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Assessing species richness of the subfamily Campopleginae (Hymenoptera, Ichneumonidae) community in Darab damask rose rain-fed plain, Fars province, Iran

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ABSTRACT. Here, the species richness of Campopleginae, a diverse subfamily of the Darwin wasps was studied in an almost organic damask rose plain located at 2600 m a.s.l., the south of Iran. Sampling was done using four Malaise traps for six months from April–October 2019. The total sampling efforts were 18 trap months. The integrated approach was used to assess the sample completeness profile, to infer true diversities of entire assemblages via asymptotic diversity estimates, to standardize the sample coverage via rarefaction and extrapolation, and to infer diversity via an evenness profile. I also used Homogenous, Homogenous (*MLE*), *Chao1*, *Chao1-bc*, *iChao1*, *ACE*, *ACE-1*, *1st order jackknife*, and *2nd order jackknife* to estimate the species richness of the studied Campopleginae community. Malaise traps yielded 491 individuals belonging to 24 morphospecies. *Diadegma majale* (Gravenhorst, 1829) included 64.7% of the total individuals collected, representing the highly dominated species. The estimated sample completeness profile showed that our data covers 59% of the total species in this community and thus 41% of species are undetected. The values for Shannon and Simpson diversity indices are 4.53 and 2.29, respectively. The models and non-parametric estimators estimated the species richness of Campoplegines from 24 – 50 species. This study provides a wealth of baseline data for the subfamily Campopleginae in the south of Iran in terms of biological control and conservation.

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INTRODUCTION

To quantify and compare biodiversity across multiple assemblages in individual-based biological surveys, it should first quantify sample completeness of the considered biological survey and assess the undetected diversity (Chao et al., 2020). Communities usually consist of some very abundant or dominant, some moderately common, and the majority remaining rare species. In poorly documented and highly diverse taxa, measuring the true species richness can be affected by limited practical sampling efforts and biodiversity inventories. The best approach is the estimate of species richness. Extrapolation of accumulation curves, parametric methods, and non-parametric estimators are the three approaches

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(Chao, 1984; Chao et al., 2009, 2014; Chao & Jost, 2012, 2015; Magurran, 2004). Recently, an integrated approach based on the framework of Hill numbers was proposed by Chao et al. (2020). This recommended novel procedure was developed in a four-step analysis to assess sample completeness based on incomplete abundance and incidence data, compare diversity and evenness among assemblages. *Step 1* assesses the sample completeness ($q = 0$), the detected and undetected species ($q = 1$) and detected highly abundant species ($q = 2$). In *step 2*, via size-based rarefaction and extrapolation analysis, the asymptotic diversity is estimated for species richness ($q = 0$), Shannon diversity ($q = 1$), and Simpson diversity ($q = 2$), the three most widely used diversity indices. In *step 3* the sample coverage is standardized for any fair comparisons among communities and finally *step 4* computes the evenness profile for the Maximum standardized coverage C_{max} , for diversity orders $0 < q \leq 2$.

The Darwin wasps of Ichneumonidae with over 100,000 estimated species are abundant and have an extremely large constitution of biodiversity and key species in functioning ecosystems (Arman et al., 2011; Hopkins, 2021). Campopleginae Förster is one of the most diverse subfamilies of this family, consisting of more than 2500 known species into 66 genera (Vas et al., 2022; Yu et al., 2016). Members of this subfamily are mainly solitary koinobiont parasitoids of Lepidoptera and less commonly Coleoptera larvae and may be known as promising biological control candidates for some agricultural pests (Quicke, 2015; Scaramozzino et al., 2018; Shaw et al., 2016; Abedi et al., 2020; Bagheri et al., 2020; Di Giovanni et al., 2021; Soroka et al., 2020). One of the most important biological characteristics of campoplegines is that they are polyphagous in their host range because of the injection of polydnaviruses along with their eggs which help them to feed on a broad spectrum of Lepidoptera species (Shaw et al., 2016; Stireman & Shaw, 2022). Ecologically, they are usually an abundant and species-rich group among the other Ichneumonidae subfamilies (Hopkins, 2021; Kendall & Ward, 2016; Mazón & Bordera, 2008, 2014; Peck et al., 2008; Riedel et al., 2021; Skillen et al., 2000; Stireman & Shaw, 2022; Veijalainen et al., 2013, 2014). This may be considered in their ecological services in agroecosystems in pest control and keeping their host populations below the economic injury level (Losey & Vaughan, 2006).

The Zagros as the biggest Mountain range in Iran is a large part of the Irano-Anatolian biodiversity hotspot and one of the main areas of endemism in Iran (Noroozi, 2020; Noroozi et al., 2021). Although plant and vegetation diversity of this wide highland territory have been discovered a long time ago, biodiversity, collection, and identification of the Darwin wasps have been limited to scattered faunistic studies. The two main surveys were conducted during 2011–2013 in Fars province (Amiri et al., 2017) and 2014–2018 in Khuzestan, Markazi, and Zanjan provinces yielded several newly recorded and new endemic species (Riedel et al., 2019a) to the ichneumonid fauna of Iran.

