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Determination of Ichneumonidae and Braconidae (Hymenoptera: Ichneumonidea) Species Using DNA Barcoding in Alfalfa Fields Around Van, Türkiye

Mehmet Salih ÖZGÖKÇE[1✍], Hilmi KARA[2], Mehmet Ramazan RİŞVANLI[3], Furkan Harun BAŞ[4]
[1,2,3]Department of Plant Protection, Faculty of Agriculture, Van Yüzüncü Yıl University, Van, Türkiye, [4]Department of Plant Protection, Faculty of Agriculture, [3]Ondokuz Mayıs University, Samsun, Türkiye
[1]https://orcid.org/0000-0002-6777-9149, [2]https://orcid.org/0000-0003-0580-0464,[3]https://orcid.org/0000-0002-5882-0533
[4]https://orcid.org/0000-0002-4764-9742
✉: msozgokce@yyu.edu.tr

ABSTRACT

Nowadays, DNA barcoding has become a powerful tool for rapid and accurate species identification, especially due to the limited number of expert taxonomists, difficulties in distinguishing very similar species, and difficulties in identifying preadult stages of species. In this study, species identification of Ichneumonidea species found in alfalfa fields in Van Province (Türkiye) and its surroundings was determined using DNA barcoding technique. Most of the Ichneumonidea are known as parasitoids of other arthropods and generally on holometabolous insects, primarily targeting insect larvae. Since they are used as natural enemies of harmful insects and have an important role in biological control, detailed studies have been conducted on this group and continue. Due to the limited use of pesticides, alfalfa fields in Van Province and its surroundings, where insect diversity is preserved, were selected as the study area to investigate Ichneumonidea species. The study was conducted in eight different districts of Van province, namely the Merkez, Ipekyolu, and Tuşba districts, Erciş, Muradiye, Özalp, Gürpınar, Edremit, and Başkale districts, where alfalfa is produced the most. Samples were collected between May and August, DNA sequences were extracted from the collected samples, and the sequences were compared with the species in NCBI, and high sequence similarities were observed. As a result of the study, two Braconidae and seven Ichneumonidae species were identified. Molecular identifications of *Aleiodes similis* (Curtis, 1834) (99.61%), *Bathyplectes curculionis* (Thomson, 1887) (98.14%), *Enizemum ornatum* (Gravenhorst, 1829) (99.80%), and *Syrphoctonus elegans* (Gravenhorst, 1829) (99.24%) were confirmed with high similarity rates and became the first record for Van province.

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Van İli (Türkiye) ve Çevresindeki Yonca Alanlarında DNA Barkodlama Yöntemi Kullanılarak Ichneumonidae ve Braconidae (Hymenoptera: Ichneumonidea) Türlerinin Belirlenmesi

ÖZET

Günümüzde, DNA barkodlama, özellikle uzman taksonomistlerin az sayıda olması, birbirine çok benzeyen türlerin ayırt edilmesindeki zorluklar ve türlerin ergin öncesi evrelerinin tanımlanmasındaki güçlükler nedeniyle hızlı ve doğru tür tanımlaması için güçlü bir araç haline gelmiştir. Bu çalışmada, Van ili (Türkiye) ve çevresindeki yonca tarlalarında bulunan Ichneumonidea türlerinin teşhisi DNA barkodlama tekniği kullanılarak belirlenmeye çalışılmıştır. Ichneumonidea'nın çoğu diğer eklembacaklıların parazitoidleri olarak bilinir ve genellikle holometebol böcekler üzerinde bulunur. Zararlı böceklerin doğal düşmaları olarak kullanıldıklarından ve biyolojik mücadeledeki önemli rolleri nedeniyle bu grup üzerinde detaylı çalışmalar yapılmıştır ve yapılmaya devam etmektedir. Pestisit kullanımının sınırlı olması sebebiyle böcek çeşitliliğinin korunduğu Van ili ve çevresindeki yonca tarlaları, Ichneumonidea türlerini araştırmak için çalışma alanı olarak seçilmiştir. Çalışma, Van ilinin Merkez, İpekyolu ve Tuşba ilçeleri ile

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yoncanın en çok üretildiği Erciş, Muradiye, Özalp, Gürpınar, Edremit ve Başkale ilçeleri olmak üzere sekiz farklı ilçesinde yürütülmüştür. Örnekler Mayıs ve Ağustos ayları arasında toplanmış, toplanan örneklerden DNA dizileri çıkarılmış ve diziler NCBI'daki türlerle karşılaştırılmış ve yüksek benzerlikler elde edilmiştir. Çalışma sonucunda iki Braconidae türü ve yedi Ichneumonidae türü tespit edilmiştir. *Aleiodes similis* (Curtis, 1834) (%99.61), *Bathyplectes curculionis* (Thomson, 1887) (%98.14), *Enizemum ornatum* (Gravenhorst, 1829) (%99.80) ve *Syrphoctonus elegans* (Gravenhorst, 1829) (%99.24) moleküler teşhisleri yüksek benzerlik oranları doğrulanmış ve Van ili için ilk kayıt olmuştur.

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INTRODUCTION

The Ichneumonidea is the largest group of Hymenoptera with 60077 described species and is distributed worldwide and even, Ichneumonidae (Hymenoptera: Ichneumonoidea) is the largest family of insects has 25285 currently described species (Yu et al., 2016; Yu, 2024; Çoruh & Kolarov, 2024; Dalan & Çoruh, 2025). It is currently composed of the three monophyletic families Ichneumonidae, Braconidae and Trachypetidae, with the majority of their species are parasitoids of other arthropods, while a few exhibit other biologies such as gall induction and seed predation (Greathead, 1986; Flores et al., 2005; Jasso-Martínez et al., 2021; Quicke & Butcher, 2021).

The identification of Ichneumonoidea species presents significant challenges due to extreme species richness, lack of specialists, low percentage of species identified, low density of ichneumonid species across the landscape, their rapid spread, and lack of detailed biological information for most of the identified species (Veijalainen et al., 2012; Meierotto et al., 2019; Sharanowski et al., 2021). Due to the vast diversity of ichneumonids and the limited knowledge of their biology for many species (Meierotto et al., 2019), traditional morphological identification methods often prove inadequate, time-consuming, and inefficient (Gomila et al., 2014; Quicke & Butcher, 2021). The dominance of two similarly sized families, Braconidae and Ichneumonidae, as well as the small, recently recognized family Trachypetidae, further complicates species identification (Quicke & Butcher, 2021). Moreover, some species within the superfamily are extremely morphologically similar, especially in males, making their identification particularly challenging (Yu et al., 1992; Klopfstein et al., 2019a).

These factors demand that alternative methods be explored for the accurate identification. Traditional phenotypic-based analyses have been demonstrated to be inadequate for reliable, definitive identifications of certain species (Gomila et al., 2014). These challenges of identification could be met by utilizing DNA barcoding for molecular identification, as some species are cryptic and difficult to distinguish based on external morphology alone (Hubert et al., 2008; Quicke et al., 2012). Furthermore, the use of polymerase chain reaction (PCR) of genomic DNA has been suggested as a method to overcome these challenges and accurately categorize species (Martinez et al., 2003; Lorenz, 2012). The application of DNA barcoding, a method utilizing a standardized, short-read DNA sequence for species identification and classification, has completely transformed insect taxonomy. DNA barcoding facilitates accurate species-level identification and contributes to phylogenetic reconstruction. Witnessing rapid advancements in recent years, it has emerged as a potent tool for diverse applications, including biodiversity investigations and monitoring, molecular phylogeny, and evolutionary studies.

The integration of molecular and morphological evidence has been emphasized as a potent tool to overcome taxonomic hurdles in diverse hymenopteran families, indicating a promising approach for resolving taxonomic impediments within the Ichneumonoidea superfamily (Vilhelmsen et al., 2010; Meierotto et al., 2019; Quicke & Butcher, 2021).

Medicago L. is a genus of flowering plants that are commonly used in agriculture as forage for livestock. The alfalfa plant (*Medicago sativa* L.), known for its high nutritional value and rich diversity, serves as a habitat for a wide range of insect species, including alfalfa weevils, aphids, alfalfa thrips, lepidopterans, and various other insects. These diverse insect populations play a natural role within the ecosystem and serve as a significant food source for their natural enemies, such as parasitoid wasps. Additionally, the presence of many flowering weeds in clover fields further enhances the attractiveness of these areas for parasitoids, providing them with abundant food

sources.

As a result, the abundance and diversity of parasitoid species in clover fields are notably high, and examining these areas is essential in faunistic studies of parasitoid species (Snyder and Ives, 2003). The interactions between pests and generalist natural enemies, including parasitoids and predators, in alfalfa fields have been studied to understand their impact on biocontrol. These interactions play a crucial role in regulating pest populations and maintaining ecological balance within agricultural ecosystems (Nelson et al., 2004). In Van province and its surroundings, where the study was conducted, the alfalfa plant is one of the most important agricultural products and constitutes approximately 9.5% of Türkiye's alfalfa production (TUIK, 2021). Pesticides are not used in alfalfa fields throughout the region, generally.

For this reason, clover areas with a rich species diversity were deemed appropriate for detecting the presence and fauna of species belonging to the Ichneumonidea in the region, which was discussed in this study.

MATERIAL and METHOD

Study area and collection of samples

The study was conducted in eight different regions of Van Province in 2021, including the districts of Ipekyolu, Tuşba, Erciş, Muradiye, Özalp, Gürpınar, Edremit, and Başkale (Figure 1). In each district, at least two alfalfa fields were chosen randomly for sample collection. Standard 200 sweep nets were employed to collect specimens weekly from May, coinciding with the first emergence of alfalfa plants, until August.



Figure 1. Study area (based on Google Earth)
Şekil 1. Çalışma alanı (Google Earth'den)

DNA extraction and PCR analysis

To generate DNA barcodes for the specimens, total genomic DNA was extracted from the legs of each individual. All legs from each specimen were placed in a microcentrifuge tube and washed with distilled water (dH_2O). After the washing process, the water was removed, and the legs were frozen in a microcentrifuge tube at -80 °C for 5 hours to harden and increase their fragility. The tubes taken from -80 °C were crushed into powder with the help of metal pestle rods. 300 µl TNES buffer (50 mM Tris-Cl, pH: 7.5; 400 mM NaCl; 20 mM EDTA, pH: 8.0; 0.5% SDS) and 5 µl proteinase-K (20 mg/ml) were added to the pulverized insect tissue, the caps of the tubes were closed and the tubes were covered with parafilm and incubated at 37 °C for 10-18 hours. Then the parafilms were opened, and 85 µl of 5 M NaCl was added to the tubes and mixed by vortexing for 15 seconds. The tubes containing NaCl were centrifuged at 14000 rpm for 5 min.

