DIVERSITY OF ARTHROPOD COMMUNITIES AS AN INDICATOR OF CHANGES PRODUCED BY THE UTILIZATION OF SILVICULTURAL TECHNIQUES

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Abstract

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The dynamics of forest arthropod communities can be completely understood only when based on their trophic connections. Given their importance in detritic food chains with their influence on the rate of decomposing organic matter and the dynamics of nutrients, terrestrial arthropods from litter and soil are useful in monitoring changes in environmental conditions in forest ecosystems. Due to their flexible diet they cannot be appropriately assigned to specific trophic modules. Their diversity frequently changes across probes mainly due to variation in micro-climatic parameters. The aim of this present study is to determine the influence of environmental changes on the diversity of epigeal fauna due to silvicultural practices. Imaginal stages of litter invertebrates were collected from two different stands in the same forest located near Bucharest. The vegetation in the first site consisted mainly of oak, which resulted from selective cuts followed by artificial regeneration, and the second one consisted of oak and other tree and shrub species. Samples were collected for one week each month from May to August and most invertebrates were classified at the family level. Sites were compared using Shannon's informational entropy and the chi-square test of goodness of fit of two empirical distributions. Results indicated greater diversity in the second site during May and June, and greater diversity in the first one during July and August, and the monthly differences were found to be significant only in May and July. Overall, the second site exhibits significantly greater diversity. Our findings suggest that the diversity of epigeal communities is greater in forests with more tree species, and therefore this sustains the hypothesis according to which these communities can indicate structural changes.

Key words: arthropods, epigeal communities, imaginal stages, diversity

Introduction

The dynamics of arthropod communities in forest ecosystems can be understood only when based on the trophic connections established between them (Scheu, 2002). Given

the importance of many of the species in detritic food chains, and the influence of their activities on the rates of decomposing organic compounds and the dynamic of nutrients (Bird et al., 2000), terrestrial arthropods from litter and soil are a useful indicator of forest ecosystem conditions and changes within them (Hole, 1982; Kopeszki, 1992; Curry, Good, 1992; Hogervorst et al., 1993; Hoekstra et al., 1995). This presented an argument for the recommendation to use soil and litter arthropods for the assessment of the biological effects of silvicultural practices of different intensities. These practices included intensive cuts, the use of pesticides and fertilizers and also soil bedding (Bird et al., 2000).

Measuring litter diversity through direct investigations is costly and therefore the use of indicators becomes necessary (Gaston, 2000; Kerr et al., 2000; Ekschmitt et al., 2003). The fact that species considered functionally redundant (according to the theory of redundancy) can gain a new functional significance due to their interaction with other species (Andrén et al., 1995), and that changes in species composition is not a random process (Andrén et al., 1995; Wolters, 2001) indicate the great stability which can be exhibited by litter biota. Therefore, species diversity is recommended as an indicator of ecosystem changes (Didham et al., 1996; Gibb, Hochuli, 2002). This argument is further strengthened by the fact that litter biota functioning is assured by the multiplication of roles maintaining a high level of specific diversity in the community (Wolters, 2001).

The basic elements of trophic webs are not strictly specialized species, but they are trophic groups of species which have equivalent roles. Detritophagous organisms consume amalgamations of particles and substances or microorganisms, and cannot be delimited by the main component of their diet (Scheu, Setälä, 2001). Since soil and litter organisms have a flexible diet they can not be appropriately assigned to a certain trophic module. Dependent on the availability of resources, these organisms can feed on algae, fungi, detritus or microorganisms, or they can be phytophagous or predators (Ponge, 1991; Walter, 1987; Maraun et al., 1998).

Although soil and microclimate parameters are generally significantly correlated with diversity, despite different measurement types, they are unsatisfactory predictors explaining less than 50% of the variation (Ekschhmitt et al., 2003). Diversity is also frequently subjected to variations across sub-samples (CV = 20–60%), mainly due to the variation in microclimatic parameters (Ekschhmitt et al., 2003). These variations can be avoided by limiting the correlation with environmental factors. Therefore, some authors suggested estimating diversity at higher taxonomical levels (Gaston, 2000; Kerr et al., 2000).

We assume that litter levels micro-climatic conditions. Therefore, the dynamics of litter communities are determined by the availability of resources and by the rates of mass and energy transfer. These rates are determined by the structure and composition of the arboretum and whether it is natural or modified.

