

# PRELIMINARY DATA ON THE PHYTOPLANKTON COMMUNITY AND SAPROBIOLOGICAL CHARACTERISTICS OF RIVER STARI BEGEJ

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*Brankovic, D. (1993): Preliminary data on the phytoplankton community and saprobiological characteristics of river Stari Begej. - Tiscia 27, 57-60.*

**Abstract.** This paper contains results on preliminary examinations of phytoplankton community and saprobiological characteristics of the protected part of river Stari Begej, within the period from April to November 1990. 274 species, varieties and forms of Cyanophyta, Pyrrophyta, Xantophyta, Chrysophyta, Bacillariophyta, Euglenophyta and Chlorophyta were collected. The phytoplankton community was characterized by domination of Chlorophyta and a sporadic occurrence of Xantophyta. Density of phytoplankton community was changeable and varied from  $4.8 \times 10^3$  ind/cm<sup>3</sup> to  $11.2 \times 10^3$  ind/dm<sup>3</sup>. Index of saprobity varied from 2.0 to 2.4 which corresponds to the beta-mesosaprobic (second category) waters.

**Key words:** *Stari Begej, phytoplankton, bioindicators, saprobity.*

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## Introduction

"Stari Begej" is a protected area located in the central part of Vojvodina province - the north of Serbia, in the aluvion of rivers Begej and Tisza. This area includes the old riverbed of river Begej (within 10 km), Tiganjica, Carska bara, Perleska bara. Present character of this area was completed with the digging of a new riverbed of river Begej. The old riverbed of river Begej is supplied with the waters from nearby fishpond and from the river Tisza.

Because no data on former examinations of the phytoplankton community and saprobiological characteristics of the protected part of river Stari Begej exist, these examinations are preliminary and baseline information for further examinations.

## Material and methods

Sampling took place from April to November 1990, and was performed monthly on three sampling sites: on 15th km-I, 10th km-II, 5th km-III of river Stari Begej. Standard limnological methods for sampling, qualitative and quantitative analyses were used (Hribar, 1978). The index of saprobity was calculated after Pantle and Buck (1955) on the

basis of phytoplankton indicator species.

## Results

274 species, varieties and forms of Cyanophyta, Pyrrophyta, Xantophyta, Chrysophyta, Bacillariophyta, Euglenophyta and Chlorophyta were recorded in the protected part of river Stari Begej in the course of the examination period. Chlorophyta were represented with 117 taxa (42.7%), Bacillariophyta with 64 (23.3%), Euglenophyta with 40 (14.6%), Cyanophyta with 24 (8.7%), Pyrrophyta with 21 (7.6%), Xantophyta with 5 (1.8%) and Chrysophyta with 3 (1.1%) taxa.

From the division Chlorophyta which was represented with the highest number of taxa, *Scenedesmus abundans* (Kirch.) Chod., *S. acutus* (Meyen) Chod., *S. denticulatus* Lagerh., *S. falcatus* Chod., *S. opoliensis* Richter, *S. quadricauda* (Turp.) Breb., *Chlorella vulgaris* Beyerinck, *Crucigenia tetrapedia* (Kirch.) W. et G.S. West, *C. quadrata* Morren, *Dicdyospherium pulchellum* Wood, *Golenkinia radiata* Chod., *Pediastrum duplex* Meyen, *P. simplex* Meyen, *P. tetras* (Ehr.) Ralfs., *Tetraedron minimum* (Al. Braun) Hansg., *T. trigonum* (Nag.) Hansg., *Tetrastrum staurogeniaeforme* (Schro.) Lemm., *Staurastrum paradoxum*

Meyen were the species with the highest frequency.

From the division Bacillariophyta, the species *Cyclotella meneghiniana* Kutz., *Melosira granulata* (Ehr.) Ralfs., *Stephanodiscus hantzschii* Grunow, *Nitzschia palea* (Kutz.) W. Smith, *Synedra acus* Kutz., *S. ulna* (Nitzsch.) Ehr. were with the highest frequency.

From the division Euglenophyta, the species *Euglena acus* Ehr., *E. oxyuris* Schmarida, *E. viridis* Ehr., *Lepocinclis ovum* (Ehr.) Lemm., *Trachelomonas hispida* (Perty) Stein, *T. volvocina* Ehr. were of highest frequency.

*acicularis* W. Smith, *N. palea* (Kutz.) Smith, *Stephanodiscus hantzschii* Grunow, *Chlamydomonas ehrenbergii* Gorosch., *Gonium pectorale* Muller. Beta mesosaprob species are *Anabaena spiroides* Klebahn, *Aphanisomenon flos-aquae* (L.) Ralfs., *Microcystis aeruginosa* Kutz., *M. flos-aquae* (Wittr.) Kirchn., *Merismopedia tenuissima* Lemm., *Peridinium aciculiferum* Lemm., *Synura uvella* Ehr., *Achnantes lanceolata* (Breb.) Grun., *Amphora ovalis* Kutz., *Cymatopleura solea* (Breb.) W. Sm., *Cymbella lanceolata* (Ehr.) v. Heurck, *C. ventricosa* Kutz., *Diatoma tenue* var. *elongatum* Lyng.,

Table 1. Dynamics of density of phytoplankton community (Nx1000 ind/cm<sup>3</sup>).

Sampling site	Month						
	IV	VI	VII	VIII	IX	X	XI
I	5.0	8.1	7.7	6.8	6.4	8.5	7.4
II	5.2	8.6	8.1	7.2	7.7	8.0	6.5
III	4.8	8.8	8.6	8.5	11.2	7.9	9.1

From the division Cyanophyta, the species *Anabaena spiroides* Klebahn, *Aphanisomenon flos-aquae* (L.) Ralfs., *Microcystis aeruginosa* Kutz., *M. flos-aquae* (Wittr.) Kirchn. were the most abundant.

The frequency of representatives of Pyrrophyta and Chrysophyta was considerably lower and the representatives of Xanthophyta were recorded only sporadically.

The monthly variation in qualitative composition of the phytoplankton community is given on Fig. 1.

The density of phytoplankton community was changeable and varied from  $4.8 \times 10^3$  ind/cm<sup>3</sup> to  $11.2 \times 10^3$  ind/dm<sup>3</sup> (Table 1.). The minimal number was recorded in April on the sampling site III, and maximal one in September, also on the sampling site III.

The recorded phytoplankton indicator species of the polysaprob level are *Anabaena constricta* (Szafer) Geitler, *Spirulina jeneri* (Hass.) Kutz., *Euglena viridis* Ehr., and the species from genus *Carteria*. Those of alpha-mesosaprob level are *Oscillatoria formosa* Bory., *O. princeps* Vauch., *O. tenuis* Agardh, *Cryptomonas erosa* Ehr., *Cyclotella meneghiniana* Kutz., *Hantzschia amphioxys* (Ehr.) Grunow, *Navicula cryptocephala* Kutz., *Nitzschia*

*Epithemia turgida* (Ehr.) Kutz., the species of the genus *Gomphonema*, *Melosira granulata* (Ehr.) Ralfs., *Nitzschia vermicularis* (Kutz.) Grun., *Rhoicospheria curvata* Grun., *Synedra acus* Kutz., *S. ulna* (Nitzsch.) Ehr., *Phacus pleuronectes* (O.F.M.) Duj., *Trachelomonas volvocina* Ehr., *Eudorina elegans* Ehr., *Pandorina morum* Bory., *Actinastrum hantzschii* Lagerh., *Coelastrium microporum* Nag., *Dictyosphaerium pulchellum* Wood, *Micratriinium pusillum* Fres., the species of genera *Pediastrum* and *Scenedesmus*. Oligosaprob species are *Ceratium hirundinella* O.F.M., *Dynobryon sertularia* Ehr., *Nitzschia linearis* W. Sm., *Synedra acus* var. *angustissima* Grun. In general the indicators of beta-mesosaprob level were dominant.

Index of saprobity (Pantle and Buck, 1955) is given in Table 2.

## Discussion

274 species, varieties and forms of algae were recorded in the protected part of river Stari Begej in the course of examinations. This differs from data on algal taxa recorded in Carska bara swamp (Pujin et al., 1987) which is a part of this protected area

Table 2. Dynamics of saprobity index

Sampling site	Month							
	IV	V	VI	VII	VIII	IX	X	XI
I	2.3	2.3	2.2	2.0	2.2	2.2	2.1	2.2
II	2.3	2.2	2.1	2.0	2.1	2.2	2.2	2.2
III	2.3	2.2	2.2	2.0	2.1	2.4	2.0	2.2

and is supplied with water from river Stari Begej. 103 algal taxa altogether were recorded in Carska bara swamp. However, there were nonsignificant differences in the qualitative composition of phytoplankton community in the protected part of river Stari Begej and in Carska bara swamp (Pujin et al., 1987). Namely, in Carska bara swamp Chlorophyta were also represented with the highest number of taxa. Bacillariophyta were the second in rank and were followed by Euglenophyta and Cyanophyta. Pyrrophyta, Xantophyta and Chrysophyta were represented with significantly lower number of taxa.

With regard to some rivers of this region, the differences in qualitative composition of phytoplankton community were noticed.

The examination of river Ponjavica (Obuškovic, 1991) showed that Euglenophyta and Chlorophyta were the dominant groups of algae and were followed by Bacillariophyta and Cyanophyta. The other groups of algae were represented with significantly lower number of taxa.

Obuškovic (1982) found that in river Bosut the representatives of Bacillariophyta were dominant and Chlorophyta, Cyanophyta and Euglenophyta taxa were subdominant. Number of taxa of other groups of algae was low.

It can be pointed out that the qualitative composition of phytoplankton community of this protected habitat was almost similar to that in Ludaš lake (Seleši, 1981) which is a protected area as well. Namely, in Ludaš lake Chlorophyta were also the dominant group of algae with the highest number of taxa. Bacillariophyta were the second and then came Euglenophyta, Cyanophyta and Pyrrophyta. Xantophyta and Chrysophyta were represented with only one taxon, respectively.

Regarding the monthly variation in the qualitative composition (Fig. 1), it can be concluded that the principal features of phytoplankton community of the protected part of river Stari Begej were the dominance of Chlorophyta and a sporadic occurrence of Xantophyta.

In the variation of density of phytoplankton community no regularity can be noticed.

The index of saprobity after Pantle and Buck (1955) varied from 2.0 to 2.4 but no regularity could be noticed in its variation, as well. On the basis of saprobity index, the waters of the protected part of river Stari Begej can be ranked as beta-mesosaprob (second category) ones.

From these examinations, it could be concluded that such qualitative composition of the phytoplankton community is often associated with eutrophic conditions.

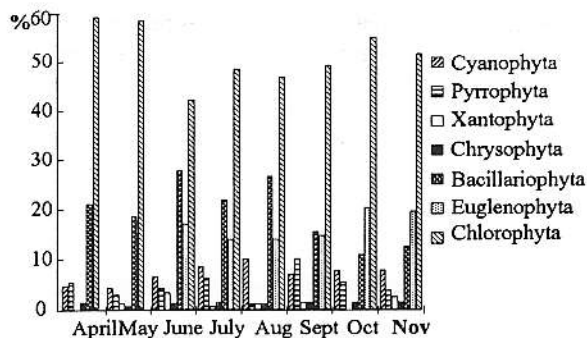


Fig. 1. Variation in phytoplankton community in Stari Begej waters during 1990.

Apart from nutrient loading, the phytoplankton community composition depends on climate and other ecological conditions. Many authors pointed out the influence of temperature and pH. Saphiro (1973) demonstrated that the phytoplankton dominance in a nutrient rich pond could be switched from dominance of blue-green algae to dominance of chlorococcal green algae by adding free carbon dioxide and lowering pH of water. Vincent and Silvester (1979) demonstrated that temperature and pH optima for *Anabaena* and *Chlorella* are divergent, 28-35 °C and 23-28 °C, respectively, and pH 9-10 and pH 7-8, respectively. So, possible explanation of Chlorophyta domination in the protected part of river Stari Begej is that carbon is never limiting factor for phytoplankton growth and, therefore, pH has not been so high that Cyanophyta growth has been selectively promoted.

Another hypothesis for Chlorophyta dominance could be that these algae oust representatives of other groups of algae by means of some growth inhibiting factors, although Vincent and Silvester (1979) demonstrated the opposite case. Namely, these authors recorded that extracellular products from *Chlorella vulgaris* promote the growth of *Microcystis* and *Anabaena* while extracellular products from *Microcystis* and *Anabaena* inhibit the growth of *Chlorella*.

Several authors (Andersson et al., 1978; Brooks and Dodson, 1965; Cronberg, 1980) recorded influence of fish stock on the phytoplankton community. Andersson et al. (1978) and Cronberg (1980) demonstrated that abundance of bream and roach in the waters affected the phytoplankton community. These fish species are very abundant in the protected part of river Stari Begej (Budakov, 1989) and so obviously have an effect on the phytoplankton community.

Taking all these facts into consideration, it

could be concluded that the phytoplankton community composition and its variation in the protected part of river Stari Begej was dependent, among other factors, and apart from nutrient loadings, on temperature, pH, allelopathic factors and fish stock.

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# THE STATE OF POPULATION OF *CROCUS BANATICUS* J. GAY IN THE TRANSCARPATHIAN REGION OF THE TISZA VALLEY

A. V. Mihály and V. I. Komendar

*Mihály, A. V. and Komendar, V. I. (1993): The state of population of Crocus banaticus J. Gay in the Transcarpathian region of the Tisza valley. - Tiscia 27, 61-63.*

**Abstract.** This paper presents the results of the investigation of a *Crocus banaticus* J. Gay population in the Transcarpathian area of the Tisza valley. Data are given about range of distribution, phytocenotic thriven species, age structure of the population and seed production. Some data are also presented on the biology of the species, and certain aspects of generative reproduction of *C. banaticus* are analyzed. We give suggestions to the protection and re-establishment of natural area of this species in Carpathian region.

**Key words:** *Iridaceae, Crocus banaticus, population biology, protection.*

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## Introduction

In order to develop the effective protection and natural area re-establishment of rare and disappearing plants, there is a need for complex studies of ecological and biological characteristics of these species. The ephemeroïd elements of the natural flora are most sensitive to anthropogenic influence. One of them is *Crocus banaticus* J. Gay that is under full destruction threat. Large quantities of its flowers are picked, corms are dugged up and transplanted. In the last decade the population size of *C. banaticus* has been drastically reduced as a consequence of wood-felling and melioration. The area decreases, some populations completely disappeared, the individual numbers in populations decreased to critical level. The *Crocus banaticus* is highly decorative, flowers in autumn, and is pollinated by bee.

## Material and Methods

Studies on *C. banaticus* were carried out in 3 isolated populations in Tisza valley:

1. Village Bushtino environs, Tyachiv district, 250 m a.s.l.;
2. Village Onok environs, Vinogradovo district, 300 m a.s.l.;
3. Village M. Kopanya environs, Vinogradovo

district, 400 m a.s.l.;

Area and state of local populations were measured, description of plant communities with the presence of *C. banaticus* was done by route method. Plants were collected to study the morphological features and seed production.

Population size, ontogeny and age structure were determined in different ecological-phytocenologic conditions with transects laid down by random method (Smirnova et al., 1976). Age classes were determined according to Rabotnov (1950a) and Smirnova et al. (1976).

Seed production was measured according to Rabotnov (1950b) and Vainagy (1974). The potential seed production (PSP) -- number of seedbuds in fruit, actual seed production -- seed number in fruit, and seeding percentage (SP) -- proportion of seedbuds developing to seed were determined on 25 randomly marked individuals in each population. Standard variance analysis statistics were calculated (Zaitsev, 1973; Schmidt, 1984).

## Results and Discussion

The *Crocus banaticus* J. Gay (syn.: *C. iridiflorus* Heuff.; *C. byzanthinus* Herb.) is an autumnal flowering ephemeroïd plant from Iridaceae A.L. de Jussieu family. As many

hysteranthous geophytes, it is also related to Mediterranean flora (Dafni et al., 1981). It is Sub-Dacian floral element (Randeljovic et al., 1990). It occurs in Rumania (Beldie, 1967), Serbia (Hayek, 1933; Jávorka, 1964; Randjelovic et al., 1990), from northern Transsylvania to the Balkans (Priszter 1974). In Ukraine it occurs only in Transcarpathia, the north-eastern border of its area. *C. banaticus* grows in zonal oak and beech forests and sometimes, for example, in Transylvanian mountains Erc, reaches 1000 m above sea-level (Bernátsky, 1911).

*C. banaticus* prefers semishaded places, grows in oak and beech forests, brushwoods. The investigated populations were in *Festuco-Quercetum roboris* association of *Quercetea robori-petraeae* Br.-Bl. et Tx. 43 class, *Fago-Carpinetum* association of *Carpino-Fagetea* Jakucs 67 class, *Robinetum pseudoacaciae* association of *Robinietea Jurko ex Hadac et Sofron* 80 class (Krichfalushiy and Mihály, 1993).

The corm of *C. banaticus* is round, slightly flattened at the top and bottom, its width varies from 14 to 16 mm, and the height from 8 to 9 mm. The colour is dirty-brown. Flowers are significantly different from those of other *Crocus* species. Size of inner petals is the half of that of outer ones, and their color is violet. Anthers are yellow, stigma is blue-violet, and is very branched (number of branches ranges up to 50). Flowers of 10-12 cm bloom in September-October (sometimes even in the beginning of November). Leaves and fruits appear next spring. The sprout is very weak and brittle during the flowering, mechanical strength is given by the associated leaves. Fruits are three-sided capsules. In each of the three cavities the seeds are arranged in two rows. Seeds are redish-brown, elliptical, lemon like acuminate at the ends, 4-4.5 mm in length. Generative individuals have three green leaves, but senile ones have only 1-2. Leaves are lanceolate, erect, 15-25 cm in length and 13-15 mm in width. Apex of leaf is slightly blunt. Fruit opens with three parts. Seeds

germinate in autumn. Flowering occurs in the 4-5th year.

Ontogenic stages of *C. banaticus* are: juvenile (j), immature (im), virgin (v), generative (g) and senile. Age structure of the populations studied is given in Table 1 and Fig. 1.

Group of juvenile plants prevails over all populations, juvenile and immature individuals are over 70 % in all populations. A rather low number of generative individuals should be explained with frequent flower picking. The Bushtino and M. Kopanya populations are fully arthrous, normal by Rabotnov (1950) scheme. The share of senile plants is very low. The three populations may be classified as young, normal, close to invasional.

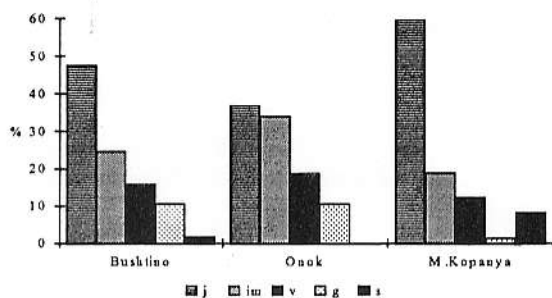


Fig. 1. Age structure of *Crocus banaticus* populations.

For the ephemeroïds, characteristic are the complete, left sided basic spectra, in which pregenerative individuals dominate over generative and senile ones. This can be explained with the long persistence of virgin period of ontogeny, as well as the dominance of seed germination over vegetative reproduction in population dynamics.

Interspecific competition has rather low effect on ephemeroïd populations, its manifestation is obvious near the border of the population distribution. In such conditions the individual number of populations decreases abruptly, and the strong deformation of their age spectra can be observed (Shorina and Smirnova, 1976).

*C. banaticus* propagates itself generatively

Table 1. Age structure of *Crocus banaticus* populations. Individual numbers per m<sup>2</sup> and percentage are given.

Population	Community	density of individuals ind/m <sup>2</sup>	Age group						
			j	im	v	g	s	j+im	v+g+s
Bushtino	Festuco-Quercetum roboris	183	87	45	29	19	3	132	51
		%	47.54	24.59	15.85	10.38	1.64	72.13	27.87
Onok	Robinetum pseudoacaciae	144	53	49	27	15	-	102	42
		%	36.80	34.03	18.75	10.42	-	70.83	29.17
M. Kopanya	Fago-Carpinetum	74	44	14	9	1	6	58	16
		%	59.46	18.92	12.16	1.35	8.11	78.38	21.62

Table 2. Potential and actual seed productions of *C. banaticus* populations studied.

Population	PSP			ASP			SP %
	$\bar{x}$	s $\bar{x}$	min-max	$\bar{x}$	s $\bar{x}$	min-max	
Bushтино	35.13	1.47	22-56	23.23	2.26	3-47	66.13
Onok	40.97	1.68	26-63	34.47	1.99	14-57	84.13
M.Kopanya	28.59	1.19	18-44	18.93	1.31	4-34	66.21

very easily and fast by means of seeds, but vegetative propagation is quite weak. The number of pregenerative individuals depends on the soil seed bank that is connected to the seed production of the population (Komendár and Némét, 1980). Table 2. summarizes the seed production of *C. banaticus* in the three populations studied.

Some conclusions of the investigations: the number of germs is considerably stable than that of seeds. Differences between germ numbers of each populations are less than those between seed numbers. Actual seed production depends mainly on environmental conditions, but potential seed production is less dependent, that refers to its genetic background.

Population of M. Kopanya is most threatened, it is situated close to the highway. Here the flowers are collected, mainly the largest ones ("artificial selection" takes place: the weakest and smallest individuals remain in the population). These facts could explain the low seed production and the small number of generative individuals in the population: this population is degrading under anthropogenic influence.

Protection of *C. banaticus* is very important in Transcarpathia, because here is the north-eastern border of its area. *C. banaticus* is present in the Red data book of Ukraine and USSR. It is a disappearing species, area of which is decreased under human pressure. *C. banaticus* is an endangered species not only in Ukrainian Carpathians but in other regions. The most effective protection and reestablishment of its populations should be in natural habitats, and with establishing nature reserves.

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# COMPARATIVE ANALYSIS OF SUCCESSIONAL STAGES OF SANDY VEGETATION - A CASE STUDY

K. Margóczy

*Margóczy, K. (1993): Comparative analysis of successional stages of sandy vegetation - a case study. - Tiscia 27, 3-8.*

**Abstract.** The vegetation of seven selected sites, representing different stages of primary succession, is analyzed in order to establish a feasible successional scheme, and to compare the traditional successional pathways and the pathway suggested by the multivariate methods.

The ordination of micro-scale coenological relevés suggests a more or less linear successional sequence of studied stands corresponding with the traditional theory.

Five typical patches were identified in each stand by classification in order to represent the internal variability of the vegetation. Ordination of these typical patches on the basis of species frequencies shows, that the primary dynamic of the sand vegetation is more complex. The linear successional sequence of studied stands is unlikely, different transitions between stages are equiprobable, and the graph structure of series is rather reticular.

