



# Comprehensive evaluation of genetic population structure for anadromous river herring with single nucleotide polymorphism data

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## ABSTRACT

Anthropogenic activities are placing increasing pressure on many species, particularly those that rely on more than one ecosystem. River herring (alewife, *Alosa pseudoharengus* and blueback herring, *A. aestivalis* collectively) are anadromous fishes that reproduce in rivers and streams of eastern North America and migrate to the western Atlantic Ocean. Here, we use data from single nucleotide polymorphisms (SNPs) to provide a comprehensive analysis of population structure for both species of river herring throughout their native ranges. We sampled river herring spawning runs in rivers from Newfoundland to Florida, examining a total of 108 locations, and genotyping over 8000 fish. We identified geographic population groupings (regional genetic groups) in each species, as well as significant genetic differentiation between most populations and rivers. Strong correlations between geographic and genetic distances (i.e., isolation by distance) were found range-wide for both species, although the patterns were less consistent at smaller spatial scales. River herring are caught as bycatch in fisheries and estimating stock proportions in mixed fishery samples is important for management. We assessed the utility of the SNP datasets as reference baselines for genetic stock identification. Results indicated high accuracy of individual assignment (76–95%) to designated regional genetic groups, and some individual populations, as well as highly accurate estimates of mixing proportions for both species. This study is the first to evaluate genetic structure across the entire geographic range of these species and provides an important foundation for conservation and management planning. The SNP reference datasets will facilitate continued multi-lateral monitoring of bycatch, as well as ecological investigation to provide information about ocean dispersal patterns of these species.

## 1. Introduction

Natural populations that are affected by anthropogenic activities require monitoring and management to avoid demographic and other risks. Genetic data allow accurate evaluation of population structure and patterns of migration, which is critical for the identification of demographic independence and appropriate management units (Palsbøll et al., 2007). When extensive population structure exists, it can be used with genetic stock identification (GSI) techniques so that individuals sampled away from their natal areas, or in mixed

aggregations, can be identified to their demographic and genetic unit of origin (Milner et al., 1981; Rannala and Mountain, 1997; Anderson et al., 2008). This is particularly relevant for anadromous fishes, as they spawn in freshwater, migrate long distances from their natal rivers and streams to the ocean and then return, and are often encountered in mixed stock aggregations while at sea. Genetic data from reference “baseline” databases of established population units can allow for the determination of which stocks are present in a mixed sample and in what proportions (Milner et al., 1981; Seeb et al., 2007; Clemento et al., 2014).

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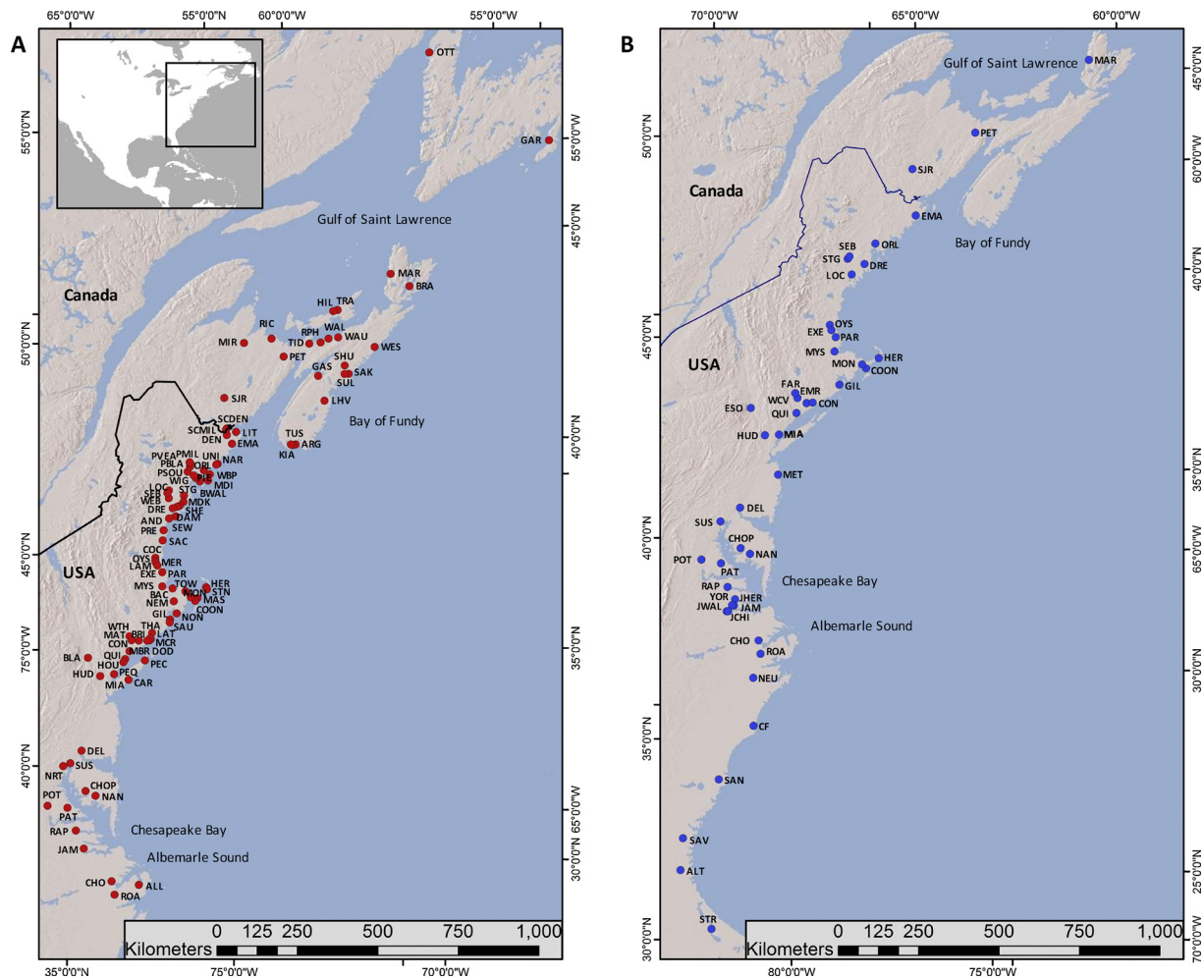


