

GENETIC STRUCTURE OF *DREISSENA POLYMORPHA* POPULATION FROM SMALL AND ISOLATED WATER BODIES

Досліджено генетичну структуру та рівень генетичної мінливості відібраних популяцій D. Polymorpha з Західної Померанії.

The zebra mussel, *Dreissena polymorpha* (Pallas, 1771), is a freshwater bivalve which has been occurring in Central and Western Europe since the beginning of the 19th century. The mussel is a typical expansive species, whose distribution area for about 200 years has gradually extended from its original range in the drainage basin of the Black, Caspian and Azov Seas to European range [1; 2]. In 1986, *D. polymorpha* invaded also the Great Lakes of North America, from where it is expected to expand to whole Nearctic [3; 4].

In Poland, the earliest records of *D. polymorpha* were made before 1824, in the area of the former Eastern Prussia (the North-Eastern part of today's Poland); in Western Pomerania the species was found in the Gulf of Szczecin as late as 1896 [1; 5]. It is suspected that the zebra mussel got to the Baltic Coast along the Nemen River, which, at the end of the 18th c., was connected with the Dnieper River by the Ogiński Canal.

The objective of my studies was to estimate the genetic structure and level of genetic variability of selected populations of *D. polymorpha* from Western Pomerania. The studies included populations from four post-glacial, small and isolated lakes (Orzechów, Duże, Płociowe and Marta), and one, also isolated but young, Lake Czarnogłowy formed in the 50s, as a remnant of a chalk quarry. The results have been compared with literature data on the genetic variation in populations of this species from large lakes of Poland and Europe, and with the first founder populations of *D. polymorpha* from the Great Lakes in North America.

Enzyme electrophoresis in starch gel was used in order to estimate the genetic structure of five populations of *D. polymorpha*. In each population 7 enzymatic loci were analysed in about 100 individuals except the smallest Lake Orzechów (surface area 28 ha) from which 20 specimens were analysed because of unevenly distributed and small population of zebra mussel in this lake.

All the analysed populations of *D. polymorpha* from Western Pomerania display a high level of genetic variability, high genetic similarity and their genotype diversity, in spite of the isolated character of the lakes that they inhabit.

In all the examined populations, variation has been found in six loci, locus Pgm 1 being always monomorphic ($H=0$). The analysis revealed 86% polymorphic loci, 2.3-3.7 alleles per locus, 2.4-5.4 genotypes per locus and the expected heterozygosity of 0.338-0.487 (Tab.1). The analysed populations show a high diversity in the mean level of variation of loci (Tab. 2). An average of 61 unique genotypes was found in the studied population, which constitutes ca. 69.3% of all genotypes (Tab. 3). The unique genotype is here defined as genotype (multilocus genotype), which was presented only once in the population. The proportion of such genotypes in particular populations ranged from 36 to 83% and was observed to depend on the number of analysed individuals (Tab. 3). The more numerous individuals were analysed, the higher was the percentage of unique genotypes. An exception in the population from Marta Lake, in which the analysis of 100 specimens revealed only 36% unique genotypes.

The genetic similarity between the populations ranged from 0.828 to 0.949 and was somewhat lower, compared to other populations of the species.

The highest value $H_S=0.487$ and proportion of unique genotypes, high number alleles and genotypes per locus in the population from the lake Czarnogłowy – chalk quarry that came into existence in the 50s – indicates the mode of invasion of new water bodies by *D. polymorph*, not accompanied by a narrowing of the gene pool of the population. On the contrary, colonisation was effected by numerous, genetically diverse individuals, or was a multiple colonisation from populations originating from various water bodies. It should be conjectured that the remaining isolated lakes were colonised in a similar way, as evidenced by similar values of the variation parameters.

The lowest values of all the analysed parameters were observed in the small population from Orzechów (Tab. 1), which is associated with the low number of analysed individuals (20), rather than with the isolated character of the population.

The genetic variation of *D. polymorpha* from small and isolated lakes does not essentially differ from those found in populations from large lakes of the Western Pomerania. The population of zebra mussel from lakes Woświn (809 ha) and Ińsko (590 ha), had the coefficient of expected heterozygosity 0.449 and 0.398 respectively [6].

The level of genetic variation in the zebra mussel from both isolated and large population from Western Pomerania is comparable to that found in the founder population from Great Lakes of North America, which have been invaded by the species since 1985 [3; 6; 7; 8]. In these American populations the coefficient of expected heterozygosity per locus per population (H_S) was high and reached values of 0.31-0.50 and no founder effect was observed in such cases [3; 9; 10; 11].

The zebra mussel from small, isolated or newly established population did not show any decrease in its genetic variation, compared to other populations of many animal species [12; 13]. Colonisation by *D. polymorpha* is not accompanied by impoverishment of gene pool resulting from founder effect. The species seems to be expanding massively, using all of its genetic potential.

Parameters of genetic variability in five populations of *D. polymorpha* from Western Pomerania (N – number of individuals analysed, A_1 – number of alleles per locus, A_2 – number of alleles per polymorphic locus, G_1 – number of genotypes per locus, P – frequencies of polymorphic loci, H_s – the mean expected heterozygosity in a population)

Population number	Population name	N	A_1	A_2	G_1	P^*	H_s^{**}
1	Orzechów	20	2.29	2.50	2.43	85.71	0.338
2	Czarnogłowy	110	3.14	3.50	5.14	85.71	0.487
3	Duże	110	3.71	4.17	5.43	85.71	0.461
4	Płociowe	100	3.29	3.29	5.43	85.71	0.362
5	Marta	100	3.00	3.33	4.29	85.71	0.412
Mean		440	3.09	3.36	4.54	85.71	0.412

* polymorphism criterion 0.99

** according to Nei (1978)[14]

Table 2.

Expected heterozygosity in a polymorphic locus (H) in 5 populations of *D. polymorpha*

Loci	Orzechów	Czarnogłowy	Duże	Płociowe	Marta	Mean
Got 1	0.565	0.720	0.351	0.390	0.658	0.537
Est 1	0.508	0.531	0.604	0.334	0.512	0.498
Pgi 1	0.476	0.640	0.481	0.679	0.325	0.520
Me 1	0.337	0.612	0.671	0.413	0.554	0.517
Mdh 1	0.431	0.394	0.539	0.165	0.377	0.381
Idh 1	0.050	0.514	0.581	0.553	0.454	0.430

Table 3.

Percentage of unique genotypes (GU) in 5 populations of *D. polymorpha*

Population number	Population name	Number of individuals	% GU
1	Orzechów	20	60.0
2	Czarnogłowy	110	82.7
3	Duże	110	80.9
4	Płociowe	100	75.0
5	Marta	100	36.0

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Сорока М. Генетическая структура популяции D. polymorpha малых и изолированных водоемов.

Исследована генетическая структура и уровень генетической изменчивости отобранных популяций D. polymorpha из Западной Померании.

Soroka M. Genetic structure of Dreissena polymorpha population from small and isolated water bodies.

The article contains the analysis of the genetic structure and level of genetic variability of selected populations of D. polymorpha from Western Pomerania.