Three groups of stands were identified by diversity ordering: (i) an initial, open grassland type with low diversity; (ii) a grassland with medium diversity; the forest herb layer also belongs to this category; (iii) the most diverse, closed grassland, and the shrubby habitat. Diversity profiles of these groups were clearly separated.

The methods employed differentiate the vegetation of the studied stands according to their species composition, diversity and complexity, but the established sequence does not necessarily reflect to the real historical development of the stands in question.

*Keywords: sandy vegetation, succession, multivariate methods, diversity ordering*

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## Introduction

One of the typical vegetation and flora types of the Hungarian Plain can be found on sandy areas between the Danube and Tisza rivers. This vegetation has been studied by many authors, among them such pioneers as Kerner (1863) and Rapaics (1918). The successional stages were described by Hargitai (1940), Zsolt (1943) and Magyar (1960). Besides this classical works, Précsényi (1981) studied the diversity changes during succession and there are several publications elucidating certain ecophysiological phenomena of such vegetation (e.g. Tuba, 1984 and Fekete et al., 1988). The spatial pattern as well as the niche relations of some species belonging to the grassland community *Festucetum vaginatae* were studied by Molnár and Nosek (1979) and Fekete et al. (1980).

Recently Fekete (1992) published a new concept of primary succession, which is different from

the traditional interpretation by the Hungarian phytosociologists. He pointed out that the primary dynamics of sandy vegetation is very complex: the vegetation-soil evolution is non-parallel; the succession is often determined by stochastic transitions between stages; the successional graph structure of the sand sere is rather reticular than linear; origin of climax stage is heterogeneous. The pioneer grassland does not accumulate sufficient humus for the establishment of steppe-meadow species, so the steppe meadow does not fit the pioneer grassland-shrub line. The stands of oak wood (the climax community in the traditional concept) are habitat-dependent.

Although the classical phytocoenological description of sandy vegetation succession is given in the above mentioned papers, no detailed multivariate analysis has been made to describe vegetation differences among the stages.

Classifications and ordinations are suitable for



analysis of succession, but the effectiveness of different methods depends on the nature of analyzed data (Mazzoleni, 1991).

Unequivocal successional sequences are not necessarily self evident to critical observer (Anderson, 1986). For example, computer based classification and ordination techniques defined a successional gradient that differed from a theoretical or assumed successional classification in the case of a big sagebrush/grass community (Tueller and Platou, 1991).

The aim of this study is to analyze the vegetation of selected habitats in a Hungarian sandy area using multivariate methods and diversity comparisons, and to evaluate the different concepts of succession according to the results.

The ant community composition and epigeic fauna of the same study plots analysed in this paper has also been studied (Járdán et al., 1993).

## Study area and Methods

### 1. Site description

The field studies were carried out in a nature reserve in the southern part of Hungary, between the rivers, Duna and Tisza near to the village Kéleshalom in June 1991. The study site is a complex of wind-blown sand dunes. Several successional stages of sandy vegetation occur here from bare sand to poplar forest. For the present study 7 plots were selected, representing these stages:

Plot 1. Almost bare sand with some plant species belonging to the association *Festucetum vaginatae*. The bare surface within the plot may derive from an abandoned sand-mine.

Plot 2. Open perennial grassland with 30-40 % plant coverage, predominating by *Festuca vaginata* (*Festucetum vaginatae danubiale*). The moss and lichen layer was also considerable.

Plot 3. Similar to plot 2, but predominated by *Stipa borysthénica*. (*Festucetum vaginatae stiptosum borysthénicae*)

Plot 4. Open perennial grassland predominated by the species belonging to the *Festucetum vaginatae* community and *Populus alba* forms a shrub storey here. Height of it is 50 cm, about 25 % cover).

Plot 5. Closed grassland with some xero-

mesophilous and mesophilous species besides the xerotolerant ones. The phytocoenological status of this stand is uncertain.

Plot 6. Shrubby habitat with 50-60 % coverage of *Crataegus monogyna*, *Juniperus communis*, *Berberis vulgaris* and *Ligustrum vulgare* shrubs

Plot 7. Closed poplar (*Populus alba*) forest with some *Robinia pseudoacacia* trees. *Crataegus monogyna* and *Juniperus communis* give a sparse shrub layer.

The areas of the study plots were about 400 m<sup>2</sup>.

### 2. Field sampling

A similar sampling procedure was applied than described by Szollát and Bartha (1991) with some modifications. Long transect of 200 contiguous small plots, each of 20x20 cm size, were used for sampling in each stand. The total transect of 40 m length was broken 4-5 times, resulting a zig-zag line "netting" the whole plot. The presence and absence of species rooting in the subplots were recorded. In the shrubby habitat and in the poplar forest only the herb layer was sampled. The presence of detectable lichen and moss species were recorded and analysed together with the higher plants.

### 3. Data analysis

The seven study sites were ordinated according to the pooled frequency of occurring species using principal coordinate analysis with Czekanowski index by the program package NuCoSA (Tóthmérész, 1991, 1993a). Virágh (1986) has found the same ordination method and similarity index to be useful for detecting vegetation differences in a similar scale study.

In order to represent the internal variability of the stands five most abundant characteristic patch types (10 contiguous 20x20 cm subplot of each) were selected in each stand by classification of all 200 subplots according to their species composition, using the Sørensen similarity index by the NCLAS2 program of SYN-TAX III. program package (Podani, 1988). These 20x100 cm<sup>2</sup> subplots, representing typical patches, were classified by NuCoSA using Czekanowski similarity index and single linkage sorting algorithm. Principal coordinate analyses (NuCoSA) of the same subplots were performed using again Czekanowski index, and the results of clustering method and ordination were combined.



Analysis of the diversity conditions were performed by diversity ordering (Tóthmérész 1993a,b). This evaluation differentiates the diversity sequence of studied communities based on

dominant versus rare species. The Hill diversity value is sensitive on rare species at low scale parameter value and it is sensitive on dominant species at high parameter value.

Table 1. The pooled frequency values of the species in the 200 20x20 cm quadrat per study plot. Data of 22 rare species, whose pooled frequency values were below 10 are not indicated. The used nomenclature is after Simon (1992).

SPECIES	STUDY PLOTS						
	1	2	3	4	5	6	7
<i>Achillea pannonica</i>	0	0	0	0	11	72	0
<i>Alyssum tortuosum</i>	30	1	5	39	0	0	0
<i>Asclepias syriaca</i>	16	0	0	0	0	0	0
<i>Asperula cynanchyca</i>	0	0	0	0	0	27	0
<i>Berberis vulgaris</i>	0	0	0	0	0	26	27
<i>Botriochloa ischemum</i>	0	0	9	9	0	0	0
<i>Bromus sterilis</i>	0	0	0	0	0	0	36
<i>Calamagrostis epigeios</i>	0	0	0	0	16	4	0
<i>Camptothecium lutescens</i>	0	0	0	0	0	54	0
<i>Carex flacca</i>	0	0	0	0	0	0	72
<i>Carex liparicarpus</i>	12	24	34	77	58	119	127
<i>Cladonia convoluta</i>	0	59	8	4	1	0	0
<i>Cladonia magyrica</i>	0	33	0	0	14	0	0
<i>Cladonia rangiformis</i>	0	0	0	0	8	56	0
<i>Cornus sanguinea</i>	0	0	0	0	0	19	10
<i>Crataegus monogyna</i>	1	0	0	0	0	9	36
<i>Cynodon dactylon</i>	0	0	14	0	0	0	2
<i>Cynoglossum officinale</i>	0	0	0	32	0	0	0
<i>Equisetum ramosissimum</i>	0	0	0	0	26	0	0
<i>Erigeron canadensis</i>	1	13	0	4	0	0	0
<i>Erysimum diffusum</i>	0	4	5	7	3	0	0
<i>Euphorbia cyparissias</i>	0	2	0	0	6	23	0
<i>Euphorbia seguieriana</i>	59	12	29	10	2	9	0
<i>Falcaria vulgaris</i>	0	0	0	0	0	14	0
<i>Festuca vaginata</i>	124	109	68	167	22	45	5
<i>Festuca wagneri</i>	0	0	0	0	73	18	0
<i>Fumana procumbens</i>	17	5	70	3	0	0	0
<i>Galium verum</i>	0	0	0	0	94	37	4
<i>Holoschoenus romanus</i>	0	0	0	0	42	0	0
<i>Kochia laniflora</i>	0	30	66	4	9	0	0
<i>Koeleria glauca</i>	12	13	36	0	2	4	0
<i>Ligustrum vulgare</i>	0	0	0	0	0	24	55
<i>Minuartia glomerata</i>	4	0	8	0	0	0	0
<i>Minuartia verna</i>	5	28	8	0	1	2	0
<i>Parmelia pokornyi</i>	0	39	58	2	1	0	0
<i>Pimpinella saxifraga</i>	0	0	0	0	0	0	10
<i>Pleurochaete squarrosa</i>	0	36	0	0	37	7	0
<i>Poa angustifolia</i>	0	0	0	0	43	51	12
<i>Polygonum arenarium</i>	0	7	5	50	12	0	0
<i>Populus alba</i>	0	0	0	33	0	0	0
<i>Potentilla arenaria</i>	0	37	18	16	23	76	0
<i>Prunus spinosa</i>	0	0	0	0	0	2	27
<i>Scabiosa ochroleuca</i>	0	0	0	0	21	55	0
<i>Sedum hillebrandii</i>	0	3	11	0	0	0	0
<i>Stipa borysthenica</i>	23	132	105	61	51	98	0
<i>Stipa capillata</i>	0	0	0	64	0	0	0
<i>Syntrichia ruralis</i>	5	70	16	34	22	0	0
<i>Taraxacum officinale</i>	0	0	0	0	1	5	4
<i>Teucrium chamaedrys</i>	0	47	0	0	113	26	48
<i>Thesium arvense</i>	0	0	0	4	6	0	0
<i>Thymus pannonicus</i>	15	46	45	0	52	101	0
<i>Torilis japonica</i>	0	0	0	0	0	0	16
<i>Viola rupestris</i>	0	0	0	0	0	32	5
Total species number	15	24	21	19	35	33	28

## Result

### *Ordination and classification of study plots*

The ordination of the seven stands according to the pooled frequency of occurring species defined a successional sequence, that did not differ considerably from a theoretical or assumed successional order, if the arch effect of the ordination method is taken into consideration; only the plot 4 does not fit well into the sequence (Fig. 1.).

The selected representative subplots of the stands were separated rather well on the PCoA scattergram (Fig. 2.), and the classification results confirm the togetherness of these subplots (Fig. 3.). There are very few overlaps between the different stands, consequently between the successional stages. Only the subplots of the shrubby habitat (plot 6) form no separate cluster and they are positioned far from each other on the central part of the scattergram. The vegetation of this stand is very heterogeneous. The identified patch types may represent different successional stages, and can be ordered in a feasible successional sequence that is parallel with the sequence of the other stands (Fig. 2.).

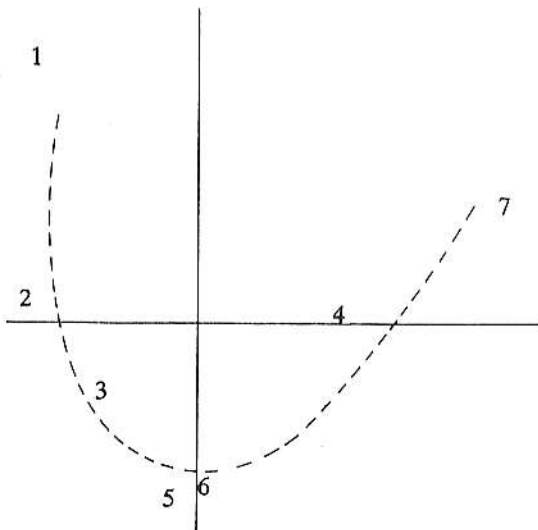


Fig. 1. Principal coordinate analysis of the study plots according to the pooled frequencies of the occurring species. For the description of the study plots indicated by numbers see the "Study area and Methods".

Some subplots do not join to any group; they represent unical patch types. On Fig. 2. the subplots of plot 1. and plot 4. are encircled together, this two plots represent the initial stage of succession in this

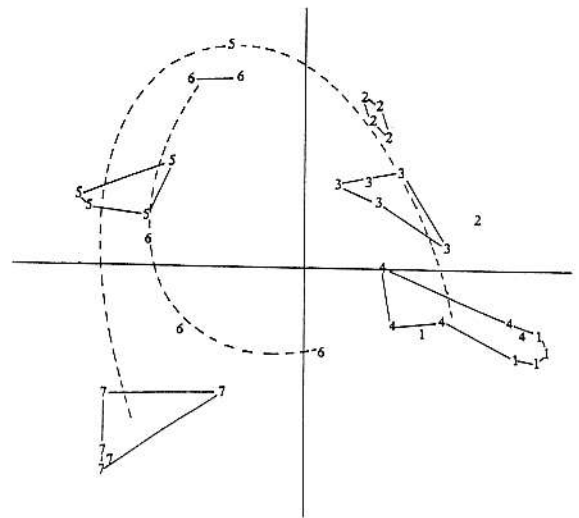


Fig. 2. Principal coordinate analysis of the representative subplots of the studied stands. Lines encircle the subplots belonging to the same cluster, indicated by stars in Fig. 3. The dashed lines sign possible orders of the samples considering the arch effect of the ordination method.

area. Inside the denoted cluster the two study sites are separated (Fig 3.).

### *Diversity*

Altogether 76 species were recorded in the 7 stands. The frequencies of species are presented on Table 1. (Data of 22 rare species, whose summed frequency values were below 10 are not indicated.)

Three groups of stands were identified by diversity ordering: (i) an initial, open grassland type with low diversity; (ii) a grassland with medium diversity; the forest herb layer also belongs to this category; (iii) the most diverse, closed grassland, and the shrubby habitat. Diversity profiles of these groups were clearly separated.

In the first group the diversity of plot 1 is unambiguously lower, than that of the plot 4. However in the medium diversity group the profile of plots 2, 3 and 7 cross each other, this means that these three communities cannot be ordered simply by their diversity. At lower scale parameter, that is, regarding the rare species the diversity of the plot 7 is the highest, but the opposite is right at the higher value of scale parameter -- regarding the dominant species.

### **Discussion**

According to the traditional interpretations (Zsolt, 1943 and Magyar, 1960) the feasible successional sequence of studied stands is the

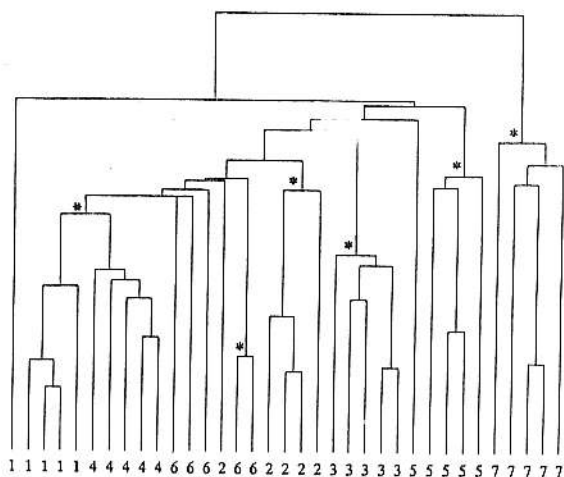


Fig. 3. Dendrogram of the representative subplots of the studied stands. The stars indicate the relevant clusters, subplots of which are encircled by lines in the ordination diagram in the Fig. 2.

following: almost bare sand (plot 1) -- *Festucetum vaginatae danubiale* (plot 2) -- *Festucetum vaginatae stipetosum sabulosae* (plot 3) -- open grassland with small poplar trees (plot 4) -- closed grassland (plot 5) -- shrubby habitat (plot 6) -- poplar forest (plot 7). On the PCoA scattergram of stands this sequence can be more or less recognized if considering the arch effect of the ordination method (Fig.1.). The arch effect is stronger when the ordinated samples have few species in common (Mazzoleni et al., 1991). The *Brometum tectorum*

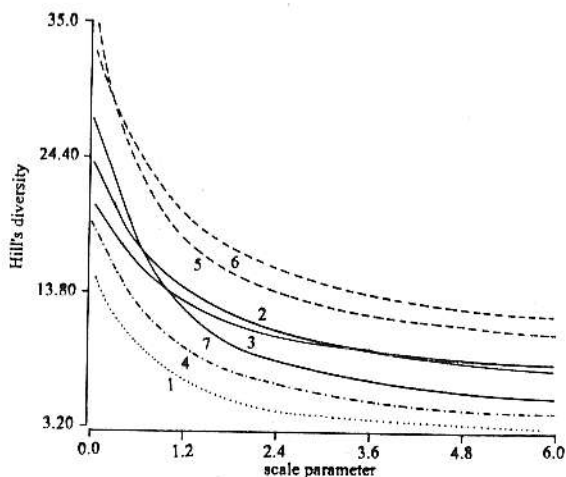


Fig 4. Diversity ordering of the study plots, according to the pooled frequency values of the occurring species. For description of the study plots indicated by numbers see the "Study area and Methods".

community, an annual grassland, which is regarded by the traditional concept as the first stage of sandy succession cannot be found in Kéleshalom site. *Festuca vaginata* is the most frequent species in the very open, presumably pioneer stages (plot 1 and plot 4). It is remarkable, that poplar can colonize even in the very initial form of *Festucetum vaginatae* community the (plot 4).

Fekete (1992) presented a different concept of primary succession on sand: the starting point is usually *Festucetum vaginatae* community. The succession terminates at the *Junipero - Populetum* along many lines; this community corresponds to the real forests in this sere. The steppe meadow (closed grassland) does not fit to the pioneer grassland -- shrub line and this makes the graph reticulated in this xereries.

The result of analysis reflecting to the internal variability of the stands (Fig. 2.) support this concept rather than the traditional, linear successional sequence. The starting point is undoubtedly the complex of the plot 1 and plot 4; plot 2, 3, 5 and 7 could be alternative endpoints of succession. Besides this an alternative explanation of the scattergram is also possible: (1-4) -- 3 - 2 - 5 - 7 plot sequence could be recognized along an arch in the Fig. 2.

The subplots of plot 6 may represent intermediate stages of alternative pathways leading from the open grassland (plot 1,4) to the closed grassland (plot 5) and poplar forest (plot 7). At the same time the subplots representing typical patches of plot 6 are ordered along an arch, parallel with the mentioned (1-4) -- 3 - 2 - 5 - 7 plot sequence in the scattergram. That is, alternative interpretations are possible when trying to identify the successional sequence on the base of the ordination result. The used methods are suitable to arrange the communities according to their complexity, and species composition but it does not mean, that the identified sequence exactly corresponds to the real historical development of the stands in question.

In a hilly area there are considerable differences in the physico-chemical condition of the soil (i.e., humus and nitrogen content, water content and soil granule size) at the top of the sand hills, in the wind grooves between them and at the relatively flat areas (Körmöcz, 1983). Such environmental differences may cause the development of alternative endpoints of succession, according to the concept of Drake (1990), who regard the environmental gradients as a filter defining which set of species is permissible to colonize.

The species diversity is the highest in the closed grassland (plot 5) and in the shrubby habitat (plot

6), but presumable because of different reasons. In the case of closed grassland community the more favourable environmental conditions of the slight wind groove habitat (higher soil humidity, lower wind effect and insolation) allow the coexistence of more species. The shrubby habitats have developed in the upper slope of a sand hill, and the shrubs stand separately providing a wide variety of microhabitats from the open, dry patches between the shrubs to the shaded sites under their canopy, where the soil is covered by litter. Here the habitat heterogeneity causes higher number of species.

Studying similar sandy vegetation Précsényi (1981) found that the species diversity was the lowest in the last stage of succession, that is in the forest. In present case the diversity of forest herb layer is high if regarding the rare species, but considerably lower if regarding the dominant species (Fig. 4.). This community does not evolve automatically from a previous grassland stage, but the light shortage (the shading effect of the growing tree canopy) drives its development. So, because of the considerable change in environmental conditions a different species pool is allowed to colonize (cf. Drake, 1990)

The vegetation of plot 4 provides an evidence, that the reforestation of open grassland is possible, but cannot be found clear transitional stages between the open grassland and forest herb layer among the studied plots.

Present paper refers to field investigations of one single time point. Direct evidences about the successional pathways can be drawn up only after several years study period on permanent plots. Result of such a long term study carried out on the vegetation of Hungarian sandy areas have not been published yet. Although better understanding of the succession is very important from the nature conservation point of view as well, because the conservation activity have to aim at maintainance of all successional stages close to each other if it is possible. But the minimal spatial scale of the successional processes is not known yet as well.

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# ANT ASSEMBLAGE COMPOSITION IN A SUCCESSIONAL HUNGARIAN SAND DUNE AREA

Cs. Járdán, L. Gallé and K. Margóczy

*Járdán, Cs., Gallé, L. and Margóczy, K. (1993): Ant assemblage composition in a successional Hungarian sand dune area. - Tiscia 27, 9-15.*

**Abstract.** In the frame of a project dealing with the succession of ant communities in sand dune areas of different geographical regions in Europe, in Kéleshalom sandy area (southern Hungary) eight study plots, representing different successional stages of vegetation, were selected for detailed sampling program. PCA analysis of the ant assemblages of study plots shows that the succession of the ant community composition follows two main pathways: one is typical to open areas, i.e. grasslands, the other is usually terminated in forests.

Comparing the successional sequence of the study plots according to their ant assemblages, vegetation composition and epigeic fauna, it is established that the initial and final successional phases are the same in each case, but there are uncoordinated successional steps in the three assemblage types in the transitional stages. The diversity of ant assemblages increases along the successional gradients, but that of the vegetation and epigeic fauna has a maximum in a transitional phase.

Microclimate, dead twigs on ground surface and vegetation architecture were identified as the main external correlates, which probably have certain role in structuring ant assemblages.

*Key words:* ant communities, primary succession, environmental correlates, sand dunes

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## Introduction

Vegetation succession has extensively been studied from the very beginning of ecology (Clements, 1916; Cowles, 1899; Gleason, 1917). The succession of animal communities, however, is one of the most neglected fields in animal ecology. Although there is a lot of information on the composition of ant communities (see e.g. Brian, 1983; Hölldobler and Wilson, 1990; as reviewing books), we know much less about the process of organization, i.e. succession of these assemblages. The succession of the ant communities is usually studied by simultaneous comparison of several habitats representing different successional stages (Szujecki et al., 1978; Vepsäläinen and Pisarski, 1982; Boomsma and Van Loon, 1982; Zorrilla et al., 1986; Gallé, 1991; Gallé et al., in preparation) and there are much fewer long-term investigations on the successional transformation of ant populations or assemblages in a particular habitat (e.g. Gallé, 1981; Gallé et al., 1993) because of the long time

span of community dynamic processes. We use the first, comparative approach in the present paper, which is a part of a project dealing with the primary succession of ant assemblages in different sand-dune areas of Europe and the Middle East, from Finland to southern Turkey. The previous papers of the series have been carried out by Gallé (1990a, 1990b, 1991) and Gallé et al. (in preparation).

