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DISTRIBUTION, GENETIC STRUCTURE AND ECOLOGICAL ROLE OF *DREISSENA POLYMORPHA* (PALLAS) IN LAKE DĄBIE, WESTERN POMERANIA, POLAND

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Abstract

Dreissena polymorpha inhabits about 46.5% of the bottom area in Lake Dąbie. It is most abundant in the northern part of the lake and sporadically occurs in its southern part. The average density of the zebra mussel is 891 individuals/m^2, while its wet weight is 1374 g/ m^2. In the settled areas the density of the zebra mussel reaches 1734 individuals/ m^2.

There were presently established 7 age-groups from 0 to 6+. The highest number of specimens occurred in the age-groups between 1+ and 3+, while the lowest number - in the groups 0, 5 and 6+. Strong eutrophication and pollution of Lake Dąbie on its southern side, combined with sedimentation of the extensive amounts of seston carried in by the Płonia and Regalica rivers, do not create favourable conditions for development of *Dreissena*.

D. polymorpha plays a very positive role in the lake ecosystem through its biofiltrating action, contributing thus to an increase of water clarity and to limitation of phytoplankton development through cumulating nutrients in its biomass.

Electrophoretic analysis of 9 enzymatic loci revealed strong polymorphism of the studied population of the zebra mussel: percent of polymorphic loci - 100, mean number of alleles in locus –

3.4, coefficient of expected heterozygosity per locus in the population, H_S - 0.335, percentage of separate genotypes - 69%, in this number unique genotypes - 58%. A very strong scattering of the alleles was stated within the entire population. In each aggregation, on average, 90% of the specimens have a separate genotype.
Each of the five defined groups of *D. polymorpha*, representing profiles I-V, respectively, had similar genetic composition. The values of the genetic similarity among the studied groups of the zebra mussel ranged from 0.96 to 0.99.

Key words: *Dreissena polymorpha*, distribution, age composition, ecological role, enzymatic polymorphism

INTRODUCTION

Dreissena polymorpha (Pall.), or the zebra mussel is a species which had been accidentally introduced to Poland along with a coelenterate *Cordylophora caspia* (Pall.) and a crustacean *Corophium curvispinum* (Sars.) from the Ponto-Caspian drainage basin in the 19th century (Urbański 1957). Mass occurrence of the zebra mussel in the brackish waters of the Odra River estuary was revealed as early as 1896 by Randt (Wiktor 1969). *Dreissena* unlike *Cordylophora* and *Corophium* plays a positive ecological role, in the water bodies of the Odra River estuary, through biofiltration and bioaccumulation. It utilizes overabundant phytoplankton as its food, creating in this way a rich food base for various animals; for example, crayfish - *Orconectes limosus* (Raf.), crabs - *Eriocher sinensis* Milne-Edwards, birds - *Fulica atra* (L.), and also economically important fishes, like roach, *Rutilus rutilus* (L.) and eel, *Anguilla anguilla* (L.) (Pęczalska 1961, Orzechowski 1966, Wiktor 1969, Piesik 1974, Stempniewicz 1974, Szlauer 1974 and Stańczykowska 1977).

The biological and ecological role of *Dreissena* in the water bodies of the Odra River estuary were studied, to name only a few, by Wiktor (1969), Hodyl (1980), Świerczyński *et al.* (1986), Janicki (1994), Piesik and Grodzicka (unpublished data).

Lake Dąbie, where the present studies on the zebra mussel were conducted, is a brackish-water basin of 56 km^2. It is naturally divided into two major parts: Dąbie Duże (about 49 km^2) and Dąbie Małe (about 7 km^2) (Fig. 1). Water volume in the lake equals 0.168 km^3 and its average depth - 2.8 m. It is supplied by the waters of the Regalica River - the eastern branch of the Odra River, by the Płonia River, and streams. Due to periodic backwater of the Baltic brackish waters through the Szczecin Lagoon and the Domiąża (the latter being a part of the Odra River), Lake Dąbie has been considered a tertiary estuary (Tadajewski *et al.* 1990). Lake Dąbie is used for transportation (barges) and fisheries. It also constitutes a convenient site for leisure activities for the Szczecin metropolis.

D. polymorpha in Lake Dąbie was hitherto studied by Piotrowski (1991), Zieliński and Wachowiak-Zielińska (1992), Piotrowski and Ochman (1993), and Janicki (1994). The aim of the present work is to the distribution of the zebra mus-

sel in Dąbie Duże Lake, determine its abundance, age composition, and genetic structure.

MATERIAL AND METHODS

Studies on the occurrence of *D. polymorpha* in Lake Dąbie were carried out from 1 to 17 August 1988 (Fig. 1). The zebra mussel was collected along five profiles traced on a east-west line. A total of 71 samples was taken. Each sample consisted of three autonomous sub-samples.

The material was gathered on the bottom of the lake using a Van Veen sampler of the area of 0.062 m^2. The samples were strained through 1-mm mesh, the mussels were separated and subsequently studied in the laboratory. Length of the mussels was measured, to the nearest 0.5 mm, using a slide caliper. Age of the mussels was determined through readings of the annual rings on their shells. The wet weight was determined based on the standards given by Wiktor (1969). Additionally, for comparative purposes, the biomass of the selected samples was determined, to the nearest 0.01 g, using a laboratory balance. Abundance and wet biomass (with water enclosed in the mantle cavity) of the samples was related to 1 m^2 of the bottom. Based on the data of Wiktor (1969) and Stańczykowska (1977) the filtration potential of *D. polymorpha* and amounts of calcium carbonate as well as phosphorus and nitrogen compounds accumulated in the biomass of the mussel, were estimated.

The occurrence constancy factor, or frequency of occurrence of *D. polymorpha* on the bottom of the lake was calculated using the following formula:

$$C\% = \frac{n}{N}100$$

where:

n—number of samples with *D. polymorpha*
N—total number of samples of *D. polymorpha* taken

Description of the profiles traced in Lake Dąbie (Figs. 1, 2):

Profile I- about 2870 m long, with 9 sampling sites in intervals of some 320 m.
Profile II- about 3850 m long, with 15 sampling sites in intervals of some 260 m.
Profile III; about 4180 m long, with 15 sampling sites in intervals of some 280 m.
Profile IV; about 3600 m long, with 25 sampling sites in intervals of some 145 m.
Profile V; about 2500 m long, with 7 sampling sites in intervals of some 360 m.