Fars province is located in the south of the Zagros Mountain range. Due to the vast fertile area, suitable and diverse climate, and topography, it has the first ranked in many agricultural products of Iran. Darab damask rose plain is the largest region in the world for cultivating *Rosa damascena* under rain-fed and almost organic conditions covering ca. 5300 hectares (Ebadzadeh et al., 2018). The high quality and commercial value of buds and flowers, rose oil, essential oil, hips, and other by-products encourage farmers to expand the area of rose cultivation by land-use changing, resulting in a negative impact on the unique species-rich natural vegetation type, *Juniperus-Amygdalus-Pistacia* Shrublands, of this region (Krashevska et al., 2022; Noroozi, 2020). On the other hand, outbreaks or increasing populations of the rose pests and diseases e.g. Rose plum moth, and Rosaceae branch borer may occur (Mohammadi-Khoramabadi & Khayrandish, 2021; Nematollahi, 2018). Good knowledge of the natural enemies and other beneficial insects may help us to conserve this ecosystem and to control pests in a sustainable approach (Bianchi et al., 2006; Letourneau et al., 2009; Losey & Vaughan, 2006). The aims of this study were (1) to provide baseline data for Campopleginae diversity in the south of Iran, Zagros Mountain ranges and (2) to quantify and estimate the species richness of Campopleginae wasps in the Darab damask rose plain.

MATERIAL AND METHODS

Study area and sampling procedure. This study was conducted at Darab damask rose plain ($28^{\circ} 41' N$, $54^{\circ} 53' E$, 2570–2650m a.s.l.), Fars province, the south of Iran (Fig. 1A). Considering the available roads and logistic facilities, we selected a 500-hectares site to install Malaise traps (Figs 1B, 1C). Malaise traps are known as effective tools for collecting Ichneumonidae (Karlsson et al., 2020; Mazón & Bordera, 2008; McCravy, 2018; van Achterberg, 2009). I installed four Malaise traps (T1: $28^{\circ}42'01''N$, $54^{\circ}54'13''E$, 2615 m a.s.l.; T2: $28^{\circ}42'15''N$, $54^{\circ}54'14''E$, 2641 m a.s.l.; T3: $28^{\circ}41'27''N$, $54^{\circ}55'21''E$, 2571 m a.s.l.; T4: $28^{\circ}42'38''N$, $54^{\circ}53'17''E$, 2646 m a.s.l. (Fig. 1B) in the Darab damask rose plain during a complete field season (6 months) from April to early October 2019 (Fig. 1D). They were aligned on a north-south axis. The 1-litter volume collection container of traps was filled with 70% ethanol as a killing and preservation medium. They were emptied at biweekly intervals. To prevent and minimize alcohol evaporation from the containers, the collecting jars were covered by an aluminum sheet. Malaise traps T3 and T4 were destroyed completely during April and May and thus the total sampling effort was 18 Malaise trap months (MTM), a convenient expressed term (Gómez et al., 2017).

Sample processing, species mounting, and identification. All Campopleginae species were dried using the AXA method and then pinned or card-mounted (van Achterberg, 2009). They were then sorted into morphospecies and identified to the species level whenever possible by Zoltán Vas (Hungarian Natural History Museum). Some campoplegine males could not be placed in morphospecies and therefore were excluded. The voucher specimens were deposited in the Hungarian Natural History Museum, Hungary, and the Insect Museum of Darab College of Agriculture and Natural Resources, Shiraz University.

