NOTE

ALLOZYMIC VARIATION IN
BYTHOTREPHES CEDERSTROEMI; A RECENT INVADER
OF THE GREAT LAKES

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ABSTRACT.

Allozymic surveys of the introduced predaceous cladoceran, *Bythotrephes cederstroemi*, were conducted on two sampling dates during July-August 1989 in the western basin of Lake Erie and lower Lake Huron. Fifteen of 16 enzyme loci that were surveyed showed monomorphic homozygous electromorph banding patterns; only phosphoglucomutase (PGM) was found to be polymorphic with two alleles present. Pooled data for the two sampling dates in Lake Erie revealed that this population was found to have heterozygote excesses. The Lake Huron population was also found to have significant heterozygote excesses on both sampling dates. In the Lake Huron population, no significant spatial heterogeneity of genotypes at the Pgm locus was observed at four transect stations (nearshore-offshore) on 21 August 1989. Additional study of the population genetic structure of this introduced species is warranted.

INDEX WORDS: Zooplankton, Lake Erie, Lake Huron, electrophoresis.

INTRODUCTION

The recent (Bur et al. 1986) introduction of the predaceous cladoceran, *Bythotrephes cederstroemi*, into the Laurentian Great Lakes has stimulated a number of investigations into the impact that this zooplankter may have on trophic dynamics in the Great Lakes pelagia (Lehman 1987). Additional studies (Berg and Garton 1988, Garton and Berg 1990) have concentrated on examining demographics of this species. To date, no one has examined the population genetic structure of this exotic species to determine the amount of genetic variation present.

Previous work that has examined the population genetic structure of large-lake cladocerans (Mort and Wolf 1986, Hebert et al. 1989, Weider 1989) indicates that these populations have a genetic structure quite similar to intermittent pond populations, as most populations are in Hardy-Weinberg (H.W.) equilibrium. These data suggest that large-lake cladoceran populations are reproducing by cyclical parthenogenesis, as their structure approximates that of a truly sexual species.

The present study represents a first attempt to categorize allozymic variation in *Bythotrephes cederstroemi*, in order to determine genotypic variation within introduced populations in the Great Lakes. Such information might provide insights into the relative number of clonal lineages that have founded these populations.
METHODS AND MATERIALS

Specimens from the western basin of Lake Erie were collected on two dates, 18 July and 10 August 1989 at a single station (41° 52'N, 82° 48'W). Multiple oblique tows were taken with a 200-µm plankton net (mouth diameter = 37 cm). Specimens from Lake Huron were collected on two additional dates, 25 July and 21 August 1989. On the 25 July, specimens were collected approximately 5 kilometers offshore from the boat launching ramp at Highland Glen Conservation Area, Ontario (43° 06'N, 82° 07'W). Samples taken on 21 August were collected at four stations extending in a transect from nearshore (approximately 1 km from shore) to offshore (approximately 10 km from shore). All samples were kept cool until they could be returned to the laboratory for electrophoretic analysis.

### TABLE 1. Genotype frequencies of *Bythotrephes cederstroemi* at the *Pgm* locus in populations from western Lake Erie (LE) and Lake Huron (LH). Alleles are designated 1 or 2, with the 2-allele migrating more anodally. N = total sample size. H. W. refers to probability of deviations from Hardy-Weinberg expectations based on Chi-square goodness-of-fit tests. * - refers to significant heterozygote excesses. Sample sizes for genotypes are given in parentheses.

<table>
<thead>
<tr>
<th>Date</th>
<th>Population</th>
<th>Genotype</th>
<th>N</th>
<th>H. W.</th>
</tr>
</thead>
<tbody>
<tr>
<td>18 July and 10 August</td>
<td>LE</td>
<td>0.095 (4)</td>
<td>691 (29)</td>
<td>214 (9)</td>
</tr>
<tr>
<td>25 July</td>
<td>LH</td>
<td>0.228 (33)</td>
<td>641 (93)</td>
<td>131 (19)</td>
</tr>
<tr>
<td>21 August</td>
<td>LH</td>
<td>0.158 (28)</td>
<td>734 (130)</td>
<td>108 (19)</td>
</tr>
</tbody>
</table>