The field studies were done in a successional sand-dune area in Middle-Hungary in order to reveal the main attributes of ant communities of different successional stages. Three main questions were addressed, as follows:

(1) What kinds of differences and similarities exist in the composition of the ant assemblages in the study plots, which represent different successional stages of vegetation?

(2) Is there any co-ordination between the pathways of ant community succession, and that of other assemblages, i.e. vegetation and the epigeic fauna?

(3) Which external conditions (habitat proper-



ties) are correlated with the structure of ant assemblages?

### Study area and methods

The study area is a complex of wind-formed sand-dunes, between the rivers Duna and Tisza in the southern part of Hungary, and it belongs to Kiskunság region near the village Kéleshalom.

For detailed studies, eight plots were selected with areas of 300 to 500 m<sup>2</sup>. The plots were parts of such habitats, which represented different stages of the sand-dune vegetation succession (Fekete, 1992) from the bare sand through open grasslands, closed grasslands, shrubby habitat to a poplar forest. Plot 1 had a low coverage (<20%) of plants, mainly *Festuca vaginata* and *Stipa borysthénica*. Although differing in exposition and total vegetation coverage, plots 2 and 3 were similar open grasslands of denser vegetation than plot 1, predominated by *Festuca vaginata*, *Stipa borysthénica* and *Koeleria glauca*. The moss and lichen layer was also considerable. Litter cover was about 40%. Plot 4 was a closed grassland, predominated by *Festuca pseudovina*, *Teucrium chamaedrys*, *Holoschoenus vulgaris*, *Galium verum* and *Poa angustifolia*. The moss and lichen cover was also considerable. Plot 5 resembled to 3, but with a *Populus alba* shrubby storey (height <50 cm, coverage about 30%). Plot 6 was a shrubby habitat with *Crataegus monogyna*, *Juniperus communis*, *Berberis vulgaris* and *Ligustrum vulgare*. *Thymus degenianus*, *Stipa borysthénica*, *Carex liparocarpos*, *Galium verum* plant species were found in the understory. Plot 7 and 8 were closed poplar (*Populus alba*) forests with some *Robinia pseudoacacia* trees. There were

shrubby storeys with *Crataegus monogyna* and *Juniperus communis*. *Carex flacca* was predominant in the herb layer. These two plots apparently differed in their red wood ants, therefore they were separately treated. A more detailed survey on the vegetation of the research area is given by Margóczy (1993).

The ant assemblages were sampled with pitfall traps. 12 traps were used in each study plot and the traps worked two times for two weeks. The same pitfall traps yielded the data on the composition of the epigeic fauna, as well. Herb layer invertebrates were collected with sweep net. 5x10 sweeps were applied in each study plot. Beside the various invertebrate groups, these samples yielded some additional information on the ant fauna of the study plots, too. All collected animals were sorted on taxonomic group level. If considerable body size differences were observed within a taxonomic group, it was subdivided into size classes.

The cover of plant species was estimated in 5 quadrates of 1 m<sup>2</sup> in every plot. Using the average values of the number of collected ant specimens, that of the other epigeic groups, and the average cover values of plant species, three resemblance matrices were set up. The percentage similarity values of Renkonen index were used in these matrices to compare the study plots according to the three different assemblages, i.e. vegetation, ants and epigeic fauna. With the help of these matrices, the possible successional sequence of study plots could be set up, because the similarity between the plots presumably represents the successional relations of them.

In order to find the main external correlates of the composition of ant assemblages, we examined

Table 1. Attributes for characterization of study plots

Core group	Habitat cores	No. of categories
[1] Vegetation architecture	1.1 Total plant cover	1
	1.2 Cover of mosses and lichens	2
	1.3 Mould thickness	1
	1.4 Plant cover at 0-5, 5-15, 15-30, 30-50... level	5
[2] Vegetation composition	2.1 Relative frequency of predominating plant species	65
[3] Size of plot		1
[4] Dead twigs on ground surface	4.1 Density of dead branches of various sizes and conditions	25
[5] Microclimate	5.1 Temperatures of soil, of air 2 cm above soil surface, and of air at 2 m height	3
	5.2 Soil water content	1
[6] Epigeic fauna	6.1 Frequency of various animal groups collected in pitfall traps	28
[7] Fauna of the herb layer	7.1 Frequency of various animal groups collected by sweep net	28
Total		160

Table 2. Frequency of ant species collected by pitfall traps (individuals/trap)

Species	Plot no.							
	1	2	3	4	5	6	7	8
<i>Myrmica rugulosa</i> Nyl.								*0.08
<i>Myrmica laevinodis</i> Nyl.							*	*
<i>Myrmica sabuleti</i> Meinert						*	+18.0	*5.66
<i>Diplorhoptum fugax</i> Latr.				0.09				
<i>Tetramorium caespitum</i> Latr.				10.27		3.58		
<i>Leptothorax nylanderi</i> Först.				0.18		+	*+3.41	*+1.66
<i>Leptothorax unifasciatus</i> Latr.						+		*0.41
<i>Leptothorax tuberum</i> Först.						0.58	*+1.75	+0.41
<i>Dolichoderus quadripunctatus</i> L.								0.08
<i>Tapinoma ambiguum</i> Em.				1.36		1.25		
<i>Plagiolepis vindobonensis</i> Lomn.	2.25	+ 8.90	+ 9.08	11.36	+ 11.1	0.91		+
<i>Plagiolepis xene</i> Starke					*			
<i>Camponotus vagus</i> Scop.						1.75		0.08
<i>Camponotus truncatus</i> Spin.						0.08		0.08
<i>Lasius alienus</i> Forst.	494.6	+181.4	+167.0	168.1	+1391.	63.33	0.08	0.16
<i>Formica sanguinea</i> Latr.		0.27		55.63		+40.58		
<i>Formica fusca</i> Latr.						0.25	4.41	4.50
<i>Formica cunicularia</i> Latr.			1.83		0.33	*2.75		
<i>Formica rufa</i> Latr.							0.08	10.66
<i>Formica pratensis</i> Retz.					2.33		64.75	4.08
<i>Cataglyphis aenescens</i> Latr.	* 11.0	+ 34.0	+ 14.83	+ 3.09	16.08			
<i>Polyergus rufescens</i> Latr.			6.41					
Total	3	4	5	7	6	13	8	14

\* = sexuals collected by hand or / and pitfall traps

+ = workers collected by sweep net

their correlation with some habitat properties. We used altogether 160 habitat attribute scores for a detailed characterization of the study plots. These habitat scores were grouped in seven: vegetation architecture, vegetation composition, size of the plot, twigs on the ground surface, microclimate, epigeic fauna and faunal composition in herb layer (Table 1).

From among the habitat attributes not mentioned above, the measurement of the microclimate was carried out in the usual ways. The number of dead twigs on the surface were counted in 0.5x0.5 m quadrates; the lengths, widths and the condition (fresh, dry, dry with holes, wet and rotten, only husks) of the twigs were measured.

In the data evaluation, PCA ordination was employed to establish relation among the studied objects (i.e. plots, ant, invertebrate and plant communities).

## Results

A total of 22 ant species were collected (Table 2). The study plots formed two main groups on the basis of the composition of their ant fauna: the ant assemblages of first three plots were predominated by *Lasius alienus*, *Plagiolepis vindobonensis* and *Cataglyphis aenescens*. These plots represented the earliest stages of ant assemblage succession, with

low species diversity. A higher number of ant species were found in the second group of plots, especially in forest habitats (Table 2).

Ordination of the Barber trap ant data by PCA yielded the following results (Fig. 1). The ant assemblages of open habitats are positioned mainly in the "a" part of the PCA; the samples from forest plots are on the opposite part of the figure ("b"); and the angle of the pipe-like figure contains the samples of transitional stages. According to these results, it seems very possible that the succession of ant community composition may follow two main pathways: one is typical to open areas, i.e. grasslands and leading to the ant assemblages of closed grasslands, the other is characteristic to the path, which leads to the ant assemblages of the forests.

A more exact successional sequence of the plots can be set up on the basis of resemblance matrices of the ant, plant and epigeic animal communities (see Fig. 2). The plots can be arranged roughly into five successional steps in all of the three community types. It is clear that the initial and final successional stages are the same in each case, but both the position of the transitional plots and the pathways show some differences. This means that there are uncoordinated steps in the succession between the different communities.

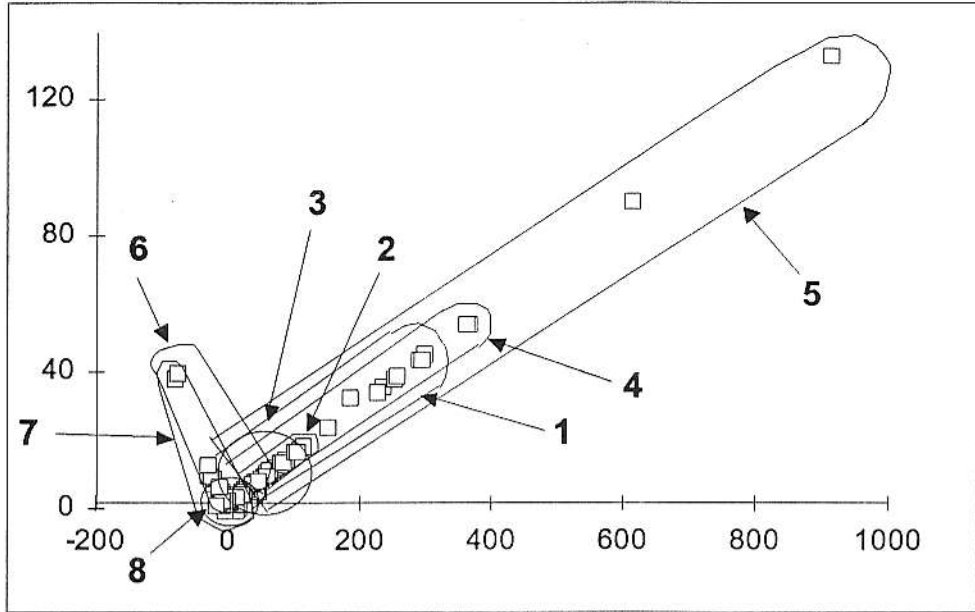


Fig. 1. Ordination of Barber trap ant data by PCA. Traps of the same plot are encircled.

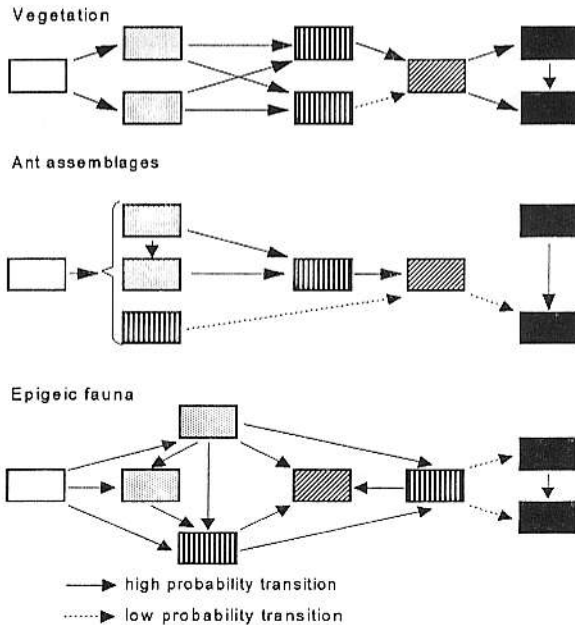


Fig. 2. Successional sequence of the study plots on the basis of resemblance matrices of the ant, plant and the epigeic animal communities.

The Shannon diversity of ant assemblages increases along the five-step successional sequence (Fig. 3.), whereas that of the vegetation and the epigeic fauna reaches a maximum in the third stage.

For the correlation analysis between ant assemblage composition and the habitat attribute scores we used the first three coordinates of each study plot in PCA factor space set up on the basis of their ant assemblage composition and the correlation were computed between these coordinates and the values of the above mentioned 160 individual habitat scores. Using this method, we found that there were 23 attributes correlated with ants, such as microclimate factors, dead twigs, some invertebrate groups and plant species (Table 3.).

There are some problems with the interpretation of these results because of the possible intercorrelation between attributes. Therefore we used also another procedure in order to determine more exactly the external correlates of ant communities. Study plots were ordinated on the basis of their ant assemblages and the different attribute groups mentioned above (Table 1.) in seven different PCA spaces. In all cases the relative position of the points representing the plots in the PCA factor spaces was measured as a set of multidimensional Euclidean distances (Pielou, 1984) from the others weighted by the variance percentage values of the PCA axes. The distances of the corresponding points in differ-

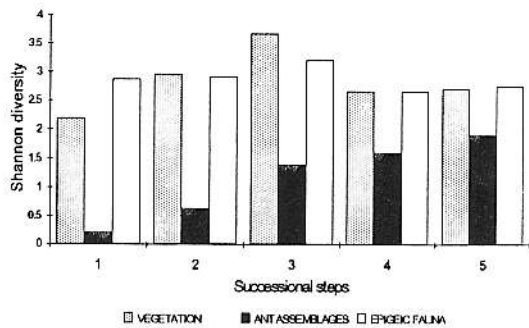


Fig. 3. Shannon diversity of vegetation, ant assemblages and epigeic fauna in five successional steps.

ent PCA spaces were compared with correlation analysis using non-parametric Spearman's coefficients. Close correlation between the relative position of plots computed from their ant assemblage composition and any other attribute group indicates that the attributes in question presumably affect the composition of the ant assemblages. Since this analysis resulted in a combined correlation table, the table-wide significance values were computed by the sequential Bonferroni test (Rice, 1989).

The dead twigs on ground surface, the microclimate and in less extent the vegetation

architecture were found to be significantly correlated with the composition of ant assemblages (Table 4.).

## Discussion

It has been demonstrated by several authors that diversity of different ecological communities shows an increasing trend during succession (Odum, 1969; Bába, 1980; Rey, 1981; Andersen, 1986; partially Boomsma and Van Loon, 1982; Györfy and Körmöczi, 1987; but not quite by Kondoh and Kitazawa, 1984). A decline of the diversity brought about by the high density of red wood ants at the final successional stages was demonstrated by Gallé et al. (in preparation) in Kampinos region, Poland. In the present study, however, the density of red wood ants was not so high in the forest plot that it could decrease the diversity of ant assemblages.

We found a negative correlation between the density of the pioneering ant species (i.e. *Lasius alienus*) and the ant community diversity ( $r = -0.76$ ,  $p < 0.05$ ) as Boomsma and Van Loon (1982) described it, likewise Gallé et al (1985) and Gallé (1991).

The above results suggest that the vegetation

Table 3. Factors correlated with PCA axes of ordination of ant assemblages.  $|r|$  = absolute value of coefficient of correlation;  $p$  = level of significance

Factors	axis	$ r $	$p$
Plant cover at 5-15 cm level	II.	0.811	< 0.02
Mould thickness	I.	0.980	< 0.001
Frequency of two plant species			
<i>Crataegus monogyna</i>	I.	0.761	< 0.05
<i>Carex flacca</i> var. <i>cuspidata</i>	I.	0.737	< 0.05
Microclimate			
Soil temperature	I.	0.820	< 0.02
Surface temperature	I.	0.836	< 0.01
Soil water content	I.	0.906	< 0.01
Dead twigs of different sizes in different conditions	I.	0.713 - 0.983	< 0.05 - < 0.001
Epigeic invertebrates			
Acaridea	I.	0.740	< 0.05
Acridoidea	I.	0.727	< 0.05
Araneidea II.	I.	0.839	< 0.01
Chilopoda	III.	0.718	< 0.05
Cicadinea	I.	0.749	< 0.05
Diplopoda	II.	0.920	< 0.01
Isopoda	I.	0.775	< 0.05
Mollusca	I.	0.976	< 0.001
Invertebrates in the herb layer			
Gastropoda	II.	0.904	< 0.01
Araneidea II.	I.	0.719	< 0.05
Diptera	III.	0.717	< 0.05
Acaridea	III.	0.762	< 0.05
Collembola	III.	0.903	< 0.01
Cicadinea	I.	0.849	< 0.01
Coleoptera I.	I.	0.903	< 0.01

Table 4. Spearman's rank correlation between PCA spaces of different groups of habitat scores and ant assemblages.  $|r|$  = absolute value of coefficient of correlation;  $p$  = level of significance

Score groups	$ r $	$p$
Vegetation architecture	0.376	<0.05
Vegetation composition	0.196	n.s.
Microclimate	0.683	<0.001
Dead twigs on ground surface	0.721	<0.001
Composition of epigeic fauna	0.199	n.s.
Fauna of the herb layer	0.199	n.s.

architecture is an important factor differentiating ant assemblages. It accords with the results of Boomsma and De Vries (1980), Johnson et al. (1983), Seifert (1986), Gallé (1991) and Gallé et al. (in preparation). The complexity of the vegetation architecture is a component of the habitat heterogeneity that can be responsible for the increasing diversity during ant community succession (Kondoh and Kitazawa, 1984; Zorrilla et al., 1986; Gallé, 1991).

Both previous studies (Gallé, 1991; Seifert, 1986) and the present results suggest that the dead twigs on the ground surface have an important effect on the composition of ant communities. The role of microclimate (Brian, 1964; Gallé, 1975, 1991) is not so equivocal.

In contrast to Johnson et al. (1983) and Seifert (1986), but according with Gallé (1991) we found that the vegetation composition does not play a significant role in structuring the composition of examined ant assemblages.

Making a comparison between the present results from Kéleshalom study site and the results of similar previous studies from other sand-dune areas studied in the course of the present project (Gallé, 1990a, 1990b, 1991; Gallé et al., in preparation) on the environmental factors which possible affect the composition of ant assemblages (Table 1.), there are some good agreements, e.g. regarding the correlation with vegetation architecture, the dead twigs on ground surface and the composition of epigeic fauna, but there are some differences, too. The comparative results of the present study with the previous ones, suggest that the microclimate has an increasing importance toward the southern geographical regions in the determination of the composition of sand-dune ant assemblages.

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# ANTS (HYMENOPTERA, FORMICIDAE) OF THE GLADES IN THE TATRA MTS (THE CARPATHIANS)

M. Woyciechowski

*Woyciechowski, M. (1993): Ants (Hymenoptera, Formicidae) of the glades in the Tatra Mts. (the Carpathians). - Tiscia 27, 17-22.*

**Abstract.** Fourteen species of ants have been found within the area of 23 glades in the Polish part of the Tatra Mts. The number of ant species and the density of nests are greater in sheep-grazed glades than in the other, non-grazed glades. The number of species is positively correlated with increasing altitude. Hitherto two ant species: *Myrmica lobicornis* and *Formica picea* have not been recorded from the Polish Tatra Mts. The preservation of Tatra glades, artificially cleared in natural forest, by moderate grazing seems to keep a greater variety of habitats and simultaneously greater diversity of ant species.

*Key words:* ant community, open habitat, glade utilization.

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## Introduction

Data concerning the distribution of ants in the Polish part of the Tatra Mts are scarce and were often compiled either in the 19th c. (Nowicki, 1864, 1867; Wierzajski, 1868, 1874) or at least 60 years ago (Kulmatycki, 1920; Lomnicki, 1931). Only few information on the distribution of previously recorded species can be found in later works (Dluski and Pisarski, 1971; Pisarski, 1971, 1975).

The distribution of ants in the Tatra Mts is limited mainly to open habitats. In forest associations, ant nests can be found almost exclusively in the vicinity of non-forest associations or, temporarily, in windfall areas.

The Tatra glades were created artificially on land formerly occupied by lower (up to ca. 1250 m a.s.l.) and upper (up to ca. 1550 m a.s.l.) mountain forest associations. Their presence there was stabilized by regular grazing or mowing, combined with organic fertilization. However, such utilization of most of the glades was abandoned in the sixties of this century. As a result, most of the glades started to become overgrown with forest relatively soon (in ca. 30 years) (Dziewolski, 1985; Michalik, 1986), thus diminishing the area of open habitats, infrequent in the mountain forest associations and primarily limited to rocks, screes or peat-bogs.

The aim of the present study was to 1) assess the species composition and quantitative relationships of the ant in glades of the Polish part of the Tatra Mts; 2) assess the influence on those insects of environmental conditions connected with the altitude and the mode of utilization (grazing, mowing) or its lack.

## Study area and methods

The research on the ants was conducted between June and August in 1982-1984. It took place in 23 of the several dozen glades situated within mountain forest associations of the Polish part of the Tatra Mts (Western Carpathians) (Fig. 1). Single stones, rocks, small, man-made mounds of stones and fallen trees were included in the study area. On the other hand, ants collected from plant associations of rocky turf-on-sprees type glades or their vicinity were not included.

The glades were selected according to their distribution within the various plant association zones and their utilization or its lack. The latter criterion helped to divide them into three groups: grazed glades, mown glades and non-utilized glades. Pasture (mostly sheep) was re-introduced in the glades of the grazed category only several years ago. Those mown were thus treated regularly in most of

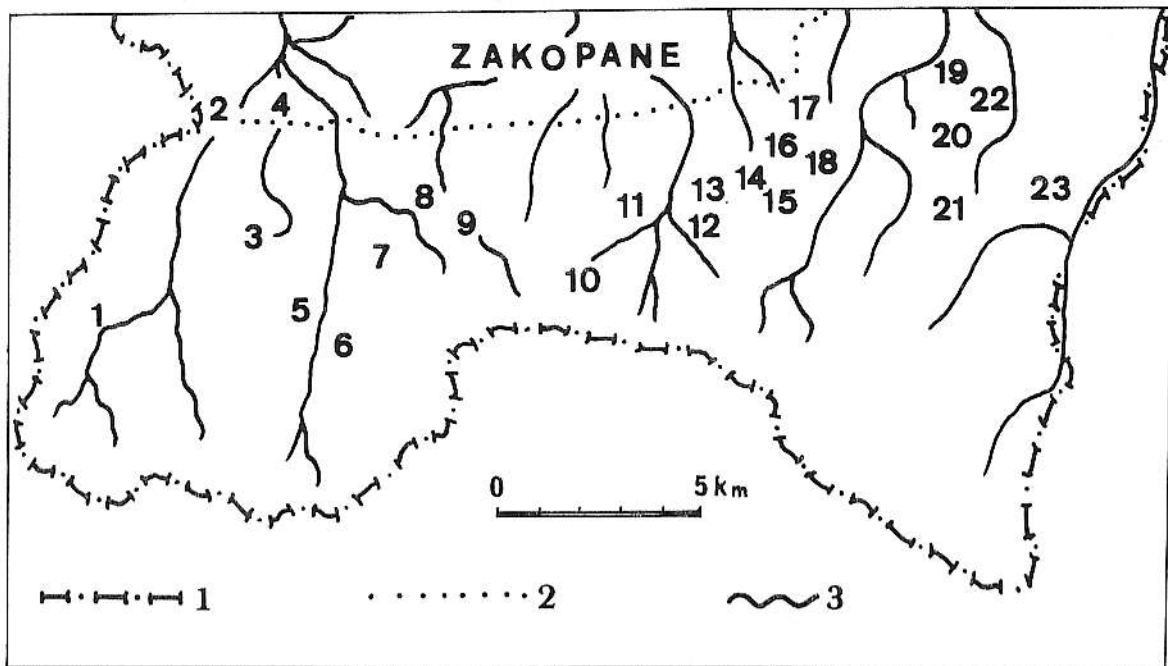


Fig. 1. The distribution of the studied glades in the Polish part of the Tatra Mts. 1 - country border, 2 - border of the Tatra National Park, 3 - streams (the number describe the glades as listed in Table 1).

their area, usually once a year. The non-utilized glades have been left non-grazed or unmown for at least a dozen or so years and were overgrown with at most single tree seedlings. Only two glades, situated outside the Tatra National Park (Fig. 1) have been mown and grazed (mostly by cattle) with no interruption for many years.

