The lobster fishery is the largest commercial fishery in Atlantic Canada. Despite its socio-economic importance, there are still significant knowledge gaps on the population structure of the species that supports it. As a consequence, the current management is based on geo-administrative areas rather than the biological ones, thus limiting the efficacy of management and measures.

Genetic differentiation may indicate reproductively distinct populations. Thus, genetic structure provides information that is greatly relevant to fishery management. In particular, there is a need for assessing the correspondence between the genetic structure of natural stocks and the 41 management units currently used.

Sustainability is one of the primary objectives of fisheries management. One prerequisite for sustainable management is the matching of biological processes and management actions; mismatch between population structure and management units could result in reduced productivity and local reduction of populations.

Furthermore, in a context of rapid climatic change, it is crucial to maintain the adaptive capacity of exploited populations.

- Fishermen, scientists and government were involved in the sampling project, both to select sites and collect samples. Site selection was based on scientific and fishermen knowledge and took into account management units design, currents circulation, salinity and temperature. This sampling was realized simultaneously with other Lobster Node projects, including those on spatial variation in female productivity and morphometric differences.

- In total, 30 sites were sampled, covering the entire range of the American lobster. At each site, 30 to 50 egg-berried female were sampled. One walking leg and several eggs were preserved for further analyses and morphometrics measurements were taken.

A pilot study was performed to test five genetic protocols on 4 individuals in order to optimize the genotyping method to be used. We found that the so-called « RAD protocol » was optimal. This allowed identifying about 12,073 molecular markers that will be used to genotype lobsters from all samples sites.

The genotyping of 756 individuals from 21 sites is currently ongoing and preliminary results will be available within the next few months.