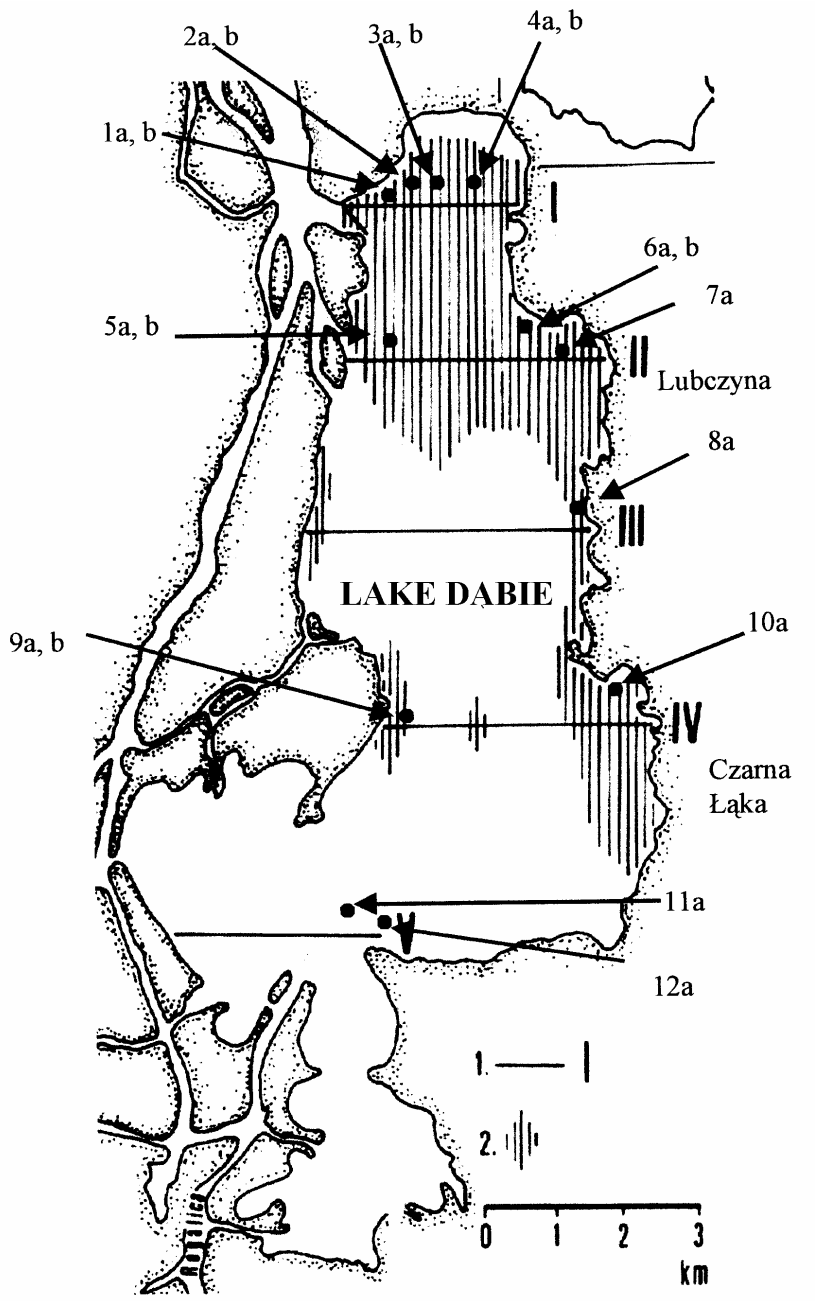

Fig. 1. *Dreissena polymorpha* distribution in Lake Dąbie.
I-V: Profiles. Marked areas denotes the presence of zebra mussel.

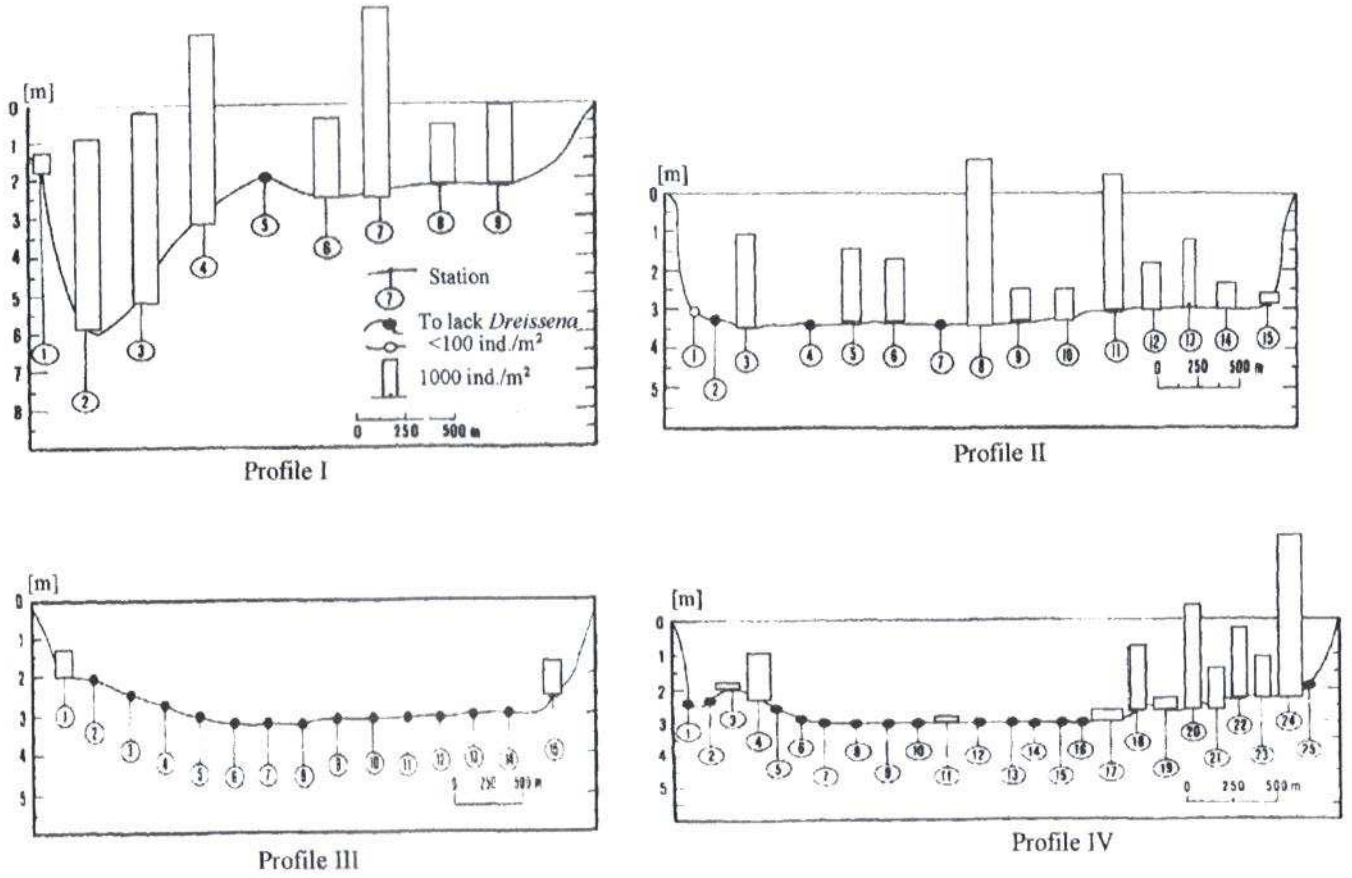

Fig. 2. *Dreissena polymorpha* distribution on profiles I-IV

At the time of the mussel sampling, pH was measured. The surface water reaction of the lake was studied on 81 sampling sites along the same profiles (Fig. 1) in August 1988. Also the water transparency was studied in August 1988, using a Secchi disk (30 cm in diameter) on 50 sampling sites, along 5 profiles (Fig. 1).

