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Small-scale distribution of psammophilic ciliates

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Abstract — Twenty-seven samples were collected along the homogeneous sandy shore of a brackish-water lake. Values of dissimilarity between all samples were calculated on the basis of qualitative and quantitative occurrences of psammophilic ciliates. Several different dissimilarity measures were used The results presented by means of cluster analysis (UPGMA) show that psammophilic ciliates are very contagiously distributed in a small scale.

Key words: Ciliates, cluster analysis, small-scale distribution, heterogeneity, psammon.

1. Introduction

In field work protozoologists often compare communities of species collected in sites representing different habitats or lying along environmental gradients. As there is no possibility to preserve the samples, their number which can be collected at a time and then worked out in the laboratory is very restricted. Hence, it often happens that samples from a number of different places are collected into a few large containers and are treated like mean samples (Bamforth 1963). Maybe this is one of the reasons why we still know very little about microspatial patterns of the distribution of Protozoans.

According to Wieser (1975) three factorial principles may be distinguished which are responsible for the „fine grained" structure of

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intertidal and shallow water marine sediments: horizontal gradients, vertical gradients and inhomogeneities. By this last term Wieser understands variations of ecological factors within a restricted site which are not due to gradients but to inhomogeneitis in sediment composition, patchiness of food and to other biotic factors. Many papers have been published which deal with psammophilic ciliates distribution along gradients between land and water or between the intertidal and the sublittoral. There are also many works concerning vertical gradients from the surface into the depth of the sediment. However, there is still lack of data about the actual role of the third of Wieser's factorial principles.

This work is a preliminary attempt at determining ciliates distribution on a homogeneous sandy shore of the brackish water lake Ptasi Raj near Gdańsk. A more detailed description of the lake may be found in a paper by Czapik and Jordan (1976).

2. Methods

2.1. Sampling and counting of the ciliates

27 samples were collected at different distances from one another along homogeneous sandy shore in June 1979. 23 samples were collected from emerged sand always about 20 cm from the shore line. Fig. 1 shows in a schematic way the localization of the places from which the samples

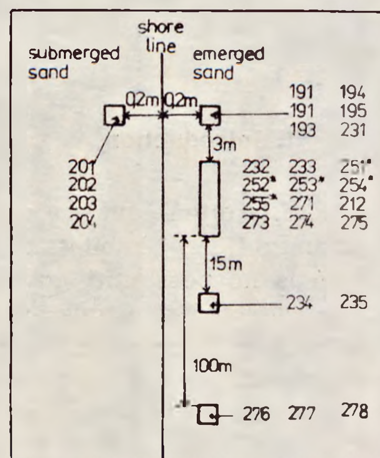

Fig. 1. Localization of sampling sites; the asterix denotes samples taken from 3×3 cm square

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were taken. Each sample is indicated by three numbers. The first and the second numbers give the day of June 1979 when the samples were collected and the third is the number of the sample in a given day. All samples were taken at random in the zones indicated in fig. 1. 12 samples were collected from the rectangle 100 × 10 cm (main sampling zone) and the remaining from squares 10 × 10 cm in the distances: 3, 15 and about 100 m along the shore. Five samples (251—255) from the main sampling zone were taken at the same time very close to each other, from the square 3 × 3 cm. All samples were taken with plexi tubes with internal diameter 0.7 cm. They were collected always about 10 a. m. and were immediately carried to the laboratory. Only 2 cm of the top of the sand column was used from each sample. As previous observations have shown below this layer only single specimens were found. Extraction of the microfauna was made by the sea-water ice method (Uhlig, 1968, Fenchel 1967, 1969). The ciliates were counted by removing them one by one with a pipette under the dissection microscope. Only very small species were ommitted like *Cyclidium* and *Aspidisca*. If the species could not be indentified without making silver preparations it was distinguished by its morphology and behaviour on the basis of earlier observations. It seems that this procedure should not lead to errors if it concerns restricted area and time and is made by one person only. Table I shows the results of the counting.

