Abstract:

White perch (*Morone americana*) are an estuarine species that ranges from South Carolina to the Miramichi River estuary in New Brunswick. This species is known to have invaded a number of lakes in the Hudson, Mohawk and St. Lawrence river drainages. Although a common species throughout most of Lake Champlain, this species was not known within Lake Champlain prior to 1984. Therefore, invasion into Lake Champlain could have been either through the Champlain Canal from the Hudson River or via the Richelieu River from the St. Lawrence. Marsden and Hauser (2009) have hypothesized that Lake Champlain was colonized from the Hudson River via the Champlain Canal only. If this hypothesis is correct the white perch in Lake Champlain will be genetically more similar to populations from the Hudson River than from populations the St. Lawrence River. DNA has been extracted from tissue samples of white perch collected from the Hudson River, two locations within Lake Champlain, and the St. Lawrence River. Five microsatellite loci are being examined. In order for the hypothesis to be examined some genetic differentiation must exist between geographically distinct white perch populations, and this is being tested for using the Excel program GenAlEx. The genotypes at each of these 5 loci are being used to determine the allele and genotypic frequencies of populations of white perch from these locations. The program GeneClass, utilizing a Bayesian statistical approach, is being used for population assignments because it can exclude all of the sampled populations as the source of the populations of interest. By identifying the source of invasion in this case, this study will be the first to characterize the population structure of the species within Lake Champlain, and provide a basis for how population genetic techniques can be used to identify water routes of invasive species.