For the electrophoretic the zebra mussel studies was sampled from five transects on 17–19 April, 19–21 June, and 6–7 July 1991. The samples were taken from 12 sites. At five sites a single scoop was taken, while at seven sites the bottom was scooped twice. A total of 19 samples was taken. Each of the samples constituted part of the aggregation (colony) of the zebra mussel.

Ten individuals of the mussel from each sample were analyzed electrophoretically. The following 8 enzymes were studied: phosphoglucomutase (PGM) leucine aminopeptidase (LAP), glutamate-oxaloacetate transaminase (GOT), esterase (EST), isocitrate dehydrogenase (IDH), phosphoglucoisomerase (PGI), malate dehydrogenase NAD-dependent (MDH), and malic dehydrogenase NADP-dependent (ME). Electrophoretic analysis of the above-mentioned enzymes as well as genetic interpretation of the acquired electrophoretic phenotypes were conducted in a similar way as it was presented in the works of Zieliński *et al.* (1996) and Soroka *et al.* (1997). Statistical calculations were performed using the following formulas (according to Nei 1972, with exclusion of Chi^2 test):

Coefficient of expected heterozygosity in locus in the population:

$$H = 1 - \sum_{i=1}^{n} p_i^p$$

where:
p_i—frequency of i^{th} allele in locus H in the population
n—number of alleles in locus H

Mean value of the coefficient of expected heterozygosity per locus in the population:

$$H_s = \frac{\sum_{i=1}^{n} H_i}{n}$$

where:
H_i—value of H in i^{th} locus
n—number of loci

Genetic similarity:

$$I_N = \frac{\sum_{i=1}^{m} p_{ix} p_{iy}}{\sqrt{(\sum_{i=1}^{m} p_{ix}^2)(\sum_{i=1}^{m} p_{iy}^2)}}$$

where:
p_{ix}—frequency of i^{th} allele in population x
p_{iy}—frequency of i^{th} allele in population y
m—number of alleles

Chi^2 test for nominal scale:

$$Chi^2 = \frac{1}{N_1 N_2} \sum_{i=1}^{k} \frac{\left(N_1 n_{i2} - N_2 n_{i1}\right)^2}{\left(n_{i1} + n_{i2}\right)}$$

where:
N_1—abundance of first population
N_2—abundance of second population
n_{i1}, n_{i2}—frequency of i^{th} allele in locus in the first and second population, respectively
k—number of alleles

RESULTS

Distribution of *D. polymorpha* in Dąbie Duże Lake

Dreissena inhabited the bottom of the lake unevenly, which was evident from its constancy of occurrence (C) in the collected samples amounting to 46.5% (on average) (Figs. 1, 2; Table 1). It was the most abundant in the northern part of the lake in the profiles I and II (88.9% and 80.0%, respectively; Fig. 2). In the profile III, the abundance of the mussel decreased, compared to the profile I by 75.6% (Table I). In this profile, the mussels were encountered only in the coastal zone, on the depths from 1.8 to 2.5 m (Fig. 2, profile III). In profile IV, the abundance of *D. polymorpha* increased a number of times, compared to profile III. The zebra mussel inhabited mainly the eastern part of this water body (Fig. 2, profile IV), with the constancy of occurrence (C) equaling 44.0%. Presence of the zebra mussel was not stated in the southern part of Dąbie Duże Lake in profile V. The values of the wet weight of the mussel in the studied profiles were presented in Table I.

The analysis of the material collected from Dąbie Duże Lake revealed the occurrence of shells of dead *Dreissena* all over the bottom and in the upper layer of the sediments of the entire lake.

Shell length of *D. polymorpha* in the individual profiles

In the material collected, length of the shell was between 4 and 35 mm. The range of the shell length in the respective profiles was as follows: profile I: 4–32 mm, profile II: 4–35 mm, profile III: 10–35 mm, and profile IV: 6–34 mm. Percentage composition of the respective length classes of *Dreissena* in the studied profiles was presented in Fig. 3. The following shell-length ranges were predominant in the respective profiles: 17.0–17.9 mm in profiles I–III (10–12%), 19.0–19.9 mm in profile IV (13.0%).