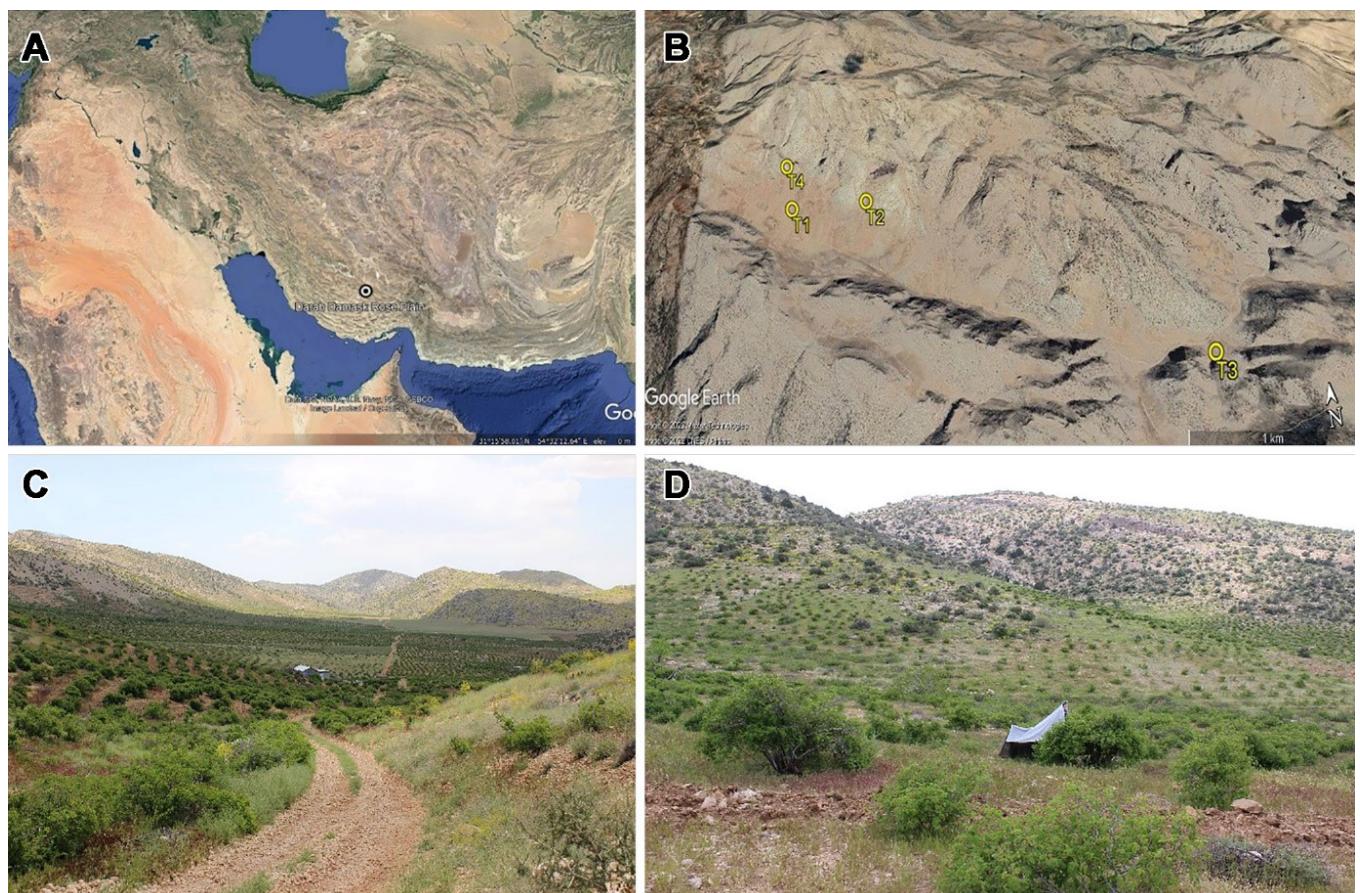


Figure 1. Darab damask rose plain, Fars province, south of Iran, 2019. **A.** Location in Iran; **B.** Location of Malaise traps; **C.** Overall vegetation; **D.** An installed Malaise trap.

Statistical analyses. The relative abundance (D) of each species was measured as:

$$D = \frac{b}{a} \times 100$$

Where, b = number of the individuals of the species and a = number of the individuals of all species. Dominance class of each species was followed Engelmann's (1978) procedure. Eudominant (Eu): species with over 32–100% of all collected individuals; dominant (Do): 32–10%; subdominant (Sd): 10–3.2%; recendent (Rc): 3.2–1%; subrecendent (Sr): 1–0.32%; and sporadic (Sp): less than 0.32% of all individuals. We used the four-step procedure proposed by Chao et al. (2020) to evaluate (a) the sampling completeness, (b) to infer the true diversity of our entire campoplegine community via asymptotic diversity estimate, (c) non-asymptotic standardization via rarefaction and extrapolation, and (d) an evenness profile (https://chao.shinyapps.io/inext_4steps). The 95% confidence intervals were obtained from a bootstrap method with 100 replications.

Non-parametric/Model estimators. Two models; Homogenous and Homogenous (MLE); and seven non-parametric estimators of *Chao1*, *Chao1-bc*, *iChao1*, ACE (Abundance-based Coverage Estimator), ACE-1, 1st order jackknife, and 2nd order jackknife were used to estimate the species richness of Campopleginae community under statistical online SPADE (Species Prediction and Diversity Estimation) (<https://chao.shinyapps.io/SpadeR/>) (Chao & Shen, 2016). The 95% confidence intervals were obtained from a bootstrap method with 100 replications.

