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## Braconidae (Hymenoptera) communities of Iranian alfalfa fields at high altitudes

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**ABSTRACT.** Braconidae (Hymenoptera) communities at high altitudes in alfalfa fields of Kerman province (Iran) were analyzed. The communities were sampled by sweep netting in 2014 and 2015. Samples were taken from three altitudinal transects: 1900–2300 m, 2400–2700 m and 2800–3100 m. A total of 1773 braconid specimens belonging to seven subfamilies were collected. Alpha, beta and gamma diversities were analyzed. The samples from 1900–2300 m and from 2400–2700 m showed similar diversity, but from 2800–3100 m had the highest number of specimens and differed considerably in diversity.

**Key words:** Parasitoid wasps, Braconidae, diversity, *Medicago sativa*, Kerman province.

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### Introduction

Braconidae is the second largest family within the Hymenoptera with 21,230 valid species described (Yu *et al.* 2012); the vast majority of the species are primary parasitoids of larvae of Lepidoptera, Coleoptera and Diptera (Sharkey 1993).

These wasps have an enormous agricultural, ecological and economical interest because of their role in controlling phytophagous insect pests, having direct effects on the size of host populations and indirect effects on the diversity and survival of the host plants (LaSalle and Gauld 1992; González and Ruíz 2000; Peris-Felipo *et al.* 2014). Additionally, they are indirect indicators for the presence or absence of the host populations (Matthews 1974; LaSalle and Gauld 1992). Despite their

importance, biology and taxonomy of most Braconidae is still largely unknown (Peris-Felipo 2013; Yu *et al.* 2012).

Although many studies have been done on diversity of Braconidae, worldwide, for example in Brazil (Cirelli *et al.* 2003; Scatolini and Penteado-Dias, 2003), Venezuela (Briceño *et al.* 2007; 2009), Andorra (Falcó-Garí *et al.* 2006) or Spain (Peris-Felipo and Jiménez-Peydró, 2011; Jiménez-Peydró and Peris-Felipo 2011, 2014; Pérez-Rodríguez *et al.* 2013; Falcó-Garí *et al.* 2013), high altitude communities have been insufficiently analysed. Within this context, this work analyses the diversity and community structure of Braconidae in the alfalfa fields located at high altitude localities in Kerman province (Southeastern Iran).

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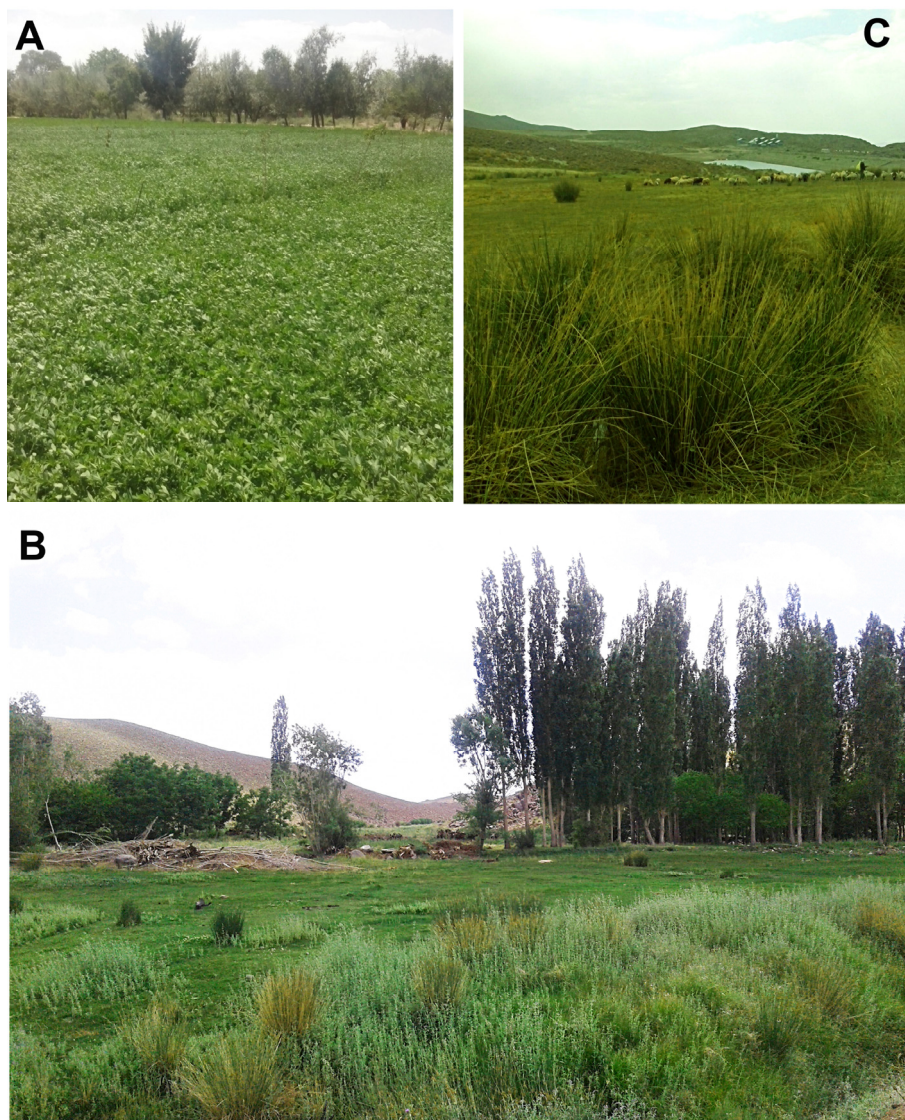
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### Material and methods