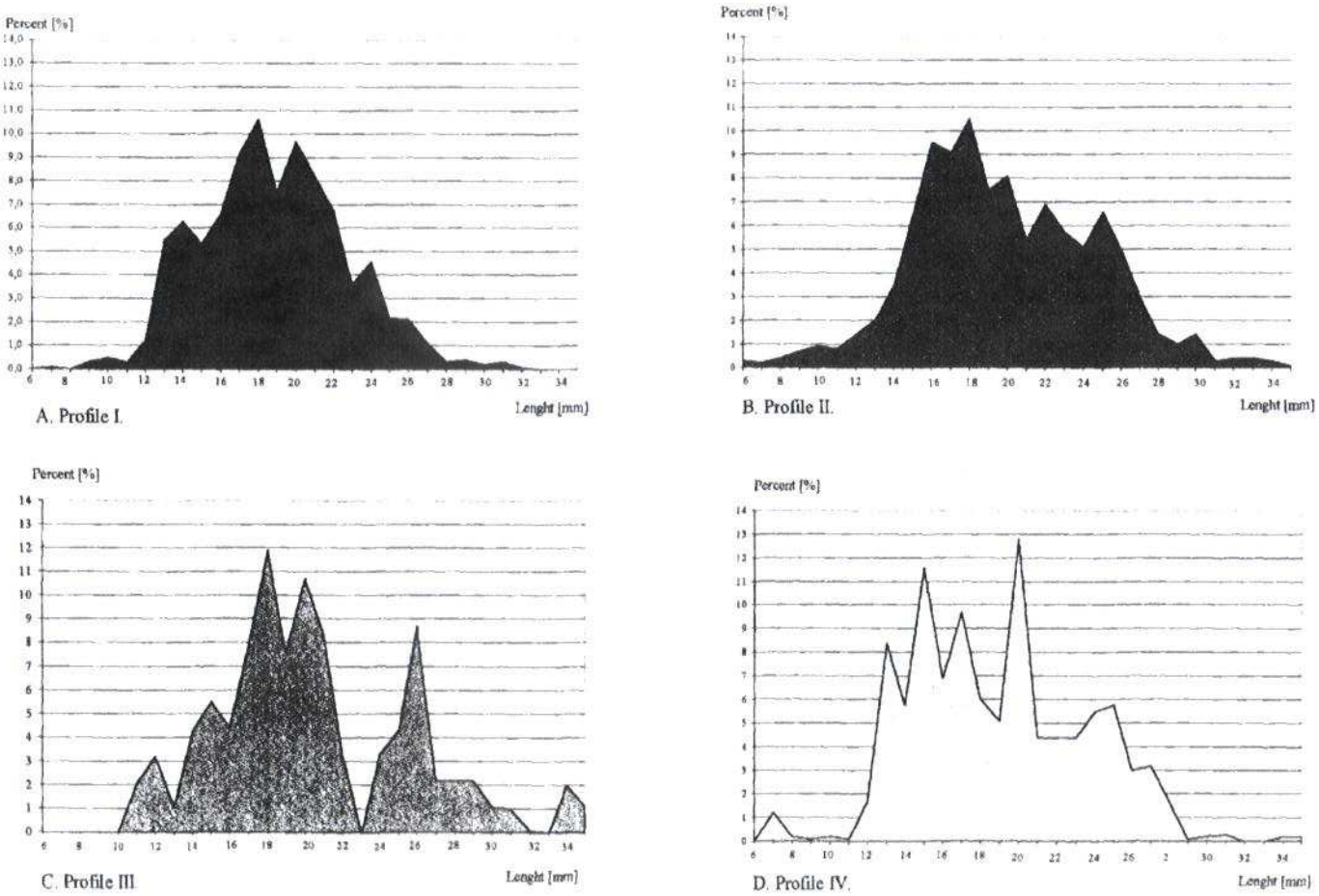

Fig. 3. Percentage composition of the lenght-classes od *D. polymorpha* shells in profiles I-IV

Table I

Abundance, wet weight and occurrence constancy (C) of *D. polymorpha* in the studied transects in Lake Dąbie.

Profile No.	No. of sampling sites	Abundance individuals/m^2			An average wet weight in g/m^2	C (%)
		range	$\bar{X}$	an average in places of occurence		
I	9	0-4754	2620	2958	4764.1	88.9
II	15	0-4205	1167	1975	1359.8	80.0
III	15	0- 892	93	700	117.2	13.3
IV	25	0-4615	574	1304	631.0	44.0
V	7	0	0	0	0	0
	71	0-4754	891	1734	1374.4	46.5

Age structure of the *D. polymorpha* population

In the age structure of the zebra mussel, a total of seven age groups was distinguished (from 0 to 6+). The percentage share of the zebra mussel in the respective age-groups in the studied profiles is shown on Fig. 4. It can be concluded from this data, that a substantial part of the zebra mussel population in Lake Dąbie is composed of specimens of the age-groups between 1+ and 3+. A smaller share in settling the bottom devoid of macrophytes had specimens of the age-groups 0 and 5+. The least abundant part of the population consisted of the older specimens representing the age-group 6+ (0–4.5% of the population). In profile III there were no juvenile specimens of the age-group 0.

Water transparency

Due to a strong phytoplankton blooming, mainly *Microcystis*, the visibility of the Secchi disk was in the range of 0.7–0.9 m (Table II).

Water pH

Mean values of the water reaction in the individual transects were as follows: profile I - 8.5, transects: II - 7.8, III - 8.1, IV - 8.3, V - 7.7.

Genetic structure of the population of *D. polymorpha*

Based on electrophoretic analysis of the 8 enzymes a total of 9 enzymatic loci was distinguished (Table III). There were from 2 to 6 alleles in each locus. The average number of alleles in locus in the studied population of *D. polymorpha* from Lake Dąbie was 3.4. In the majority of loci there was one allele that exhibited substantially higher frequency than the remaining alleles. The value of the expected heterozygosity coefficient (H) in the analyzed loci was relatively high due to higher number of alleles occurring in the loci. In the loci Est1 and Pgi1, the frequencies of the two most frequent alleles were similar, which resulted in the highest values of H in those loci (0.503 and 0.617, respectively).

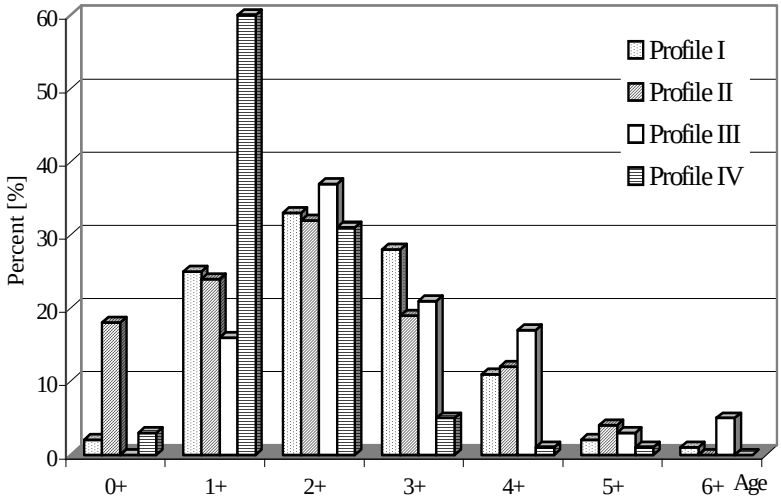

Fig. 4. Age structure of *D. polymorpha* in profiles I-IV

Table II

Abundance and occurrence constancy of *D. polymorpha* in selected areas of the Odra River estuary during summer season

Sampling sites	Abundance in individals/m^2			Range of visibility of Secchi disk (m)	An average visibility of Secchi disk (m)	Occurence constancy C (%)	Filtration (*)	Reference
	range	$\overline{X}$	An average in places of occurence					
Stepnicka Bay (Szczecin Lagoon)	0-4754	1984	3223	0.9-1.2	1.1	65.4	10	Grodzicka (unpublished)
Roztoka Odrzańska (Szczecin Lagoon)	44-6354	952	1704	0.3-1.2	0.8	56.0	78	Świerczyński *et al.* (1986)
Dąbie Duże Lake	0-4754	890	1734	0.7-0.9	0.8	46.5	27	own data
Dąbie Małe Lake	0-2960	177	670	0.4-0.9	0.7	22.7	134	Janicki (1994)

