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Preliminary phylogeny of the thrips parasitoids of Turkey based on some morphological scales and 28S D2 rDNA, with description of a new species

Oğuzhan DOĞANLAR[1,*], Mikdat DOĞANLAR[2], Anne FRARY[3]

[1]Ağrı İbrahim Çeçen University, Faculty of Science and Arts, Department of Biology, Ağrı - TURKEY

[2]Mustafa Kemal University, Faculty of Agriculture, Department of Plant Protection, Antakya, Hatay - TURKEY

[3]İzmir Institute of Technology, Department of Molecular Biology and Genetics, Urla, İzmir - TURKEY

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Abstract: Species of the *Ceranisus* thrips-attacking genus are difficult to distinguish morphologically. The phylogenetic relationships within the *Ceranisus* species were explored using nucleotide sequences of the 28S D2 expansion region of the rDNA gene. Bayesian, maximum likelihood, and parsimony inference methods were employed to construct the phylogenetic relationships. Principal component analysis on the Turkish species of *Ceranisus*, namely *antalyacus*, *menes*, *bozovaensis*, *hirsutus, planitianus* (a new record for Turkey), *pacuvius*, and a new species, provided supporting evidence. All known data concerning hosts and geographical distribution are presented. A new species, *C. onuri* O. Doganlar, sp.n., was described from Turkey.

Key words: Thrips, parasitoids, *Ceranisus*, phylogeny, 28S rDNA, Turkey

Türkiye thrips parazitoitlerinin bazı morfolojik ölçümler ve 28S D2 rDNA özelliklerine dayanarak oluşturulan ön filogenisi ile yeni bir türün tanısı

Özet: Thripsler üzerinde doğal düşman olan, *Ceranisus* cinsinin morfolojik olarak teşhis edilmeleri oldukça zordur. Bu sebeple çalışmada bu böceklerin rDNA'sına ait genişlemiş 28S D2 bölgesinin gen dizisi kullanılarak, *Ceranisus* türleri için bir filogenetik ilişki ortaya konmuştur. Filogenetik ilişki oluşturulurken Bayesian, Maximum likelihood ve Parsimony metodları kullanılmıştır. Morfolojik ölçümler kullanılarak *Ceranisus*, viz., *antalyacus*, *menes*, *bozovaensis*, *hirsutus, planitianus* (Türkiye için yeni kayıt), *pacuvius* ve yeni bir tür üzerinde temel bileşenler analizi yapılmış ve sonuçlar bu yeni türün farklı tür olduğunu desteklemiştir. Türler üzerinde coğrafik yayılış, ilişkide olduğu konak bitkiler ile ilgili bilinen tüm bilgiler verilmiştir. Türkiye'den yeni bir tür *C. onuri* O. Doganlar, sp.n. tanımlanmıştır.

Anahtar sözcükler: Thrips, parazitoit, *Ceranisus*, filogeni, 28S rDNA, Türkiye

* E-mail: doganlaro@yahoo.com.tr

Introduction

Thrips (Thysanoptera: Thripidae) are very small insects distributed worldwide with approximately 5000 species identified so far. Approximately a few hundred thrips species are serious pests of crops due to the injury they cause by feeding on flowers or seed capsules, which results in bruising, deformity, and reduced yield of the crop (Lewis, 1997). Due to their small size, special behavior, and high rate of biotic potential, thrips are difficult to control by classical control methods. Only the species in 2 families, Eulophidae: Entedontinae and Trichogrammatidae, of parasitoid Hymenoptera are known to parasitize their larvae and eggs, respectively. All of the thrips parasitoids belonging to Entedontinae are found in 5 genera (Boucek, 1976, 1988; Schauff, 1991; Triapitsyn and Headrick, 1995; Doğanlar, 2003; Noyes, 2007).

