VIRGINIA SALTWATER RECREATIONAL FISHING DEVELOPMENT FUND
SUMMARY PROJECT APPLICATION*

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NAME AND ADDRESS OF APPLICANT:	PROJECT LEADER (name, phone, e-mail):
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PRIORITY AREA OF CONCERN:	**PROJECT LOCATION:**
Research and Data Collection	Old Dominion University Norfolk, VA

DESCRIPTIVE TITLE OF PROJECT:

Examining Stock Composition of Migratory Striped Bass (*Morone saxatilis*)

PROJECT SUMMARY:

This project will perform a Mixed Stock Analysis of migratory striped bass within and outside Chesapeake Bay. The analysis will be performed using a recently developed and validated panel of microsatellite DNA markers, as well as a baseline data set previously generated from young-of-year striped bass from Hudson River to South Carolina. These markers and baseline data allow determination of the population of origin of striped bass from mixed stocks (e.g. the coastal migratory fishery) with a high degree of accuracy. The goal of the proposed work is to determine the contributions of major production areas (i.e Hudson River, Chesapeake Bay, North and South Carolina) to the migratory striped bass fishery in Chesapeake Bay and in coastal waters of Virginia.

EXPECTED BENEFITS:

A healthy, well-managed striped bass stock is beneficial to both recreational and commercial fishermen. Recovery of the stock in the mid-1990s represents a success story in fisheries research and management, however the abundance of striped bass along the Atlantic coast undergoes long-term fluctuations, and recent data indicates natural mortality is increasing. It will therefore be necessary to maintain and refine effective management practices to sustain successes in rebuilding the stock. Our knowledge of the contribution of various production areas to the coastal migratory stock is based primarily on 20+ year-old information collected before or during major population declines and a rebuild of the stock. Up-to-date information on this topic is necessary, as current treatment of striped bass as a single, genetically homogeneous population ignores potentially major differences in yield from individual populations. This project will provide a current, sensitive analysis of the coastal migratory stock composition, and will therefore be of use in effective management of the resource. The project will also have significant angler involvement through sample collections and public outreach.

COSTS:

Funds are requested for support of project personnel (Drs. David Gauthier and Jens Carlsson), as well as a graduate student at ODU. We request funds for supplies related to sample processing and limited funds for travel to fishing tournaments and to present results of our work. Indirect costs are also requested per ODU requirements.

VMRC Funding:	82,351
Recipient Funding:	15,337
Total Costs:	**97,688**

Detailed budget must be included with proposal.

Updated 11/12/08

***This form alone does not constitute a complete application, see application instructions or contact Sonya Davis at 757-247-8155 or sonya.davis@mrc.virginia.gov**

Old Dominion University Research Foundation

April 15, 2011

Virginia Marine Resources Commission
2600 Washington Avenue, Third Floor
Newport News, VA 23607

Re: Virginia Saltwater Recreational Fishing Development Fund

Dear Sir or Madam:

Old Dominion University Research Foundation is pleased to submit its Proposal entitled "Examining Stock Composition of Migratory Striped Bass (Morone saxatilis)". The proposal is submitted on behalf of the principal investigator Dr. David Gauthier, Department of Biological Sciences, Old Dominion University.

Please note that if an award is made as a result of this proposal, it should be made payable to the Old Dominion University Research Foundation. The Research Foundation is the fiscal and administrative agent for Old Dominion University for sponsored agreements. The Foundation is a not-for-profit corporation, and it is tax exempt under Section 501 (c) (3) of the Internal Revenue Code.

We are pleased to forward this proposal for your review and consideration. Please address any questions of a technical nature to Dr. David Gauthier at (757) 683-3822. Contractual questions should be addressed to Chankia Nelson, Grant & Contract Administrator, at (757) 683-4293 ext 613.

Sincerely,

Carole E McPhillips

Carole E. McPhillips
Manager, Sponsored Programs

Enclosure: Original via email
ODU Research Foundation Prop. No. 11-583

Cc: David Gauthier
Wayne Hynes
Chris Osgood

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Examining Stock Composition of Migratory Striped Bass (*Morone saxatilis*)

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I. Need:

The anadromous striped bass is one of the most commercially and recreationally important finfishes in Chesapeake Bay. In 2008, recreational and commercial landings in Maryland and Virginia totaled 4.4 and 4.7 million pounds, respectively (Atlantic States Marine Fisheries Commission data). The striped bass is also a keystone predator species with very high ecological importance to the Chesapeake Bay ecosystem as a whole. Striped bass spawn during spring in most major estuarine systems from the St. Lawrence River in Quebec to northern Florida, and undergo major coastal migrations, generally northward in summer, and southward in winter. Stocks south of Albemarle Sound are thought to be considerably less migratory than northern stocks, however some limited tagging evidence suggests that southern fish may join coastal migrations [1]. There is also evidence that a portion of adult striped bass populations may remain resident in headwaters of major tributaries, forgoing coastal migration [2-4].

