CAC-C10</i>	<i>CAC-C28</i>	<i>CAC-C040</i>
Negret	211/217	236/248	291/297	219/223	256/268	122/130	138/155	182/184	275/275	131/144	186/192
Pauetet	211/215	234/248	277/297	219/227	256/256	118/130	153/155	182/182	275/275	131/141	186/192
Tomasina	211/213	236/244	277/291	211/219	256/256	118/118	138/140	184/186	275/275	131/134	186/192
Francoli	211/213	234/248	277/291	211/223	256/256	118/122	140/155	182/184	275/275	131/134	186/186
TGdL	215/221	234/244	277/291	219/219	256/262	118/122	155/155	182/182	275/275	131/131	186/186
Cosford	211/217	236/236	277/281	211/211	266/270	116/128	148/153	182/182	278/278	131/141	186/186
Daria	215/217	234/236	281/291	211/219	262/270	116/122	148/155	182/182	278/278	131/141	186/186
Montebello	215/219	244/244	291/295	219/227	254/262	122/122	155/155	182/188	278/278	131/141	186/186
Willamette	217/219	236/244	291/295	219/223	254/270	122/128	153/155	182/188	278/278	131/131	186/186
Tombul Ghi.	211/215	244/244	279/291	219/225	262/262	122/122	155/155	182/184	281/281	134/141	186/186
Willamette	217/219	236/244	291/295	219/223	254/270	122/128	153/155	182/188	278/278	131/131	186/186
Clark	215/217	244/244	279/295	219/225	262/270	122/128	153/155	182/184	278/278	131/141	186/186
Barcelona	215/219	234/248	291/295	211/223	254/262	122/128	153/155	182/182	275/278	131/141	186/186
Tombul Ghi.	211/215	244/244	279/291	219/225	262/262	122/122	155/155	182/184	281/281	134/141	186/186
Lewis	215/217	236/244	279/291	219/223	262/270	122/122	155/155	182/182	278/278	131/134	186/186
Barcelona	215/219	234/248	291/295	211/223	254/262	122/128	153/155	182/182	275/278	131/141	186/186
Gasaway	215/215	236/244	277/297	211/219	256/278	116/135	153/157	192/192	275/278	144/144	186/189
Zimmerman	215/219	234/236	277/291	211/219	254/278	122/135	153/155	182/192	278/278	141/144	186/189
Tonda Roma.	211/217	238/248	277/291	211/219	262/268	122/122	155/161	182/182	275/275	131/141	183/186
Tombul Ghi.	211/215	244/244	279/291	219/225	262/262	122/122	155/155	182/184	281/281	134/141	186/186
Zimmerman	215/219	234/236	277/291	211/219	254/278	122/135	153/155	182/192	278/278	141/144	186/189
Epsilon	215/217	236/248	277/291	219/225	262/278	122/122	153/155	184/192	275/275	141/144	183/186
Casina	211/217	244/244	277/281	219/227	268/278	118/122	140/155	182/184	275/275	131/141	186/192
Riccia di Tala.	215/219	242/244	277/291	219/223	254/262	122/122	155/155	182/184	275/275	131/141	186/186
Gasaway	215/215	236/244	277/297	211/219	256/278	116/135	153/157	192/192	275/278	144/144	186/189
Gamma	215/217	244/244	277/277	219/223	262/268	122/135	140/157	184/192	275/275	131/144	186/186
Ruby	217/251	236/236	279/281	211/217	264/264	118/130	136/144	184/184	278/278	134/147	186/192
Fusco Rubra	215/217	236/246	277/279	217/219	264/266	116/118	136/140	184/186	272/278	134/134	186/189

Table 2.4 Continued

Cultivars	CAC-C115	CAC-C118	CAC-C119	CaT-B107	CaT-B502	CaT-B504	CaT-B505	CaT-B507	CaT-B508	CaT-C504
Negret	182/214	179/185	258/258	120/134	189/189	176/182	114/126	191/195	157/159	161/161
Pauetet	193/214	179/185	258/258	120/134	187/189	176/176	114/126	181/195	157/159	158/161
Tomasina	173/214	179/185	264/264	120/134	195/195	170/182	106/122	181/191	157/159	161/161
Francoli	182/214	179/185	258/264	120/134	189/195	170/182	106/114	191/191	157/159	161/161
TGdL	173/173	179/179	258/258	134/151	185/189	170/182	114/126	185/191	146/163	158/161
Cosford	193/214	179/179	256/258	134/144	187/195	172/176	106/116	189/195	148/161	152/164
Daria	173/214	179/179	258/258	134/134	187/189	176/182	116/126	191/195	148/163	158/164
Montebello	173/196	179/179	258/260	112/122	183/189	158/182	120/126	181/191	157/157	158/167
Willamette	193/196	179/179	258/258	122/144	189/195	158/182	120/126	189/191	157/161	167/167
Tombul Ghi	173/182	179/179	260/260	116/134	187/187	168/182	118/126	189/197	157/163	158/161
Willamette	193/196	179/179	258/258	122/144	189/195	158/182	120/126	189/191	157/161	167/167
Clark	173/193	179/179	258/258	134/144	187/195	158/168	118/126	189/191	161/163	158/167
Barcelona	173/193	179/179	258/258	112/134	187/189	158/182	106/120	181/191	157/157	155/158
Tombul Ghi.	173/182	179/179	260/260	116/134	187/187	168/182	118/126	189/197	157/163	158/161
Lewis	193/193	179/179	258/258	134/144	187/189	168/182	120/126	181/191	157/161	155/155
Barcelona	173/193	179/179	258/258	112/134	187/189	158/182	106/120	181/191	157/157	155/158
Gasaway	214/217	179/182	258/264	122/128	183/195	174/174	114/120	179/190	146/165	161/164
Zimmerman	173/214	179/182	258/264	128/134	187/195	174/182	106/114	190/191	146/157	158/164
Tonda Romana	173/196	176/179	258/258	134/142	187/191	160/182	118/126	185/189	157/157	152/158
Tombul Ghi.	173/182	179/179	260/260	116/134	187/187	168/182	118/126	189/197	157/163	158/161
Zimmerman	173/214	179/182	258/264	128/134	187/195	174/182	106/114	190/191	146/157	158/164
Epsilon	173/196	176/179	258/258	128/134	187/195	160/182	114/118	190/197	146/157	152/158
Casina	173/196	179/185	256/258	130/134	187/187	176/176	118/126	189/191	167/161	158/158
Riccia di Tala.	182/196	179/179	258/258	118/134	187/197	168/182	118/126	181/185	157/167	155/158
Gasaway	214/217	179/182	258/264	122/128	183/195	174/174	114/120	179/190	146/165	161/164
Gamma	173/196	179/179	258/258	130/134	183/187	168/176	118/126	179/189	161/167	158/161
Ruby	188/214	179/185	260/264	120/122	191/195	164/176	106/122	176/198	144/165	152/152
Fusco Rubra	214/214	179/182	256/264	120/122	189/195	164/174	114/122	189/198	165/165	152/164

Conclusions

The polymorphism and somatic stability of SSR markers and UPGMA cluster analysis in combination with the proportion of shared alleles seems to be a very powerful method to analyze genetic diversity in European hazelnut and other clonally propagated crops. Unlike other distance methods, it makes no assumptions about the nature of the population under study. Especially for a clonally propagated crop like hazelnut, the ‘proportion of shared alleles’ distance method is appropriate (Dangl et al., 2001).

The low probability of randomly matching genotypes (PI index) in this study gives great confidence that our SSRs detected synonyms, identified mislabeled accessions and confirmed pedigree information. The phenogram revealed some tight geographically clustered groups and 70 synonyms in the population. However, SSR markers could not differentiate some synonyms that differ in pellicle color [e.g ‘White Filbert’ (brown pellicle), ‘Purple Fortrin’(red-purple pellicle), ‘Purple Aveline’(red-purple pellicle), ‘Pellicule Rouge’(red-purple pellicle), ‘Istarski Debeloplodna ’(brown pellicle), ‘Fructo Albo’(brown pellicle), ‘Barbarella’ (red-purple pellicle) and ‘Aveline Rouge’(red-purple pellicle)].

Some of the cultivars (e.g. ‘Purple Aveline’, ‘White Filbert’, ‘Webb’s Prize Cob’, ‘DuChilly’, ‘Gunslebert’, ‘Garibaldi’, ‘Ennis’, ‘Butler’, ‘Istarski Duguljasti’ and ‘Pellicle Rouge’) are placed by various taxonomic source in a different species, *Corylus maxima*. However, these cultivars did not cluster together as a separate group; rather they are mixed with other *C. avellana* cultivars. So, our results indicate that *C. maxima* is not a distinct taxonomic group.

SSR markers revealed a great diversity in the Turkish hazelnut cultivars.

However, German and Italian cultivars are less diverse. The lack of genetic diversity was especially striking in the Sicilian group where 11 cultivars were synonyms.

This study included some low informative SSR markers with low H_o and H_e values and with only a few alleles. For small scale fingerprinting studies, loci with high H_o and H_e values and with many alleles are suggested (O'Reilly and Wright, 1995; Testolin et al., 2000).

A second set of DNA samples was extracted from four trees ('Bard', 'Karidaty', 'Istarski Debeloplodna' and 'Riekchen's Zellernuss') and included as checks. PCRs of all controversial fragment sizes such as null allele containing loci or cultivars that differ from each other only at one locus were redone at least once to make sure that the fragment size was correct. The presence of null alleles is a known problem associated with the use of SSR markers (Callen et al., 1993). Null alleles are usually not detected and individuals are scored as homozygous at that locus. This results in a loss of information. The presence of null alleles can be expected in large homogeneous populations, when the observed heterozygosity (H_o) is markedly less than the expected heterozygosity (H_e). The expected null allele frequencies at three loci (CAC-C010, CaT-C504 and CaT-B508) have high positive values and the occurrence of null alleles at these three loci was detected by comparing the pedigree information of some cultivars.

We used 21 SSR loci to characterize 270 hazelnut accessions. The map locations of 16 of these were identified (Chapter 3). We recommend that a subset of these loci be used in future fingerprinting studies, with a preference for loci with high heterozygosity

as indicated by high PIC and PEP values, low PI values, and a low frequency of null alleles. Furthermore, loci in different linkage groups are preferred as they would give better coverage of the genome. According to these criteria, we suggest CAC-B029b and CAC-A040 on chromosome 1, CAC-B010 on chromosome 3, CAC-C115 on chromosome 4, CAC-A014a and CAC-B028 on chromosome 5, CaT-B504 and CAC-C005 on chromosome 7, CAC-C119 on chromosome 8, CaT-B507 on chromosome 9 and CaT-B502 on chromosome 10. These loci generate fragments of different sizes. The use of different florescent labels would allow their use in 3 to 4 multiplexes.

Synonyms are a big problem in the management of hazelnut germplasm collections. Of the 270 accessions screened in this study, 70 (26%) turned out to be synonyms. The high percentage of synonyms might be due to mistakes during propagation and points to a need to verify that the plants in the USDA-ARS-NCGR and OSU hazelnut collections and in other collections around the world are true-to-name.. The SSR loci used in this study could be used to amplify DNA extracted from other collections, and morphological and phenological traits could be compared to those in published descriptions. We encourage the adoption of the standard set of 11 markers listed above for this purpose.

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CHAPTER 3

INTEGRATION OF TWENTY-NINE SSR MARKERS INTO A LINKAGE MAP OF HAZELNUT

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Abstract

Thirty-three simple sequence repeat (SSR) markers were scored in a population of European hazelnut (*Corylus avellana* L.) 144 seedlings from a controlled cross of OSU 252.146 x OSU 414.062. Twenty-nine of them were successfully integrated into the RAPD marker-based linkage map for this population. Two of these loci showed aberrant segregation ratios and were not placed on the map, and two loci remained unlinked. The linkage map, constructed using the two-way pseudo-testcross approach, identified eleven linkage groups for each parent, corresponding to the haploid chromosome number of hazelnut ($2n=2x=22$). The map spanned a total distance of 668 cM in the susceptible parent and 813 cM in the resistant parent. The order of homologous SSR loci in the two parents was collinear in most cases. Placement of these SSR “anchor loci” on the hazelnut linkage map will make it useful in other populations.

Introduction

Hazelnut is a general name used for the nuts of all *Corylus* species. The genus *Corylus* is a member of the Betulaceae or Birch family and includes other important forest tree species and ornamentals (Erdogan and Mehlenbacher, 2000). The European hazelnut, *Corylus avellana* is one of the 25 described species in the genus, all of which produce edible nuts, which are collected from the wild by humans. All *Corylus* species are diploid with $2n = 22$ chromosomes (Kasapligil, 1968; Thompson et al., 1996).

The European hazelnut, *Corylus avellana* L., is grown in many regions of Europe and western Asia and has been used as a food source by humans since prehistoric times. *Corylus avellana*, the species of commerce, is native to Europe and Asia Minor (Kasapligil, 1972).

Hazelnut is clonally propagated and highly heterozygous (Mehlenbacher, 1995). It has a unique floral biology, which was reviewed in detail by Germain (1994). It is monoecious, dichogamous and wind-pollinated (Thompson et al., 1996). The male flowers are borne in catkins, and female inflorescences have no perianth. They appear as a tuft of red stigmatic styles protruding from the apex of compound buds located on shoots or catkin peduncles. The hazelnut tree is self-incompatible, which enforces cross-pollination. Incompatibility is of the sporophytic type, which is under the control of a single locus (the S-locus) with multiple alleles (Mehlenbacher, 1997).

Among the various DNA-based molecular markers, random amplified polymorphic DNA (RAPD) markers are the most commonly used in hazelnut. RAPD markers linked to eastern filbert blight resistance (Davis and Mehlenbacher, 1997;

Mehlenbacher et al., 2003) and to self-incompatibility (Pomper et al., 1998) have been identified at Oregon State University. Furthermore, a linkage map based on RAPD markers was recently developed by Mehlenbacher et al. (2005 a&b). RAPDs are dominant markers. Polymorphism is the result of presence or absence of the priming site in the genomic DNA. RAPD is a fast, easy and inexpensive technique. However, it has some reliability problems. Results are very sensitive to changes in reaction conditions and even different equipment in different laboratories may give different results (Powell et al., 1996).

Microsatellites have become the marker of choice for germplasm “fingerprinting” because of their advantages over other types of markers. Microsatellites or simple sequence repeats (SSRs) are tandemly repeated 1-6 bp sequence motifs found in both eukaryotic and prokaryotic genomes. They are abundant and dispersed throughout the genome and they can be found in both coding and non-coding regions. They are present mostly in the latter due to the fact that non-coding DNA can accumulate mutations more easily than coding DNA (Ahmad et al., 2003). Although the mechanism of microsatellite evolution is not known exactly, it appears most likely due to the slippage of DNA polymerase during DNA replication or unequal crossing-over between homologous chromosomes during recombination (Schlötterer and Tautz, 1992). The majority of microsatellites are dinucleotide repeats located in non-coding regions of the genome (Li et al., 2002). On the other hand, microsatellites found in coding regions are mainly trinucleotide and hexonucleotide repeats, probably due to negative-selection against frameshift mutations in coding regions (Morgante et al., 2002).

Microsatellite markers have been extensively used in fingerprinting (Thomas and Scott, 1993), linkage map construction (Bowcock et al., 1994; Hazan et al., 1992), forensic DNA research, and population genetic studies (Jarne and Lagoda, 1996). Valuable characteristics of SSR markers include a high level of polymorphism, they are co-dominant, only a small quantity of DNA is needed for PCR, loci are usually conserved between related species and even sometimes across genera, they do not require the use of radioactivity and data are scored easily and reproducibly (Zane et al., 2002). The exchange of primer sequences instead of probes allows other labs to work with the same loci and is another advantage of SSR markers. The only disadvantages of microsatellite markers are that they must be isolated *de novo* from most species being examined for the first time and the development of SSRs requires a considerable investment and technical expertise (Zane et al., 2002; Jauhar, 1996).

