RESOLVING THE TAXONOMIC STATUS OF THE MYSTERIOUS „GREEN OAK“ (QUERCUS × VIRIDIS TRINAJSTIĆ) FROM CROATIA BASED ON PHYLOGENETIC ANALYSIS

TAKSONOMSKI STATUS MISTERIOZNOGA „ZELENOGA HRASTA“ (QUERCUS × VIRIDIS TRINAJSTIĆ) IZ HRVATŠKE, TEMELJEN NA FILOGENETSKOJ ANALIZI

Martina TEMUNOVIĆ¹, Jozo FRANJIĆ¹*, Federico VESSELLA², Marco C. SIMEONE²

Summary

The “green oak” is a well-known specific individual oak tree of unknown origin growing near Zadar in Croatia. Depending on the authors, it was described either as a hybrid taxon between Quercus cerris L. and Q. ilex L. (named Q. × viridis Trinajstić) or alternatively as a presumed hybrid between Q. cerris and Q. suber L. To finally resolve the origin of this taxon, we performed molecular analyses and investigated the phylogenetic relationships between the “green oak” and other closely related oak taxa from the surrounding area, including all putative parental species. A total of 16 individuals representing nine Quercus L. taxa were investigated based on both plastid (trnK-matK and trnH-psbA) and nuclear (5.8S + ITS2) DNA sequence variation. Placement of the green oak in the phylogenetic relationships between the studied oak taxa does not support Q. ilex as one of its parental species but rather indicates that this taxon is in fact Q. cerrana Lam., reaffirming previous alternative hypothesis that the green oak is a hybrid between Q. cerris and Q. suber. We therefore confirm the presence of Q. cerrana in the Croatian flora and based on historical literature survey, we explore and discuss the implication of its occurrence and possible hybridogenic origin in the Croatian territory.

KEY WORDS: Green oak, Quercus × viridis, Quercus cerrana, hybrids, phylogeny, taxonomy

INTRODUCTION

UVOD

Oak taxonomy has been an unfailing research topic for decades and continues to be so. This comes as no surprise since oaks (genus Quercus L., Fagaceae) are among the most important forest trees in the Northern hemisphere from ecological, economic, biodiversity and social points of view. In addition, oaks offer an emblematic example of problematic taxonomy and species status due to extensive hybridization among several taxa (Muir, 2000). Although challenging the classical biological species concept (Burger,

¹ Dr. sc. Martina Temunović, Prof. dr. sc. Jozo Franjić, Sveučilište u Zagrebu – Šumarski fakultet, Zavod za šumarsku genetiku, dendrologiju i botaniku, Svetošimunska 25, HR-10000 Zagreb, Croatia, e-mail: martina.temunovic@gmail.com, *franijc@sumfak.hr
² Federico Vessella, PhD, Marco C. Simeone PhD, Dipartimento di Scienze Agrarie e Forestali (DAFNE), Università della Tuscia, 01100, Viterbo, Italy, e-mail: vessella@unitus.it, mcsimeone@unitus.it
hybridization in oaks has greatly contributed to their extremely high variation and plasticity; it constitutes an important mechanism of their dispersal and is suggested to play a crucial role in their adaptive potential to changing climate (Rushton, 1993; Petit et. al., 2004; Aitken et. al., 2008).

Our case study focused on resolving the taxonomic status of a specific semi-evergreen oak tree described and known in literature as the “green oak” due to persistence of its thick green leaves deep into the winter (up to end of February). This individual tree grows in the village of Islam Latinski (Zadar County), Northern Dalmatia, Croatia, and has been protected as a nature monument since 1957 (HTRS96 x: 414861.9036, y: 4895526.4636) (Figure 1). It is estimated to be more than 200 years old (Borzan et. al., 1997). To the best of our knowledge, the first literature mention of the “green oak” was by Jedlowski (1955) who presumed that the individual is a probable hybrid between Q. cerris L. and Q. suber L. Later, Trinajstić (1974a) described this particular individual tree as a hybrid Quercus × viridis Trinajstić, hybr. nov. suggesting that it is in fact a hybrid probably between Quercus cerris f. austriaca and Q. ilex (Figure 2). He based his description on morphological characters and the fact that Q. suber is not growing in the surrounding area.

