POPULATION GENETIC STRUCTURE OF *ORTHOTOMICUS EROSUS* (WOLLASTON, 1857) (COLEOPTERA: CURCULIONIDAE, SCOLYTINAE) IN PINE FORESTS OF THE MEDITERRANEAN REGION OF TURKEY

SARIKAYA, O.[1*] – ŞEN, I.[2*]

[1]*Suleyman Demirel University, Faculty of Forestry, 32260, Isparta, Turkey*

[2]*Suleyman Demirel University, Technology Faculty, 32260, Isparta, Turkey*

**Corresponding authors*
e-mail: oguzhansarikaya@sdu.edu.tr; ismailsen32@gmail.com
(phone: +90-246-211 39 64; fax: +90-246-211 39 48)

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Abstract. *Orthotomicus erosus* (Wollaston, 1857) (Coleoptera: Curculionidae: Scolytinae) is one of the principal pests of Eurasian forests. Gathering data from this study concerning population genetic structure of *O. erosus* would help improving new strategies to control the pest by giving new insights on forest management. The aims of the study were to resolve the population genetic structure of *Orthotomicus erosus* which distributes Mediterranean Region of Turkey and to determine the factors (such as host pine species and geographic barriers) that contributed to the current distribution of genetic diversity. The beetle samples were collected from 20 stands from the pine forests included in the Mediterranean Region of Turkey. 67 samples were studied using mitochondrial cytochrome oxidase subunit I (COI) gene and Neighbor Joining (NJ) and Maximum Likelihood (ML) analyses were performed. As a result of the study, thirty-seven distinct haplotypes from sixty-seven samples were determined. The species did not form any phylogroup in populations depending on the geographical location according to the NJ and ML analysis. The NJ and ML trees revealed that those *O. erosus* individuals that fed on different pine species did not have genetic variations. Consequently, NJ and ML analysis results reveals that different populations of the species across the Mediterranean Region were not disconnected and isolated geographically either.
Keywords: *Orthotomicus erosus, mtDNA, Neighbour Joining, Maximum Likelihood, Turkey*

Introduction

Forests have played a very important role for all organisms since the existence of human-beings. However, forestlands have shrunk and have been destroyed due to overutilization and misuse for centuries. Particularly the growing world population in the last century and thus the social pressure as well as the negative impacts such as environmental pollution, forest fire and insect damage have resulted in the shrinkage of forest areas, which still prevails at the same pace (Sarıkaya and Avcı, 2006).

There are several factors that led to shrinkage of forest areas and reduction of their productivity in the Mediterranean Region located in the south of Turkey. Among these factors, harmful insect species play a very important role. Bark beetles are among the most important insect groups that lead to significant economic loss due to the damage they cause in forest trees. The bark beetles that damage the forests in the Mediterranean Region include Mediterranean pine engraver *Orthotomicus erosus* (Wollaston, 1857), which is highly important because of its damage in pine forests. Although these beetles cause secondary damage, they may cause primary damage just after the dry periods. In this region, especially *Pinus brutia* is one of most widely distributed species (Karatepe et al., 2014). *Orthotomicus erosus* (Wollaston) was found in pine (*Pinus* spp.), fir (*Abies*

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spp.), spruce (*Picea orientalis*) and cedar (*Cedrus libani*) species in Turkey (Schedl, 1961; Tosun, 1975; Selmi, 1989 and 1998; Çanakçıoğlu and Mol, 1998). Studies conducted in other countries demonstrated that *O. erosus* caused damage in pine species in primarily Mediterranean countries and Middle and South Europe, Iran, Israel, Morocco, Tunisia, Algeria, Crimea, Caucasia, South and North America (Mendel and Halperin, 1982; Mendel, 1983; Pfeffer, 1995; Henin and Pavia, 2004; Lee, 2004; Haack, 2004; Jamaa et al., 2007; Amini et al., 2013; Gómez and Martínez, 2013).

Molecular tests have been increasingly used in systematic and taxonomic studies conducted on insects and contributed to the solution of taxonomic problems thanks to the recent developments, enzymatic amplification of specific regions of a DNA strand In Vitro (PCR), (Mullis et al., 1986), introduction of automatic devices for DNA sequence analysis and superfast computers (Brower and De Salle, 1994; Roderick, 1996; Simon et al., 1994). Current population structure of a species reflects both historic and contemporary ecological and evolutionary forces (Hewitt, 2000). These processes left their signatures in the genomes of species. Thus, current population genetic structure can be used to infer past evolutionary and demographic events within species (Avise, 2000).