Table III

Frequency of alleles, mean value of the coefficient of expected heterozygosity in locus H and in locus of population H_S and average number of genotypes in locus in population of *D. polymorpha* from Lake Dąbie

	Alleles	Frequency of alleles	H	Average number of genotypes in locus
Pgm1	1 2	0.842 0.158	0.266	2
Lap1	1 2	0.932 0.068	0.126	2
Lap2	1 2	0.879 0.121	0.212	3
Got1	1 2 3	0.932 0.021 0.047	0.129	3
Est1	1 2 3	0.477 0.518 0.005	0.503	3
Idh1	1 2 3 4	0.674 0.026 0.292 0.008	0.458	5
Pgi1	1 2 3 4	0.368 0.487 0.077 0.068	0.617	7
Mdh1	1 2 3 4	0.705 0.245 0.027 0.005 0.018	0.441	7
Me1	1 2 3 4 5 6	0.729 0.134 0.008 0.024 0.045 0.060	0.444	10
$\overline{X}$	3.4		H_S 0.335	4.67

The average value of the expected heterozygosity coefficient per locus in the population (H_S) was very high and reached 0.335. The least variable were loci: Lap1 - 0.126 and Got1 - 0.129 (Table III). The number of genotypes in the respective loci ranged from 2 to 10 and it was 4.67 in average. The lowest number of genotypes occurred in the loci Lap1 and Pgm1 - two genotypes in each, while the highest number - in the loci Mdh1 and Pgi1 - seven genotypes in each. Locus Me had 10 genotypes. The number of genotypes in locus increased along with the increase in the number of alleles in locus (Table III).

Only because of the concurrent analysis of each individual for 8 enzymes, was it possible to determine a combined genotype, considering 9 enzymatic loci. A total of 131 separate genotypes were distinguished among 190 of the specimens studied. Numeric distribution of the genotypes in the population studied was as follows: among 131 separate genotypes, 21 occurred a number of times (2 to 9 times), while the remaining 110 were unique genotypes. The percentage of the separate genotypes, expressed with G% coefficient was 69% (131/190), while that of the unique genotypes GI%—0.58 (110/190).

The scattering of alleles in the population was extensive and it increased with the increase of alleles frequency. The alleles representing the highest frequencies in individual loci were present in all aggregations. The alleles of lower frequencies occurred in the majority of aggregations. Low-frequency alleles occurred in few aggregations only a (Fig. 5). Each of 19 aggregations studied was polymorphic concurrently for 6 loci out of 9 analyzed. Some of the loci namely: Mdh1, Pgi1, and Idh1 were polymorphic in each aggregation, while locus Me - in 18, Lap2 - in 10, Pgm - in 9, Lap1 - in 8, Est - in 5, and Got - in 4 aggregations.

Frequency of alleles and genotypes in the aggregations were subject of fluctuations, caused probably by a small number of analyzed individuals from a given aggregation.

Very extensive genetic variability was stated among the specimens composing aggregations. In each aggregation there were on average 9 separate genotypes out of 10 analyzed individuals. Only in profile IV, aggregation 9b had as few as 5 separate genotypes (Table IV).

Table IV

Genotype variability of *D. polymorpha* specimens in aggregations.
Number of studied specimens in aggregation N = 10

Profile I	N 80	Profile II	N 50
aggregations:		aggregations:	
1/a	10	5/a	9
b	10	b	9
2/a	9	6/a	10
b	10	b	7
3/a	9	7/a	10
b	9		
4/a	10		
b	8		
Profile III	N 10	Profile IV	N 30
aggregations:		aggregations:	
8/a	8	9/a	10
		b	5
		10/a	7
Profile V	N 20		
aggregations:			
11/a	10		
12/a	10		