**Area of study:** Kerman is the second largest province of Iran with an area of 180,726 km<sup>2</sup>. Kerman is located on the mountainous margin of the Kavir-e Lut (= Lut Desert) (Kerman Management and Planning Organization 2007). This region possesses a wide range of climates depending on the relief of the area. The north, northwest and central areas have a dry and moderate climate, whereas in the south and southeast, the weather is warm and relatively humid.

The average temperature during March-June is 20–25°C (with a maximum and minimum average temperature of 39.6°C and -7°C, respectively) (Kerman Management and Planning Organization 2007).

**Sampling design and data collection:** Eight localities (Bardsir, Kuhpayeh, Sirch, Kuhbanan, Baft, Sarduyeh, Lalehzar and Qaleh-Askar) were selected in order of altitudinal transects (1900–2300 m, 2400–2700 m and 2800–3100 m). The specimens were sampled from June 2014 to August 2015 (Fig. 1).



**Figure 1.** Sampling points; A. 1900–2300 m. B. 2400–2700 m. C. 2800–3100 m.

Transects differ by a distance of 100 m of slope to separate the sampled communities. Specimens were captured by sweep net and secured by aspirator, and killed directly in ethyl alcohol (75%). Subsequently, braconids were identified to subfamily level in accordance with van Achterberg's keys (1990, 1993). Specimens are deposited in the insect collection of the Department of Biology, Shahid Bahonar University of Kerman, Iran (ZMSBUK).

**Data Analysis:** Diversity indices analyses were performed to identify possible relationships between taxa distributions within each sampled habitat; similarity/dissimilarity analyses were performed in order to identify the relationship between taxa. All analyses were carried out using PAST (Hammer *et al.* 2001). Alpha diversity reflects the richness in species of a homogeneous community. This sort of diversity was measured by taxa richness, abundance and dominance.

**Taxa richness:** used for valuing richness of sampling areas. It was measured using the Margalef index, a measure of specific richness that transforms the number of species per sample into the proportion to which the species are added by expansion of the sample, establishing a functional relationship between number of species and total number of specimens (Moreno 2001).

**Abundance:** used for valuing faunal composition of a given area (Magurran 1991). This was undertaken using the Shannon-Wiener index because it measures equity, indicating the degree of uniformity in species representation (in order of abundance) while considering all samples. This index measures the average degree of uncertainty that predicts which species an individual randomly picked from a sample belongs to (Magurran 1991; Moreno 2001; Villareal *et al.* 2004).

**Dominance:** occurrence of genera or dominance value was calculated with the Simpson index, often used to measure

species dominance values in a given community, its negative thus representing equity. It measures the representativity of the most important species without considering the other species present. It expresses the probability that two individuals randomly picked from a sample will belong to the same species (Magurran 1991).

**Community structure:** In order to complement the diversity analyses and enquire into community structure, *log-series*, *log-normal* and *broken-stick* models were also applied (Magurran 1991). The *log-series* model represents a community composed of a few abundant species and a high number of rare species. The *broken-stick* model refers to maximum occupation of an environment with equitable sharing of resources between species. Finally, the *log-normal* reflects an intermediate situation between the two (Soares *et al.* 2010). Using the data obtained from the parks, each of these models was applied to calculate the expected number of species,  $\log_2$  grouping species according to abundance (Magurran 1991; Tokeshi 1993; Krebs 1999). To test the significance of the models, the expected species values were compared with those of the observed species through chi-square analysis (Zar 1999).