Afterwards, the peculiar green oak has been investigated several times including botanical, biological, taxonomical, detailed morphological as well as wood and leaf anatomy points of view (Siegrist, 1995; Vranković and Pernar, 1995; Borzan et. al., 1997; Borzan and Pfeifhofer, 1998; Borzan, 2000; Guttenberger, 2000; Borzan and Stabentheiner, 2002). For example, Borzan (2000) has reported hermaphroditic unseasonal flowering in the green oak which lead to the detailed study of pollen and leaf hairs morphology of this individual compared to the putative ancestors Q. cerris and Q. ilex by scanning electron microscopy (Borzan and Stabentheiner, 2002). The latter study implied that the green oak does not share any similarities with Q. ilex based on these traits. Likewise, Guttenberger (2000) who has also performed measurements of the DNA content of the green oak and related oak species concluded that Q. ilex does not seem to be one of the parental species of the green oak.

Finally, the latest review on the origin of this particular oak by Muller et. al. (2003) suggested that this individual shares much more similarities with Q. cerris compared to Q. ilex; the authors conclude that all gathered studies of this taxon support the opinion given by Jedlovski (1955) and not the description by Trinajstić (1974a). However, the origin of this intriguing taxon remains still uncertain to date, and all

Figure 1. The „Green oak“ (Quercus × viridis Trinajstić) individual growing in Islam Latinski near Zadar, Croatia.
Slika 1. Stablo „zelenoga hrasta“ (Quercus × viridis Trinajstić), Islam Latinski pored Zadra u Hrvatskoj.
cited authors recommended the use of molecular data and DNA analysis to definitely assess its taxonomic status.

In this study, we carried out for the first time a phylogenetic analysis of the “green oak” in comparison to other closely related oak species from the surrounding region, including all putative parental species: *Q. cerris*, *Q. ilex* and *Q. suber*. A further oak tree from Croatia displaying similar morphology to the “green oak” individual, as well as members of *Q. crenata* Lam., i.e. the supposed stable hybrid between *Q. cerris* and *Q. suber* (Bellarosa et al., 2005; Cristofolini et al., 2005; Conte et al., 2007) from Italy and Slovenia, were included in the dataset. To finally resolve the origin of the green oak tree, we combined both plastid and nuclear DNA markers widely used for DNA barcoding in plants and which have proven to be helpful in taxonomic identification and delimitation of some closely related Euro-Mediterranean oak taxa (Simeone et al., 2013).

**MATERIALS AND METHODS**

**MATERIJAL I METODE**

**Plant material – Biljni materijal**

We collected leaf samples from the “green oak” individual (*Q. × viridis* Trinajstić) growing in the village of Islam Latinski near Zadar, as well as from another putative green oak growing near Rijeka (Donje Jelenje) where unusual evergreen oak individuals of unknown origin have been observed (J. Franjić, personal observation) (Table 1). In addition, leaf samples from 1-3 individuals were collected from all closely related oak taxa (*Q. cerris*, *Q. suber*, *Q. ilex*, *Q. coccifera* L. and *Q. crenata*) from Croatia, Slovenia, Italy and Greece to maximally cover the geographic area surrounding the target “green oak”. Finally, samples from single individuals of three more distant oak species belonging to the infrageneric group *Quercus* (*Q. robur* L., *Q. petraea* /Matt./ Liebl. and *Q. pubescens* Willd.) were also investigated and used as outgroups. In total, nine *Quercus* taxa were included in the analyses (Table 1).

**DNA extraction and amplification – Izolacija i umnažanje DNK**

DNA extractions from silica-gel dried leaves were performed with the DNeasy Plant Minikit (QIAGEN), following the manufacturer’s instructions. In a search for maximum variability in our taxon-based study, we used two highly variable plastid regions (*trnK-matK* and *trnH-psbA*), and the nuclear ribosomal region 5.8S + ITS2 (Simeone et al., 2013). Plastid primers were the same as in Piredda et al. (2011); ribosomal oligonucleotides were designed as follows: 5’-ACG ACT CTC GGC AAC GGA TA-3’ (5.8S_Fw), 5’-CAG CGG GTA GTC CCG CCT GA-3’ (25S_Rev). DNAs (ca. 40 ng) were amplified with RTG PCR beads (GE Healthcare) in 25 µl final volume according to the manufacturer’s protocol. Thermocycling conditions were: 94° for 3 min, followed by 35 cycles of 94° for 30 sec, 53° for 40 sec and 72° for 40 sec, with a final extension step of 10 min at 72° (plastid loci), and 98° for 3 min, followed by 35 cycles of 98° for 30 sec, 60° for 30 sec and 72° for 30 sec, with a final extension step of 5 min at 72° (ITS region). PCR products were cleaned with Illustra DNA and Gel Band Purification Kit (GE Healthcare), and eluted in 30 µl type 6 elution buffer. Standardized aliquots were then submitted to Eurofins MWG Operon (https://www.eurofinsgenomics.eu) for sequencing. Electropherograms were edited with CHROMAS 2.3 (www.techne lysium.com.au) and checked visually.

