

GENETIC STRUCTURE OF THE POLYTYPIC SPECIES *IDOTEA BALTHICA* (ISOPODA VALVIFERA)

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Abstract

Allozyme variation among 15 populations belonging to the 4 subspecies, *I. b. basteri*, *I. b. stagnea*, *I. b. tricuspidata* and *I. b. balthica* of the polytypic *I. balthica* and collected from the Mediterranean to the Baltic Sea were analysed using polyacrylamide gel electrophoresis. Genetic structural analysis was performed assaying four polymorphic loci. Nei's genetic distance (D) varied from 0 to 0.567 showing low divergence within populations of the same subspecies, except for *I. b. basteri*, while the highest distance was recorded between the Nordic and the Mediterranean groups. Fst and gene flow were estimated and revealed a gene flow restriction between the geographical groups.

Keywords : *Crustacea, Enzymes.*

Introduction

The sublittoral Isopod *Idotea balthica*, occurred in the Baltic Sea, on the Atlantic coast, on the and on the Mediterranean coasts and lagoons, is relatively widely distributed. Based on the interbreeding tests and the morphological features in parents and hybrids, [1] considered this species as a polytypic species composed of four subspecies: *Idotea b. balthica* from the Baltic Sea, *Idotea b. tricuspidata* from the European Atlantic coasts, *Idotea b. basteri* from the Mediterranean Sea and *Idotea b. stagnea* from some Mediterranean French lagoons.

In the present paper, we report the allozyme variation analysis based only on the polymorphic loci of natural populations of the polytypic species *Idotea balthica*: 1) to analyse the genetic variability within populations, 2) to estimate the gene flow between these populations 3) to calculate the genetic distance and the level of genetic divergence among populations and subspecies, 4) to reconstruct the evolutionary history of this species. The analysis was conducted on 15 populations of the polytypic species *Idotea balthica* from different geographical areas: *I. b. balthica* from Baltic Sea, *I. b. tricuspidata* from the European Atlantic coasts, *I. b. basteri* from the Western Mediterranean basin and Adriatic Sea and *I. b. stagnea*, from some Mediterranean French lagoons.

Materials and Methods

The enzymatic polymorphism was performed on polyacrylamide gels. More than 30 enzyme assays were tried; ten yielded scorable results and only the four polymorphic loci (Amy-2, Est-2, Ldh-1 and Pgi-1) were considered.

For each population, mean sample size per locus, average number of alleles per locus, mean heterozygosity observed and mean heterozygosity expected under Hardy-Weinberg equilibrium were calculated using Biosys-1 program of [2]. The genetic structure within and among populations was evaluated using F-statistics (Fit, Fis and Fst).

Results and Discussion

The mean number of alleles ranged from 1.7 ± 0.2 to 3.2 ± 0.7 . Mean direct count heterozygosity gene (Ho) varied from 0.071 ± 0.059 to 0.201 ± 0.090 and the expected average heterozygosity from 0.081 ± 0.052 to 0.286 ± 0.125 . Considering the subspecies, the highest level of genetic variability was observed in *I. b. stagnea* (Ho=0.171), followed by *I. b. tricuspidata* (Ho=0.144), *I. b. basteri* (Ho=0.131), whereas the lowest belonged to *I. b. balthica* (Ho=0.088). The Fis values ranged from 0.0140 for Ldh to 0.898 for Pgi. The average value was high (0.280) showing that the populations were not in Hardy-Weinberg equilibrium.

Fst varied from 0.045 to 0.861 with an average of 0.433 and the amylase-3 locus exhibited most gene flow restriction. Among the fixation indices, Fit shows the highest value (0.590) indicating a high differentiation between populations.

Genetic distance values were low $0 < D < 0.024$ within populations of the same subspecies except from *I. b. basteri* populations where D rose to 0.217. D ranged from 0.084 to 0.164 between *I. b. balthica* and *I. b. tricuspidata* with the average value $D_m=0.120$, and from 0.010 to 0.118 between *I. b. basteri* and *I. b. stagnea* ($D_m=0.063$). The average genetic distance values among *I. balthica* subspecies showed a higher mean value among Nordic subspecies than Mediterranean ones. However, an average high value ($D_m=0.137$) within *I. b. basteri* was observed when comparing Adriatic and western Mediterranean populations and a lower value between *I. b. stagnea* and *I. b. basteri* ($D_m=0.063$).

The clustering pattern using the UPGMA and the NJ methods, respec-

tively requiring or not requiring, equal rates of evolution, showed two main groups, the Nordic and the Mediterranean ones. In the first group, the two subspecies can be clearly separated confirming morphological features. In contrast, within the Mediterranean group more than two subspecies could be distinguished; the Adriatic populations seem to be genetically different.

References

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