

Proposal for Funding made to:
Atlantic Coastal Cooperative Statistics Program
Operations and Advisory Committees
1050 N. Highland Street, Suite 200 A-N
Arlington, VA 22204

**Creation of a Genetic Stock Identification program for
Atlantic coast striped bass (*Morone saxatilis*)**

Submitted by:

Benjamin Gahagan
Massachusetts Division of Marine Fisheries
30 Emerson Avenue
Gloucester, MA 01930

Applicant Name: Massachusetts Division of Marine Fisheries

Project Title: Creation of a Genetic Stock Identification program for Atlantic coast striped bass (*Morone saxatilis*)

Project: Type: New Project

Principal Investigator: Benjamin Gahagan

Co-Principal Investigators: Dr. Scott Pavey, Dr. Andrew Whiteley, Dr. Adrian Jordaan

Requested Award Amount: \$99,820

Requested Award Period: For one year, beginning after receipt of funds

Date Submitted: Aug. 11, 2020

Objective: We propose to deliver a data program plan and methodology that would allow management agencies on the Atlantic coast to efficiently and accurately estimate the catch and harvest of migratory striped bass (*Morone saxatilis*) caught in mixed stock fisheries back to three spawning populations. The project's primary objectives focus on the biological module (70%) but our products have relevance to the catch and effort (15%) and bycatch (15%) modules.

Within the scope of the project, the following specific deliverables will be met:

- Processing and classification of 5,000 striped bass tissue samples collected from coastal commercial and recreational fisheries between 2015 and 2020
- Power analysis of data set to determine adequate sample sizes needed to estimate annual population specific mortality in a specified region
- Finalization and publication of an affordable, open access genomic method for accurate and precise classification of striped bass caught in mixed stock fisheries
- Report providing sampling and processing recommendations and protocols for the establishment of a coastal sampling program that can be integrated into ACCSP data collection and interstate management

Need: Striped bass fisheries comprise the most popular and economically significant recreational fisheries on the northern half of the Atlantic coast and contribute more than six billion dollars of economic activity annually (Southwick Associates 2005). In Massachusetts alone, the National Marine Fisheries Service estimated that roughly 1.1 billion dollars was spent on recreational fishing in 2016, with 60% of trips targeting striped bass. This suggests that as much as 600 million dollars was spent by recreational fishers to target striped bass in just Massachusetts in 2016 (NMFS 2018). Striped bass also support important commercial fisheries in several states. As anadromous migratory fish that routinely cross among jurisdictions, and the target of commercial fisheries in several states, striped bass are managed on an interstate basis by the Atlantic States Marine Fisheries Commission (ASMFC), which considers them a high priority species (ASMFC 2018b). Indeed, the Atlantic Striped Bass Conservation Act (1984) and Atlantic Coastal Fisheries Cooperative Management Act (ACFCMA, 1993), codifying state and federal agency partnerships to manage coastal fisheries, established striped bass as a flagship species for multi-partner management on a coastal scale.

Due to data limitations, the ASMFC continues to manage coastal striped bass fisheries, which are in fact made up of a mixture of bass from several spawning areas, as a homogeneous 'stock'. A methodology to assign catch from coastal mixed stock fisheries to the populations from which they originate fulfills ASMFC Modeling/Quantitative as well as Fishery-Independent Priorities (ASMFC 2018a, 2018b). This project also meets the criteria for the ACCSP Recreational Technical Committee funding prioritization as it implements Biological sampling for recreational fisheries separate from MRIP APAIS. Striped bass are relevant to the ACCSP Bycatch Sampling Priority Matrix because they are bycatch in many of the fisheries and gear types listed, including New England Mid-Water Otter Trawl, New England Gillnet, New England Otter Trawl, and Mid-Atlantic Small Mesh Bottom Trawl.

Striped bass can be found seasonally in many coastal rivers and estuaries within their range but only a few estuaries (i.e., Chesapeake Bay, Hudson River, Delaware Bay, and the Roanoke River/Albemarle Sound) are thought to substantially contribute to the abundance of coastal migrants (Boreman and Lewis, 1987). Currently, seine surveys are used in estuaries with spawning populations of striped bass to estimate age-1 recruitment. However, as recruits leave natal rivers and estuaries, there is a lack of any ability to partition migrants to spawning populations. This problem is exacerbated by diverse behaviors, where significant portions of individuals within a population display resident or migratory behaviors which can shift as striped bass grow and mature (Secor et al 2001, Gahagan et al 2015, Secor et al 2020). These behavioral complexes, known as partial migration (Secor 2015), can uncouple observable trends between juvenile production and coastal abundance. Recruitment potential to the migratory stock may be further complicated by ongoing climate change, which is anticipated to alter the migratory pathways, habitats, and productivity of many fish (Perry et al. 2005, Nye et al. 2009, Lucey and Nye 2010, Lynch et al. 2015) and may change the phenology of spawning (Ellis and Vokoun 2009, Fincham et al. 2013, McQueen and Marshall 2017) with resulting effects on striped bass mortality (Peer and Miller, 2014).