RESULTS

Observed species richness and community structure. Out of 631 Ichneumonidae specimens collected, 491 individuals were Campopleginae, belonging to the genera *Diadegma* (8), *Hyposoter* (4), *Casinaria* (2), *Campoletis* (2), *Campoplex* (2), *Alcima* (1), *Venturia* (1), *Meloboris* (1), *Melalophacharops* (1), *Enythus* (1), *Lemophagus* (1), totally 24 species. Table 1 lists the species recorded, including their raw abundance and the degree of dominance. *Diadegma majale* (Gravenhorst, 1829) was highly dominant (Eudominant). Four species including *Campoletis scyticus* Riedel, 2017, *Casinaria ischnogaster* Thomson, 1887, *Diadegma* sp.1, and *Venturia canescens* (Gravenhorst, 1829) with 9.57–3.46% of the collected individuals were subdominant (Table 1). Singletons and doubletons were represented by 10 (41.67%) and 3 (12.5%) of all species sorted, respectively (Fig. 2). The flight period of the most abundant Campopleginae species (relative abundance $\geq 1\%$ of total collected individuals) of Darab damask rose plain showed that with one exception in *V. canescens*, the others (*D. majale*, *C. scyticus*, *C. ischnogaster*, *D. semiclausum* and *M. collector*) are active during May and June (Table 2). The integrated four-step procedure was implemented for the evaluation of (a) the sampling completeness, (b) to infer the true diversity of our entire campoplegine community via asymptotic diversity estimate, (c) non-asymptotic standardization via rarefaction and extrapolation, and (d) an evenness profile.

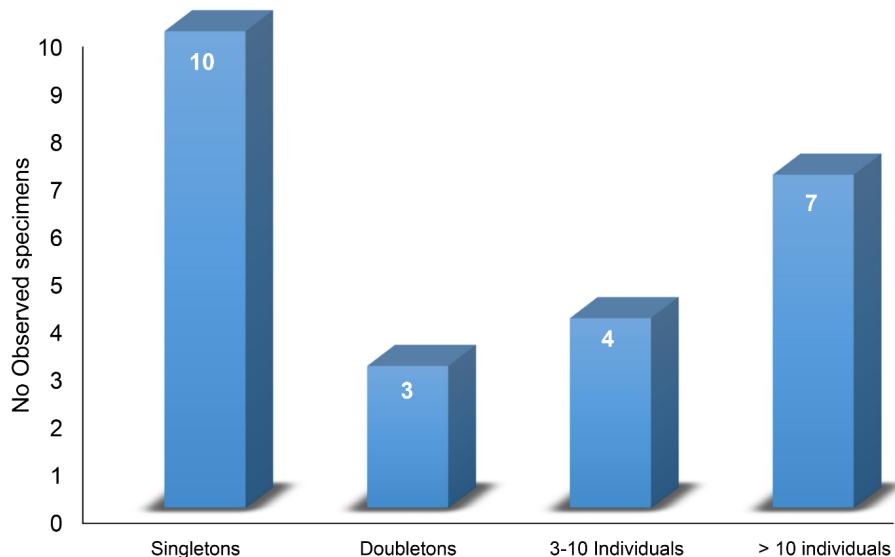
Step 1. Assessment of Sample completeness Profiles (Fig. 3A, Table 3). Figure 3A shows that the estimated sample completeness profile is increasing with diversity order, indicating that there are many undetected species within the dataset. Based on the corresponding values for $q = 0$, our data covers 59% of the total species in this community and thus 41% of species are undetected (Table 3). The detected and undetected species cover 98% and 2% of this community's individuals ($q = 1$, 98%), respectively. Almost all of the highly abundant species of Campopleginae are detected ($q = 2$, 99.9%).

Step 2. Size-based rarefaction and extrapolation analysis and the asymptotic diversity profiles (Figs 3B, 3C, Table 3). The size-based rarefaction and extrapolation curve for a diversity of order $q = 0$, extrapolated up to double the reference sample size (982), does not stay at a fixed level (Fig. 3B) suggesting that the current data do not contain sufficient information to accurately estimate the true species richness in our community. However, the curves for the diversity of orders $q = 1$ and 2 stabilize, indicating that our asymptotic diversity estimates for these two measures work satisfactorily to infer true diversities.

Table 1. Campopleginae of Darab damask rose plain, Fars province, ranked in order of abundance, 2019.

	Species	Raw abundance (No.)	Relative abundance (%)	Dominance*
1	<i>Diadegma majale</i> (Gravenhorst, 1829)	318	64.77	Eu
2	<i>Campolethis scyticus</i> Riedel, 2017	47	9.57	Sd
3	<i>Casinaria ischnogaster</i> Thomson, 1887	34	6.92	Sd
4	<i>Diadegma</i> sp.1	18	3.67	Sd
5	<i>Venturia canescens</i> (Gravenhorst, 1829)	17	3.46	Sd
6	<i>Diadegma semiclausum</i> (Hellén, 1949)	12	2.44	Rc
7	<i>Hyposoter</i> sp.1	11	2.24	Rc
8	<i>Meloboris collector</i> (Thunberg, 1822)	7	1.43	Rc
9	<i>Diadegma fenestrale</i> (Holmgren, 1860)	4	0.81	Sr
10	<i>Campoplex</i> sp.1	4	0.81	Sr
11	<i>Diadegma</i> sp.2	3	0.61	Sr
12	<i>Alcima orbitale</i> (Gravenhorst, 1829)	2	0.41	Sr
13	<i>Melalophacharops persicus</i> Vas, 2022	2	0.41	Sr
14	<i>Enythus apostatus</i> (Gravenhorst, 1829)	2	0.41	Sr
15	<i>Casinaria trochanterator</i> Aubert, 1960	1	0.20	Sp
16	<i>Campoletis zonata</i> (Gravenhorst, 1829)	1	0.20	Sp
17	<i>Lemophagus foersteri</i> (Tscheck, 1871)	1	0.20	Sp
18	<i>Campoplex</i> sp.2	1	0.20	Sp
19	<i>Diadegma</i> spp. (3 species)	3	0.20	Sp
20	<i>Hyposoter</i> spp. (3 species)	3	0.20	Sp
24 morphospecies		491	100	-