The ants were collected in 10 to 30 plots (10 m<sup>2</sup>) in each glade, according to the size of the glade. The plots were combed as precisely as possible for all ant nests. This method was used in 13 glades of a total of 3100 m<sup>2</sup>. Additionally, in all the 23 glades, it was attempted to find as many nests as possible on the whole area of each glade, with particular care in the places where the probability of discovering them was the greatest. It is latter method that yielded a qualitatively richer material. The altitudes were recorded for each nest found. Also, foraging ants were collected during the search for nests. If a species was represented in a glade by foraging individuals only, this information was treated as if one nest of the foraging species were found, without any data on its altitude. Single representatives of sexual castes were not included in the results.

## Results

A total of 14 ant species was recorded from 23 Tatra glades. Of those, *Myrmica ruginodis*, *Formica lemni*, *M. scabrinodis* and *M. rubra* were the most numerous and present in the greatest number of the glades. Nests of the remaining species were found in lesser numbers and in less than a half of the glades studied (Table 1.).

Two of the species recorded, *M. lobicornis* and *F. picea* have not been reported so far from the Tatra Mts. *M. lobicornis* was found in seven glades. Two nests of *F. picea* were found in a tall peat-bog called Molkowka.

It was established that the number of ant species present in the glades is positively correlated with the area of the glades (Sperman test;  $r_s=0.586$ ,  $df=20$ ,  $P<0.01$ ; Table 1.). The Bialy Potok glade was excluded from the evaluation of this correlation, as its area was greater than almost twice that of the other large glades, and because of its situation in the vicinity of busy roads and settlements.

The greatest number of ten species was recorded in the non-utilized Przyslop Mietusi glade, standing apart from the other glades because of its

greatest habitat differentiation. The nests of most of those species were found on the southern slopes of the glade, among scant vegetation covering dry, shallow, rocky terrain. Excluding this glade from the considerations, the average number of species

found in all grazed glades was 6.1, in mown glades 4.8 and in non-utilized glades 3.1. The difference in the number of species inhabiting the three glade groups is of statistic significance (Kruskal-Wallis test;  $T=6.392$ ,  $df=2$ ,  $P<0.05$ ).

Table 1. Percentage of ant species and number of nests (N) found in the Tatra glades (each glade with its approximated area in ha, type of utilization: g - grazed, m - mown, n - non-utilized, and the average altitude of nests found, respectively).

Glade	a	b	c	d	e	f	g	h	i	j	k	l	m	n	N		
1. Chochołowska	19 g	1139	21	38	15	2	2	15	7						47		
2. Molkowka	15 g	940	57	17			10	8	9	9					23		
3. Niznia Kominiarska	8 g	1144	3	5	52	10		5	15						40		
4. Biały Potok	40 g	920	20	60				20							5		
5. Stara	3 n	1100	100												1		
6. Smytnia	5 n	1125	17	50								33			6		
7. Uplaz	12 n	1280		50								50			4		
8. Przysłop Mietusi	11 n	1152	4	4	50	4	4	4	4	11		4			26		
9. Małej Łaki	12 n	1183	4	64			4	4	8		4	16			25		
10. Kondratowa	13 m	1367	4	32	4	7	14	4				35			28		
11. Kalatówki	13 g	1179	2	2	45	30	17					4			53		
12. Kasprowa	4 n	1231	11	89											9		
13. Jaworzynka	10 n	1091	11	22	56							11			9		
14. Oleczysko	8 m	1075	38	8	4	4	8				21	17			24		
15. Krolowa	4 n	1300		100											1		
16. Sucha	5 g	1130		61	8	8	8					15			13		
17. Szalasiska	2 g	1115	9	9	37			27				18			1		
18. Kopieniec	9 g	1249	3	67		3	3				6	18			33		
19. Wawrzeczkowa Cyrhla	9 m	915	8	25	50						8	42			24		
20. Przednia Soltysia	5 n	1314	4	8	25	13					8	42			24		
21. Wąskmundzka	12 m	1358		69	8							23			13		
22. Szalasiska Kopy	2 n	1140		57		42									7		
23. Rusinowa	17 g	1235	17	44	14	3			8	3	8	3			36		
Total number of nests			10	51	189	57	4	19	4	15	1	6	16	14	62	2	450

a - *Manica rubida*; b - *Myrmica rubra*; c - *M. ruginodis*; d - *M. scabrinodis*; e - *M. rugulosa*; f - *M. lobicornis*; g - *M. sulcinodis*; h - *Leptothorax acervorum*; i - *L. muscorum*; j - *Camponotus herculeanus*; k - *Lasius niger*; l - *L. flavus*; m - *Formica lemni*; n - *F. picea*

The evaluation of ant nest density was performed for 13 glades (Table 2.); only 9 species, of which 4 were represented by single nests, were found on 3100 m<sup>2</sup>. 39 nests of the most numerous species, *M. ruginodis*, were found in 7 grazed glades over a total of 1540 m<sup>2</sup>. Only 20 nests of that species were found in the other glade categories

over a total of 1560 m<sup>2</sup>; this would point to a significant difference of their density in both types of the glades ( $\chi^2 = 5.360$ ,  $df = 1$ ,  $P < 0.05$ ). As the number of the nests of the other ant species was insignificant, they were treated jointly; thus, only 7 nests were found in the non-grazed glades, while 52 in the grazed ones. In view of the study area, this

Table 2. Density of ant nests per 100 m<sup>2</sup> and total number of nests found (N) in the Tatra glades (each glade with its type of utilization - as in Table I. - and area in which the search was conducted, in m<sup>2</sup>).

Glade	a	b	c	d	e	f	g	h	i	N
1. Chochołowska	g 300	1.7	2.0	1.7	0.3		0.3	0.3	0.3	20
3. Niznia Kominiarska	g 240	0.4	1.7	1.3						8
8. Przysłop Mietusi	n 300	1.0	2.7							11
9. Małej Łaki	m 300		1.7							5
10. Kondratowa	m 300		1.3			0.3			0.7	7
11. Kalatówki	g 300	0.3	5.3	4.3	3.0					39
13. Jaworzynka	n 130		0.3							1
14. Oleczysko	m 130									0
15. Krolowa	n 100									0
16. Sucha	g 100									0
18. Kopieniec	g 300	0.3	3.0						1.3	14
21. Wąskmundzka	g 300		0.7						0.3	3
23. Rusinowa	g 300	0.7	1.3	1.0	0.3					10

a - *Myrmica rubra*; b - *M. ruginodis*; c - *M. scabrinodis*; d - *M. rugulosa*; e - *M. lobicornis*; f - *M. sulcinodis*; g - *Leptothorax acervorum*; h - *Lasius niger*; i - *Formica lemni*.

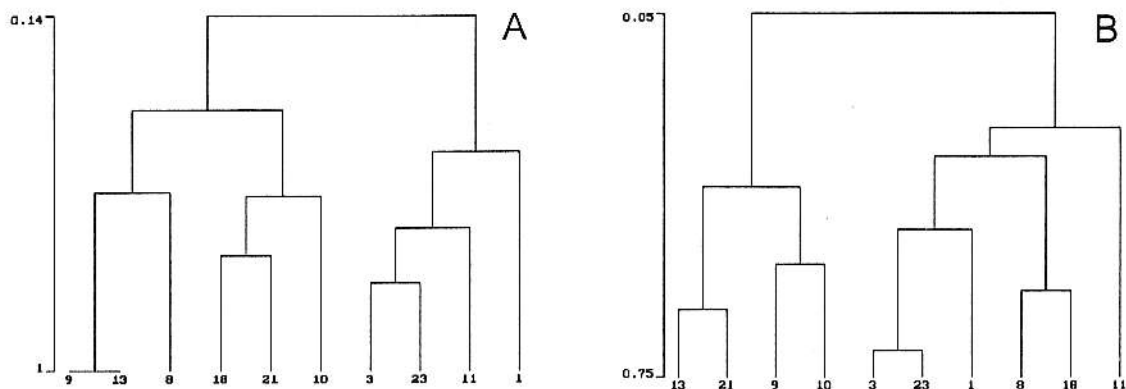


Fig. 2. Similarity of myrmecofauna of 10 Tatra glades evaluated basing on the search of plots, resulting from species presence (A) and nest density (B).

yields a highly significant difference in density ( $\chi^2 = 29.728$ ,  $df = 1$ ,  $P < 0.001$ ).

The results obtained in nest density evaluation (the glades with zero trials were excluded) were used in a dendrogram of glade similarity, calculated basing on the information of the species' presence (Fig. 2A) or on their nests' density per 100 m<sup>2</sup> (Fig. 2B). In both dendrograms, the glades grouped into two categories, the grazed and the non-grazed, with two exceptions: the Kopieniec glade (18), which entered the non-grazed group (Fig. 2A) and the non-utilized Przyslop Mietusi glade (8) among the grazed glades (Fig. 2B).

In order to establish the influence of the altitude on the distribution of the particular species, the nests were categorized according to their situation below or above the altitude of 1250 m a.s.l. (Table 3.). Only the Molkowka glade was excluded from these considerations, its being a natural peat-bog and not an artificially created glade. Of the 13 spe-

cies, all were found below 1250 m a.s.l., while only 9 above that altitude.

### Discussion

Two of the 14 ant species recorded in the glades (Table 1.) were not mentioned in the list of the 16 species reported by Lomnicki (1931) from the Polish part of the Tatra Mts. The first of these is *F. picea* from the Molkowka peat-bog, now utilized as grazing ground, though it is a natural non-forest association, with a preserved, typically peat-bog floras. *F. picea* is rare in Poland, only found in peat-bogs (Dluski and Pisarski, 1971). This species has been so far unrecorded from the Polish part of the Carpathians. The nests of the second species, *M. lobicornis*, were found in almost one in three of the glades. It is thus a species frequent in the glades; it can be surmised that the reports on the presence of the morphologically related *M. schencki*, reported

Table 3. Percentage of ant nests found in the Tatra glades below and above 1250 m a.s.l., with (parenthesized) the number of studied nests of each species (the lowest altitude of a nest was 915, the highest - 1450 m a.s.l.).

Species		Up to 1250	Above 1250
1. <i>Manica rubida</i>	(9)	78	22
2. <i>Myrmica rubra</i>	(37)	97	3
3. <i>M. ruginodis</i>	(189)	85	15
4. <i>M. scabrinodis</i>	(53)	79	21
5. <i>M. rugulosa</i>	(4)	25	75
6. <i>M. lobicornis</i>	(14)	83	17
7. <i>M. sulcinodis</i>	(1)	100	
8. <i>Leptothorax acervorum</i>	(14)	100	
9. <i>Lep. muscorum</i>	(1)	100	
10. <i>Camponotus herculeanus</i>	(6)	100	
11. <i>Lasius niger</i>	(15)	93	7
12. <i>L. flavus</i>	(14)	86	14
13. <i>Formica lemni</i>	(59)	54	46



by Lomnicki (1931) from the Tatra Mts, the region of Zakopane and Toporowa Cyrhla, concern in fact *M. lobicornis*.

The severe climatic conditions of the Tatra Mts are the reason for the poverty of the ant fauna there, in comparison with the other parts of the Carpathians, e.g. with the much smaller Pieniny Mts (46 species; Koehler, 1951; Czechowska, 1976), Male Pieniny Mts (38 species; Woyciechowski, 1985, and unpublished) or Bieszczady Mts (30 species; Parapura and Pisarski, 1971). Four species are the most frequent ones in Tatra glades, whether these are utilized or not: *M. ruginodis*, *F. lemami*, *M. scabrinodis* and *M. rubra*. Both the dominant species and the complete list (Table 1.) are similar to those of the glades in the Bieszczady Mts, which, similarly to the Tatra glades, were created in primarily for the scant forest terrain. The Tatra glades are characteristic for the scant presence of the nests of *L. niger* and *L. flavus*, dominant in glades and pastures of the other regions of the Carpathians (Parapura and Pisarski, 1971; Petal, 1974; Czechowska, 1976; Woyciechowski and Misztka, 1976; Woyciechowski, 1985).

The parts of the glades overgrown with rich grassy vegetation are usually completely deprived of ant nests. This can be observed in most non-utilized and mown glades. Also empty of ants are the fragments of glades covered with compact *Alchemilla* sp. or *Rumex alpinus*, as sheep rarely graze on those species. Such associations can be observed not only in non-utilized glades such as Przyslop Mietusi or mown ones such as Mala Laka, but also in grazed ones such as Niznia Kominiarska. The diversity of habitats of particular importance for the ants was mostly impoverished in the glades mown now or in the past. Large fragments of those glades have been deprived of single rocks or stones and nests of many ant species can be found on mounds made of those stones or on small embankments. In some glades, e. g. Chocholowska, such places yield much higher nest densities, and are the almost sole habitats occupied by the ants in some other ones, e. g. Mala Laka or Olczyška.

Parts of many glades, especially steep, insolated slopes of shallow, rocky terrain, are convenient habitats for ant nests whether they are presently utilized or not. This is the case in glades such as Przyslop Mietusi, Kopieiniec or Szalasiska Kopy.

The above-mentioned reasons make more difficult a straightforward evaluation of the type of glade utilization on the ants. It can be stated, however, that the number and density of their nests is higher in grazed glades than in mown or non-utilized ones (Table 2, Fig. 2). In spite of that it has not

been determined that there exist species avoiding or preferring glades of any type of utilization. It seems then that the mode of glade utilization or its lack could determine a particular ant species composition (Table 1.). This is due to the fact that grazing increases the area of habitats adequate for the ant nests. The size of the glades and its altitude further complicate the evaluation of the influence of grazing or mowing. The result to the effect that the area of a glade is of some significance for the diversity of the species which inhabit it is not surprising; the probability of finding different type habitats in a given glade increases with its area. Also increase the odds for survival of such local, small populations, endangered with elimination in the extreme environmental conditions. These conditions become worse with the altitude, so that less species are found in higher glades, or even higher parts of glades (Table 3.). Particularly invulnerable to altitude-connected factors is *F. lemami*, a species significantly increasing its domination in higher glades (Tables 1. and 3.).

The preservation of the Tatra glades is of aesthetic, cultural and economic value, and does not strives to preserve the natural biocenoses. The biological factors are significant because of the fact that the glades increase the area of the non-forest habitats, the natural associations of which occupy only a small part of the mountain forest zone. The preservation of the glades would thus increase the diversity of the local ants.

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# SOME REMARKS ON THE FORAGING STRATEGY IN *CATAGLYPHIS AENESCENS* NYL. (HYMENOPTERA, FORMICIDAE)

I. Z. Petrov

Petrov, I. Z. (1993): Some remarks on the foraging strategy in *Cataglyphis aenescens* Nyl. (Hymenoptera, Formicidae). - *Tiscia* 27, 23-28.

**Abstract.** The frequency of exits and entries, the maximal distance of foraging trips from the nest, as well as the foraging route shape of a marked ant, in the connection with the temperature of sand were observed twice in 1981.

The number of exits of the marked ant was similar in both cases (12 and 10 times). The maximal distances were similar in both cases (10 m and 10.6 m). The marked ant spent similar time in the nest between two exits (on the average 20.25 min. and 25.3 min. respectively). There is a difference in the time spent out of the nest (13.94 min. and 21.6 min. respectively).

The marked ant shows the site-fidelity, by running in the same direction chosen by the first exit.

*Key words:* ant foraging strategy, diurnal activity, *Deliblatska pescara*.

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## Introduction

This paper continues the series of works on *Cataglyphis aenescens* Nyl. (formerly called *C. cursor* Fonsc. or *C. c. aenescens* Nyl.) (Petrov 1984, 1985, 1986, 1988, 1990; Petrov and Gallé 1986).

According to its morphological and ethological characteristics such as: somewhat upward raised gaster, long legs and high running speeds, this species is adapted to arid habitats. Concerning the peculiarities of the habitats which *C. aenescens* inhabits (semidesert and desert), as well as its importance and role in such habitats, *C. aenescens* (*C. cursor*) arose interest of many authors (Cagniant 1973, 1976, 1979, 1980, 1980a, 1984; Dlussky 1962, 1981; Marikovski 1973, 1977; Reznikova 1983; Lenoir 1987; Lenoir et al. 1988; Schmid-Hempel 1987).

Since the data on foraging strategy of this species, under poor trophic conditions of semidesert and desert, are scarce (Petrov, 1990), it seemed of interest to continue relevant investigations to illustrate some aspects of the foraging mode of one desert ant species such as *C. aenescens*.

## Material and methods

Investigations on the foraging mode of *C. aenescens* have been carried out in the locality Cardak (Deliblatska pescara, Serbia), about 70 km northeast of Belgrade, twice in 1981.

Both times the investigations of frequency of exits and entries, began with the first exit of the marked ant and lasted 507 minutes each. The ant was marked by using the light colour, in the afternoon of the previous day.

The foraging route and the maximal distance from the nest was established by using coloured sticks, which were pined into the sand on each 15-20 cm behind the marked ant, and drawing the routes later. Out of 22 observations of two marked ants from two different nests, it was possible to draw the routes of 13.

## Result and discussion

*C. aenescens*, like the other *Cataglyphis* species, is strictly diurnal forager, leaving the nest individually and never undertaking mass foraging.

The first observation of July 19, began at 5.30 a.m. and lasted until 2.15 p.m. It can be noticed that the marked ant left the nest 12 times (Tab. 1). The first leaving was at 6.37 a.m., at the temperature of sand of 26 °C, and the last leaving was at 12.31 p.m., when the sand temperature was 57°C. Out of the nest, this ant spent from 2 to 26 minutes. The total out time was 167.3 minutes (13.94 min. on the average) (Tab. 1).

This ant spent from 1 to 48 minutes in the nest between two exits. the total nest time was 243 minutes (20.25 min. on the average) (Tab. 1).

The maximal distance observed was from 0.1 m to 10 m (the average 3.95 m) (Tab. 1).

The marked ant was loaded three times, or 25% of the total exits (Tab. 1). Although this ant used to find certain particles which it began to carry toward the nest, it did not bring them into the nest twice, but lost them and returned unloaded.

The second observation of August 4, was carried out between 5.30 a.m. and 2.15 p.m. The marked ant left the nest 10 times. It left the nest the first time at 6.05 a.m. at the sand temperature of 22.5°C. The last leaving was at 1.15 p.m., when the sand temperature was 62.5°C. This ant spent from 1

minute to 2 hours out of the nest. The total out time was 216 minutes (the average 21.6 min.) (Tab. 2).

This ant spent from 1 minute to 2 hours in the nest between two exits (the average 25.3 min.). The maximal distance was from 0.1 m to 10.6 m (the average 3.93 m) (Tab. 2). In this observation, the marked ant returned loaded only once.

These observations confirm some statements about the related species *C. bicolor* F. Namely, Harkness (1977) stated that *C. bicolor* on its foraging trips spent 17 minutes out of the nest on the average, and 8-24 minutes in the nest.

Wehner et al. (1983) stated that "the foraging range of a colony can be approximated by a circular area centered around the nest". Their investigations showed that the radius of a circular area within which the ants spend the most of the time doing foraging trips, was 13 m in Greece and 32 m in Tunisia irrespective whether a food item has been found.

Their investigations on *C. bicolor* showed that the number of foraging trips was 10 runs in Greece and only 4 runs in Tunisia. They explained that with the fact that *C. bicolor* in Greece started its exits earlier in the morning and finished them later in the evening.

Table 1. Frequency of exits and entries, maximal distances, out nest and in nest time of the marked ant (19.7.1981.): food (f).

No. of exit	hours (h)	out nest time (min)	in nest time (min)	max.distance (m)	sand temp. (°C)
1f	6 <sup>37</sup> -6 <sup>49</sup>	12		1.20	26
2f	6 <sup>50</sup> -7 <sup>09</sup>	19	1	1.80	29
3	7 <sup>15</sup> -7 <sup>20</sup>	5	6	1.70	31
4	8 <sup>02</sup> -8 <sup>21</sup>	19	42	9.00	36
5	9 <sup>09</sup> -9 <sup>28</sup>	19	48	10.00	45
6f	9 <sup>37</sup> -9 <sup>45</sup>	8	12	7.80	47
7	10 <sup>32</sup> -10 <sup>40</sup>	8	47	1.40	50
8	11 <sup>20</sup> -11 <sup>40</sup>	20	48	2.30	56
9	11 <sup>48</sup> -11 <sup>58</sup>	10	8	3.20	57
10	12 <sup>00</sup> -12 <sup>03</sup>	3	2	0.10	56
11	12 <sup>28</sup> -12 <sup>30</sup>	2	28	2.20	57
12	12 <sup>31</sup> -12 <sup>57</sup>	26	2	6.80	57
TOTAL	507 min.	167.3	243	47.50	547
$\bar{x}$	-	13.94	20.25	3.95	45.50

Table 2. Frequency of exits and entries, maximal distances, out nest and in nest time of the marked ant (04.8.1981.): food (f.).