There is any study concerning population genetics of *O. erosus* (Hughes and Vogler 2004) although the species has been included in several molecular studies (Cognato and Felix, 2000; Cognato and Vogler, 2001; Jordal et al., 2008; Cognato, 2013; Jordal and Kambestad, 2014). *O. erosus* is one of the most damaging bark beetle species to pine forests at the Mediterranean shore latitude in Turkey. Generally a secondary pest, it can immediately gain a primary character especially after the arid periods in the Mediterranean and Aegean regions of Turkey. However, population structure of the species is also unknown in Turkey. Information concerning its population structure could help in the future control of this pest. The aims of the study were to resolve the population genetic structure of *O. erosus* in the Mediterranean Region of Turkey and to determine the factors (such as host pine species and geographic barriers) that contributed to the current distribution of genetic diversity.

Material and Methods

In order to collect *Orthotomicus erosus* samples, sampling plots were selected in the stands where the Brutian pine and black pine grew under different habitat conditions in the Mediterranean Region and the damage caused by the bark beetle was intense and beetle samples were collected from these areas. The adult samples of *Orthotomicus erosus* were collected from different locations across the Mediterranean Region in 2013. The locations where *O. erosus* samples were collected are presented in *Table 1* and *Figure 1*.

Table 1. *Pinus brutia and P. nigra stands where Orthotomicus erosus samples were collected. (Host tree species were symbolised with capital letter N: P. nigra; B: P. brutia in the Abbreviation column)*

Samples No	Abbreviation	Location	Coordinates	Altitude (m)	Host species
1	B-AntKem	Kemer-Karabucak	N 36° 58′ 31′′ E 30° 53′ 45′′	44	*Pinus brutia*
2	B-AntAks	Akseki-Küser	N 37° 10′ 86′′ E 31° 74′ 35′′	1127	*P. brutia*
3	B-AntKum	Antalya-Kumluca	N 36° 23′ 56′′ E 30° 19′ 22′′	300	*P. brutia*

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4	N-AntAksCam	Akseki-Çambeleni	N 37° 14′ 87′′ E 31° 83′ 85′′	1367	*P. nigra*
5	N-BurAkc	Burdur-Akçaören	N 37° 41′ 64′′ E 30° 19′ 91′′	1305	*P. nigra*
6	B-BurBuc	Burdur-Bucak Gündoğdu	N 37° 35′ 10′′ E 30° 61′ 66′′	892	*P. brutia*
7	B-IspEgiAsa	Eğirdir-Aşağıgökdere	N 37° 32′ 88′′ E 30° 48′ 45′′	250	*P. brutia*
8	B-MrsTarCam	Tarsus Çamalanı Akarca	N 37° 31′ 28′′ E 34° 78′ 45′′	1200	*P. brutia*
9	B-MerGl	Mersin-Gülnar	N 36° 32′ 97′′ E 33° 40′ 40′′	956	*P. brutia*
10	B-MerAna	Anamur-Demirören village	N 36° 06′ 57′′ E 32° 65′ 62′′	254	*P. brutia*
11	B-MerTar	Mersin-Tarsus	N 37° 13′ 04′′ E 34° 54′ 36′′	950	*P. brutia*
12	B-MrsDav	Mersin-Davultepe	N 36° 48′ 49′′ E 34° 22′ 14′′	760	*P. brutia*
13	N-MerGz	Mersin-Gözne	N 37° 04′ 30′′ E 34° 33′ 30′′	1200	*P. nigra*
14	N-MrsTarCam	Tarsus- Çamalanı, Tekir	N 37° 31′ 28′′ E 34° 78′ 45′′	1325	*P. nigra*
15	B-AdaCuk	Adana-Çukurova Karahan Köyü-Tapan Tepe	N 37° 08′ 18′′ E 35° 17′ 82′′	141	*P. brutia*
16	B-AdaKad	Osmaniye-Kadirli-Börklüler	N 37° 47′ 17′′ E 36° 20′ 26′′	627	*P. brutia*
17	B-OsmYar	Osmaniye-merkez Yarpuz-Yemşen	N 37° 07′ 21′′ E 36° 33′ 94′′	728	*P. brutia*
18	N-AdaKar	Karaisalı-Damlama	N 37° 35′ 76′′ E 34° 96′ 76′′	1271	*P. nigra*
19	B-KmrAnd	Andırın-Efirağızlı	N 37° 51′ 78′′ E 36° 37′ 74′′	625	*P. brutia*
20	N-KmrAndSar	Andırın-Sarıtanışmanlı	N 37° 67′ 44′′ E 36° 45′ 80′′	1436	*P. nigra*