After centrifugation, the supernatant was carefully transferred to a new tube, and a volume of 99% cold ethanol was added. These tubes, to which ethanol was added, were centrifuged in a refrigerated centrifuge (4 °C) at 15000 rpm for 7 min. After this application, all the liquid in the tube was drained without touching the pellet, and 70% cold ethanol was added for re-washing and centrifuged again in a refrigerated centrifuge (4 °C) at 15000 rpm for 2-3 min. After the ethanol remaining after centrifugation was removed entirely and the pellet was allowed to dry, 30 µl 1x TE (10 mM Tris-Cl, pH: 7.5; 1 mM EDTA) buffer was added to dissolve the DNA, and the tubes containing total genomic DNA were stored at -20 °C.

The COI (*cytochrome oxidase I*) region in mitochondrial DNA, which is the gene region of the samples whose DNA was obtained, was aimed to be amplified using various universal primers (Table 1).

Table 1. Primers used in this study for mtDNA-COI gene amplification.
Çizelge 1. Bu çalışmada mtDNA-COI geninin amplifikasyonu için kullanılan primerler.

Gene Region	Primer	Sequence	Source
COI	LCO1491	GGTCAACAAATCATAAAGATATTGG	Forward
COI	HCO2198	TAAACTTCAGGGTGACCAAAAAATCA	Reverse

RESULTS

Distance Analyses and Genetic Diversity

DNA sequence analyses showed that all final sequences selected were of good quality, and the selected COI sequences represent 11 nominal species from seven genera (Table 2). A barcode sequence length ranging from 511 to 669 base pairs (Table 2) was employed for the examination of the COI sequences, which is regarded as a sufficient length (Ratnasingham and Hebert 2013). COI gene sequences derived from the specimens were analyzed using the Maximum Likelihood (ML) analysis, along with their closest matches retrieved from the NCBI GenBank database. Pairwise genetic distances were calculated between the collected sequences and closest matches from GenBank, with similarity values ranging from 87.2% to 99.8% at the species level (Table 3). While 8 of the sequences matched the full species name, 3 of them matched at the genus level. Five species had similarity rates ranging from 99.22% to 99.80% at the species level, while three species had similarity values of 98.14%, 92.89%, and 87.20%, respectively. The three species' respective genus-level similarity percents were found to be 99.43%, 96.92%, and 91.71%. DNA sequences of the species have been deposited in NCBI, and accession numbers obtained are given in column 3 of Table 2.

A total of 11 different species, 9 ichneumonids and 2 braconids, were identified across all samples collected from around the Van province region. While 2 species belonging to the Braconidae family were found to belong to the Rogadinae subfamily, 3 of the 9 species belonging to the Ichneumonidae family were determined to belong to the Campopleginae subfamily, 2 species to the Cryptinae subfamily, and two species to the Diplazontinae subfamily. It was determined that 1 species each belonged to the Pimplinae and Tryphoninae subfamilies.

The genetic distances of the species identified in this study and the species taken from the gene bank according to their sequences (species with which they match best according to their similarity ratios) are given in Table 3. Accordingly, the genetic similarity between B1 and *Aleiodes coxalis* (EF115459.), B2 and *A. similis* (MN968703.1), I1 and I2, I1 and *Bathyplectes curculionis* (MN729637.1), I1 and *Bathyplectes* sp. (KY837888.1), I2 and *B. curculionis* (MN729637.1), I2 and *Bathyplectes* sp. (KY837888.1), I3 and *Campoletis* sp. (MF902636.1), I6 and *Enizemum ornatum* (KT960000.1), I7 and *Syrphoctonus elegans* (JN626329.1), I8 and *Itoplectis maculator* (MZ627044.1), *B. curculionis* (MN729637.1) and *Bathyplectes* sp. (KY837888.1) was found to be statistically significant. According to these results, the probability that *B. curculionis* (MN729637.1) and *Bathyplectes* sp. (KY837888.1) identified with I1 and I2 are the same species may be quite high.

Phylogenetic Analyses

The phylogenetic analysis revealed that all samples clustered with their corresponding species in the phylogenetic tree, supported by high bootstrap values (Figure 2). A high bootstrap value (typically > 70%) suggests strong statistical support for the monophyly of the group of taxa branching from that node. Notably, the clustering pattern demonstrates a high confidence level in the genetic relatedness of the studied species, as evidenced by the 100% bootstrap values for the ten represented species and a 99% bootstrap value for *Cryptinae* sp. This clustering pattern suggests a clear separation and evolutionary divergence among the species, reflecting their unique genetic signatures and evolutionary histories. A high bootstrap value (like 95 or 100) means that a particular clade appeared in a high percentage of the resampled trees. This indicates a very high degree of confidence in the evolutionary relationship shown at that node. The evolutionary analysis conducted using the Maximum Likelihood method and the General Time Reversible model further elucidates the genetic relationships among the species.

Table 2. Braconidae and Ichneumonidae species collected from clover fields in Van and its districts.
Çizelge 2. Van ve ilçelerindeki yonca tarlalarından toplanan Braconidae ve Ichneumonidae türleri.

Top species match	Similarity (%), Accession Number (NCBI)	Code in samplings/ Accession Number (NCBI)	Sequence length of samplings (base pairs)	Family	Subfamily	Tribe	Genus	Sampling location
Aleiodes coxalis	99.52, (EF115459.1)	B.1 PV056080	632	Braconidae	Rogadinae		*Aleiodes*	6
Aleiodes similis	99.61, (MN968703.1)	B.2 PV056081	512				*Aleiodes*	11
Bathyplectes curculionis	98.14, (MN729637.1)	I.1 PV056082	669	Ichneumonidae	Campopleginae		*Bathyplectes*	11
Bathyplectes sp.	99.43, (KY837888.1)	I.2 PV056083	526				*Bathyplectes*	8
Campoletis sp.	96.92, (MF902636.1)	I.3 PV056084	523					6
Stibeutes brevicornis	87.20, (MZ609096.1)	I.4 PV056085	530		Cryptinae	*Phygadeuontini*	*Stibeutes*	6
Cryptinae sp.	91.71, (KR791419.1)	I.5 PV056086	523					11
Enizemum ornatum	99.80, (KT960000.1)	I.6 PV056087	512		Diplazontinae		*Enizemum*	8
Syrphoctonus elegans	99.24, (JN626329.1)	I.7 PV056088	683				*Syrphoctonus*	11
Itoplectis maculator	99.22, (MZ627044.1)	I.8 PV056089	512		Pimplinae	Pimplini	*Itoplectis*	9
Netelia testacea	92.89, (MZ628742.1)	I.9 PV056090	511		Tryphoninae	Phytodietini	*Netelia*	11

* Locations: 1: Bahçesaray, 2: Başkale, 3: Çaldıran, 4: Çatak, 5: Edremit, 6: Erciş, 7: Gevaş, 8: Gürpınar, 9: İpekyolu, 10: Muradiye, 11: Özalp, 12: Saray, 13: Tuşba.

Table 3. The mean pairwise interspecific genetic distances.
Çizelge 3. Türler arası ortalama genetic mesafe.

	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]	[10]	[12]	[13]	[14]	[15]	[16]	[17]	[18]	[19]	[20]	[21]	[22]
[1] B.1																					
[2] B.2	0.0688																				
[3] I.1	0.5322	0.4909																			
[4] I.2	0.5533	0.5120	0.0444																		
[5] I.3	0.5078	0.4665	0.1422	0.1634																	
[6] I.4	0.6478	0.6065	0.4096	0.4308	0.3852																
[7] I.5	0.5808	0.5395	0.3426	0.3637	0.3182	0.3705															
[8] I.6	0.5242	0.4829	0.2583	0.2794	0.2339	0.4016	0.3346														
[9] I.7	0.5389	0.4975	0.2729	0.2941	0.2485	0.4163	0.3492	0.1615													
[10] I.8	0.5641	0.5228	0.2982	0.3193	0.2738	0.4415	0.3745	0.2200	0.2347												
[11] I.9	0.6426	0.6013	0.3767	0.3978	0.3523	0.5200	0.4530	0.3153	0.3299	0.3552											
[12] EF115459.1 *Aleiodes coxalis*	0.0049	0.0737	0.5371	0.5582	0.5127	0.6527	0.5856	0.5291	0.5437	0.5690	0.6475										
[13] MN968703.1 *Aleiodes similis*	0.0722	0.0034	0.4942	0.5154	0.4699	0.6099	0.5428	0.4863	0.5009	0.5262	0.6047	0.0770									
[14] MN729637.1 *Bathyplectes curculionis*	0.5283	0.4870	0.0193	0.0405	0.1383	0.4057	0.3387	0.2544	0.2690	0.2943	0.3728	0.5332	0.4903								
[15] KY837888.1 *Bathyplectes* sp.	0.5495	0.5082	0.0406	0.0039	0.1595	0.4270	0.3599	0.2756	0.2903	0.3155	0.3940	0.5544	0.5116	0.0367							
[16] MF902636.1 *Campoletis* sp.	0.5078	0.4665	0.1422	0.1633	0.0343	0.3852	0.3182	0.2339	0.2485	0.2738	0.3523	0.5127	0.4698	0.1383	0.1595						
[17] KR791419.1 *Cryptinae* sp.	0.5426	0.5013	0.3044	0.3256	0.2800	0.3323	0.1051	0.2964	0.3111	0.3363	0.4149	0.5475	0.5047	0.3005	0.3218	0.2800					
[18] KT960000.1 *Enizemum ornatum*	0.5263	0.4850	0.2604	0.2815	0.2360	0.4037	0.3367	0.0021	0.1635	0.2221	0.3173	0.5312	0.4883	0.2565	0.2777	0.2360	0.2985				
[19] MZ627044.1 *Itoplectis maculator*	0.5600	0.5186	0.2940	0.3152	0.2696	0.4374	0.3703	0.2159	0.2305	0.0079	0.3510	0.5648	0.5220	0.2901	0.3114	0.2696	0.3322	0.2180			
[20] MZ628742.1 *Netelia testacea*	0.6270	0.5857	0.3610	0.3822	0.3367	0.5044	0.4374	0.2996	0.3142	0.3395	0.0868	0.6319	0.5890	0.3571	0.3784	0.3366	0.3992	0.3017	0.3353		
[21] MZ609096.1 *Stibeutes brevicornis*	0.6103	0.5690	0.3721	0.3933	0.3478	0.2039	0.3330	0.3642	0.3788	0.4040	0.4826	0.6152	0.5724	0.3682	0.3895	0.3477	0.2948	0.3662	0.3999	0.4669	
[22] JN626329.1 *Syrphoctonus elegans*	0.5389	0.4975	0.2729	0.2941	0.2485	0.4163	0.3492	0.1615	0.0000	0.2347	0.3299	0.5437	0.5009	0.2690	0.2903	0.2485	0.3111	0.1635	0.2305	0.3142	0.3788