Linkage map construction by the double pseudo-testcross strategy

Mapping and sequencing of full plant genomes would provide a more complete understanding of gene function, gene regulation and expression. Marker-saturated high-density linkage maps have useful applications in both fundamental and applied genetic research. Molecular markers are extensively used in identification and isolation of genes of interest, and linkage analysis is one of the basic and central techniques in genetics. Linkage can define the genetic distances between polymorphic loci which may be expressed as differences in appearance of enzyme activities, restriction fragment lengths or nucleotide sequences at an allelic locus (Mohan et al., 1997). In the past few years

linkage maps have been constructed for woody perennial plants including *Citrus* (Sankar and Moore, 2001), *Prunus* (Joobeur et al., 1998), cacao (*Theobroma cacao* L.) (Pugh et al., 2004), apple (*Malus x domestica*) (Hemmat et al., 1994; Liebhard et al., 2003), grape (*Vitis vinifera*) (Dalbo et al., 2000, Fischer et al., 2004; Riaz et al., 2004), coniferous forest trees (Scott et al., 1999) and olive (*Olea europae* L.) (Wu et al., 2004). Among the nut crops, linkage maps have been constructed for European hazelnut (*Corylus avellana* L.) (Mehlenbacher et al., 2005 a&b), European chestnut (*Castanea sativa* L.) (Casasoli et al., 2001) and *Macadamia* (Peace et al., 2003).

Construction of a genetic linkage map is a useful step in identifying markers linked to genes controlling traits of interest, and genetic maps can also be used to identify loci that control quantitative traits (Paterson et al., 1991). Similar to other perennial tree crops, the juvenile period of hazelnut ranges from three to six years, with five years being the median (Mehlenbacher and Smith, 1992) and genotypes exhibit sporophytic self-incompatibility (Mehlenbacher, 1997). The 'two-way pseudo-testcross strategy' involves linkage analysis of an F₁ population produced by crossing two highly heterozygous (diploid) parent clones. The first linkage map using this method and PCR-based markers was constructed for *Eucalyptus* (Grattapaglia and Sederoff, 1994). Genetic linkage maps can be constructed using software packages such as MapMaker (Lander et al., 1987), JoinMap 3.0 (van Ooijen and Voorrips, 2001) or GMendel (Holloway et al., 1994). The two important issues in linkage map construction are locus order and distance. The likelihood odds (LOD) score is the test statistic used to test the hypothesis that there is no linkage against the alternative hypothesis that there is linkage. A LOD score of 3.00 is

roughly equal to $P=0.001$. So, if $LOD \geq 3.00$, it is very likely that two loci are linked (Li et al., 2003). Linkage distances with the highest LOD scores are the best estimates of real linkage distances.

The objective of this study was to score 33 SSR markers in a population of 144 seedlings and to place them on the RAPD marker-based linkage map constructed by Mehlenbacher et al. (2005 a&b). Because of their ease of use, high information content and co-dominant nature, SSR markers are valuable additions to dominant markers and RFLP markers in mapping projects (Dib et al., 1996). Placement of SSR markers on the hazelnut linkage map would allow them to serve as “anchor loci” that are useful in other segregating populations.

Materials and Methods

Plant material and DNA extraction

The mapping population, a total of 144 seedlings, was generated in 1993 from a controlled cross of two heterozygous clones. The maternal parent, OSU 252.146, is susceptible to eastern filbert blight, while the paternal parent, OSU 414.062, is heterozygous resistant. Two sets of fresh young leaves for each of 144 seedlings and the two parents were collected in the spring of 2004 from the collection of Oregon State University in Corvallis, Oregon. DNA was extracted according to Lunde et al. (2000) with minor modifications and RNA was removed by incubation with RNase A (Sigma, St. Louis, MO) at 37 °C for one hour in a shaker, followed by extraction with 25 phenol: 24 chloroform: 1 isoamyl alcohol. The DNA concentrations were determined spectrophotometrically, adjusted to 5 ng/μl and the DNA was stored at -18 °C until used for PCR.

Amplification and allele sizing

Primer pairs for 24 loci developed in Corvallis (CAC) (Bassil et al., 2005) and for 9 loci developed in Torino (CaT) (Boccacci et al., 2005) (Table 3.1) were chosen for this study. Reverse primers were purchased from Operon Technologies (Qiagen, Valencia, CA). Forward primers fluorescently labeled with FAM and HEX were purchased from Operon Technologies and with NED from Applied Biosystems (Foster City, CA). PCR reactions were performed in a total volume of 10 μl and the reaction mixture contained 1X Biolase NH₄ reaction buffer, 2 mM MgCl₂, 200 μM each of dATP, dCTP, dGTP, and

dTTP, 0.3 μ M each of forward and reverse primers, 0.25 units of Biolase DNA polymerase (Bioline Inc., Randolph, MA), and 2.5 ng of template DNA. The PCR program consisted of 35 cycles of a 40 s denaturation step at 94 °C, a 40 s annealing step at the optimum annealing temperature (Table 3.1), and a 40 s extension step at 72 °C. Finally one 30-min extension step at 72 °C was run to maximize non-templated adenosine addition to the 5' ends. PCRs were run in Perkin-Elmer model 9700 thermocyclers (PE Applied Biosystems, Foster City, CA). PCR amplification and approximate fragment sizes were confirmed on 3% agarose gels using 4 μ l of aliquot and 5 μ l of loading dye (15% Ficoll® 400, 0.03% xylene cyanol FF, 0.4% orange G, 10mM Tris-HCL pH 7.5, and 50 mM EDTA). Gels were stained with ethidium bromide and photographed under UV-light by an imaging system (UVP, Upland, CA). Amplified PCR products were diluted forty times with nanopure water and kept as stock for multiplexing. Stock solutions were further diluted 2 to 16 (Table 3.1) times and 1 μ l of mix of four to five (Appendix A) PCR products were separated on an ABI 3100 capillary electrophoresis instrument (Applied Biosystems, Foster City, California) at the OSU Central Services Laboratory (CSL), and DNA fragments were sized using GeneScan and Genotyper software.

Integration of SSR markers into a linkage map of hazelnut

The software package JoinMap 3.0 (van Ooijen and Voorrips, 2001) was used to construct the linkage map by integrating the SSR loci reported in this chapter with the RAPD markers previously mapped in hazelnut by Mehlenbacher et al. (2005 a&b).

Table 3.1 Description of 33 microsatellite loci: the repeat motif, sequence of the fluorescent forward primer (*FAM*, *NED*, *HEX*) and the reverse primer (*R*), the optimum annealing temperature (*T_m*), dilution cofactor in multiplex, allele size range and linkage group*

SSR Locus	Motif	Primers (5' – 3')	T _m	Dilution	Allele Size Range	Linkage Gr ^c
CAC-A014a	(CA) ₁₃	<i>FAM</i> -GGTTTGTACAGAAATTCAGACG <i>R</i> -GCGTGTGGTTAATGTTTTCTTT	60°C	1:640	203-251	5S, 5R
CAC-A24b	(GA) ₁₈ (AT) ₇	<i>NED</i> -CACAACATGCAACGTCTATGTA <i>R</i> -AGGTACGTATTGACAGGCTTTT	62°C	1:120	118-138	7R
CAC-A040	(CA) ₁₃	<i>NED</i> -TGCTCAAGCAAATATTGCAC <i>R</i> -GTTTGGGATCCAATTAACCCTCT	62°C	1:213	234-248	1S, 1R
CAC-A102	(AG) ₁₆ (AC) ₁₅	<i>HEX</i> -AAACTGTGACGAACGAAAACAC <i>R</i> -TTGCACTTCCATAACTGTCAAA	62°C	1:80	269-307	9S, 9R
CAC-B005	(GA) ₂₂	<i>FAM</i> -CAAACCTATGATAGGCATGCAA <i>R</i> -TGTCACCTTGGGAAGACAAGAGA	62°C	1:320	277-297	7R
CAC-B010	(GA) ₁₆	<i>FAM</i> -AGCTTCCAAATCACACATTACC <i>R</i> -GAAGAGCATCCGTATGATTGAG	62°C	1:320	211-227	3S, 3R
CAC-B011	(GA) ₁₁	<i>NED</i> -CACTGGTGATCTCACAGGTTTA <i>R</i> -GTCCTCAAAAAGCTAAGCACAAG	62°C	1:240	131-157	2S, 2R
CAC-B020	(GA) ₁₉	<i>HEX</i> -GGGAAAATACTCCAAATCGCT <i>R</i> -TCACCGAGCCGTCATAATC	60°C	1:240	273-289	7R
CAC-B028	(AG) ₁₆	<i>NED</i> -ATGGACGAGGAATATTTTCAGC <i>R</i> -CCTGTTTCTCTTTGTTTTCGAG	55°C	1:213	252-288	5S, 5R

Table 2.2 Continued

SSR Locus	Motif	Primers (5' – 3')	T _m	Dilution	Allele Size Range	Linkage Gr ^e
CAC-B029b	(GA) ₁₃	<i>NED</i> -CAATTTACACCTCAGGGAAGAG <i>R</i> -AAGTTCACCCAAGAAATCCAC	58°C	1:160	114-139	1S, 1R
CAC-B101	(AG) ₁₄	<i>HEX</i> -GCAGACCAGAGTCTGTTATTCA <i>R</i> -AGACAATTTCTGACTGGGTAT	62°C	1:480	135-180	unlinked
CAC-B105	(GA) ₁₆	<i>HEX</i> -AAAGGAGCAAGCATGTTAGG <i>R</i> -GTTTGTACGGATGATCCACTGAG	62°C	1:320	125-163	10S, 10R
CAC-B109	(GA) ₂₁	<i>HEX</i> -AATCCAAGCCTTTTCACTACC <i>R</i> -ACCCATCAAGTTCACCAATC	58°C	1:320	145-155	9S
CAC-B113	(GA) ₁₄	<i>HEX</i> -TTGAGGAAGTCCAGGAAAAT <i>R</i> -GCCAGAGAGAGCAAGAGTTAG	60°C	1:320	167-179	2R
CAC-B114	(GA) ₁₄	<i>HEX</i> -TTCCCCTCTCAAAGCCAC <i>R</i> -GAAGGTTGAAGAAGAGCAACAG	64°C	1:480	138-153	not placed
CAC-C001a	(CACAGAG) ₃	<i>FAM</i> -CCCGTAACTAACCAATCACAAT <i>R</i> -TGGAGAAGAGGAGAGCTTAGTG	58°C	1:320	200-220	9S, 9R
CAC-C005	(GAA) ₈	<i>NED</i> -GCTCTGAAACTATCGCTAGACG <i>R</i> -GTCTGCCATTTGTGGTCTGT	58°C	1:320	97-127	not placed
CAC-C008	(AAG) ₁₁	<i>FAM</i> -TTTCCGCAGATAATACAGGG <i>R</i> -TCCTTTGCTTTGGACCAG	58°C	1:320	200-245	4S, 4R

Table 2.2 Continued

SSR Locus	Motif	Primers (5' – 3')	Tm	Dilution	Allele Size Range	Linkage Gr ^e
CAC-C028	(GAA) ₁₀	<i>NED</i> -CTACCCCATCGCTTGACAC <i>R</i> -GGAGACTTGTTTGCCACAGA	60°C	1:213	131-147	10R
CAC-C040	(GAA) ₈ (GGA) ₅	<i>FAM</i> -AGCCCCATTAGCCTTCTTAG <i>R</i> -GTTTCCAGATCTGCCTCCATATAAT	62°C	1:320	168-192	4R
CAC-C114	(TTC) ₆	<i>HEX</i> -TCTCCCTCTCCCTCTCTTCTAC <i>R</i> -GAAAGGAAAAAGCACATAGCAA	60°C	1:400	255-279	5S, 5R
CAC-C115	(TAA) ₅ (GAA) ₁₂	<i>FAM</i> -CATTTTCCGCAGATAATACAGG <i>R</i> -GTTTCCAGATCTGCCTCCATATAAT	60°C	1:320	167-225	4S, 4R
CAC-C118	(AAG) ^b	<i>HEX</i> -AGCAACAGAGGTTAGGTGTG <i>R</i> -GCCCCATTAGCCTTCTTA	60°C	1:320	162-185	4R
CAC-C119	(GA) ₇ (GA) ₉	<i>NED</i> -CTCACCTTTACCCCTTCATTTT <i>R</i> -GTTTCCTCATCTTCTGAGAACCATC	62°C	1:213	256-264	8R
CaT-A114	(TG) ₁₇	<i>FAM</i> -CGCCTTGATAGTATGTTCAAAC <i>R</i> -CGGCAGAATGTAGAAGTCCCC	60°C	1:320	165-181	4S, 4R
CaT-B106	(AG) ₁₇ AA(AG) ₆	<i>HEX</i> -CCAATCGCCAATGAATCATC <i>R</i> -CCCTTTCCAAACTGGGCAT	60°C	1:320	156-181	unlinked
CaT-B107	(CT) ₁₄	<i>NED</i> -GTAGGTGCACTTGATGTGCTTTAC <i>R</i> -AACACCATATTGAGTCTTTCAAAGC	58°C	1:160	112-151	10R

Table 2.2 Continued

SSR Locus	Motif	Primers (5' – 3')	Tm	Dilution	Allele Size Range	Linkage Gr ^e
CaT-B501	(GA) ₂₁	<i>NED</i> -GAAATTCAATCACACCAATAAAGCA <i>R</i> -CCTCCCTTGTCTCATCACTG	64°C	1:160	117-137	2R
CaT-B502	(CT) ^c	<i>FAM</i> -CTCATGACTGCCCCATTTCTCG <i>R</i> -AGGCATGCAGGCTTCACAC	62°C	1:400	183-211	10S, 10R
CaT-B504	(CT) ₁₈	<i>HEX</i> -CGCCATCTCCATTTCCCAAC <i>R</i> -CGGAATGGTTTTCTGCTTCAG	60°C	1:400	158-184	7R
CaT-B507	(GA) ^d	<i>FAM</i> -CTA AGCTCACCAAGAGGAAGTTGAT <i>R</i> -GCTTCTGGGTCTCCTGCTCA	62°C	1:400	176-198	9S, 9R
CaT-B509	(GA) ₁₄	<i>HEX</i> -GTCTGGCATGGTTTTGAGAAGA <i>R</i> -CTTTCCCGCCCAAACCAC	62°C	1:320	109- 119	7R
CaT-C502	(CTT) ^e	<i>HEX</i> -GCATGCAAGGTGGTCGGT <i>R</i> -TTTGGCACCCAACAACCTCTAGA	62°C	1:320	151-166	9R

^a (GAA)₇GGA(GAA)₂N₂₁(GAA)₂ATT(GAA)₄N₁₅(GAA)₃

^b (AAG)₃(GAA)₃(AAG)₈N₆(AAG)₄

^c GA)₁GC(GA)₂GC(GA)₁₄

^d (CT)₁₆GCTTTTC(CT)₅

^e Figure 3.1

JoinMap requires a certain format for entering the data. Marker data were scored as 1 for the presence of an allele, 0 for the absence of an allele, or n for unknown, according to the parental origin of the alleles of each marker. For SSR loci, data were scored for each allele. Presence of one allele in a seedling meant absence of the other allele from that parent at that locus. Two data sets were obtained, one for the susceptible maternal parent OSU 252.146 (S) and one for the resistant paternal parent OSU 414.062 (R). Afterward, the marker data sheets were recoded as “h” for 1, “a” for 0 and “u” for n, and then saved as a tab-delimited text file and imported into JoinMap 3.0. For loci segregating with 1:2:1 ratios, the parental origin of alleles in heterozygous seedlings could not be determined. Therefore, the indicator variable for each allele was coded as “u” for unknown.

Four segregation patterns were expected for the SSR loci: 1 : 1 from the maternal parent, 1 : 1 from the paternal parent, and 1 : 2 : 1 or 1 : 1 : 1 : 1 from both parents (heterozygous in both parents). Observed segregation ratios were compared to the expected Mendelian segregation ratios using a chi-square (χ^2) goodness-of-fit test. Computed χ^2 values were compared to the critical values from theoretical distributions. The appropriate degrees of freedom (df) were calculated by subtracting one from the number of genotypic classes (Table 3.2). The Yates correction factor was not used.

A preliminary analysis was performed using a small group of about 250 RAPD markers for each parent to allow assignment of the SSR markers to a linkage group on the preliminary map (Mehlenbacher et al., 2005 a&b). A critical LOD value ≥ 5 and the default recombination frequency of 0.40 were used to detect linkage and minimize the merging of groups at lower values. After linkage group assignment, individual SSR

marker data were appended to the RAPD marker data for the same linkage group. To be able to distinguish the SSR markers from RAPD markers on the map, an asterisk sign “*” was placed before the label of each SSR marker. Linkage maps were constructed independently for each group using the “LOD grouping tree” command. Following the first mapping attempt, JoinMap listed the RAPD markers and linked SSR alleles, followed by an error message, “insufficient linkage to above group”, and a second group of SSR alleles. The first group includes SSR alleles linked in coupling to the RAPD markers and the second group consists of markers that are linked in repulsion. The second group was removed and JoinMap created a map for each linkage group. The Kosambi mapping function was used to convert the recombination frequencies into map distance (Kosambi, 1944). JoinMap tests each marker with a chi-square test for goodness-of-fit. The highest chi-square value allowed was arbitrarily set at 6 and markers with larger values were removed in stepwise fashion until all markers in each linkage group had a value of less than 6.