Beta diversity is the degree of change or substitution in species composition between different communities within the same landscape.

**Cluster analysis:** employed to calculate the degree of correlation based on similarity/dissimilarity. For the calculation of these values, statistics-processing software PAST was used (Hammer *et al.* 2001).

Finally, gamma diversity measurement indicates the diversity value of all environments under study, as expressed in the richness indexes for each area (alpha diversity) and the difference between them (beta diversity) (Villareal *et al.* 2004)

## Results

During the sampling period, a total of 1773 braconid specimens were collected belonging to seven subfamilies: Alysiinae (434 specimens), Aphidiinae (854), Blacinae (73), Braconinae (32), Euphorinae (112), Microgastrinae (185) and Opiinae (83) (Table 1). These subfamilies were present in all samples.

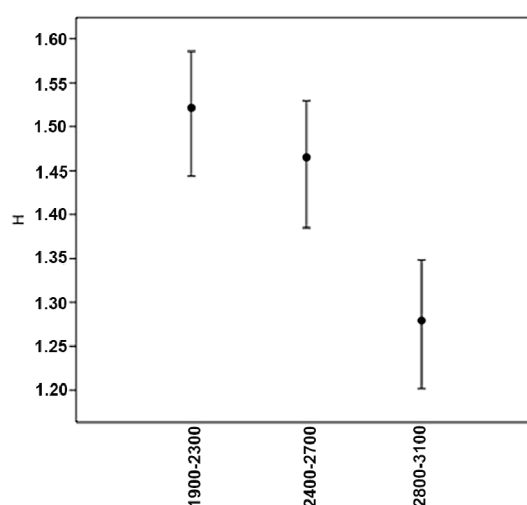
The abundance of Braconidae per altitude-transect was highest (762 specimens) at the highest altitude (2800–3100 m), followed by 1900–2300 m and 2400–2700 m (with 528 and 483 specimens, respectively) (Table 1).

For analysing the community structure proportional abundance indices and parametric models were used. The proportional abundance indices consist of dominance indices (e.g. the used Simpson index) and equity indices (as the Shannon-Wiener index).

The analysis obtained with the Simpson index (Table 2) showed a dominance by one or more subfamilies with a high abundance. These predominant subfamilies were also found by the Shannon index (Table 2) and the results showed that the samples of the 1900–2300 m and 2400–2700 m transects are very similar (Fig. 2).

**Table 1.** Subfamily distribution and specimen numbers per altitudinal transect.

Subfamily	Altitude			Total
	1900–2300	2400–2700	2800–3100	
Alysiinae	190	143	101	434
Aphidiinae	190	201	463	854
Blacinae	16	14	43	73
Braconinae	20	8	4	32
Euphorinae	26	22	64	112
Microgastrinae	47	72	66	185
Opiinae	39	23	21	83
<b>TOTAL</b>	<b>528</b>	<b>483</b>	<b>762</b>	<b>1773</b>



**Figure 2.** Graphical representation of Shannon-Wiener analysis by altitude localities.

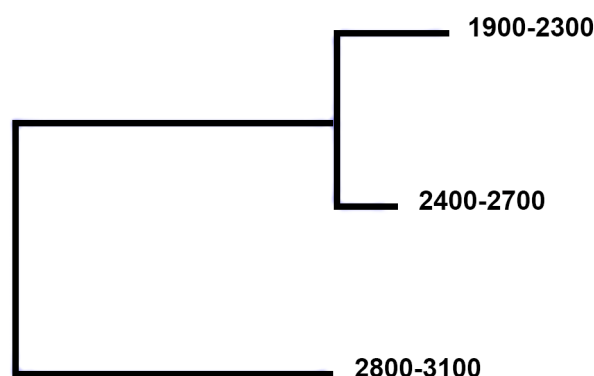
The application of parametric models showed the compliance with log-series, log-normal and broken-stick models (Table 3). The results indicate that the communities are unstable and composed by a few abundant species and a large number of rare species, with a maximum environment occupation and equitability in resources sharing, and with a very specific botanical and faunal composition as well as climatic conditions of the sampled areas.