* Dominance class is indicated by: Eu (eudominant), Sd (subdominant); Rc (recedent); Sr (subrecedent); Sp (sporadic).

**Figure 2.** Community structure of Campopleginae in Darab damask rose plain, Fars province, 2019.

The undetected species richness for this dataset is at least 16.63 (40.63–24) ($\geq 40.9\%$) (Species richness for $q = 0$) (Fig. 3C, Table 3). The values for Shannon ($q = 1$) and Simpson ($q = 2$) diversity indices are 4.53 and 2.29, respectively. The undetected Shannon and Simpson diversity within the data are 0.19 and 0 (Table 3), implying that nearly all abundant and highly abundant species were detected through our sampling.

Table 2. The flight period of the most abundant Campopleginae species (relative abundance $\geq 1\%$ of total collected individuals) in Darab damask rose plain, Fars province, Malaise trapping, 2019.

Species	April	May	June	July	August	September
<i>Diadegma majale</i>						
<i>Campolethis scyticus</i>						
<i>Casinaria ischnogaster</i>						
<i>Diadegma</i> sp.1						
<i>Venturia canescens</i>						
<i>Diadegma semiclausum</i>						
<i>Hyposoter</i> sp.1						
<i>Meloboris collector</i>						

Step 3. Non-asymptotic coverage-based rarefaction and extrapolation analysis. Based upon the previous step, our sampling data do not contain sufficient information to accurately infer true diversity for any comparisons. For any fair comparisons among Campopleginae communities, the sample coverage was standardized in this step (comparing diversity for a standardized fraction of an assemblage's individuals). The value for C_{max} was defined as 98.9% (the level of coverage reached by the sample that attains the lowest coverage when all samples are extrapolated to double the reference sample size) (Table 3, Step 3). At the Maximum standardized coverage $C_{max} = 98.9\%$, the values for $q = 0$ (species richness), $q = 1$ (Shannon diversity) and $q = 2$ (Simpson diversity) were 31.51, 4.44 and 2.29, respectively (Table 3, Fig. 3D).

Step 4. For diversity orders $0 < q \leq 2$, the evenness profile (Fig. 3E) are computed for $C_{max} = 98.9\%$. The value for Pielou J' is low (0.43) (Table 3).

Non-parametric estimators. The models and non-parametric estimators estimated the species richness of campoplegines in the studied area as following: Homogenous model (31.08 ± 4.89); Homogenous (MLE): (24.00 ± 1.65); Chao1 (Chao, 1984): (40.63 ± 14.82); Chao1-bc: (35.23 ± 9.54); iChao1 (Chiu et al. 2014): (41.79 ± 11.79); ACE (Chao & Lee, 1992): (40.64 ± 12.02); ACE-1 (Chao & Lee, 1992): (50.04 ± 22.91); 1st order jackknife: (33.98 ± 4.47); 2nd order jackknife: (40.96 ± 7.73) (Fig. 4). This implies that additional sampling would yield a considerable number of new species to the local campoplegine richness. The reason for the highly increased value of estimation is the high number (17) of rare species with ≤ 10 individuals (cut-Off point=10) in the reference sample data (Table 1, Fig. 2).

Table 3. The numerical values for the three special cases $q = 0, 1$ & 2 for abundance-based Campopleginae collected from Darab damask rose plain, Fars province, 2019.

Step 1. Sample completeness profile			
Sample completeness	$q = 0$	$q = 1$	$q = 2$
	59%	98%	99.9%
Step 2. Asymptotic analysis			
Diversity	$q = 0$ (species richness)	$q = 1$ (Shannon diversity)	$q = 2$ (Simpson diversity)
Asymptotic estimator	40.63	4.53	2.29
Empirical	24	4.34	2.29
Undetected	16.63	0.19	0
Step 3. Non-asymptotic coverage-based rarefaction and extrapolation			
Maximum standardized coverage $C_{max} = 98.9\%$			
Diversity	$q = 0$ (species richness)	$q = 1$ (Shannon diversity)	$q = 2$ (Simpson diversity)
	31.51	4.44	2.29
Step 4. Evenness among species abundance			
Evenness	Pielou J'	$q = 1$	$q = 2$
	0.43	0.11	0.04