No. of exit	hours (h)	out nest time (min)	in nest time (min)	max.distance (m)	sand temp.(°C)
1	6 <sup>05</sup> -6 <sup>25</sup>	20		6.00	22.5
2	6 <sup>30</sup> -8 <sup>30</sup>	120	5	10.00	25
3	8 <sup>47</sup> -8 <sup>48</sup>	1	14	0.10	46
4	8 <sup>49</sup> -8 <sup>50</sup>	1	1	0.20	46.5
5	8 <sup>50</sup> -9 <sup>28</sup>	38	0.30	10.60	47
6	9 <sup>40</sup> -9 <sup>41</sup>	1	28	0.30	51
7f	9 <sup>47</sup> -10 <sup>15</sup>	28	6	6.50	51
8	11 <sup>05</sup> -11 <sup>10</sup>	5	50	2.80	59
9	11 <sup>14</sup> -11 <sup>15</sup>	1	14	4.00	60
10	13 <sup>15</sup> -13 <sup>16</sup>	1	120	3.00	62.5
TOTAL	507 min.	216	253	43.5	470.5
$\bar{x}$	-	21.6	25.3	3.93	47.5

A small percentage of successful foraging trips in our investigations can be explained with poor trophic conditions in habitats which *C. aenescens* inhabits (semidesert or desert), although Wehner et al. (1983) stated that in their both investigated sites (Greece and Tunisia) about half of the foragers returned with a solid prey (dead arthropod).

These investigations in some way, as well as some others, concerning the activity of workers (Petrov 1988), confirm the statement given by Harkness (1977), Dlussky (1981), Wehner et al. (1983) that at any time in a colony, there are not more than a few hundred foragers, which is the smaller part of the colony.

In the first observation, the routes of nine exits was established (Fig. 1). It is obvious that although the routes are winding, and the maximal distance is different, the marked ant always foraged in the same direction. The route shapes by its foraging trips are more or less similar (triangular, elongated, elliptic).

The first exit was different from the others. Namely, the ant wandered across the bulwark at first, and then suddenly started to run in one direction in which it ran for the rest of its foraging time.

In the second observation four routes were established (Fig. 2). On that occasion, the marked

ant went through one turf of *Festuca vaginata* on the way from and to the nest. Generally, the route shapes of this ant were almost identical. On the way out, in front of the *F. vaginata* turf, the marked ant stopped for a while, or turned around itself before it entered the turf.

It is obvious that in both cases, the minimal, the maximal and the mean distance were similar. The ants were always going in the same direction chosen by the first exit. Such a behavior of workers confirms the site-fidelity, present in ant species and mentioned by several authors (Rosengren 1977, 1977A; Harkness 1979; Wehner et al. 1983). Making its foraging trips, *C. aenescens* is hunting over the desert ground at the hottest time of the day. Like all *Cataglyphis* species, *C. aenescens* is a scavenger. Its diet consists mainly of dead arthropods (chiefly insects). Small xerophilic snails of the family *Cepaeidae* were also found to be items of its dietary resources. Plant material and plant saps account for smaller portion of dietary resources of *C. aenescens* (Petrov, 1990).

These investigations stimulate, of course, the question of navigation in this and other individually searching desert ants. That problem has not been investigated by the author up till now. But, Wehner and R aber (1979) and Wehner (1982) stated that the navigational strategies employed by *C. bicolor* are



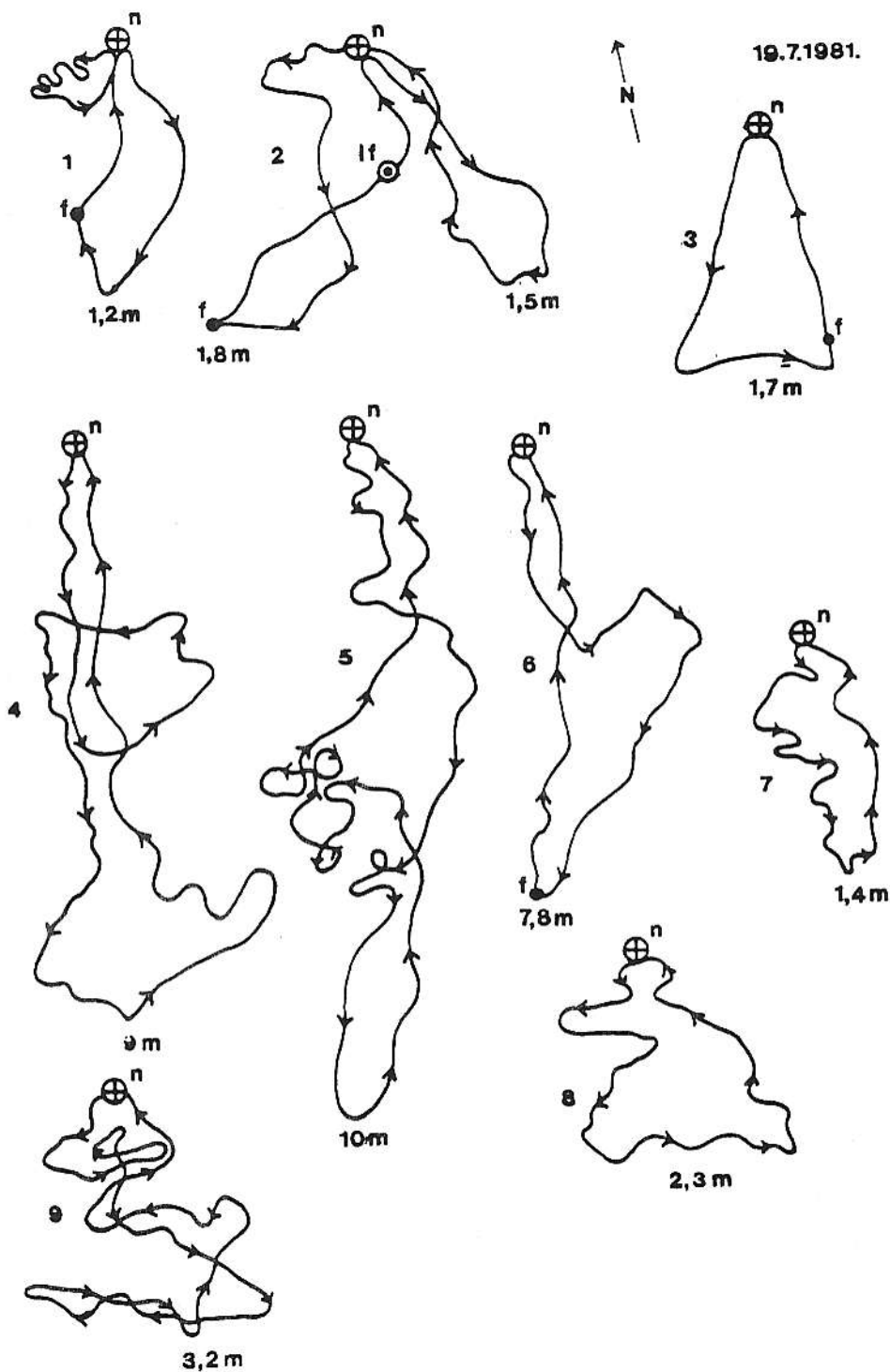


Fig. 1. Route shape and the maximal distance of the marked ant: nest (n), food (f), lost food (lf).

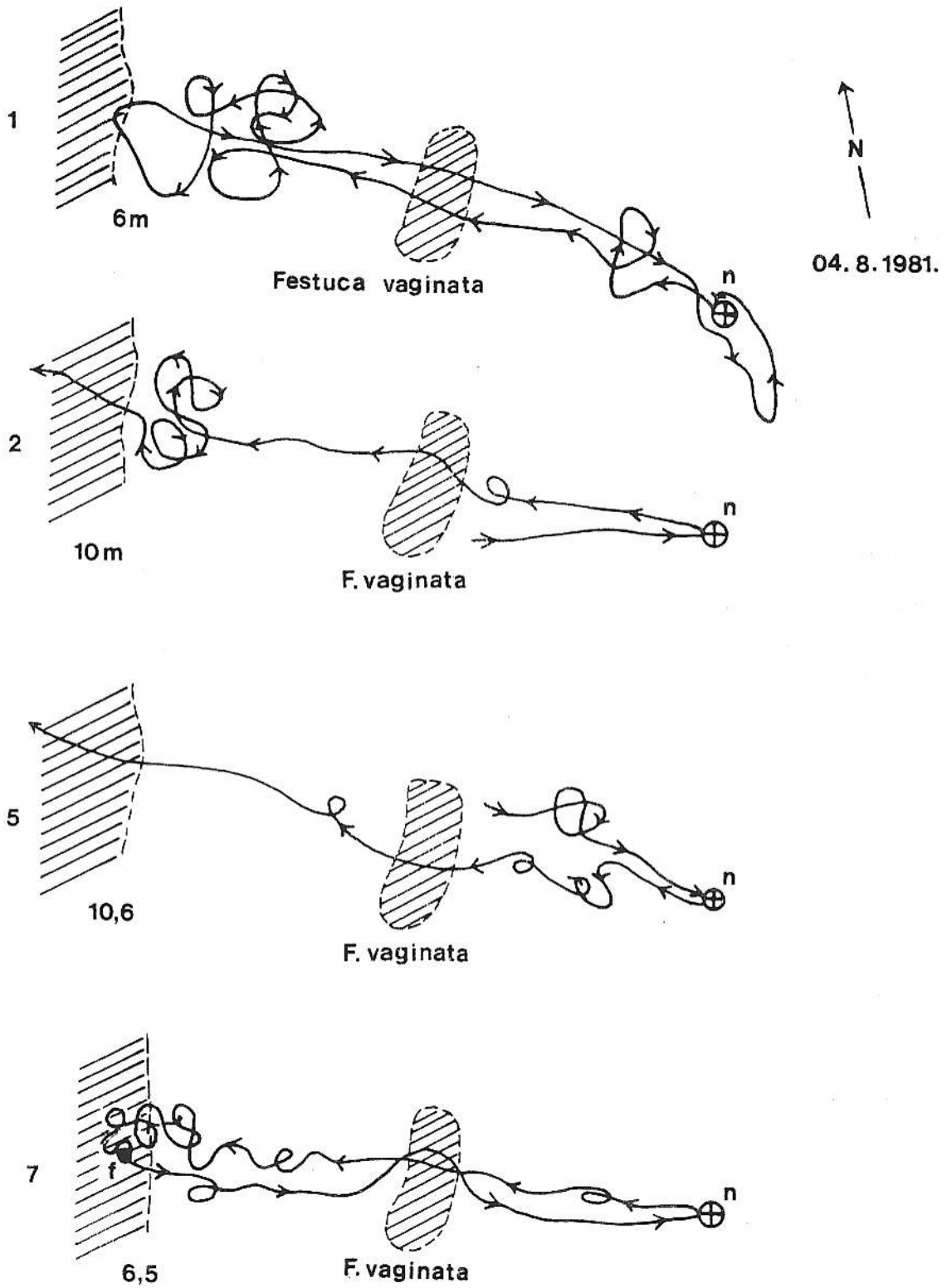


Fig. 2. Route shape and the maximal distance of the marked ant: nest (n), food (f).

"dead-reckoning (vector navigation by means of celestial compass) and piloting by landmarks". It means that "they rely nearly exclusively on visual cues including sunlight patterns and landmarks panoramas".

## Conclusions

On the basis of present investigations it may be concluded that *Cataglyphis aenescens* is diurnal individually foraging desert ant.

The number of exits and entries were similar in both cases (12 and 10 times).

The maximal distances by foraging trips were similar in both cases (10 m and 10.6 m).

The average time spent in the nest between two exits of the marked ant was similar (20.25 min. and 25.3 min.).

The average time spent out of the nest was different (13.94 min. and 21.6 min.).

*C. aenescens* shows the site-fidelity by doing its foraging trips.

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# STUDIES ON ANTS AND THEIR COMMENSAL INSECTS

## D. Paraschivescu

*Paraschivescu, D. (1993): Ecological studies on ants and their commensal insects. - Tiscia 27, 29-31.*

**Abstract.** In Dobrudja (Roumania, South-West Europe) *Atelura formicaria* Heyder and *A. pseudolepisma* Grassi (Tisanura) were found in the nest of *Messor structor* Latr. *Formica pratensis* Retz. was proved to be the host species of *Lepisma aurea* Dufour (Tisanura) and *Lomechusa strumosa* F. (Coleoptera: Staphilinidae). *Atropos formicaria* Hagen (Psocoptera) was present in the nest of *Lasius fuliginosus* (Latr.). Experimental laboratory researches were carried out on behavioural and ecological aspects of the relations between *M. structor* and *A. formicaria*.

*Key words: commensal insects.*

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## Introduction

Among the papers dealing with myrmecophily, Jannet (1897), Halifman (1964), Hölldobler (1967) and Gösswald (1989) gave summarizations and reviews. Bernard (1968) enumerated 241 commensal insect species from the nests of 193 ant species in Western and Southern Europe. Our previous studies described the trophic relations between Lachnidae and Formicidae (Paraschivescu, 1973; 1975; 1976a, c).

This paper presents the results of the field and laboratory studies on commensal insect of ants in Dobrudja, Rumania, from the period of 1968-1991, focused mainly onto the first part of it.

## Material and Methods

The observations were carried out in South-Western Dorudja (Rumania) in the localities of Valului Traian and Palas-Constanta Agigea. The nest populations of ants and their commensal insect guests were collected in the field by excavating the nests and preserved in 70 % ethanol. The commensal insects were studied from the nests of *Messor structor* (Latr.), *Formica pratensis* Retz. and *Lasius fuliginosus* Latr. Altogether ten nests of these species were sorted and the guest insects were identi-

fied. Field observations were compared with the results of laboratory studies.

Artificial nests (Jannet, 1897; Paraschivescu, 1972) were used to maintain ant colonies with their guest insects in laboratory conditions. The nest walls were made of plexiglass and paraffin oil was employed to prevent ants to leave the nest.

## Results

### (1) Field observations

*Atelura formicaria* Heyder was found in the nests of *Messor structor* (Table 1) together the ant workers, usually in the oval chambers with the remnants of Gramineae plants, the seeds of which are collected by *Messor*. Its flattened body helps to disappear very rapidly among ant workers if the nest is disturbed as well as to approach regurgitating ants to collect food drops from them during trophallaxis. The other species collected from *Messor* nests was *A. pseudolepisma* Grassi and Roseli.

The other three species of commensal insects (*Lepisma aurea* Dufour, *Lomechusa strumosa* F. and *Atropos formicaria* Hagen) were found in the nests of *Formica pratensis* and *Lasius fuliginosus* (Table 1) in a number much less than in the case of *Atelura formicaria*.

Table 1. Number of individuals of commensal insects found in nests of different ant species.

species	date		commensal species	individual number of commensal species
<i>Messor structor</i> Latr.	15.06.1979	1*	<i>Atelura formicaria</i> Heyder	14
"	"	2*	"	13
<i>Messor structor</i> Latr.	17.06.1979	1*	"	9
"	"	2*	"	6
"	"	3*	"	15
"	"	4*	"	7
"	"	5*	<i>Atelura pseudolepisma</i> Grassi and Roselli	3
<i>Formica pratensis</i> Retz.	17.06.1979	1**	<i>Lepisma aurea</i> Dufor	2
"	"	2**	<i>Lomechusa strumosa</i> F.	9
<i>Lasius fuliginosus</i> Latr.	17.06.1979	1**	<i>Atropos formicaria</i> Hagen	3
Total 3 species			5 commensal insect species	81 individuals

\* nest built in the soil; \*\* nest with middle mound

## (2) Laboratory experiments

In each of the three artificial nests of *Messor*, there were particular chambers, where *Atelura formicaria* individuals were seen. Since the total number of *Atelura* specimens was 49 with 589 ants, their appearance and activity rates were high in these chambers, therefore a tendency of aggregation is established. All the pairs of food changing ants were surrounded by two or three *Atelura* as a rule, and the ratio of food taken from the ants is high. Their high efficiency is explained by the high speed of *Atelura* movement.

## Acknowledgment.

Commensal insects were identified in the Taxonomic Laboratory of Institute of Biology, Jassy University. Author would like to thank for this courtesy.

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# DIVORD 1.50: A PROGRAM FOR DIVERSITY ORDERING

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*Tóthmérész, B. (1993): DivOrd 1.50: A Program for Diversity Ordering. - Tiscia 27, 33-44.*

**Abstract.** The methods of diversity ordering, based on diversity profiles, have been developed as an improvement on diversity comparisons based on numerical valued diversity indices. A community A is said to be more diverse than that of B when the curve of the diversity profile of A is above of B on the whole range of a scale parameter. A program, DivOrd, is presented to calculate and display the diversity profiles of communities. Eight methods are included in the package. Mathematical background of the methods is also discussed. New results about the diversity index families are presented concerning their relations and characteristic features. Their usefulness is also assessed and a guideline is presented how to use and interpret the results during ecological studies. Density dependent and density independent representations are proposed and the effect of spatial pattern is also stressed. Their relations towards the direct spatial series analysis are also mentioned.

The program is written in Turbo Pascal and it is executable on any IBM-compatible PC having 640 Kbyte memory or more and VGA, EGA or Hercules graphics card. The program is completely menu-controlled.

*Keywords one-parameter diversity index families, diversity profile, diversity ordering, density dependent and density independent representations, direct spatial series analysis*

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## Why should we use diversity profiles for diversity comparisons?

Different diversity indices may rank inconsistently a given pair of communities (Hurlbet, 1971). For example, two communities with the following abundances

A = (33, 29, 28, 5, 5), 5 species community

B = (42, 30, 10, 8, 5, 5), 6 species community

are ranked differently by the Shannon, H, and Simpson, D, indices:

$$H(A) = 1.3808 < 1.4574 = H(B),$$

$$D(A) = 0.7309 > 0.7194 = D(B).$$

Values of Shannon diversity was calculated by  $H = -\sum p_i \log p_i$  using natural logarithm. Simpson diversity was calculated by  $D = 1 / [\sum n_i(n_i - 1)] / [N(N - 1)]$ .  $n_i$  is the abundance and  $p_i$  is the relative abundance of the  $i$ -th species;  $N = \sum n_i$ . There are many reasons for this mis-ordering. Patil and Taillie (1979) emphasized that such inconsistencies are inevitable whenever one attempts to reduce a multidimensional concept to a single number; a community is a multidimensional entity and its diversity is only a scalar quantity. A more straightforward illumination

of the problem, provided by them, is related to the different sensitivities of diversity indices. The Shannon index is more sensitive to the effect of rare species; while the Simpson index tend to stress the effect of dominant species. A possible solution is to use parametric families of diversity indices instead of a numerical-valued diversity index. An important property of the family of diversity indices is their variable sensitivity to rare and abundant species. This means that communities can be compared for different "dominance levels" as a scale parameter changes. When we use a one-parameter family  $\{D_\alpha; \alpha \text{ real}\}$  of diversity indices then the family may be portrayed graphically by plotting diversities  $D_\alpha$  against the scale parameter  $\alpha$ . This curve, the graph of  $\{D_\alpha; \alpha \text{ real}\}$ , is frequently mentioned as the diversity profile of the community (Patil and Taillie, 1979, 1982). In fact,  $\alpha$  serves as a scale parameter; members of the  $D_\alpha$  family have varying sensitivities to the rare and abundant species as  $\alpha$  changes. Diversity profiles of communities A, B and

C = (32, 21, 16, 12, 9, 6, 4)

are presented in Fig. 1.

Using diversity profiles we can define the diversity ordering of communities in the following way: Community A is more diverse than community B (written  $A > B$ ) when the diversity profile of A is above or equal to the diversity profile of B on the whole range of the scale parameter.

It can be shown that diversity ordering is a partial order so that if  $A > B$  and  $B > C$  then  $A > C$ . However, it is not true that for every A, B, either  $A > B$  or  $B > A$ ; i.e. curves of two diversity profiles may intersect. In this case the two communities are not comparable; this means that we can find at least two diversity indices which order the communities differently. This situation might reflect important ecological processes which can be interpreted clearly; see for example Matus and Tóthmérész (1992), Tóthmérész et al. (1993). In Fig. 1 we can see that A and B are non-comparable, but that  $C > A$  and  $C > B$ .

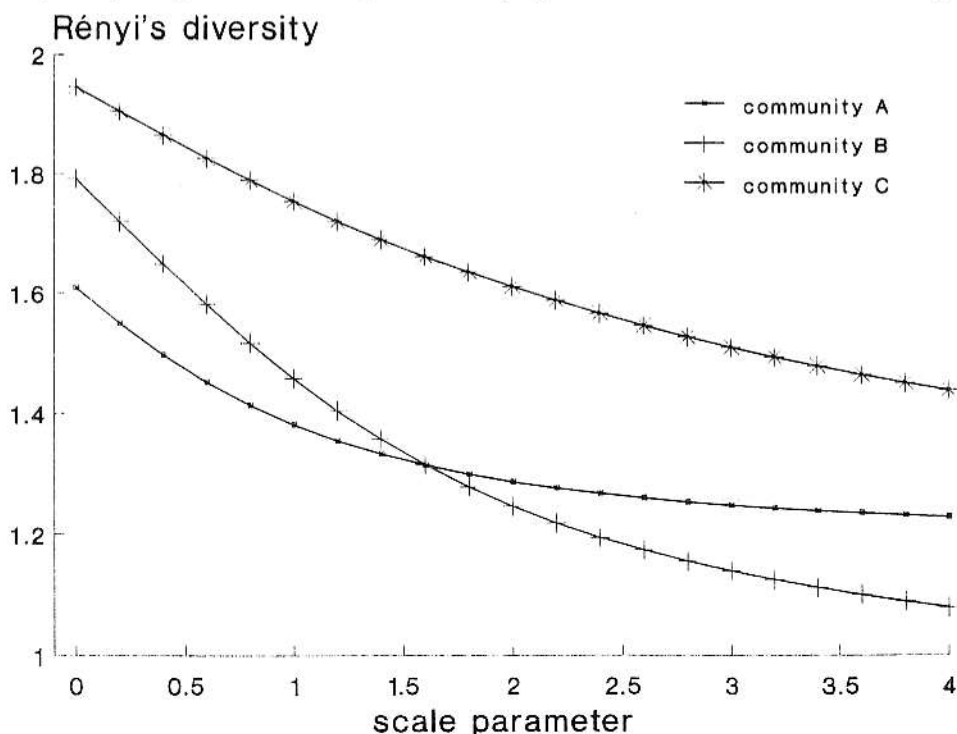
While calculating diversities is very popular in theoretical and field ecology, diversity ordering based on parametric families of diversity indices is not frequently used. These methods involve more calculations than a simple diversity index. On the other hand they are relatively simple and more straightforward than the multivariate statistical methods. However, none of these are included in standard computer packages. NuCoSA might be an

exception (Tóthmérész, 1991, 1993c). This software gap has delayed the spread of these methods.

## Overview of diversity orderings

### Historical notes

There are a long history and tradition of diversity in ecology. Tremendous lot of indices were published to measure it. These statistics were also used in other sciences, especially in physics. Statisticians also looked into the details of the characterization of "diversity". Rényi (1961) has published the first generalized entropy function. Generalized entropies are heavily used in physics nowadays (Hentschel and Procaccia, 1983). Based on this paper Hill (1973) derived a family of diversity indices and examined the usefulness of this unified notation. This index family is a straightforward derivation of the Rényi's entropy. Daróczy (1970) published another generalized entropy which also includes the Shannon diversity as a special case. At that time, ecologists did not recognize one of the most useful properties of these index families; i.e. they can be used for diversity ordering. It was recognized and emphasized by Patil and Taillie (1979); see also Solomon (1979). They had a very important contribution to the idea of diversity. They also proposed other families of diversity ordering.