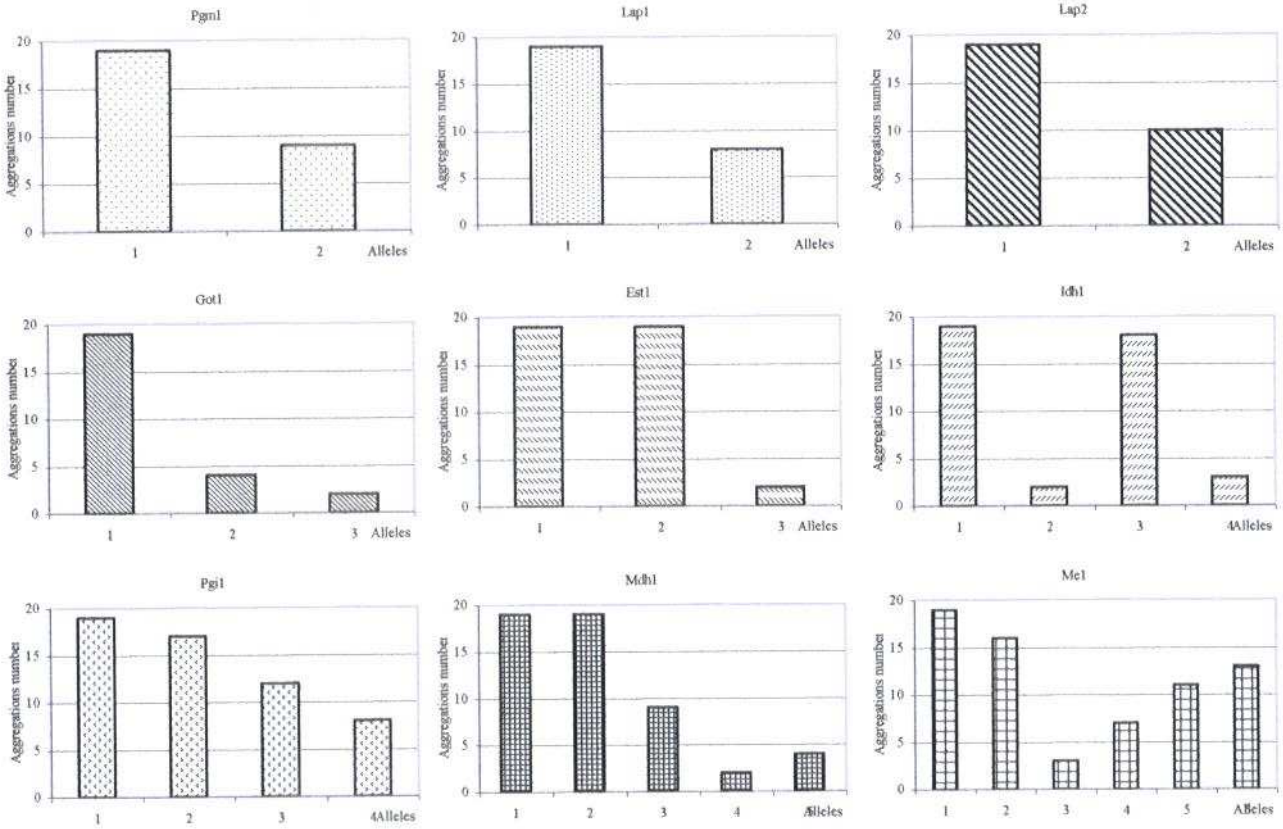

Fig. 5. Distribution of alleles in aggregation of D. polymorpha

The studied population of the zebra mussel was relatively homogeneous genetically. Usually the same alleles of similar frequencies occurred in the analyzed profiles (Table V). The profiles compared in the respect of individual loci exhibited extensive genetic similarity with exclusion of the locus Pgi (Fig. 6). In locus Est, the value of this similarity exceeded 0.99, while in locus Lap1 - 0.98, loci Lap2 and Me - 0.97, locus Got 0.96, locus Mdh - 0.94, locus Pgm - 0.92, locus Idh - 0.90, and in locus Pgi - 0.75. In locus Pgi, the lowest value of genetic similarity was 0.78 and it occurred between the profiles III and V.

Based on Chi^2 calculations, statistically significant differences in alleles frequency in five transects in relation to the following enzymatic loci were demonstrated: Idh, Pgm, Got and Lap2. In locus Idh those differences concerned the profiles I and IV, while in locus Pgm - I and II, I and IV, I and V, in locus Got - I and IV, locus Lap2 - I and II (Table VI). The profiles analyzed in respects of all enzymatic loci also exhibited close similarity. The values of genetic similarity coefficients for the studied transects were between 0.96 and 0.99 (Table VII, Fig. 7).

Table V

Frequency of alleles of *D. polymorpha* in five profiles of Lake Dąbie

Loci	Alleles	Profile I N 80	Profile II N 50	Profile III N 10	Profile IV N 30	Profile V N 20
Pgm1	1	0.725	0.900	0.900	0.930	1.000
	2	0.275	0.100	0.100	0.070	0.000
Lap1	1	0.925	0.940	1.000	0.970	0.850
	2	0.075	0.060	0.000	0.030	0.150
Lap2	1	0.813	0.940	1.000	0.900	0.900
	2	0.187	0.060	0.000	0.100	0.100
Got1	1	0.975	0.900	1.000	0.770	1.000
	2	0.025	0.040	0.000	0.200	0.000
	3	0.000	0.060	0.000	0.030	0.000
Est1	1	0.463	0.500	0.500	0.500	0.450
	2	0.537	0.500	0.500	0.500	0.500
	3	0.000	0.000	0.000	0.000	0.050
Idh1	1	0.587	0.780	0.750	0.584	0.850
	2	0.000	0.020	0.000	0.133	0.000
	3	0.400	0.190	0.250	0.283	0.150
	4	0.013	0.010	0.000	0.000	0.000
Pgi1	1	0.381	0.300	0.200	0.400	0.525
	2	0.425	0.520	0.800	0.550	0.400
	3	0.100	0.100	0.000	0.050	0.000
	4	0.094	0.080	0.000	0.000	0.075
Mdh1	1	0.637	0.710	0.750	0.834	0.750
	2	0.318	0.210	0.200	0.133	0.200
	3	0.019	0.050	0.000	0.000	0.050
	4	0.013	0.000	0.000	0.000	0.000
	5	0.013	0.030	0.050	0.033	0.000
Me1	1	0.719	0.660	0.750	0.870	0.725
	2	0.119	0.200	0.200	0.083	0.075
	3	0.006	0.010	0.000	0.000	0.025
	4	0.025	0.040	0.000	0.000	0.025
	5	0.056	0.050	0.050	0.000	0.050
	6	0.075	0.040	0.000	0.050	0.100