Results and Discussion

Microsatellite map position

The genotypes of each of the 144 seedlings and the two parents were successfully determined at all 33 SSR loci. Analysis of segregation ratios showed that two of thirty-three SSR markers (6%) (CAC-B114, CAC-C005) displayed a significant deviation from expected ratios ($P < 0.05$) (Table 3.2). JoinMap assigned both of these markers to linkage groups. CAC-B114 could be placed only on chromosome 11 of the susceptible parent, although both parents are heterozygous at this locus. On the other hand, CAC-C005 was mapped on chromosome 6 of both resistant and susceptible parents, but did not show perfect colinearity. Because of these aberrations, both were removed from the map. CAC-B101 and CaT-B106 had low chi-square values but could not be placed on the map and are listed as unlinked loci.

After adding the SSR loci to the map, two RAPD markers (487-500 on chromosome 2 of the resistant parent and 217-750 on chromosome 1 of the susceptible parent) showed high chi-square values and were removed from the maps. Of the 33 SSR primers, 29 of them (88%) were successfully integrated into a RAPD marker-based hazelnut linkage map at LOD scores of 5.0 and 7.0 (Figure 3.1). Eleven linkage groups were identified for each parent, corresponding to the haploid chromosomes number of hazelnut ($2n=2x=22$) and spanning a total distance of 668 cM in the susceptible parent and 813 cM in the resistant parent. 270 markers, 19 of which are SSRs, were placed on

Table 3.2 Segregation analysis of microsatellite markers

SSR Locus	♀ x ♂	Expected ratio	Progeny segregation	χ^2	df	P
CAC-A24b	(130/130) x (126/134)	1 : 1	73 : 71	0.028	1	0.867
CAC-B005	(295/295) x (279/291)	1 : 1	70 : 74	0.444	1	0.505
CAC-C028	(131/131) x (141/144)	1 : 1	63 : 81	2.25	1	0.134
CAC-B109	(149/151) x (151/151)	1 : 1	70 : 74	0.111	1	0.739
CAC-B113	(173/173) x (173/175)	1 : 1	59 : 85	4.694	1	0.03
CAC-B101	(173/175) x (173/173)	1 : 1	69 : 75	0.25	1	0.617
CAC-C040	(186/186) x (186/189)	1 : 1	62 : 82	2.777	1	0.096
CAC-C118	(179/179) x (179/182)	1 : 1	61 : 83	3.361	1	0.067
CAC-C119	(258/258) x (260/264)	1 : 1	71 : 73	0.027	1	0.869
CaT-C502	(155/155) x (155/159)	1 : 1	71 : 73	0.027	1	0.869
CaT-B504	(158/158) x (168/182)	1 : 1	69 : 75	0.25	1	0.617
CaT-B106	(168/180) x (180/180)	1 : 1	71 : 73	0.027	1	0.869
CaT-B107	(112/112) x (112/128)	1 : 1	68 : 76	0.444	1	0.505
CAC-A14a	(215/219) x (215/219)	1 : 2 : 1	27 : 80 : 37	1.917	2	0.383
CAC-A102	(289/303) x (289/303)	1 : 2 : 1	41 : 73 : 30	1.708	2	0.426
CAC-B028	(254/262) x (254/262)	1 : 2 : 1	36 : 81 : 27	3.375	2	0.185
CAC-C005	(110/116) x (110/116)	1 : 2 : 1	31 : 40 : 73	52.944*	2	<0.001
CAC-A040	(233/244) x (244/248)	1 : 1 : 1 : 1	27 : 33 : 40 : 44	4.722	3	0.193
CAC-B010	(208/219) x (215/221)	1 : 1 : 1 : 1	30 : 38 : 41 : 35	1.833	3	0.608
CAC-B011	(135/152) x (143/152)	1 : 1 : 1 : 1	38 : 30 : 43 : 33	2.722	3	0.437

Table 3.2 Continued

SSR Locus	♀ x ♂	Expected ratio	Progeny segregation	χ^2	df	P
CAC-B020	(283/285) x (277/283)	1 : 1 : 1 : 1	38 : 31 : 41 : 34	1.611	3	0.657
CAC-B029b	(116/128) x (116/122)	1 : 1 : 1 : 1	35 : 38 : 37 : 34	0.277	3	0.964
CAC-B105	(153/155) x (155/159)	1 : 1 : 1 : 1	33 : 35 : 30 : 46	4.055	3	0.256
CAC-B114	(144/149) x (142/144)	1 : 1 : 1 : 1	55 : 9 : 69 : 11	77.889*	3	<0.001
CAC-C001a	(210/212) x (210/214)	1 : 1 : 1 : 1	35 : 40 : 39 : 30	1.722	3	0.632
CAC-C008	(206/215) x (206/239)	1 : 1 : 1 : 1	32 : 45 : 29 : 38	4.166	3	0.244
CAC-C114	(270/273) x (264/273)	1 : 1 : 1 : 1	39 : 24 : 42 : 39	5.5	3	0.139
CAC-C115	(182/193) x (182/214)	1 : 1 : 1 : 1	33 : 46 : 29 : 36	4.388	3	0.223
CaT-A114	(165/171) x (169/173)	1 : 1 : 1 : 1	30 : 37 : 31 : 46	4.5	3	0.212
CaT-B501	(115/129) x (121/129)	1 : 1 : 1 : 1	37 : 31 : 40 : 36	1.166	3	0.761
CaT-B502	(189/195) x (183/187)	1 : 1 : 1 : 1	40 : 30 : 42 : 32	2.888	3	0.409
CaT-B507	(181/191) x (191/197)	1 : 1 : 1 : 1	38 : 31 : 34 : 41	1.611	3	0.657
CaT-B509	(109/111) x (107/109)	1 : 1 : 1 : 1	34 : 36 : 43 : 31	2.166	3	0.539

* $P < 0.05$

eight chromosomes of the susceptible parent and 305 markers, 33 of which are SSRs, were placed on nine chromosome of the resistant parent. No SSR markers other than CAC-C-005 as mentioned above could be placed on chromosome 6, where the eastern filbert blight resistance gene from ‘Gasaway’ is located.

The order of homologous loci was collinear in most cases. JoinMap initially placed four SSR loci, CAC-A024b, CaT-B504, CAC-B005 and CAC-B113 on both chromosome 2 and chromosome 7 of the resistant parent. A similar problem was encountered with RAPD markers by Mehlenbacher et al. (2005 b) who reported that JoinMap created 11 linkage groups in the susceptible parent but only 10 linkage groups in the resistant parent. The RAPD markers initially placed on large linkage group 2 in the resistant parent were separated by MapMaker into linkage group 2 and linkage group 7. Indeed, CAC-B011 and CaT-B501 were placed on chromosome 2 of the susceptible parent indicating that group 2R is the correct assignment for these loci. Likewise, CaT-B509 and CAC-B020 were placed on chromosome 7 of the susceptible parent indicating that group 7R is the correct assignment for these loci. To identify the correct location of the other four loci (CAC-A024b, CAT-B504, CAC-B005 and CAC-B113), another linkage analysis was performed with MapMaker. MapMaker removed CAC-B113 from chromosome 7R and placed it on 2R. Loci CAC-B005 and CaT-B504 were positioned on both 2R and 7R. However, chi-square values for linkage on 7R were lower, which indicates a better fit, so they were placed on chromosome 7R. Locus CAC-A024b was also placed on chromosome 2R and 7R, but since it was tightly linked to loci CAC-B005 and CaT-B504 it was also placed on chromosome 7R.

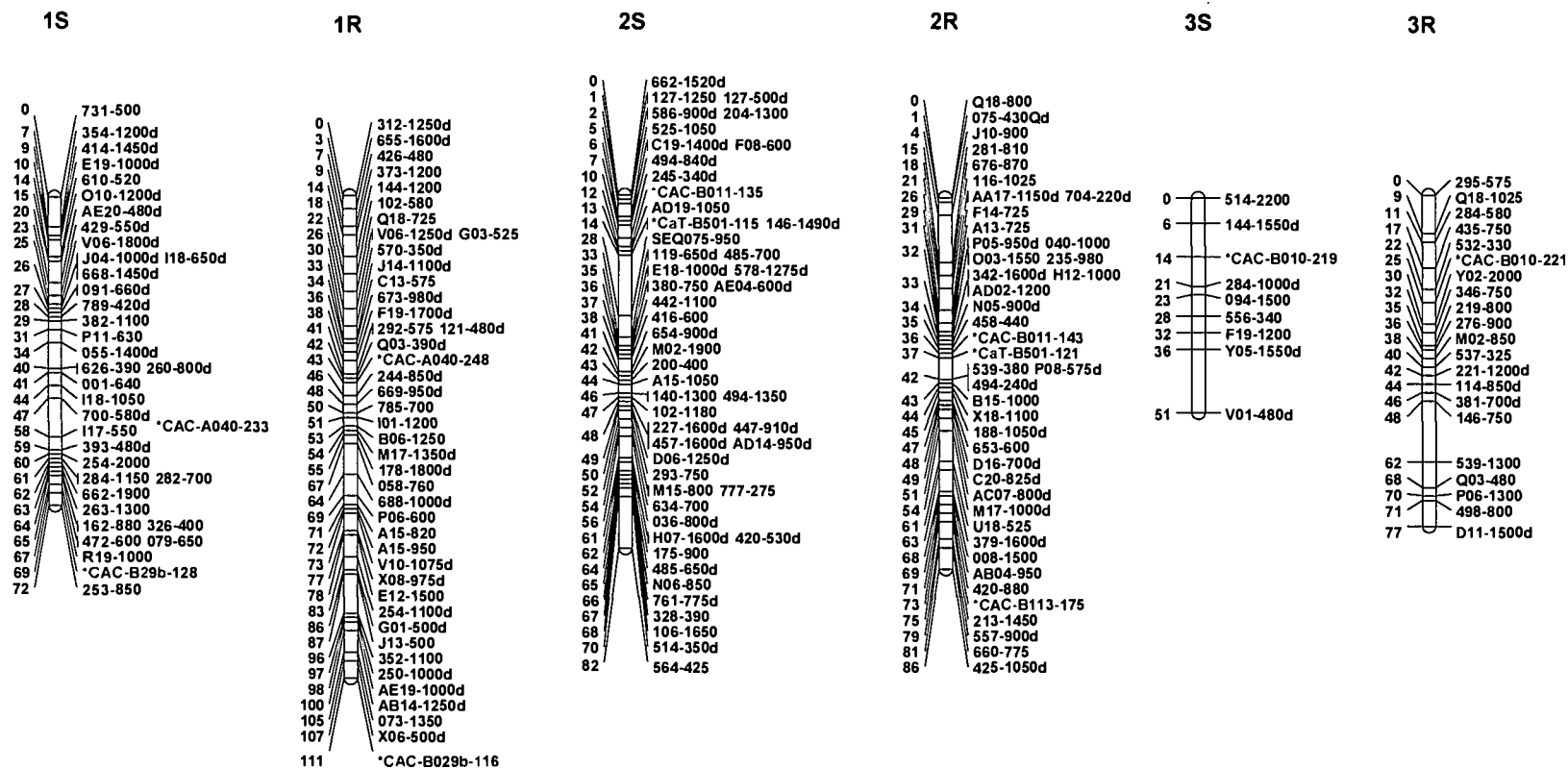


Figure 3.1 Genetic linkage map of European hazelnut (*Corylus avellana*) based on SSR and RAPD markers. The linked allele size is shown for each SSR locus. For each linkage group marker names are shown on the right and distance between markers in cM is shown on the left. SSR markers are indicated with an asterisk (*).