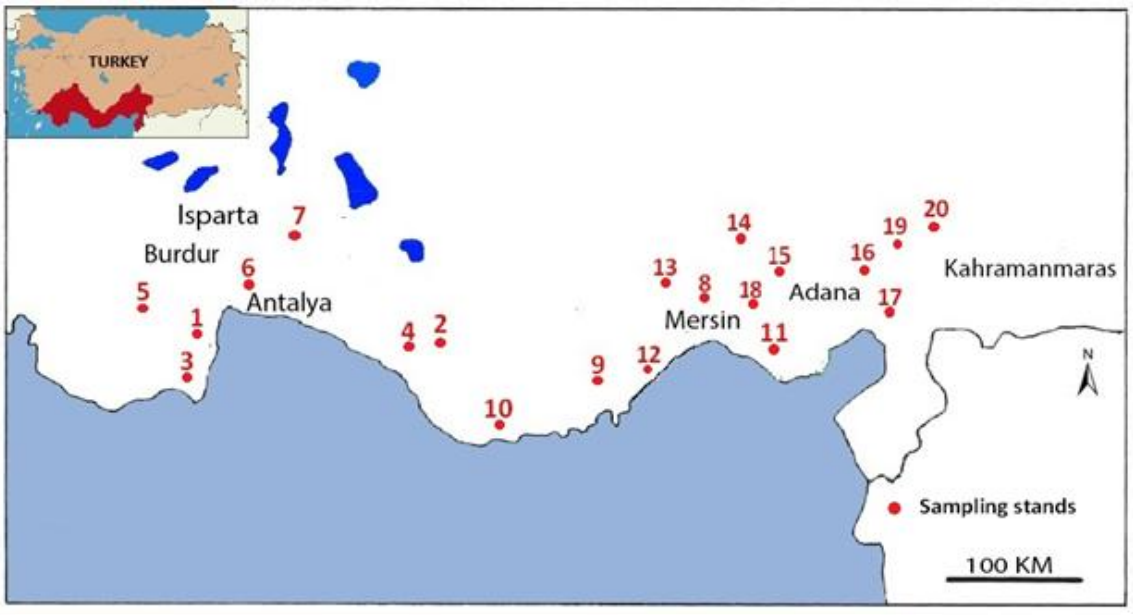

Figure 1. *Sampling stands of Orthotomicus erosus specimens*

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Trap woods were placed in the sampling plots before the flying period in order to collect the samples. Traps were composed of 12 woods each with a length of 1 m. The samples collected from the trap trees were soaked in pure alcohol of 99% and stored.

Furthermore, pheromone traps were placed in the sampling plots before flying periods and the samples were collected from these traps. Pheromone preparations containing 1500 mg methyl butanol + 100 mg cis-verbanol + 30 mg Ipsdienol were used in the pheromone traps to capture *O. erosus*. Moreover, samples were collected from trunks maintained in the forest storages and production areas across the region through observation. The collected samples were placed and stored in tubes containing pure alcohol. The tubes where the samples were placed were stored in deep freezer until the performance of genomic DNA (gDNA) isolation.

Genomic DNA isolation

gDNAs of *O. erosus* samples collected during the field study were isolated from the head and thorax of the beetles. Abdominal and elytra of the samples from which gDNA was isolated were stored at the laboratory for morphological analysis. gDNAs of the samples were isolated with Qiagen DNeasy Blood and Tissue Kit (Qiagen).

Polymerase Chain Reaction (PCR) and DNA sequencing

The isolated gDNAs were controlled using 0.8% agarose gel electrophoresis and the gDNA quantity of the samples was diluted to the concentration level that was appropriate for PCR according to their gel appearance. The primers S1718 (5'-GGAGGATTTGGAAATTGATTAGTTCC-3') and A2237 (5'-CCGAATGCTTCTTTTTTACCT CTTTCTTG-3') were used for the amplification of mitochondrial cytochrome oxidase subunit I (COI) regions of the samples through PCR (Simon et al., 1994; Normark et al. 1999). Thirty cycles of amplification were performed as follows: denaturation step at 94°C for 30 seconds, annealing at 48°C for 1 min, and extension at 72°C for 90 seconds. PCR products were purified with QIAquick PCR purification kit (QIAgen) and sequenced.

Population Genetic Analyses

The phylogenetic relationships between the haplotypes were analysed and phylogenetic trees were created using Neighbour Joining (NJ) and Maximum Likelihood (ML) algorithms. The best substation model according to the DNA sequencing data was determined using the hierarchical likelihood ratio test (hLRT) and Akaike information criterion (AIC) in MODELTEST v. 3.7 (Posada and Crandall, 1998). The substitution model for the two abovementioned statistics was found to be TIM3+I for upon *Orthotomicus erosus* by consensus and these criteria were entered as substitution model while constructing the Maximum Likelihood (ML) tree. ML trees were questioned according to the heuristic search approach. The branch support values of ML trees were evaluated through 1000 non-parametric bootstrap analysis (Felsenstein, 1985).