**Phylogenetic analyses – Filogenetske analize**

All sequences were first aligned with MUSCLE (Edgar, 2004) and checked by eye. We calculated summary statistics of the aligned sequences (number of variable sites – V,
number of haplotypes – h, and nucleotide diversity - \( \pi \) using Arlequin v. 3.5.2.2 (Excoffier and Lischer, 2010). The phylogenetic analyses were performed separately on the combined plastid DNA dataset (\( trnK-matK + trnH-psbA \)) sequences and on the nuclear dataset (5.8S + ITS2). We first constructed a plastid haplotype and a nuclear ribotype networks, based on the median-joining network algorithm (Bandelt et. al., 1999) as implemented in the PopArt software (Leigh and Bryant, 2015). Next, to assess the phylogenetic relationships among the studied oak taxa based on the nuclear sequence dataset, we constructed a phylogenetic tree using a maximum parsimony (MP) method with bootstrap analyses of 1000 replicates to test for the branch support. The analysis was carried out using the MEGA v. 7.0.26 and Seaview v4.6.2 software (Gouy et. al., 2010; Tamura et al. 2016) with default parameters (gaps were treated as unknown states). Finally, because the position of hybrid species in a classic phylogenetic tree is often doubtful, we also computed a rooted consensus cluster network based on nuclear sequences to identify putative hybridization events leading to the formation of the "green oak". This network was based on a set of 1000 original trees obtained with a MP analysis and with a 20 % threshold (minimum support) for a cluster to be included in the procedure using Dendroscope v. 3.5.9 (Huson and Scornavacca, 2012).

**RESULTS**

Our dataset included 16 sequences of both plastid and nuclear regions for nine oak taxa. Alignment of the \( trnH-psbA \) region had 538 characters (bp) in length, 22 variable sites and 7 parsimony informative sites. Alignment of the \( trnK-matK \) region displayed 694 characters, 14 variable sites and 12 parsimony informative sites, while the alignment of the combined plastid DNA dataset resulted in a total length of 1232 sites, 36 of which were variable and 19 parsimony informative (Table 2). The alignment of the nuclear dataset resulted in the total length of 371 sites of which 21 were variable and 13 parsimony informative (Table 2). In total, five haplotypes were identified based on the combined plastid sequences with a low nucleotide diversity \( \pi = 0.0073 \) (Table 2). The plastid DNA haplotype network showed that one haplotype was shared among 11 studied individuals representative of four oak taxa, namely Q. cer-
TEMUNOVIĆ, M. et al.: RESOLVING THE TAXONOMIC STATUS OF THE MYSTERIOUS „GREEN OAK“ (Quercus × Viridis Trinajstić) ...

ris, Q. suber, Q. crenata and Q. × viridis (Figure 3a). Another plastid haplotype was shared between Q. robur and Q. petraea individuals while Q. ilex, Q. coccifera and Q. pubescens displayed different, unique haplotypes. The haplotype network showed that the five haplotypes are arranged according to three lineages, each representing the three main infrageneric groups encompassing the here studied oaks: Group Cerris (Q. cerris, Q. suber, Q. crenata), Group Ilex (Q. ilex and Q. coccifera) and Group Quercus (Q. robur, Q. petraea and Q. pubescens). Interestingly, Q. × viridis individuals were all included in the only haplotype of the Cerris group, diverging from the Q. ilex haplotype by 27 mutational steps (Figure 3a).