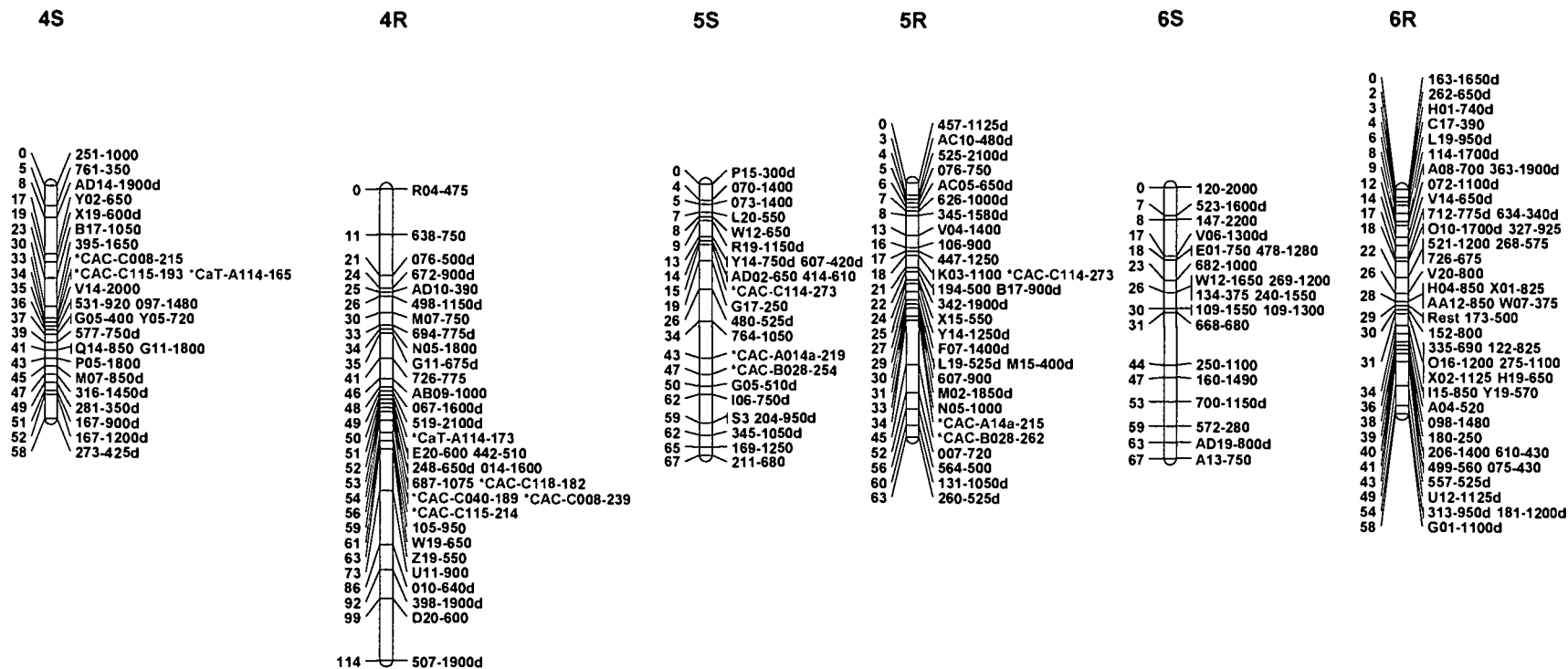


Figure 3.1 Continued

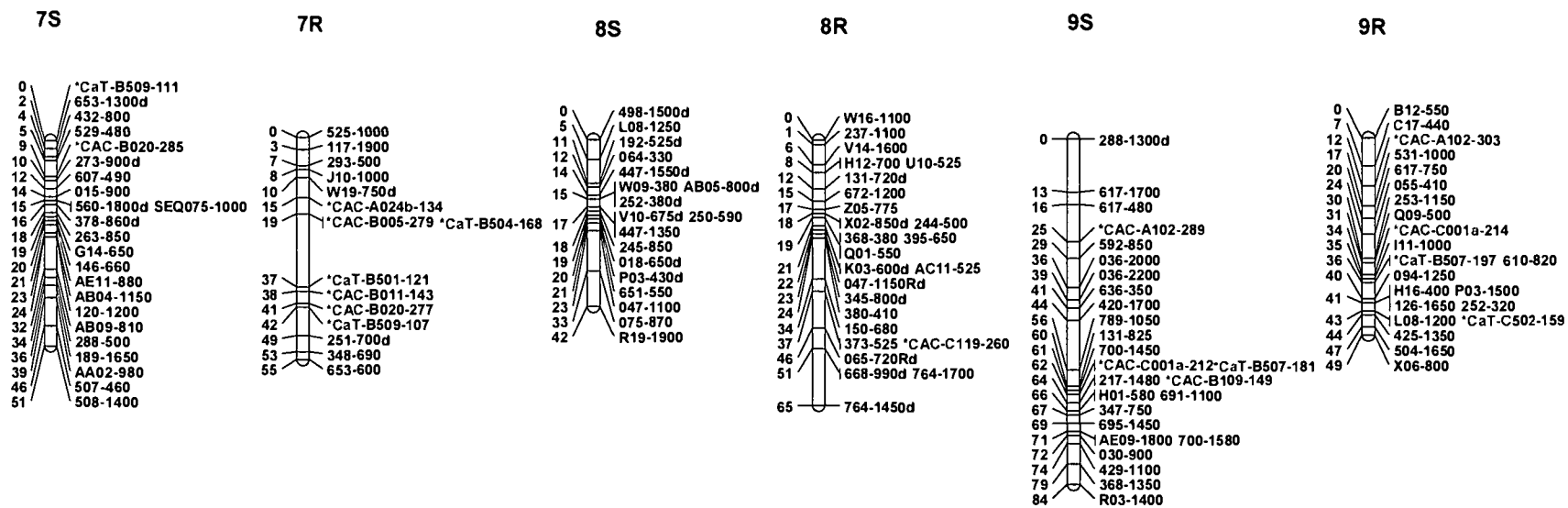


Figure 3.1 Continued

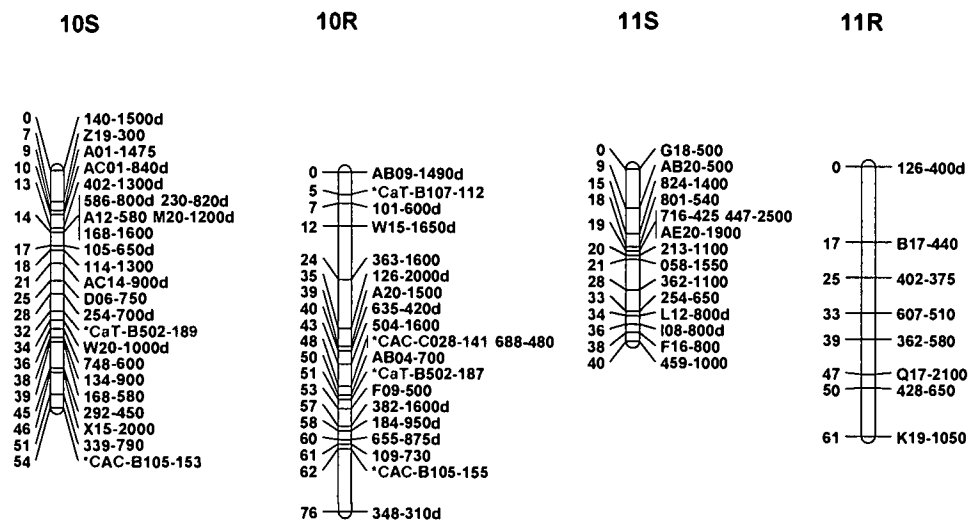


Figure 3.1 Continued

Conclusion

In this study we placed 29 of 33 SSR markers on the RAPD-based hazelnut linkage map. Although the percentage is high (88%), the number of loci is low and no SSR loci were placed in group 6 where the eastern filbert blight resistance gene is located. Identification of additional SSR loci and their placement on the linkage map will allow development of a more saturated microsatellite-based framework linkage map. Placement of these SSR and additional “anchor loci” on the hazelnut linkage map will make it more useful, as their locations are highly conserved and transferable to other populations. Such a map could be used in studies of genome structure, the localization of genes of interest, and allow identification of quantitative trait loci (QTLs) (Liebhard et al., 2003). SSR loci may also be useful in marker assisted selection (MAS) in breeding programs.

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CHAPTER 4

SUMMARY

Twenty-one pairs of simple sequence repeat (SSR) primers were used to investigate genetic diversity in 270 accessions of European hazelnut (*Corylus avellana*) representing a wide geographic range. A total of 211 alleles were amplified and the number of alleles detected ranged from 5 to 15 per locus with an average of 10.05. The observed heterozygosity (H_o) for individual loci ranged from 0.24 to 0.88, with an average of 0.67 over all loci. A genetic similarity matrix based on possible pair-wise combinations of accessions using the “proportion of shared alleles” was generated. UPGMA cluster analysis was used to construct a phenogram from the genetic similarity matrix using. The phenogram revealed geographically tight clusters and some synonyms among European hazelnut cultivars. Of the 274 accessions in the population, 200 are unique cultivars, 70 are suspected synonym accessions (different trees), as they are morphologically identical, but were imported from different collections under different names, and 4 are duplicate DNA templates from the same tree included as checks. 22 of 211 total alleles amplified were unique, as they were detected only in one cultivar. Nine of the unique alleles were amplified in genetically diverse cultivars, outside of the tightly clustered cultivar groups. A subset of 11 loci is recommended for use in future fingerprinting studies in hazelnut.

This study showed that the polymorphism and somatic stability of SSR markers and UPGMA cluster analysis in combination with the proportion of shared alleles seems

to be a very powerful method to analyze genetic diversity in European hazelnut. Unlike other distance methods, it makes no assumptions about the nature of the population under the study. Especially for a clonally propagated crop like hazelnut, the ‘proportion of shared alleles’ distance method is appropriate. The low probability of randomly matching genotypes (PI index) in this study gives great confidence that our SSRs detected synonyms, identified mislabeled accessions and confirmed pedigree information.

This study also showed that SSR markers can be successfully placed on the RAPD-based hazelnut linkage map. Total of 144 seedlings from a controlled cross OSU 252.146 x OSU 414.062 were scored for 33 SSR markers, and 29 of them (88%) were integrated into the hazelnut linkage map. Two additional loci showed aberrant segregation ratios and remained unlinked. The linkage map was constructed using the two-way pseudo-testcross approach from the mapping population. Eleven linkage groups were identified for each parent, corresponding to the haploid chromosomes number of hazelnut ($2n=2x=22$) and spanning a total distance of 668 cM in the susceptible parent and 813 cM in the resistant parent. The order of homologous SSR loci in the two parents was collinear in most cases.

Placement of these SSR “anchor loci” on the hazelnut linkage map will make it useful in other populations. Although most loci were assigned to a map location, only a small number of SSR loci were included in this study and no SSR was assigned to linkage group 6 where the resistance gene is located. Development of new SSR loci and their placement on the linkage map will lead to a more microsatellite-based framework linkage map. Placement of these SSR and additional “anchor loci” on the hazelnut

linkage map will make it useful in other populations, as they are highly conserved and transferable to other populations. Such a map could be used in studies of genome structure, localization of genes of interest, and identification of quantitative trait loci (QTLs). Furthermore, the map locations of SSR markers would be useful in future fingerprinting studies. SSR loci on different chromosomes rather than ones linked to each other would provide a better genomic coverage. Placement of SSR loci on the linkage map may also makes them useful in marker-assisted selection (MAS) in breeding programs.

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APPENDICES

Appendix A Multiplexing of fluorescently labeled SSR primers

Table A.1 Suggested multiplexing of fluorescently labeled SSR primers in Chapter 2

Ned	Hex	Fam	Ned	Hex	Fam
100-150	151-180	181-250	251-280	281-300	>300
CaT-B107 (112-151)	CAC-B111 (170-192)	CAC-A014a (203-251)			B005 (277-297)
CAC-C28 (131-147)	CaT-C504 (152-173)	CaT-B502 (183-211)			
	CaT-B508 (142-167)	CaT-B507 (176-198)	CAC-C119 (256-264)		
CAC-B029b (114-139)		CAC-C040 (62,168-192)	CAC-B028 (252-288)		
CaT-B505 (106-139)	CAC-B105 (125-163)	CAC-C115 (60,167-225)	CAC-A040 (234-248)		
	CaT-B504 (158-184)	CAC-B010 (62, 211-227)	CAC-C010 (272-319)		
	CAC-C118 (162-185)				

Table A.2 Suggested multiplexing of fluorescently labeled SSR primers in Chapter 3

Ned	Hex	Fam	Ned	Hex	Fam
100-150	151-180	181-250	251-280	281-300	>300
CAC-C005 (97-127)	CAC-B114 (138-153)	CaT-A114 (165-181)	CAC-A040 (234-248)	CAC-A102 (269-307)	
CaT-B107 (112-151)	CAC-B113 (167-179)	CAC-A014a (203-251)	CAC-B020 (273-289)		B005 (277-297)
CAC-C028 (131-147)	CaT-B106 (156-181)	CaT-B502 (183-211)	CAC-C114 (255-279)		
CAC-A024b (118-138)	CAC-B109 (145-155)	CaT-B507 (176-198)	CAC-C119 (256-264)		
CAC-B029b (114-139)	CaT-B504 (158-184)	CAC-C040 (168-192)	CAC-B028 (252-288)		
CaT-B501 (117-137)	CAC-C118 (162-185)	CAC-B010 (211-227)			
CAC-B011 (131-157)	CAC-B105 (125-163)	CAC-C001a (200-220)			
	CaT-B509 (109-119)	CAC-C115 (167-225)			
	CAC-B101 (135-180)	CAC-C008 (200-245)			
	CaT-C502 (151-166)				

Appendix B Allelic composition of 274 European hazelnut cultivars

Table B.1 Allele numbers (n), expected heterozygosity (H_e), observed heterozygosity (H_o), polymorphism information content (PIC), probability of identity (PI), parental exclusion probability (PEP) and frequency of null alleles (r) of 21 SSR studied in 274 European hazelnut cultivars

SSR Locus	n	H_e	H_o	PIC	PI	PEP	r
CAC-A014a	12	0.75	0.69	0.71	0.18	0.53	0.035
CAC-A040	8	0.72	0.73	0.68	0.20	0.49	-0.003
CAC-B005	10	0.78	0.84	0.75	0.14	0.58	-0.029
CAC-B010	7	0.78	0.78	0.75	0.14	0.58	-0.002
CAC-B028	15	0.84	0.69	0.82	0.08	0.69	0.082
CAC-B029b	13	0.80	0.74	0.77	0.12	0.62	0.033
CAC-B105	15	0.70	0.64	0.68	0.16	0.51	0.039
CAC-B111	8	0.69	0.59	0.65	0.23	0.46	0.059
CAC-C010	5	0.59	0.23	0.52	0.39	0.31	0.222
CAC-C028	6	0.68	0.77	0.63	0.27	0.43	-0.051
CAC-C040	5	0.27	0.27	0.26	0.56	0.15	-0.001
CAC-C115	14	0.80	0.81	0.77	0.12	0.61	-0.007
CAC-C118	5	0.28	0.29	0.28	0.54	0.16	0.002
CAC-C119	5	0.54	0.49	0.50	0.34	0.31	0.032
CaT-C504	7	0.78	0.62	0.75	0.14	0.58	0.094
CaT-B107	15	0.86	0.88	0.85	0.06	0.73	-0.006
CaT-B508	13	0.76	0.68	0.74	0.11	0.59	0.045
CaT-B502	12	0.76	0.76	0.73	0.15	0.56	0.004
CaT-B504	13	0.82	0.83	0.80	0.09	0.65	-0.007
CaT-B505	9	0.82	0.90	0.80	0.10	0.65	-0.044
CaT-B507	14	0.84	0.82	0.82	0.08	0.69	0.012
Total	211	14.86	14.05	14.26			
Average	10.05	0.71	0.67	0.68			

Appendix C Phenotypic profiles of 110 hazelnut accessions

Table C.1 Nut size, nut shape and husk length

Gr.	Cultivars	Nut Size	Nut Shape	Husk Length
1	Maria	Large	Long	Intermediate
	Lenka #4	Large	Long	Intermediate
2	Bard	Small to medium	Long	Short
	Barr's Zellernuss	Small to medium	Long	Short
	Bearn	Small to medium	Long	Short
3	Obrovsky Novy	Medium	Long and compressed	Short
	Liegel's Zellernuss	Medium	Long and compressed	Short
	Kunzenmuller Zellernuss	Medium	Long and compressed	Short
	Jeeve's Samling	Medium	Long and compressed	Short
4	Kadetten Zellernuss	Medium	Large	Short
	Early Long Zellernuss	Medium	Large	Short
5	Mogulnuss	Large	Long	Intermediate
	Riekchen's Zellernuss	Medium to large	Long	Intermediate
6	Italian Red	Medium to large	Long	Short
	Heynick's Zellernuss	Medium to large	Long	Short
	Gustav's Zellernuss	Medium to large	Long	Short
7	<i>C. multiflorum</i>	Large	Long	Short
	Cosford	Large	Long	Short
	Prolofique a Coque Serrée	Large	Long	Short
	Petoka (not)	Large	Long	Short
	Multiflora	Large	Long	Short
8	Little Poland	Large	Long	Short
	Pruhovany	Large	Long	Short
	Daviana	Large	Long	Short
9	Korthaset Zellernuss	Medium	Very long	Long tubular
	Du Chilly	Medium	Very long	Long tubular
10	Red Filbert	Medium	Very long	Short
	Princess Royal	Medium	Very long	Short
11	Bandnuss	Large	Long	Short
	A Pellicola Bianca	Large	Long	Short
	Apolda	Large	Long	Short
12	Pearson's Prolific	Small	Very long	Intermediate
	Nottingham	Small	Very long	Intermediate
13	White Filbert	Small	Long	Long tubular
	Purple Fortrin	Small	Long	Long tubular
	Purple Aveline	Small	Long	Long tubular
	Pellicle Rouge	Small	Long	Long tubular
	Istarski Debeloplodna	Small	Long	Long tubular
	Fructo Albo	Small	Long	Long tubular
	Barbarella	Small	Long	Long tubular
	Aveline Rouge	Small	Long	Long tubular

Table C.1 Continued

Gr.	Cultivars	Nut Size	Nut Shape	Husk Length
14	Noce Lungha	Large	Long	Long tubular
	Istarski Duguljasti	Large	Long	Long tubular
	B-4	Large	Long	Long tubular
15	Sivri Ocak #5	Medium	Long and pointed	Very long husk
	Kerasund Dlinnyi	Medium	Long and pointed	Very long husk
16	Frizzled Filbert	Small	Long	Long
	Downton Long #2	Small	Long	Long
17	Ganja	Small to medium	Slightly oblate to round	Long
	Romavel	Small to medium	Slightly oblate to round	Long
	San Benedetto	Small to medium	Slightly oblate to round	Long
	Palaz	Small to medium	Slightly oblate to round	Long
	54.056	Small to medium	Slightly oblate to round	Long
18	Karidaty	Large	Round	Intermediate
	Vilcea 22	Large	Round	Intermediate
	Wanliss Pride	Large	Round	Intermediate
	Imperial de Trabizonde #1	Large	Round	Intermediate
	Imperial de Trabizonde #2	Large	Round	Intermediate
19	Nemsa (not)	Large	Round	Long
	Kudryavchik (not)	Large	Round	Long
	Kudryavchik	Small	Round	Long
20	Tombul Ocak 1	Small	Pointed	Very long
	Extra Ghiaghli	Small	Pointed	Very long
21	Restiello	Small	Slightly long	Short
	Negret	Small	Slightly long	Short
22	Istarski Okrogloplodna	Large	Round	Short
	Fruttogrosso	Large	Round	Short
	Romische Nuss	Large	Round	Short
	Romai	Large	Round	Short
	Payrone	Large	Round	Short
23	Segorbe	Small	Slightly long	Intermediate
	Comun Aleva	Small	Slightly long	Intermediate
	Gironenc Coldejou	Small	Slightly long	Intermediate
24	Louisen's Zellernuss	Very large	Round	Short
	Rimsky	Very large	Round	Short
25	Quiros	Small	Slightly long	Intermediate
	Espinaredo	Small	Slightly long	Intermediate
	Casina	Small	Slightly long	Intermediate
	Amandi	Small	Slightly long	Intermediate
26	Molar	Medium	Round	Intermediate
	Ceret	Small	Round	Long
27	Rosetta	Large	Round	Intermediate
	Barrettona	Large	Round	Intermediate