**Fig. 1.** Diversity ordering of three artificial communities using Rényi's index family. Community C is the most diverse ( $C > A$  and  $C > B$ ). Communities A and B are non-comparable because the diversity profiles intersect.

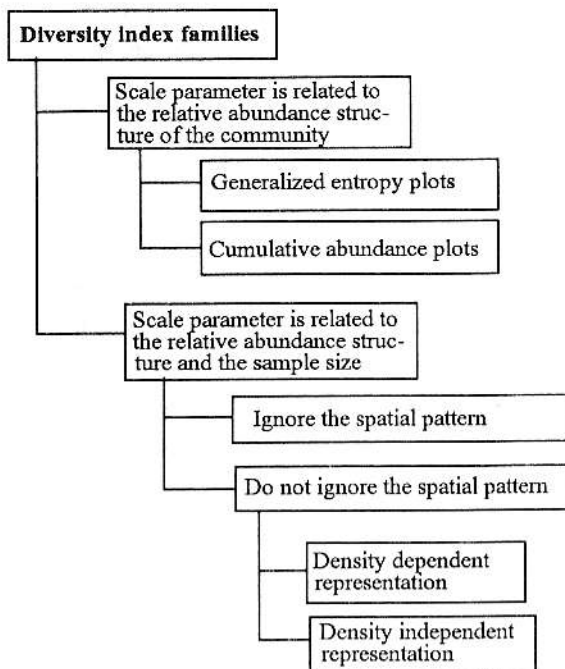


Fig. 2. Tree diagram of one-parameter diversity index families (diversity orderings).

Tóthmérész (1993b) reviewed the families which may be useful for diversity ordering; he also proposed a new one.

The story of rarefaction diversity, which also can be used for diversity ordering, is even more interesting. This is usually attributed to Saunders (1968) and/or Hurlbert (1971). A minimum variance unbiased estimation of it was published by Smith and Grassle (1977). However, this is nothing else just a species-individual curve which was invented in botany during the 1920's (Arrhenius, 1921; Gleason, 1922). That time there was a lot of discussion about the role of species-area and species-individual curves (Ashby and Stevens, 1935; Blackman, 1935). They even published many of the numerical formulas re-invented later in the same or a somewhat different context.

#### Types of diversity orderings

There are two main groups of diversity index families (Fig. 2). In the first group the scale parameter is related to the dominance structure of the community. In the second group there is a straightforward interpretation of the scale parameter related to different sample sizes. Thus, the meaning of the scale parameter is somewhat different for the two groups.

There are two subgroups of the first group; they

can be mentioned as *generalized entropy plots* (GenE plots) and *cumulative relative abundance plots* (CuRe plots). All the diversity index families included in a subgroup are closely related; see the proofs in Tóthmérész (1993b). The first one includes the methods of Rényi, Hill, Daróczy, and Patil & Taillie; the second one contains the logarithmic dominance plot and right-tail-sum diversity plots. For the members of the first subgroup there is a scale parameter which is usually larger than 0 or -1; see Table 1. For the members of the other subgroup the range of the scale parameter is "automatically" the number of species.

Table 1. One-parameter diversity index families useful for diversity ordering. The name of the families is in the first column. The graph of an index family is displayed in the second column in the form of (x-coordinate, y-coordinate) which curve is the diversity profile. The third column contains the range of the family where the result is relevant from mathematical and ecological point of view.

Name	Graph	Range
<b>Generalized Entropy Plots (GenE Plots)</b>		
Rényi	$(\alpha, H(\alpha))$	$\alpha \geq 0, \alpha \neq 1$
Hill	$(\alpha, \exp H(\alpha))$	$\alpha \geq 0, \alpha \neq 1$
Daróczy	$(\alpha, DH(\alpha))$	$\alpha \geq 0, \alpha \neq 1$
Patil & Taillie	$(\beta, D(\beta))$	$\beta \geq -1, \beta \neq 0$
<b>Cumulative Relative Abundance Plots (CuRe Plots)</b>		
Logarithmic dominance plot	$(\log i, T(i))$	$i=1, \dots, S$
Right tail sum plot	$(i, T(i))$	$i=1, \dots, S$
<b>Rarefaction Diversity Plots</b>		
Logarithmic species-individual plot	$(\log m, S(m))$	$m > 0$
Logarithmic species-area plot	$(\log A, S(A))$	$A > 0$

There is a sophisticated relationship between the diversity orderings of the second group and the direct spatial series analysis. It is evident that the diversity of a community also depends on the spatial structure. Strongly aggregated or segregated appearance of the species may heavily decrease the diversity. It is not possible to represent the effect of pattern in diversity comparisons except for the members of the second group. In the traditional form these methods also ignore the spatial structure of the community. Indeed, when the spatial structure is included we should speak about direct spatial series analysis. The spatial series analysis, however, needs special sampling techniques (Juhász-Nagy, 1976; Juhász-Nagy and Podani, 1983; Tóthmérész and Erdei, 1992); thus, these are not included in the package. This needs a special package like MULTIPATTERN (Erdei and Tóthmérész, 1993).

It can be proved that all these families are equivalent from the point of view of ordering (Patil and Taillie, 1979). It does not involve, however,

that there is no reason to use the others. Tóthmérész (1993b) demonstrated studying the graphical properties of the diversity orderings that different methods may be useful for different data sets depending on the community structure, sample size, number of species, etc. Another important feature of the species-area and species-individual relations the possibility of the density dependent and density independent representations and the close relationship to the direct spatial processes (Tóthmérész, 1993a).

#### Diversity orderings implemented in the program

Generally, a community A may be identified with the ordered pair  $A=(S_A, n_A)=(S(A), n(A))$ , where  $S_A$  is the number of species that are present and

$n_A=(n_1, n_2, \dots, n_i, \dots, n_{S(A)})$  is the abundance vector of the community and  $n_i$  is the abundance of the  $i$ -th species of the community. Frequently enough to know the relative abundances of species; thus a community may be identified by a pair  $(S_A, p_A)$ , where  $p_A$  is the relative abundance vector of the species.

Patil and Taillie (1979) stressed the view that community diversity can be defined to be the average species rarity. Many different rarity functions, and thus many different diversity functions can be defined. The one-parameter diversity index families implemented in the program are displayed in Table 1. The diversity index families are defined in the following way.

Entropy of order  $\alpha$  (Rényi, 1961):

$$H(\alpha) = \left( \log \sum_{i=1}^S p_i^\alpha \right) / (1-\alpha)$$

Entropy of type  $\alpha$  (Daróczy, 1970; Aczél and Daróczy, 1975)

$$DH(\alpha) = \left( \sum_{i=1}^S p_i^\alpha - 1 \right) / (2^{1-\alpha} - 1)$$

Diversity index of degree  $\beta$  (Patil and Taillie, 1979):

$$D(\beta) = \left( 1 - \sum_{i=1}^S p_i^{\beta+1} \right) / \beta$$

Right-tail-sum diversity (Patil and Taillie, 1979; Solomon, 1979):

$$T(i) = p_{(i+1)} + \dots + p_{(S)} = \sum_{j=i+1}^S p_{(j)}$$

where  $p_{(1)}, \dots, p_{(S)}$  are the relative abundances of the species of a community arranged in descending order.

Rarefaction diversity (Saunders, 1968; Hurlbert, 1971) or species-individual curve:

$$S(m) = S - \sum_{i=1}^S (1-p_i)^m$$

The expected number of individuals in an area is proportional to the size of the area. Therefore, we can calculate the species-area curve (Blackman 1935) using the following relationship where  $N$  is the total number of individuals on the area.

Smith and Grassle (1977) presented the minimum variance unbiased estimation of  $S(m)$  as:

$$\hat{S}(m) = S - \sum_{i=1}^S \binom{N-n_i}{m} / \binom{N}{m}$$

where

$$\binom{N}{m} = \frac{N!}{(N-m)!m!}$$

An important property of family of indices is its variable sensitivity to rare and abundant species. A precise definition of sensitivity is given by Patil and Taillie (1982). For large values of the scale parameter, GenE plots are sensitive to abundant species, whereas they are sensitive to rare species for smaller values of the scale parameter.

Table 2. The relation of the magnitude of scale parameter and the sensitivity of diversity orderings.

Name	Value of the scale parameter	
	small	large
GenE plots	sensitive to effect of rare species	sensitive to the effect of dominant species
CuRe plots	sensitive to effect of dominant species	sensitive to the effect of rare species
Rarefaction plots	sensitive to effect of dominant species	sensitive to the effect of rare species

The pattern of sensitivity of the CuRe plots are opposite to that of GenE plots: they are sensitive to abundant species for small "i" and to rare species for large "i". In the case of rarefaction curves the



pattern of sensitivity is the same as with CuRe plots.

### Special cases and interpretation of index families

It is important to know some special cases of diversity index families to interpret the result of diversity orderings.

For the Rényi's diversity ordering the following relations are valid.

$H(-\infty)$  = logarithm of the reciprocal of the relative abundance of the rarest species. This is mentioned just because of the completeness of the special values because it was proposed not to use scale parameter values less than 0.

$H(0)$  = logarithm of the total number of species;

$H(\alpha > 1)$  = Shannon index;

$H(2)$  = logarithm of the reciprocal of Simpson's index;

$H(+\infty)$  = logarithm of the reciprocal of the relative abundance of the commonest species. This is the logarithm of the reciprocal of Berger-Parker index (Berger and Parker, 1970).

The following special cases can be mentioned for the Patil and Taillies's diversity index family.

$D(-1)$  = total number of species - 1

$D(\beta > 0)$  = Shannon index

$D(1)$  = Simpson index

Finally for the species-individual relationship the following cases may be mentioned.

$S(2)$  = (1 + Simpson index);

$S(+\infty)$  = total number of species.

When  $m$  is a positive integer,  $S(m)$  is the expected number of species to be found in a hypothetical random sample of size  $m$ . For a given community, the plot of this index versus  $m$  is the expected species-individual curve. There is mathematical sense of  $S(m)$  for a noninteger  $m$  value. In direct spatial series analysis there is ecological sense as well (Tóthmérész, 1993a).

$D(\beta)$  of Patil and Taillie can be interpreted as the number of species that a completely even community would need to have its diversity to be the same as that of the studied community. Thus, sometimes it is mentioned as *equivalent number of species*.  $expH(\alpha)$  also can be interpreted this way.

### How to use the program

Place the DivOrd diskette into the A: disk drive. Copy the DIVORD.EXE file to your hard disk. From the root directory, type COPY A:DIVORD.EXE then press <ENTER>. Preferable

you should copy the program into a subdirectory instead of the root directory.

To activate the program, type DIVORD and press <RETURN>. Then one page of information appears, and if you press any key you can see the main menu (Fig. 3).

```
1 - Data Input

Generalized Entropy Plots (GenE Plots)
2 - Rényi
3 - Hill
4 - Daróczy
5 - Patil & Taillie

Cumulative Relative Abundance Plots (CuRe Plots)
6 - Logarithmic Dominance Plot
7 - Right-Tail-Sum Diversity Plot

Rarefaction Diversity Plots
8 - Species-Individual Curve (Density Independent)
9 - Species-Area Curve (Density Dependent)

10 - Other Samples to Compare
11 - Result to Disk in HG Format

12 - Exit

Your choice :
```

Fig. 3. The main menu of the DivOrd program.

The program takes data from data files and not directly from the keyboard. The instructions for the arrangement of data input files are in the "Arrangement of input data" Chapter. This version of the program can handle data matrices containing 50 samples and 200 species (50 rows and 200 columns). The "Data Input" option is used to load data matrices into the program in the following way. First the name of the file is requested (Fig. 4).

```
Name of Input File = DEMO.DAT

There are 3 sample units.

How many curves do you want to draw (less than or equal to 4) ? 2

Please type the identity number of the sample sites:
1.: 1
2.: 3
```

Fig. 4. Data Input screens of the DivOrd program. In the "DEMO.DAT" file there are 3 samples and the diversity profile of the 1st and 3rd samples (communities) are asked to draw.

Then, the computer informs you about the

number of communities (sampling units) contained in the data matrix and then the number of communities (sampling units) to be compared is asked (Fig. 4).

The computer informs you when the data file cannot be found, for example, owe to mistyping of the file name. Then you have to use again the "Data Input" option to load data into the program. After finishing the data input procedure successfully you are in the main menu again and you can select a diversity ordering.

```

Range of the scale parameters during the previous run :

Start = 0.000

End   = 4.000

Step  = 0.250

New run with other range <y/RETURN> ?
  
```

Fig.5. The menu of changing the range of scale parameter and the steps of calculations.

In the case of the GenE plots the pre-defined range of the scale parameter is the [0,4] interval for Rényi's and Hill's ordering, [0,2] for Daróczy's, and [-1,2] for Patil & Taillie's. If you press any key the diversity profiles disappear and you can choose another range of the scale parameter (Fig. 5). You can also change the step-size of the calculations; using larger steps the calculation is faster but the curve

might not be as smooth as using an optimal step size. There is no reason to use a scale parameter higher than 10. Very frequently 4 or 6 is excellent as an upper bound; sometimes 3 is enough. For practical reasons the program is designed not to use parameter values higher than 15 or 20.

Finally, the "Other Samples to Compare" option allows you to choose other communities (sampling units) to be compared from the same data set. First the program informs you again about the number of communities (sampling units) in the data matrix as in the case of choosing the "Data Input" menu and then you proceed in exactly the same way as before.

The figures presented by the DivOrd program can be included into papers directly using the GRAB.EXE utility of WordPerfect or any other utility distributed with high quality word processors. There is a special option in the DivOrd to save the results into as ASCII file in a special format which can be used directly to import into the HarvardGraphics program package. Thus, you can produce high quality figures comfortably. You should consult the documentation how to use HarvardGraphics. We present a short description how to import ASCII data into the HarvardGraphics.

1. Select "Create new chart" at the main menu and then "bar/line chart". There you must select "number" as X data type. Finally press F10; see Fig. 6.
2. At the Main Menu, select Import/Export.
3. At the "Import/Export" menu, select Import ASCII data.

The Select File screen appears. (a) Select an

```

Bar/Line Chart Data
-----
Title:
Subtitle:
Footnote:

X Data Type Menu
-----
Pt | Name | Day | Week | Month | Quarter | Year
   | Month/Day | Month/Yr | Qtr/Yr | Time | Number |
-----
X data type:  Number
Starting with:
Increment:
Ending with:

-----
F1-Help      F3-Save      F5-Set X type  F9-More series
F2-Draw chart F4-Draw/Annot F6-Calculate   F8-Options    F10-Continue
  
```

Fig. 6. "Bar/line chart" menu of the HarvardGraphics.



	species 1	species 2	species 3
sample 1	33	29	5
sample 2	42	30	10
sample 3	32	21	16

Fig. 9. The arrangement of data items in the data file used by the DivOrd program.

## Guideline to the applications of the methods

### *Graphical comparison of diversity orderings*

Tóthmérész (1993b) compared the diversity orderings according to their effectiveness in displaying the differences of community structures. He was stressing a practical point of view: which methods were the most useful during the graphical inspection of data comparing the diversity of communities.

One of the best method for ordering communities was Rényi's index family irrespectively of the species number of the communities; the intersection of the diversity profiles was well-indicated by this method. Logarithmic dominance ordering also produced clear, well-interpretable figure for communities of all size. For species-poor and moderately species-rich communities Hill's index family was useful; for species-poor communities the right tail sum ordering also performed well.

When the differences between the species number of communities are medium or high (i.e. when one of the compared communities are much richer in species than the others) then also the Rényi's index family or logarithmic dominance plot was useful.

Calculation of rarefaction diversities was overly time-consuming compared with the others in the case of unbiased minimum variance estimation. The curves produced by rarefaction diversities clearly indicated the relation of sample size and the number of species but it was not especially effective in reflecting the intersection of diversity profiles. The logarithmic scaling of the x-axis, however, highly improved the figure. Plotting them this way they were also very useful for both small and large communities.

### *Density dependent and density independent representations*

Evidently the number of species in a sample depends on the number of individuals which can be found in the sample. The density of vegetation, however, is frequently different for the compared

communities. We are interested in the diversity pattern of the communities and the density has a "scaling" effect. Therefore, depending on the goal of the study, it may be useful a density independent representation of the rarefaction diversity profiles. Density dependent and density independent representations evidently may produce different diversity ordering relations as it is demonstrated by Fig. 10. Here  $B > A$ , but the density of community B was higher. Using a density independent or density-free representation of the rarefaction diversity profiles, we can see that the communities are non-comparable. The possibility of density dependent and density independent representations are extremely useful in ecological research; see an application in Tóthmérész and Matus (1993). There is no such possibility for GenE and CurE plots.

### *Complementarity of GenE and CuRe plots*

GenE plots depend strongly on the number of species because at the starting point of the diversity profile they take the value of the number of species or a value directly related to it, like  $S-1$  or  $\log S$ . CuRe plots are heavily depend on the abundance of the most abundant species. From this point of view these methods are exactly complementary. Lets compare the diversity of the communities of the first Chapter to a community

$$A' = (29, 29, 28, 5, 5)$$

which is almost identical with A; the abundance of the first species is 29 instead of 33. Using one of the GenE plots evidently  $A < B$  but it is rather difficult to recognize that  $A' < B$ . The diversity profiles intersect for a scale parameter value which is larger than 16 and it is almost impossible to recognize the intersection. On the other hand the non-comparability is evident using one of the CuRe plots; see Fig. 11.

It is easy to produce an example which is the "opposite" of the above mentioned. Lets compare the following communities:

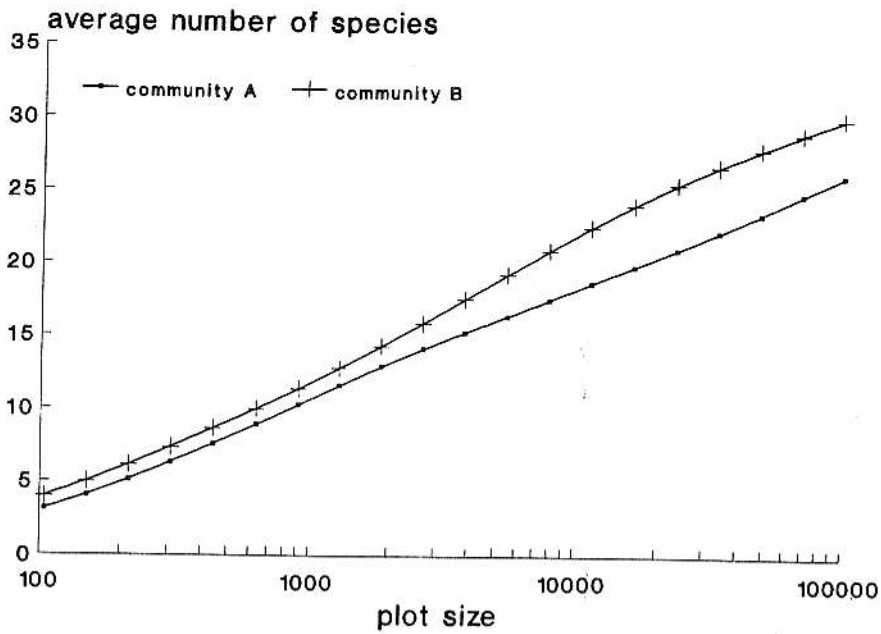
$$E1 = (790, 74, 19, 123, 50, 3, 25, 13, 28, 37),$$

$$E1' = (790, 74, 19, 123, 50, 3, 25, 13, 28, 37, 1, 1),$$

$$E2 = (8, 60, 55, 45, 8, 7, 14, 4, 1, 75, 45).$$

The first and the third communities are almost identical; the only difference is that in the community E1' two new species are included with 1-1 individuals. Using a CuRe plot it is rather difficult to detect that  $E1' < E2$ , however, it is evident using a GenE plot; see Fig. 11.

density dependent representation



density independent representation

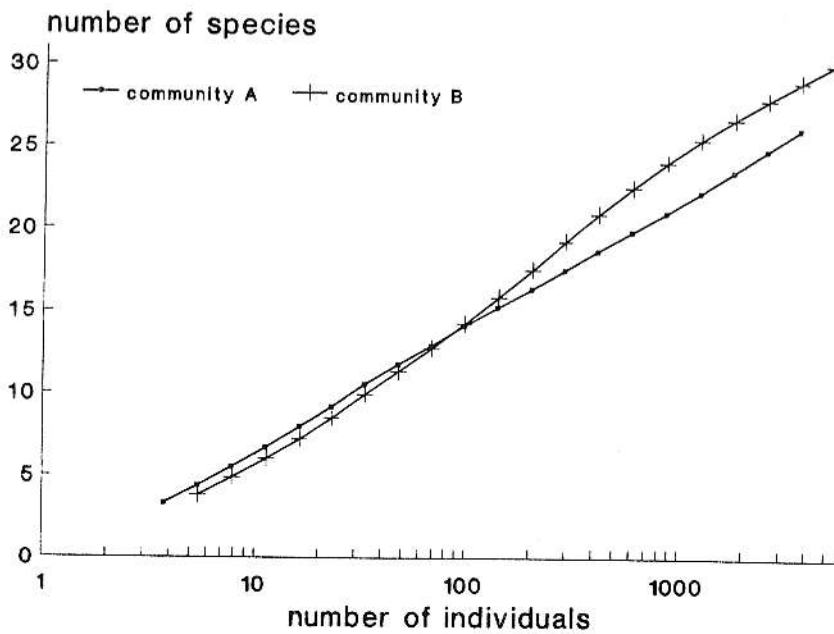


Fig. 10. Density dependent and density independent representation of the diversity profiles of the same communities.