2.2. Data analysis

The values of dissimilarity between all samples were calculated on the basis of the data from Table I. The results were shown by means of cluster analysis. This method can be applied to the cases in which the conditions of rigorous statistical methods are not properly met, and thus where tests of significance may be meaningless (Kaesler 1966). The unweighted pair group method (UPGMA) with arithmetic average was chosen for this study as it produces clusters with less distortion than other commonly used clustering methods (Boyce 1969, Farris 1969, Kaesler, Cairns 1972). As there are not any objective criteria to decide which of the known dissimilarity measures will give the „best" results, several different coefficients were used both for quantitative and for presence-absence form of the data. Four coefficients, commonly used in ecological work, which assume values from 0 (similarity) to 1 (dissimilarity) were chosen: Canberra metric, Bray-Curtis measure, one complement of Jaccard and of Simple Matching coefficients. The description of the properties of these coefficients may be found in Clifford and Stephenson (1975). Canberra metric was used in two variants: normal, involving double zero records and modified so as to ignore them

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Table 1. Number of specimens of each species in the samples

Species	Samples																										
	191	192	193	194	195	231	232	235	234	233	251	252	253	254	255	276	277	278	274	275	271	272	273	205	204	201	202
Blepharisma sp.	3	2	2	2	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	-	-	-
Condylostoma sp.	-	-	-	-	-	-	-	-	1	-	-	1	-	-	3	-	-	-	-	-	-	-	-	23	3	52	85
Climacostomum virens	3	2	-	1	2	-	4	-	-	7	4	2	8	3	14	1	-	-	30	8	-	13	2	-	-	-	-
Climacostomum sp.	2	-	-	-	-	-	-	-	-	-	-	2	4	2	2	2	1	-	3	-	-	-	-	1	-	-	-
Diophrys sp.	-	-	-	-	-	-	-	-	-	-	1	-	3	7	3	11	2	2	15	1	2	1	-	136	21	67	119
Euplotes 2	-	2	1	1	-	3	-	-	-	-	1	1	1	3	4	-	-	6	-	3	1	1	4	-	1	-	-
Gruberia 1	6	7	-	1	-	-	6	3	12	6	-	-	-	-	-	-	-	-	-	13	3	2	2	1	15	92	19
Gruberia 2	-	2	1	1	-	-	1	-	-	-	-	-	2	-	-	-	-	-	35	-	-	33	-	-	-	3	-
Hypotricha 1	1	-	2	-	-	-	40	27	13	10	4	7	4	14	8	50	100	34	15	20	3	-	3	23	10	9	8
Hypotricha 2	5	1	8	1	-	4	78	-	4	47	23	8	11	130	83	11	37	73	137	75	325	384	79	12	1	2	6
Hypotricha 4	-	-	-	-	-	-	-	1	1	1	-	-	-	-	-	116	22	166	-	-	-	-	-	-	-	-	-
Lacrymaria sp.	-	-	1	-	5	-	-	3	-	1	-	-	-	-	-	-	-	-	2	1	-	-	-	-	-	1	2
Lacrymaria olor	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	10	1	2	8	10	4	-	-	9	11	1	18
Loxophyllum multinucleatum	4	2	2	2	4	1	18	2	1	1	2	3	2	7	5	-	1	1	13	11	-	14	-	1	2	-	2
Loxophyllum sp.	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	-	-	-	-	2	-	-	-	1	1	2	-
Paramecium aurelia	1	-	2	-	-	-	-	10	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
Plagiopogon sp.	-	-	1	-	-	-	-	144	13	-	-	-	-	-	-	-	-	-	-	-	-	2	-	28	30	12	21
Pleuronema sp.	2	1	1	2	17	8	44	73	32	28	21	6	18	48	103	3	2	1	7	50	-	13	-	46	63	24	60
Prorodon discolor	3	6	4	2	-	1	12	13	-	3	-	1	1	4	2	22	36	30	-	5	1	-	-	22	67	7	9
Prorodon raabei	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	1	3	-	-	-	-	-	-	-	8	1	-
Spathidium sp.	-	-	-	-	-	-	3	1	1	2	1	1	-	3	2	-	-	1	-	7	-	-	-	-	-	-	-
Urosoma sp.	5	9	10	1	7	-	35	13	11	9	-	-	4	1	9	-	-	-	15	8	1	2	-	60	51	298	193
Urostyla sp.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7	-	-	-	-	17	13	4	9
Diophrys scutum	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20	81	17	86
Trachelostyla sp.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	11	100	4
Euplotes 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	17	9	57	44
Frontonia sp.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	439	115	540	141
Hypotricha 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	28	1	9	24