Individual females were assayed electrophoretically for allosyme phenotypes using cellulose acetate electrophoresis (Helena Scientific, Beaumont, Texas) following the protocols of Hebert and Beaton (1989). Sixteen enzyme systems were surveyed initially: *Acon* (aconitase, ACON, EC 4.2.1.3), *Amy* (amylase, AMY), *Ao* (aldehyde oxidase, AO, EC 1.2.3.1), *Apk* (arginine phospho-kinase, APK, EC 2.7.3.3), *Fum* (fumarate hydratase, FUM, EC 4.2.1.2), *Got* (glutamate oxaloacetate transaminase, GOT, EC 2.6.1.1), *Gpdh* (glycerol-3-phosphate dehydrogenase, GPDH, EC 1.1.1.8), *Hex* (hexokinase, HEX, EC 2.7.1.1), *Idh* (isocitrate dehydrogenase, IDH, EC 1.1.1.42), *Ldh* (lactate dehydrogenase, LDH, EC 1.1.1.27), *Mdh* (malate dehydrogenase, MDH, EC 1.1.1.37), *Me* (malic enzyme, ME, EC 1.1.1.40), *Mpi* (mannose phosphate isomerase, MPI, EC 5.3.1.8), *Pgi* (phosphoglucomutase, PGI, EC 5.3.1.9), *Pgm* (phosphoglucomutase, PGM, EC 2.7.5.1), and *6pgdh* (6-phosphogluconate dehydrogenase, 6PGDH, EC 1.1.1.44). All enzyme exhibited monomorphic homozygous electromorph banding patterns, with the exception of the *Pgm* locus. Two alleles were detected at the *Pgm* locus.

RESULTS AND DISCUSSION

Results (Table 1) from chi-square tests for deviations from Hardy-Weinberg (H. W.) equilibrium at the *Pgm* locus indicated that sample sizes for the Lake Erie population were too small on each sampling date to allow for separate analysis. A G-test revealed that the two samples were not significantly different from each other (G = 0.95, df = 1, n.s.), and they therefore were pooled. Analysis of the pooled Lake Erie data revealed that this population was not in H.W. equilibrium, and exhibited significant heterozygote excesses (Table 1). Data from Lake Huron indicated that on both sampling dates, significant deviations from H.W. expectations in the form of heterozygote excesses were also observed. No significant spatial heterogeneity in *Pgm* genotype frequencies was observed across the four Lake Huron stations sampled on 21 August (G-test, d.f. = 6, G = 5.47, P = 0.50).

The few data that have been gathered from this study indicate that *Bythotrephes cederstroemi* exhibits low levels of enzyme polymorphisms, when compared with other cladoceran species (Hebert...
1987). This low genetic variability could be the result of founder effect. Little can be said about the genetic structure of the Lake Erie population due to small sample sizes and limited sampling on only two dates. In contrast, data from the Lake Huron population indicate that random mating was not occurring in this population, at least during July and August 1989. The Lake Huron population was characterized by heterozygote excesses. Hebert (1987) suggested that heterozygote excesses may reflect the existence of genomic heterosis, associated with interbreeding of distinct inbred lines. Other potential explanations could be invoked as well (e.g., isolate breaking resulting in Wahlund effect).

The Lake Huron data are in direct contrast to results obtained for another predaceous cladoceran, Polyphemus pediculus (Weider 1989). Weider (1989) noted that European populations of P. pediculus were generally in H.W. equilibrium, thus indicating that reproduction is via cyclical parthenogenesis. The few deviations that were observed represented heterozygote deficiencies.

Future work needs to be conducted to assay additional enzyme systems to determine whether other polymorphic loci exist in this species. In addition, more extensive collections need to be conducted to determine the extent of temporal and/or spatial fluctuations in gene/genotype frequencies. The introduction of Bythotrephes cederstroemi into the Great Lakes affords an unique opportunity to track the population genetic structure of an invader species, at an early stage of the invasion process.

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REFERENCES