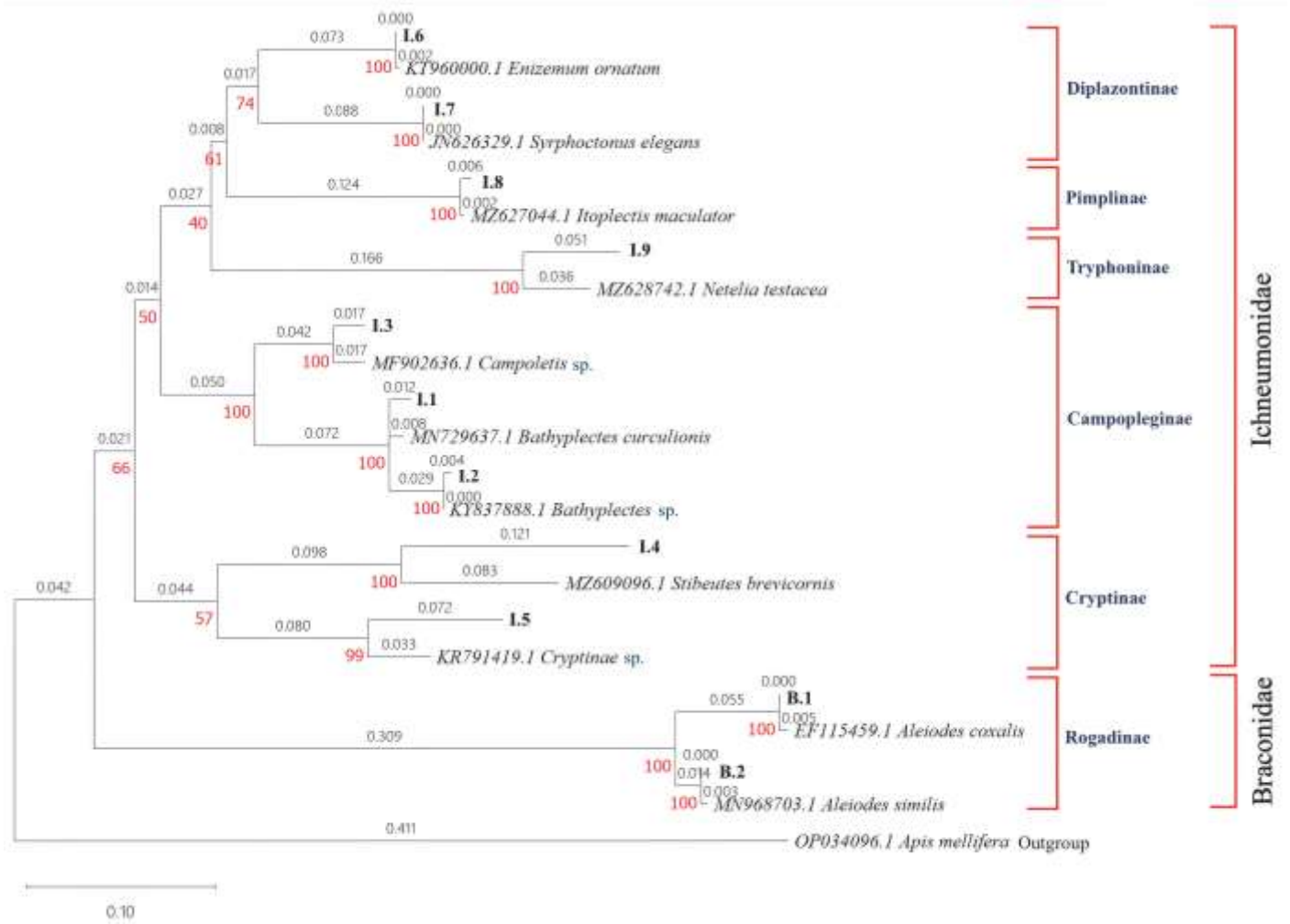


Figure 2. Maximum Likelihood phylogeny based on the DNA barcoding region COI for Ichneumonidae and Braconidae species.

Şekil 2. Ichneumonidae ve Braconidae türleri için DNA barkodlama bölgesi COI'ye dayalı Maksimum Olabilirlik filogenisi.

Distribution and habitats of the ichneumonids and braconids around the Van

Braconidae

B.1. *Aleiodes coxalis* (Spinola, 1808)

Synonyms: =*Aleiodes kolthoffi* (Fahringer, 1929), =*Aleiodes nunbergi* (Noskiewicz, 1956), =*Aleiodes tristis* (Wesmael, 1838), ≡*Bracon coxalis* (Spinola, 1808), ≡*Rhogas nunbergi* (Noskiewicz, 1956), =*Rogas nunbergi* (Noskiewicz, 1956).

The genus *Aleiodes* is distributed worldwide but is particularly species-rich in the Holarctic region. The species of *Aleiodes* are koinobiont endoparasitoids of Lepidopteran larvae, especially of Noctuidae and Geometridae. The host caterpillar is mummified (Shaw et al., 1997). The genus *Aleiodes* comprises 215 species and about 126 species in the Palaearctic (Yu et al., 2005).

Examined: Van, Erciş (N39° 00.871' E43° 27.542').

Distribution in Türkiye: Ankara (Gölbaşı), Bingöl (Adaklı, Hasbağlar, Ahlat, Tatvan, Reşadiye), Muş (Mercimek, Varto), Sivas (Gürün), Van (Erciş) (Beyarslan and Çakici, 2021).

Global Distribution: Palaearctic, Oriental. Albania, Belgium, Bulgaria, China, Croatia, Czech Republic, England, France, Germany, Greece, Hungary, Kazakhstan, Italy, Iran, Japan, Korea, Madeira Islands, Mongolia, Montenegro, Netherlands, Poland, Romania, Russia, Serbia, Slovakia, Slovenia, Spain, Sweden, Switzerland, Ukraine, Turkmenistan, former Yugoslavia, Austria, Finland (Shenefelt 1975 as *A. tristis* Wesmael), Siberia (Watanabe 1937 as *Rhogas tristis*; Shenefelt 1975 as *A. tristis* Wesmael) (Quicke et al., 2006; Beyarslan et al., 2017; Yu et al. 2012).

Ecological Role

The ecological role of *Aleiodes coxalis* lies primarily in controlling the populations of pest insects. Parasitoids are highly valuable for pest management in agricultural ecosystems. As natural enemies, they provide an environmentally friendly alternative to chemical insecticides. Moreover, parasitoids prevent the overpopulation of host insects, thereby protecting plant health.

Hosts: Lepidoptera, Crambidae: *Cnaphalocrocis medinalis* (Guenée, 1854); *Ostrinia nubilalis* (Hübner, 1796). Geometridae: *Eupithecia pimpinellata* (Hübner, 1813); *Scopula nigropunctata* (Hufnagel, 1767). Hesperiidae: *Thymelicus lineola* (Ochsenheimer, 1808) (Yu et al., 2012). Noctuidae: *Sideridis rivularis* Fabricius, 1775. Nymphalidae: *Coenonympha pamphilus* (Linnaeus, 1758); *C. tullia* (Müller, 1764); *Erebia* sp.; *Limenitis populi* (Linnaeus, 1758); *Maniola jurtina* (Linnaeus, 1758); *Melanargia lachesis* Hübner, 1790; *Mycalesis gotama* Moore, 1857; *Pyronia tithonus* (Linnaeus, 1767). Pterophoridae: *Emmelina monodactyla* (Linneaus, 1758) (Yu et al., 2012).

DNA barcoding: The specimen B.1 exhibits a high degree of similarity (99.52%) to *A. coxalis* according to the BLAST comparison in the NCBI database (accession number EF115459.1). This high similarity percentage indicates a close genetic relationship between the sampled specimen and the reference species, supporting the accurate identification of *A. coxalis* in the study.

B.2. *Aleiodes similis* (Curtis, 1834)

Synonyms: =*Aleiodes fuscomaculatus* (Ashmead, 1906), =*Aleiodes japonicus* (Ashmead, 1906), =*Aleiodes ochraceus* Hellen, 1927, =*Aleiodes rossicus* (Kokujev, 1898), =*Aleiodes spathuliformis* (Curtis, 1834), ≡*Ichneumon gastritor* (Thunberg, 1822) ≡*Rhogas rossicus* Kokujev, 1898, ≡*Rogas similis* (Curtis, 1834).

Examined: Van, Muradiye (N38° 57.933' E43° 42.289').

Distribution in Türkiye: Ardahan (Posof), Bitlis (Tatlı kaynak village, Adilcevaz), Edirne (Güllapoğlu), Kars (Sarıkamış, Büyükkumru) Muş (Bulanık, Güllüova village) (Beyarslan and Çakici, 2021).

Global Distribution: Holarctic, Oceanic, Oriental (Beyarslan and Çakici, 2021).

Ecological Role

Aleiodes similis primarily targets the larvae of butterflies and moths as a parasitoid. These insect groups are among the pests that can damage agricultural crops and forests. *Aleiodes similis* provides natural biological control by parasitizing the larvae of these pests. Parasitoids develop inside or on the host insect, suppressing the pest's population and preventing it from damaging plants. This offers an environmentally friendly method for both agricultural production and the preservation of natural vegetation.

Hosts: Lepidoptera, Crambidae: *Ostrinia nubilalis* (Hubner, 1796), *Phlyctaenia coronata* (Hufnagel, 1767), Drepanidae: *Cilix glaucata* (Scopoli, 1763), Elachistidae: *Depressaria absynthiella* (Herrich-Schaffer, 1865), Geometridae: *Alsophila pometaria* (Harris, 1841), *Apocheima cinerarius* (Erschoff, 1874), *A. hispidaria* (Denis & Schiffermuller, 1775), *Chiasmia clathrata* (Linnaeus, 1758), *Chloroclystis v-ata* (Haworth, 1809), *Digrammia gnophosaria* (Guenee, 1857), *Epirrita autumnata* (Borhausen, 1794), *Erannis defoliaria* (Clerck, 1759), *Eupithecia alliaria* (Staudinger, 1870), *E. miserulata* (Grote, 1863), *E. pusillata* (Denis & Schiffermuller, 1775), *Glena cribrataria* (Guenee, 1858), *Hylaea fasciaria* (Linnaeus, 1758), *Hypagyrtis unipunctata* (Haworth, 1809), *Isturgia limbaria* (Fabricius, 1775), *Lycia hirtaria* (Clerck, 1760), *Lycia pomonaria* (Hubner, 1790), *Operophtera brumata* (Linnaeus, 1758), *Phthonandria atrilineata* (Butler 1881), *Tephrina arenacearia* (Denis & Schiffermuller, 1775), Lasiocampidae: *Malacosoma neustria* (Linnaeus, 1758), Erebidae: *Euproctis chrysorrhoea* (Linnaeus, 1758), *E. similis* (Fuessly, 1775), *Hypena scabra* (Fabricius, 1798), *Leucoma salicis* (Linnaeus, 1758), Noctuidae: *Agrapha agnata* (Staudinger, 1892), *Autographa gamma* (Linnaeus, 1758), *Harpyia hermelina* (Stephens, 1829), *Helicoverpa armigera* (Hubner, 1808), *Pseudaletia unipuncta* (Haworth, 1809), *Spodoptera exigua* (Hubner, 1808), *Trichoplusia ni* (Hubner, 1803), Notodontidae: *Cerura vinula* (Linnaeus, 1758), *Thaumetopoea processionea* (Linnaeus, 1758), Yponomeutidae: *Prays oleae* (Bernard, 1788), Tortricidae: *Archips rosana* (Linnaeus, 1758), *Lobesia botrana* (Denis & Schiffermuller, 1775) (Beyarslan and Çakici, 2021).