The genus *Ceranisus* Walker (Hymenoptera: Eulophidae), the most important monophyletic group in Entedontinae, are larval parasitoids of thrips, some of which are used for biological control of thrips pests (Schauff, 1991; Loomans and van Lenteren, 1995; Triapitsyn and Headrick, 1995; Loomans and Pakozdi, 1996; Loomans, 2003). The Nearctic species of *Ceranisus* were reviewed by Triapitsyn and Headrick (1995), and Triapitsyn (2005) gave a world taxonomic revision of *Ceranisus* and listed their known host associations. Noyes (2007) listed 16 species of *Ceranisus* in world fauna. The identification key of European species of *Ceranisus* was first provided by Graham (1963), who also described *Ceranisus lepidotus* Graham (Hymenoptera: Eulophidae) from England. Erdös (1966) described *Ceranisus planitianus* Erdös (Hymenoptera: Eulophidae) from Hungary. The first thrips parasitoids species in Turkey was found by Doğanlar (2003), who described *Urfacus bozovaensis* Doğanlar (Hymenoptera: Eulophidae), which was recently synonymized by Doğanlar and Triapitsyn (2007) as *Ceranisus bozovaensis* (Doğanlar). Cameron et al. (2004) described a new species, *C. antalyacus* S. Triapitsyn, 2004, from the western Mediterranean region of Turkey. Doğanlar and Triapitsyn (2007) published a taxonomic revision of Turkish species of *Ceranisus* and provided identification keys to both sexes of the European and Turkish species of *Ceranisus*. They also described a new species, *Ceranisus hirsutus* Doganlar and S. Triapitsyn (Hymenoptera: Eulophidae), and redescribed *C. bozovaensis*, including the female.

Morphology alone may not be enough to distinguish all species clearly, and molecular data provide an additional useful tool for identification of species. Molecular data have proven to be very powerful for resolving difficult problems (Chen et al., 2004). Using DNA sequence data, Campbell et al. (2000) intended to resolve the relationships of Chalcidoidea. Sequence data for 28S D2 rDNA were used to construct a phylogeny of the family Eulophidae (Gauthier et al., 2000). However, there are very few studies using molecular data of rDNA for *Ceranisus* species; only the Kenyan isolate of *C. menes* was previously sequenced by Gauthier et al. (2000).

This paper is the first phylogenetic study of *Ceranisus* based on DNA sequence data from the second expansion segment (D2) of the 28S ribosomal subunit. The goals of the study were to perform a modern phylogenetic classification of Turkish species of the genus, and to distinguish and identify species based on their morphology, including morphometrics, by performing principal component analysis.

Materials and methods

Taxon sampling

Our study focused on the species of *Ceranisus* that parasitize larvae of some thrips pests in Turkey. Insect sampling and collection details are listed in Table 1. During 2005-2007, a total of 174 *Ceranisus* specimens were collected from thrips larvae on their hosts in southern and southeastern Turkey. The specimens were killed in ethanol and subsequently stored in a freezer (–20 °C), and some were slide-mounted in Canada balsam. The examined specimens were deposited in the Insect Museum of the Plant Protection Department (ICMKU), Faculty of Agriculture, Mustafa Kemal University, Antakya, Hatay, Turkey.

Principal component analyses of morphological measurements

Specimens were examined for a range of discrete and continuous morphological variables. The morphological character measurements of the antennae, wings, and ovipositors of females were used to determine the factors of the principal components.

All data were found to be normally distributed, and principal component analyses were undertaken using the PCA option of XLSTAT software (Addinsoft Ltd, Paris, France).

