What's Difference Between Faunistic and Biodiversity Studies?

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Abstract: While faunistic studies give information about the distribution of animals in a region, the diversity (number and variety of species) studies give information about diversity of plant and animal life within a region of which they are part. In other words; faunistic studies prove the existence of animals in that habitat or region with systematically or by random sampling. The number of individuals of the sampled species is not that important. Faunistic studies are essential scientific studies, especially for the detection of new species and their introduction to the inventory. There is no doubt as to the great desirability of faunistic studies on the geographical distribution of animals. Biological diversity is the variability among living organisms from all sources (including terrestrial, marine, and other aquatic ecosystems) and the ecological complexes. This includes diversity within species (alpha), between species (beta), and of ecosystems (gamma). The importance of this description is that it draws attention to the many dimensions of biodiversity (Genetic, species, habitat, and ecosystem). Studies of biological diversity and its measurement necessarily require systematic and homogenous sampling methods. Especially when comparing two or more habitats in terms of species richness, diversity, evenness, similarity, etc. Such biodiversity indices are often used to measure the diversity in habitats destroyed by human. Four pasture ecosystems, two of which are natural and two of which are grazed by sheep and goats, were chosen as the study area in Atabey district of Isparta province. Pitfall trap and sweep net sampling methods were used in selected habitats. While the pitfall trap sampling method was applied homogeneously in the habitats, the sweep net sampling method was not applied homogeneously. The data obtained from these two sampling methods, homogeneous and non-homogeneous, were used in the calculation of biodiversity parameters. We desire to call attention in this manuscript to the differences between faunistic and biodiversity studies (specially its measurement) with reference to the previous studies.
Key words: insect, species richness, dominancy, similarity, evenness

Faunistik ve Biyoçeşitlilik Çalışmaları Arasındaki Fark Nedir?

Özet: Faunistik çalışmalar, hayvanların bir bölgedeki dağılımı hakkında bilgi verirken, çeşitlilik (tür sayısı ve çeşitliliği) çalışmaları, parçası oldukları bir bölgedeki bitki ve hayvan yaşamının çeşitliliği hakkında bilgi verir. Diğer bir deyişle; Faunistik çalışmalar, sistematik veya rastgele örnekleme ile o habitatta veya bölgede hayvanların varlığını kanıtlamaktadır. Örneklenen türün birey sayısı o kadar önemli değildir. Faunistik çalışmalar, özellikle yeni türlerin tespiti ve envantere girişi için gerekli bilimsel çalışmalardır. Hayvanların coğrafi dağılımına ilişkin faunistik çalışmaların büyük arzu edildiği konusunda hiçbir şüphe yoktur. Biyolojik çeşitlilik, tüm kaynaklardan (karasal, deniz ve diğer su ekosistemleri dahil) ve ekolojik komplekslerden gelen canlı organizmalar arasındaki değişkenliktir. Bu, türler içindeki (alfa), türler arasındaki (beta) ve ekosistemlerdeki (gama) çeşitliliği içerir. Bu tanımlamanın önemi, biyolojik çeşitliliğin birçok boyutuna (Genetik, türler, habitat ve ekosistem) dikkat çekmesidir. Biyolojik çeşitlilik çalışmaları ve ölçümü, mutlaka sistematik ve homojen örnekleme yöntemleri gerektirir. Özellikle iki veya daha fazla habitatı tür zenginliği, çeşitlilik, eşitlik, benzerlik vb. açısından karşılaştırırken. Bu tür biyolojik çeşitlilik indeksleri genellikle insanlar tarafından yok edilen habitatlardaki çeşitliliği ölçmek için kullanılır. Çalışma alanı olarak Isparta ili Atabey ilçesinde ikisi doğal, ikisi koyun ve keçilerin otladığı dört mera ekosistemi seçilmiştir. Seçilen habitatlarda tuzak ve süpürme ağı örnekleme yöntemleri kullanılmıştır. Habitatlarda tuzak tuzak örnekleme yöntemi homojen olarak uygulanırken, taramalı ağ örnekleme yöntemi homojen olarak uygulanmamıştır. Biyoçeşitlilik parametrelerinin hesaplanmasında homojen ve homojen olmayan bu iki örnekleme yönteminden elde edilen veriler kullanılmıştır. Bu yazıda, daha önceki çalışmalara atıfta bulunarak, faunistik ve biyoçeşitlilik çalışmaları (özellikle ölçümü) arasındaki farklılıklara dikkat çekmek istiyoruz.
Anahtar kelimeler: Havaalanı yüzey akış suları, düşük masraflı arıtma, yapay sulakalanlar, çöktürme havuzları, yüzey akış suları arıtımı