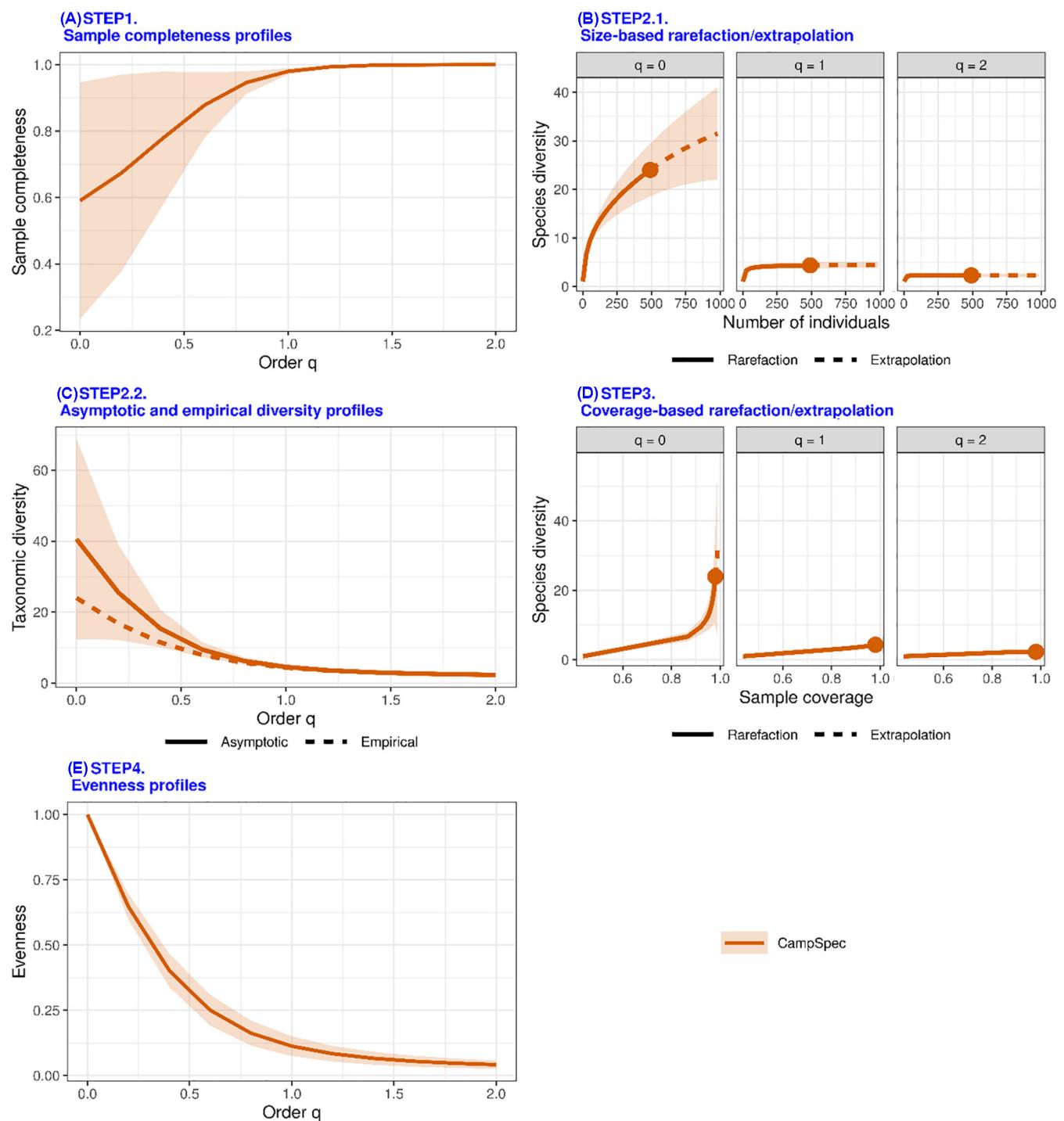


Figure 3. A. The plot of sample completeness curve as a function of order q between 0 and 2 in the reference sample data ($S_{obs} = 24$, $n = 491$) for Campopleginae of Darab damask rose plain, Iran, 2019; **B.** Sample-size-based rarefaction (solid lines) and extrapolation curves (dashed lines) up to size 982 for Campopleginae sample data to allow better visualization; **C.** The asymptotic estimates of diversity profiles (solid lines) and empirical diversity profiles (dotted lines); numerical values refer to the estimated asymptotic diversities; **D.** Coverage-based rarefaction (solid lines) and extrapolation (dashed lines) curves up to the corresponding coverage value for size 982; **E.** Evenness profile as a function of order q , for $0 < q \leq 2$, based on the normalized slope of Hill numbers. Solid dots and triangles denote observed data points. All shaded areas in **A-D**. Denote 95% confidence bands obtained from a bootstrap method with 100 replications.