The nuclear dataset was characterized by 11 ITS2 + 5.8S ribotypes (Figure 3b) and higher nucleotide diversity $\pi = 0.01617$ (Table 2). In contrast to the obtained plastid haplotypes, the majority of the included Quercus taxa as well as some individuals of the same species showed private ITS2 + 5.8S sequence variants. In total, nine ribotypes occurring in single individuals were detected. Two variants were shared among different taxa: one between Q. suber, Q. crenata and Q. × viridis (from Rijeka) and the other between Q. crenata and Q. × viridis (from Zadar) (Figure 3b). Three ribotypes were detected in Q. cerris and two in Q. suber and in Q. × viridis. Similar to the cpDNA network, lineages corresponding to the three infrageneric groups could be recognized. Ribotypes found in the Q. × viridis individuals were included in the Cerris lineage, separated from the ribotype displayed by Q. ilex by at least 10 mutational steps.

The reconstructed MP phylogenetic relationships of the nuclear ribosomal sequences revealed three main clades, still corresponding to the three Quercus infrageneric groups (Figure 4). Within the Cerris clade, the putative Q. × viridis individual from Islam Latinski (Zadar) and the other putative Q. × viridis individual from Donje Jelenje (Rijeka), formed a subclade together with Q. suber and Q. crenata individuals from Croatia, Slovenia and Italy, with no or very low resolution, and separated from the Q. cerris sequences. In particular, Q. × viridis individual from Zadar (Croatia) was placed as a sister taxon next to the sampled Q. crenata from the Latium region in Italy (Figure 4). Separation of the Q. × viridis individuals from those belonging to the
ris and Q. suber, as first suggested by Jedlowski (1955). However, the two putative Q. × viridis individuals included in this study did not show identical phylogenetic pattern. Both putative Q. × viridis individuals shared the same cpDNA haplotype (Figure 3) which was also present in all other cerroid oaks included in this study (Q. cerris, Q. suber and Q. crenata). This is however not surprising as the used cpDNA barcoding regions (trnK-matK and trnH-psbA) were shown to have low differentiation rates below the infrageneric level and thus relatively low efficiency to discriminate between closely related Quercus taxa, particularly for the Group Cerris (Simeone et. al., 2013). Interspecific sharing of plastid haplotypes is also well documented for the white oaks of the infrageneric groups Quercus and Ilex across wide geographic areas (Petit et. al., 2002; Slade et. al., 2007; Vitelli et al., 2017).

On the other hand, the nuclear 5.8S + ITS2 region has shown to have a better discriminatory power in oak phylogeny compared to the used plastid regions (Bellarosa et. al., 2005). In this study, the two Q. × viridis individuals displayed slightly different ribotypes, separated by only one mutational step (Figure 3). In addition, the "famous" green members of the Ilex infrageneric group, Q. ilex and Q. cocifera, was evident. Finally, the rooted consensus cluster network clearly indicated close relationships between all members of the Cerris subclade, and further suggested the hybrid origin of the Q. × viridis with Q. suber as one of the parental species (Figure 5).

**DISCUSSION**

Our work represents the first attempt to resolve the taxonomic status of the "green oak" (Q. × viridis), described by Trinajstić (1974a) as a putative hybrid between Q. cerris and Q. ilex, based on molecular data. We used both plastid and nuclear DNA sequences to carry out a phylogenetic analysis involving a total of nine oak taxa from a wide geographic range surrounding the investigated oak, including all possible parental species. All our results of phylogenetic relationships among the studied oak taxa do not support Q. ilex as one of the parental species of the green oak. Rather, they confirm that the investigated green oak individuals are actually Q. crenata Lam., a presumed hybrid between Q. cerris and Q. suber, as first suggested by Jedlowski (1955). However, the two putative Q. × viridis individuals included in this study did not show identical phylogenetic pattern.

Both putative Q. × viridis individuals shared the same cpDNA haplotype (Figure 3) which was also present in all other cerroid oaks included in this study (Q. cerris, Q. suber and Q. crenata). This is however not surprising as the used cpDNA barcoding regions (trnK-matK and trnH-psbA) were shown to have low differentiation rates below the infrageneric level and thus relatively low efficiency to discriminate between closely related Quercus taxa, particularly for the Group Cerris (Simeone et. al., 2013). Interspecific sharing of plastid haplotypes is also well documented for the white oaks of the infrageneric groups Quercus and Ilex across wide geographic areas (Petit et. al., 2002; Slade et. al., 2007; Vitelli et al., 2017).