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(Clifford, Stephenson 1975). In both variants in the case when one element of any comparison was zero it was replaced by one-fifth of the lowest entry in the data matrice. Both raw and log (a + 1) transformed data were used. (This transformation is frequently used to reduce the influence of extremely high values). In general the same set of data was analysed in eight different ways:

A. Complement of Jaccard Coefficient
B. Complement of Simple Matching Coefficient

C.	Bray-Curtis measure	
D.	Canberra metric	Raw data
E.	„Canberra metric" ignoring conjoint absences	
F.	Bray-Curtis measure	
G.	Canberra metric	Transformed data
H.	„Canberra metric" ignoring conjoint absences	

The amount of distortion produced by averaging in the course of the clustering procedure was estimated by the cophonetic correlation coefficients (r_{cc}) (Sokal, Sneath 1963, Boyce 1969, Cairns, Kaesler 1969). The correlation coefficients were computed between all half Q-matrices.

3. Results and discussion

3.1. Comparison of the methods

Table II shows the correlation coefficients computed between eight half Q-matrices of dissimilarity values. On the basis of this table a dendrogram (UPGMA) was computed (fig. 2). The used procedures form two distinct clusters. There are all coefficients which ignore conjoint absences in the first cluster and those which involve them in the second. The values of Bray-Curtis measure computed from raw data form the third distinct category. This coefficient tends to be greatly influenced by occasional outstanding values and after transformation of the data it gives results nearer to the other coefficients ignoring conjoint absences. Canberra metric, on the contrary, does not come to be dominated by extremely high values (Clifford, Stephenson 1975) and gives very similar results on raw and on transformed data (fig. 2).

The significance of negative matches (conjoint absences) is discussed

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Table II. Correlation coefficients between all half Q-matrices

	/A/	/B/	/C/	/D/	/E/	/F/	/G/	/H/
/A/	-							
/B/	0.759	-						
/C/	0.560	0.561	-					
/D/	0.771	0.723	0.773	-				
/E/	0.529	0.929	0.566	0.716	-			
/F/	0.839	0.724	0.847	0.883	0.622	-		
/G/	0.906	0.770	0.749	0.955	0.674	0.948	-	
/H/	0.631	0.969	0.598	0.747	0.988	0.701	0.746	-

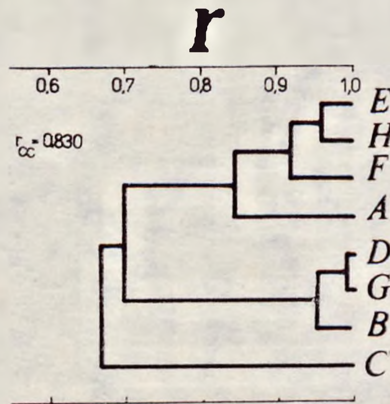

Fig. 2. Dendrogram (UPGMA) based on the matrix of correlation coefficients (Table II)

by K a e s l e r (1966). According to that author negative matches should be given equal weight with positive ones in forming biotopes if sampling is adequate and the study area behaves as an environmental unit. In this work the study area is small and visually quite homogeneous. Maybe negative matches give in this case information as good as positive ones. However, as we do not have any sort of spatial relationship model for protozoans (C a i r n s, Y o n g u e 1977) we cannot admit it. Each of the eight analyses yielded somewhat different results. Only four characteristic dendrograms were presented in fig. 3.