DNA barcoding: The specimen B.2 exhibits a high similarity of 99.61% to *A. similis* (MN968703.1) in the NCBI database. The high similarity percentage suggests that the sampled specimen likely belongs to the same species as *A. similis*, confirming the accuracy of species identification through DNA barcoding.

Ichneumonidae

I.1. *Bathyplectes curculionis* (Thomson, 1887).

Synonym: ≡*Canidia curculionis* (Thomson, 1887).

Examined: Van, Muradiye (N39° 05.154' E43° 48.018').

Distribution in Türkiye: Adana, Ankara, Diyarbakır, Edirne, Iğdır, İçel, İstanbul, Mardin, Şanlıurfa (Kolarov, 1989; Öncüer, 1991; Kolarov, 1995; Kolarov & Beyarslan, 1995; Çoruh et al., 2013; Gözüaçık & Kolarov, 2016; Çoruh et al., 2017; Efil, 2018; Gözüaçık, 2019).

Global Distribution: It is widespread throughout the Palearctic region, encompassing more than 71 countries in North America, Europe, Northeast Africa and Asia, including Bulgaria, Egypt, England, Greece, Ireland, Iran, Iraq, Scotland, Serbia – Srbobran, Spain and Türkiye (Kolarov, 1989; Gonzalez et al., 1980; Thomson, 1887; Radcliffe and Flanders, 1998; Ribes, 2012; Rand, 2013; Broad, 2016; Yu et al., 2016; Plećaš et al., 2023; Levi-Mourao et al., 2025).

Ecological Role

Bathyplectes curculionis is an effective parasitoid of weevil pests, particularly in alfalfa farming. Its distribution is closely tied to its host, the alfalfa weevil. The females lay their eggs on the host insect's larvae, and the emerging larva develops inside the host, ultimately killing it. This process suppresses pest populations and reduces the damage caused to agricultural crops. This biological control mechanism offers an environmentally friendly alternative by reducing the need for chemical pesticides. In the production of key crops such as alfalfa, these parasitoid wasps help manage pest populations naturally

Hosts: *Apion pisi* (Fabricius, 1801) (Coleoptera: Apionidae), *Hypera postica*, *Hypera* spp. (Coleoptera: Curculionidae) (Soroka et al., 2020; Plećaš et al., 2023).

DNA barcoding: The specimen I.1 shows a similarity of 98.14% to *B. curculionis* (MN729637.1) in the NCBI database. While slightly lower than the previous matches, this similarity percentage still indicates a close genetic relationship between the sampled specimen and *B. curculionis*, supporting its identification at the species level.

I.2. *Bathyplectes* sp.

Examined: Van, Gevaş (N38° 22.222' E43° 11.302').

DNA barcoding: Specimen I.2 demonstrates a high similarity of 99.43% to *Bathyplectes* sp. (KY837888.1) in the NCBI database. Specimen I.2 demonstrates a high similarity of 99.43% to *Bathyplectes* sp. (KY837888.1) in the NCBI database. The closest species-level sample to this sample, which was identified at the genus level at a high rate, was *B. curculionis* with accession number MN729638.1, with a percentage of 97.84%.

Ecological role

Bathyplectes sp. lay their eggs on the larvae of the host insect. The larvae that emerge from the eggs develop inside the host, ultimately killing it. This process suppresses pest populations and prevents damage to agricultural crops. As natural enemies, these species have the potential to reduce the use of chemical pesticides and serve as an important tool for sustainable agricultural practices.

I.3. *Campoletis* sp.

Examined: Van, Erciş (N39° 04.074' E43° 17.827').

DNA barcoding: The specimen I.3 exhibits a similarity of 96.92% to *Campoletis* sp. (MF902636.1) in the NCBI database. This similarity percentage indicates a moderate genetic relationship between the sampled specimen and *Campoletis* sp., supporting the identification of the specimen at the genus level. *Campoletis chlorideae* showed the highest match rate to this sample at the species level in the NCBI genebank, with a rate of 95.94% and accession number 0Q710106.1.

Ecological Role

Campoletis sp. typically parasitize the larvae of Lepidoptera (butterflies and moths). The female wasp lays her eggs on the larvae of the host insect. The larva that emerges from the egg develops inside the host, ultimately killing it. This process suppresses pest populations and thereby reduces the damage caused to agricultural crops.

These species provide an environmentally friendly alternative by reducing the use of chemical pesticides. In agricultural practices, these natural enemies can be an important resource for managing pest populations.

I.4. *Stibeutes brevicornis* (Lange, 1911).

Synonym: ≡*Stilpnus brevicornis* (Lange, 1911).

Examined: Van, Edremit (N38° 22.222' E43° 11.302').

Distribution in Türkiye: -

Global distribution: Austria, Canada, Croatia, Finland, Germany, Sweden, United Kingdom (Horstmann, 2010; Broad, 2016; Yu et al., 2012; Anonymous, 2024).

Hosts: Caterpillars, beetle larvae, spiders, and various other insects (Anonymous, 2024)

DNA barcoding: Specimen I.4 shows a similarity of 87.20% to *St. brevicornis* (MZ609096.1) in the NCBI database. While this similarity percentage is lower compared to other matches, it still suggests a genetic relationship between the sampled specimen and *St. brevicornis*, aiding in the species identification process.

Ecological Role

Stibeutes brevicornis typically parasitizes harmful larvae, such as leafroller insects. The females lay their eggs on the larvae of the host insect; the larva that emerges from the egg develops inside the host and ultimately kills it. This process suppresses pest populations and reduces the damage caused to agricultural crops. This species provides an environmentally friendly alternative by reducing the use of chemical pesticides. In agriculture, it serves as an important tool for the natural control of pest populations.

I.5. *Cryptinae* sp.

Examined: Van, Muradiye (N39° 05.154' E43° 48.018')

DNA barcoding: The specimen I.5 exhibits a similarity of 91.71% to *Cryptinae* sp. (KR791419.1) in the NCBI database. This similarity percentage indicates a moderate genetic relationship between the sampled specimen and *Cryptinae* sp., providing insights into the taxonomic classification of the specimen at the subfamily level. No species was matched to this sample at the species level in the sequence matching made in NCBI and BOLD gene banks.

Ecological Role

Cryptinae sp. typically parasitize the larvae of harmful insects such as Lepidoptera and Coleoptera. The female lays her eggs on the larvae of the host insect; the larva that emerges from the egg develops inside the host and ultimately kills it. This process suppresses pest populations and reduces the damage caused to agricultural crops. These species provide an environmentally friendly alternative by reducing the use of chemical pesticides. In agricultural practices, these natural enemies can be an important resource for managing pest populations.

I.6. *Enizemum ornatum* (Gravenhorst, 1829).

Synonyms: *≡Bassus ornatum* (Gravenhorst, 1829), *=Enizemum carinulatum* (Ruthe, 1859), *=Enizemum deplanatum* (Gravenhorst, 1829), *=Enizemum deplinatum* (Gravenhorst, 1829), *=Enizemum frenator* (Desvignes, 1862), *=Enizemum neomexicanum* Brues, 1908, *=Enizemum sumptuosum* (Schmiedeknecht, 1926).

Examined: Van, Gevaş (N38° 18.050' E43° 06.909').

Distribution in Türkiye: Isparta (Birol, 2010), Bolu, Isparta (Klopfstein, 2014).

Global distribution: England, Iran-Qazvin, Sistan-Beluchestan (Mohammadi-Khoramabadi et al. 2013), Scotland, Wales, Ireland, Isle of Man (Broad, 2016), Switzerland (Klopfstein et al., 2019b), Afghanistan, Austria, Belgium, Bulgaria, Canada, China, Czech Republic, Czechoslovakia, Finland, France, Germany, Greenland, Hungary, Iceland, India, Ireland, Italy, Latvia, Lithuania, Moldova, Mongolia, Netherlands, Norway, Poland, Romania, Russia, Spain, Sweden, Switzerland, Türkiye, U.S.A., United Kingdom (Yu et al., 2012).

Hosts: *Syrphidae* species (Yu et al., 2012; 2016).

DNA barcoding: Specimen I.6 demonstrates a high similarity of 99.80% to *E. ornatum* (KT960000.1) in the NCBI database. The high similarity percentage suggests a close genetic relationship between the sampled specimen and *E. ornatum*, supporting its accurate identification at the species level.

Ecological Role

Enizemum ornatum typically parasitizes the larvae of various harmful insects. The female lays her eggs on the larvae of the host insect; the larva that emerges from the egg develops inside the host and ultimately kills it. This process suppresses pest populations and reduces the damage caused to agricultural crops. This species provides an environmentally friendly alternative by reducing the use of chemical pesticides. In agriculture, it serves as an important tool for the natural control of pest populations.

I.7. *Syrphoctonus elegans* (Gravenhorst, 1829).

Synonyms: ≡ *Bassus elegans* (Gravenhorst, 1829), =*Syrphoctonus affinis* (Szepligeti, 1898), =*Syrphoctonus rufonotatus* (Holmgren, 1858).

Examined: Van, Muradiye (N38° 57.933' E43° 42.289').

Distribution in Türkiye: Afyon, Ankara, Burdur, Isparta (Özdemir, 2001; Klopfstein et al., 2019b).

Global distribution: Holarctic regions (Abdinbekova, 1963; Klopfstein, 2014), Afghanistan, Austria, Azerbaijan, Belgium, Canada - Ontario - Quebec, former Czechoslovakia, Finland, France, Germany, Greenland, Georgia, Hungary, Ireland, Isle of Man, Iran, Ireland, Italy (Country), Italy - Sicily Lithuania, Moldova, Mongolia, Morocco, Netherlands, Norway - main, Poland, Romania, Russia, Russia-Kamchatka Oblast - Sakhalin Oblast-Sankt Petersburg, Scotland, Spain, Sweden, Switzerland, Türkiye, United Kingdom, Wales, Western Sahara (Horstmann, 2010; Khayrandish et al., 2014; Klopfstein, 2014; Broad, 2016; Vas, 2020; Reijo et al., 2021; Riedel & Japoshvili, 2021).