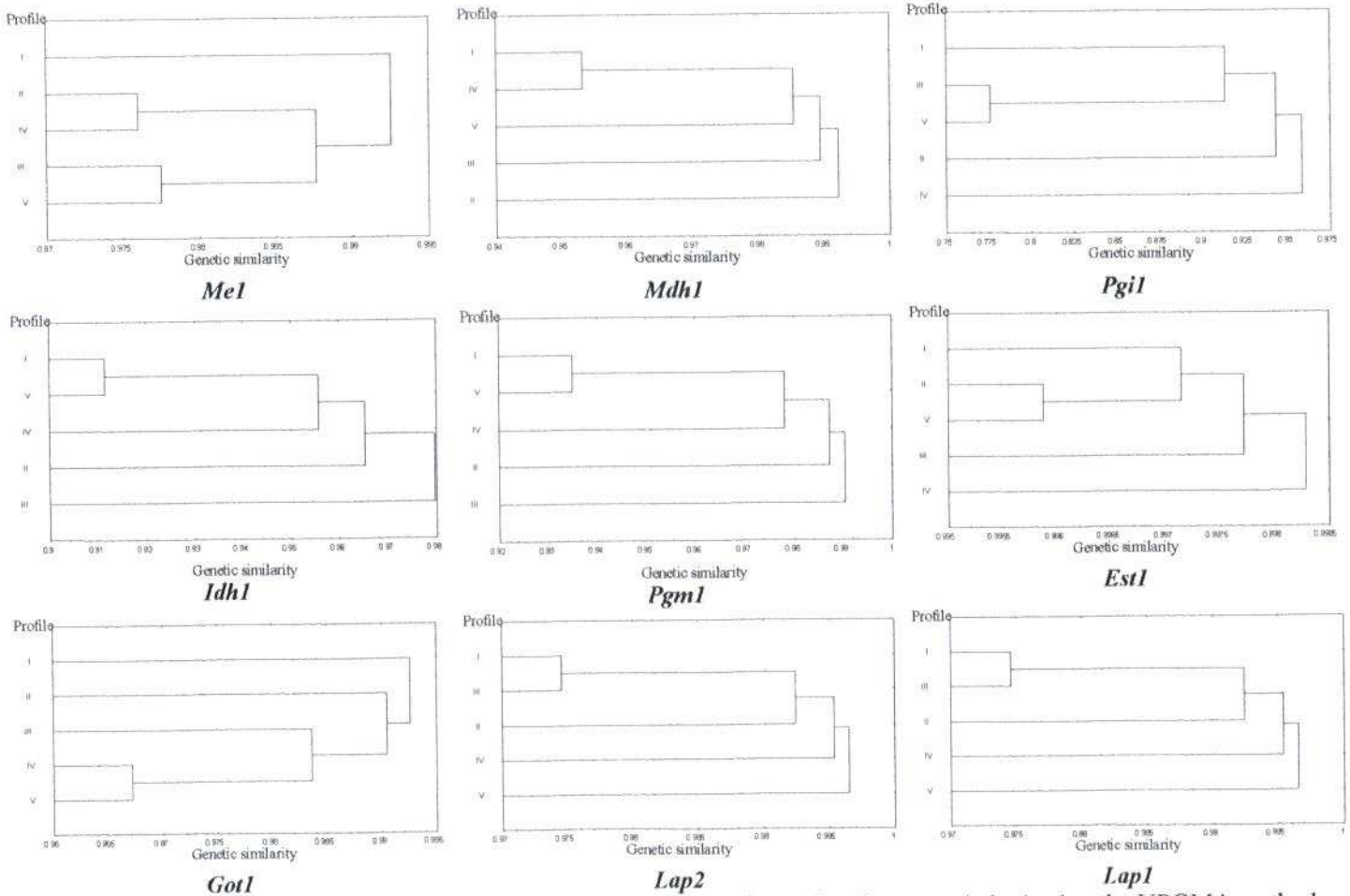

Fig. 6. Grouping of *D. polymorpha* from profiles I-V, according to the analysed enzymatic loci using the UPGMA method, based on the values of coefficients of genetic similarity

Table VI

Values of Chi^2 test of the analyzed loci of *D. polymorpha* for five profiles of Lake Dąbie

	Profiles						Profiles				
Me1	I	II	III	IV	V	Est1	I	II	III	IV	V
I	0.000	2.422	1.524	3.718	1.007	I	0.000	0.169	0.052	0.12	4.041
II	2.422	0.000	0.993	5.798	2.663	II	0.169	0.000	0.002	0.000	2.569
III	1.524	0.993	0.000	3.032	2.388	III	0.052	0.002	0.000	0.001	0.533
IV	3.718	5.798	3.032	0.000	3.741	IV	0.12	0.000	0.001	0.000	1.559
V	1.007	2.663	2.388	3.741	0.000	V	4.041	2.569	0.533	1.559	0.000
Mdh1						Got1					
I	0.000	3.603	1.609	5.442	2.189	I	0.000	5.205	0.256	12.583	0.509
II	3.603	0.000	0.622	2.498	0.636	II	5.205	0.000	1.086	5.518	2.149
III	1.609	0.622	0.000	0.349	1.493	III	0.256	1.086	0.000	2.774	0.001
IV	5.442	2.498	0.349	0.000	2.592	IV	12.583	5.518	2.774	0.000	5.330
V	2.189	0.636	1.493	2.592	0.000	V	0.509	2.149	0.001	5.330	0.000
Pgi1						Lap2					
I	0.000	1.247	5.419	4.212	2.895	I	0.000	4.168	2.240	1.209	0.86
II	1.247	0.000	3.241	3.561	4.411	II	4.168	0.000	0.629	0.432	0.345
III	5.419	3.241	0.000	2.119	4.437	III	2.240	0.629	0.000	1.079	1.069
IV	4.212	3.561	2.119	0.000	4.212	IV	1.209	0.432	1.079	0.000	0.000
V	2.895	4.411	4.437	4.212	0.000	V	0.86	0.345	1.069	0.000	0.000
Idh1						Lap1					
I	0.000	7.603	1.042	11.835	4.849	I	0.000	0.107	0.804	0.751	1.099
II	7.603	0.000	0.455	5.876	0.811	II	0.107	0.000	0.632	0.364	1.477
III	1.042	0.455	0.000	1.688	0.447	III	0.804	0.632	0.000	0.307	1.667
IV	11.835	5.876	1.688	0.000	4.812	IV	0.751	0.364	0.307	0.000	2.403
V	4.849	0.811	0.447	4.812	0.000	V	1.099	1.477	1.667	2.403	0.000
Pgm1											
I	0.000	5.726	1.431	5.359	7.051						
II	5.726	0.000	0.000	0.209	2.154						
III	1.431	0.000	0.000	0.094	2.069						
IV	5.359	0.209	0.094	0.000	1.461						
V	7.051	2.154	2.069	1.461	0.000						

Table VII

Values of genetic similarity coefficients of *D. polymorpha* between five profiles of Lake Dąbie

Profiles	I	II	III	IV	V
I	1.000	0.980	0.966	0.970	0.977
II	0.980	1.000	0.987	0.975	0.986
III	0.966	0.987	1.000	0.969	0.965
IV	0.970	0.975	0.969	1.000	0.968
V	0.977	0.986	0.965	0.968	1.000

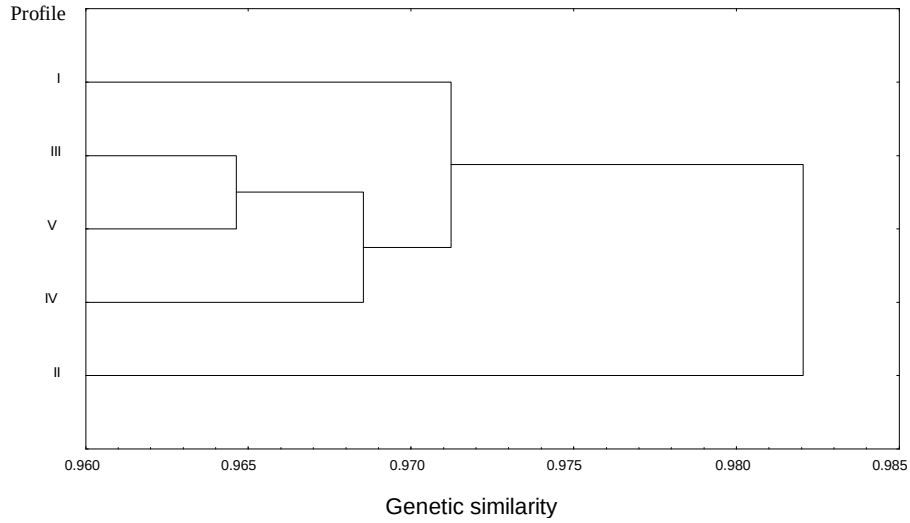

Fig. 7. Grouping of *D. polymorpha* from profiles I–V, according to 9 enzymatic loci, using the UPGMA method, based on the values of genetic similarity coefficients.