There is currently a major gap in our knowledge regarding the genetic composition of the Atlantic migratory striped bass stock. The document "Status of Stock Assessment Knowledge Used to Manage Important Virginia Finfish Species" [5] currently indicates an "Acceptable State of Knowledge" regarding Stock Identification of striped bass, however this judgment requires examination. Contributions of various areas to the migratory striped bass stock have been previously estimated by analysis of morphometric characters [6] and eye proteins [7]. These analyses, however, did not explicitly address genetic composition, and as baseline data was derived from spawning adults, these methods make important assumptions about natal stream fidelity. That is to say, by creating a baseline for population identification based on adults sampled within a breeding ground, this assumes that the adults on that breeding ground: a)

originated in that area, and b) are not admixed with fish from other areas. Given the highly migratory nature of striped bass, these assumptions are open to question. Further, the use of morphometric characters, as in [6], has the drawback that these features are under both genetic and environmental control, and therefore may be confounded by fish migration. Genetic studies have advantages over morphometric studies in that the environmental variable is removed, and one such study using mitochondrial DNA has been performed to examine the stock structure in the eastern Long Island coastal fishery [8]. This study found a mixture of fish from Chesapeake Bay and Hudson River origin, supporting the idea that multiple production areas contribute to the migratory stock.

Regardless of experimental methodology, the most recent [8] of these studies examined fish collected in 1989, and focused on fish from New York waters. The next most recent focused on the 1982 year class in Rhode Island waters, and the only study including migrants collected south of New York [6] was performed on samples collected during 1975. There is therefore a 30+ year gap in our knowledge about genetic composition of migratory striped bass in/around Chesapeake Bay, and a 20+ year gap in our knowledge about the subject along the Atlantic coast. It is generally assumed [9] but not well-supported, that the contribution of various production areas to the coastal stock varies from year to year, and given the fact that the striped bass stock on the Atlantic coast has undergone a major collapse and rebuild in the last three decades, the need to reassess this issue is clear. It is worth noting here that a common statistic on the contribution of the Chesapeake Bay to the coastal migratory stock (70%-90%, see [1, 10]) is apparently derived from morphometrics-based work performed in the 1970s [6, 11].

Knowledge of the genetic composition of the migratory striped bass stock is important for several reasons. First, current virtual population analysis-based management assessment of striped bass does not take into account genetically differentiated populations of these fish along the mid-Atlantic coast. While major production areas are managed separately, our knowledge about the contribution of various populations of striped bass (e.g. Hudson River, Chesapeake Bay) to these areas is outdated and this information can essentially be considered unknown. Treatment of striped bass as a single, genetically homogeneous population for management therefore ignores potentially major differences in yield from individual populations. This is significant, as low recruitment from populations that are in need of more active management efforts will not be detected, due to high recruitment from populations reproducing under more

favorable conditions. Second, while current juvenile recruitment surveys being performed in major north Atlantic production areas (Hudson River, Delaware River, Chesapeake Bay, North Carolina) are excellent tools for gauging local recruitment, there is currently no methodology by which the propagation of those juveniles to the coastal fishery may be measured. That is, there is a disconnect between measurement of local productivity and how many of those juveniles actually recruit to the migratory stock and contribute to subsequent generations. This is important for gauging success of production areas throughout the life of the fish they produce, and also provides an important metric by which habitat restoration efforts may be assessed. A recent ASMFC report (Habitat Management Series #9, [1]) identified habitat protection and restoration as a major priority for continuing health of diadromous species including striped bass. In order to truly measure the success of these efforts, it is important to have a viable way by which their impacts not only on juveniles, but on the adult portion of the stocks, be assessed. Finally, the striped bass stock is currently considered healthy along the Atlantic coast, and the latest stock assessment indicates it is not overfished [12]. A decline in stock abundance since 2004 has been observed, however, and there is evidence for increased natural mortality in Chesapeake Bay [13] and elsewhere along the Atlantic coast [12], possibly due to the effects of mycobacteriosis [12, 14]. If regional rises in natural mortality are in fact occurring, accurate modeling of their affects on overall stock health will require determination of the relative contributions of various areas to the coastal stock. For example, if disease-related natural mortality is considerably higher in Chesapeake Bay than in other areas, this would be expected to have a large effect on the overall stock, depending on the relative contribution of Chesapeake Bay to this overall stock. This relative contribution, however, is currently unknown, so effects of natural mortality in specific regions cannot be adequately assessed.