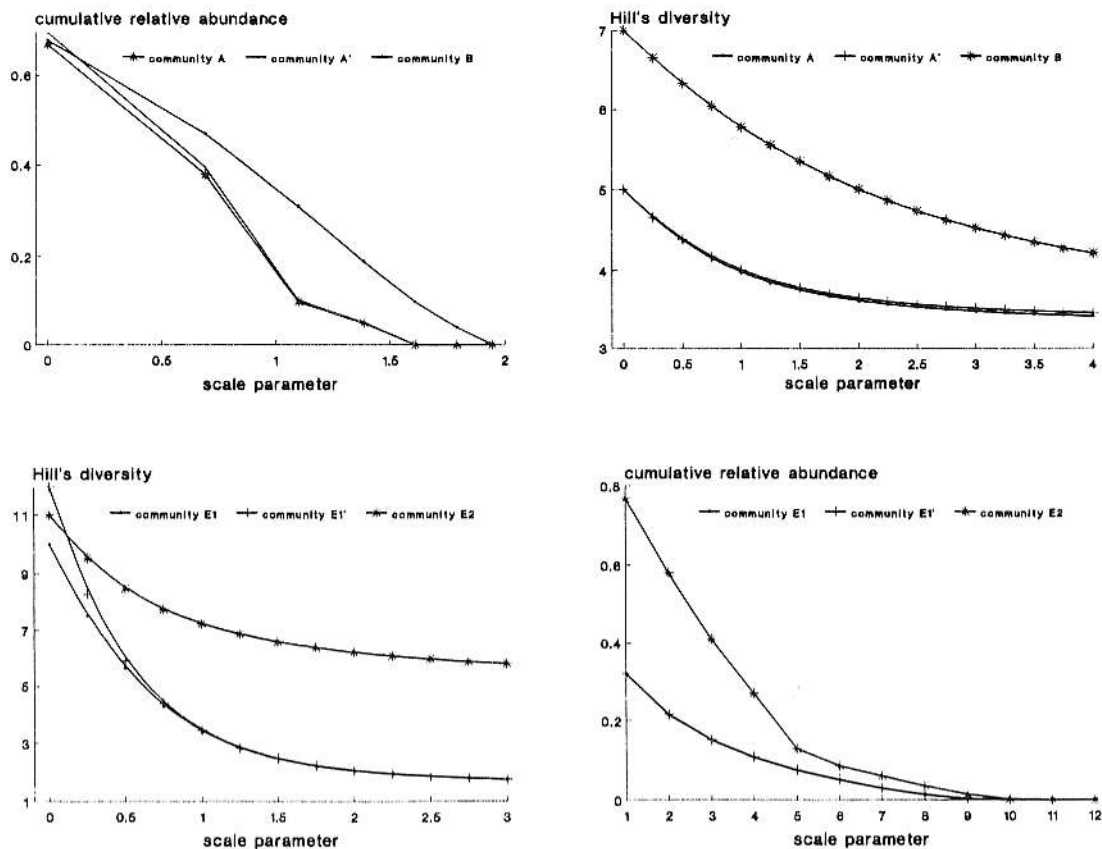


Fig. 11. Complementarity of the GenE and CuRe plots from the point of view of displaying the non-comparability of communities.

### The effect of grazing

Matus and Tóthmérész (1992) and Tóthmérész and Matus (1993) studied the effect of moderate cattle grazing to the structure of a sandy grassland in Eastern Hungary. This region is characterized by inland dunes having been formed during the Pleistocene. The studied meadow is not sustained or stabilized by the grazing; the grazing is not part of the ecosystem here.

There were 33 species in the ungrazed case and 36 in the grazed one. 30 species were detected in both transects. The species-individual diversity of the ungrazed community was 2.2757 and 2.2269 for the grazed community using the corrected Shannon formula proposed by Hutcheson (1970), the difference is not high, yet it is significant in statistical sense using the analog of t-test developed for comparing diversities. Another interesting fact was that the grazed community was more species rich while the ungrazed community was more diverse. The diversity profiles of the communities intersected;

for the rare species the cattle grazed community was more diverse while the ungrazed community was more diverse for the dominant and subdominant species. Therefore, the moderate grazing decreased the diversity of dominant species; the abundance of these species also decreased. At the same time the number of rare species and their diversity increased. The situation was much more sophisticated using rarefaction diversity ordering with special emphasis on the effect of the distributional pattern (Tóthmérész et al., 1993).

### Diversity orderings and spatial processes

The rarefaction curves are well known in botany and zoology as species-area and species-individual curves; more exactly these are the species-area or species-individual curves of a "random" or unstructured community. However, the diversity of a community heavily depends on the pattern. The importance of the patchiness on the community level was recognized very early in botany; see

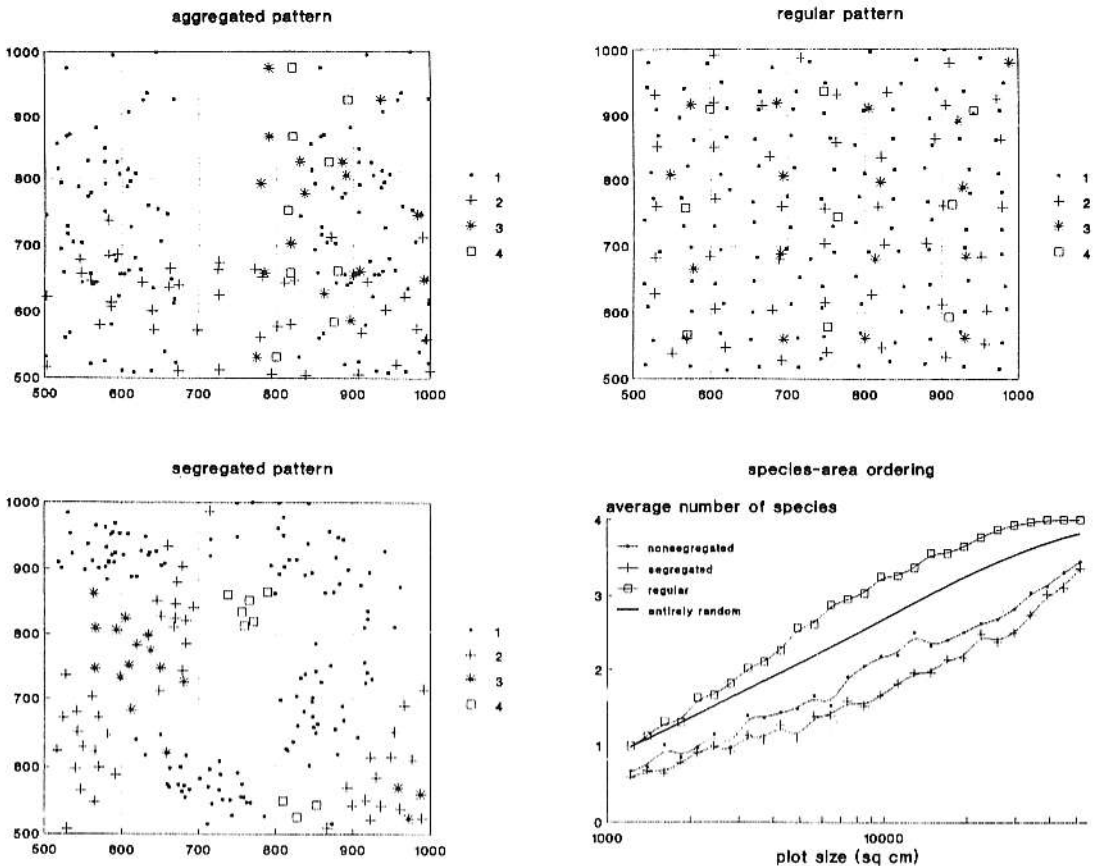


Fig. 12. The effect of spatial pattern on rarefaction diversity ordering.

Godwin and Conway (1939), Watt (1925, 1937). Watt (1947) suggested that plant communities are comprised of a mosaic pattern of patches which are dynamically related to each other. Ecologists always professed the importance of multispecies patterns; see Watt (1947). This is also confirmed by the fact that Watt's seminal paper is the most frequently cited paper in the ecological literature (McIntosh, 1989).

The effect of pattern to the species richness is demonstrated by the Fig. 12. Each community has exactly the same number of species and the same number of individuals; therefore the  $S(m)$  curve is the same for each community if we ignore the spatial pattern. The distribution of individuals, however, are strikingly different. The number of species was counted for 50 plots for each plot size and the average number of species was plotted against the plot size. The communities are well ordered; the community having regular pattern is the most diverse; the aggregated community is less diverse than the totally random, unstructured community.

The less diverse is the segregated community where the distribution of individuals is aggregated and there is a strong segregation between the species; i.e. the patches usually contain one or only few species.

Table 3. The relation of rarefaction diversity orderings and direct spatial series analysis.

	density dependent	density independent
expected (random)	species-area curve	species-individual curve
observed (field)	direct spatial series analysis: location-type statistics for number of species in the plots	direct spatial series analysis: location-type statistics for the number of species in a sample of $N$ individuals

That is a very significant feature of the rarefaction diversity orderings. All the other methods ignore the spatial pattern of the communities. To utilize this important feature of the rarefaction diversity ordering we need a special sampling tech-

nique which reflect the spatial arrangement of the individuals. The relation of rarefaction diversity orderings and direct spatial series analysis is demonstrated by Table 3. A more detailed discussion of direct spatial series analysis can be found in Tóthmérész (1993a).

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# MULTI-PATTERN 1.00. PROGRAM PACKAGE TO ANALYZE AND SIMULATE COMMUNITY-WIDE PATTERNS

Zs. Erdei and B. Tóthmérész

*Erdei, Zs. and Tóthmérész, B. (1993): MULTI-PATTERN 1.00. Program package to analyze and simulate community-wide patterns. - Tiscia 27, 45-48.*

**Abstract:** MULTI-PATTERN is a program package developed for IBM-compatible PC's to simulate multi-species point patterns and to calculate direct and indirect spatial statistics for real and simulated point patterns. The program is entirely menu controlled. The program package is supported by detailed graphical display of the results.

**Keywords:** multispecies point patterns, direct and indirect spatial series analysis, computerized sampling, simulation.

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## General description of the package

MULTI-PATTERN is written in Turbo Pascal. It may be run on IBM-compatible PC's with at least 640 Kbytes available memory. Because of the extensive input and output manipulations and of the large amount of simulated data, a hard disk is inevitable. At least 2 Mbytes free space is recommended to store the simulated data sets. The graphics routines can run on any graphics card, but EGA or VGA are preferred. To carry out an extensive simulation study a mathematical coprocessor is highly recommended. Each procedure is planned to minimize computing time and maximize the size of data set.

The package has two separate goals; one of these is to analyze the pattern of multispecies communities in direct and indirect spatial series analysis and the second one is to simulate multispecies point patterns which may be useful to test other techniques which are frequently used in ecology.

Graphical display of the field and/or simulated point patterns (Fig. 1) and the result of spatial series analysis is included in the package (Fig. 2).

## Spatial statistics included in the package

There is a long tradition of the analysis of one- and two-species patterns in botany and ecology (Greigh-Smith, 1952, 1983; Kershaw, 1957, 1961). It is incredibly time-consuming, however, to study

multispecies spatial patterns quantitatively; Erdei et al. (1993) published results about computing times. Before the widespread availability of fast computers, the calculations even for species poor communities would have been a formidable task.

During a spatial series analysis the spatial pattern is analyzed using a series of different sized plots. For each plot size  $n$  plots are placed randomly to the studied community. The importance of such spatial analysis of the vegetation, when a series of increasing plot size is used, was recognized and emphasized very early by Juhász-Nagy (1967, 1976). According to the method developed by him the number of plots having different species list are counted first and after that the statistics describing

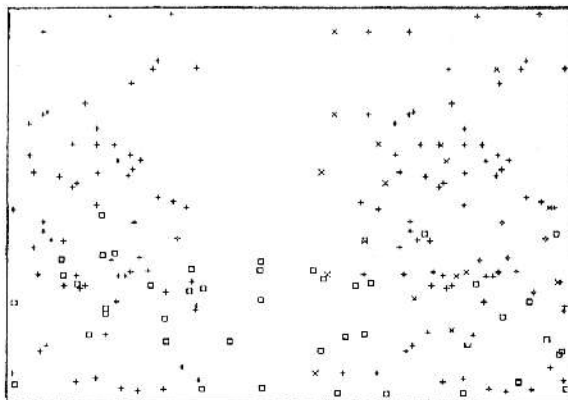


Fig. 1. A community containing four species. The distribution of the individuals are strongly aggregated for each species.

the spatial structure of the vegetation are calculated from this derived data set. Therefore, it might be mentioned as an indirect spatial series analysis. In the case of direct spatial series analysis for each plot a characteristics, like number of species or diversity, is calculated and the spatial pattern is described this way (Tóthmérész, 1993a).

Two statistics are included in the package for direct spatial series analysis; the average and variance of the number of species (Tóthmérész, 1993a). There are five indirect spatial statistics in the program: number of species combinations, florula diversity, florula evenness, preferential information heterogeneity or local distinctiveness and associatum (Juhász-Nagy and Podani, 1983; Podani, 1984a, 1984b).

### Neutral models and complete spatial randomness

It is natural to use as a neutral or null model the hypothesis of Complete Spatial Randomness (CSR). CSR is frequently used in ecology and elsewhere to the formulation of hypotheses concerning the pattern and its genesis (Diggle, 1983; Ripley, 1981). The CSR hypothesis can be stated as follows: Given the occurrence of  $m$  individuals in a finite region  $A$ , the location of those individuals are a random sample of size  $m$  from the uniform distribution on  $A$ . There are alternative characterizations of CSR related to Poisson distribution.

Multispecies point patterns can be constructed by extending univariate models. The simplest such models are those compound of independent components. In many respects, the role of independence is analogous to the role of CSR in the univariate case (Cressie, 1991).

Juhász-Nagy stressed very early the importance of null models in ecology (Juhász-Nagy, 1970). Nowadays, the significance of these models is generally accepted (Caswell, 1976; Harvey et al., 1983). There are two possibilities to generate neutral models for a spatial series analysis. It is possible to calculate the "theoretical" value of a spatial statistics for a random community. The theoretical null model is calculated for "infinitely large" community where the ratio of the species is the same as for the studied community. Another possibility is to simulate a random community where the number of species and the number of individuals is the same as for the studied community, and then to calculate the statistics for that pattern; that produce a realized null model (see Fig. 2). Because of the finite number of individuals the realized and the

theoretical null model may produce strikingly different result. In the case of rare and subdominant species Tóthmérész and Erdei (1992) demonstrated that the association, which should be zero for a random community, is much higher than zero for realized random models.

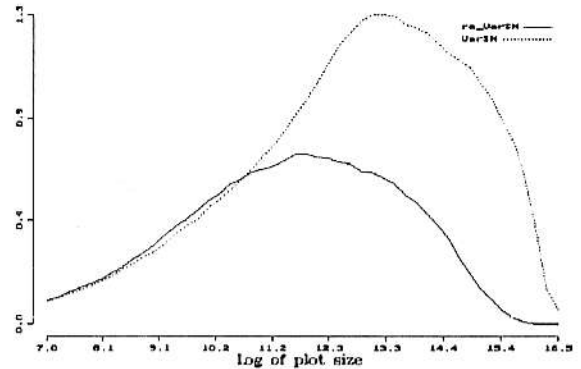


Fig. 2. Variance of the average number of species (*re\_varSN*) in a direct spatial series analysis for the community presented in Fig. 1 and the realized null model of it (*varSN*).

Both theoretical and realized random models can be calculated by the package. Calculation of the theoretical values is included in the package as an option. The realized random model also can be simulated by the package and then, the realized values of the spatial statistics can be calculated.

### Format of data files

The program works with the two-dimensional euclidean coordinates of the individuals. The default extension of the data files is "\*.COO". The first line of the data file is a label which helps to identify the data-file. The second line contains the x-size and y-size of the studied area. The third line contains the number of individuals. In the following lines are the coordinates of the individuals; one individuals in one line. The first figure in the line is an integer value to identify the species. The second figure is the x-coordinate and the third figure is the y-coordinate of the individual. This data format is compatible with the format used by the SYN-TAX III (Podani, 1988); the only difference is that the first three lines of the files, which provide additional information from the data, are missing in the case of SYN-TAX and the file directly starts with the species identification and the coordinates of the data.



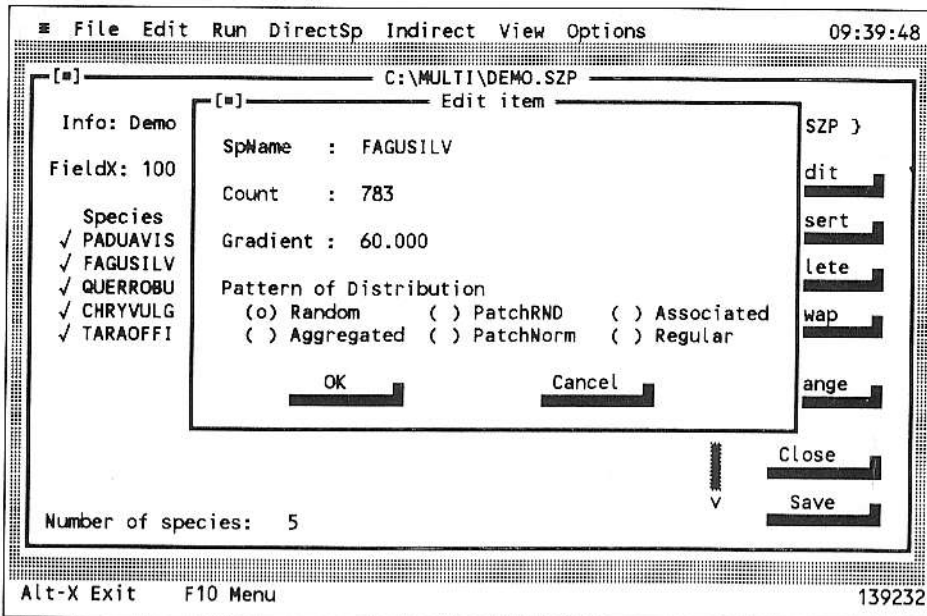


Fig. 3. The menu-controlled built-in editor of the program package to create a file containing the parameters of simulation.

### Parameter files of simulation and sampling

Parameters of a simulation are proposed to store in a file having a "\*.SIM" extension. This is the default extension. The first line of the file contains information about the data included in the file. The second line contains two figures: the length and width of the area where the individuals are located. The third line contains the number of species. Then each consecutive line contains the number of individuals of a species and some other parameters describing the distributional pattern of the individuals. The following patterns can be generated: (i) uniformly random; (ii) uniformly random along a gradient; (iii) aggregated pattern; (iv.a) patchy distribution with 2-dimensional normal distribution within the patches; (iv.b) patchy distribution with uniformly random distribution within the patches; (v) association between the species; (vi) regular distribution. The file can be generated by any general-purpose editor or it is generated automatically by the program using the menu options (see Fig. 3). It is stored as an ASCII file.

It is also possible to create communities with pre-defined abundance-dominance structure; the following abundance-dominance distributions are included: (i) MacArthur's broken stick model; (ii) Zipf model; (iii) Zipf-Mandelbrot model. The

abundance-dominance structure can be modified or entirely created by the built-in editor of the package.

The point pattern resulted in by the simulation can be displayed by symbols of different form and colour using the "View" option of the program.

The program package is able to simulate sampling procedure. It can be used by the data set generated by the package or any other data set (e.g. by a real point map of a forest or any other communities). Total random and regular sampling may be carried out. Sampling units with the shape of square, rectangle, circle and ellipse can be used.

"\*.PLP" is the default extension of a parameter file which describes the sampling technique of the spatial series analysis. This is also generated automatically by the program. The shape and size of the plots are included in the file.

There are two options for sampling. In the case of binary sampling just the presence/absence of species is recorded while in the case of quantitative sampling the number of individuals are also recorded. The result of sampling is saved to disk in a file with a user-defined file-name in the form of a two-way table. Thus it can be used by other programs or program packages. Data format of this file is identical with the data-format used by the NuCoSA program package (Tóthmérész, 1993c).

## Availability.

Executable program and demo files for IBM-compatible PC's are available from the authors on request sending a formatted disk (3.5" or 5.25"). It is also available on E-mail.

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# OLIGOCHAETA COMMUNITY AS INDICATOR OF EUTROPHICATION IN LOWER STREAM OF RIVER TISZA

N. Djukic, S. Maletin and B. Miljanovic

*Djukic, N., Maletin, S. and Miljanovic, B. (1993): Oligochaeta community as indicator of eutrophication in lower stream of river Tisza. - Tiscia 27, 49-52.*

**Abstract.** Analyses of Oligochaeta community in Backwater Tisza (during 1983-1991) and lower stream of river Tisza (from 1985 to 1991) established a rapid increase in number and biomass, especially for species which are indicators of eutrophic environment. According to relative abundance in Backwater Tisza, *Limnodrilus hoffmeisteri* (up to 50 %) and *Brachiura sowerbyi* (13 %) were dominants. Average annual number of individuals ranged from 88.8 (in 1983) to 12,457 (in 1990) ind/ m<sup>2</sup>, and biomass from 0.3 to 29.15 g/ m<sup>2</sup>. The significant increase of population density in river Tisza was stated upstream from the dam which is a consequence of slower flow and enrichment of substrate with organic compounds. Maximum number of individuals ranged up to 2,908 ind/m<sup>2</sup> and biomass up to 10.21 g/m<sup>2</sup> with predomination of genera *Limnodrilus* and *Branchiura*. Disturbed relationship in the structure of Oligochaeta community, rapid increase of individual number and biomass, and high rate of eutrophic species indicate a rapid process of eutrophication.

*Key word: backwater, river-bed, population, density, biomass.*

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## Introduction

Scientists have begun to be interested in the problem of eutrophication of stagnant waters at the beginning twentieth century (Weber, 1907). Lots of papers have shown that eutrophication develops in large mountain lakes as well in Switzerland, Sweden, USA and other countries (Milbrink, 1980; Lang and Lang-Dobler, 1980; Lang and Hutter, 1981; Lang, 19484; Goldman and Byron, 1986). Investigation of Oligochaeta community and estimation of eutrophication in Backwater Tisza until 1987 are shown by Dukic (1989) indicating accelerated eutrophication process in this environment. However, hydrotechnical measures in river Tisza bed, as various regulations including locks and dams, slowing the water flow, decreasing the water quality and increasing eutrophication process, too. In lots of papers it was clarified that the construction of reservoirs and other anthropogenic influences have caused changes in the bottom fauna (Petran and Kothe, 1975; Russev, 1982; Herzig, 1984; Djukic and Kilibarda, 1985).

Therefore new assignments are posed to investigators including research on occurrence of eutrophication in rivers (Owens, 1970; Guseva and Anisimova, 1971; Kozova, 1974; Labutina, 1974; Chernogolovska, 1974; Lee and Jones, 1978; Sirenko and Gavrilenko, 1978).

Investigations of Oligochaeta community in this sector of Tisza valley are continued so this work gives insight to results obtained for stagnant and running water.

## Methods

Samples were collected seasonally in 1983-1991 period for analysis of Oligochaeta fauna from Backwater Tisza and river Tisza (near the bank). Study site at Backwater Tisza is situated near Curug village, and those at river Tisza vere near Martonos (border profile), Novi Becej (dam) and Titel (at the mouth). Mud was taken by "Ekman-Bridge" dredge. Collected material was prepared in laboratory by American standard methods. Determination was carried out on live Oligochaeta specimens. Number

of individuals is given as average annual value per  $m^2$  of surface examined, and biomass as fresh mass of specimens in  $g/m^2$ .