Epigeal communities remain an effective measure of changes at the ecosystem level. This study emphasizes the beneficial use of diversity in epigeal communities as an instrument for investigating changes in ecological systems as a result of silvicultural practices. Here, we used litter invertebrate fauna which is richer than the invertebrate fauna in the fermentation layer (Evans et al., 2003). Important differences between the

larval and imaginal stage with respects to their belonging to a certain trophic category determined that the focus on the diversity of epigeal fauna should be placed on the latter stage.

The overall goal of the study is to compare the diversity of epigeal fauna in two forest stands, one subject to stronger anthropic interventions over a longer period, and thus hypothesizing that the greater diversity of the fauna will correspond to a greater diversity in flora and to less human intervention. If results confirm the hypothesis, this will offer practitioners arguments for selecting near-natural techniques in silvicultural management.

Material and methods

Study sites

The study was conducted in two stands situated in a mixed lime-oak-hornbeam forest (Doniță et al., 1990) located in the plain region of Southern Romania near Bucharest (40°38'7.77" N, 26°9'18.76" E). The stands have the following structure: (1) oak wood (*Querceta roboris*), with a dense litter and highly covered soil, less shrubbery with average-developed vegetation characteristic of the plains: *Arum orientale* M. B i e b. and *Pulmonaria officinalis* L.; (2) oak wood (*Querceta roboris*) with derived arboreta: *Acer campestre* L., and *Carpinus betulus* L., dense litter, with average-developed shrubbery containing mostly *Crataegus nomogyna* J a c q.*,* and *Ligustrum vulgare* L., and vegetation consisting of associations of *Brachypodium sylvaticum* (H u d s.) B e a u v., *Geum urbanum* L., *Pulmonaria officinalis* L.*, Asperula* sp., and *Dentaria bulbifera* L. A more detailed comparison of the two stands is presented in Table 1.

T a b l e 1. Displaying a brief comparison of the forest stands.

Characteristic	Site A	Site B
Type	artificial	natural
Productivity	high	low
Age structure	homogeneous	homogeneous
Surface (ha)	2.0	11.8
Landform	average plane plain	average plane plain
Elevation	90 m from the sea level	90 m from the sea level
Soil	typical brown-red	typical brown-red
Litter	continuous, thin	continuous, normal
Composition of shrub layer	*Cornus sanguinea*, *Ligustrum vulgare*, density 0.9/0.6	*Corylus avellana*, *Crataegus monogyna*, *Cornus sanguinea*, *Ligustrum vulgare*, density 0.9/0.8
Composition of tree layer	*Ouercus robur, Tilia tomentosa*, ratio 9:1, density 0.7	*Quercus robur, Carpinus betulus, Acer campestre, Quercus cerris*, ratio 7:1:1:1, density 1.0
Type of flora	*Arum-Pulmonaria*	*Brachypodium-Geum-Pulmonaria*

Treatments

Both stands form part of a forest created as an artificial regeneration plantation 70 years ago. Vegetation in the first stand (referred as "site A") consists mainly of *Quercus robur* L. pedunculate oak, resulting from selective cuts and artificial regeneration, so that other species were replaced by this pedunculate oak.

The vegetation of the second stand (referred as "site B") consists of pedunculate oak and other tree and shrub species, which are present in different proportions, thus generating the characteristic mosaic of mixed oak forests.

Sampling

Pitfall traps were used to collect epigeal fauna. Traps consisting of transparent plastic containers with a diameter of 15 cm, containing a preserving liquid consisting of a small quantity of detergent added to 4% formaldehyde solution, to modify the surface tension of the liquid, were buried completely up to the container top. For each site, traps were placed in lines of ten at a distance of 1.5 m apart. This configuration ensured the best representation of fauna in the probes. Sampling was performed in May, June, July, and August, which corresponded to the vernal and estival periods. Traps were installed for a period of one week each month. These periods reflect the main stages in the vegetation cycle of leafing, blooming and fruiting.

Samples were transported to a laboratory and the arthropods were identified and stored in 80% isopropyl alcohol. All invertebrates were classified to the family level, except for *Pseudoscorpiones*, *Araneae*, *Opiliones, Acari, Isopoda*, *Diplopoda* and *Chilopoda* which are considered recognizable taxonomical units. Individuals considered to be at the same taxonomical level were assigned to functional groups (Bird et al., 2000). The insects were also determined up to the order level, except for beetles (*Coleoptera*), flies (*Diptera*), wasps (*Vespoidea*), and true bugs (*Heteroptera*). The abundance of each taxon was recorded. Due to the fact that the trophic category can differ between larval and imaginal stages, the larvae were not accounted for.