Ecological Role

Syrphoctonus elegans typically parasitizes the larvae of various harmful insects. The female lays her eggs on the larvae of the host insect; the larva that emerges from the egg develops inside the host and ultimately kills it. This process suppresses pest populations and reduces the damage caused to agricultural crops.

Hosts: The diversity of host interactions, which can range from specific associations with particular host species to more generalist activities directed at a wider range of hosts, includes those of the Tephritidae and Bombycidae families (Savaris et al., 2015; Tokuhira et al., 2022)

DNA barcoding: The specimen I.7 shows a high similarity of 99.24% to *S. elegans* (JN626329.1) in the NCBI database. This high similarity percentage indicates a strong genetic resemblance between the sampled specimen and *S. elegans*, confirming its identification at the species level.

I.8. *Itoplectis maculator* (Fabricius, 1775).

Synonyms: ≡*Ichneumon maculator* Fabricius, 1775, =*Itoplectis arlequinata* (Geoffroy, 1785), =*Itoplectis lateratoria* (Thunberg, 1822), =*Itoplectis maculatrix* (Schulz, 1906), =*Itoplectis plaesseus* (Geoffroy, 1785), =*Itoplectis scanica* (Villers, 1789), =*Itoplectis vincta* (Vollenhoven, 1873).

Examined: Van, Gürpınar (N38° 20.014' E43° 25.016').

Distribution in Türkiye: Adana, Ankara, Afyon, Artvin, Balıkesir, Bitlis, Bolu, Çanakkale, Çorum, Denizli, Eastern Mediterranean Region, Edirne, Eskişehir, Erzurum, Gümüşhane, Isparta, İçel, İstanbul, İzmir, Kars, Kastamonu, Kırklareli, Kırşehir, Konya, Manisa, Nevşehir, Niğde, Muğla, Rize, Sinop, Tekirdağ, Van, Yozgat, Zonguldak (İren, 1952; 1960; 1977; Kasparyan, 1973; 1974; Ulu, 1983; Kansu et al., 1986; Doğanlar, 1987; Kolarov, 1987; Özdemir and Kılınçer, 1990; Kolarov and Beyarslan, 1994; Kolarov, 1995; Erol and Yaşar, 1996; Kolarov et al., 1997, 1999, 2002; Özdemir and Özdemir, 2002; Gürbüz, 2004; Çoruh, 2005; Gürbüz, 2005; Kolarov and Gürbüz, 2004; Çoruh, 2005; Yurtcan and Beyarslan, 2005; Çoruh et al., 2007, 2014; Okyar and Yurtcan, 2007; Gürbüz et al., 2009; Birol, 2010; Çoruh and Kolarov, 2010; Çoruh and Kolarov, 2010; Eroğlu et al., 2011; Çoruh et al., 2014; Kolarov et al., 2016; Çoruh, 2016; Kondur and Şimşek, 2016; Aydoğdu and Kanev, 2017; Narmanlıoğlu and Çoruh, 2017; Sarı and Çoruh, 2018; Tek and Okyar, 2018; Kolarov et al., 2020; Yurtcan et al., 2021; Korukcu and Çoruh, 2024).

Global distribution: It is distributed across Europe and North Africa, and it has been introduced in North America (Yefremova et al., 2007).

Ecological Role

Itoplectis maculator is a polyphagous endoparasitoid that typically attacks different small members of Lepidoptera, Coleoptera, Hymenoptera and Diptera (Menken, 1982). The females lay her eggs on the host's larvae; when the eggs hatch, the larvae feed on the host from the inside, ultimately killing it. This parasitic behavior helps to regulate pest populations, reducing the damage these pests can inflict on crops.

Hosts: *Archips rosana* (Linnaeus, 1758), Tortricidae (Lepidoptera). It is effective on more than 150 known hosts (especially Lepidoptera) (Chambon, 1974; Aydoğdu, 2014).

DNA barcoding: Specimen I.8 exhibits a high similarity of 99.22% to *I. maculator* (MZ627044.1) in the NCBI database. The high similarity percentage suggests a close genetic relationship between the sampled specimen and *I. maculator*, supporting its accurate identification at the species level.

I.9. *Netelia testacea* (Gravenhorst, 1829)

Synonyms: =*Netelia ambiguator* Aubert, 1969, =*Netelia deserta* (Kokujev, 1915), =*Netelia fuscicarpus* (Kokujev, 1899), =*Netelia maltractata* (Roman, 1938), =*Netelia valvator* (Aubert, 1969), =*Paniscus fuscicarpus* (Kokujev, 1899), ≡*Paniscus testaceus* (Gravenhorst, 1829).

Examined: Van, Muradiye (N38° 57.082' E43° 39.849').

Distribution in Türkiye: Adana, Afyon, Adana, Bursa, Edirne, Elazığ, Erzincan, Eskişehir, Hatay, Istanbul, Izmir, Kayseri, Kırıkkale, Kırklareli, Manisa, Malatya, Muğla, Nevşehir, Osmaniye, Tekirdağ, Trabzon and Tunceli (Öncüer 1991; Kolarov, 1995; Kolarov et al., 1997; Özdemir, 2001; Yurtcan et al., 2006; Yaman, 2014; Yurtcan et al., 2021).

Global distribution: This species is distributed in more than 104 countries in Europe, Asia and Australia, such as Korea, the U.K. and Northern Ireland, Spain, France, Belgium, Germany, Iran, Sweden, Norway, Belarus, Finland (Yu et al., 2016; Riedel & Japoshvili, 2021; Anonymous, 2024).

Ecological Role

Netelia testacea typically parasitizes the larvae of various insects, often targeting pests that can be detrimental to crops. The female wasp lays her eggs on or inside the host larvae. Once the eggs hatch, the larvae of Netelia testacea develop within the host, eventually leading to the host's death. This process effectively helps control pest populations and mitigates the damage caused to agricultural crops.

Hosts: It has more than 62 hosts, such as *Polygonia egea* Cr. (Lepidoptera: Nymphalidae), *Acronicta rumicis* L. (Lepidoptera: Noctuidae) (Fahringer, 1922), *Pectinophora gossypiella* Saund. (Lepidoptera: Gelechiidae) (Yu et al., 2016).

DNA barcoding: The specimen I.9 shows a similarity of 92.89% to *N. testacea* (MZ628742.1) in the NCBI database. This similarity percentage indicates a moderate genetic relationship between the sampled specimen and *N. testacea*, aiding in the species identification process.

DISCUSSION and CONCLUSION

DNA barcoding has become a crucial tool for rapid and highly accurate identification of insect species, particularly in cases where there is a lack of expert taxonomists, time-consuming traditional methods, challenges in identifying immature stages, and difficulties distinguishing closely related species (Pentinsaari et al., 2014; Szyp-Borowska & Sikora, 2019; Yılmaz & Yeltekin, 2025). One of the key advantages of DNA barcoding is its ability to provide a more permanent and easily accessible inventory of species data. Unlike traditional morphological methods, which rely on physical specimens that can degrade over time, DNA barcodes are stored digitally and can be shared globally through databases such as the Barcode of Life Data System (BOLD) and NCBI. This digital permanence ensures that species data remain accessible for future research, conservation efforts, and biodiversity monitoring. Research has demonstrated that DNA barcoding can offer a standardized and efficient tool for insect species identification, with high success rates and substantial interspecific divergences (Pentinsaari et al., 2014). This method has proven especially effective in identifying insects where the vast diversity presents a significant challenge, such as the Ichneumonoidea, to conventional identification methods (Pentinsaari et al., 2014). A key benefit of DNA barcoding is its capacity to overcome the limitations of morphological identification, especially when dealing with morphologically similar species or different life stages (Virgilio et al., 2010). This capability is crucial in situations where precise identification is critical, such as in the context of insect pests and their natural enemies in agricultural environments (Pongen et al., 2023).

DNA barcoding has become a crucial tool for rapid and highly accurate insect species identification, particularly in cases where traditional morphological methods face limitations such as a critical shortage of expert taxonomists, unresponsiveness or excessive delays from specialists, time-consuming procedures, and difficulties in distinguishing closely related or cryptic species (Pentinsaari et al., 2014). In the present study, Ichneumonoidea species identification was conducted exclusively through DNA barcoding due to these compounding challenges, with specimens showing high sequence similarity to reference data in NCBI and BOLD databases—a methodology widely validated and accepted in contemporary taxonomy (Hebert et al., 2003; Smith et al., 2005). This method proves particularly valuable for taxonomically challenging groups like Ichneumonoidea, where small body size, morphological ambiguity, and cryptic diversity complicate conventional identification. The approach is further validated by studies showing 94% agreement between molecular and morphological identifications (Meier et al., 2006). Beyond overcoming expertise gaps, DNA barcoding generates permanent, digitally accessible species records in global databases (BOLD, NCBI), ensuring data availability for future research and conservation.

This study focused on the identification of species belonging to the Ichneumonoidea in alfalfa fields in Van and its surroundings and the effectiveness of DNA barcoding in overcoming taxonomic difficulties. Firstly, the study's meticulous sampling across various districts provided a comprehensive repository, aiding in the identification process. Weekly sweep net collections from May to August ensured that the sampling encompassed a broad spectrum of the species' active period. This approach clearly emphasizes the need for temporal comprehensiveness in faunistic studies. The genetic analysis revealed significant percentages of similarity between the collected samples and reference sequences in the NCBI database, and the species were distributed in their appropriate places on the phylogenetic tree with high bootstrap values. The collected samples exhibited strong molecular matches with the NCBI-registered species *Enizemum ornatum, Aleiodes similis*, *A. coxalis*, *Syrphoctonus elegans, Itoplectis maculator,* and *Bathyplectes curculionis*, with similarity rates of 99.80%, 99.61%, 99.52%, 99.24%, 99.22%, and 98%, respectively. This high genetic compatibility confirms the utility of DNA barcoding in rapidly identifying samples using NCBI-registered species. The study presented new records for Van Province, such as *A. similis*, *B. curculionis, E. ornatum,* and *S. elegans*. However, the two species whose definitive species identification could not be confirmed were found to be most similar to *Stibeutes brevicornis* and *Netelia testacea* with rates of 87.20% and 92.89%. Identifying these species marks a significant extension of their known geographical distributions, contributing to the biogeographical knowledge of Ichneumonoidea.

This augments the region's biodiversity inventory and provides crucial data for future ecological and conservation-oriented research. In addition, the phylogenetic analyses conducted reinforced the reliability of the species identification. The clustering pattern exhibited in the phylogenetic tree, supported by high bootstrap values, delineates clear genetic separations and evolutionary divergences among the species. Such robust phylogenetic frameworks are critical for understanding the evolutionary dynamics and ecological roles of parasitoids in agroecosystems.