DNA amplification and sequencing

Genomic DNA was extracted from single specimens, using the DNeasy Tissue Kit (QIAGEN), by freezing and heating methods (QIAGEN, Leusden, the Netherlands). Sequence fragments displaying an increasing degree of variability were analyzed in the conserved D2 expansion of the 28S nuclear gene. Standard 50 µL PCR reactions were performed using 0.2 U Taq DNA polymerase (Fermentas), 5 µL of 10× Taq buffer with KCl (Fermentas), 3 µL of 25mM $MgCl_2$ (Fermentas), 1 µL of 10× dNTPs (Fermentas), 1 µL of each primer, 2 µL of template DNA, and 36.8 µL of dH_2O (Sigma). Primer sequences for the 28S rDNA D1F (ACC CGC TGA ATT TAA GCA TAT) and D2R (TTG GTC CGT GTT TCA AGA CGG) were from Harry et al. (1998) and Campbell et al. (1993), respectively. PCR conditions for *C. bozovaensis*, *C. hirsutus*, and *C. antalyacus* were 30 cycles of 94 °C denaturation (30 s), 55 °C annealing (30 s), and 72 °C elongation (90 s), with an initial 94 °C denaturation (3 min) and a final 72 °C extension (30 min). For *C. menes*, *C. planitianus*, and the new species, the conditions were 30 cycles of 94 °C denaturation (30 s), 62 °C annealing (30 s), and 72 °C elongation (60 s), with an initial 94 °C denaturation (3 min) and a final 72 °C extension (10 min). After DNA amplification, 5 µL of product with 1 µL of loading dye (Fermentas) was loaded onto 1% agarose gel to check the DNA amplification. The remaining DNA was loaded onto a 1.5% agarose gel with ethidium bromide, separated by electrophoresis at 140 V for 1 h, and visualized under UV light. The amplified product was purified using a QIAquick Gel Extraction Kit (QIAGEN). DNA fragments were run on an ABI 3100 Avant Genetic Analyzer (Applied Biosystems, Foster City, CA, USA).

Sequence alignment and gene analysis

Sequences were aligned with the program ClustalW (Thompson et al., 1994) in MEGA 3.1 (Kumar et al., 2004) using the default setting (Open gap penalty = 15, extend gap penalty = 6.66). The alignments were checked manually.

Equally weighted maximum parsimony (MP) and maximum likelihood (ML) analyses were performed using PAUP (4.0 beta version) (Swofford, 2000). For MP analysis, a heuristic search procedure was used with the following default settings: 10 replicates of random taxon addition, tree-bisection-reconnection branch swapping, multiple trees retained, no steepest descent, and accelerated transformation. Gaps were treated as missing data. For ML analysis, the appropriate substitution model of DNA evolution that best fit (GTR-gamma model) the dataset was determined by Akaike's information criterion with Model Test 3.06 (Posada and Crandall, 1998) as follows: 28S rDNA, base frequencies = (A: 0.1468; C: 0.3033; G: 0.3321; T: 0.2178), rate matrix = (1.9391; 2.1793; 1.2682; 0.3533; 3.9780; 1.0000), and gamma distribution shape parameter = 0.2806. Bootstrap analysis with 1000 replicates was calculated as a measure of support for individual clades for the MP and ML trees. A Bayesian analysis was conducted on each dataset using Metropolis-coupled Markov chains Monte Carlo (MCMCMC) implemented in the MrBayes software (Huelsenbeck and Ronquist, 2001). Each Bayesian analysis consisted of 4 chains, random starting trees, a uniform prior distribution of parameters, and the GTR+I+_ model of nucleotide substitution. The chains were run for 2 million generations, and trees were sampled every 100 generations. The best tree was determined by visual examination of the log-likelihood plots and the burn-in trees were discarded. As the MP and ML analyses usually gave multiple trees, we reduced the set of trees to one consensus tree. The sequences of *Galeopsomyia* sp. (AJ274458) and *Cirrospilus* sp. (Eulophidae: Eulophinae) (AJ274438; Gauthier et al., 2000) were used as out-groups for these analyses.

Results

Examination of morphological characters

Three factors were retained for the principle component analyses (PCA), and their cumulative percentages were calculated as 54.69%, 69.51%, and 82.87%, respectively. The first 2 factors, accounting for 69.51% of the cumulative variance, were plotted against each other (Figure 1). The eigenvalues, variance and cumulative variance, analysis result, eigenvectors, and factor loading values of the 3

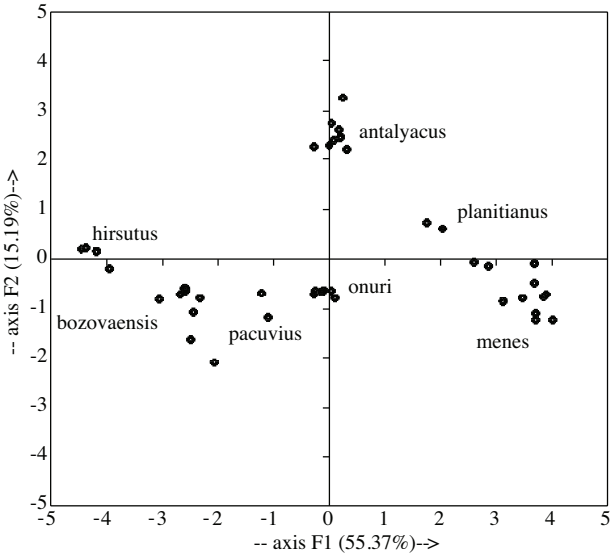

Figure 1. Scatter plot for *Ceranisus* individuals distributed on a coordinate system of the first 2 factors resulting from principal component analysis.