Table C.1 Continued

Gr.	Cultivars	Nut Size	Nut Shape	Husk Length
28	Pinyolenc #1a	Medium	Round	Intermediate
	Pinyolenc #1b	Medium	Round	Intermediate
	Ros de la Selva	Medium	Round	Intermediate
29	Pinyolenc #2a	Small	Slightly long	Intermediate
	Pinyolenc #2b	Small	Slightly long	Intermediate
30	Macrocarpa	Large	Round	Intermediate
	Turk	Large	Round	Intermediate
	Kruse	Large	Round	Intermediate
31	D'Algers	Large	Round	Intermediate
	Barcelona	Large	Round	Intermediate
	Grande	Large	Round	Intermediate
32	Atlas	Large	Round	Short
	Belle di Giubilino	Large	Round	Short
33	Racinante Clone G	Medium	Round and oblate	Short
	Nostrale	Medium	Round and oblate	Short
	Montebello	Medium	Round and oblate	Short
	Minnolora	Medium	Round and oblate	Short
	Barettona (not)	Medium	Round and oblate	Short
	Avellana Speciale	Medium	Round and oblate	Short
	Siciliana	Medium	Round and oblate	Short
	Mansa	Medium	Round and oblate	Short
	Locale di Piazza Armerina	Medium	Round and oblate	Short
	Commune di Sicilia	Medium	Round and oblate	Short
	Carello	Medium	Round and oblate	Short
	Nocchione	Medium	Round and oblate	Short
34	Rosset de Valls	Medium	Round and compressed	Short
	Artellet	Medium	Round and compressed	Short

Appendix D SSR profiles of 274 hazelnut accessions at 21 loci

Table D.1 Fragment sizes of 274 hazelnut accessions determined by 21 SSR loci

Cultivar	CAC-A14a	CAC-A40	CAC-B005	CAC-B010	CAC-B028	CAC-B29b
A pellicola Bianca	211/217	236/244	277/281	211/211	266/268	116/124
Acorn Hazel	217/217	236/246	281/281	211/221	270/270	116/116
Alcover	211/217	236/248	277/291	219/223	256/256	122/130
Alli	215/215	236/244	277/281	219/227	256/262	116/132
Amandi	211/217	244/244	277/281	219/227	268/278	118/122
Apolda	211/217	236/244	277/281	211/211	266/268	116/124
Arneson's Rootstock	211/215	244/248	277/295	223/223	254/262	118/122
Artellet	215/215	234/246	277/291	211/227	256/256	118/128
Ata Baba Ganja	211/213	236/244	279/279	211/219	262/264	116/128
Atlas	217/219	244/248	291/295	211/223	254/268	118/122
Aurea	213/213	236/238	277/277	219/219	258/278	124/130
Aveline d'Angleterre	215/215	244/246	279/281	219/227	256/256	124/128
Aveline Rouge	217/217	244/248	279/281	211/219	268/268	116/124
Avellana Speciale	215/219	244/244	291/295	219/227	254/262	122/122
B-3	213/215	238/248	277/281	223/225	262/266	116/124
B-4	211/215	244/248	281/291	211/225	260/268	116/122
Badem	215/215	244/248	281/291	219/225	262/262	122/124
Bandnuss	211/217	236/244	277/281	211/211	266/268	116/124
Barbarella	217/217	244/248	279/281	211/219	268/268	116/124
Barcelona	215/219	234/248	291/295	211/223	254/262	122/128
Barcelonner Zellernuss	215/215	236/236	277/277	223/227	256/268	116/118
Bard #1	211/215	236/248	277/277	211/211	258/266	124/128
Bard #2	211/215	236/248	277/277	211/211	258/266	124/128
Barrettona	213/215	236/244	277/281	211/211	256/262	116/122
Barrettona-not	215/219	244/244	291/295	219/227	254/262	122/122
Barr's Zellernuss	211/215	236/248	277/277	211/211	258/266	124/128
Bearn	211/215	236/248	277/277	211/211	258/266	124/128
Belle di Giubilino #1	217/219	244/248	291/295	211/223	254/268	118/122
Belle di Giubilino #2	217/219	244/248	291/295	211/223	254/268	118/122
Bergeri	211/217	236/236	277/281	211/225	256/268	116/128
Bianca	215/219	244/244	277/295	219/223	254/262	116/122
Blumberger Zellernuss	215/217	236/236	281/287	211/221	256/280	118/128
Brixley's New	215/219	234/246	277/291	223/227	254/256	128/137
Brixnut	213/219	234/244	281/291	223/223	254/254	128/137
Bulgaria XI-8	211/215	244/244	281/297	211/219	262/262	116/128
Burchardt's Zellernuss	211/215	236/244	277/279	219/223	256/262	116/126
Butler	217/219	234/248	277/295	211/211	254/270	116/128
Buttner's Zellernuss	211/213	236/248	277/281	211/211	254/266	116/118
C. multiflorum	211/217	236/236	277/281	211/211	266/270	116/128
C.avellana AL55	215/215	236/236	277/279	223/227	254/264	124/128
C.avellana Swe.	203/213	236/236	277/277	219/223	254/256	128/135
Camponica	211/215	236/244	281/295	219/223	262/278	118/122
Carello	215/219	244/244	291/295	219/227	254/262	122/122
Casina	211/217	244/244	277/281	219/227	268/278	118/122
Ceret	215/217	244/248	281/291	211/219	262/268	122/122
Clark	215/217	244/244	279/295	219/225	262/270	122/128
Closca Molla	215/217	244/244	277/291	211/219	256/262	122/130

Table D.1 Continued

Cultivar	CAC-B105	CAC-B111	CAC-C010	CAC-C28	CAC-C040	CAC-C115
A pellicola Bianca	148/155	182/186	278/281	131/131	186/186	193/193
Acorn Hazel	140/148	182/188	278/278	141/141	186/186	214/214
Alcover	138/138	182/182	275/275	131/131	186/186	173/182
Alli	138/146	182/184	275/275	131/134	186/186	214/214
Amandi	140/155	182/184	275/275	131/141	186/192	173/196
Apolda	148/155	182/186	278/281	131/131	186/186	193/193
Arneson's Rootstock	155/155	182/182	275/275	131/141	186/186	173/214
Artellet	140/153	182/182	275/275	131/141	186/186	193/193
Ata Baba Ganja	155/157	170/182	275/281	131/141	186/186	193/193
Atlas	155/155	182/182	275/278	131/141	186/186	173/196
Aurea	138/153	186/188	275/275	131/134	183/189	214/214
Aveline d'Angleterre	146/148	186/188	281/281	131/134	186/186	193/193
Aveline Rouge	155/155	186/186	281/281	131/141	186/186	173/193
Avellana Speciale	155/155	182/188	278/278	131/141	186/186	173/196
B-3	146/155	182/186	275/275	131/141	186/189	173/214
B-4	142/155	186/186	275/281	131/141	186/192	173/193
Badem	140/155	182/186	275/278	131/134	186/189	173/217
Bandnuss	148/155	182/186	278/281	131/131	186/186	193/193
Barbarella	155/155	186/186	281/281	131/141	186/186	173/193
Barcelona	153/155	182/182	275/278	131/141	186/186	173/193
Barcelonner Zellernuss	148/157	182/182	275/275	131/134	189/189	193/214
Bard #1	148/159	184/186	275/278	131/134	186/186	176/193
Bard #2	148/159	184/186	275/278	131/134	186/186	176/193
Barrettona	155/155	182/182	278/278	131/134	186/186	173/193
Barrettona-not	155/155	182/188	278/278	131/141	186/186	173/196
Barr's Zellernuss	148/159	184/186	275/278	131/134	186/186	176/193
Bearn	148/159	184/186	275/278	131/134	186/186	176/193
Belle di Giubilino #1	155/155	182/182	275/278	131/141	186/186	173/196
Belle di Giubilino #2	155/155	182/182	275/278	131/141	186/186	173/196
Bergeri	138/140	184/186	275/275	137/141	186/186	173/214
Bianca	140/155	188/188	278/278	131/141	186/186	173/196
Blumberger Zellernuss	140/148	182/184	275/275	131/141	186/186	179/214
Brixley's New	140/153	182/186	275/275	131/141	186/186	173/214
Brixnut	140/153	182/186	275/278	131/144	186/186	173/193
Bulgaria XI-8	155/157	182/186	275/281	131/144	186/189	173/182
Burchardt's Zellernuss	140/155	170/182	275/275	131/137	186/186	193/193
Butler	153/153	182/182	278/278	131/131	186/186	193/193
Buttner's Zellernuss	140/148	182/186	278/278	131/141	186/186	193/193
C. multiflorum	148/153	182/182	278/278	131/141	186/186	193/214
C.avellana AL55	146/159	182/182	275/275	131/144	186/186	193/193
C.avellana Swe.	148/148	182/182	275/275	131/134	189/189	214/214
Camponica	155/155	182/184	275/275	141/141	186/186	173/196
Carello	155/155	182/188	278/278	131/141	186/186	173/196
Casina	140/155	182/184	275/275	131/141	186/192	173/196
Ceret	155/155	182/182	275/275	131/141	186/186	173/182
Clark	153/155	182/184	278/278	131/141	186/186	173/193
Closca Molla	148/155	182/182	275/275	131/141	186/186	182/214

Table D.1 Continued

Cultivar	CAC-C118	CAC-C119	CaT-B107	CaT-B502	CaT-B504	CaT-B505
A pellicola Bianca	179/179	258/258	122/142	189/195	176/176	106/126
Acorn Hazel	179/179	256/264	130/134	187/187	176/176	116/118
Alcover	179/179	256/264	134/134	189/189	176/182	116/128
Alli	179/179	258/264	128/130	199/209	174/176	114/116
Amandi	179/185	256/258	130/134	187/187	176/176	118/126
Apolda	179/179	258/258	122/142	189/195	176/176	106/126
Arneson's Rootstock	179/179	258/258	112/134	183/189	158/168	114/118
Artellet	179/179	258/264	122/134	187/195	176/182	106/114
Ata Baba Ganja	179/179	258/264	122/122	183/189	168/170	106/120
Atlas	179/179	258/260	112/134	183/189	158/182	106/114
Aurea	176/182	260/260	120/120	187/195	174/176	118/120
Aveline d'Angleterre	179/179	258/264	130/134	201/201	170/176	118/126
Aveline Rouge	179/179	258/258	122/134	187/189	168/176	106/126
Avellana Speciale	179/179	258/260	112/122	183/189	158/182	120/126
B-3	179/182	258/258	116/120	189/189	176/182	118/122
B-4	179/185	258/258	134/134	187/189	176/182	106/118
Badem	179/182	258/258	116/122	187/189	172/176	118/126
Bandnuss	179/179	258/258	122/142	189/195	176/176	106/126
Barbarella	179/179	258/258	122/134	187/189	168/176	106/126
Barcelona	179/179	258/258	112/134	187/189	158/182	106/120
Barcelonner Zellernuss	182/182	256/256	122/134	187/195	174/176	116/120
Bard #1	179/179	258/264	120/122	195/195	176/176	106/118
Bard #2	179/179	258/264	120/122	195/195	176/176	106/118
Barrettona	179/179	258/258	122/142	183/189	176/176	106/122
Barrettona-not	179/179	258/260	112/122	183/189	158/182	120/126
Barr's Zellernuss	179/179	258/264	120/122	195/195	176/176	106/118
Bearn	179/179	258/264	120/122	195/195	176/176	106/118
Belle di Giubilino #1	179/179	258/260	112/134	183/189	158/182	106/114
Belle di Giubilino #2	179/179	258/260	112/134	183/189	158/182	106/114
Bergeri	179/179	260/264	122/130	187/189	168/176	106/114
Bianca	179/179	258/258	120/122	183/187	158/176	114/118
Blumberger Zellernuss	179/179	258/260	128/144	187/195	176/176	106/139
Brixley's New	179/179	258/264	122/130	187/189	174/182	114/118
Brixnut	179/179	258/258	112/122	189/195	176/182	114/120
Bulgaria XI-8	179/182	258/258	122/134	187/209	176/176	106/118
Burchardt's Zellernuss	179/179	258/264	120/130	183/183	168/178	126/128
Butler	179/179	258/258	112/134	189/189	158/172	106/114
Buttner's Zellernuss	179/179	256/258	134/142	187/195	176/176	106/106
C. multiflorum	179/179	256/258	134/144	187/195	172/176	106/116
C.avellana AL55	185/185	260/260	128/132	187/187	176/176	114/120
C.avellana Swe.	182/182	258/264	142/142	187/187	174/176	118/120
Camponica	179/179	258/258	112/134	183/189	158/176	118/126
Carello	179/179	258/260	112/122	183/189	158/182	120/126
Casina	179/185	256/258	130/134	187/187	176/176	118/126
Ceret	179/179	258/258	122/134	187/189	176/182	106/126
Clark	179/179	258/258	134/144	187/195	158/168	118/126
Closca Molla	179/179	258/264	122/134	187/201	176/182	106/114

Table D.1 Continued

Cultivar	Ca T-B507	Ca T-B508	Cat-C504
A pellicola Bianca	185/195	153/165	158/164
Acorn Hazel	189/189	144/161	152/164
Alcover	191/191	157/163	164/164
Alli	179/195	161/165	152/152
Amandi	189/191	157/161	158/158
Apolda	185/195	153/165	158/164
Arneson's Rootstock	181/185	157/161	155/155
Artellet	181/191	157/165	152/158
Ata Baba Ganja	191/191	142/157	173/173
Atlas	181/191	157/157	158/167
Aurea	179/179	161/165	152/152
Aveline d'Angleterre	189/189	157/161	164/164
Aveline Rouge	185/197	157/157	158/164
Avellana Speciale	181/191	157/157	158/167
B-3	185/189	144/163	158/164
B-4	197/197	157/157	164/164
Badem	185/191	153/163	161/164
Bandnuss	185/195	153/165	158/164
Barbarella	185/197	157/157	158/164
Barcelona	181/191	157/157	155/158
Barcelonner Zellernuss	189/189	144/161	152/158
Bard #1	195/195	161/161	152/164
Bard #2	195/195	161/161	152/164
Barrettona	191/193	146/157	158/158
Barrettona-not	181/191	157/157	158/167
Barr's Zellernuss	195/195	161/161	152/164
Bearn	195/195	161/161	152/164
Belle di Giubilino #1	181/191	157/157	158/167
Belle di Giubilino #2	181/191	157/157	158/167
Bergeri	195/195	165/165	161/164
Bianca	185/191	161/161	158/167
Blumberger Zellernuss	189/195	159/159	152/152
Brixley's New	185/190	144/157	152/152
Brixnut	181/185	157/157	158/164
Bulgaria XI-8	189/191	157/157	161/173
Burchardt's Zellernuss	187/195	153/159	158/158
Butler	181/195	157/161	152/155
Buttner's Zellernuss	195/195	161/165	158/164
C. multiflorum	189/195	148/161	152/164
C.avellana AL55	197/197	157/157	152/152
C.avellana Swe.	195/195	146/161	161/164
Camponica	181/191	157/167	155/158
Carello	181/191	157/157	158/167
Casina	189/191	157/161	158/158
Ceret	185/191	157/163	164/164
Clark	189/191	161/163	158/167
Closca Molla	191/195	157/165	158/164