3.2. Distribution of ciliates

Three conclusions may be drawn from the dendrograms:

1. The submerged and the emerged sand represent two qualitatively

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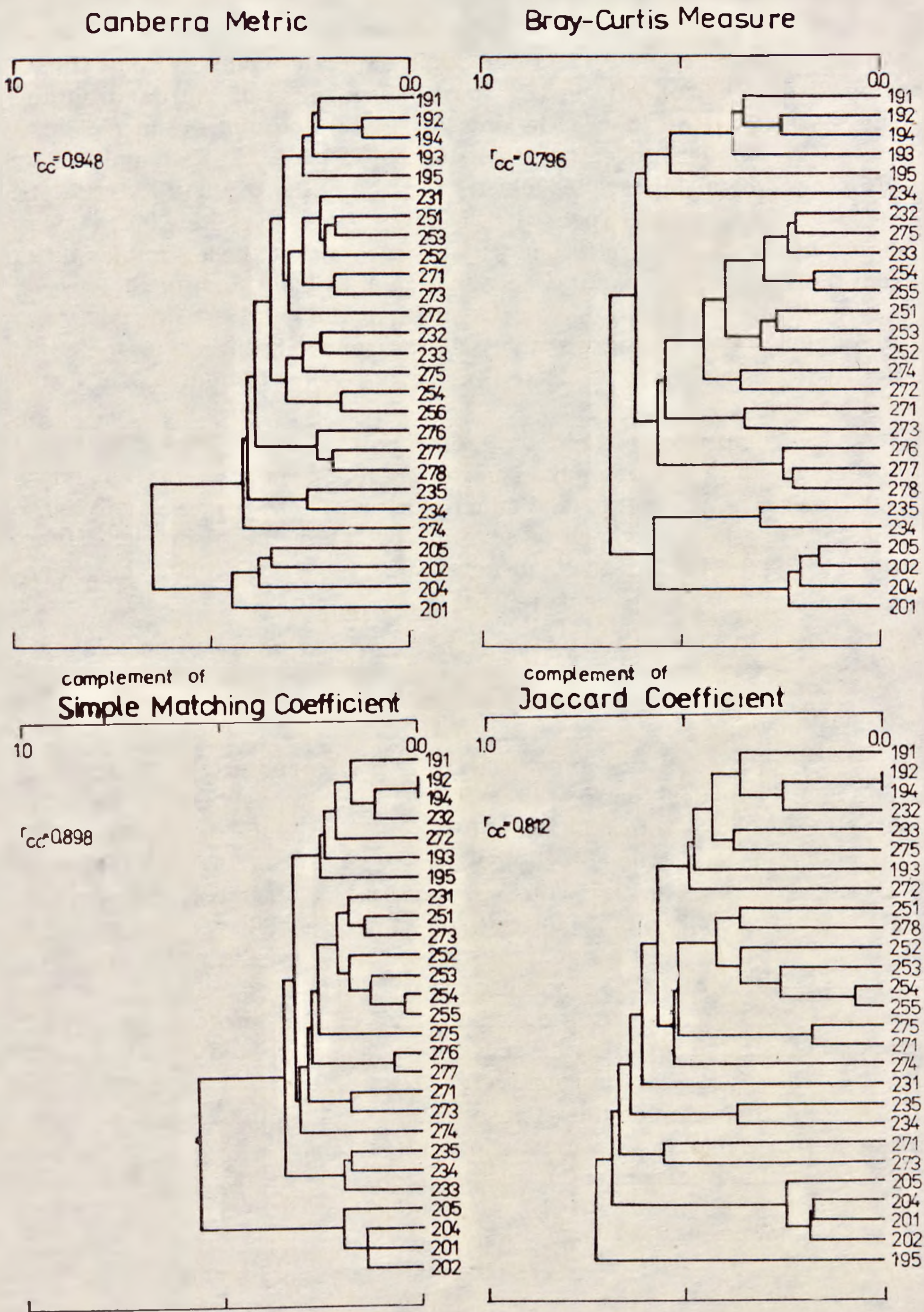