In order to determine the polymorphism and diversity level of *Orthotomicus erosus*, the number of within populations and among populations average nucleotide differences and nucleotide diversity (π) were analysed. In order to determine the significance of the differences between the populations of the species, pairwise Fst values were calculated.

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In order to determine if the populations of the species showed the cases such as enlargement/bottleneck in the past, historical demographic pattern of both species were analysed. To this end, Tajima's D (Tajima, 1989) and Fu's FS (Fu, 1997) neutrality tests were performed for the COI gene regions that were studied. Moreover, sum of squared differences (SSD) and Harpending's Raggedness index (Hri) mismatch distribution analysis were used to check if the sequence data of the species deviated from the possible enlargement model estimation.

Results and Discussion

67 samples were analysed for *Orthotomicus erosus* in this study. The DNA sequences of the samples that were studied were aligned, the impractical regions were removed, and a sequence of 488 base pairs that could be used for statistical analysis was obtained. 49 bases out of the sequence of 488 base pairs had mutations. 37 different haplotypes were found in 67 samples that were analysed due to the abovementioned mutations. Some haplotypes were represented more than once.

The within populations and among populations genetic variations of *Orthotomicus erosus* were analysed through AMOVA (*Table 2*). The analysis showed that the within populations genetic variation of the species was higher than the among populations variation.

Table 2. *Spatial analysis of molecular variance of Orthotomicus erosus. df degrees of freedom*

	d.f.	Sum of squares	Variance components	Percentage of variance
among populations	18	242.876	3.11977 Va	55.07
within populations	48	122.183	2.54549 Vb	44.93
Total	66	365.060	5.66525	

The genetic diversity of 67 samples from different populations of *Orthotomicus erosus* collected from the Mediterranean Region and intraspecific genetic diversity were determined with Neighbour Joining (*Figure 2*) and Maximum Likelihood (*Figure 3*) methods. According to the base data obtained prior to the Maximum Likelihood analysis, the substitution model in the COI sequence of the species was found to be TIM3+I in Model test software and the tree was constructed according to that substitution model. To construct both trees, *O. erosus*, *O. proximus* and *O. suturalis* were used as the outgroup.

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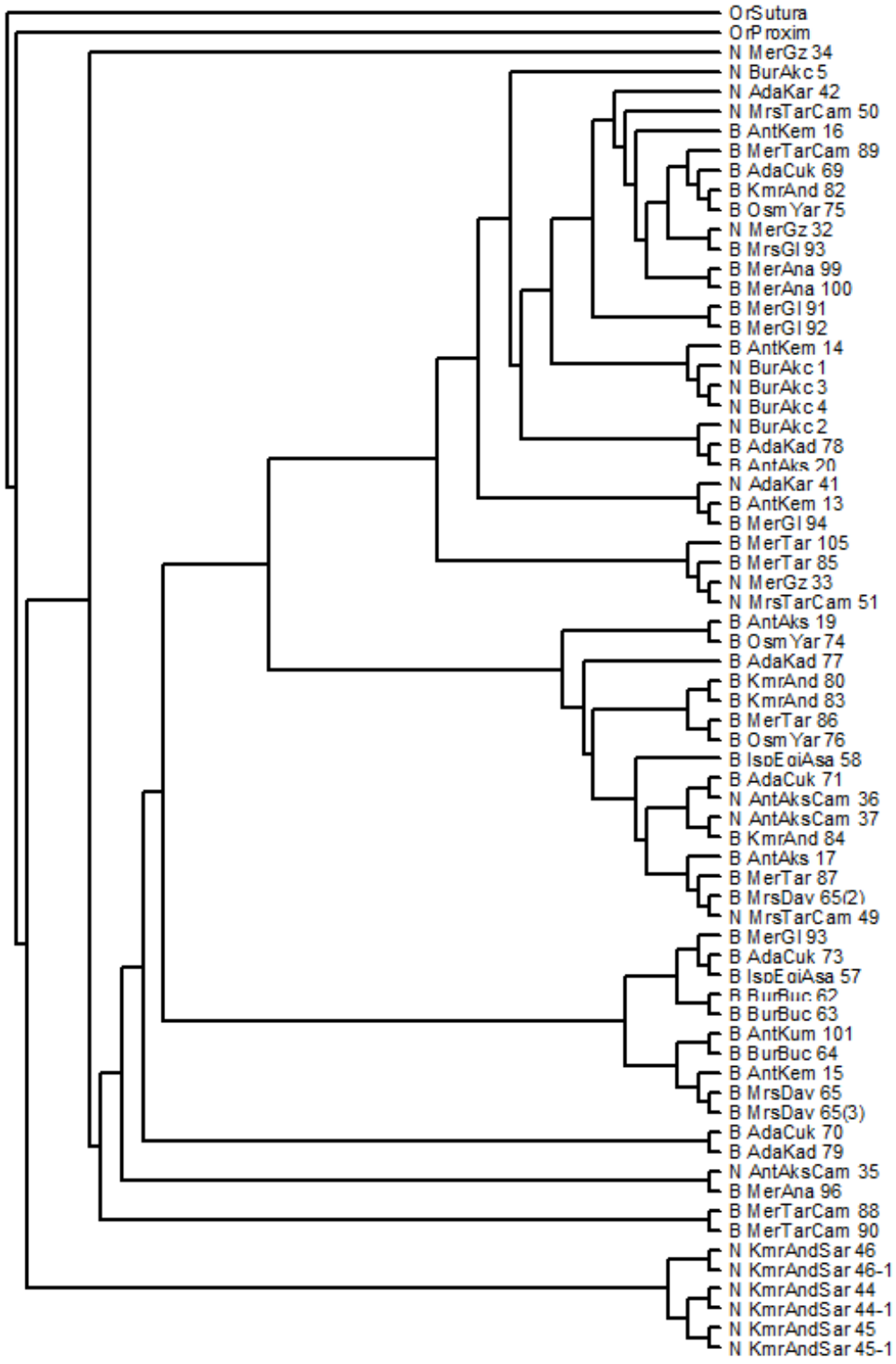