The Mixed Stock Analysis (MSA) proposed in this work will provide data on the genetic composition of the migratory striped bass stock within and outside of Chesapeake Bay as well as in other coastal Atlantic areas. The work will therefore provide a linkage between studies of recruitment in major production areas and propagation of those fish into coastal waters. Because we will collect age data in addition to genetic information, variation in genetic structure by age-class will also be addressed, so strong year-classes in individual areas may be followed into the coastal stock. If this project is successful in the first year, as we anticipate, we intend to seek funding for further study so that temporal patterns of age-classes from individual populations of

origin may be examined. This study will also provide information relevant to understanding the effects of increased natural mortality in individual areas on the overall stock.

II. Objectives:

This work has two major objectives:

1) Use a previously developed and validated panel of molecular DNA markers to examine contributions of different production areas (Hudson River, Delaware/Chesapeake/North Carolina complex, South Carolina) to the composition of coastal/migratory striped bass stocks.

2) Engage the fishing community in research on striped bass stock composition via interaction with anglers at tournaments and return of origin and age data on collected fish.

A timeline for completion of these objectives is shown below:

Project activity	**O**	**N**	**D**	**J**	**F**	**M**	**A**	**M**	**J**	**J**	**A**	**S**
Prepare for sample processing	X	X	X									
Receive/process samples			X	X	X	X	X	X	X	X	X	
Data analysis/return of information to anglers				X	X	X	X	X	X	X	X	X
Final analysis/preparation of final report											X	X

III. Expected Results or Benefits:

A healthy, well-managed striped bass stock is beneficial to both recreational and commercial fishermen. The proposed study will therefore be of roughly equal importance to both user groups. Information from the proposed study will be of significant value for increasing our

understanding of striped bass biology and will be of particular interest for managers. Striped bass are of great economic importance, and efforts to rebuild the stock in the late 1980s and early 1990s represent a success story in fisheries research and management [9]. The abundance of striped bass along the Atlantic coast is characterized by substantial long-term fluctuations, therefore it will be necessary to maintain and refine effective management practices to sustain recent successes in rebuilding the stock. These practices must be based on sound biological information, including the contribution of various production areas to the migratory stock.

The MSA approach has turned out to be a very effective management tool for the Pacific salmon fishing industry in Alaska. Alaska Department of Fish and Game managers in the Bristol Bay can now use genetic data from 2,000 fish taken in a test fishery, compare them to a baseline of 10,000 fish, and assign them to a source population, allowing managers to estimate stock compositions and set stock-specific fishing targets within 24 hours [15]. Without this up-to-date information, particular stocks, which are superficially identical and may mix in open water, could be disproportionately overexploited, leading to the collapse of geographically isolated spawning populations. Genetic stock identification also allows for proactive management in which stocks that are known to have declining spawning populations can be protected from overfishing because it allows for real time management of stocks and populations [16]. We expect that the approach described in this proposal will allow for effective monitoring of stock composition both spatially and temporally and will facilitate more effective management of the striped bass resources. This will help to ensure the longtime health and sustainability of striped bass along the US eastern seaboard.

The proposed work will focus primarily on the migratory striped bass stock in and around Virginia waters, and will thus provide information directly relevant to the VA coastal and migrant fishery. A limited number of fish from further north along the Atlantic coast will be collected by the NEAMAP survey, so comparisons to fish stocks in more northern locations can be made. Importantly, we will be collecting samples from migratory striped bass at different times of year (Fall 2011, Spring 2012), which will allow for examination of whether the composition of the migratory stock with respect to fish origin changes over a fishing season. In other words, multiple sampling seasons will indicate whether fish from different coastal stocks are arriving as migrants in the VA fishery at different times of year.