In order to obtain beta diversity values (similarity/dissimilarity) between localities under consideration, the Euclidean index was calculated (Table 4). The resulting values indicated that the habitats at 1900–2300 m and 2400–2700 m are very similar in subfamily distribution (IE = 58.09), while 2800–3100 m is clearly different from 1900–2300 m (IE = 292.51) and 2400–2700 m (IE = 270.31). These results were also found in the Euclidean cluster obtained through cluster

analysis, of which the level of correlation was  $r = 0.99$  (Fig. 3). Finally, gamma diversity reached a value of 7, which is identical to the value of the total subfamily richness caught in the three habitats (subfamily number = 7).

### Discussion

The greatest abundance of Braconidae was found at the 2800–3100 m transect, followed by the 1900–2300 and 2400–2700 m, where the subfamily composition is very similar. The most abundant subfamilies in all areas were Aphidiinae and Alysiinae with a total of 48.16% and 24.47%, respectively. The relative abundance is very interesting due to the relationships that these parasitic wasps have with their hosts. Aphidiinae are parasitoids of aphids and Alysiinae of Diptera-Cyclorrapha, both are the main pests in alfalfa fields in Iran (Farahani *et al.* 2016).



**Figure 3.** Cluster of Euclidean analysis reflecting relationship between habitats.

**Table 2.** Diversity and abundance values for collected Braconidae.

	1900–2300	2400–2700	2800–3100
Number of subfamilies	7	7	7
Number of specimens	528	483	762
Simpson Index	0.7229	0.7115	0.5947
Shannon-Wiener Index	1.522	1.465	1.279



**Table 3.** Community structure analysis. Values of  $\chi^2$  and p-value by model per habitat.

Habitat		<i>log-series</i>	<i>log-normal</i>	<i>broken-stick</i>
1900–2300	$\chi^2$	5.488	8.515	6.411
	p-value	0.600	0.289	0.492
2400–2700	$\chi^2$	4.992	11.246	6.205
	p-value	0.669	0.128	0.516
2800–3100	$\chi^2$	5.06	0.722	6.480
	p-value	0.750	0.999	0.593

**Table 4.** Values of Euclidean analysis of similarity/dissimilarity.

	1900–2300	2400–2700
1900–2300		
2400–2700	58,09	
2800–3100	292,51	270,31

The structure analysis showed that all altitude transect samples comply with log-series, log-normal and broken-stick models. This indicates that these communities are unstable and composed by a few abundant species and large number of rare species, with a maximum environment occupation and equitability in resource sharing, and with a very specific botanical and faunal composition as well as climatic conditions of the sampled areas.

A previous study carried out in the Sierra Calderona (Valencia, Spain), where the Braconidae subfamily community from *Pinus* and *Quercus* forests were analysed with the same models with exception of the broken-stick model (Falcó-Garí *et al.* 2014). Iranian results could be explained by the reduced number of subfamilies because of only seven subfamilies were found in all localities and by the single-crop farming of alfalfa (*Medicago sativa* L.).

In conclusion, studies conducted to determine the biodiversity are important because they increase the limited knowledge about the faunal composition and the community structure in our landscapes. The insights could be important for the application of biocontrol.

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## جامعه گونه‌ای خانواده (Hymenoptera) Braconidae مزارع یونجه در مناطق مرتفع ایران

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**چکیده:** جامعه گونه‌ای خانواده (Hymenoptera) Braconidae مزارع یونجه واقع در مناطق کوهستانی استان کرمان مورد بررسی قرار گرفت. نمونه های این خانواده توسط تور دستی در طی سال‌های ۱۳۹۳ و ۱۳۹۴ جمع آوری شدند. نمونه ها از سه ارتفاع شامل ۱۹۰۰-۲۳۰۰ متر، ۲۴۰۰-۲۷۰۰ متر و ۲۸۰۰-۳۱۰۰ متر جمع‌آوری شدند. در مجموع ۱۷۷۳ نمونه متعلق به هفت زیرخانواده به دست آمد. تنوع آلفا، بتا و گاما محاسبه شد. نمونه‌های دو ارتفاع اول تنوع مشابهی نشان دادند، در صورتی که نمونه‌های مربوط به ارتفاع ۲۸۰۰-۳۱۰۰ متر دارای بیشترین تعداد نمونه بودند و از نظر تنوع به طور قابل ملاحظه‌ای متفاوت بودند.

**واژگان کلیدی:** زنبورهای پارازیتوئید، تنوع گونه‌ای، یونجه، استان کرمان