principle components are shown in Table 2. Six *Ceranisus* species were clearly separated in the coordinate systems. *C. antalyacus*, *C. menes*, *C. onuri* sp.n., and *C. hirsutus* were located in 4 different poles of the scatter plot. *C. planitianus* was intermediate between *C. antalyacus* and *C. menes*, while *C. bozovaensis* was located between *C. onuri* sp.n., *C. pacuvius*, and *C. hirsutus*. While the different specimens of most *Ceranisus* species were closely clustered, the *C. bozovaensis* samples were more widely distributed in the coordinate system. The scape and first flagellar segment length to width ratio and wing characteristics were of primary importance for the first principle components. Ovipositor length and antennal characters were determined by PCA as the second principle components (Table 2) for identification of the *Ceranisus* species of Turkey.

28S D2 rDNA sequence data of *Ceranisus*

The size of the amplified 28S D2 expansion region of the rDNA gene fragment ranged from 415 to 576 bp. The base composition of the sequence had a strong bias toward cytosine and guanine, which constituted approximately 62.3% of the total. The alignment of the sequenced fragment resulted in 464 characters, including gaps. Of these, 345 characters were constant, 59 characters were variable and parsimony-uninformative, and 60 characters were parsimony-informative. The alignment was relatively straightforward and did not require insertion gaps. The base composition of the 28S D2 region was as follows: A, 0.143; C, 0.301; G, 0.322; T, 0.233. The slight G bias evident in the 28S sequences was noted in Chalcidoidea by Gillespie et al. (2005) and can be attributed to guanine's ability to base pair with both cytosine and uracil in RNA molecules (Gutell et al., 1994).

Maximum parsimony analysis of the amplified 28S D2 expansion region of the rDNA gene fragment produced 156 equally parsimonious trees [consistency index (CI) = 0.9038, retention index (RI) = 0.8421] and bootstrap (1000 replicates). The 50% majority rule strict consensus tree is given in Figure 2. The heuristic search yielded one single tree with a score of -Ln likelihood = 1395.15050 (Figure 2b). There are some differences between the consensus trees generated under maximum parsimony and maximum likelihood, but in general, the topologies of these reconstructions are similar. The 50% majority rule consensus tree inferred from the Bayesian analysis is very similar to the results of the parsimony and likelihood analyses (Figure 2c). There is one conflict between the Bayesian trees and the parsimony trees; they merely differ in the separation of *C. hirsutus*. The Bayesian posterior probabilities offered a slightly higher nodal support in comparison with the bootstrap analysis.

Parsimony, maximum likelihood, and Bayesian analyses produced similar topologies (Figure 2). The main differences were in the position of the group including *C. menes*, *C. planitianus*, *C. pacuvius*, and *C. onuri* sp.n., and the other group including *C. antalyacus*, *C. hirsutus*, and *C. bozovaensis*. In the analysis, high bootstrap values (91%-100%) were determined between *C. menes* and *C. planitianus*, and they were located on different branches of the trees. In addition, 2 species were clearly separated from other *Ceranisus* species, with 100% bootstrap and Bayesian posterior probabilities scores. *Ceranisus pacuvius* and *C. onuri* sp.n. occurred in one group and were located on the same branch in all trees, but they were clearly separated by bootstrap values (100%) and 20 bp differences in maximum parsimony analyses. The parsimony tree showed 29 bp differences between

Table 1. The number of *Ceranisus* species, sampling localities, altitude, collection date, associated plants, most common thrips species on host plants, the EMBL GenBank accession number of Turkey thrips parasitoids, and their DNA sequences.