The lack of a reliable method to partition coastal harvest has led to uncertainty in assessments, potentially inaccurate quotas, possible overharvest of less productive populations and underharvest of productive ones, and difficulty enacting regulations that are widely supported (ASMFC 2013, 2015). We propose a research project that will provide an easily implemented and accurate genomic-based sampling program and enable estimates of coastal mortality to be assigned to three spawning areas on the Atlantic coast of the U.S. for mixed stock fisheries throughout the migratory range of Atlantic coast striped bass.

The outstanding need for an accurate assignment method is a result of the inability of many traditional methods to adequately describe striped bass migratory behaviors. Studies based on conventional tags (e.g. spaghetti or loop tags) have provided important details of broader migratory patterns (Chapoton and Sykes 1961, Clark 1968, Boreman and Lewis 1987) but lack an adequate number of returns and frequently relied on fish of unknown origin tagged during oceanic migrations. In the past decade researchers have increasingly relied on acoustic telemetry tags (Wingate and Secor 2007, Wingate et al. 2011, Kneebone et al. 2014, Gahagan et al. 2015), which can provide highly detailed migration patterns and rates of mortality but their high cost prevents deploying the number of tags required to cover all natal populations. Attempts to use early genetic markers (Waldman et al. 1988, Waldman et al. 2011) produced variable results while more recent genetic-based studies have been partially successful in discerning stock structure in smaller portions of the coast-wide species distribution (Roy et al. 2000, Brown et al. 2005, Gauthier et al. 2013) but have not been able to confidently estimate the assignment of coastal migrants with enough precision for management use. Wirgin et al. (2020) recently completed a microsatellite-based genetic baseline that is broad in coverage and appears to offer accurate results, but it's applicability may be limited by difficulty in transferring microsatellite markers among genetics laboratories.

4

MA Division of Marine Fisheries

ACCSP Funding Proposal: Creation of a Genetic Stock Identification program for Atlantic coast striped bass (*Morone saxatilis*)

Sections of the proposal identified to help with the ranking process are in highlighted in green with a summary on page 13. All changes to initial proposal are highlighted in yellow.

The problem facing striped bass management is neither unique nor without solutions. On the West Coast, state and federal agencies, along with academic researchers, have successfully taken advantage of recent genomic advances, especially the development of Single Nucleotide Polymorphism (SNP) markers, to implement Genetic Stock Identification (GSI) sampling programs. The successful implementation of these programs has allowed agencies to manage anadromous mixed stock fisheries using nearly real-time information about population specific harvest (Habicht et al. 2010, Dann et al. 2013, Satterthwaite et al. 2014, Bradbury et al. 2016). These GSI programs typically take advantage of the improved speed and accuracy that is a by-product of SNP based panels for high throughput Next Generation Sequencing (NGS). Another substantial benefit of SNP based approaches is that they are generally easily replicated among labs, allowing many labs to simultaneously process samples with consistent results and making our project applicable over the entire region occupied by migratory striped bass.

Accordingly, we have already assembled and analyzed a SNP baseline spanning the entire range of migratory striped bass from North Carolina through the Canadian Maritimes. Our results (LeBlanc et al. 2020) indicate that the baseline can be used to classify striped bass back to six spawning areas, three of which are in Canada and three in the United States (U.S.). The U.S. complexes include the Hudson and Kennebec Rivers, the Delaware and Chesapeake Bays, and the Roanoke River and Albermarle Sound. We are now in the process of identifying the most informative SNPs for stock assignment and creating a GT-seq panel (Campbell et al. 2015) for fast and efficient assignment of mixtures and individual striped bass caught in coastal fisheries at reasonable costs (\$25-30 per sample). This project would have an important regional impact by providing complementary biological data to what is already collected, would address important coastwide management and stock assessment needs throughout the migratory range of the species, provide a baseline of data for future studies, and complement potential future advances such as close-kin mark-recapture (Bravington et al. 2016a and 2016b).

Results and Benefits: The creation of a GSI program for striped bass addresses multiple priorities for the ASMFC and ACCSP while providing new biological sampling data and addressing urgent stock assessment needs. The successful implementation of the program would allow for population specific management of mixed stock fisheries creating fisheries that are more sustainable while maximizing fishing opportunities.

The GSI program will provide two types of data: estimation of mixture proportions (Grant et al. 1980; Anderson et al. 2008) and assignment of individuals to natal populations (Manel et al. 2005; Anderson et al. 2008). For striped bass, accurate estimates of mixture proportions and individual assignments serve different purposes and are both essential for understanding stock-specific age structure and migratory patterns required by management agencies and for assessments. Mixture estimates will provide the basic information required to partition the coastal catch to specific populations. Accurate individual assignments will allow managers and researchers to incorporate a variety of individual-level attributes to that mortality. These characteristics include attributes essential to stock assessment data, such as sex, migratory

history, and age. Since striped bass can have highly variable life histories (Secor et al. 2001, Gahagan et al. 2015, Secor et al. 2020), these data will create unparalleled opportunities to understand their life history and apply that knowledge to management actions.