Figure 2. *Neighbour Joining tree of O. erosus populations*

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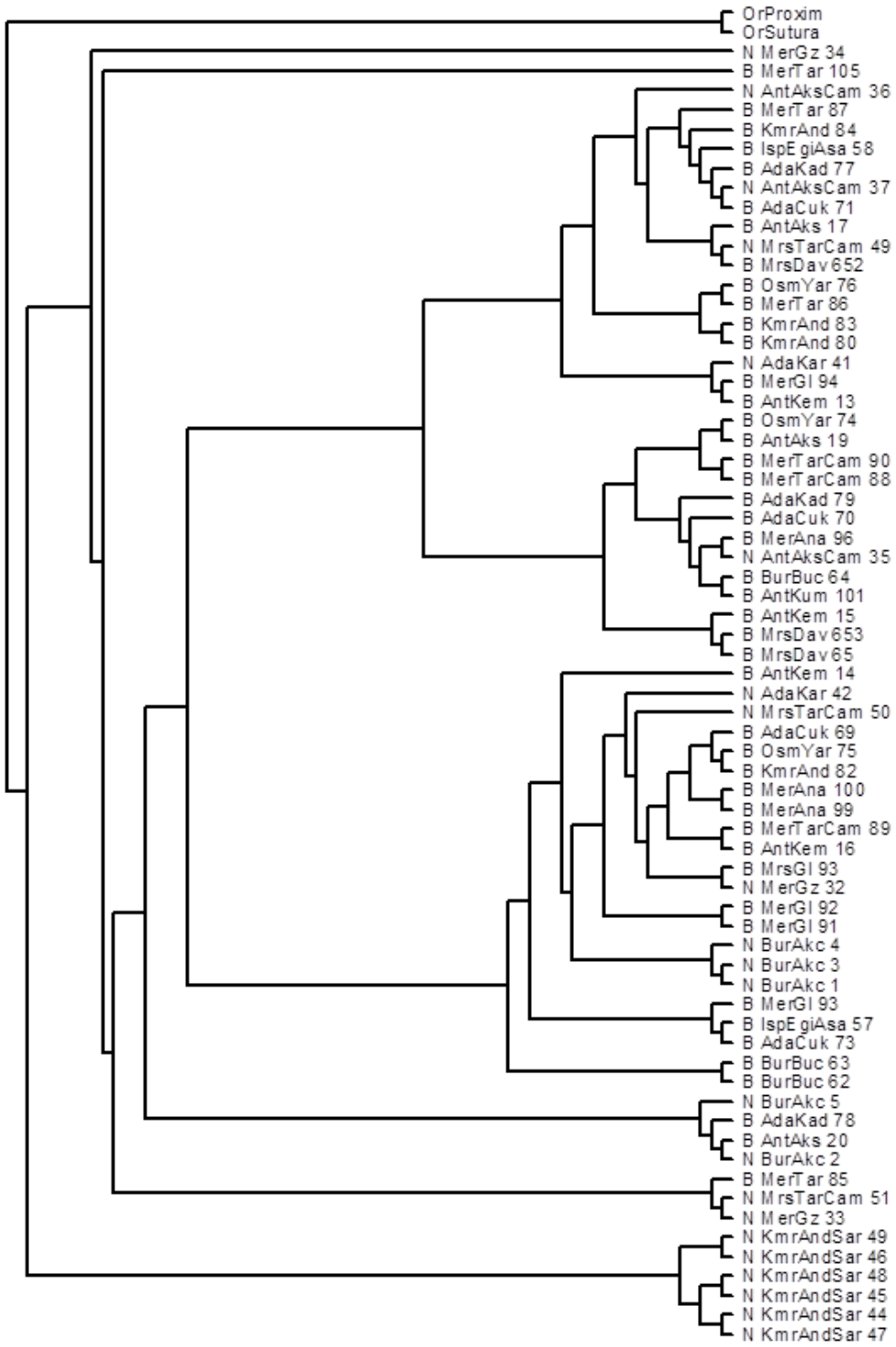