Species	Locality		Coordinate (°,' and N:E)	Alt. (m)	Date	Speci.	Thrips	Host plant	Access. no.
Ceranisus antalyacus	Hatay	Altınözü-Yanıkpınar	36 01: 36 13	720	10.04.07	2♂, 2♀	*Taeniothrips inconsequens*	*Arbutus inconsequens*	EU557271
		Yayladağı	-		10.04.07	5♀			
		Yayladağı	-		20.04.07	4♀			
Ceranisus onuri	Niğde	Maden-Karagöl	37 25: 34 33	2425	17.06.06	11♀	*Thrips meridionalis*	*Asphodeline damascena*	EU557272
		Bolkar Mountains	37 26: 34 35	2182	17.06.06	23♀			
Ceranisus bozovaensis	Şanlıurfa	Bozova	37 22: 38 29	685	07.04.07	1♂,3♀	*Thrips tabaci,*	Wheat, lentil, chickpea	EU557273
					07.04.07	3♂,5♀;	*Haplothrips tritici,*		
					23.04.06	2♀	*Haplothrips reuteri*		
		Kangörmez	36 26: 38 11	445	04.05.06	3♀			
	Adıyaman	Gölbaşı	37 37: 37 30	857	25.07.06	1♀			
Ceranisus hirsutus	Şanlıurfa	Kangörmez	36 26: 38 11	445	06.04.07	2♂,5♀	Unknown	Wheat, lentil, leek	EU557274
	Adıyaman	Fırat river	37 27: 38 15	402	25.03.07	2♀		plants, and some grasses	
Ceranisus pacuvius	K.maraş	Center			14.05.03	2♀	Unknown	Medicago sativa and	EU557275
	Şanlıurfa	Birecik-Arat Mou.	37 03: 38 08	800	06.05.05	2♂,9♀		lentil plants	
		Bozova	37 22: 38 29	685	07.04.07	3♂,5♀;			
		Aslanlı village	37 46: 39 26	937	04.05.06	3♀			
Ceranisus planitianus	Gaziantep	Akyokuş	37 10: 36 58	1100	25.03.07	2 ♀	Unknown	Leek plants and	EU557276
	Hatay	Payas-Sincan Yaylası	36 43: 36 14	490	05.05.07	2♀		some grasses	
Ceranisus menes	Gaziantep	Islahiye	36 56: 36 34	518	16.03.07	1♀	*Thrips tabaci,*	Wheat, lentil, chickpea,	AJ234445
		Araban-Y.mülk	37 27: 37 26	921	23.05.07	1♀	*Haplothrips tritici*	leek plants, and some	
	Adıyaman	Gölbaşı	37 37: 37 30	857	24.07.06	1♀		grasses	
	Hatay	Atçana	36 14: 36 22	96	30.04.07	14♀			
		Teknepınar	36 07: 35 56	260	30.04.07	2♀			