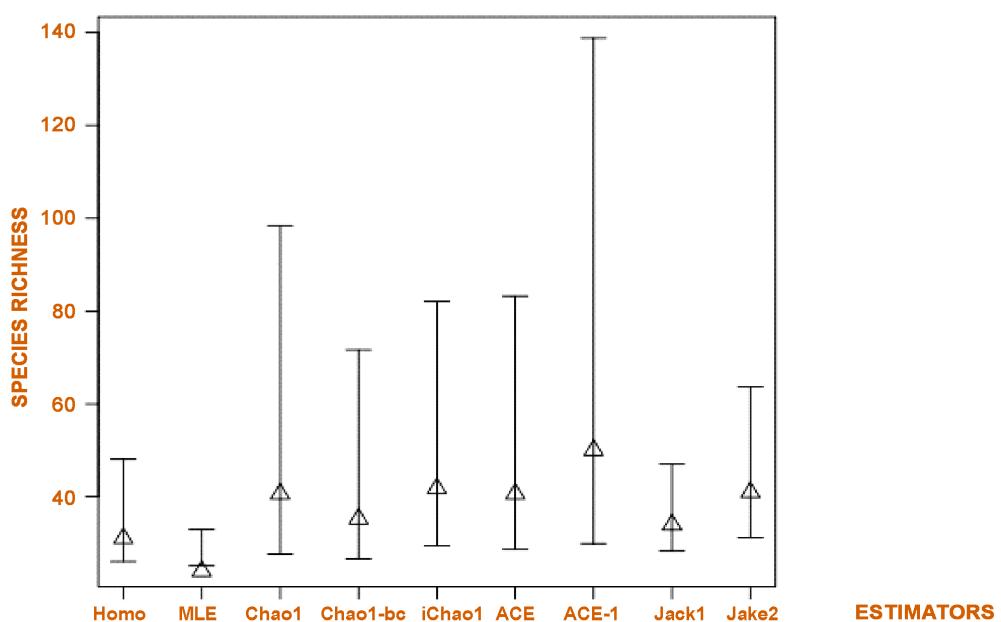


Figure 4. Comparison of estimators for Campopleginae community in Darab damask rose plain, Fars province (Iran), 2019. Triangles represent the estimated species richness \pm 95% confidence intervals obtained from a bootstrap method with 100 replications.

DISCUSSION

This study provides the first biodiversity overview of the Campopleginae species in Darab damask rose plain, a unique organic plantation at the high elevation of ca. 2600 m a.s.l. in Iran. The number of observed species was 24, making up 26.96% of the Iranian Campopleginae fauna (89 known Iranian Campopleginae species) (Barahoei et al., 2012; Riedel et al., 2019a; 2019b). It is about 60% of the estimated species richness (about 40 species) of this subfamily (Fig. 4), here. This may be a sign of a wide and intensive discovery of the fauna of Campopleginae in the high mountain ranges of Zagros, Iran. The asymptotic (Table 3, Step 2) and non-parametric estimators (Fig. 4) assumed a significantly higher value of species richness than the reference collecting data during 2019. This is because of the high percentage (70.83%) of rare species (cutting-off point = 10) and low sample size (491 individuals). The highly-abundant and abundant species were most likely captured (Table 3, Steps 1 and 2), but, it may suggest that our four Malaise trap-years cannot provide sufficient data to estimate the true species richness of the megadiverse Campopleginae community. Skillen et al. (2000) found 1487 Campopleginae individuals during 1992–1993 using 10 Malaise traps in five old-growth forests (two in each forest site). They collected 95 Campopleginae species ranging from 9–49 species with their corresponding abundance of 20–572 individuals in their surveyed sites. Using non-parametric estimators, the median species richness of the Campopleginae community was estimated at 43, 47, 67, 42, and 27 species in Shaw woods (Ontario), Patuxent (Maryland), Hitchiti (Georgia), Tall timbers (Florida), and San Felasco (Florida), respectively. Due to the small population size and being seasonal activity of rare Ichneumonid species, and very variable catches of Ichneumonidae by Malaise traps (Gómez et al., 2017), getting a better picture of Campopleginae life in this region and any other site, require more extensive and long-term samplings.

In term of biological control, the five most abundant Campopleginae in the studied area were two species of the genus *Diadegma*, *C. scyticus*, *C. ischnogaster*, and *V. canescens* (Table 1). Reliable identification of the collected *Diadegma* spp. need future taxonomical and revision studies on this diverse genus in the Palaearctic. *Diadegma majale* is a well-known and effective biological control agent for some Microlepidopteran agricultural pests, such as DBM (*Plutella xylostella* (L.) (Fathi et al., 2012). *Campoletis*