Despite the significant advantages provided by DNA barcoding, its effectiveness can be limited by incomplete databases, technical challenges, and resolution issues. Therefore, it is best used as a complementary tool alongside the traditional method. The ecological implications of this study are manifold. The province of Van, with its pesticide-free or low-pesticide-use alfalfa fields, has a high density of parasitoid species, which play a key role in natural pest control. The identification of numerous Ichneumonoid species emphasizes their potential in sustainable agricultural practices. These parasitoids could be harnessed as biological control agents, reducing the dependency on chemical pesticides and promoting agroecological balance.

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Contribution Rate Statement Summary of Researchers

The authors declare that they have contributed equally to the article.

Conflict of Interest

The authors of the article declare that there is no conflict of interest between them.

REFERENCES

REFERENCES

Abdinbekova, A. (1963). The Ichneumonid fauna of the Kuba-Khachmassk zone of Azerbaidzhan. *Izvestiya Akademii Nauk Azerbaidzhanskoi SSR, 5*, 43-51.

Anonymous. (2024). *Open access to biodiversity data*. Global Biodiversity Information Facility, Copenhagen, Denmark. https://www.gbif.org/ (Accessed: 12.09.2024).

Aydoğdu, M. (2014). Parasitoid abundance of *Archips rosana* (Linnaeus, 1758) (Lepidoptera: Tortricidae) in organic cherry orchards. *North-Western Journal of Zoology, 10*(1), 42-47.

Aydoğdu, M., & Kanev, M. O. (2017). Üç Pestisitin Parazitoit Itoplectis maculator (Fabricius, 1775) (Hymenoptera: Ichneumonidae) Üzerine Toksisitesi. *Düzce Üniversitesi Bilim ve Teknoloji Dergisi, 5*(1), 184-192.

Beyarslan, A., Gadallah, N.S. & Ghahari, H. (2017). An annotated catalogue of the Iranian Microtypinae and Rogadinae (Hymenoptera: Braconidae). *Zootaxa, 4291*(1), 99-116. https://doi.org/10.11646/zootaxa.4291.1.6

Beyarslan, A. & Çakıcı, M. (2021). Contribution to the Rogadinae (Hymenoptera, Braconidae) fauna of Turkey. *Natura Somogyiensis, (37)*, 65-78. https://doi.org/10.24394/NatSom.2021.37.65

Birol, O. (2010). *Isparta İli Davraz Dağı Ichneumonidae (Hymenoptera) Faunası Üzerine Bir Araştırma (Tez no 268749)*. [Yüksek Lisans Tezi, Süleyman Demirel Üniversitesi Fen Bilimleri Enstitüsü]. Yükseköğretim Kurulu Ulusal Tez Merkezi.

Broad, G.R. (2016). Checklist of British and Irish Hymenoptera-Ichneumonidae. *Biodiversity Data Journal, 4*, e9042. https://doi.org/10.3897/BDJ.4.e9042

Chambon, J. (1974). Permanent Laboratory Rearing of *Itoplectis maculator* (Hym-Ichneumonidae) Parasite of *Cnephasia pumicana* Zell (Lep-Tortricıdae) on *Anagasta kuhniella* Zell (Lep-Pyralidae). *Revue De Zoologie Agricole Et De Pathologie Vegetale, 73*(4), 117-128.

Çoruh, S. (2005). *Erzurum ve Çevre İllerdeki Pimplinae (Hymenoptera: Ichneumonidae) Türleri Üzerinde Faunistik, Sistematik ve Ekolojik Çalışmalar (Tez no 171171).* [Doktora Tezi, Atatürk Universitesi Fen Bilimleri Enstitüsü]. Yükseköğretim Kurulu Ulusal Tez Merkezi.

Çoruh, S., Özbek, H., & Kolarov, J. (2007). Aras Vadisi (Kars)'ne yerleştirilen malezya tuzağından elde edilen Ichneumonidae (Hymenoptera) türleri. Türkiye II. Bitki Koruma Kongresi, Isparta, Türkiye, (27-29 Ağustos 2007).

Çoruh, S. (2016). Biogeography and host evaluation of the subfamily Pimplinae (Hymenoptera: Ichneumonidae) in Turkey. *Journal of the Entomological Research Society, 18*(2), 33-60.

Çoruh, S., Gürbüz, M.F., Kolarov, J., Yurtcan, M. & Özdan, A. (2013). New and Little-Known Species of Ichneumonidae (Hymenoptera) for the Turkish Fauna. *Journal of the Entomological Research Society, 15*(3), 71-83.

Çoruh, S., Kolarov, J. & Çoruh, İ. (2014). Ichneumonidae (Hymenoptera) from Anatolia. II. *Turkish Journal of Entomology, 38*(3), 279-290. http://dx.doi.org/10.16970/ted.15518

Çoruh, S. & Kolarov, J. (2010). Ichneumonidae (Hymenoptera) from Northeastern Turkey. I. *Bulletin of the Natural History Museum, 3*, 177-186.

Çoruh, S. & Kolarov, J. (2024). A taxonomical and biogeographical analysis of the fauna Metopiinae (Hymenoptera: Ichneumonidae) of Türkiye. *Kahramanmaraş Sütçü İmam Üniversitesi Tarım ve Doğa Dergisi, 27*(3), 622-634. https://doi.org/10.18016/ksutarimdoga.vi.1330418

Çoruh, S., Kolarov, J. & Özbek, H. (2014). The fauna of Ichneumonidae (Hymenoptera) of eastern Turkey with zoogeographical remarks and host data. *Journal of Insect Biodiversity, 2*(16), 1-21.

Dalan, M. & Çoruh, S. (2025). Türkiye Karlıova (Bingöl) Ichneumonidae (Hymenoptera) Biyoçeşitliliği. *Kahramanmaraş Sütçü İmam Üniversitesi, Tarım ve Doğa Dergisi, 28*(1), 132-153. https://doi.org/10.18016/ksutarimdoga.vi.1578935

Doğanlar, M. (1987). Erzurum ve çevresindeki elma ve armut ağaçlarında bulunan yaprakbükenler ve benzer şekilde beslenen diğer lepidopter'ler ile bunların parazitleri üzerinde araştırmalar. *Doğa Dergisi, 11*(1), 86-93.

Efil, L. (2018). The damage status of Alfalfa Weevil *Hypera variabilis* (Herbst, 1795) (Coleoptera: Curculionidae) in the alfalfa areas of Diyarbakır, Şanlıurfa, and Mardin provinces, and parasitoid *Bathyplectes curculionis* (Thomson, 1887) and parasitization. *Turkish Journal of Agricultural and Natural Sciences, 5*, 86-89.

Eroğlu, F., Kıraç, A. & Birol, Ö. (2011). A faunistic study on Ichneumonidae (Hymenoptera) in Türkmen Mountain, Turkey. *Linzer biologische Beiträge, 43*(2), 1219-1228.

Erol, T. & Yaşar, B. (1996). Van ili elma bahçelerinde bulunan zararlı türler ile doğal düşmanları. *Türkiye Entomoloji Dergisi, 20*(4), 281-293.

Flores, S., Nassar, J. M. & Quicke, D. L. (2005). Reproductive phenology and pre-dispersal seed-feeding in *Protium tovarense* (Burseraceae), with a description of the first known phytophagous "Bracon" species (Hymenoptera: Braconidae: Braconinae). *Journal of Natural History, 39*(42), 3663-3685. https://doi.org/10.1080/00222930500392659

Gomila, M., Prince-Manzano, C., Svensson-Stadler, L., Busquets, A., Erhard, M., Martínez, D. L., Lalucat, J. & Moore, E.R.B. (2014). Genotypic and Phenotypic Applications for the Differentiation and Species-Level Identification of Achromobacter for Clinical Diagnoses. *PLOS ONE, 9*(12), e114356. https://doi.org/10.1371/journal.pone.0114356

Gonzalez, D., Etzel, L., Esmaili, M., El-Heneidy, A. & Kaddou, I. (1980). Distribution of *Bathyplectes curculionis* and *Bathyplectes anurus* [Hym.: Ichneumonidae] from Hypera [Col.: Curculionidae] on alfalfa in Egypt, Iraq, and Iran. *Entomophaga, 25*, 111-121. https://doi.org/10.1007/BF02374313

Gözüaçık, C. & Kolarov, J. (2016). The Investigation on larval parasitoids of *Hypera postica* Gyllenhal, 1813) (Coleoptera: Curculionidae) and its parasitism rates in alfalfa Fields of Iğdır. *Bitki Koruma Kongresi*, 5-8.

Gözüaçık, C. (2019). Iğdır ili yonca alanlarında *Hypera postica* Gyllenhal (Coleoptera: Curculionidae)'nın larva parazitoiti *Bathyplectes curculionis* (Thompson) (Hymenoptera: Ichneumonidae) ve parazitlenme oranları. *Harran Tarım ve Gıda Bilimleri Dergisi, 23*(3), 295-300. https://doi.org/10.29050/harranziraat.515168

Greathead, D. J. (1986). Parasitoids in classical biological control. *Insect Parasitoids*, 289-318.

Gürbüz, M.F. (2004). *Isparta İli Ichneumonidae (Hymenoptera) Familyası Türleri Üzerine Faunistik ve Sistematik Araştırmalar (Tez no 184313)*. [Doktora Tezi, Süleyman Demirel Üniversitesi, Fen Bilimleri Enstitüsü]. Yükseköğretim Kurulu Ulusal Tez Merkezi.

Gürbüz, M.F. (2005). A survey of the Ichneumonidae (Hymenoptera) of Isparta in Turkey. *Linzer biologische Beiträge, 37*(2), 1809-1817.

Gürbüz, M.F., Aksoylar, M.Y. & Boncukçu, A. (2009). A faunistic study on Ichneumonidae (Hymenoptera) in Isparta, Turkey. *Linzer biologische Beiträge, 41*(2), 1969-1984.

Hebert, P.D., Cywinska, A., Ball, S.L., & DeWaard, J.R. (2003). Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London. Series B: Biological Sciences, 270*(1512), 313-321.

Horstmann, K. (2010). Revision der europäischen Arten von Stibeutes Förster, 1850 (Hymenoptera, Ichneumonidae, Cryptinae). *Entomofauna, 31*(15), 229-264.

Hubert, N., Hanner, R., Holm, E., Mandrak, N. E., Taylor, E., Burridge, M., Watkinson, D., Dumont, P., Curry, A., Bentzen, P., Zhang, J., April, J. &. Bentzen, P. (2008). Identifying Canadian freshwater fishes through DNA barcodes. *PLOS ONE, 3*(6), e2490. https://doi.org/10.1371/journal.pone.0002490

İren, Z. (1952). Türkiye'de yeni bulunan *Hyponomeuta padella* L. ve *Carpocapsa pomonella* L. parazitleri. *Bitki Koruma Bülteni, 4*, 16-18.

İren, Z. (1960). Ankara Bölgesinde Ağ Kurtları (Yponomeuta) Türleri, Arız Olduğu Bitkiler, Bu Türlerin Kısa Biyolojisi ve Mücadelesi Üzerinde Araştırmalar. *Zirai Vekili İlmi Rapor ve Araştırmalar, Seri. C, 4*, 141.