Figure 3. *Maximum Likelihood tree of O. erosus populations*

The intra-population genetic diversity of different populations of *Orthotomicus erosus* in the Mediterranean Region and the results of the neutrality test are presented in *Table 3*. The mismatch distribution analysis of different populations of *Orthotomicus erosus* in the Mediterranean Region is shown in *Table 4*; and the FST values of those populations are shown in *Table 5*.

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Table 3. *Genetic diversity of Orthotomicus erosus populations in the Mediterranean Region and the results of the neutrality test; h: haplotype diversity, π: nucleotide diversity*

	B_AdaCuk	B_AdaKad	N_AdaKar	B_AntAks	N_AntAksCam	B_AntKem_Kum	N_BurAkc	B_BurBuc	B_IspEgiAsa	B_KmrAnd	N_KmrAndSar
Individual number	4	3	2	3	3	5	5	3	**2**	**4**	**6**
3h3	1.0000 +/- 0.1768	1.0000 +/- 0.2722	1.0000 +/- 0.5000	1.0000 +/- 0.2722	1.0000 +/- 0.2722	1.0000 +/- 0.1265	1.0000 +/- 0.1265	1.0000 +/- 0.2722	1.0000 +/- 0.5000	1.0000 +/- 0.1768	1.0000 +/- 0.0962
π	0.016052 +/- 0.011315	0.013661 +/- 0.011061	0.016393 +/- 0.017388	0.010929 +/- 0.009016	0.002732 +/- 0.002807	0.013525 +/- 0.008996	0.002049 +/- 0.001908	0.008197 +/- 0.006966	0.010246 +/- 0.011224	0.012295 +/- 0.008853	0.005464 +/- 0.003896
Theta (*S*)	8.18182	6.66667	8.00000	5.33333	1.33333	7.20000	0.96000	4.00000	5.00000	6.54545	2.18978
Theta (*S*) s.d.	4.74042	4.32784	6.0000	3.52767	1.09834	3.92508	0.75803	2.72554	3.87298	3.85876	1.34160
Theta (*π*)	7.83333	6.66667	8.00000	5.33333	1.33333	6.60000	1.00000	4.00000	5.00000	6.00000	2.66667
Theta (*π*) s.d.	5.52152	5.39776	8.48528	4.39978	1.36987	4.38999	0.93095	3.39935	5.47723	4.32049	1.90127
Tajima's D	-0.43306	0.00000	0.00000	0.00000	0.00000	-0.60926	0.24314	0.00000	0.00000	-0.84046	121.883
Tajima's D p-value	0.48700	0.70900	100.000	0.75600	0.94000	0.36800	0.76000	0.77100	100.000	0.09800	0.89200
FS	0.04321	0.70320	207.944	0.45758	-121.640	-0.91837	-477.912	0.13353	160.944	-0.28768	-357.660
FS p-value	0.28900	0.44400	0.53600	0.38100	0.06600	0.15800	0.00000	0.28300	0.50100	0.23600	0.00400
	B_MerAna	N_MerGz	B_MerGl	B_MerTar	B_MerTarCam	B_MrsDav	N_MerTarTek	B_OsmYar	Mean	s.d.	
Individual number	**3**	3	5	4	3	3	3	3			
h	1.0000 +/- 0.2722	1.0000 +/- 0.2722	1.0000 +/- 0.1265	1.0000 +/- 0.1768	1.0000 +/- 0.2722	1.0000 +/- 0.2722	1.0000 +/- 0.2722	1.0000 +/- 0.2722			
π	0.016393 +/- 0.013103	0.012295 +/- 0.010039	0.010656 +/- 0.007249	0.005464 +/- 0.004352	0.015027 +/- 0.012082	0.009563 +/- 0.007992	0.016393 +/- 0.013103	0.015027 +/- 0.012082			