As part of the proposed work, we will develop methodology to extract DNA from uncleaned scales sampled by many agencies for ageing and frequently stored without undergoing any processing such as removal of tissues. The ability to use scales confers several advantages for future examinations of striped bass harvest. Importantly, most states already collect many scale samples, thus GSI analysis would integrate well into current collecting protocols. These existing sampling programs and potential archived samples will allow our methods to be easily expanded in the future to important areas like the Chesapeake Bay, Delaware Bay, and Hudson River estuary. All of these estuaries have resident populations and understanding the fluctuations in resident and coastal population segments, as well as potential for difference in mixed stock contributions to fisheries seasonally, are important factors in striped bass management. Existing scale collections also have the potential to be used for retrospective analyses to answer many pertinent management issues if agencies have archived uncleaned scales. This information could help inform managers on how the overall stock has responded to large scale climactic forcing, how the productivity of individual estuaries has influenced coastal fisheries over the past several decades, fluctuations in population level contributions to specific fisheries seasonally, and potentially how stocks have diverged since widespread stocking in the late 1800s. Finally, many volunteer angler groups already collect scale samples for state agencies or academic institutions. Scale collection protocols have a wide acceptance and use in the angling community and should be a productive source of genetic samples without the need for educating the public about new collection methods. These provide numerous citizen science opportunities for future work.

The proposed project is complementary to current biological as well as catch and effort sampling programs. The preferred method of collecting of tissue samples for GSI, typically dried fin clips, is simple and quick. Adding sample collection to current fishery dependent and independent sampling is easily accomplished and little different than collecting scale samples. As discussed above, scale samples can be used in many situations if necessary. Thus, the biological data collected and the interface between that data and catch and effort data that already exists, can be easily and directly paired with GSI results to better understand biological factors that influence population specific migration and residence in coastal waters as well as the proportionality of catch and effort on populations.

Data Delivery Plan: The proposed project will include plans for the creation of data formatting for delivery into relevant ACCSP Biological Data Modules on an annual basis by any partner who conducts GSI sampling in the future. Wherever possible, population assignment data will be paired with all biological data (i.e., total length, age) and metadata (e.g., capture date, capture location, fishery type) from assigned individuals, allowing for analysis of biological indicators of stock composition. The potential for data generated by this project to be compatible with current Catch and Effort Data housed by ACCSP exists and can be investigated in the future.

6

MA Division of Marine Fisheries

ACCSP Funding Proposal: Creation of a Genetic Stock Identification program for Atlantic coast striped bass (*Morone saxatilis*)

Sections of the proposal identified to help with the ranking process are in highlighted in green with a summary on page 13. All changes to initial proposal are highlighted in yellow.

Approach: Fisheries dependent samples consisting of fin clips and scales from mixed stock fisheries in the waters off Massachusetts were collected in the summers of 2015 through 2020 (Fig. 3). Fin clips from striped bass landed in the commercial fishery were collected via portside sampling by Massachusetts Division of Marine Fisheries (MADMF) staff. Fin clips or scales were collected from recreationally caught striped bass by MADMF staff or participants in MADMF voluntary Sportfish Angler Data Collection Team program. Samples from Long Island Sound will be collected in the summer of 2020 by Connecticut Department of Energy and Environmental Protection (CTDEEP) Long Island Sound Trawl Survey. These will be fishery independent samples, but they are assumed to be reflective of striped bass available to local fisheries by the ASMFC. All samples were collected using established protocols to preserve DNA in samples and avoid cross-contamination during collection. No archived samples will be used in this study, but the methods developed and shared will allow future work to be conducted using archived materials.

In collaboration, the project partners will assess the ability of the GT-seq panel of baseline populations to be accurately identified in GSI applications using the most robust methods developed by Pacific salmon researchers at Alaska Department of Fish and Game (ADFG), who will participate in the analyses. We will perform GSI with models with mixed stock striped bass implemented in the R package *rubias* (Moran and Anderson 2019). We will use the conditional model in *rubias*, with fixed allele frequencies in the reference (baseline) samples to obtain an initial estimate of mixture proportions for each sample. We will then use these initial mixture proportion estimates as priors for the full Bayesian model in *rubias*, which is more time intensive because allele frequencies are updated at each step in the MCMC chain. This combined approach performed best in a comprehensive evaluation of GSI methods (Habicht et al. 2007). Posterior distributions from the Bayesian model will provide stock composition estimates. Results will be summarized by the mean, median, and posterior quantiles of posterior distributions from BAYES.