DISCUSSION

As presently stated, the distribution of *D. polymorpha* on the bottom of Dąbie Duże Lake was not homogeneous (Fig. 1). The observed location of the congregations of *D. polymorpha* in the northern and eastern part of the lake might have been caused by the sandy or sandy-muddy bottom, reinforced with dead shells of mollusks, as well as by its gentle drop. In the southern part of Dąbie Duże Lake, living mussels were not encountered, which might have been an outcome of large amounts of seston brought by the Regalica and the sedimentation of detritus due to deceleration of the current in the lake. In this flow-through water body, sediment itself extensive amounts of seston, also in the deeper part of the lake. *Dreissena* occurs sporadically on the bottom, covered with thick layer of detritus, and only as an epizoic form settling *Anodonta*. Due to a relatively low depth of the water body, waves - induced by strong winds-cause elevation of the detritus up to the water column. The other factor contributing to the re-suspension of the detritus is the impact of the propellers of the barges navigating the channel. Periodic changes in the water level in the entire Odra River estuary approaching 80 cm (Majewski 1980) limit the occurrence of *Dreissena* in the most shallow parts of Lake Dąbie. Organic and inorganic pollutants carried in by the waters of the Regalica and Płonia in a specified and adverse way influence the development of the zebra mussel in this area. It can be presumed that those contaminants have the most extensive impact in the southern part of Dąbie Duże Lake, where they are intensively deposited

in the sediments. These assumptions are confirmed by the absence of alive specimens of the zebra mussel in this part of the lake. The pollutants brought to the lake undergo sedimentation resulting from the deceleration of the water current. Subsequently, they undergo a self-purification process, the latter becoming stronger in a northward direction. Because of the convenient substrate and the advance stage of the water purification process, *Dreissena* finds the most convenient conditions for its development in the northern part of the lake. This is evident from its abundance, wet weight and occurrence constancy factor (C) exceeding 80%. High degree of eutrophication of the waters of Lake Dąbie caused by the constant process of nutrients inflow, mainly from the Regalica creates convenient conditions for excessive phytoplankton growth. In summer, the latter was dominated by blue-green algae (93000 colonies/m^3 - *Microcystis aeruginosa* Kütz, and *Oscilatoria* - 55000 colonies/m^3; Piesik, unpublished data). A substantial part of the phytoplankton constituted also diatoms 53000 colonies/m^3. The remaining taxa constituted between 1 to 5 thousand cells/m^3. Phytoplankton, mainly blue-green algae are carried in with the waters of Regalica, and after the current slows down in the lake, they rapidly develop blooming intensively in the warmer seasons of the year. Despite the biofiltration performed by *Dreissena*, the abundance of phytoplankton increases in the northern part of the lake. It is confirmed by high pH with values reaching 9.9, which can be attributed to the intensive photosynthesis. Strong alkalization of the water creates favorable conditions for outbreaks of alkaline disease posing a threat to hydrobionts in this number and also to the zebra mussel (Piesik 1992a). High reaction of the water, exceeding pH 9.0 occurred in July 1986 on some 7% of the lake area (Piesik, unpublished data), to cover 12% in August 1988. High-degree eutrophication of Dąbie Duże Lake (up to 1.2 mg P-PO_4, Tadajewski *et al.* 1990) is also confirmed by the water transparency readings using Secchi disk (Table II). Stańczykowska *et al.* (1983) noticed, that the abundance of *Dreissena* was lower in those Masurian lakes which contained a higher concentration of phosphorus. The presence of pollutants may be in the future the cause of the zebra mussel retreat also from the northern part of the lake, as was the case in the 1980s in the Great Lagoon - a part of the Szczecin Lagoon.

Significant impact of pollutants and eutrophication manifests itself while comparing the abundance of *Dreissena* in Dąbie Duże and Dąbie Małe lakes (Table II). It is evident from the recalculation of the present data and those of Janicki (1994), that the average abundance of *D. polymorpha* in Dąbie Małe Lake is five times lower, compared to the abundance of this mussel in Dąbie Duże Lake, while the average wet weight is as much as 10 times lower.

It is evident from the data contained in Table II, that in the selected areas of the Odra River estuary, the abundance of *Dreissena* decreases with the decrease of the visibility of Secchi disk.

Dreissena as an important species in the benthos community of Dąbie Duże Lake plays a positive ecological role, not only in the bottom area, but also affects the pelagic zone. In the course of its activity, through processes of biofiltration, biosedimentation, and bioaccumulation, the *Dreissena* contributes to the elimina-

tion of seston, and mineral substances from the water, participating in the creation of the bottom sediments and contributes to creation of the rich food base utilized by a number of animal species (Orzechowski 1966; Piesik 1992b; Szlauer 1974; Wiktor 1969; Wiśniewski and Dusoge 1983).

In the process of biofiltration, *Dreissena* eliminates seston from the water, especially phytoplankton - excessively developing and poorly utilized by planktonic animals. Elimination of the mass-growing blue-green algae probably limits their toxicity and inhibits dangerous alkalization of the water. Water clarity increase, through elimination of seston, may contribute to widening of the phytobenthos range, which declines along with poor water visibility. The filtration potential of *Dreissena* is diversified in the respective parts of the Odra River estuary (Table II), which is dependent on a number of factors. Lake Dąbie, being a natural retention reservoir for certain part of the Odra River waters, exchanges its volume 50 times a year (Mikulski 1974). This explains why despite the significant abundance and the biomass of *Dreissena* and its extensive filtration potential, the effect of its action concerning water clarity is hardly noticed in Lake Dąbie in connection with mass development of phytoplankton and meaningful water exchange. In the process of bioaccumulation, *Dreissena* in Dąbie Duże Lake accumulates 28420 t of $CaCO_3$, 560 t of nitrogen, and 129 t of P_2O_5. Accumulation of the nutrients in the biomass of *Dreissena* limits the amount of the nutritive salts accessible to phytoplankton which in turn limits its development. This influences the process of eutrophication reversal of the water column (Piesik 1992b). The above-mentioned data indicate the multilateral positive action of *D. polymorpha* on the biotope and biocoenosis of Dąbie Duże Lake.

The electrophoretic studies revealed that *Dreissena* from Lake Dąbie is strongly polymorphic. This population is also relatively homogenous genetically, because there were no differences in the genetic structure of the zebra mussel collected from the five profiles in different parts of the lake. It is then justified to treat *D. polymorpha* in Lake Dąbie as a homogeneous population of the panmictic system of reproduction. Eutrophication increases in Lake Dąbie and periodical inflows of brackish waters, as well as a continuous reduction in *D. polymorpha* abundance in this area, particularly visible in its southern part have not hitherto caused changes in the genetic structure of this population.

Genetic structure of the analyzed aggregations from different parts of the lake was similar and the differences concerned only the alleles of low frequencies.
It can be presumed, that strong genetic variability of the studied population, combined with the lack of spatial variability are the result of biological features of this mussel, in particular: the production of extensive numbers of gametes, external fertilization, free-swimming veliger larva and random pattern of larvae settlement.

The population of the zebra mussel from Lake Dąbie is similar in its genetic composition to the other populations of this species, inhabiting relatively clean and periodically salt-free environments (Zieliński *et al.* 1996). It is very likely, that the populations of *D. polymorpha* exhibit high genetic homeostasis, which along

with its extensive polymorphism constitute a wide adaptive potential of the studied species contributing to the increase of its dispersal abilities.

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