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Theta (*S*)	8.00000	6.00000	5.76000	2.72727	7.33333	4.66667	8.00000	7.33333	5.53847	2.33498	
Theta (*S*) s.d.	5.12696	3.92792	3.20568	1.78962	4.72749	3.12694	5.12696	4.72749	3.57554	1.47199	
Theta (π)	8.00000	6.00000	5.20000	2.66667	7.33333	4.66667	8.00000	7.33333	5.45439	2.24756	
Theta (π) s.d.	6.39444	4.89898	3.53761	2.12374	5.89622	3.89998	6.39444	5.89622	4.45448	1.93464	
Tajima's D	0.00000	0.00000	-0.70314	-0.21249	0.00000	0.00000	0.00000	0.00000	-0.07034	0.42527	
Tajima's D p-value	0.70000	0.72500	0.32700	0.59100	0.71100	0.76200	0.70200	0.69600	0.68395	0.23034	
FS	0.90079	0.58779	-128.257	-141.422	0.80681	0.30830	0.90079	0.80681	-0.21775	169.616	
FS p-value	0.44400	0.39300	0.10600	0.06300	0.44200	0.37000	0.44600	0.39600	0.29253	0.17609	

Table 4. *Mismatch distribution analysis of Orthotomicus erosus*

	B_AdaCuk	B_AdaKad	N_AdaKar	B_AntAks	N_AntAksCam	B_AntKem_Kum	N_BurAkc	B_BurBuc	B_IspEgiAsa	B_KmrAnd	N_KmrAndSar
SSD	0.15942	0.20122	0.00000	0.22311	0.26508	0.04733	0.00764	0.36418	0.00000	0.17790	0.09176
SSD p-value	0.26000	0.26000	0.00000	0.45000	0.14000	0.74000	0.83000	0.13000	0.00000	0.15000	0.15000
Hri	0.16667	0.66667	0.00000	0.66667	100.000	0.12000	0.11000	111.111	0.00000	0.33333	0.32444
Hri p-value	0.73000	0.54000	0.00000	0.56000	0.54000	0.68000	0.88000	0.27000	0.00000	0.64000	0.17000

	B_MerAna	N_MerGz	B_MerGl	B_MerTar	B_MerTarCam	B_MrsDav	N_MerTarTek	B_OsmYar	Mean	s.d.
SSD	0.44599	0.36835	0.07231	0.29711	0.44161	0.13406	0.14034	0.21895	0.19244	0.14260
SSD p-value	0.02000	0.10000	0.39000	0.02000	0.01000	0.46000	0.41000	0.27000	0.25211	0.24310
Hri	100.000	111.111	0.20000	111.111	100.000	0.44444	0.22222	0.66667	0.53971	0.41232
Hri p-value	0.49000	0.36000	0.34000	0.02000	0.54000	0.83000	0.91000	0.60000	0.47895	0.28614

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Table 5. *Pairwise Fst values of Orthotomicus erosus populations*

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0,000																		
2	-0,056	0,000																	
3	-0,214	-0,136	0,000																
4	-0,072	-0,080	-0,063	0,000															
5	-0,031	0,000	0,172	0,000	0,000														
6	0,074	0,128	-0,007	0,089	0,184	0,000													
7	0,138	0,271	0,286	0,152	0,544	0,228	0,000												
8	0,114	0,186	0,213	0,208	0,273	0,161	0,545	0,000											
9	-0,094	-0,031	-0,083	-0,076	0,138	0,115	0,441	0,204	0,000										
10	-0,085	0,031	-0,072	-0,068	0,061	0,134	0,211	0,250	0,016	0,000									
11	0,875	0,895	0,901	0,903	0,936	0,878	0,944	0,917	0,916	0,895	0,000								
12	0,129	0,305	0,040	0,221	0,425	0,249	0,483	0,400	0,222	0,190	0,880	0,000							
13	-0,038	0,123	-0,017	0,105	0,233	0,093	0,326	0,297	0,136	0,122	0,892	0,100	0,000						
14	0,001	0,155	-0,137	0,073	0,249	0,127	0,099	0,305	0,129	0,115	0,894	0,166	0,035	0,000					
15	0,000	0,045	0,158	-0,009	0,045	0,177	0,348	0,373	0,141	0,037	0,924	0,366	0,077	0,210	0,000				
16	0,059	0,171	0,010	0,136	0,304	0,198	0,357	0,320	0,210	0,193	0,884	0,127	0,032	0,149	0,295	0,000			
17	0,093	0,105	0,152	0,118	0,182	0,213	0,503	0,250	0,128	0,168	0,910	0,406	0,200	0,281	0,181	0,325	0,000		
18	-0,066	0,000	-0,091	0,016	0,067	0,095	0,348	0,182	-0,050	0,014	0,884	0,143	-0,125	0,100	0,020	0,138	0,081	0,000	
19	-0,185	-0,068	-0,267	-0,213	0,000	0,032	0,160	0,177	-0,099	-0,167	0,890	0,068	0,000	-0,041	-0,063	0,015	0,069	-0,078	0,000