1. Introduction

Biodiversity refers to all living things living in an environment (Hoffman, et al., 2021). The measurement of biodiversity parameters of a habitat does not always exactly reflect the biodiversity of that habitat (Jabopsen, et al., 2007). In determining the fauna of a habitat, many different sampling methods can be applied according to the biology of the insect. Which sampling methods will be applied for which type of insects should be specified in the scientific studies? For example; the pitfall trap sampling method which have been used as one of the most used sampling method is generally used to estimating arthropod diversity and detect mostly epigean species, while the light trap is used to identify light-sensitive heliophiles (Hohbein and Conway, 2018). However, to use an expression such as "the biodiversity value of that habitat has been determined" is not correct while carrying out such faunistic studies.

Measurement of the biological diversity necessarily requires homogeneity, especially for sampling methods (Kvålseth, 1991). The sampling methods applied for the comparison of the biodiversity parameters of the habitats cannot be different from each other. For example, sweep net sampling method applied in the morning times in habitat A, should be done at the same time in habitat B so that the parameters work correctly and give the correct result. Otherwise, insects caught in habitat A will include groups of insects caught in the morning times, and those caught in habitat B will represent groups of insects caught in different times, for example the evening.

This study was carried out with the aim of "measurement of biodiversity parameters and comparison of faunistic studies, which have not been studied much in our country" in order to find answers to such questions. For these purposes the data obtained from different sampling methods, homogeneous and non-homogeneous, were used in the calculation of biodiversity parameters.

2. Material and Method

2.1. Study area and sampling methods:

Two natural (MrN_1; MrN_2) and two destroyed (cattle grazing) (MrY_1; MrY_2) pasture ecosystems were selected as the study area in Atabey district of Isparta province. In the study, two different sampling methods, homogeneous and non-homogeneous, were evaluated in terms of biodiversity.

Epigean species, living on the soil surface, were collected by pitfall trap sampling method between April and October 2020.

Plastic containers with a diameter of 15 cm and a depth of 20 cm were placed in the selected habitats for the sampling of Epigean hexapod species, keeping the open parts at the same level with the soil surface, 10 pieces in each habitat at 5 meters intervals were located and checked once a week (New, 1988; Ward, et al., 2001).

In the same ecosystems, the sweep net sampling method was applied once a month (HongFan, et al., 2017). For the sweep net sampling method, the weep net was shaken 100 times on the plants in the habitats with 3 replications. The sweep net sampling method was carried out in the early morning in natural ecosystems and in the evening hours in destroyed pasture ecosystems in order to disrupt the homogeneity.

The data obtained from both sampling methods were used in the calculation of biodiversity parameters.

2.2. Evaluation of data

The basic biodiversity parameters of the habitats were obtained using the EvenDiv 1.1 program (Heimann, 2004), the parameters used and their calculation methods are given below.

Species diversity measurements

Shannon-Wiener and Simpson diversity indices were used to determine species diversity.

-Shannon-Wiener diversity index;

$$H' = -\Sigma pi \ln (pi) \qquad (1)$$

pi: The ratio of the number of individuals of the ith species to the total number of individuals

ln: natural logarithm (Magurran, 1998; Magurran, 2004).