Statistical analysis

To compare the diversity of the two sites, we used three indices: species diversity and two indices of similarity, Jaccard's and Sorensen's (Magurran, 1998).

Jaccard's index: $nc / (nA + nB - nc)$ [Equation 1]

Sorensen's index: $2 nc / (nA + nB)$ [Equation 2]

where nA and nB are the number of species in sites A and B, and nc = number of common species.

In addition, similar to methods employed in the study by Petrişor (2000), we computed diversities using Shannon's informational entropy and compared them for the two communities using a test proposed by Magurran (Magurran, 1998). In addition, the specific frequency distributions during each month individually and for the entire period of study were calculated using the $\chi2$ test for "goodness of fit" of the two empirical distributions (Hutcheson, 1970). Shannon's informational entropy is defined as

$$h = -\sum_{i=1}^{s} p_i (\ln(p_i)),$$ [Equation 3]

where h is the informational entropy, expressed in this case as nits; p_i represents the relative frequency of the species i; and s represents the total number of species in the community (Petrişor, 2000; Magurran, 1998; Hutcheson, 1970).

The comparison of two empirical entropies is performed using the following test

$$t = \frac{h_1 - h_2}{\sqrt{\operatorname{var}(h_1) + \operatorname{var}(h_2)}}$$ [Equation 4]

where,

$$\text{var}(h) = \frac{\sum\limits_{i=1}^{s} p_i (\ln(p_i))^2 - \left(\sum\limits_{i=1}^{s} p_i (\ln(p_i)) \right)^2}{n} - \frac{s-1}{4n^2}$$ [Equation 5]

Under the null hypothesis (i.e., no difference between the two distributions, tested against the alternative "any difference"), the test follows a t (Student) distribution which contains the following number of degrees of freedom (Petrişor, 2000; Magurran, 1998; Hutcheson, 1970)

$$df = \frac{(\text{var}(h_1) + \text{var}(h_2))^2}{\frac{(\text{var}(h_1))^2}{n_1} + \frac{(\text{var}(h_2))^2}{n_2}}$$ [Equation 6]

Hutcheson (1970) proposed a chi-square (^{2}) test for comparing specific frequency distributions of two communities. The ^{2} test is computed using the formula

$$\chi_{n-1}^2 = \sum_{i=1}^{s} \frac{(O_i - R_i)^2}{R_i} \, ,$$ [Equation 7]

where χ_{n-1}^2 is the test statistic; under the null hypothesis, its distribution is ^{2} with n-1 degrees of freedom; Ri is the frequency of species i, in the reference period; and Oi is the frequency of species i, in the studied period (Petrişor, 2000; Hutcheson, 1970).

All computations were performed using an Excel® spreadsheet, except for the p-values which were computed by a software application implemented via the Internet (Arsham, 2004).

Results

Taxonomic considerations

Individuals collected in all samples were found to belong to five classes of arthropods: *Arachnida (Pseudoscorpiones, Araneae, Opiliones, Acari)*, *Malacostraca* (*Isopoda*: *Oniscidea*), *Diplopoda, Chilopoda* and *Insecta*. Over the entire period, 9439 individuals were collected in May (6932 in Site A and 2507 in Site B), 4638 in June (2640 in Site A and 1998 in Site B), 5125 in July (2231 in Site A and 2894 in Site B), and 265 (81 in Site A and 187 in Site B) in August (Fig. 1 and Table 4). This gave totals of 11884 individuals collected at Site A and 7583 at Site B (Fig. 2). For the distribution at the order and family level, please refer to Table 2. From this, 12 taxons were present in site A only, 12 in site B only, while 51 were found in both sites.