Table D.1 Continued

Cultivar	CAC-A14a	CAC-A40	CAC-B005	CAC-B010	CAC-B028	CAC-B29b
Comen	215/217	234/248	277/291	219/223	262/262	122/128
Comun	217/217	236/236	277/291	219/227	268/268	116/137
Comun Aleva	211/211	236/248	277/281	211/219	266/278	122/135
Comune di Sici.	215/219	244/244	291/295	219/227	254/262	122/122
Contorta	217/217	244/248	277/277	219/223	268/268	116/128
Corabel	211/215	234/236	277/295	211/223	262/266	128/128
Cosford	211/217	236/236	277/281	211/211	266/270	116/128
Cozia	215/215	244/246	279/291	219/227	256/256	116/122
Creswell	215/217	236/244	277/279	219/225	262/268	124/128
Culpla	213/217	236/244	277/291	219/227	256/268	118/122
Cutleaf	215/217	236/244	277/277	221/227	254/270	122/124
Da Viega	215/217	236/248	277/291	219/219	266/268	116/122
Dal Rosso	211/211	244/248	277/279	211/219	270/270	116/118
D'Algers	215/219	234/248	291/295	211/223	254/262	122/128
Daria	215/217	234/236	281/291	211/219	262/270	116/122
Daviana #1	217/217	236/248	277/281	211/211	270/270	116/116
Daviana #2 = Cosford	211/217	236/236	277/281	211/211	266/270	116/128
Delta	215/215	244/244	281/297	219/221	256/262	116/122
Des Anglais	211/217	236/248	277/279	211/219	256/256	124/128
Dowton Long #1	213/215	236/244	277/281	223/223	254/256	116/137
Dowton Long #2	215/217	236/244	277/281	219/227	256/268	116/118
DuChilly	213/217	244/244	281/281	211/223	254/268	124/137
Early Long Zel.	215/215	236/246	277/281	211/227	256/256	116/128
Ennis	217/219	234/248	277/295	211/223	254/264	116/128
Epsilon	215/217	236/248	277/291	219/225	262/278	122/122
Espinaredo	211/217	244/244	277/281	219/227	268/278	118/122
Extra Ghiaghli	211/215	244/244	279/291	211/225	262/262	116/130
Finland	212/217	236/244	279/279	219/221	258/270	135/137
Fitzgerald	217/219	234/236	277/295	211/223	254/270	116/128
Fitzgerald #20	215/215	234/236	285/295	211/211	262/262	116/122
Francoli	211/213	234/248	277/291	211/223	256/256	118/122
Frango #2	211/215	236/246	277/277	211/221	266/266	116/128
Frango #4	215/215	236/246	277/281	219/221	254/256	116/128
Frango #5	211/215	236/244	277/281	211/221	256/266	116/116
Freehusker	211/219	236/248	277/291	211/211	254/266	116/122
Frizzled Filbert	215/217	236/244	277/281	219/227	256/268	116/118
Fructo Albo	217/217	244/248	279/281	211/219	268/268	116/124
Fruttogrosso	211/217	236/248	277/281	219/223	268/278	122/124
Fusco Rubra	215/217	236/246	277/279	217/219	264/266	116/118
Gamma	215/217	244/244	277/277	219/223	262/268	122/135
Ganja	211/215	236/244	277/279	211/225	262/276	122/130
Garibaldi	211/211	236/244	277/281	219/219	266/266	124/128
Garrofi	215/219	234/248	291/295	211/225	254/262	122/122
Gasaway	215/215	236/244	277/297	211/219	256/278	116/135
Gem	213/215	234/244	281/291	223/223	256/262	128/137
Ghirara	211/215	236/244	277/291	219/219	256/262	122/132
Gironenc Coldejou	211/211	236/248	277/281	211/219	266/278	122/135
Gironenc Vermellet	211/215	244/248	277/291	219/223	258/262	122/128

Table D.1 Continued

Cultivar	CAC-B105	CAC-B111	CAC-C010	CAC-C28	CAC-C040	CAC-C115
Comen	140/155	182/182	275/275	131/131	186/189	173/214
Comun	140/151	182/182	275/275	131/134	186/186	173/182
Comun Aleva	155/155	182/182	275/275	141/141	186/186	173/196
Comune di Sici.	155/155	182/188	278/278	131/141	186/186	173/196
Contorta	146/155	186/186	281/281	131/131	186/186	185/214
Corabel	148/153	182/182	275/278	131/141	186/186	193/193
Cosford	148/153	182/182	278/278	131/141	186/186	193/214
Cozia	140/155	170/188	275/275	134/134	186/189	193/217
Creswell	153/155	182/186	281/281	131/131	186/186	173/205
Culpla	148/155	182/186	275/278	131/131	186/186	182/205
Cutleaf	155/155	178/178	275/278	134/134	186/189	214/214
Da Viegá	140/155	182/182	275/275	134/141	186/186	173/193
Dal Rosso	138/155	186/188	275/275	131/141	186/189	173/196
D'Algers	153/155	182/182	275/278	131/141	186/186	173/193
Daria	148/155	182/182	278/278	131/141	186/186	173/214
Daviana #1	153/155	182/186	278/278	131/131	186/186	173/193
Daviana #2	148/153	182/182	278/278	131/141	186/186	193/214
Delta	140/157	182/192	275/275	141/144	186/186	196/214
Des Anglais	151/155	186/186	281/281	131/134	186/189	185/193
Downton Long #1	140/140	186/186	278/278	131/144	186/186	173/193
Downton Long #2	151/155	186/188	275/281	141/147	186/186	173/205
DuChilly	140/155	186/186	278/281	131/144	186/186	173/193
Early Long Zel.	138/140	184/186	275/275	131/141	183/186	214/214
Ennis	153/155	182/182	278/278	131/141	186/186	173/193
Epsilon	153/155	184/192	275/275	141/144	183/186	173/196
Espinaredo	140/155	182/184	275/275	131/141	186/192	173/196
Extra Ghiagli	155/155	184/186	275/275	134/141	186/186	182/193
Finland	148/153	182/186	278/278	131/131	186/186	214/214
Fitzgerald	155/155	182/186	278/278	131/131	186/186	173/193
Fitzgerald #20	153/155	182/186	275/275	131/131	186/186	173/193
Francoli	140/155	182/184	275/275	131/134	186/186	182/214
Frango #2	140/148	182/188	275/278	141/141	186/186	193/214
Frango #4	140/159	182/188	275/278	131/141	186/192	214/217
Frango #5	140/148	182/184	275/278	141/141	186/186	193/214
Freehusker	148/153	182/182	278/278	131/141	186/186	173/193
Frizzled Filbert	151/155	186/188	275/281	141/147	186/186	173/205
Fructo Albo	155/155	186/186	281/281	131/141	186/186	173/193
Fruttogrosso	155/155	182/188	275/278	141/141	186/186	173/196
Fusco Rubra	136/140	184/186	272/278	134/134	186/189	214/214
Gamma	140/159	184/192	275/275	131/144	186/186	173/196
Ganja	155/157	170/186	281/281	141/141	186/186	193/193
Garibaldi	155/159	182/186	278/281	131/144	186/186	173/193
Garrofi	140/155	182/186	275/278	134/141	186/189	193/214
Gasaway	153/157	192/192	275/278	144/144	186/189	214/217
Gem	140/153	182/186	275/278	131/144	186/186	173/193
Ghirara	140/155	182/188	275/275	131/141	186/186	196/217
Gironenc Coldejou	155/155	182/182	275/275	141/141	186/186	173/196
Gironenc Vermellet	140/153	182/182	275/275	131/134	186/186	173/205

Table D.1 Continued

Cultivar	CAC-C118	CAC-C119	Ca T-B107	Ca T-B502	Ca T-B504	Ca T-B505
Comen	179/185	258/258	122/134	189/195	172/182	120/126
Comun	179/179	256/258	122/134	189/195	174/182	114/122
Comun Aleva	179/179	258/264	112/134	183/187	174/176	106/114
Comune di Sici.	179/179	258/260	112/122	183/189	158/182	120/126
Contorta	179/179	258/264	122/130	189/189	174/176	114/118
Corabel	179/179	258/258	112/134	187/189	158/172	106/120
Cosford	179/179	256/258	134/144	187/195	172/176	106/116
Cozia	179/182	258/264	130/130	187/201	168/184	118/126
Creswell	179/179	258/260	122/134	189/189	168/174	116/128
Culpla	179/179	258/258	124/134	183/189	170/182	114/126
Cutleaf	179/182	264/264	122/134	201/209	170/176	126/128
Da Viega	179/179	256/258	122/134	187/187	172/182	114/126
Dal Rosso	179/182	258/258	124/134	183/187	168/176	106/106
D'Algers	179/179	258/258	112/134	187/189	158/182	106/120
Daria	179/179	258/258	134/134	187/189	176/182	116/126
Daviana #1	179/179	258/258	134/134	189/195	172/176	106/116
Daviana #2	179/179	256/258	134/144	187/195	172/176	106/116
Delta	179/179	258/264	122/130	183/187	176/182	118/126
Des Anglais	179/182	258/258	120/134	189/201	168/174	106/114
Dowton Long #1	179/179	260/264	120/122	195/195	174/176	114/114
Dowton Long #2	179/179	258/264	122/130	183/187	176/176	118/126
DuChilly	179/179	258/264	122/130	189/195	176/176	106/114
Early Long Zel.	176/179	258/264	122/128	187/209	176/176	106/114
Ennis	179/179	258/258	134/134	187/195	158/172	116/120
Epsilon	176/179	258/258	128/134	187/195	160/182	114/118
Espinaredo	179/185	256/258	130/134	187/187	176/176	118/126
Extra Ghiaghli	162/179	260/260	116/116	187/187	168/182	106/118
Finland	179/179	258/264	126/126	199/199	168/178	116/118
Fitzgerald	179/179	258/258	112/134	189/189	158/172	106/120
Fitzgerald #20	179/179	258/258	112/134	189/189	158/176	106/106
Francoli	179/185	258/264	120/134	189/195	170/182	106/114
Frango #2	179/179	256/264	130/144	187/187	172/174	106/118
Frango #4	179/185	258/258	120/130	187/187	162/176	114/118
Frango #5	179/179	258/264	130/134	187/187	172/176	116/118
Freehusker	179/179	256/258	112/134	187/189	172/182	116/120
Frizzled Filbert	179/179	258/264	122/130	183/187	176/176	118/126
Fructo Albo	179/179	258/258	122/134	187/189	168/176	106/126
Fruttogrosso	179/179	258/260	122/134	183/187	174/176	114/126
Fusco Rubra	179/182	256/264	120/122	189/195	164/174	114/122
Gamma	179/179	258/258	130/134	183/187	168/176	118/126
Ganja	179/179	258/258	134/134	187/187	168/168	106/118
Garibaldi	179/179	258/258	134/142	183/187	176/176	118/126
Garrofi	179/182	258/258	112/126	187/195	158/182	114/120
Gasaway	179/182	258/264	122/128	183/195	174/174	114/120
Gem	179/179	258/264	112/130	189/195	176/182	114/120
Ghirara	179/179	258/258	112/112	183/185	176/182	118/126
Gironenc Coldejou	179/179	258/264	112/134	183/187	174/176	106/114
Gironenc Vermellet	179/179	256/258	112/120	185/189	176/182	120/126

Table D.1

Cultivar	CaT-B507	CaT-B508	Cat-C504
Comen	191/195	157/165	158/158
Comun	191/195	146/157	155/155
Comun Aleva	179/191	157/165	155/158
Comune di Sici.	181/191	157/157	158/167
Contorta	185/189	146/157	158/161
Corabel	181/195	157/161	152/158
Cosford	189/195	148/161	152/164
Cozia	189/189	144/161	158/161
Creswell	191/197	146/157	161/161
Culpla	191/197	144/157	152/152
Cutleaf	185/195	159/167	161/161
Da Viega	191/195	157/165	158/158
Dal Rosso	197/197	157/157	161/161
D'Algers	181/191	157/157	155/158
Daria	191/195	148/163	158/164
Daviana #1	185/195	161/161	152/164
Daviana #2	189/195	148/161	152/164
Delta	189/189	144/165	161/161
Des Anglais	185/189	153/161	152/152
Dowton Long #1	185/189	157/159	158/167
Dowton Long #2	185/195	153/163	158/161
DuChilly	185/189	157/165	164/164
Early Long Zel.	193/195	159/165	152/152
Ennis	185/191	157/157	152/155
Epsilon	190/197	146/157	152/158
Espinaredo	189/191	157/161	158/158
Extra Ghiaghli	189/197	157/163	161/161
Finland	179/193	150/165	152/158
Fitzgerald	181/195	157/157	152/155
Fitzgerald #20	181/185	157/157	155/164
Francoli	191/191	157/159	161/161
Frango #2	189/195	148/165	152/152
Frango #4	195/195	144/144	152/158
Frango #5	190/195	144/161	152/152
Freehusker	181/195	157/161	152/158
Frizzled Filbert	185/195	153/161	158/161
Fructo Albo	185/197	157/157	158/164
Fruttogrosso	191/195	157/167	155/158
Fusco Rubra	189/198	165/165	152/164
Gamma	179/189	161/167	158/161
Ganja	191/198	144/157	152/158
Garibaldi	185/190	157/165	152/164
Garrofi	181/191	157/157	155/158
Gasaway	179/190	146/165	161/164
Gem	181/185	157/157	158/164
Ghirara	191/195	146/157	155/158
Gironenc Coldejou	179/191	157/165	155/158
Gironenc Vermellet	181/189	157/165	158/158

Table D.1

Cultivar	CAC-A14a	CAC-A40	CAC-B005	CAC-B010	CAC-B028	CAC-B29b
Goc	217/217	244/244	277/277	211/211	264/264	116/128
Grande	215/219	234/248	291/295	211/223	254/262	122/128
Grifoll	211/215	248/248	277/291	219/227	256/262	122/124
Gubener Barcelloner	211/215	236/242	277/295	223/225	256/278	116/118
Gunslebert	215/215	244/246	277/295	223/227	262/262	116/118
Gustav's Zellernuss	215/215	236/246	277/277	221/227	256/264	128/128
Hall's Giant	215/215	244/246	277/279	221/227	256/264	116/128
Henneman #3	213/213	244/248	279/279	219/225	264/270	116/137
Heynick's Zell.	215/215	236/246	277/277	221/227	256/264	128/128
Iannusa Racinante	215/219	244/244	277/291	219/227	254/256	122/122
Imp. de Trebizonde #1	215/217	244/244	279/291	211/219	262/268	116/122
Imp. de Trebizonde #2	215/217	244/244	279/291	211/219	262/268	116/122
Imperatrice Eugenie	217/217	236/244	281/281	211/211	268/270	124/128
Istarski Debeloplodna #1	217/217	244/248	279/281	211/219	268/268	116/124
Istarski Debeloplodna #2	217/217	244/248	279/281	211/219	268/268	116/124
Istarski Okrogloplodna	211/217	236/248	277/281	219/223	268/278	122/124
Istrski Duguljasti	211/217	244/248	281/291	211/225	260/268	116/122
Italian Red	215/215	236/246	277/277	221/227	256/264	128/128
Jean's	215/217	244/248	277/279	219/223	262/268	116/116
Jeeve's Samling	215/215	244/246	279/281	227/227	256/256	116/116
Kadetten Zellernuss	215/215	236/246	277/281	211/227	256/256	116/128
Kalinkara	211/221	236/244	279/279	219/221	262/266	116/122
Karidaty #1	215/217	244/244	279/291	211/219	262/268	116/122
Karidaty #2	215/217	244/244	279/291	211/219	262/268	116/122
Karol	215/215	236/246	277/277	211/221	256/256	116/116
Kerasund Dlin.	217/217	244/244	279/291	219/225	262/268	116/122
Korthaset Zellernuss	213/217	244/244	281/281	211/223	254/268	124/137
Kruse	215/219	236/248	291/295	219/219	254/262	122/122
Kudryavchik #1	211/215	244/244	279/291	219/225	262/262	122/122
Kudryavchik #2	211/215	244/248	279/279	211/225	262/262	114/126
Kunzemuller Z	215/215	244/246	279/281	227/227	256/256	116/116
Lange Landsberger	215/215	236/244	277/279	221/227	256/256	128/128
Lech	215/215	244/246	277/277	221/227	256/264	116/116
Lenka #3	217/217	236/246	277/281	211/221	270/270	128/128
Lenka #4	211/211	236/246	277/279	211/227	256/266	116/116
Lewis	215/217	236/244	279/291	219/223	262/270	122/122
Liegel's Z	215/215	244/246	279/281	227/227	256/256	116/116
Liegel's Zellernuss	215/219	244/244	291/295	219/227	254/262	122/122
Little Poland	217/217	236/244	277/277	211/227	270/270	116/116
Lluenta	211/211	236/244	277/291	219/223	256/258	128/130
Louisen's Zellernuss	217/217	246/248	277/281	223/227	256/268	116/124
Ludolph's Zellernuss	215/215	246/246	279/281	227/227	256/264	116/116
Lyons	215/217	234/244	281/291	223/223	262/268	122/137
Macrocarpa	215/219	236/248	291/295	219/219	254/262	122/122
Mansa	215/219	244/244	291/295	219/227	254/262	122/122
Maria	211/211	236/246	277/279	211/227	256/266	116/116
Martorella	211/213	236/248	277/277	223/227	256/256	122/130
Mincane	211/217	244/244	279/279	219/223	262/268	122/126
Minnolara	215/219	244/244	291/295	219/227	254/262	122/122