-Simpson diversity index;

$$S = 1 - \Sigma ni(ni - 1)/N(N - 1) \qquad (2)$$

i: number of species

ni: number of individuals belonging to a species

N: The total number of individuals of the species in a region (Magurran, 1998, Magurran, 2004).

-Dominance measurements

Simpson dominance index was used to determine dominance.

- Simpson dominance (Sd)

$$Sd = \Sigma ni(ni - 1)/N(N - 1) \qquad (3)$$

i: Number of species

ni: The number of individuals belonging to a species

N: The total number of individuals of the species in a region (Magurran, 1998, Magurran, 2004).

-Evenness measurements

Shannon and Simpson Evenness indices were used to determine the population density relationships of the species.

- Shannon Evenness (EsH)

$$EsH = H' / \ln(N) \qquad (4)$$

H': Shannon-Wiener diversity index

ln: natural logarithm

N: The total number of individuals of the species in a region (Magurran, 1998, Magurran, 2004)

-Simpson Evenness (Esm)

$$Esm = (1/D) / S \qquad (5)$$

1/D: Simpson diversity

S: The total number of species (Magurran, 1998, Magurran, 2004).

-Similarity indexes

Percent similarity indices were used to determine similarity relationships.

Percent similarity (S)

$$S = \sum \min(a, b, \ldots \ldots x) \qquad (6)$$

$\sum \min$: Percentage ratios in the habitat represent the sum of the smallest values calculated with the smallest values in the other habitat whose similarity was calculated (Southwood, 1971; Krebs, 1999; Magurran, 1988; Magurran, 2004).

Multi Variate Statistical Package (MVSP) 3.11c program was used to classify selected habitats (Kovach, 1999). In the evaluation of the data obtained, the arithmetic group average (Unweighted Pair Group Method with Arithmetic Mean - UPGMA) was chosen as the classification method. The distance between similarities or differences is shown by the Sörensen coefficient. Considering that it will facilitate the interpretation of the Sörensen similarity value, the percent similarity values of the habitats were calculated by choosing the arithmetic group averages.

3. Result and Discussion

A total of 638 individuals belonging to 17 species were sampled by pitfall trap and sweep net sampling method. Most of the species caught by the pitfall trap sampling method belong to the Carabidae, followed by the Scarabaeidae, Tenebrionidae, Curculionidae,

Staphylinidae families. In the sweep net sampling method, species belonging to Diptera, Hymenoptera and Orthoptera species were found the most.

It was already expected that the selected sampling methods would capture the targeted insect species and give similar results to previous studies (Lang, 2000; Mommertz, et al., 1996).

The biodiversity parameter results calculated using the data obtained from the insect species caught by the pitfall trap sampling method calculated the expected values and the Shannon-Wiener and Simpson diversity results were found to be the highest in natural pasture ecosystems (Shannon-Wiener results: MrD_1: 2,6586; MrD_2: 2,6256; Simpson Results: MrD_1: 0,9244 ve MrD_2: 0,9204). As expected, Simpson dominance values were recorded as 0.1873 and 0.159, respectively, in destroyed pasture ecosystems with the highest MrY_1 and MrY_2 codes (Table 1). Both Shannon and Simpson Evenness indices were calculated higher in natural ecosystems in parallel with diversity indices (Shannon-Evenness results: MrD_1: 0,9589; MrD_2: 0,947; Simpson evenness results MrD_1: 0,8267; MrD_2: 0,7852).

Contrary to expectations, Shannon-Wiener biodiversity parameter results calculated using the data obtained from insect species caught by sweep net sampling method were calculated higher in the destroyed MrY_1 ecosystem than in the natural MrD_2 ecosystem. Similarly, Simpson diversity parameter results show that MrY_2 destroyed pasture ecosystem is calculated higher than the naturally selected MrD_1 pasture ecosystem (Table 1). When both Shannon and Simpson Evenness density indices are evaluated, unexpected results appear (Table 1).