İren, Z. (1977). Önemli Meyve Zararlıları, Tanınmaları, Zararlıları, Yaşayışları ve Mücadele Metodları. *T.C. Gıda-Tarım ve Hayvan Bakanlığı, Ankara Bölge Zirai Mücadele Araştırma Enstitüsü Yayınları Mesleki Eserler Serisi, 36*, 167 pp.

Jasso-Martínez, J.M., Quicke, D.L., Belokobylskij, S.A., Meza-Lázaro, R.N. & Zaldívar-Riverón, A. (2021). Phylogenomics of the lepidopteran endoparasitoid wasp subfamily Rogadinae (Hymenoptera: Braconidae) and related subfamilies. *Systematic Entomology, 46*(1), 83-95. https://doi.org/10.1111/syen.12449

Kansu, A., Kılınçer, N., Uğur, A. & Gürkan, O. (1986) Ankara, Kırşehir, Nevşehir ve Niğde illerinde kültür bitkilerinde zararlı lepidopterlerin larva ve pupa asalakları, Türkiye I. Biyolojik Mücadele Kongresi (12-14 Şubat, Adana), 146-161.

Kasparyan, D. (1973). Review of Palearctic Ichneumonids of the tribe Pimplini (Hymenoptera, Ichneumonidae). The genera Itoplectis Foerster and Apechtis Foerster. *Entomologicheskoe Obozreniye, 52*(3), 665-681.

Kasparyan, D. (1974). On the fauna of ichneumonids (Hymenoptera, Ichneumonidae) of the Mongolian people's Republic. Tribes Pimplini, Tryphonini, genus Lycorina. *Insect of Mongolia, 2*, 250-258.

Khayrandish, M., Bakhtiarynasab, F. & Mohammadi-Khoramabadi, A. (2014). First record of *Homotropus elegans* (Hym.: Ichneumonidae: Diplazontinae) from Iran. *Journal of Entomological Society of Iran, 34*(2), 77. http://www.entsociran.ir/journal/browse.php?a_id=488&sid=1&slc_lang=en

Klopfstein, S. (2014). Revision of the Western Palaearctic Diplazontinae (Hymenoptera, Ichneumonidae). *Zootaxa, 3801*(1), 1-143. https://doi.org/10.11646/zootaxa.3801.1.1

Klopfstein, S., Langille, B., Spasojevic, T., Broad, G. R., Cooper, S. J., Austin, A. D. & Niehuis, O. (2019a). Hybrid capture data unravel a rapid radiation of pimpliform parasitoid wasps (Hymenoptera: Ichneumonidae: Pimpliformes). *Systematic Entomology, 44*(2), 361-383. https://doi.org/10.1111/syen.12333

Klopfstein, S., Riedel, M. & Schwarz, M. (2019b). Checklist of ichneumonid parasitoid wasps in Switzerland (Hymenoptera, Ichneumonidae): 470 species new for the country and an appraisal of the alpine diversity. *Alpine Entomology, 3*, 51-81. https://doi.org/10.3897/alpento.3.31613

Kolarov, J. (1987) Ichneumonidae (Hymenoptera) from Balkan peninsula and some adjacent regions. I. Pimplinae, Tryphoninae and Cryptinae. *Turkish Journal of Entomology, 11*(1), 11-26.

Kolarov, J. (1989). Ichneumonidae (Hymenoptera) from Balkan peninsula and some adjacent regions. II. Lissonotinae, Ctenopelmatinae, Tersilochinae, Cremastinae and Campopleginae. *Turkish Journal of Entomology, 13*(2), 67-84.

Kolarov, J. (1995). A Cataloque of the Turkish Ichneumonidae (Hymenoptera). *Entomofauna, 7*, 137-188.

Kolarov, J. & Beyarslan, A. (1994). Investigations on the Ichneumonidae (Hym.) fauna of Turkey. 1. Pimplinae and Tryphoninae. *Turkish Journal of Entomology, 18*(3), 133- 140.

Kolarov, J. & Beyarslan, A. (1995). New and little known Turkish Campopleginae (Hymenoptera: Ichneumonidae) 18-21. III. National Scientific Conference of Entomology (18-20 September, Sofia, Bulgaria) Proceedings.

Kolarov, J., Beyarslan, A. & Yurtcan, M. (1997). Ichneumonidae (Hymenoptera) from the Gokceada and Bozcaada Islands - Turkey. *Acta Entomologica Bulgarica, 3*(4), 13-15.

Kolarov, J., Özbek, H. & Yıldırım, E. (1999). New distributional data of the Turkish Ichneumonidae (Hymenoptera). I. Pimplinae and Tryphoninae. *Journal of the Entomological Research Society, 1*(2), 9-15.

Kolarov, J., Yurtcan, M. & Beyarslan, A. (2002). Ichneumonidae species of the Turkish Aegean Region. Parasitic wasps: evolution, systematics, biodiversity and biological control. International Symposium (14-17 May. 2001, Agroinform, Keszthely-Hungary), 299-305.

Kolarov, J., Coruh, S. & Coruh, I. (2016). Contribution to the knowledge of the Ichneumonidae (Hymenoptera) fauna of Turkey from northeastern Anatolia, Part I., *Turkish Journal of Zoology, 40*(1), 40-56. https://doi.org/10.3906/zoo-1501-38

Kolarov, J., Çoruh, S., & Çoruh, İ. (2020). Ichneumonidae (Hymenoptera) species from Anatolia, Part III. *Atatürk Üniversitesi Ziraat Fakültesi Dergisi, 51*(2), 168-175. https://doi.org/10.17097/ataunizfd.635494

Kolarov, J., Gürbüz, M.F. (2004). A study of the Turkish Ichneumonidae (Hymenoptera). Pimplinae. *Linzer biologische Beiträge, 36*(2), 841-845.

Korukcu, K. H. & Çoruh, S. (2024). Aras Vadisi Ichneumonidae (Hymenoptera) Biyoçeşitliliğine Katkılar. *Turkish Journal of Agricultural and Natural Sciences, 11*(4), 933-949. https://doi.org/10.30910/turkjans.1469845

Kondur, Y. & Şimşek, Z. (2016). Pupal Parasitoids of Green Oak Tortrix [*Tortrix viridana* L. (Lepidoptera: Tortricidae)] in Çankırı, Turkey. International Forestry Symposium, IFS2016, Kastamonu, Turkey.

Levi-Mourao, A., Lazarević, M., Parés-Casanova, P.M., Meseguer, R., Pons, X. & Žikić, V. (2025). Differentiation of two *Bathyplectes species, B. anurus* and *B. curculionis*, parasitoids of the Alfalfa weevil (*Hypera postica*) in Spain. *Bulletin of Entomological Research, 115*(6), 1-8. https://doi.org/10.1017/S000748532510028X

Lorenz, T. C. (2012). Polymerase chain reaction: basic protocol plus troubleshooting and optimization strategies. *Journal of Visualized Experiments, 63*, e3998. https://doi.org/10.3791/3998

Martinez, E., Alonso, V., Quispe, A., Thomas, M., Alonso, R., Pinero, J., Gonzalez, A. C., & Valladares, B. (2003). RAPD method useful for distinguishing Leishmania species: design of specific primers for L. braziliensis. *Parasitology, 127*(6), 513-517. https://doi.org/10.1017/S0031182003004104

Meier, R., Shiyang, K., Vaidya, G. & Ng, P. K. (2006). DNA barcoding and taxonomy in Diptera: a tale of high intraspecific variability and low identification success. *Systematic biology, 55*(5), 715-728. https://doi.org/10.1080/10635150600969864.

Meierotto, S., Sharkey, M.J., Janzen, D.H., Hallwachs, W., Hebert, P.D., Chapman, E. G. & Smith, M. A. (2019). A revolutionary protocol to describe understudied hyperdiverse taxa and overcome the taxonomic impediment. *Deutsche Entomologische Zeitschrift, 66*(2), 119-145. https://doi.org/10.3897/dez.66.34683

Menken, S. (1982). Enzymatic characterization of nine endoparasite species of small ermine moths (Yponomeutidae). *Experientia, 38*, 1461-1462.

Narmanlıoğlu, H. K. & Çoruh, S. (2017). Parasitoids of the apple ermine moth, *Yponomeuta malinellus* Zeller, 1838 (Lepidoptera: Yponomeutidae), in the Çoruh Valley, Erzurum Province, Turkey. *Turkish Journal of Entomology, 41*(4), 357-365. https://doi.org/10.16970/entoted.316858

Nelson, E. H., Matthews, C. E. & Rosenheim, J. A. (2004). Predators reduce prey population growth by inducing changes in prey behavior. *Ecology, 85*(7), 1853-1858. https://doi.org/10.1890/03-3109

Okyar, Z. & Yurtcan, M. (2007). Phytophagous Noctuidae (Lepidoptera) of the Western Black Sea Region and their ichneumonid parasitoids, *Entomofauna, 28*, 377-388.

Öncüer, C. (1991). Türkiye Bitki Zararlısı Böceklerinin Parazit ve Predatör Kataloğu. *Ege Üniversitesi, Ziraat Fakültesi Yayınları, 505*, 354.

Özdemir, Y. (2001). İç Anadolu Bölgesi'nde saptanan Diplazontinae ve Tryphoninae (Hymenoptera: Ichneumonidae) altfamilyası türleri. *Türkiye Entomoloji Dergisi, 25*(3), 183-191.

Özdemir, Y. & Kılınçer, N. (1990). İç Anadolu Bölgesinde Saptanan Pimplinae ve Ophioninae (Hym: Ich) Türleri. Türkiye II. Biyolojik Mücadele Kongresi, 26-29 Eylül Ankara, s: 309-318.

Özdemir, Y. & Özdemir, M. (2002). Orta Anadolu Bölgesinde *Archips* türlerinde (Lep.: Tortricidae) saptanan Ichneumonidae (Hym.) türleri. *Bitki Koruma Bülteni, 42*(1-4), 1-7.