We will assess GSI performance using proof tests (Habicht et al. 2010). Proof tests will be implemented by creating training and holdout sets of individuals. The training group will incorporate 50 striped bass per spawning population. GSI tests will use the training set as the baseline, with an additional 50 individuals per baseline population as “unknown”. The holdout group “unknowns” will be analyzed as a mixture sample initially with the conditional model in *rubias*, with the rebuilt data set as the baseline. Mixture proportion estimates from the conditional model in *rubias* will serve as a prior for the Bayesian model in *rubias*. We will consider a baseline population as ‘identifiable’ if the 90% credible interval exceeds 90% correct allocation in the proof test. This approach of a training and hold out data set is similar to the rigorous approach used by Koljonen et al. (2005), which they termed a ‘repeat baseline test’. Accuracy for both stock composition and individual assignment will be noted for both overall and population-specific performance.

Individual assignment tests will be used to estimate the origin of each fish in the fishery sample. We will use the likelihood and Bayesian approach implemented in the R package *rubias* (Moran and Anderson 2019) to assign individuals in the mixture sample to the baseline population with the highest probability of producing the given genotype in the mixture. Thus, genotype frequencies and mixture proportions are used to estimate the origin of individuals. This method is different from other assignment tests because it takes estimated mixture proportions into account and therefore is most appropriate for use in mixed-stock fishery context. We will conservatively use an assignment probability cutoff of 0.95 for further analysis of fish assigned to either stock.

We will use a jackknife approach, referred to as the “leave one out” test in the GSI literature, to evaluate the accuracy of assignment tests, as implemented in *rubias*. Each fish in each baseline population will be sequentially removed from the baseline and its origin estimated using the rest of the baseline. Individuals with complete genotypes at greater than 90% of loci will be included in the analysis. We will also perform realistic fishery simulations of various mixture proportions of fish from baseline populations to test how well the baseline data can identify the origin of each individual.

Following all GSI analyses, the project partners and CTDEEP will perform power analyses to examine the effects of factors such as overall sample size, seasonality, fish age, and fish length on results. These sensitivity analyses will be incorporated into a report describing the sampling protocols, the GT-seq panel, and GSI analytical methods to create recommendations for the creation of a coast-wide biological sampling program. The project partners anticipate that this program will complement current fisheries independent and dependent biological sampling completed by states in the migratory range of striped bass. The methods and results will also be prepared in manuscript format and submitted to an open-access peer-reviewed journal so that they are widely available to all interested parties. All genomic information will be made available in a Dryad repository or similar online storage and access warehouse.

Geographic Location: Over 5,000 striped bass tissue samples have been collected from Massachusetts state waters since 2015. CTDEEP will collect 200 samples from Long Island Sound in the fall of 2020. Sample processing will be completed by Dr. Scott Pavey, an international partner, at the University of New Brunswick – Saint John, Canada. Data analysis will be performed in Gloucester, Massachusetts, Missoula, Montana, and Anchorage, Alaska by all project partners. Report and manuscript preparation will occur in Gloucester, Massachusetts with contributions from all project partners, including CTDEEP. The project investigators believe that if travel can safely be performed to work in collaboration and attend meetings that the project will be conducted more efficiently. However, if travel costs or COVID-19 related safety measures prevent travel, meetings and collaborative work can be accomplished remotely.

Milestone Schedule:

The milestone schedule is based on the starting month of the project as month “1.”

Task	Month												
	1	2	3	4	5	6	7	8	9	10	11	12	13
Sample processing													
Genomic Stock Identification													
Sensitivity analyses for sampling protocols													
Manuscript and report writing													

Project Accomplishments Measurement:

Project Goal	Measure of Accomplishment
Sample processing	DNA extraction and preparation for sequencing of 5,000 tissues samples.
Genomic Stock Identification	Analysis of all 5,000 samples and assignment back to spawning population using <i>rubias</i> and other applicable programs.
Sensitivity analyses for sampling protocols	Use analyzed data to create recommendations for sampling levels and frequency to accurately describe mixed stock coastal fisheries.
Manuscript and report writing	Submit a manuscript to an open access, peer reviewed journal that includes the GT-seq panel, methodology, GSI analysis, and results. Create a report describing best practices and recommendations for sample collection design, sample processing and sequencing, and analysis.

Cost Summary:

ITEM	QUANTITY	UNIT PRICE	REQUEST	IN-KIND
MA DMF				
c. TRAVEL			\$4,467	\$365
Gahagan travel to Saint John (hotel, per diem, mileage) for six days			\$780	\$365
Gahagan travel to University of Montana (airfare, hotel, car rental, and per diem) for six days			\$1,538	
Gahagan travel to Anchorage, AK (airfare, hotel, car rental, and per diem) for seven days			\$2,149	
f. CONTRACTUAL			\$89,338	\$57,712
(University of New Brunswick - Saint John (UNB-STJ))			\$86,567	\$57,712
a. PERSONNEL			\$26,897	\$17,931
Lab Technician, monthly salary	6	\$4,482.80	\$26,897	
Lab Technician, monthly salary	4	\$4,482.80		\$17,931
b. FRINGE			\$3,093	\$2,062
Fringe Benefits at UNB-STJ rate	11.50%		\$3,093	
Fringe Benefits at UNB-STJ rate	11.50%			\$2,062
h. OTHER			\$49,080	\$32,720
DNA Extraction and GT-seq library construction	3000	\$16.36	\$49,080	
DNA Extraction and GT-seq library construction	2000	\$16.36		\$32,720
i. TOTAL UNB-STJ DIRECT COSTS			\$79,070	\$52,713
j. UNB-STJ INDIRECT (on salary and fringe)			\$7,497	\$4,998
k. UNB-STJ Total			\$86,567	\$57,712
University of Montana (Dr. Whiteley)			\$2,771	\$0
c. TRAVEL			\$1,885	
Dr. Whiteley (co-PI) travel to Anchorage, AK (airfare, hotel, per diem) for 6 days			\$1,885	
j. UNIVERSITY OF MONTANA INDIRECT			\$886	
k. University of Montana Total			\$2,771	\$0
h. OTHER			\$6,015	\$3,015
Open access publication costs	1	\$1,500	\$1,500	
Genetic sequencing for 1,000 samples	3	\$1,500	\$4,500	
Genetic sequencing quality control (\$15)	1	\$15	\$15	
Genetic sequencing for 1,000 samples	2	\$1,500		\$3,000
Genetic sequencing quality control (\$15)	1	\$15		\$15
i. TOTAL DIRECT COSTS			\$99,820	\$61,091
j. INDIRECT - MA DMF rate (on salary)			\$0	\$0
k. TOTAL REQUESTED			\$99,820	\$61,091
Total Project Cost			\$160,911	38%

MA Division of Marine Fisheries

ACCSP Funding Proposal: Creation of a Genetic Stock Identification program for Atlantic coast striped bass (*Morone saxatilis*)

Sections of the proposal identified to help with the ranking process are in highlighted in green with a summary on page 13. All changes to initial proposal are highlighted in yellow.

Cost Details (\$99,820 Requested; \$61,091 In-Kind):

c. Travel (\$4,467 Requested; \$365 In-Kind)

Travel costs are requested for three trips that will facilitate the processing and analysis of samples:

1. Benjamin Gahagan to the University of New Brunswick – Saint John (\$1,145): Mr. Gahagan will travel to co-PI Dr. Scott Pavey’s lab to help process samples, prepare libraries, and process data. He will drive a state vehicle to Saint John (810 miles @ \$0.45/mile; \$365 total in-kind) and stay in a hotel for five nights (\$120/night; total \$600). His meals stipend request (\$180) has been calculated at Mr. Gahagan’s union employee per diem rate of \$36/day for five days.
2. Benjamin Gahagan to the University of Montana (\$1,538): Mr. Gahagan will fly (\$450) to Bozeman, MT to work directly with co-PI Dr. Whiteley to prepare and analyze data using the *rubias* program. This trip will coincide with the annual ConGen conference at University of Montana where Mr. Gahagan will be able to interface and network with leaders in the conservation genetics and mixed stock assignment field while working directly with the project data. While in Montana, Mr. Gahagan will stay in a hotel for five nights (\$100/night; total \$500) and rent a car for transportation (six days at \$68/day; total \$408). His meals stipend request (\$180) has been calculated at Mr. Gahagan’s union employee per diem rate of \$36/day for five days.
3. Benjamin Gahagan to Anchorage, AK (\$2,149): Mr. Gahagan will fly from Boston, MA (\$525) to work directly with staff from the Alaska Department of Fish and Game’s Gene Conservation Laboratory (ADFG) to analyze data, correct any analytical issues, and help design sampling protocols. The staff of ADFG have extensive experience designing sampling programs and enacting genetic stock identification programs to monitor anadromous fisheries and their expertise will benefit this project. While in Anchorage, Mr. Gahagan will stay in a hotel for six nights (\$160/night; total \$960) and rent a vehicle for seven days (\$64/day; total \$448). Mr. Gahagan’s meals stipend request (\$216) has been calculated at Mr. Gahagan’s union employee per diem rate of \$36/day for six days.

f. Contractual (\$89,338 Requested; \$57,712 In-Kind)

University of New Brunswick – Saint John (\$86,567 Requested; \$57,712 In-Kind)

Processing and preparation of all samples will occur in the lab of Dr. Scott Pavey at University of New Brunswick – Saint John (UNB-STJ). This work will require six months of technician time, which are subject to UNB-STJ’s fringe (11.5%) and requested indirect (25.0%) rates (total technician cost = \$26,897 salary, \$3,093 fringe, and \$7,497 indirect). Other items that will be purchased by UNB-STJ include plates and reagents to prepare samples for high throughput sequencing (\$16.36 per sample for 3,000 samples; total of \$49,080) and are not subject to fringe or indirect costs. In FY 2021, MADMF has allocated money to pay Dr. Pavey’s lab to prepare 2,000 samples from the same pool of collected

tissues discussed in this grant. We are including the costs for four months of technician time at identical fringe and indirect rates (total technician cost = \$17,931 salary, \$2,062 fringe, and \$4,998 indirect) and other items (\$16.36 per sample for 2,000 samples; total of \$32,720) to process those samples as **in-kind** in this proposal. UNB-STJ's indirect rate agreement is attached for reference, which shows a higher rate than the requested 25% rate.