In both sites, the *Insecta* had the highest relative abundance: 84.77% in site A and 77.54% in site B. The groups of arthropods with high relative abundance were: *Collembola* (67.96% in site A and 51.64% in site B), *Araneae* (7.20% in site A and 8.25% in site B), *Formicidae* (4.19% in site A and 7.39% in site B), *Acari* (3.95% in site A and 4.19% in site B), *Opiliones* (1.63% in site A and 6.04% in site B), *Carabidae* (2.64% in site A and 3.44% in site B), *Sci-*
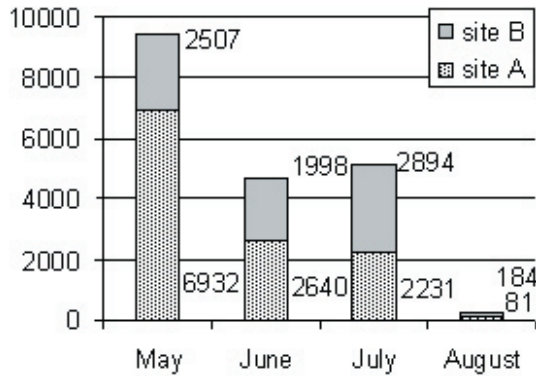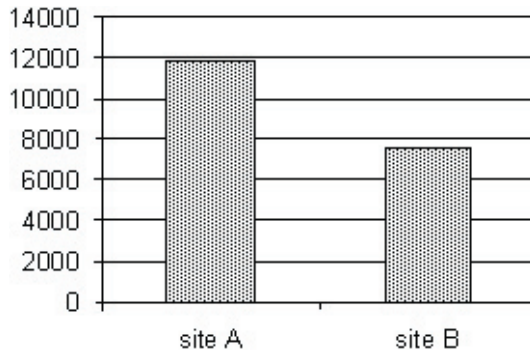
Fig. 1. Total number of individuals by month.

Fig. 2. Total number of individuals by site.

aridae (2.99% in site A and 2.29% in site B), *Isopoda* (1.64% in site A and 3.08% in site B), *Tipulidae* (1.03% in site A and 1.71% in site B) and *Phoridae* (0.72% in site A and 2.34% in site B). All these taxonomic groups, except for the three families of *Diptera* (*Sciaridae*, *Tipulidae* and *Phoridae*), are characteristic of the epigeal fauna. We assume that the high abundance of the families of *Diptera* in our captures was a result of sampling bias; we used pitfall traps without covers.

Community considerations

Table 3 displays a simple comparison of diversity in the two sites based on species richness, and similarity measured using Jaccard's and Sorenson's indices. The values indicate that the

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T a b l e 2. Taxonomic groups identified: Bold: site A only (12), Italics: site B only (12), normal: both (51).

Acari	Chironomidae	Drosophilidae	Mycetophilidae	Rhizophagidae
Agromyzidae	Chloropidae	Dryomyzidae	**Nabidae**	**Scarabaeidae**
Anthicidae	Chrysomelidae	Elateridae	Nitidulidae	*Scatopsidae*
Anthomyiidae	Cicadina	*Empididae*	Opiliones	Sciaridae
Aphididae	Cinipoidaea	Formicidae	Orthoptera	**Scutelleridae**
Apoidea	Coccinelidae	Heleomyzidae	*Panorpidae*	Silphidae
Araneae	Collembola	Histeridae	**Pentatomidae**	**Simuliidae**
Byrrhidae	Cryptophagidae	Ichneumonoidea	Phoridae	Syrphidae
Byturidae	*Culicidae*	Isopoda	**Platypezidae**	Sphaeroceridae
Calliphoridae	Curculionidae	**Lathridiidae**	Proctotrupoidea	Staphylinidae
Carabidae	Cydnidae	Lepidoptera	Pseudoscorpiones	Stratiomyidae
Cerambicidae	Cynipoidea	Lucanidae	Psocoptera	*Symphita*
Cecidomyiidae	**Dermaptera**	Lygaeidae	Psychodidae	*Tabanidae*
Chalcidoidea	Diplopoda	**Miridae**	*Ptiliidae*	Tipulidae
Chilopoda	Dolichopodidae	Muscidae	*Rhagionidae*	Vespoidea

T a b l e 3. Simple comparison of the two sites based on species richness and indices of similarity.

Month	Species richness		Index of diversity	
	Site A	Site B	Jaccard	Sorenson
May	40	40	0.58	0.74
June	37	37	0.53	0.69
July	38	38	0.60	0.75
August	14	14	0.50	0.67
Overall	61	61	0.69	0.82

T a b l e 4. Comparison of specific diversities expressed as Shannon's informational entropy between the two investigated communities, for each month individually, and for the entire period of study. The table displays the values of entropy (in nits), its variance and corresponding total number of species. The values of the t test, corresponding number of degrees of freedom (df) and associated p-values (p) are displayed for each comparison.

Period	Site A			Site B			Comparison		
	Entropy	Variance	N	Entropy	Variance	N	t test	df	p
All	2.34	0.001	11884	2.94	0.002	7583	-10.29	16490	< 0.0001
May	1.01	0.001	6932	2.04	0.003	2507	-16.74	4977	< 0.0001
June	1.82	0.003	2640	1.92	0.003	1998	-1.21	4531	0.226
July	1.80	0.003	2231	1.48	0.002	2894	4.39	4927	< 0.0001
August	1.91	0.040	81	1.68	0.026	184	0.89	187	0.376

sites are more than 50% similar, regardless of the period or index used in comparison. The results of comparing informational entropy for the two communities are presented in Table 4. Tests were significant at 0.001 in May, July and overall, but not in June (p = 0.226) and

T a b l e 5. Comparison between the specific frequency distributions of the two communities using the chi-square test for each month individually, and for the entire period of study. The table displays values of the chi-square test, corresponding number of degrees of freedom and associated p-values (p) in two scenarios, corresponding to the use of each community as a reference.