Pentinsaari, M., Hebert, P.D. & Mutanen, M. (2014). Barcoding beetles: a regional survey of 1872 species reveals high identification success and unusually deep interspecific divergences. *PLOS ONE, 9*(9), e108651. https://doi.org/10.1371/journal.pone.0108651

Plećaš, M., Žikić, V., Kocić, K., Čkrkić, J., Petrović, A. & Tomanović, Ž. (2023). Diversity of parasitoid wasps (Insecta, Hymenoptera) in oilseed rape fields in Serbia. *Biodiversity Data Journal, 11*. https://doi.org/10.3897/BDJ.11.e110118

Pongen, A., Behere, G., Firake, D., Sharma, B. & Rajesh, T. (2023). DNA barcoding of major insect pests and their natural enemies from cucurbitaceous crops in northeast India. *Indian Journal of Entomology, 85*(1), 150-154. https://doi.org/10.55446/IJE.2022.4404

Quicke, D.L., Mori, M., Zaldivar-Riverón, A., Laurenne, N.M. & Shaw, M.R. (2006). Suspended mummies in Aleiodes species (Hymenoptera: Braconidae: Rogadinae) with descriptions of six new species from western Uganda based largely on DNA sequence data. *Journal of Natural History, 40*(47-48), 2663-2680. https://doi.org/10.1080/00222930601121288

Quicke, D.L., Alex Smith, M., Janzen, D.H., Hallwachs, W., Fernandez-Triana, J., Laurenne, N. M., & Klopfstein, S. (2012). Utility of the DNA barcoding gene fragment for parasitic wasp phylogeny (Hymenoptera:

Ichneumonoidea): data release and new measure of taxonomic congruence. *Molecular Ecology Resources, 12*(4), 676-685. https://doi.org/10.1111/j.1755-0998.2012.03143.x

Quicke, D.L. & Butcher, B.A. (2021). Review of venoms of non-polydnavirus carrying ichneumonoid wasps. *Biology, 10*(1), 50. https://doi.org/10.3390/biology10010050

Radcliffe, E. B. & Flanders, K. L. (1998). Biological control of alfalfa weevil in North America. *Integrated Pest Management Reviews, 3*, 225-242.

Rand, T.A. (2013). Host density drives spatial variation of the alfalfa weevil, *Hypera postica*, across dryland and irrigated alfalfa cropping systems. *Environmental Entomology, 42*, 116-122.

Ratnasingham, S. & Hebert, P.D.N. (2013). A DNA-based registry for all animal species: the Barcode Index Number (BIN) system. *PLOS ONE 8*, e66213. https://doi.org/ 10.1371/journal.pone.0066213

Ribes, A. (2012). Himenòpters de Ponent. http:// ponent.atspa ce.org/ fauna/ ins/ index.htm.

Reijo, J.N.S., Jin-Kyung, C., Hamid, S. & Angélica, M.P.D. (2021). A contribution to the study of Ichneumonidae (Hymenoptera: Ichneumonoidea) of Iran. *Iran Egyptian Journal of Plant Protection Research Institute, 4*(3), 458-472.

Riedel, M. & Japoshvili, G. (2021). New records of Ichneumonidae from Northwestern Sakartvelo (Georgia), with additions to the fauna of Lagodekhi reserve. *Linzer biologische Beiträge, 53*(1), 241-288.

Sarı, Ü. & Çoruh, S. (2018). Ichneumonidae (Hymenoptera) from Northeastern Anatolia Region (Erzurum, Aşkale). *Turkish Journal of Entomology, 42*(3), 215-228.

Savaris, M., Lampert, S., Lorini, L.M., Pereira, P.R.V.S. & Marinoni, L. (2015). Interaction between Tephritidae (Insecta, Diptera) and plants of the family Asteraceae: new host and distribution records for the state of Rio Grande do Sul, Brazil. *Revista Brasileira de Entomologia, 59*(1), 14-20. https://doi.org/10.1016/j.rbe.2014.11.002

Sharanowski, B.J., Ridenbaugh, R.D., Piekarski, P.K., Broad, G.R., Burke, G.R., Deans, A.R., Lemmon, A. R., Emily, C. Moriarty Lemmon, Gloria J. Diehl, & Whitfield, J.B. (2021). Phylogenomics of Ichneumonoidea (Hymenoptera) and implications for evolution of mode of parasitism and viral endogenization. *Molecular Phylogenetics and Evolution, 156*, 107023. https://doi.org/10.1016/j.ympev.2020.107023

Shaw, S., Marsh, P. & Fortier, J. (1997). Revision of North American Aleiodes Wesmael (Part 1): the pulchripes Wesmael species-group in the New World (Hymenoptera: Braconidae, Rogadinae). *Journal of Hymenoptera research, 6*, 10-35.

Smith, M.A., Fisher, B.L., & Hebert, P.D. (2005). DNA barcoding for effective biodiversity assessment of a hyperdiverse arthropod group: the ants of Madagascar. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *360*(1462), 1825-34. https://doi.org/10.1098 /rstb. 2005.1714. PMID: 16214741; PMCID: PMC1609228.

Snyder, W.E. & Ives, A.R. (2003). Interactions between specialist and generalist natural enemies: parasitoids, predators, and pea aphid biocontrol. *Ecology, 84*(1), 91-107. https://doi.org/10.1890/0012-9658(2003)084[0091:IBSAGN]2.0.CO;2

Soroka, J., Bennett, A.M., Kora, C. & Schwarzfeld, M.D. (2020). Distribution of alfalfa weevil (Coleoptera: Curculionidae) and its parasitoids on the Canadian Prairies, with a key to described species of Nearctic Bathyplectes (Hymenoptera: Ichneumonidae). *The Canadian Entomologist, 152*(5), 663-701. https://doi.org/10.4039/tce.2020.35

Szyp-Borowska, I. & Sikora, K. (2019). DNA barcoding: A practical tool for taxonomy and species identification of entomofauna. *Leśne Prace Badawcze / Forest Research Papers, 80*(3), 227-232. https://doi.org/10.2478/frp-2019-0021

Tek, S. E. & Okyar, Z. (2018). A contribution to the knowledge of parasitoids of insects associated with Rosaceae species from Edirne province, European Turkey. *Acta Biologica Turcica, 31*(3), 86-101.

Thomson, C.G. (1887). Opuscula. Entomologica*, 13,* 1301-1302.

Tokuhira, T., Ono, S., Fernández-Triana, J.L., Shımızu, S., Yokoyama, T. & Maeto, K. (2022). Discovery of a New Endoparasitoid Wasp (Hymenoptera: Braconidae: Microgastrinae) on Bombyx Larvae (Lepidoptera: Bombycidae) from Japan. *Esakia, 55*, 31-40. https://doi.org/10.5109/6610220

TUIK. (2021). Turkish Statistical Institute Reports. Retrieved from http://www.tuik.gov.tr. Access date: 15.03.2023:

Ulu, O. (1983). *Archips* (Cacoecia) spp. (Lepidoptera, Tortricidae) as a Pest on Some Fruit Trees in İzmir and Manisa province; Investigations on its Species, Their Identifications, Hosts, Distributions and Biologies. Bornova Bölgesi, Zirai Mucadele Arastirma Enstitüsü Müdürlüğü, Araştırma Eserleri, 45: 165 pp.

Vas, Z. (2020). New species and records of Ichneumonidae (Hymenoptera). *Folia entomologica hungarica, 81*, 95-104. https://doi.org/10.17112/FoliaEntHung.2020.81.95

Vilhelmsen, L., Miko, I. & Krogmann, L. (2010). Beyond the wasp-waist: structural diversity and phylogenetic significance of the mesosoma in apocritan wasps (Insecta: Hymenoptera). *Zoological Journal of the Linnean Society, 159*(1), 22-194. https://doi.org/10.1111/j.1096-3642.2009.00576.x

Veijalainen, A., Wahlberg, N., Broad, G.R., Erwin, T.L., Longino, J. T. & Sääksjärvi, I. E. (2012). Unprecedented ichneumonid parasitoid wasp diversity in tropical forests. *Proceedings of the Royal Society B: Biological Sciences, 279*(1748), 4694-4698. https://doi.org/10.1098/rspb.2012.1664

Virgilio, M., Backeljau, T., Nevado, B. & De Meyer, M. (2010). Comparative performances of DNA barcoding across insect orders. *BMC Bioinformatics, 11*, 1-10. https://doi.org/10.1186/1471-2105-11-206

Yaman, G. (2014). *Türkiye Tryphoninae (Hymenoptera: Ichneumonidae) türlerinin kontrol listesi (Tez no 373024)*. [Yüksek Lisans Tezi, Trakya Üniversitesi Fen Bilimleri Enstitüsü]. Yükseköğretim Kurulu Ulusal Tez Merkezi.

Yefremova, Z., Ebrahim, E. & Yegorenkova, E. (2007). The subfamilies Eulophinae, Entedoninae and Tetrastichinae in Iran, with description of new species (Hymenoptera: Eulophidae). *Entomofauna, 28*, 321-356.

Yılmaz, A. & Yeltekin, Y. (2023). Phylogenetic Relationships of The Trifolium L. Species Based on cpDNA Sequences. *Kahramanmaraş Sütçü İmam Üniversitesi Tarım ve Doğa Dergisi, 26*(2), 299-306. https://doi.org/10.18016/ksutarimdoga.vi.1095219

Yu, D.S., Kokko, E.G., Barron, J.R., Schaalje, G.B. & Gowen, B.E. (1992). Identification of ichneumonid wasps using image analysis of wings. *Systematic Entomology, 17*(4), 389-395. https://doi.org/10.1111/j.1365-3113.1992.tb00558.x

Yu, D.S., Van Achterberg, K. & Horstmann, K. (2005). Taxapad, World Ichneumonoidea 2004. Taxonomy, Biology, Morphology, and Distribution. (CD-ROM).

Yu, D. S., van Achterberg, C. & Horstmann, K. (2012). Taxapad, World Ichneumonoidea 2011. Database on a flash drive. Ottawa, Canada.

Yu, D.S., Van Achterberg, C. & Horstmann, K. (2016). Taxapad, Ichneumonoidea. 09.05.2022, https://www.catalogueoflife.org/data/dataset/1068.

Yu, D.S. (2024). Taxapad Ichneumonoidea (version May 2009). In O. Bánki, Y. Roskov, M. Döring, G. Ower, D. R. Hernández Robles, C. A. Plata Corredor, T. Stjernegaard Jeppesen, A. Örn, T. Pape, D. Hobern, S. Garnett, H. Little, R. E. DeWalt, K. Ma, J. Miller, T. Orrell, R. Aalbu, J. Abbott, C. Aedo, et al., Catalogue of Life (Version 2024-12-19). Catalogue of Life, Amsterdam, Netherlands. https://doi.org/10.48580/dgjc7-39v

Yurtcan, M. & Beyarslan, A. (2005). Polysphinctini and Pimplini (Hymenoptera: Ichneumonidae: Pimplinae) from the Thrace region of Turkey. *Fragmenta Faunistica*, *48* (1), 63-72.

Yurtcan, M., Kolarov, J. & Beyarslan, A. (2006). Tryphoninae Species from the Turkish Aegean Region (Hymenoptera, Ichneumonidae). *Linzer biologische Beiträge, 38*(1), 985-990.

Yurtcan, M., Çoruh, S., Kolarov, J., Özdan, A.B., Gürbüz, M.F. & Erkaya, I. (2021). Ichneumonidae (Hymenoptera) Fauna of Natural Protection Areas in the Eastern Mediterranean Region of Turkey, Part II. *Entomological News, 129*(5), 453-471. https://doi.org/10.3157/021.129.0501