University of Montana (\$2,771 Requested; \$0 In-Kind)

Dr. Andrew Whiteley will accompany Mr. Gahagan to Anchorage, AK where they will work directly with staff from ADFG (see trip description above). Travel costs for Dr. Whiteley include a flight from Bozeman, MT (\$625) to Anchorage, AK, hotel stay for six nights (\$160/night; total \$960), and a per diem stipend of \$50/day for six days (\$300 total), which has been calculated based on the University of Montana's out-of-state rate. University of Montana applies a 47% indirect rate to all incoming funds. Their indirect rate agreement is attached for reference.

- h. Other (\$6,015 Requested; \$3,015 In-Kind)** The co-PIs will prepare results of the GT-Seq panel construction, GSI methodology, and results for publication in an open access, peer reviewed journal (\$1,500). This will maximize exposure of the project and make it completely accessible to any groups wishing to use it.

MADMF will also pay Genome Quebec for high throughput sequencing services and quality control measures. The cost for each lane of 1,000 samples in the sequencer is \$1,500 (\$4,500 total for 3,000 samples) and there is a onetime cost of \$15 for quality control measures when setting up the panel to be sequenced. We have included the cost of sequencing services for the 2,000 samples being prepared separately in FY 2021 as **in-kind** (\$3,015 = \$1500 x 2 lanes of samples + \$15 quality control measures).

- i. Direct (\$99,820 Requested; \$61,091 In-Kind)**
- j. Indirect (\$0 Requested; \$0 In-Kind)**
There are no indirect charges from MADMF in this proposal.
- k. Total Project Costs \$160,911 (\$99,820 Requested; \$61,091 In-Kind)**
Requested from ACCSP: 99,820 (62% of total costs)
MADMF in-kind: \$61,091 (38% of total costs)

Summary of Proposal for Ranking Purposes

Proposal Type: *New Project*

Primary Program Priority:

Biological Sampling (100%): This proposal focuses on the creation of a biological sampling program that uses genomic data to assign striped bass caught in mixed stock coastal fisheries back to spawning populations. Data generated will be reviewed for compatibility with the ACCSP Biological Data Module and a plan to add this type of data will be investigated.

Project Quality Factors:

Multi-Partner/Regional impact including broad applications:

This project is collaboration between state agencies and multiple academic institutions over a broad area. The broader work in the project stretches across jurisdictions. Connecticut Department of Energy and Environmental Protection will provide mixed stock samples from Long Island Sound to compare to those collected in coastal Massachusetts. The project is supported by other agencies with management authority over striped bass as evidenced by two letters of support from Northeast partners. The results will have range-wide applicability and can be used by any interested and capable group.

Contains funding transition plan/defined end-point:

This is a one-year project with a defined end goal. The goal is to create genomic based method to assign striped bass caught in coastal fisheries to a spawning population and provide recommendations for a coast-wide sampling program.

In-kind contribution:

This proposal includes \$61,091 of in-kind funding which equates to 38% of the total budget.

Improvement in data quality/quantity/timeliness:

Providing spawning population assignment for coastal mixed stock striped fisheries would provide a new and important data stream for management and stock assessment.

Potential secondary module as a by-product:

Catch and effort: This proposal focuses on the creation of stock identification data that could be integrated with catch and effort data already collected by ACCSP.

Bycatch/Species Interactions: This proposal focuses on the creation of stock identification data that can be used to assign striped bass caught as bycatch in many fisheries identified in the Bycatch Priority Matrix.

Impact on stock assessment:

The genetic stock identification tool proposed here directly answers the recognized need for a method to partition coastal mortality of striped bass that has been pointed out in recent stock assessments. This proposal would allow future stock assessments to cease managing coastal striped bass as a

separate stock and instead allow them to manage striped bass on a population by population basis, the preferred method for mixed stock fisheries.

Innovative:

SNP based GSI, a proven technique in mixed stock fisheries for migratory anadromous fish, has not been completed for striped bass. This project will provide the opportunity to apply innovative technology that will benefit the resource, management, and fishery participants.

Properly prepared:

This project has been prepared as per the Funding Decision Document.