Table D.1 Continued

Cultivar	CAC-B105	CAC-B111	CAC-C010	CAC-C28	CAC-C040	CAC-C115
Goc	148/155	182/182	275/275	141/141	186/186	173/214
Grande	153/155	182/182	275/278	131/141	186/186	173/193
Grifoll	155/155	182/184	275/275	131/144	186/186	182/185
Gubener Barcelloner	155/157	182/184	275/275	131/141	186/186	196/214
Gunslebert	140/155	184/186	275/275	141/141	186/186	196/214
Gustav's Zellernuss	138/140	186/188	275/275	131/141	186/186	214/214
Hall's Giant	140/148	186/188	275/275	134/141	186/186	193/214
Henneman #3	148/155	182/186	278/278	134/141	186/186	173/214
Heynick's Zell.	138/140	186/188	275/275	131/141	186/186	214/214
Iannusa Racinante	155/155	182/182	278/278	131/141	183/186	193/196
Imp. de Trebizonde #1	155/155	170/186	275/275	134/137	186/189	193/217
Imp. de Trebizonde #2	155/155	170/186	275/275	134/137	186/189	193/217
Imperatrice Eugenie	148/155	182/186	278/281	131/141	186/186	193/193
Istarski Debeloplodna #1	155/155	186/186	281/281	131/141	186/186	173/193
Istarski Debeloplodna #2	155/155	186/186	281/281	131/141	186/186	173/193
Istarski Okrogloplodna	155/155	182/188	275/278	141/141	186/186	173/196
Istrski Duguljasti	142/155	186/186	275/281	131/141	186/192	173/193
Italian Red	138/140	186/188	275/275	131/141	186/186	214/214
Jean's	140/155	170/186	275/281	131/141	186/186	173/193
Jeeve's Samling	140/140	186/186	278/278	131/141	183/186	214/225
Kadetten Zellernuss	138/140	184/186	275/275	131/141	183/186	214/214
Kalinkara	146/155	182/182	275/278	141/144	186/189	176/182
Karidaty #1	155/155	170/186	275/275	134/137	186/189	193/217
Karidaty #2	155/155	170/186	275/275	134/137	186/189	193/217
Karol	148/155	186/186	275/275	131/134	186/186	193/193
Kerasund Dlin.	155/155	184/186	275/278	131/134	186/186	173/193
Korthaset Zellernuss	140/155	186/186	278/281	131/144	186/186	173/193
Kruse	155/155	182/184	275/275	131/141	186/186	196/196
Kudryavchik #1	155/155	182/184	281/281	134/141	186/186	173/182
Kudryavchik #2	142/155	170/188	275/275	134/141	186/189	167/193
Kunzemuller Z	140/140	186/186	278/278	131/141	183/186	214/225
Lange Landsberger	140/140	186/188	275/275	131/141	186/186	214/214
Lech	140/140	182/188	275/275	131/144	186/186	193/214
Lenka #3	140/153	182/186	278/278	141/141	186/186	193/214
Lenka #4	140/153	182/188	278/278	131/144	186/186	214/214
Lewis	155/155	182/182	278/278	131/134	186/186	193/193
Liegel's Z	140/140	186/186	278/278	131/141	183/186	214/225
Liegel's Zellernuss	155/155	182/188	278/278	131/141	186/186	173/196
Little Poland	140/153	182/184	278/278	131/144	186/186	193/193
Lluenta	153/155	182/182	275/275	131/131	186/186	182/205
Louisen's Zellernuss	140/155	184/188	275/275	141/141	183/186	196/214
Ludolph's Zellernuss	138/140	186/186	275/275	131/134	186/186	193/214
Lyons	153/155	182/186	278/281	131/131	186/186	193/193
Macrocarpa	155/155	182/184	275/275	131/141	186/186	196/196
Mansa	155/155	182/188	278/278	131/141	186/186	173/196
Maria	140/153	182/188	278/278	131/144	186/186	214/214
Martorella	140/155	182/182	275/275	131/134	186/192	173/214
Mincane	144/155	170/186	275/281	141/144	186/186	182/193
Minjolara	155/155	182/188	278/278	131/141	186/186	173/196

Table D.1 Continued

Cultivar	CAC-C118	CAC-C119	Ca T-B107	Ca T-B502	Ca T-B504	Ca T-B505
Goc	179/179	256/264	130/134	187/201	172/174	106/116
Grande	179/179	258/258	112/134	187/189	158/182	106/120
Grifoll	179/179	258/258	120/122	189/189	162/182	118/126
Gubener Barcelloner	179/179	258/258	112/130	187/199	158/176	118/118
Gunslebert	179/179	258/264	112/122	183/187	158/174	118/118
Gustav's Zellernuss	179/179	258/264	128/130	187/209	174/176	114/118
Hall's Giant	179/179	264/264	122/130	187/201	170/174	120/120
Henneman #3	179/179	258/260	120/134	187/195	168/176	114/126
Heynick's Zell.	179/179	258/264	128/130	187/209	174/176	114/118
Iannusa Racinante	176/179	258/258	112/132	183/189	176/182	118/120
Imp. de Trebizonde #1	179/182	258/258	120/120	183/187	168/184	114/126
Imp. de Trebizonde #2	179/182	258/258	120/120	183/187	168/184	114/126
Imperatrice Eugenie	179/179	258/264	122/134	187/189	176/176	106/106
Istarski Debeloplodna #1	179/179	258/258	122/134	187/189	168/176	106/126
Istarski Debeloplodna #2	179/179	258/258	122/134	187/189	168/176	106/126
Istarski Okrogloplodna	179/179	258/260	122/134	183/187	174/176	114/126
Istrski Duguljasti	179/185	258/258	122/134	187/189	176/182	106/118
Italian Red	179/179	258/264	128/130	187/209	174/176	114/118
Jean's	179/179	258/258	120/122	183/187	168/178	126/128
Jeeve's Samling	176/179	258/264	122/128	187/195	168/176	114/118
Kadetten Zellernuss	176/179	258/264	122/128	187/209	176/176	106/114
Kalinkara	179/182	258/258	128/128	187/187	168/172	114/126
Karidaty #1	179/182	258/258	120/120	183/187	168/184	114/126
Karidaty #2	179/182	258/258	120/120	183/187	168/184	114/126
Karol	179/179	258/264	122/134	189/201	172/174	116/118
Kerasund Dlin.	179/179	258/258	130/130	187/189	168/182	118/126
Korthaset Zellernuss	179/179	258/264	122/130	189/195	176/176	106/114
Kruse	179/179	258/258	118/134	183/189	158/182	114/126
Kudryavchik #1	179/179	258/260	116/134	187/187	168/182	118/126
Kudryavchik #2	179/182	258/260	120/124	183/187	168/168	114/114
Kunzemuller Z.	176/179	258/264	122/128	187/195	168/176	114/118
Lange Landsberger	179/179	264/264	128/130	187/187	170/176	114/118
Lech	179/179	264/264	122/122	187/195	174/176	106/118
Lenka #3	179/179	258/264	122/134	187/187	174/176	106/118
Lenka #4	179/179	258/264	122/144	187/195	170/172	106/118
Lewis	179/179	258/258	134/144	187/189	168/182	120/126
Liegel's Z.	176/179	258/264	122/128	187/195	168/176	114/118
Liegel's Zellernuss	179/179	258/260	112/122	183/189	158/182	120/126
Little Poland	179/179	258/258	128/134	187/195	172/174	106/116
Lluenta	179/179	258/258	120/134	189/189	176/182	120/126
Louisen's Zellernuss	176/179	258/260	122/134	187/187	174/176	114/114
Ludolph's Zellernuss	179/179	264/264	128/130	187/209	170/176	114/118
Lyons	179/179	258/264	122/134	189/189	176/182	114/120
Macrocarpa	179/179	258/258	118/134	183/189	158/182	114/126
Mansa	179/179	258/260	112/122	183/189	158/182	120/126
Maria	179/179	258/264	122/144	187/195	170/172	106/118
Martorella	179/185	258/258	120/122	185/195	170/178	114/122
Mincane	179/179	258/258	134/134	187/187	168/168	126/128
Minnolara	179/179	258/260	112/122	183/189	158/182	120/126

Table D.1 Continued

Cultivar	CaT-B507	CaT-B508	Cat-C504
Goc	197/197	148/157	155/164
Grande	181/191	157/157	155/158
Grifoll	185/195	159/159	158/161
Gubener Barcelloner	179/181	159/159	155/164
Gunslebert	181/189	157/165	152/152
Gustav's Zellernuss	190/195	144/165	152/164
Hall's Giant	189/189	144/161	152/164
Henneman #3	179/197	157/161	161/161
Heynick's Zell.	190/195	144/165	152/164
Iannusa Racinante	181/191	146/157	152/158
Imp. de Trebizonde #1	187/191	157/159	158/161
Imp. de Trebizonde #2	187/191	157/159	158/161
Imperatrice Eugenie	185/189	148/157	152/164
Istarski Debeloplodna #1	185/197	157/157	158/164
Istarski Debeloplodna #2	185/197	146/157	158/164
Istarski Okrogloplodna	191/195	157/167	155/158
Istrski Duguljasti	197/197	157/157	164/164
Italian Red	190/195	144/165	152/164
Jean's	185/195	153/153	158/158
Jeeve's Samling	195/195	144/159	152/164
Kadetten Zellernuss	193/195	159/165	152/152
Kalinkara	185/197	150/157	158/161
Karidaty #1	187/191	157/159	158/161
Karidaty #2	187/191	157/159	158/161
Karol	185/190	161/161	152/152
Kerasund Dlin.	179/197	157/157	161/161
Korthaset Zellernuss	185/189	157/165	164/164
Kruse	179/185	157/167	155/158
Kudryavchik #1	189/197	157/163	161/161
Kudryavchik #2	191/193	150/157	161/161
Kunzemuller Z	195/195	144/159	152/164
Lange Landsberger	189/195	159/161	152/164
Lech	181/190	144/165	152/152
Lenka #3	190/195	161/161	152/164
Lenka #4	189/195	161/161	152/152
Lewis	181/191	157/161	155/158
Liegel's Z	195/195	144/159	152/164
Liegel's Zellernuss	181/191	157/157	158/167
Little Poland	190/195	144/161	152/152
Lluenta	189/191	157/157	158/158
Louisen's Zellernuss	191/195	157/159	152/155
Ludolph's Zellernuss	189/195	144/165	152/164
Lyons	181/185	157/157	158/164
Macrocarpa	179/185	157/167	155/158
Mansa	181/191	157/157	158/167
Maria	189/195	161/161	152/152
Martorella	185/195	157/159	161/164
Mincane	191/197	150/157	158/158
Minnolara	181/191	157/157	158/167

Table D.1 Continued

Cultivar	CAC-A14a	CAC-A40	CAC-B005	CAC-B010	CAC-B028	CAC-B29b
Ratoli	215/217	236/248	277/291	211/221	262/268	122/122
Red Filbert	211/213	236/244	281/281	211/223	254/266	124/128
Red Fortrin	215/217	234/244	281/295	211/211	262/264	128/128
Restiello	211/217	236/248	291/297	219/223	256/268	122/130
Ribet	215/215	246/248	277/281	211/221	256/262	122/122
Riccia di Talanico	215/219	242/244	277/291	219/223	254/262	122/122
Riekchen's Zellernuss #2	215/215	236/246	277/281	211/227	256/256	116/128
Riekchen's Zellernuss #1	215/215	236/246	277/281	211/227	256/256	116/128
Rimsky	217/217	246/248	277/281	223/227	256/268	116/124
Rode Zeller	211/217	236/244	277/281	211/219	264/266	116/128
Romai	211/217	236/248	277/281	219/223	268/278	122/124
Romavel	215/215	243/248	279/279	211/219	262/262	122/128
Romische Nuss	211/217	236/248	277/281	219/223	268/278	122/124
Ros de la Selva	211/215	236/248	277/291	211/211	262/262	122/122
Rosetta	213/215	236/244	277/281	211/211	256/262	116/122
Rosset de Valls	215/215	234/246	277/291	211/227	256/256	118/128
Royal	217/219	236/248	277/291	211/211	254/270	116/122
Ruby	217/251	236/236	279/281	211/217	264/264	118/130
Ryan	217/219	234/236	277/291	211/223	254/254	116/122
San Benedetto	211/215	238/244	279/279	211/219	262/262	116/130
San Giovanni	213/215	234/248	291/295	219/223	254/262	116/122
Sant Jaume	211/219	236/248	281/291	219/223	254/258	122/122
Sant Joan	211/215	236/244	277/291	219/223	256/262	122/128
Sant Pere	211/217	248/248	277/291	219/219	256/256	130/135
Segorbe	211/211	236/248	277/281	211/219	266/278	122/135
Siciliana	215/219	244/244	291/295	219/227	254/262	122/122
Sickler's Zel.	215/215	236/244	277/281	211/221	256/256	116/128
Simon	211/215	234/236	295/297	211/223	256/262	122/130
Sivri Ghiaghli	211/211	244/244	279/291	219/225	262/262	116/122
Sivri Ocak 5	217/217	244/244	279/291	219/225	262/268	116/122
Skorspelka	213/217	236/244	279/279	211/219	258/262	116/116
Syrena	215/217	244/244	279/281	211/221	256/264	116/128
Tapparona di SCC	211/215	244/248	277/291	211/223	262/276	118/122
Tonda Gentile d. Langhe	215/221	234/244	277/291	219/219	256/262	118/122
The Shah	211/213	236/244	277/281	211/223	254/264	124/124
Tokolyi Cosford	211/211	242/248	279/295	219/223	268/268	116/118
Tomasina	211/213 234	236/244	277/291	211/219	256/256	118/118
Tombul	211/217	244/244	279/279	219/223	262/268	122/126
Tombul Ghiaghli	211/215	244/244	279/291	219/225	262/262	122/122
Tombul Ocak 1	211/215	244/244	279/291	211/225	262/262	116/130
Tonda Bianca	211/219	236/242	277/291	219/223	254/278	118/122
Tonda di Giffoni	211/215	236/248	291/295	219/223	262/278	118/122
Tonda Romana	211/217	238/248	277/291	211/219	262/268	122/122
Tonda Rossa	211/215	242/244	277/295	219/223	268/278	122/122
Tonnolella	211/215	236/244	291/295	219/223	262/266	118/128
Trenet	217/219	234/248	277/291	211/219	256/262	122/122
Truchsess	219/219	236/244	277/277	221/227	256/256	128/128
Turk	215/219	236/248	291/295	219/219	254/262	122/122
Ugbrooke	211/211	236/244	277/279	219/221	256/256	124/128

Table D.1 Continued

Cultivar	CAC-B105	CAC-B111	CAC-C010	CAC-C28	CAC-C040	CAC-C115
Ratoli	140/155	182/182	275/275	131/144	186/186	173/182
Red Filbert	153/155	182/186	278/278	131/131	186/186	193/214
Red Fortrin	153/155	182/182	275/275	141/141	186/189	173/214
Restiello	138/155	182/184	275/275	131/144	186/192	182/214
Ribet	151/155	182/182	278/278	134/141	186/186	173/214
Riccia di Talanico	155/155	182/184	275/275	131/141	186/186	182/196
Riekchen's Zellernuss #2	138/148	186/188	275/275	131/134	183/186	193/214
Riekchen's Zellernuss #1	138/148	186/188	275/275	131/134	183/186	193/214
Rimsky	140/155	184/188	275/275	141/141	183/186	196/214
Rode Zeller	153/155	182/184	275/278	131/141	186/189	193/214
Romai	155/155	182/188	275/278	141/141	186/186	173/196
Romavel	153/155	182/186	278/278	131/134	186/186	173/193
Romische Nuss	155/155	182/188	275/278	141/141	186/186	173/196
Ros de la Selva	155/159	182/182	278/278	134/141	186/186	173/193
Rosetta	155/155	182/182	278/278	131/134	186/186	173/193
Rosset de Valls	140/153	182/182	275/275	131/141	186/186	193/193
Royal	153/153	182/182	278/278	131/144 ¹²³	186/186	193/193
Ruby	136/144	184/184	278/278	134/147	186/192	188/214
Ryan	153/155	182/182	275/275	131/141	186/186	173/193
San Benedetto	155/155	182/184	281/281	131/141	186/186	173/196
San Giovanni	148/155	182/182	275/275	131/131	186/186	173/196
Sant Jaume	140/153	182/182	275/278	131/141	186/189	173/214
Sant Joan	148/155	182/182	275/275	131/141	186/189	182/214
Sant Pere	138/144	182/184	275/275	131/134	186/186	173/182
Segorbe	155/155	182/182	275/275	141/141	186/186	173/196
Siciliana	155/155	182/188	278/278	131/141	186/186	173/196
Sickler's Zel.	140/140	186/188	275/275	141/141	183/183	193/214
Simon	155/155	182/182	275/275	131/134	186/186	182/193
Sivri Ghiaghli	155/155	182/186	278/281	131/141	186/186	173/182
Sivri Ocak 5	155/155	184/186	275/278	131/134	186/186	173/193
Skorspelka	144/157	170/186	275/275	131/141	186/186	176/182
Syrena	140/159	184/186	275/275	141/141	186/186	193/214
Tapparona di SCC	155/159	182/182	278/278	131/137	186/192	173/185
Tonda Gentile d. Langhe	155/155	182/182	275/275	131/131	186/186	173/173
The Shah	155/155	186/188	278/278	131/134	186/186	173/205
Tokolyi Cosford	155/155	184/186	275/275	131/141	186/186	193/214
Tomasina	138/140	184/186	275/275	131/134	186/192	173/214
Tombul	144/155	170/186	275/281	141/144	186/186	182/193
Tombul Ghiaghli	155/155	182/184	281/281	134/141	186/186	173/182
Tombul Ocak 1	155/155	184/186	275/275	134/141	186/186	182/193
Tonda Bianca	155/155	182/184	275/275	131/141	186/186	196/214
Tonda di Giffoni	155/155	182/182	275/275	141/141	186/186	173/214
Tonda Romana	155/161	182/182	275/275	131/141	183/186	173/196
Tonda Rossa	155/155	184/184	275/275	141/141	186/186	196/214
Tonnolella	140/155	182/182	275/275	134/141	186/186	214/214
Trenet	138/140	182/182	275/278	131/134	186/186	173/193
Truchsess	138/148	186/186	275/275	131/134	183/186	214/214
Turk	155/155	182/184	275/275	131/141	186/186	196/196
Ugbrooke	148/155	178/186	275/275	131/141	186/186	193/214