Table 1. Biodiversity parameter values of insect species (MrD-1 and MrD_2: natural pasture; MrY_1 and MrY_2: destroyed pasture) of the insect species caught by pitfall trap and sweep net sampling methods in the studied ecosystems.

	Pitfall Trap				Sweep Net			
Habitats	MrD_1	MrD_2	MrY_1	MrY_2	MrD_1	MrD_2	MrY_1	MrY_2
Species richness	16	16	13	12	12	9	11	9
Number of individuals	73	78	152	117	89	69	37	23
Diversity indexes								
Shannon-Wiener[H]	**2.6586**	**2.6256**	2.0588	2.1233	**2.3214**	1.9514	**2.1808**	1.9941
Simpson Index[Sd]	0.0756	0.0796	**0.1873**	**0.159**	0.1107	**0.1766**	0.1381	**0.1607**
Simpson Diversity [S]	**0.9244**	**0.9204**	0.8127	0.841	**0.8893**	0.8234	**0.8619**	0.8393
Evenness indexes								
Shannon-Evenness [EsH]	**0.9589**	**0.947**	0.8027	0.8545	**0.9342**	0.8881	**0.9095**	0.9076

Simpson-Evenness [Esm]	**0.8267**	**0.7852**	0.4107	0.5241	**0.7528**	0.6292	0.6583	**0.6914**

The percent similarity parameter results calculated from the data obtained from the individuals caught by the pitfall trap sampling method showed that the naturally selected pasture ecosystems were the most similar to each other (79.74%). Destroyed pasture ecosystems, on the other hand, are 78,067% similar to each other. These two groups, formed by natural and destroyed pasture ecosystems, were found to be similar to each other by 39.257%. The most dissimilar habitats were found MrY_2 and MrD_2 with 35.897% and, MrY_1 and MrD_2 with 36.522 % respectively (Figure 1).

The percent similarity parameter results calculated based on the data obtained from the individuals caught by the sweep net sampling method showed that the most similar habitats were in the naturally selected pasture ecosystems at a rate of 65.823%. This rate has been calculated as 60% in destroyed pasture ecosystems. The similarity rate of the groups formed by natural and destroyed pasture ecosystems with each other was calculated as 34,424%. The most dissimilar group was seen in MrY_1 and MrD_2 ecosystems with 28.302%, followed by MrY_2 and MrD_2 ecosystems with 32.609% (Figure 1).
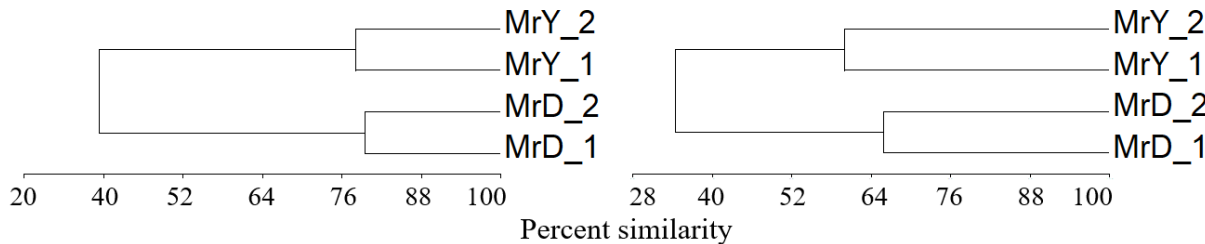

Figure 1. Percent similarity dendrogram calculated from insect species obtained by pitfall trap sampling method (left) and sweep net sampling method (right).

As a result, similarity parameters calculated from individuals caught by both pitfall trap and sweep net sampling method, it was determined that natural and unnatural pasture habitats form groups among themselves. However, when the results of the pitfall trap sampling method are compared with the results of the sweep net sampling method, it has been shown that these groups formed by natural and unnatural grassland ecosystems are more similar to each other.