Literature Cited

- Anderson, E.C., R.S. Waples, and S.T. Kalinowski. 2008. An improved method for predicting the accuracy of genetic stock identification. *Canadian Journal of Fisheries and Aquatic Sciences* 65:1475-1486.
- Atlantic States Marine Fisheries Commission. 2013. Atlantic Striped Bass stock assessment update. Vol. B. 57th Northeast Regional Stock Assessment Workshop of the Atlantic States Marine Fisheries Commission. ASMFC, Washington, D.C.
- Atlantic States Marine Fisheries Commission. 2015. Atlantic Striped Bass benchmark stock assessment. ASMFC, Washington, D.C.
- Atlantic States Marine Fisheries Commission. 2018a. Atlantic States Marine Fisheries Commission Research Priorities and Recommendations to Support Interjurisdictional Fisheries Management. ASMFC, Arlington, VA 93pp.
- Atlantic States Marine Fisheries Commission. 2018b. 2019 Action Plan. ASMFC, Arlington, VA. 18pp.
- Boreman, J. and R. Lewis. 1987. Atlantic coastal migration of striped bass. *American Fisheries Society Symposium* 1:331-339.
- Bradbury, I.R., L.C. Hamilton, G. Chaput, M.J. Robertson, H. Goraguer, A. Walsh, and T. King. 2016. Genetic mixed stock analysis of an interceptory Atlantic salmon fishery in the Northwest Atlantic. *Fisheries Research* 174: 234-244.
- Bravington, M.V., P.M. Grewe, and C.R. Davies. 2016a. Absolute abundance of southern bluefin tuna estimated by close-kin mark-recapture. *Nature Communications* 7:13162.
- Bravington, M.V., H.J. Skaug, and E.C. Anderson. 2016b. Close-kin mark-recapture. *Statistical Science* 31(2):259-274.
- Brown, K.M., G.A. Baltazar, and M.B. Hamilton. 2005. Reconciling nuclear microsatellite and mitochondrial marker estimates of population structure: breeding population structure of Chesapeake Bay striped bass (*Morone saxatilis*). *Heredity* 94:606-615.
- Campbell, N.R., S.A. Harmon, and S.R. Narum. 2015. Genotyping-in-Thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing. *Molecular Ecology Resources* 15:855-867.
- Clark, J. 1968. Seasonal movements of striped bass contingents of Long Island Sound and the New York Bight. *Transactions of the American Fisheries Society* 97:320-343.
- Chapoton, R.B. and J.E. Sykes. 1961. Atlantic coast migration of large striped bass as evidenced by fisheries and tagging. *Transactions of the American Fisheries Society* 90:13-20.
- Dann, T. H., C. Habicht, T.T. Baker, and J.E. Seeb. 2013. Exploiting genetic diversity to balance conservation and harvest of migratory salmon. *Canadian Journal of Fisheries and Aquatic Sciences* 70: 785-793.
- Debevec, E.M., R.B. Gates, M. Masuda, J. Pella, J. Reynolds, and L. W. Seeb. 2000. SPAM (version 3.2): statistics program for analyzing mixtures. *Journal of Heredity* 91:509-511.

- Ellis, D.E. and J.C. Vokoun. 2009. Earlier spring warming of coastal streams and implications for alewife migration timing. *North American Journal of Fisheries Management* 29(6):1584-1589.
- Fincham, J.I, A.D. Rijnsdorp, and G.H. Engelhard. 2013. Shifts in the timing of spawning in sole linked to warmer sea temperatures. *Journal of Sea Research* 76:69-76.
- Gahagan, B.I, D.A. Fox, and D.H. Secor. 2015. Partial migration of striped bass: revisiting the contingent hypothesis. *Marine Ecology Progress Series* 525:185-197.
- Gauthier, D.T., C.A. Audemard, J.E.L. Carlsson, T.L. Darden, M.R. Denson, K.S. Reece, and J. Carlsson. 2013. Genetic Population Structure of US Atlantic Coastal Striped Bass (*Morone saxatilis*). *Journal of Heredity* 104:510-520.
- Grant, W.S., G.B. Milner, P. Krasnowski, and F.M. Utter. 1980. Use of biochemical genetic variants for identification of sockeye salmon *Oncorhynchus nerka* stocks in Cook Inlet, Alaska. *Canadian Journal of Fisheries and Aquatic Sciences* 37:1236-1247.
- Habicht, C., W.D. Templin, T.M. Willette, L.F. Fair, S.W. Raborn, and L.W. Seeb. 2007. Postseason stock composition analysis of upper Cook Inlet sockeye salmon harvest, 2005–2007. Alaska Department of Fish and Game, Fishery Manuscript 07-07, Anchorage. Available: <http://www.sf.adfg.state.ak.us/>. (April 2010).
- Habicht, C., L.W. Seeb, K.W. Myers, E.V. Farley, and J.E. Seeb. 2010. Summer–fall distribution of stocks of immature sockeye salmon in the Bering Sea as revealed by single-nucleotide polymorphisms. *Transactions of the American Fisheries Society*, 139: 1171-1191.
- Kneebone, J., W.S. Hoffman, M.J. Dean, D.A. Fox, and M.P. Armstrong. 2014. Movement patterns and stock composition of adult striped bass tagged in Massachusetts coastal waters. *Transactions of the American Fisheries Society* 143:1115-1129.
- Koljonen, M.L., J. J. Pella, and M. Masuda. 2005. Classical individual assignments versus mixture modeling to estimate stock proportions in Atlantic salmon (*Salmo salar*) catches from DNA microsatellite data. *Canadian Journal of Fisheries and Aquatic Sciences* 62:2143–2158.
- Leblanc, N.M. , B.I. Gahagan, S.N. Andrews, T.S. Avery, G.N. Puncher, B.J. Reading, C. Buhariwall, R.A. Curry, A.R. Whiteley, and S.A. Pavey. 2020. Genomic population structure of striped bass (*Morone saxatilis*) from the Gulf of St. Lawrence to the Cape Fear River. *Evolutionary Applications* <https://doi.org/10.1111/eva.12990>
- Lucey, S.M. and J.A. Nye. 2010. Shifting species assemblages in the Northeast US Continental Shelf Large Marine Ecosystem. *Marine Ecology Progress Series* 415:23-33.
- Lynch, P.D. J.A. Nye, J.A. Hare, C.A. Stock, M.A. Alexander, J.D. Scott, K.L. Curti, and K. Drew. 2015. Projected ocean warming creates a conservation challenge for river herring populations. *ICES Journal of Marine Science* 72(2):374-387.