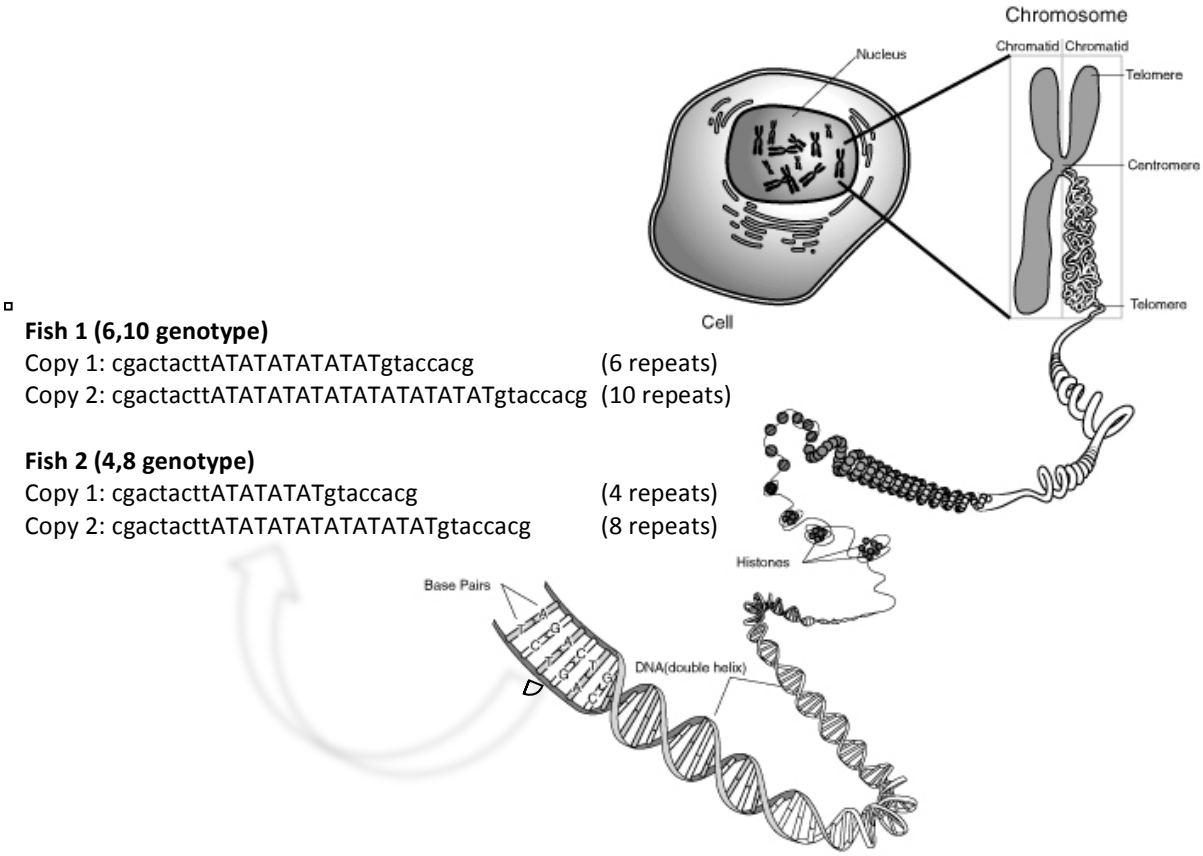
Results of this study will be made available to fisheries and management communities

through annual reports, publication in peer-reviewed journals, and presentations to ASMFC committees. Dr. Gauthier has presented before the ASMFC Striped Bass Management Board (2010) and will do so again if invited. This information will be of direct relevance and importance to resource managers, therefore we consider it a high priority to present the results of the proposed work to this group. This project includes a major component of recreational angler participation, and we will be directly disseminating genotype and age information on individual fish to the collectors. Through public outreach efforts about the project, we anticipate a great deal of contact with the fishing community, which will naturally lead to dissemination of the results of this work. We will also seek to contribute to articles targeted to the local fishing community in publications such as the CCA Tide bimonthly issue.

IV. **Approach**:

Population of origin of individual striped bass will be determined with microsatellite markers. Microsatellites are stretches of repetitive DNA found in eukaryotic organisms (organisms with a cell nucleus). Microsatellites typically consist of a simple repeat of 2-6 base pairs, with between 10-100 repeats present for a given microsatellite. For example, the sequence ATATATATATATAT would be an AT dinucleotide repeat microsatellite with 7 repeats (**Fig. 1**).