On the other hand, the nuclear 5.8S + ITS2 region has shown to have a better discriminatory power in oak phylogeny compared to the used plastid regions (Bellarosa et. al., 2005). In this study, the two Q. × viridis individuals displayed slightly different ribotypes, separated by only one mutational step (Figure 3). In addition, the "famous" green
TEMUNOVIĆ, M. et al.: RESOLVING THE TAXONOMIC STATUS OF THE MYSTERIOUS „GREEN OAK“ (Quercus × Viridis Trinajstić) ...

...oak individual near Zadar shared its ribotype with Q. crenata from Italy (Latium), while the putative green oak individual from Rijeka exhibited the same ribotype as Q. suber from Croatia (Pula) and Italy (Latium) as well as Q. crenata from Slovenia and Italy (Trentino). Likewise, placement of both Q. × viridis from Zadar and Rijeka as sister taxa to Q. crenata and Q. suber in the MP tree indicates that these taxa (Q. suber, Q. crenata and Q. × viridis) are indeed highly related at the nuclear level. Borzan (2002) already pointed out that “a visit to the Herbarium Patavinum, Padua (Italy), and to the Erbario Centrale Italiano »Filippo Parlatore«, Sezione di Botanica, Museo di Scienze Naturali, Firenze (Italy), revealed that the herbarium samples of the “green oak” from Zadar are very similar to those kept in these Italian botanical institutions under the name Q. crenata and Q. pseudosuber Santi”. Individuals assigned to the complex Q. crenata – Q. pseudosuber are in fact traditionally acknowledged as stabilised hybrids between Q. cerris × Q. suber and the latest paper on this topic concluded that Q. crenata Lam. is the correct name for this nothospecies (Cristofolini and Crema 2005; Cristofolini et. al., 2017). This oak taxon (the “false cork oak”) is known to occur in southern France and Italy where the two supposed parental species are found in sympatry; however, scattered Q. crenata individuals can be also found in Northeastern Italy, western Slovenia and Croatia, where Q. suber is currently out of its distribution range (Cristofolini and Crema 2005; Bellarosa et. al., 2005). Thus, the origin of these Q. crenata individuals is still under debate (Cristofolini and Crema, 2005; Conte et. al., 2006; Schirone et. al., 2015).

For example, some authors included Croatia in the natural range of Q. suber (Muller, 1900; see references in Schirone et. al., 2015 and Euro+Med PlantBase) because this oak species has been well documented in older floristic literature from several localities across Croatia. These include Istria and particularly the Šijana forest, near Pula, where the largest and oldest known cork oak stand in Croatia occurs (Trinajstić, 2006 and references therein). In addition, isolated Q. suber trees are known from several localities in Dal-

Table 2. Summary statistics of the aligned sequences.

<table>
<thead>
<tr>
<th></th>
<th>tmH-psbA</th>
<th>tmK-matK</th>
<th>cpDNA</th>
<th>5.8S + ITS2</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
<td>16</td>
<td>16</td>
<td>16</td>
<td>16</td>
</tr>
<tr>
<td>Length (bp)</td>
<td>538</td>
<td>694</td>
<td>1232</td>
<td>371</td>
</tr>
<tr>
<td>V</td>
<td>22 (4.3 %)</td>
<td>14 (2 %)</td>
<td>36 (3 %)</td>
<td>21 (5.7 %)</td>
</tr>
<tr>
<td>Pi</td>
<td>7 (1.4 %)</td>
<td>12 (1.7 %)</td>
<td>19 (1.6 %)</td>
<td>13 (3.5 %)</td>
</tr>
<tr>
<td>π</td>
<td>0.0082</td>
<td>0.0067</td>
<td>0.0073</td>
<td>0.0162</td>
</tr>
</tbody>
</table>

N – number of sequences, V – number of variable sites, Pi – number of Parsimony informative sites, π – nucleotide diversity.


Figure 5. Rooted consensus network based on nuclear sequences (5.8S + ITS2 region) computed using Dendroscope from a set of 1000 of trees obtained with a Maximum Parsimony analysis. The resulting network represents clusters occurring, at least, in the 20 % of all trees in their full resolution. Putative hybridization events are represented by blue lines.