Table D.1 Continued

Cultivar	CAC-C118	CAC-C119	CaT-B107	CaT-B502	CaT-B504	CaT-B505
Ratoli	179/179	258/264	130/134	185/189	172/182	106/114
Red Filbert	179/179	258/264	122/144	189/195	176/176	106/116
Red Fortrin	179/182	258/264	134/134	187/187	158/176	106/106
Restiello	179/185	258/258	120/134	189/189	176/182	114/126
Ribet	179/179	258/260	122/134	185/187	174/176	106/114
Riccia di Talanico	179/179	258/258	118/134	187/197	168/182	118/126
Riekchen's Zellernuss #2	176/179	264/264	128/130	201/209	174/176	106/118
Riekchen's Zellernuss #1	176/179	264/264	128/130	201/209	174/176	106/118
Rimsky	176/179	258/260	122/134	187/187	174/176	114/114
Rode Zeller	179/182	256/264	130/134	187/195	168/176	106/126
Romai	179/179	258/260	122/134	183/187	174/176	114/126
Romavel	179/179	258/258	134/134	187/189	168/168	114/126
Romische Nuss	179/179	258/260	122/134	183/187	174/176	114/126
Ros de la Selva	179/179	258/258	120/134	189/189	162/182	106/114
Rosetta	179/179	258/258	122/142	183/189	176/176	106/122
Rosset de Valls	179/179	258/264	122/134	187/195	176/182	106/114
Royal	179/179	258/258	112/132 ¹⁵⁴	189/195	172/182	106/116
Ruby	179/185	260/264	120/122	191/195	164/176	106/122
Ryan	179/179	258/258	134/134	187/195	172/182	116/120
San Benedetto	179/179	258/260	134/134	187/189	168/168	106/126
San Giovanni	179/179	258/258	118/134	189/211	158/182	118/126
Sant Jaume	179/182	258/264	112/134	187/189	176/182	120/120
Sant Joan	179/182	258/260	122/130	187/189	176/182	120/126
Sant Pere	179/179	258/258	118/134	189/201	170/182	118/126
Segorbe	179/179	258/264	112/134	183/187	174/176	106/114
Siciliana	179/179	258/260	112/122	183/189	158/182	120/126
Sickler's Zel.	176/179	258/264	122/122	187/187	174/176	106/118
Simon	179/179	258/258	126/134	187/189	158/176	114/120
Sivri Ghiaghli	179/179	258/260	116/116	187/199	168/182	118/126
Sivri Ocak 5	179/179	258/258	130/130	187/189	168/182	118/126
Skorspelka	179/179	258/264	120/120	189/197	168/180	106/106
Syrena	179/179	264/264	130/134	187/187	170/176	116/118
Tapparona di SCC	179/185	258/264	122/124	185/187	162/182	106/126
Tonda Gentile d. Langhe	179/179	258/258	134/151	185/189	170/182	114/126
The Shah	179/179	258/258	120/130	189/189	168/176	114/114
Tokolyi Cosford	179/179	258/258	118/134	187/197	158/168	118/126
Tomasina	179/185	264/264	120/134	195/195	170/182	106/122
Tombul	179/179	258/258	134/134	187/187	168/168	126/128
Tombul Ghiaghli	179/179	260/260	116/134	187/187	168/182	118/126
Tombul Ocak 1	162/179	260/260	116/116	187/187	168/182	106/118
Tonda Bianca	179/179	258/258	112/118	183/197	158/168	114/118
Tonda di Giffoni	179/179	258/258	118/134	183/187	158/182	118/126
Tonda Romana	176/179	258/258	134/142	187/191	160/182	118/126
Tonda Rossa	179/179	258/258	112/118	183/183	158/174	114/114
Tonnolella	179/179	258/258	118/120	183/199	158/182	126/128
Trenet	179/179	258/264	130/134	185/189	176/182	106/126
Truchsess	176/179	258/264	128/130	201/209	174/176	114/118
Turk	179/179	258/258	118/134	183/189	158/182	114/126
Ugbrooke	179/179	260/260	122/134	187/199	168/174	114/126

Table D.1

Cultivar	Ca T-B507	Ca T-B508	Cat-C504
Ratoli	189/191	157/165	164/164
Red Filbert	185/189	157/161	164/164
Red Fortrin	189/191	157/157	158/164
Restiello	191/195	157/159	161/161
Ribet	191/195	157/165	158/158
Riccia di Talanico	181/185	157/167	155/158
Riekchen's Zellernuss #2	189/195	144/159	152/152
Riekchen's Zellernuss #1	189/195	144/159	152/152
Rimsky	191/195	157/159	152/155
Rode Zeller	189/197	148/157	158/164
Romai	191/195	157/167	155/158
Romavel	191/197	157/157	158/158
Romische Nuss	191/195	157/167	155/158
Ros de la Selva	188/191	146/157	158/158
Rosetta	191/193	146/157	158/158
Rosset de Valls	181/191	157/165	152/158
Royal	181/189	148/157	152/158
Ruby	176/198	144/165	152/152
Ryan	191/195	157/161	152/158
San Benedetto	191/197	157/167	158/161
San Giovanni	181/191	157/167	155/158
Sant Jaume	181/191	157/165	158/158
Sant Joan	185/189	157/165	164/164
Sant Pere	181/191	157/159	158/158
Segorbe	179/191	157/165	155/158
Siciliana	181/191	157/157	158/167
Sickler's Zel.	189/195	159/161	152/152
Simon	181/191	157/157	161/161
Sivri Ghiaghli	179/197	157/163	158/161
Sivri Ocak 5	179/197	157/157	161/161
Skorspelka	191/197	157/161	158/158
Syrena	189/197	148/157	152/164
Tapparona di SCC	181/185	163/163	158/158
Tonda Gentile d. Langhe	185/191	146/163	158/161
The Shah	185/189	157/165	158/164
Tokolyi Cosford	179/197	157/167	155/158
Tomasina	181/191	157/159	161/161
Tombul	191/197	150/157	158/158
Tombul Ghiaghli	189/197	157/163	158/161
Tombul Ocak 1	189/197	157/163	161/161
Tonda Bianca	179/181	167/167	155/155
Tonda di Giffoni	181/191	157/157	155/158
Tonda Romana	185/189	157/157	152/158
Tonda Rossa	179/181	146/146	155/155
Tonnolella	191/195	157/163	167/167
Trenet	189/191	157/163	158/164
Truchsess	189/195	161/165	152/152
Turk	179/185	157/167	155/158
Ugbrooke	189/197	157/159	158/158

Table D.1 Continued

Cultivar	CAC-A14a	CAC-A40	CAC-B005	CAC-B010	CAC-B028	CAC-B29b
Unknown #3	211/215	244/244	279/291	219/225	262/262	122/122
Vilcea 22	215/217	244/244	279/291	211/219	262/268	116/122
Volski Round	211/215	236/244	277/277	211/221	256/266	116/116
Wanliss Pride	215/217	244/244	279/291	211/219	262/268	116/122
Warsaw Red	213/219	248/248	279/295	223/225	254/270	116/128
Webb's Prize Cob	212/214	236/244	277/283	211/219	260/276	116/124
White Filbert	217/217	244/248	279/281	211/219	268/268	116/124
Whiteheart	217/217	244/248	281/295	219/219	262/268	116/130
Willamette	217/219	236/244	291/295	219/223	254/270	122/128
Woodford	217/219	248/248	281/291	211/211	254/270	116/122
Zeta	219/219	236/244	281/291	211/227	254/254	118/135
Zimmerman	215/219	234/236	277/291	211/219	254/278	122/135
26.072	215/215	244/248	277/281	211/225	254/254	126/139
54.021	215/221	244/244	279/279	211/221	262/266	116/130
54.039	209/215	244/244	279/291	225/225	254/262	118/130
54.041	211/215	236/244	277/279	219/225	262/262	116/122
54.056	211/215	238/244	279/279	219/225	262/266	116/130
408.04	212/217	236/236	277/277	223/225	256/256	122/122
495.049	217/217	238/244	277/281	219/219	262/274	118/128
495.072	215/215	236/236	279/295	225/227	254/264	120/124
556.019	215/215	244/244	289/291	219/219	262/274	122/122
556.027	215/215	236/244	279/283	219/223	256/262	120/122
622.051	211/211	236/244	277/279	211/221	262/264	116/118
681.074	211/219	244/244	279/279	219/225	256/262	122/126
681.078	211/213	236/244	277/279	219/221	256/266	114/114
686.124	215/217	244/244	285/287	223/223	262/262	116/135
693.073	211/217	236/244	277/291	211/221	262/262	116/130
693.117	213/215	238/244	277/291	219/219	262/270	118/122
702.041	211/215	244/244	277/291	219/225	262/262	118/122
717.087	211/215	244/244	277/279	219/221	262/270	116/122

Table D.1 Continued

Cultivar	CAC-B105	CAC-B111	CAC-C010	CAC-C28	CAC-C040	CAC-C115
Unknown #3	155/155	182/184	281/281	134/141	186/186	173/182
Vilcea 22	155/155	170/186	275/275	134/137	186/189	193/217
Volski Round	148/148	182/188	275/278	134/141	186/186	193/214
Wanliss Pride	155/155	170/186	275/275	134/137	186/189	193/217
Warsaw Red	148/153	182/182	278/278	131/134	186/186	173/173
Webb's Prize Cob	155/157	184/186	275/275	131/131	186/186	193/225
White Filbert	155/155	186/186	281/281	131/141	186/186	173/193
Whiteheart	155/155	182/186	281/281	131/144	186/186	193/193
Willamette	153/155	182/188	278/278	131/131	186/186	193/196
Woodford	153/153	182/182	278/278	131/131	186/186	193/193
Zeta	155/155	182/182	275/278	131/141	186/192	173/196
Zimmerman	153/155	182/192	278/278	141/144	186/189	173/214
26.072	140/153	184/188	275/275	131/141	186/192	173/214
54.021	155/155	184/186	275/275	134/141	168/186	182/193
54.039	155/163	184/190	278/278	131/141	168/186	193/193
54.041	155/155	182/182	281/281	131/144	186/189	173/176
54.056	138/155	182/186	275/281	131/144	186/186	167/193
408.04	140/157	182/182	275/278	131/134	183/186	193/214
495.049	136/153	182/182	275/275	131/144	186/192	176/191
495.072	153/159	170/186	275/281	144/144	186/189	214/217
556.019	155/155	182/184	275/275	141/141	186/186	173/214
556.027	140/155	170/184	278/281	141/141	186/186	182/217
622.051	125/155	182/186	275/281	131/141	186/186	193/214
681.074	155/155	182/184	278/281	141/144	186/186	167/182
681.078	148/161	182/182	275/275	131/131	186/186	217/225
686.124	155/155	182/190	275/275	137/141	168/186	193/193
693.073	155/155	182/186	275/275	134/141	168/189	176/193
693.117	155/155	182/182	281/281	134/141	186/189	182/217
702.041	155/155	182/186	278/278	134/141	186/189	182/217
717.087	153/155	182/184	281/281	134/141	186/186	173/182

Table D.1 Continued

Cultivar	CAC-C118	CAC-C119	CaT-B107	CaT-B502	CaT-B504	CaT-B505
Unknown #3	179/179	260/260	116/134	187/187	168/182	118/126
Vilcea 22	179/182	258/258	120/120	183/187	168/184	114/126
Volski Round	179/179	256/264	130/134	187/201	172/174	116/118
Wanliss Pride	179/182	258/258	120/120	183/187	168/184	114/126
Warsaw Red	179/179	258/260	120/134	189/195	158/168	106/114
Webb's Prize Cob	179/179	258/258	120/142	185/189	178/178	114/120
White Filbert	179/179	258/258	122/134	187/189	168/176	106/126
Whiteheart	179/179	258/258	112/134	187/189	158/176	118/126
Willamette	179/179	258/258	122/144	189/195	158/182	120/126
Woodford	179/179	258/258	134/134	189/195	176/182	106/106
Zeta	179/185	256/256	128/130	187/189	176/182	106/118
Zimmerman	179/182	258/264	128/134	187/195	174/182	106/114
26.072	179/185	258/264	120/128	183/187	174/176	118/128
54.021	162/179	260/260	120/120	187/187	168/172	106/114
54.039	162/179	258/260	134/134	183/187	168/182	118/118
54.041	179/182	258/258	130/130	187/189	172/178	118/126
54.056	179/179	258/258	122/134	189/195	168/168	118/126
408.04	176/179	260/260	120/130	183/187	168/172	114/116
495.049	179/185	258/262	132/132	187/189	170/176	120/122
495.072	179/182	258/260	126/126	185/187	164/174	118/120
556.019	179/179	258/260	124/134	183/187	176/182	126/126
556.027	179/179	258/260	120/134	187/187	162/168	126/128
622.051	179/179	258/258	122/134	187/187	168/174	106/114
681.074	179/179	258/264	116/120	187/193	168/168	114/126
681.078	179/179	258/258	120/122	189/209	168/176	116/116
686.124	162/179	258/258	120/134	183/187	176/180	106/114
693.073	162/182	258/260	120/120	187/187	176/182	106/118
693.117	179/182	260/260	116/124	187/187	168/182	126/126
702.041	179/182	260/260	116/124	187/187	168/182	126/126
717.087	179/179	258/258	116/134	187/209	168/176	118/126

Table D.1 Continued

Cultivar	CaT-B507	CaT-B508	Cat-C504
Unknown #3	189/197	157/163	158/161
Vilcea 22	187/191	157/159	158/161
Volski Round	189/189	144/161	152/164
Wanliss Pride	187/191	157/159	158/161
Warsaw Red	191/197	157/157	155/158
Webb's Prize Cob	185/195	157/157	164/164
White Filbert	185/197	157/157	158/164
Whiteheart	185/193	157/157	158/164
Willamette	189/191	157/161	167/167
Woodford	185/191	157/157	158/164
Zeta	189/189	146/157	158/158
Zimmerman	190/191	146/157	158/164
26.072	181/197	159/159	152/161
54.021	185/195	157/157	158/161
54.039	179/189	163/163	161/161
54.041	179/197	157/157	158/164
54.056	191/197	157/157	158/161
408.04	179/179	150/161	152/158
495.049	179/183	153/157	152/158
495.072	179/191	157/165	158/164
556.019	189/197	163/163	158/161
556.027	189/197	157/163	158/158
622.051	185/193	155/157	158/161
681.074	189/195	163/163	158/158
681.078	183/189	153/165	152/152
686.124	183/191	157/157	161/164
693.073	189/197	155/163	161/161
693.117	179/197	159/163	161/161
702.041	179/197	159/163	161/161
717.087	193/197	144/157	164/164