Period	Chi-square (using community B as reference)	df	p	Chi-square (using community A as reference)	df	p
All	5872.74	54	< 0.0001	3888.19	63	< 0.0001
May	18645.17	23	< 0.0001	4845.27	42	< 0.0001
June	1035.94	37	< 0.0001	652.67	45	< 0.0001
July	870.82	38	< 0.0001	691.65	35	< 0.0001
August	98.79	19	< 0.0001	382.76	15	< 0.0001

August (p = 0.376), thus indicating greater diversity in site B in May, June, and overall, and in site A in the remaining periods. Table 5 presents the results of the comparison performed using the chi-square test to compare the specific distributions. All tests exhibited significance at 0.001, indicating significantly different distributions for each month individually, and also for the entire study period.

Discussion

Species richness appears to be greater in community A for each month individually and also overall. However, comparisons based on informational entropy indicate greater diversity in community B during May and June, and greater diversity in community A during July and August. Monthly differences are significant only in May and July. For the entire period of study, community B exhibits significantly greater diversity. While results appear to be different when using the two methods, it is worth mentioning that comparisons based on Shannon's entropy index lead to sound results and are sustained by statistical significance. Specific distributions significantly differ for all months, for the entire period of study and also in all scenarios.

Our findings suggest that epigeal community diversity is greater in forests with increased tree species, and sustain the hypothesis according to which these communities can indicate structural changes (Evans et al., 2003).

The biodiversity data shifts with proportional increase in taxonomic resolution (Doledec et al., 2000). The literature reviews identified numerous papers in which sites, samples or treatments are compared based on ordinal-level abundance data, similar to this study. Since many of these processes operate at the species level, although there are some exceptions (New, 1996), few of these studies make a significant contribution to our understanding of the processes at work. A good practice is to allocate material to the species or morpho-species level if possible. Similarly, a beneficial practice is to treat all samples as separate entities throughout processing unless there is a very good reason to aggregate them before processing. Keeping them separate provides greater flexibility to the analysis. This is especially appropriate to detect levels of between-sample variation or species turnover, or to estimate species

richness by examining the rate of species accumulation by sample (Brose, 2002; Cam et al., 2002). An additional issue arises when material from a single species includes a mixture of developmental stages. This occurs in insect taxa which undergo incomplete metamorphosis, including bugs and grasshoppers, and also in many other invertebrate taxa, such as millipedes and molluscs. Presuming that data refers only to adults, when creating a database for such material it is important not to aggregate them if subsequent analysis treats all material as having equal status. At the macro-taxonomical level of order and family, a similar number of individuals or, otherwise a significant difference can be obtained from two compared sites (Grove, 2003; Krebs, 1989; Nitzu et al., 2009).

From an ecological viewpoint, we conclude that the greater diversity of site B, correlated with the fact that its structure is the closest to the natural one, suggests that silvicultural practices closer to the natural model provide for greater diversity, and this leads to increased stability under pressures induced by anthropogenic impact (Tomescu, Savu, 2002).

Finally, from a statistical methodology viewpoint, the results herein emphasize the utility of using the t-test in the comparison of Shannon's informational entropy index when comparing diversity (Magurran, 1998).

Conclusion

The functions of forest ecosystems change gradually from forests with a structure closer to the natural one to those subject to silvicultural interventions such as selective cuts and artificial regeneration across the gradient of anthropogenic impact; the endpoints can easily be distinguished functionally based on the structure of plant communities, and herbivorous and detritivorous organisms.

Our results indicate that diversity in epigeal communities is greater in forest sites with more tree species, suggesting that silvicultural practices closer to the natural model increase the diversity of forest ecosystems. Therefore, forest management has an effect on the richness and diversity of litter fauna, due to the interactions of trophic guilds. Consequently, the surrogacy of higher taxa can be seen as a valuable approach when it is impossible to identify the specimens at a low taxonomic level in a reasonable period of time, and in a context of limited financial resources. However, further studies are required to test whether the results herein are specific to the studied systems or if they can be generalized to "different" types of forest management.

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