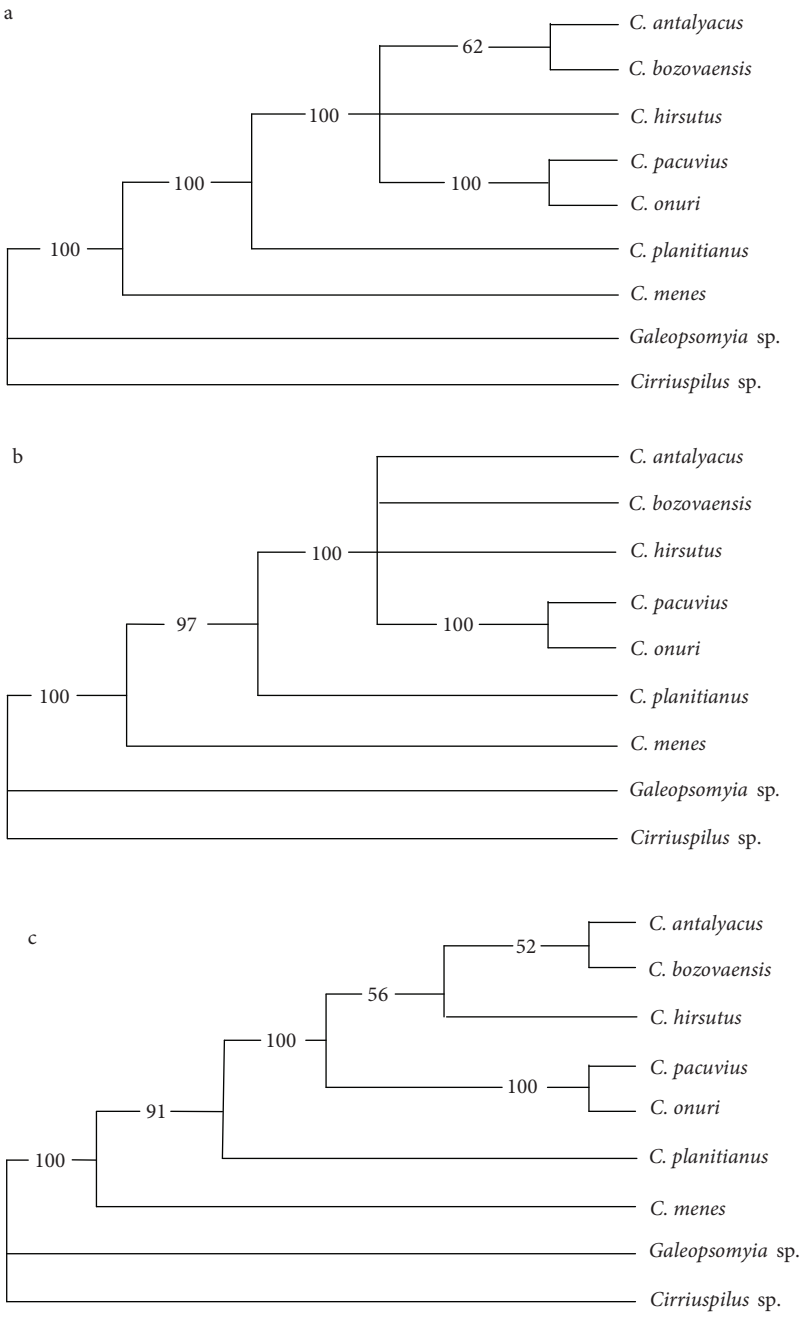

Figure 2. a) Bayesian tree, using MCMCMC method and GTR+I+_ model; b) Bootstrap 50% majority rule consensus tree inferred by maximum likelihood analyses of the 28S D2 rDNA gene (GTR-gamma model, -Ln likelihood = 1395.15050); c) The strict consensus most parsimonious tree, inferred by 28S D2 rDNA sequences. Numbers above lines represent bootstrap values from 1000 replicates on all parsimony-informative characters, and only bootstrap values >50% are shown. Tree length is 156, CI is 0.9038, HI is 0.1630, RI is 0.8421.

Table 2. The eigenvalues, variance, statistics, eigenvectors, and factor loading values for the first 3 factors resulting from principle component analysis.

	F1	F2	F3
Eigenvalue	6.645	1.823	1.522
% variance	55.373	15.192	12.684
Cumulative %	55.373	70.565	83.248
Chi-square (observed value)	693.300		
Chi-square (critical value)	85.965		
DF	66		
One-tailed P-value	<0.0001		
Alpha	0.05		

	Eigenvectors			Factor loadings		
	F1	F2	F3	F1	F2	F3
Scape	0.121	0.338	0.640	0.311	0.456	0.790
Pedicel	0.145	–0.310	0.398	0.375	–0.419	0.491
F1	0.271	–0.299	0.164	0.699	–0.403	0.202
F2	0.357	–0.065	0.192	0.922	–0.087	0.237
Clava	0.308	–0.332	0.209	0.795	–0.448	0.257
C1	0.303	0.416	–0.097	0.782	0.561	–0.119
C2	0.361	0.184	–0.001	0.930	0.249	–0.001
Specula	0.314	–0.009	–0.410	0.808	–0.012	–0.506
Forewing	0.287	–0.170	0.008	0.740	–0.229	0.009
Longest marginal cilia	0.332	–0.238	–0.253	0.855	–0.321	–0.312
Hind wing	0.334	0.115	–0.274	0.860	0.156	–0.338
Ovipositor	0.208	0.529	0.089	0.537	0.715	0.110

populations of the *C. onuri* sp.n. and *C. planitianus* group and group 1, and the likelihood analyses demonstrated a 12-base difference between the same populations of *Ceranisus* species. In likelihood analyses, a single 28S substitution supporting the relationship between *C. hirsutus*, *C. bozovaensis*, and *C. antalyacus* was homoplasious, with very low bootstrap support and 1 or 5 bp differences.