1	B-AdaCuk	6	B-AntKem-Kum	11	N-KmrAndSar	16	B-MerTarCam
2	B-AdaKad	7	N-BurAkc	12	B-MerAna	17	B-MrsDav
3	N-AdaKar	8	B-BurBuc	13	N-MerGz	18	N-MerTarTek
4	B-AntAks	9	B-IspEgiAsa	14	B-MerGl	19	B-OsmYar
5	N-AntAksCam	10	B-KmrAnd	15	B-MerTar	20	

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The intraspecific diversity of *Orthotomicus erosus* was determined by using COI gene sequence that had 488 base pairs. The species did not form any phylogroup in populations depending on the geographical location according to the NJ and ML analysis. The genetic variations of *O. erosus* populations in *Pinus brutia* and *P. nigra* were also analysed. The NJ and ML trees revealed that those *O. erosus* individuals that fed on different pine species did not have genetic variations. Moreover, NJ and ML trees also showed that different populations of the species across the Mediterranean Region were not disconnected and isolated geographically either.

The number of the haplotypes shared by the populations of *O. erosus* was low. AMOVA results also revealed that the variations within and among populations were very similar. This indicates that the intraspecific genetic diversity was very high.

High genetic diversity of genetic lineages were also reported for other animal species from Turkey (Gündüz et al., 2005; Stone et al., 2007; Bardakçı et al., 2006, Mutun, 2011). High haplotype diversity might be due to the continuous introduction of individuals from different locations.

The highest nucleotide diversity was found in the populations distributed in *Pinus brutia* trees in Adana-Çukurova Karahan Village, Mersin-Anamur-Demirören Village and Mersin-Tarsus and in *P. nigra* trees in Adana Karaisalı-Damlama district, Mersin-Tarsus-Çamalanı, Tekir and Mersin-Gözne.

According to the FST values of *O. erosus*; there was a gene flow between the populations in Adana-Çukurova Karahan village and Adana-Kadirli Börklüler, Antalya-Akseki-Küser district, Akseki-Çambeleni, Adana Karaisalı-Damlama; Isparta, Eğirdir-Aşağıgökdere, Kahramanmaraş Andırın-Efirağızlı, Mersin-Gözne, Mersin-Tarsus-Çamalanı- Tekir and Osmaniye- Yarpuz-Yemşen; populations in Adana-Kadirli Börklüler and Adana Karaisalı-Damlama district; populations in Antalya-Akseki-Çambeleni, Isparta, Eğirdir-Aşağıgökdere, Osmaniye-Yarpuz-Yemşen; populations in Adana Karaisalı-Damlama and Antalya-Akseki-Küser district, Antalya Kemer and Kumluca, Isparta, Eğirdir-Aşağıgökdere, Kahramanmaraş Andırın-Efirağızlı, Mersin-Gözne, Mersin-Gülnar, Mersin-Tarsus- Çamalanı, Tekir and Osmaniye-Yarpuz-Yemşen; populations in Antalya-Akseki-Küser and Isparta, Eğirdir-Aşağıgökdere, Kahramanmaraş Andırın-Efirağızlı and Mersin-Tarsus; populations in Mersin-Tarsus Çamalanı-Tekir and Isparta, Eğirdir-Aşağıgökdere and Mersin-Gözne, populations in Osmaniye-Yarpuz-Yemşen and Isparta, Eğirdir-Aşağıgökdere, Kahramanmaraş Andırın-Efirağızlı, Mersin-Gülnar and Mersin-Tarsus. The topologies of NJ and ML trees and negative FST values indicated that *O. erosus* could be distributed in quite long distances.

D and FS test results of *O. erosus* showed that the populations in Antalya- Kemer and Antalya-Kumluca, Kahramanmaraş-Andırın Efirağızlı, Mersin-Gülnar and Mersin-Tarsus had an enlargement in the past. Furthermore, the sum of squared differences (SSD) and Raggedness index (Hri) results revealed that the populations only in Antalya-Kemer, Antalya-Kumluca and Mersin-Gülnar had enlargement.

Conclusion

Knowing of the genetic variations of bark beetles at local and regional level will provide highly useful data for forest management. The findings of this study, in which the genetic variations of *Orthotomicus erosus* that damaged pine trees including primarily the Brutian pine in the Mediterranean Region were analysed, show that there

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were not significant within population genetic variations or differences. These findings indicate that the concerned harmful bark beetles are highly mobile.

It was found that individuals of *O. erosus* that can feed on different pine species in the Mediterranean Region did not have any genetic variations and different populations were not disconnected and isolated geographically. This indicates that change of host does not result in dependence on a specific host for *O. erosus*; therefore, there is no barrier before the distribution of this species.

O. erosus does not have any sub-species. On the other hand, there is a need for further studies to explore if *O. erosus* depends on a specific geographical location and specific host species across Turkey considering its wide distribution in the country.

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