- Manel, S., O.E. Gaggiotti, and R.S. Waples. 2005. Assignment methods: matching biological questions techniques with appropriate techniques. *Trends in Ecology & Evolution* 20:136-142.
- Moran, B.M. and E.C. Anderson. 2019. Bayesian inference from the conditional genetic stock identification model. *Canadian Journal of Fisheries and Aquatic Sciences* 76(4):551-560.
- National Marine Fisheries Service. 2018. Fisheries Economics of the United States, 2016. U.S. Department of Commerce, NOAA Technical Memorandum NMFS-F/SPO-187a, 243p.
- Nye, J.A., J.S. Link, J.A. Hare, and W.J. Overholtz. 2009. Changing spatial distribution of fish stocks in relation to climate and population size on the Northeast United States continental shelf. *Marine Ecology Progress Series* 393:111-129.
- Peer, A.C. and T.J. Miller. 2014. Climate change, migration phenology, and fisheries management interact with unanticipated consequences. *North American Journal of Fisheries Management* 34:94-110.
- Pella, J. and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. *Fishery Bulletin* 99:151-167.
- Perry, A.L., P.J. Low, J.R. Ellis, and J.D. Reynolds. 2005. Climate change and distribution shifts in marine fishes. *Science* 308:1912-1915.
- Roy, N.K., L. Maceda, and I. Wirgin. 2000. Isolation of microsatellites in striped bass (*Morone saxatilis*) and their preliminary use in population identification. *Molecular Ecology* 9:827-829.
- Satterthwaite W.H., M.S. Mohr, M.R. O'Farrell, E.C. Anderson, M.A. Banks, S.J. Bates, M.R. Bellinger, L.A. Borgerson, E.D. Crandall, J.C. Garza, and B.J. Kormos. 2014. Use of genetic stock identification data for comparison of the ocean spatial distribution, size at age, and fishery exposure of an untagged stock and its indicator: California coastal versus Klamath River Chinook Salmon. *Transactions of the American Fisheries Society* 143:117-133.
- Secor, D.H. 2015. Migration ecology of marine fishes. Johns Hopkins University Press, Baltimore, MD. 292 pp.
- Secor, D.H., J.R. Rooker, E. Zlokovitz, and V.S. Zdanowicz. 2001. Identification of riverine, estuarine and coastal contingents of Hudson River striped bass based upon otolith elemental fingerprints. *Marine Ecology Progress Series* 211:245-253.
- Secor, D.H., M.H.P. O'Brien, B.I. Gahagan, J.C. Watterson, D.A. Fox. 2020. Differential migration in Chesapeake Bay striped bass. *PLoS ONE* 15(5):e0233103.
- Southwick Associates, Inc. 2005. The Economics of Recreational and Commercial Striped Bass Fishing.

- Storer, C.G., C.E. Pascal, S.B. Roberts, W.D. Templin, L.W. Seeb, and J.E. Seeb. 2012. Rank and order: evaluating the performance of SNPs for individual assignment on a non-model organism. PLoS ONE 7: e49018.
- Waldman, J.R., J. Grossfield, and I. Wirgin. 1988. Review of stock discrimination techniques for striped bass. North American Journal of Fisheries Management 8:410-425.
- Waldman, J., L. Maceda, and I. Wirgin. 2012. Mixed-stock analysis of wintertime aggregations of striped bass along the Mid-Atlantic coast. Journal of Applied Ichthyology 28:1-6.
- Wingate, R.L. and D.H. Secor. 2007. Intercept telemetry of the Hudson River striped bass resident contingent: Migration and homing patterns. Transactions of the American Fisheries Society 136:95-104.
- Wingate R.L., D.H. Secor, D.H., and R.T. Kraus. 2011. Seasonal patterns of movement and residency by striped bass within a subestuary of the Chesapeake Bay. Transactions of the American Fisheries Society 140:1441-1450.
- Wirgin, I., L. Maceda, M. Tozer, J. Stabile, and J. Waldman. 2020. Atlantic coastwide population structure of striped bass *Morone saxatilis* using microsatellite DNA analysis. Fisheries Research 226:105506