Discussion

C. menes and *C. planitianus* are morphologically different from other *Ceranisus* species of Turkey as they have almost smooth heads and mesosoma and bear distinct semioval bare areas at the posterior margin behind the base of the marginal vein. *C. menes* is a solitary endoparasitoid of thrips larvae and is found on a wide range of host plants in different biotopes around the world (Loomans, 1991; Goodwin and Steiner, 1996; Triapitsyn, 2005; Doğanlar and Triapitsyn, 2007). In Turkey, it was collected from weeds, vegetable crops, barley, lentils, chickpeas, leeks, and some grasses in approximately all sampling localities of the Mediterranean region. *C. planitianus* is distributed in Canada, the USA, Israel, Turkey (new record), and Europe (Loomans and Van Lenteren, 1995; Triapitsyn, 2005; Triapitsyn and Morse, 2005), but was rarely found in collection areas in Turkey. In

our study, *C. planitianus* was found on *Raphanus* sp. with white flowers in only 2 localities with 4 female specimens. *C. menes* differs from *C. planitianus* in having the malar groove whole and straight, and metasoma yellow or light brown (in *C. planitianus*, the malar groove is Y-shaped and the metasoma is dark brown or black). Our PCA and molecular analyses support the morphological data. Thus, this difference was clearly shown in PCA results; the points based on the morphological characters of specimens of each of these species were closely grouped and the species clusters were located in different areas of the scatter plots. Additionally, the divergence between *C. menes* and *C. planitianus* was strongly supported by MP, ML, and Bayesian analyses with high bootstrap values (91%, 97%, and 100% respectively) and by concordant base changes in the 28S D2 rDNA region. Although *C. onuri* sp.n. specimens were collected from different habitats, climatic conditions, and geographic regions of Turkey compared to *C. pacuvius* (Table 1), genetic analyses show good bootstrap support for the high (94%) association between *C. onuri* sp.n. and *C. pacuvius*. An adjusted distance matrix shows that *C. onuri* sp.n. and *C. pacuvius* differ in 5 characters (base pairs), indicating that these 2 species are related. These results were corroborated by PCA analyses based on selected morphological characters of *C. menes* and *C. pacuvius*. These 2 species were separated from other *Ceranisus* species under the effect of the first principle components, which were length of the spicula of C2, long marginal setae, and forewing length to width ratio, and were located in the positive pole of the F1 axis. According to the morphological characters of this species, *C. onuri* sp.n. differs from *C. lepidotus* in having an almost smooth body, while *C. lepidotus* has a reticulated body. These differences were clearly shown in the PCA scatter plot and the MP, ML, and Bayesian analyses consensus trees. The other 3 species were placed in the same group by the genetic analyses, but all examined species have quite different morphological characters. *C. hirsutus* has 3 segmented clavae of female antenna and 17 setae on the mesosoma, *C. antalyacus* has a very different female antennal scape with C1 longer than C2 (Cameron et al., 2004; Doğanlar and Triapitsyn, 2007), and *C. bozovaensis* has a notably expanded marginal vein of the male forewing. *C. hirsutus* and *C. bozovaensis* have similar habitat choices, e.g., weeds, wheat, lentils, and alfalfa plants, whereas *C. antalyacus* was obtained from different habitat in Turkey. Only this species was collected together with *Taeniothrips inconsequens*, feeding on flowers of pear and *Arbutus andrachne*. Those differences were shown only in the MP analyses of the *Ceranisus* species. *C. antalyacus*, *C. bozovaensis*, and *C. hirsutus* were separated by MP analyses with 52 and 56 bootstrap scores and 8, 2, and 5 base pair differences, respectively. However, these differences were not supported by the maximum likelihood or Bayesian analyses (Figure 2).

