River Herring Technical Expert Working Group

Genetics subgroup – Brainstorming from 1st call

Final Draft May 12, 2014

Molecular Marker development

- Genome wide Single Nucleotide Polymorphism (SNP) discovery and development
  Benefits:
  -easy data standardization across laboratories
  -an improved degree of resolution through a greater number of independent molecular markers confers increased statistical power for addressing key questions (highlighted below)
  -broad applications (bycatch, marine ecology, life history, stocking effects) allows integration among TEWG subgroups
  -minimal investment in specialized equipment due to 'out-sourcing' to key laboratories that routinely conduct similar work

  Approach:
  -identify a single ideal platform for marker development (i.e., Illumina MiSeq) and future sequencing (i.e., Fluidigm)
  -identify a central location where samples could be submitted from multiple labs for genotyping across a singular platform and in a single location (e.g., NOAA/NMFS: Southwest Fisheries Science Center, Santa Cruz, CA; WHOI in the future?)

- Adaptive genetic variation (RAD tags)
  - An understanding of the magnitude and spatial distribution of adaptive genetic variation is required to determine whether the loss of stock complexes (or riverine populations; as identified through the examination of neutral genetic markers) is 'significant' and thereby comprise DPSs (ESA listing decision pg 48950).
  -examination of adaptive genetic variation may enhance resolution of stock structure
  - helps resolve capacity of populations/stocks to respond to current/future perturbations and environmental variability (e.g., climate change, various sources of mortality, etc.)

Otolith microchemistry

- Obtain baseline information for specific rivers (to be identified)

- Investigate methods by which otolith microchemistry and molecular markers could be integrated to provide complementary information about river herring ecology and evolution

Life history and Freshwater Ecology

- Conduct a truly rangewide study of genetic population structure by considering collections from Canada and the US in a single analysis
  - integrate information from otolith microchemistry, otolith shape and microstructure, and body morphology (where possible and appropriate) for resolving fine spatial scale structure

- Determine natural straying rates
  -crucial life history information that is not currently understood for either species
  -valuable for identifying time frames for natural recolonization of habitat following dam removal
  -valuable for understanding connectivity and for setting reasonable expectations for (re-) colonization
  -allows the identification of the source of migrants for future northward range expansion (i.e. new habitat colonization) as a consequence of climate change

- Assess relative contribution of populations (i.e., river level spawning stocks) to species level genetic diversity
  -provides insight about the amount of standing genetic variation and relative evolutionary potential of each population and their intrinsic capacity to respond to future perturbations (e.g., climate change)
  -provides insight on whether large river populations contain the most diversity or whether we need to be concerned about extirpations from small coastal drainages

- Identify contemporary changes to species distributions (i.e., range shifts, contractions)

- Assess whether adaptive genetic diversity varies within a population across life history stages (from larvae to returning adults)
  - provides an opportunity to examine the effects of selection at various life history stages
- Identify genetic structure of life history variants (freshwater residents)

- integrate information from otolith microchemistry to resolve migratory patterns within drainages where appropriate

Demography

- Determine effective population size (N_e)
  -provides insight about the relative abundance of spawning runs
  -promotes immediate integration with the Stock Status sub-group as they grapple with determining census population size (N_c)

Incidental harm

- Determine which stocks and populations are susceptible to bycatch in open ocean fisheries (e.g., Atlantic herring and mackerel)

- Determine the extent to which specific stocks and populations are impacted by other sources of mortality (dams, etc.)

- Combine genetic and otolith microchemistry data for improved resolution of assignment to stock and population (i.e., river; where appropriate)

Marine ecology (An important issue because factors that influence the population dynamics for the freshwater portion of their life history can not readily be separated from marine factors)

- Determine spatiotemporal distributions of stocks/populations and thereby habitat preferences in the marine environment

- Determine migratory routes for stocks/populations

- Resolve ocean migration and mixing patterns
  - mixed stock or single stock groups?
  -segregation by sex/age class?

- Assess extent of intermixing among Canadian and US populations and stocks

- Assess extent of intermixing among stocks and populations from across species' ranges

Restoration

- Evaluate the performance of hatchery fish in river herring restoration
  -assess the relative contribution of hatchery broodstock to overall production

- Resolve the impacts of stocking activities on population genetic structure and levels of standing neutral genetic variation (i.e., genetic diversity)

- Identify the source of migrants for natural recolonization of habitat following dam removal

- Assess the extent of artificial selection in hatchery programs and potential impacts on natural populations

Hybrids

- To what extent do anadromous hybrids successfully breed with other anadromous hybrids and purebred alewife and blueback herring?

- Is there selection against hybrids in the marine realm (i.e., are proportionally more hybrids produced in freshwater than what make it back to spawn; relative to purebreds).
  -need controlled laboratory trials to experimentally create hybrids and back crosses

- Using archival collections, determine whether there has been a shift in the proportion of hybrids in anadromous populations as a consequence of dam construction

- Assess the extent to which alewife and blueback herring hybridize with American shad and Hickory shad

- Determine whether hybrids do well in the marine environment because of 'hybrid vigor'

- Determine whether parallel evolutionary processes (reflective of hybridization) occur in replicated systems where both alewife and blueback herring have become landlocked

Additional

- Assess predation effects on river herring by using genetics to identify stomach contents

- Monitoring genetic diversity at different life history stages: larvae vs. YOY/juveniles vs spawning adults. Is genetic diversity being lost at a specific stage in the life cycle?

- Is there a need for individual level identifications? Parentage analyses?

- Generate a standardized (lethal and non-lethal) sampling protocol to be used for all future river herring research that can be adopted by every state/province involved in regular monitoring efforts

- We need dedicated monitoring at range edges (alewife: North Carolina and Quebec/Newfoundland; blueback herring: Florida and New Brunswick/Nova Scotia) - the genotyping of larvae provides large sample sizes and information on presence/absence of successful reproduction in drainages

- Identify sources and availability of archival river herring tissues (MA, ME state archives, others?) that could be used for setting baseline information about important parameters (e.g., N_e, gene flow, etc.)

- Assess evolutionary implications of admixture between landlocked alewife and blueback herring and anadromous conspecifics