Fig. 1. Maps of sampling locations from coastal rivers for river herring (A) sampling sites for alewife (B) blueback herring. Sampling location codes correspond to Table 1.

Population structure for anadromous fishes is typically understood by sampling populations in freshwater spawning habitat. Populations of anadromous fishes often show signals of hierarchical structure and patterns of isolation by distance, due to high rates of homing to natal rivers, with migration usually to proximate river basins (Garza et al., 2014; Ozerov et al., 2017). This restricted gene flow among river basins, and among tributaries within larger river systems, leads to population structure even when individuals move thousands of kilometers over their lifetimes. The resulting population structure allows individuals sampled in the ocean to be assigned back to rivers and regional stocks of origin using GSI techniques (Anderson et al., 2008; Seeb et al., 2007; Clemento et al., 2014). Such information can provide insight about differential exploitation of populations or regional demographic units and patterns of marine migration and distribution in space and time (e.g., Larson et al., 2012; Bradbury et al., 2016; Anderson et al., 2017).

River herring is the collective name given to alewife (*Alosa pseudoharengus*) and blueback herring (*A. aestivalis*). These anadromous sister species, native to eastern North America and the northwestern Atlantic Ocean, have similar life-history characteristics, including spawning in freshwater during spring and spending two to five years in the marine environment, where they undertake migrations along the continental shelf, following food resources and schooling with other species such as Atlantic herring and Atlantic mackerel (Turner et al., 2016, 2017), and then return to their natal rivers to spawn (Scott and Crossman, 1973). Hasselman et al. (2014) and McBride et al. (2014) documented hybridization between alewife and blueback herring

populations spawning in the same rivers. River herring are of significant ecological and conservation concern due to declining populations and the effects of habitat loss, pollution and harvest (Limburg and Waldman, 2009; Atlantic States Marine Fisheries Commission [ASMFC] 2012; Palkovacs et al., 2014; McBride et al., 2015; Hasselman et al., 2016).

Previous population genetic studies of river herring have provided important insights into the species biology, conservation, and management (McBride et al., 2014; Palkovacs et al., 2014; Turner et al., 2015; Hasselman et al., 2014; Hasselman et al., 2016; Ogburn et al., 2017). Palkovacs et al. (2014), examining populations from rivers south of the US-Canada border, identified three regional genetic units of alewife and four genetic units of blueback herring. McBride et al. (2014), examining populations from Canadian rivers, detected weak differentiation among populations of alewife. These studies provided important information to facilitate the conservation and management of river herring, but derived their genetic data from microsatellite markers. Despite their high variability and extensive use in the study of fish and wildlife over the last several decades, microsatellites have important limitations when applied to fisheries management. Primary among them are a lack of portability across laboratories and instruments, which prevents the integration of datasets without extensive standardization efforts (Seeb et al., 2007; Clemento et al., 2011; Seeb et al., 2011). To overcome this limitation, single nucleotide polymorphism (SNP) genetic markers have been developed to assess population structure and employ GSI techniques for the study of anadromous fishes and other migratory species. SNP markers can be

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