In conclusion, molecular data for the amplified 28S D2 expansion region of the rDNA gene fragment produced an informative phylogeny of the genus *Ceranisus*. The molecular data are consistent with the morphological data for supporting the differences of *C. menes*, *C. planitianus*, *C. onuri* sp.n., and *C. pacuvius*. In contrast, the phylogenetic relationships among members of *C. antalyacus*, *C. hirsutus*, and *C. bozovaensis* are not completely supported by the morphological data and results of PCA analysis and further analyses are needed. However, the 28S D2 rDNA phylogeny obtained by maximum parsimony, maximum likelihood, and Bayesian analyses generally agreed with the relationships based on previous morphological criteria.

***Ceranisus onuri* O. Doğanlar, sp.n.**

(Figures 3–7.)

Types. Holotype ♀ (on slide), labeled: "TURKEY, Niğde, Maden, Karagöl, 37°25′N, 34°33′E, 2425 m, 05.05.2005, O. Doganlar. Mounted at ICMKU by the first author 2007 in Canada balsam." Paratypes, 11 ♀♀, same data as the holotype; 23 ♀♀, Niğde, Bolkar Mountains, 37°26′N, 34°35′E, 2182 m, 17.06.2006, M. Doğanlar: stored at –20 °C in 96% alcohol, ICMKU.

Description

Female: Body length 0.7-1.16 mm (holotype 1.06 mm). Head and mesosoma brown; antenna, legs, venation, and metasoma light brown; wings hyaline.

Head. Vertexal suture broadly V-shaped (Figure 3). Antenna (Figure 4) sparsely setaceous with scape slender, about 6.5× as long as wide, pedicel notably shorter than scape, 2.6× longer than wide, F1 almost cylindrical and without sensillae, shorter and narrower than F2, 0.43× as long as and 0.4× as wide as F2; F2 with

Figures 3-7. *Ceranisus onuri* sp.n. female. 3) Head, 4) Antenna, 5) Mesoscutum and scutellum, 6) Forewing, 7) Gaster and genitalia.

1 sensillum; clava 2-segmented, including spicula 3.02× as long as wide, C1 slightly shorter than C2.

Mesosoma (Figure 5) 0.69× as long as metasoma; pronotum and mesoscutum in 1/5 apical area with light engraved reticulation; each side lobe of mesoscutum with one seta; midlobe of mesoscutum with 2 pairs and scutellum with 1 pair of setae. Forewing (Figure 6) 3× as long as wide; uniformly covered with numerous microtrichia; longest marginal cilia about one-fourth maximal width of forewing; submarginal vein with 2 long macrochaetae and 3 hypochaetae opposite to basal macrochaetae;

postmarginal vein 1.98× as long as stigmal vein, marginal vein and parastigma 6.04× as long as stigmal vein. Hind wing about 6.87× as long as wide; blade uniformly setaceous.

Metasoma (Figure 7) with petiole almost as long as wide. Ovipositor occupying about two-thirds length of gaster, slightly exserted; ovipositor to metatibia length ratio 1:1.2.

Relative measurements, as length or length/width: Antenna scape: 13/2, pedicel: 6.5/2.5, F1: 3/2, F2: 7/5, clava: 9.6+1.3/3.5, C1: 4, C2: 5.5, spicula: 1.3, forewing 50/17, longest marginal cilia 4.2, hind wing 44/6.4, ovipositor: 22.3.

Diagnosis:

By following the key of Doğanlar and Triapitsyn (2007) for the European and Turkish species of *Ceranisus,* the new species*, C. onuri*, runs to the female of *C. pacuvius*, but it differs from *C. pacuvius* in having a vertexal suture broadly V-shaped (Figure 3) (in *C. pacuvius*, a vertexal suture broadly C-shaped); clava, including spicula 3.02× as long as wide (in *C. pacuvius*, clava including spicula 2.2× as long as wide); and forewing (Figure 7) 3× as long as wide (in *C. pacuvius*, forewing 2.5× as long as wide).

Male: unknown.

Biology: larval parasitoid of *Thrips meridionalis* (Priesner) (Thysanoptera: Thripidae) living on *Asphodeline damascena* (Boiss.) at 2500 m elevation in the Taurus (Bolkar) Mountains.

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