Microsatellites have a higher mutation rate than most other regions of the genome, and therefore will show considerable variability. In fact the number of alleles within populations is much higher in microsatellites compared to many other types of molecular markers (e.g. Single Nucleotide Polymorphism, mitochondrial sequences, allozymes or Restriction Fragment Length Polymorphisms). This is a useful quality that can be employed for such uses as determination of parentage, assessing levels of genetic differences between populations, and crime-scene forensics. The latter application is familiar to many via depictions on popular television, in which blood or other tissue from a crime scene can be linked back to an individual. In the U.S., this procedure uses a standardized panel of 16 microsatellite markers, for which virtually every individual on earth (excluding identical twins) will have a unique pattern.



Fish 1 (6,10 genotype)
Copy 1: cgactacttATATATATATATgtaccacg (6 repeats)
Copy 2: cgactacttATATATATATATATATATATgtaccacg (10 repeats)

Fish 2 (4,8 genotype)
Copy 1: cgactacttATATATATgtaccacg (4 repeats)
Copy 2: cgactacttATATATATATATATATgtaccacg (8 repeats)

Figure 1: Illustration of a microsatellite locus. DNA contained within cell nuclei (top) is organized into chromosomes. Microsatellites within chromosomes are composed of flanking regions (lowercase) and repeats (uppercase, AT). There are two chromosomes in each individual, so there are two copies of the microsatellite position (locus). Each individual fish therefore has two copies of a microsatellite variant (allele). In this case, Fish 1 has a 6 repeat allele and a 10 repeat allele at the other. Fish 1 can be distinguished from Fish 2, which has a 4 and 8 copies at the same locus. By comparing many microsatellite loci in a fish from unknown origin with baseline data generated from fish of known origin, one may "assign" the unknowns to natal population.

Recently, Gauthier and Carlsson created and validated a panel of 14 microsatellite markers for striped bass, and used these markers to perform a large-scale analysis of striped bass population structure along the Atlantic coast of the United States, ranging from Hudson River to South Carolina. This study examined young-of-year striped bass in order to establish baseline location-specific information about population structure. In addition to large-scale structure (e.g. Hudson River vs. Chesapeake Bay), more fine-scale structure (e.g. within Chesapeake Bay) and,

importantly, temporal variation in structure over two years was addressed. We also deployed the microsatellite panel for preliminary Mixed Stock Analysis of a limited number of adult fish from within Chesapeake Bay (collected by Chesapeake Bay Multispecies Monitoring and Assessment Program, ChesMMAP) as well as in coastal waters (North-East Area Monitoring and Assessment Program, NEAMAP). The results of these studies are being prepared for submission to a peer-reviewed journal, but some highlights are presented here:

1. F_{ST} analyses indicated that there was significant population structure among the five major regions examined (Hudson River, Delaware River, Chesapeake Bay, Albemarle Sound (NC), Santee-Cooper system (SC). Genetic differentiation was consistent with isolation-by-distance.

2. Analysis of data with STRUCTURE indicated highest support for separating genotypes into three population clusters, namely Hudson River, Delaware River/Chesapeake Bay/Albemarle Sound complex, and South Carolina (**Fig. 2**).

3. Analysis of contemporary gene flow indicated unequal gene flow between populations, with the Chesapeake Bay contributing significantly to other stocks with minimal return inputs.

4. Using a stringent assignment score cutoff (80%) in the Structure software, we were able to assign 58% of fish from within Chesapeake Bay to source populations, and with the same cutoff were able to assign 62% of fish collected in coastal waters to source populations. Fish from Hudson River, and from Delaware River/Chesapeake Bay/Albemarle Sound complex were identified in both samples. The accuracy of the assignment was evaluated by using 10 individuals from each of the three regions as test samples. Of these 26 (87%) could be assigned with a stringent cutoff (at least 80% assignment score). All 26 (100%) of the test fish assigned correctly to their source population (**Fig. 3**).

These findings, especially #4, are highly significant to the proposed study and to striped bass management. *The results clearly indicate that it is possible with our microsatellite panel to assign fish from a mixed stock to population of origin with high accuracy.*

The microsatellite panel deployed in the previous study is an important tool for future examination of striped bass genetic population structure. More important still is the large baseline dataset generated by this work. By comparing microsatellite profiles of fish collected from mixed stocks (e.g. the coastal fishery) to this baseline, we can, with a high degree of accuracy, assign these fish to natal population. The methodology behind microsatellite

amplification and size determination is already well-established, therefore we anticipate no future technical development and minimal laboratory troubleshooting. Further, we have demonstrated that assignment testing with these markers works in practice, therefore the project methodology has a very high chance of success.