## Results

Two families, Naididae and Tubificidae, and seven genera were identified by qualitative analysis of Oligochaeta community in Backwater Tisza. During the last three years of investigated period, eutrophic species dominated. According to relative abundance analysis, percent share of *Psammoryctides barbatus* decreased, and that of *Limnodrilus hoffmeisteri* increased up to 50%. *Branchiura sowerbyi* species was not recorded in previous period, but it was found in further researches with average share of 13%. All these data are in favour of conclusion that this river lake is rich in organic compounds and eutrophic (Fig. 1).

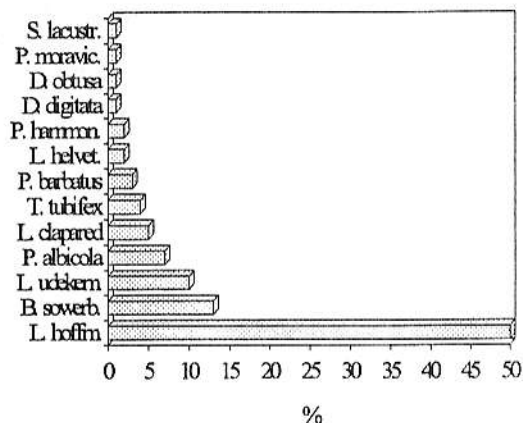


Fig. 1. Average percentage presence values of Oligochaeta species. Period: 1988-1990.

Examination of quantitative Oligochaeta share in benthic community shows distinct increase in number of individuals -- from  $88.8 \text{ ind}/m^2$  in 1983 to  $12,457 \text{ ind}/m^2$  in 1990 (Fig. 2). At the same time, biomass ranged from  $0.3 \text{ g}/m^2$  in 1983 to  $29.15 \text{ g}/m^2$  in 1990 (Fig. 3). Number of individuals increased 141-fold, and biomass 97-fold, which is characteristic for eutrophic waters.

The differences between these extreme values are highly significant ( $p < 0.01$ ), as well as majority inter alia years, especially in consideration for first three years in relation to the next period.

In qualitative analysis of Oligochaeta community in lower stream of river Tisza, 16 species were found from 10 genera and 2 families,

Naididae and Tubificidae (Table 1). Changes in percent share of certain species were noted on locality near Novi Becej, close to dam. On this section species from Tubificidae family are dominant from genera *Limnodrilus* and *Brachiura*. Percent share of these species ranges up to 50% in comparison to other species in the Oligochaeta community.

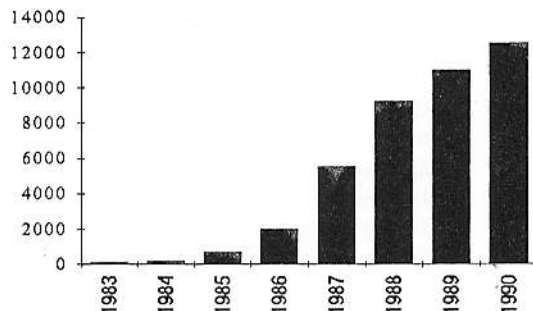


Fig. 2. Mean annual values ( $\text{ind}/m^2$ ) of the Oligochaeta number in backwater Tisza.

The period of investigation (1985-1991) is characterized by visible increase of individual number. Extremely high values were found upstream from the dam. Maximum number ranged up to  $2,908 \text{ ind}/m^2$  which represents 44-fold increase in comparison to results from 1976, and 4.3-fold in comparison to maximum value from 1984. At the same time, maximum average annual biomass was recorded in 1990 ( $10.21 \text{ g}/m^2$ ). These increases are also significant ( $p < 0.05$ ), particularly in comparison to values at the beginning (1985) and the end (1991) of studied period. The increased dynamics in number of individuals and biomass is discernibly connected to time when dam begun to function (Fig. 4 and 5).

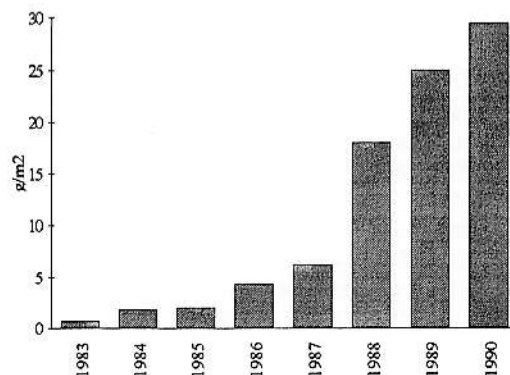


Fig. 3. Mean annual values of the Oligochaeta biomass.

Table 1 Qualitative analysis of Oligochaeta in lower stream of river Tisza (1985-1991).

Species	Martonos	Localities Novi Becej	Titel
<i>NAIDIDAE</i>			
<i>Dero digitata</i>	+	+	+
<i>Dero obtusa</i>	+	+	+
<i>Nais communis</i>	+		
<i>Nais elinguis</i>	+		
<i>Paranais litoralis</i>	+		
<i>Uncinialis uncinata</i>	+		
<i>TUBIFICIDAE</i>			
<i>Branchiura sowerbyi</i>	+	+	+
<i>Limnodrilus claparedeanus</i>	+	+	+
<i>Limnodrilus hoffmeisteri</i>	+	+	+
<i>Limnodrilus udekemianus</i>	+	+	+
<i>Peloscolex velutinus</i>	+		
<i>Potamothrix hammoniensis</i>	+		+
<i>Potamothrix moldaviensis</i>	+		
<i>Psamocitides barbatus</i>	+		+
<i>Tubifex montanus</i>	+		
<i>Tubifex tubifex</i>	+		+

## Discussion

Oligochaeta community of Backwater Tisza was investigated as a very good indicator of eutrophication level (Djukic, 1989). In vicinity of backwater, agricultural fields are located, influencing nutrient content of the water, as well as increasing of primary and secondary production. Drastic increase of Oligochaeta number and biomass is a warning that equilibrium in the community is disturbed.

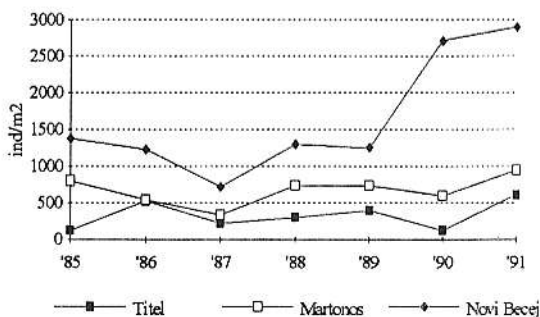


Fig. 4. Mean annual values of Oligochaeta number

This highly productive ecosystem should be used more rational. It is suggested that planned stocking of benthophagic fish species (*Cyprinus carpio* and *Tinca tinca*) would enhance exploitation

of this part of food resource. In that way, existing food chains, established by permanent introduction of planktophagic fish species as well as predators, would be supplemented.

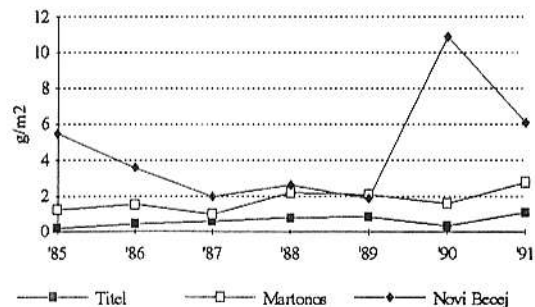


Fig. 5. Mean annual values of Oligochaeta biomass

First data on Oligochaeta from lower stream of river Tisza were published by Pujin and Maric (1961). They stated that river bottom was sandy and clayey with small amount of organic compounds and sparse number of Oligochaeta in bottom fauna. On the basis of complex physico-chemical and hydrobiological investigations, they concluded that this river was not polluted, water quality ranging within limits of  $\beta$ -mesosaprobic, even oligosaprobic, during summer. Twenty years later Djukic and Kilibarda (1985) found that dam, built in 1977, caused significant change in number of Oligochaeta individuals. Slower river stream and enrichment of



substrate in organic compounds contributed to intensive increase of individual number. At the same time, number of species found during the analyzed period has not changed significantly in comparison to former results (Djukic and Stanojevic, 1981, 1983; Djukic and Kilibarda, 1985). However, these species (from genera *Limnodrilus* and *Branchiura*) are very numerous in waters which are rich in organic compounds. According to Carroll and Dorris (1972), waters with slower flow and high organic compounds content are favourable for growth and development of *Branchiura sowerbyi*.

Disturbed relationships in Oligochaeta community structure, increase of number of individuals and biomass, and dominance of eutrophic species, are warning of accelerated process of eutrophication in studied water ecosystems.

## Conclusion

Investigations of Oligochaeta community in Backwater Tisza during 1983-1990 and in lower stream of river Tisza from 1985 to 1991 show that this hydroecosystems have very accelerated eutrophication process. The significant increase of individual number and biomass was established in analyzed backwater, as well as in river Tisza upstream (near dam), which is consequence of slowed water flow and substrate enriched in organic compounds. In the whole research period, eutrophic Oligochaeta species dominated, therefore they are characteristic for this environment. This points to disturbance of biological equilibrium in this part of Tisza valley. Authors suggest that this backwater should be used more rationally by increase of fish production of benthophagic fish species. All facts considered in the case of lower stream of river Tisza point out on disturbance of biological balance and increased eutrophication process, especially in river part upstream from dam.

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# CHARACTERISTICS OF FEEDING AND GROWTH OF PIKE PERCH AND PIKE IN THE PROTECTED PART OF RIVER BEGEJ

L. Budakov

*L. Budakov (1993): Characteristics of feeding and growth of pike perch and pike in the protected part of river Begej. - Tiscia 27, 53-56.*

**Abstract.** Material was collected through 1990 up to October 1991 in the regional park "Stari Begej" of river Begej. Altogether 80 specimens of pike perch and 94 specimens of pike were investigated.

The aim of the study was the analysis of relationship between predators and prey concerning their growth and length.

The age of pike was between 2<sup>+</sup> and 6<sup>+</sup>, and that of pike perch between 2<sup>+</sup> and 5<sup>+</sup>. Age class 3<sup>+</sup> was dominant in the case of both species. The values of body length increase are in the limits reported by Maletin and Budakov (1984), and Budakov (1989) as shown for both predators in Vojvodina rivers.

Pike and pike perch have limited variation concerning feeding. Fish predominated their food, 4 and 6 fish species, respectively. The highest proportion is linked with *Carassius auratus gibelio*. Both species are on the list of Serbian "Red book".

*Key words:* pike, pike perch, Stari Begej, feeding, growth.

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## Introduction

The Regional Park "Stari Begej" is situated in alluvial flat land of rivers Begej and Tisza.

Today's aspect of Stari Begej is the result of digging and its artificial separation on the fifteenth kilometer. In the length of about ten kilometers, river Begej is today in the limit of protected area separated from the rest of rivers Begej and Tisza. Separated part of river Begej is cut from Tisza by water gate. Natural and seasonal variation of water level is regulated by the water gate system on the northern and southern parts.

It represents last and modest remnants of marsh area in the low stream of rivers Begej and Tisza.

Stari Begej is occupied by 24 fish species from 7 families: Esocidae, Cyprinidae, Cobitidae, Siluridae, Ictaluridae, Centrarchidae and Percidae. The greatest is Cyprinidae family with 16 species (Budakov, 1989).

Ichthyofauna of Stari Begej has been investigated in the last few years. Predators (*Silurus glanis*, *Stizostedion lucioperca*, *Esox lucius*, *Perca fluviatilis*) are abundant and consequently their in-

fluence on the other species is important.

## Material and Methods

Studied material was collected in Stari Begej within the limits of protected area - Regional Park Stari Begej. Catching of pike and pike perch was done through 1990 up to October 1991 by electrofishing.

Material - 94 pike and 80 pike perch individuals - were investigated in fresh condition. Age and reconstruction of body length were determined on the basis of scales. Body weight was estimated from body length. Annual cycle of food composition was established from the stomach content, depending on season, age and sex.

## Results

In the studied sample, age classes of pike were labeled 2<sup>+</sup> - 4<sup>+</sup> in 1990 and 2<sup>+</sup> - 6<sup>+</sup> in 1991. Within the period of both years, the age class 3<sup>+</sup> was dominant.

Averages of body length (without caudal fin) were 369.75 and 438.33 mm, respectively (Table 1). According to the calculated values, length was duplicated after the second year, showing an intensive increase in the first years of life. It increased with age and became larger in individuals from 1991. Annual increase of body length gradually depressed, but after age 5<sup>+</sup> it increased prominently. Growth rate and growth constant are the highest in age 2<sup>+</sup> (C=0.03; K=4.07 or 3.57). Decrease of growth constant was noticed from 3<sup>+</sup> (K=2.07 or 1.74) related to approaching maturity.

Table 2. shows average values of body length (without caudal fin) for pike perch ranging from 337.86 to 342.69 mm. Estimated values of growth of body length are the same during the first year. This parameter increased gradually with age but the

values are slightly larger in individuals from 1990. In the ages 1<sup>+</sup> and 2<sup>+</sup>, annual increase of length growth and growth rate were very similar for both years, then gradually decreased but from age 4<sup>+</sup> they abruptly increased.

Growth of weight of pike and pike perch is shown in Fig. 1. These values prominently increased for pike after fifth and for pike perch after fourth year.

On the basis of the seasonal analysis of feeding of pike from 93 stomachs (Table 3.), the highest mass was noticed in Spring and the smallest in Summer. Seven fish species were determined in stomach content, as well as young fish were separated. The largest proportion belonged to *Carassius auratus gibelio*, followed by *Rutilus rutilus*. Pikes of ages 2<sup>+</sup> to 4<sup>+</sup> feed with *Perca fluviatilis* and

Table 1. Longitudinal growth of *Esox lucius* in Stari Begej, on the basis of samples from 1990 and 1991. Data are given in mm.

age class	generation	N	length mm	L1	L2	L3	L4
2 <sup>+</sup>	1990	11	327.64	154.86	258.07		
3 <sup>+</sup>	1989	42	352.02	135.29	233.70	307.22	
4 <sup>+</sup>	1988	19	433.32	134.69	235.67	323.40	386.84
average			369.75	138.12	237.97	312.26	386.84
annual increase				138.12	99.84	74.3	74.58

age class	generation	N	length mm	L1	L2	L3	L4	L5	L6
2 <sup>+</sup>	1991	1	377.00	150.80	282.75				
3 <sup>+</sup>	1990	14	421.71	159.47	278.90	370.23			
4 <sup>+</sup>	1989	4	464.00	143.73	262.85	359.41	420.70		
5 <sup>+</sup>	1988	1	448.00	135.76	203.64	271.51	339.39	407.27	
6 <sup>+</sup>	1987	1	620.00	155.00	258.33	344.44	413.33	482.22	551.11
average			438.33	154.72	271.46	361.84	405.92	444.75	551.11
annual increase				154.72	116.74	90.38	44.08	38.83	106.36

Table 2. Longitudinal growth of *Stizostedion lucioperca* in Stari Begej, on the basis of samples from 1990 and 1991. Data are given in mm.

age class	generation	N	length mm	L1	L2	L3	L4	L5
2 <sup>+</sup>	1990	9	283.11	115.82	217.36			
3 <sup>+</sup>	1989	18	335.44	119.74	215.40	284.75		
4 <sup>+</sup>	1988	9	399.78	116.32	207.47	285.38	347.85	
5 <sup>+</sup>	1987	2	530.00	147.86	259.29	345.71	422.14	478.57
average			337.86	119.6	216.3	289.16	361.36	478.57
annual increase				119.6	96.81	72.86	72.21	117.21

age class	generation	N	length mm	L1	L2	L3	L4	L5
2 <sup>+</sup>	1991	9	333.78	143.49	255.48			
3 <sup>+</sup>	1990	22	339.41	118.61	216.09	287.79		
4 <sup>+</sup>	1989	8	339.25	99.14	175.71	242.05	296.74	
5 <sup>+</sup>	1988	3	402.67	96.04	180.12	260.20	320.50	363.36
average			342.69	118.6	214.3	274.2	303.2	363.4
annual increase				118.6	95.7	59.9	29.2	60.1

*Rutilus rutilus*. Young fish is eaten in the largest amount by age class 2+. From age class 2+ to 4+ range of food is very wide and includes five species. *Carassius auratus gibelio* was prey of pike of age 4+.

In Spring, after pike's spawning, female are more active in searching food, but the proportion of individuals with not empty stomach is almost the same for male and female.

From 78 studied stomachs of pike perch, 56 had one component - fish and young fish. The determination of the latter was not possible. Increasing number of species were noticed from Spring to Autumn, but *Carassius auratus gibelio*, *Rutilus rutilus* and *Lepomis gibbosus* were present during all seasons. *Carassius auratus gibelio* and *Rutilus rutilus* are main components of food of pike perch in age classes 2+ to 5+. Males and females have practically the same demands for food after spawning.

## Discussion

Data related to the growth of length are contribution to the knowledge of ecology of pike and pike perch which are very important in economy as well as in sport fishing.

Age and growth of pike in Vojvodina waters were investigated by Ristic (1968), Jankovic (1973), Budakov and Maletin (1982a, 1982b, 1984), Maletin and Budakov (1983) and Budakov (1989), and those of pike perch by Maletin and Budakov (1984).

Table 3. Composition of prey species in the food of studied predators.

<i>Esox lucius</i>	season			growth					Spring sex	
	Spring	Summer	Autumn	2+	3+	4+	5+	6+	female	male
number of estimated stomachs	58	14	21	12	54	21	1	1	43	14
Number of full stomachs	30	3	17	4	28	16	1	1	23	7
<i>Rutilus rutilus</i>	24.39	-	20.00	42.86	25.96	9.09	-	100.00	22.58	30.00
<i>Scardinius erythrophthalmus</i>	2.44	-	10.00	-	-	18.18	-	-	3.23	-
<i>Abramis ballerus</i>	-	50.00	-	-	3.70	-	-	-	-	-
<i>Carassius auratus gibelio</i>	46.30	-	40.00	-	-	54.55	-	-	45.16	50.00
<i>Misgurnus fossilis</i>	4.88	-	-	-	7.41	-	-	-	6.54	-
<i>Lepomis gibbosus</i>	7.32	50.00	10.00	-	14.81	-	100.00	-	6.45	10.00
<i>Perca fluviatilis</i>	2.44	-	10.00	14.29	44.44	9.09	-	-	3.23	-
Young fish	12.19	-	10.00	42.86	7.41	9.09	-	-	12.90	10.00

<i>Stizostedion lucioperca</i>	season			growth				Summer sex	
	Spring	Summer	Autumn	2+	3+	4+	5+	female	male
number of estimated stomachs	16	37	25	17	40	16	5	23	14
Number of full stomachs	10	24	22	10	28	14	4	13	11
<i>Rutilus rutilus</i>	41.67	42.42	13.79	30.77	31.15	28.57	16.67	43.75	41.18
<i>Alburnus alburnus</i>	-	3.03	-	-	-	7.14	-	6.25	-
<i>Carassius auratus gibelio</i>	50.00	33.33	41.38	69.23	26.83	42.86	50.00	31.25	35.29
<i>Misgurnus fossilis</i>	-	3.03	3.45	-	2.44	-	16.67	-	5.88
<i>Lepomis gibbosus</i>	8.33	9.09	10.34	-	12.20	14.29	-	18.75	-
<i>Perca fluviatilis</i>	-	-	6.90	-	4.88	-	-	-	-
Young fish	-	9.09	24.14	-	19.51	7.14	16.67	-	17.65

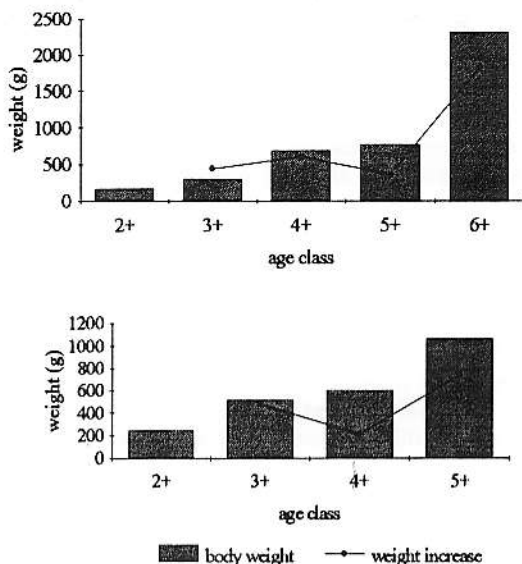


Fig. 1. Estimated growth of weight of *Esox lucius* (upper) and *Stizostedion lucioperca* (lower) in Stari Begej.

The growth of length of pike in Stari Begej is similar to the those in Danube, Sava and Tisza, but larger than those in Obedska bara and Koviljski rit (Budakov, 1989a, 1989b), and opposite to the results of Pankratova (1980).

Maletin and Budakov (1984) reported the largest longitudinal growth of pike perch from Sava and weaker than that from Danube. The values of this parameter were similar for Tisza and Tamis. These

results show that longitudinal growth of pike perch from Stari Begej was better related to that from Danube but smaller concerning pike perch from Sava, Tisza and Tamis.

Food composition of predators in waters of different type depends on the abundance of prey fish species, as well as their availability, dimensions, body shape, behaviour and water regime (Nikoljski, 1974). Feeding characteristics of pike and pike perch change with season and age (Domanevskij, 1958; Rudzjanskene, 1987), as well as related to sex, especially after spawning (Ivanova, 1965).

Spectrum of food of pike and pike perch in Stari Begej is poor, and includes nonvaluable species. Stomach content of pikes from Danube, Sava, Tisza, Koviljski rit consisted of 11 to 17 species. System of feeding is similar to that in Obedska bara (Budakov, 1988, 1990). In the food of pike perch, the primary species are similar to those of pike (Ivanova, 1965). Kirillov et al. (1977) reports that food composition depends on availability of different species as well as on their length and ecological characteristics (Rudzjanskene, 1987).

Spectrum of predator's feeding depending on age is less investigated. Pervazvanskij et al. (1977) reports that predators of age group up to 4<sup>+</sup> are characterized by different food. On the other hand, individuals labeled from 5<sup>+</sup> to 9<sup>+</sup> replace small littoral species with larger ones.

Intensive feeding of pike and pike perch females after spawning (Zajcev, 1956) could not be totally accepted according to our results.

The feeding biology of pike and pike perch are different and because of that there is no interspecific competition between these two fish species. Although *Carassius auratus gibelio* is predominant in their feeding, this resulted from its large abundance in this river. The role of these predators is related to decrease of allochthonous species in the protected area.

Our results show (Budakov, 1989) that pike and pike perch are exposed to enough food, since this factor has no limitation for their longitudinal growth. It is obvious that dependence exists between growth and environmental conditions, but it is very hard to separate any special factor concerning their complex effect.

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