scyticus have been distributed in Iran, Afghanistan, Bulgaria, Turkey, Kazakhstan, Kyrgyz Republic, Turkmenistan, and Morocco (Vas, 2019). Although it has not been documented any host record for this species, it may attack some Lepidoptera in the families Noctuidae, Nymphalidae, or Pterophoridae, similar to other species of the genus *Campoletis* (Bhosale & Salunkhe, 2022; Shaw et al., 2016). Considering the potential for mass rearing of some species of this genus in biological control programs of major agricultural pests (Bhosale & Salunkhe, 2022), future attempts to the determination of the host (s) of this species will be valuable. *Casinaria ischnogaster* has been recorded in some European countries, Far Eastern Russia, and recently Iran with some known hosts in the families Noctuidae and Geometridae (Glavendekić, 2010; Riedel, 2018). *Venturia canescens* is a well-studied and laboratory-reared parasitoid attacking a broad range of moths of the family Pyralidae in both stored products and fruits (Andreadis et al., 2014; Bagheri et al., 2020). The high abundance of *V. canescens* in this agroecosystem, may indicate its adaptability to the environmental conditions of this region and thereby potential use for inundative release programs against caterpillars if any outbreaks occur.

In recent decades, the natural vegetation type of this region has been under great pressure from anthropogenic activities such as land-use changing, grafting almond trees, plowing, fire, deforestation, and cutting down trees resulting in habitat fragmentation and reducing plant resources, nectar, shelter and alternative suitable hosts for this species-rich parasitoids. Considering that Campopleginae species may be more susceptible to habitat destruction (Skillen, 2002), to sustainably maintain the high population size of abundant species and endemic rare species of this community, of which one species has been recently described (Vas et al., 2022), need a strong policy of conservation and preservation of the remaining natural plant patches, preventing any chemical compound usage and developing a practical training system to the farmers and residents (Noroozi, 2020; Rodríguez & Medianero, 2022).

AUTHOR'S CONTRIBUTION

The author confirm his contribution in the paper as follows: A.M.K: Managed the project, data curation, designing methodology, formal analysis, and preparation of the original manuscript. The author read and approved the final version of the manuscript.

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AVAILABILITY OF DATA AND MATERIAL

Not applicable.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

Not applicable.

CONSENT FOR PUBLICATION

Not applicable.

CONFLICT OF INTERESTS

The author declare that there is no conflict of interest regarding the publication of this paper.

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ارزیابی غنای گونه‌ای جامعه زنبورهای زیرخانواده *Campopleginae* (Hymenoptera, Ichneumonidae) در دشت گل محمدی دیم داراب، استان فارس، ایران

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چکیده: در این مطالعه، غنای گونه‌ای زنبورهای زیرخانواده *Campopleginae*، یک زیرخانواده متنوع از زنبورهای داروین در دشت گل محمدی دیم ارگانیک داراب در ارتفاع ۲۶۰۰ متر از سطح دریا در جنوب ایران ارزیابی شد. نمونه‌برداری با استفاده از چهار تله مالیز به مدت شش ماه از فوروردین تا مهر ۱۳۹۸ انجام شد. مجموع نمونه‌برداری انجام شده، ۱۸ تله/ماه بود. بهمنظور ارزیابی کامل بودن نمونه‌برداری، روش تلفیقی برای تعیین تنوع حقیقی جامعه مورد نظر با استفاده از تخمین تنوع مماسی، استانداردسازی پوشش نمونه‌برداری از طریق روش تنکسازی و بروندیابی، و استخراج تنوع از طریق نمودار یکنواختی، به کار گرفته شد. مدل‌های همگنی، همگنی (ام ال ای) و روش‌های چائو ۱، چائو ۱-بی سی، آی چائو ۱، ای سی ای، ای سی ای ۱، مرتبه اول جکنایف و مرتبه دوم جکنایف، به منظور تخمین حداکثر غنای گونه‌ای جامعه زنبورهای زیرخانواده *Campopleginae* استفاده شدند. تله‌های مالیز، ۴۹۱ فرد متعلق به ۲۴ گونه ریخت‌شناختی را شکار کردند. گونه *Diadegma majale* (Gravenhorst, 1829)، با ۶۴٪/۷ از کل افراد شکار شده، به عنوان گونه فراغالب معرفی گردید. نمودار تخمینی کامل بودن نمونه‌برداری نشان داد که داده‌ها، ۵.۹٪ از غنای گونه‌ای را در بردارند و ۴۱٪ گونه‌ها کشف نشده‌اند. مقادیر شاخص‌های تنوع گونه‌ای شانون و سیمپسون به ترتیب ۴/۵۳ و ۲/۲۹ تعیین شدند. برآوردگرهای مدلی و ناپارامتری، غنای گونه‌ای زنبورهای زیرخانواده *Campopleginae* را ۵۰-۲۴ گونه تخمین زدند. این مطالعه اطلاعات پایه ارزشمندی از زنبورهای زیرخانواده *Campopleginae* برای اهداف کنترل زیستی و حفاظت در جنوب ایران فراهم آورده است.

واژگان کلیدی: ساختار جامعه، حفاظت، تنوع، ایکنئومونیده، تنکسازی، بروندیابی، غنای گونه‌ای