In addition, when all the data obtained from both pitfall trap and sweep net sampling methods are shown on the dendrogram, it is seen that the natural pasture areas where the pitfall trap sampling method is applied are 54.041% similar to the natural pasture areas where the sweep net sampling method is applied. This group, on the other hand, is 41.784% similar to the group of destroyed pasture ecosystems in which the sweep net sampling method is applied. Finally, the similarity of the group consisting of destroyed pasture ecosystems to which the

pitfall trap sampling method was applied to all other groups was calculated as 30.226% (Figure 2).
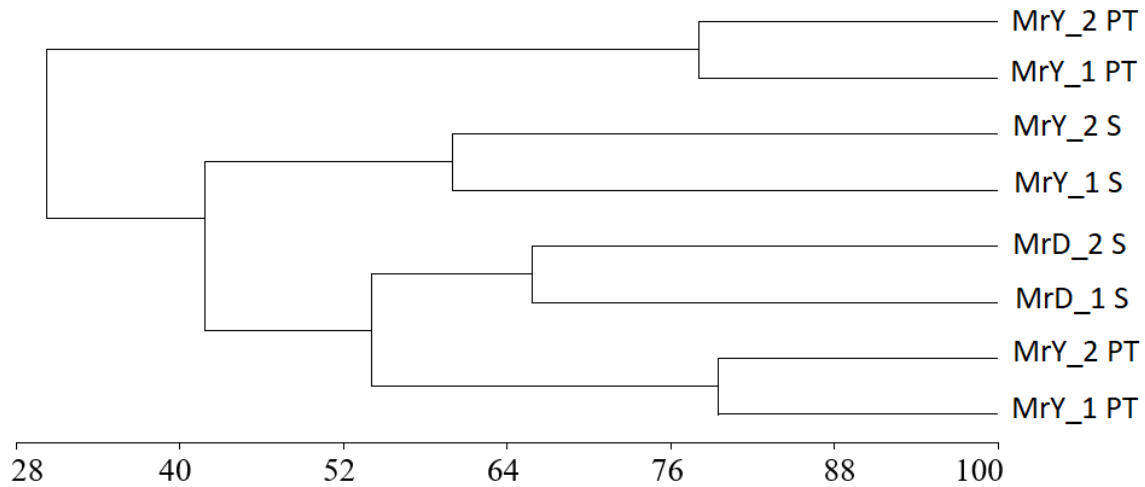

Figure 2. Percent similarity dendrogram calculated from insect species obtained by both pitfall and sweep net sampling methods (PT: Pitfall trap; S: Sweep net sampling method)

Chang et al. (2004) found that with increasing altitude, the Shannon-Wiener species diversity index increased from 1.432 to 1.832 although Simpson diversity index was found complicated. Wang et al. (2009) declared that the intercropped pasture had more beneficial insects than the non-intercropped site ($P < 0.05$). Numerous examples of biodiversity results can be given from previous studies (Aydın & Şen, 2020; Aydın & Karaca, 2018). However, it is normal for the results to be different due to the ecological differences in the regions where the studies were conducted. The important thing in this study is that the biodiversity parameters obtained in the pasture areas where the inhomogeneous sweep net sampling method was applied could not be calculated as expected. When these data are compared with the pasture areas where the homogeneous pitfall trap sampling method is applied, completely different results were obtained, as if the biodiversity values in the destroyed pasture habitats were calculated higher. The same can be mentioned for similarity parameters. The dissimilarity of destroyed and unworn pasture areas with non-homogeneous sweep net sampling method draws attention.

4. Conclusion

As a result, insect species obtained from sampling methods applied by ignoring homogeneity can sometimes give misleading results in the calculation of biodiversity parameters and similarities. For this reason, it should be noted that selected sampling method must be homogeneous. Sampling methods chosen by ignoring the homogeneity should only be

used in the determination of fauna, and should not be used in the biodiversity parameters to be calculated especially for the sustainability and protection of the habitat.

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