Ah Receptor Sequence Variation from Shiner Surfperch (Cymatogaster aggregata) Populations in Polychlorinated Biphenyl Contaminated and Reference Sites around San Francisco Bay

Jeffrey N. Schinske (jeffs@sfsu.edu) and Sarah Cohen (sarahcoh@sfsu.edu)
Romberg Tiburon Center for Environmental Studies, Dept. of Biology
San Francisco State University

ABSTRACT

Genetics-based methodologies can play an important role in studying the effects of environmental pollutants on natural populations. We are employing a candidate gene approach to investigate the persistence of shiner surfperch (Cymatogaster aggregata) in PCB-contaminated areas. We aim to sequence portions of two candidate genes, AHR1 and AHR2, to determine whether PCB-contaminated populations exhibit different AHR allele patterns compared to reference populations. We are additionally sequencing part of the mitochondrial D-loop locus to aid in differentiating selection from genetic drift. Preliminary analyses have failed to identify significant population subdivision for shiner surfperch from 3 northern California sites spanning a range of approximately 200 km. This could enable our ability to detect selection at AHR1 or AHR2. Thus far, 4 AHR1 alleles have been identified, suggesting surprisingly low genetic diversity at that locus.

EXPERIMENT DESIGN

SELECTION OF CANDIDATE MODEL ORGANISM

Shiner surfperch (C. aggregata) is a viviparous estuarine fish native to San Francisco Bay. The following table describes the factors considered in selecting C. aggregata as a candidate model organism for toxicity-related population genetics work.

<table>
<thead>
<tr>
<th>Site</th>
<th>SNP Haplotypes</th>
<th>Length Variation Haplotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Big River</td>
<td>(n=18)</td>
<td></td>
</tr>
<tr>
<td>Bodega</td>
<td>(n=10)</td>
<td></td>
</tr>
<tr>
<td>San Francisco</td>
<td>(n=19)</td>
<td></td>
</tr>
</tbody>
</table>

Preliminary Estimates of Gene Flow

Surprisingly Low Genetic Diversity at AHR1 Suggests Role of Lower Fitness of Candidate Genes in Conferring PCB Resistance

FUTURE DIRECTIONS

We feel that the available natural history information and preliminary indications of population connectivity make C. aggregata an interesting prospective model species for candidate gene studies. We hope to:

- Identify additional field sites of toxicological interest for incorporation into the study
- Continue sequencing current samples for AHR1 and AHR2
- Compare gene flow estimates and search for linkage between SNP and repeat D-loop regions
- Design primers to amplify and sequence AHR2

We hope that a better understanding of how marine organisms are affected by polluted environments will assist in the future management of the biotic resources of San Francisco Bay.