

## ABSTRACT

Genetic variation among Atlantic herring spawning groups and larval assemblages was assessed at a range of spatial (1000's, 100's, 10's km) and temporal (year, week, day) scales, using micro satellite DNA markers (short, tandemly repeated DNA sequences in the nuclear genome that are highly variable in repeat number). It is shown that 5 Pacific herring dinucleotide microsatellites can be amplified in Atlantic herring, and there is measurable differentiation between putative species (Pacific vs Atlantic herring;  $F_{ST} \sim 0.045$ ), among populations at ocean basin scales (NE vs NW Atlantic;  $F_{ST} \sim 0.040$ ), and at regional management scales ( $F_{ST} \sim <0.01$ ), in the Scotia-Fundy herring stock complex.

Nine tetranucleotide microsatellites, the first microsatellites developed for Atlantic herring, were isolated using magnetic bead hybridization selection and were used to study 17 collections of herring ( $N > 1400$ ) drawn from the Scotian Shelf, the Celtic Sea, the Baltic Sea, and coastal Iceland. Differentiation was observed between NE and NW Atlantic herring ( $F_{ST} \sim 0.065$ ) and significant genetic variability was observed within NW Atlantic herring spawning groups (max  $F_{ST} = 0.018$ ), at a relatively small spatial scale on the Scotian Shelf. Genetic variation between Bras d'Or Lakes herring and all other collections was sufficient to hypothesize that an event associated with a small effective population size (e.g. population bottleneck) had occurred in Bras d'Or Lakes.

Temporal stability of genetic pattern, using annual collections and age data showed that among-location genetic variation was  $\sim 1.4$  fold greater than within-location annual variation on the Scotian Shelf. It is shown that overlapping generations, when used for population structure analyses, may explain inconsistencies in estimates of temporal stability in marine fishes, particularly herring. There was no relationship between number of alleles found at a locus and the ability of the locus to resolve differences among the herring collections. Herring spawning waves were virtually indistinguishable from a population genetic-structure perspective, though a small difference ( $F_{ST} = 0.0043$ ,  $P = 0.013$ ) was revealed on the Scotian Shelf (Devastation Shoal) between spawners separated by 6 days within the same year class. Herring in the 2<sup>nd</sup> spawning wave were larger at age within a year-class (t-test;  $P < 0.001$ ). These analyses suggest that the differences can be explained by either: 1) genetically distinct Devastation Shoal populations that are temporally separated; 2) sub-annual temporal genetic patchiness; or 3) transient use of the spawning ground by different populations.

Near genetic homogeneity was observed among 14 larval herring ( $N > 1200$ ) collections, drawn from across the central Scotian Shelf. Genetic patterns and circulation associated with sampling locations could not easily be used to reconcile the hypothesis that larval retention or larval mixing has generated, or maintained, patterns of population structure in Scotia-Fundy herring. A suite of genetic and morphometric analyses of larval collections (coastal and offshore) indicate the larvae were likely produced by few parents. This last finding is consistent with sweepstake events, especially in light of the conflicting results (differences and lack thereof), in comparisons between larvae and the spawning adults that are presumed to have produced them.