Slika 5. Ukorijenjena dogovorna mreža temeljem jezgrinih sekvenci (5.8S + ITS2 regija) dobivena u programu Dendroscope od 1000 originalnih stabala maksimalne štedljivosti. Prikazana filogenetska mreža predstavlja klastere koji se pojavljuju u barem 20 % svih ulaznih stabala. Potencijalni procesi/putevi hibridizacije prikazani su plavim linijama.
matia: Dundo forest on the island of Rab, on Mljet and in Blato on the island of Korčula (Hirc, 1903-1912; Trinajstić, 2006). Moreover, individuals of *Q. pseudosuber* (= *Q. crenata*) were historically reported from many sites across Istria and the Kvarner region (Šijana forest, Strobl, 1872; Pericin 2001, Veruda forest, Freyn, 1877; Dragonja, Tinjan, Pazin, Mirna river, Lovran and Volosko, Ascherson and Graebner, 1908-1913; Pula and Volosko, Schneider, 1906; Cres, Hirc, 1916; Kvarner, Hayek, 1924; Cres and Rab island, kanjon Rječine, Lovrić, 1981), as well as from Dalmatia (Richter, 1897; Adamović, 1911; Hayek, 1924, 1927). Later, Trinajstić (2006) suggested that in fact all *Q. pseudosuber* individuals reported from Croatia belong to *Q. suber* and concluded that the taxon *Q. crenata* is not present in Croatian flora. However, our results provide clear evidence that *Q. crenata* individuals do occur in Croatia and confirm similar findings of previous studies (Lovrić, 1981; Cristofolini and Crema, 2005; Perinčić, 2010; Simeone *et al.*, 2009, 2013; Schirone *et al.*, 2015). For example, more recently *Q. crenata* was recorded in Zadar, nevertheless it was cultivated in the Vladimir Nazor Park which dates from the end of the 19th century (Perinčić, 2010; Nikolić 2017). Thus, it remains an open question whether this taxon could have been established in Croatia naturally or has been man-mediated.

Based on similar findings of *Q. suber* and *Q. crenata* individuals on the eastern side of the Adriatic sea, several authors hypothesized that *Q. suber* first originated in the Eastern Mediterranean (probably surviving in the Balkan Peninsula), expanded westward and finally got extinct in the East Mediterranean (Bellarosa *et al.*, 2005; Simeone *et al.*, 2009; Schirone *et al.*, 2015). Under this hypothesis, *Q. suber* and *Q. cerris* would have been naturally co-occurring until a recent past, possibly giving rise to occasional hybridizations. However, up to date this scenario has not been generally accepted due to lack of strong scientific evidence and is a subject of ongoing debate (c.f. Magri *et al.*, 2007).

The two “green oak” individuals included in this study did not show identical genetic patterns, indicating a different descent. If we assume an hybridogenic origin, the phylogenetic position of *Q. × viridis* from Rijeka, clustering among *Q. crenata* individuals from Slovenia and Trentino (Northern Italy) and *Q. suber* (Figure 3, Figure 4) suggest that, at least for the region of Istra and Kvarner, it is plausible to infer a natural origin of this tree, since both parental species (*Q. cerris* and *Q. suber*) grow in this area since, at least, four generations (Trinajstić, 2006). On the other hand, it is highly unlikely that the “green oak” from Islam Latinski (Zadar) is a natural hybrid of the two parental species, since *Q. suber* is absent from the surrounding area and the nearest known cork oak trees grow on the island of Rab (cca 90 km away), where they were planted at the beginning of the 20th century (Šurić, 1933), thus after the “green oak” individual was already established. Placement of this green oak individual in the phylogenetic relationships with *Q. crenata* from Latium in Italy indicates a possibility that this particular oak originated from this region where *Q. crenata* is particularly widespread. It was likely planted in the village of Islam Latinski a long time ago since long distance pollen dispersal from *Q. crenata* and /or *Q. suber* from Central Italy does not seem highly probable. However, extinction/progressive rarefaction of its wild, close-by relatives that were part of a common, little differentiated gene pool is also probable, and more extensive samplings would be clearly needed to accurately establish autochthony or the provenance origin of this important tree.

**REFERENCES**

**LITERATURA**


• Šušić, S., 1933: Opis i osnova gospodarenja u držav. šumi “Dundó” na otoku Rabu. Šum. list, 57(4): 259–264.


Šažetak


KLJUČNE RIJEČI: zeleni hrast, Quercus × viridis, Quercus crenata, hibridi, filogenija, taksonomija