Fig. 3. Dendrograms (UPGMA) based on four different Q-matrices

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different habitats. The samples taken from the submerged zone (201, 202, 204, 205) differ distinctly from the rest both in qualitative and quantitative composition of the ciliates. As one could expect the dendrograms (fig. 3) show distinctly isolated clusters, particulary those of the dendrograms which are based on the coefficients involving conjoint absences.

2. The samples collected in distances 15 m (235, 234) and 100 m (276, 277, 278) make isolated clusters in the cases of quantitative data. However, one might expect that samples from the site 100 m away should be much more different. Table I shows that these samples differ from the rest rather quantitatively than qualitatively and for that reason they are somewhat mixed with the other in the dendrograms computed from binary data. This means that with presence-absence data one could not distinguish samples collected in the distance of about 100 m in the studied area.

3. The samples collected from the square 3 × 3 cm (251—255) are not more similar to each other than those taken at greater distances and on other days. They do not form distinct clusters. There is a relatively large variation in the occurrence of several species in these samples (*Hypotricha* 2: 23, 8, 11, 130, 83, *Pleuronema* sp.: 21, 6, 18, 48, 103). The distances between these samples were from 0.5 to 1.5 cm.

4. Conclusion

The results mentioned above show that psammophilic ciliates are very contagiously distributed in a small scate. This is consistent with the observations quoted from other habitats. Cairns and Yongue (1968) found that on a presumably homogeneous substrate the individuals of various protozoan species were not uniformly distributed. Samples collected from visually similar habitats or within a small area may show no tendency to be similar in their protozoan fauna (Cairns et. al. 1974, Taylor 1979). Taylor and Berger (1980) tried to quantify microspatial heterogeneity in the distribution of ciliated protozoa in a small pond. They found mean patch size and mean interpatch distance as 1.5 to 2 cm and 3 to 4 cm respectively. According to these authors the ephemeral character of these clusters may be due to behavioral aggregation around the non-continuous food sources.

The problem of microspatial heterogeneity in the distribution of psammophilic ciliates calls for a quantitative determinations of this phenomenon. This seems to be indispensable both to understand protozoan communities and to collect the samples in a proper way.

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5. Polish summary

Rozmieszczenie orzęsków psammonowych w małej skali

W ciągu kilku dni czerwca 1979 r. pobrano 27 prób ze słonawego jeziora Ptasi Raj koło Gdańska. Próby pobierano w różnych wzajemnych odległościach wzdłuż jednorodnego piaszczystego brzegu. Większość prób pochodzi ze strefy piasku wynurzonego, w odległości ok. 20 cm od linii wody.

Na ryc. 1 przedstawiono schematycznie lokalizację miejsc poboru prób. Na podstawie jakościowego i ilościowego występowania orzęsków psammonowych obliczono liczbowe podobieństwa między wszystkimi próbami. Zastosowano kilka różnych używanych w ekologii współczynników, a wyniki przedstawiono graficznie metodą analizy skupień (UPGMA). Posłużono się danymi (tabela I) jakościowymi i ilościowymi zarówno w formie surowej, jak i transformowanej (log(a+1)). Poszczególne metody porównano obliczając współczynniki korelacji między wszystkimi pół-Q-macierzami (tabela II i ryc. 2). Otrzymane wyniki (ryc. 3) wskazują na bardzo skupiskowe rozmieszczenie orzęsków psammonowych w małej skali i sugerują konieczność dużej ostrożności przy interpretowaniu danych ilościowych.

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