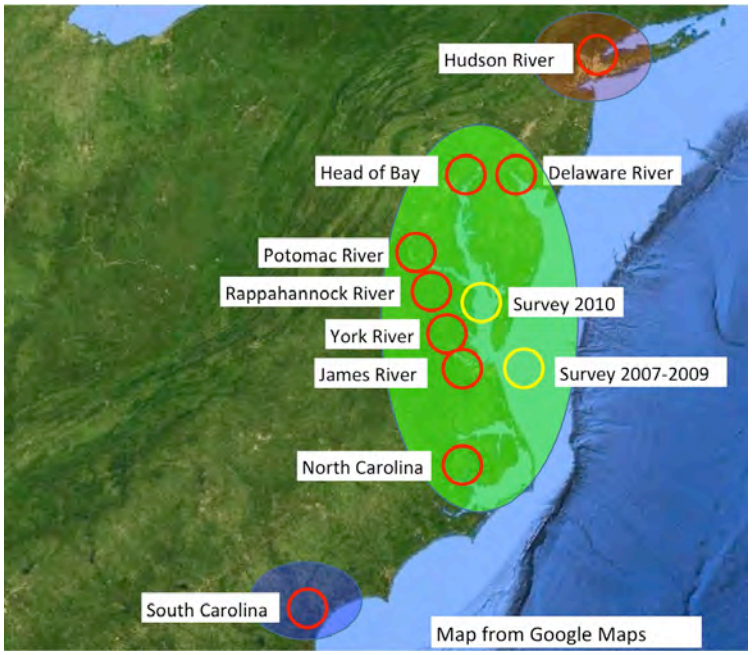


Figure 2. Genetic groups resolved using Structure. Transparent red, green and blue ovals denote clusters identified by Structure. Red circles denotes samples used for the Structure baseline and yellow circles are adult striped bass from surveys used in a preliminary assignment test.

Figure 3. Structure clustering of striped bass (a) and quality control by assigning ten known individuals per cluster (b). The graph is composed of a series of bars. Each bar represents one individual and the colors of the bar represent the proportional origin of individuals. Red indicates Hudson River origin, green indicates origin in the Delaware River/Chesapeake Bay/North Carolina cluster, and blue indicates South Carolina origin. a) contains three potential source clusters and a fourth group that consisting of striped bass with unknown origin (assignment). b) contains seven groups, the three indicated by previous Structure analysis, ten individuals from each of these three clusters (test), and the seventh group consisting of individuals with unknown origin (assignment).

We will deploy the aforementioned microsatellite panel to perform Mixed Stock Analysis of approximately 700 adult striped bass. These will include individuals collected from the coastal fishery, as well as large (age 4+) striped bass collected during spawning migrations within Chesapeake Bay. Several sampling strategies will be employed. First, striped bass within Chesapeake Bay will be sampled via the Chesapeake Bay Multispecies Monitoring and Assessment Program (ChesMMAP, R. Latour and C. Bonzek co-PIs). This survey samples adult finfishes throughout the bay five times per year, and we have an established collaboration with the survey for sampling of striped bass. We will target age 4+ fish, which can be presumed to be migratory based on previous work [17, 18]. Sampling younger fish would also yield interesting scientific data, as it may indicate the amount of current genetic contribution of outside areas to Chesapeake Bay recruitment, however the migratory status of age 1-3 fish is difficult to determine, and we wish to focus our efforts on older migratory animals. An additional benefit to ChesMMAP based sampling is that all collected fish will be worked up for sex and otolith-based age determination as part of normal operating procedures on that survey. The former may be used to determine if there are sex-based biases in the genetic composition of migratory striped bass within the Bay, while the latter may be used to confirm scale-based age determination. Based on prior experience, we anticipate approximately 100-200 striped bass ranging from 4-10+ years will be sampled by this platform during this study. To more specifically target offshore migratory striped bass, we will collect samples using the NorthEast Area Monitoring and Assessment Program (NEAMAP) survey (R. Latour and C. Bonzek, co-PIs). The NEAMAP program collects adult and juvenile finfishes in coastal waters from Cape Cod, MA to Cape Hatteras, NC during spring and fall cruises. These fish can be definitively classed as migratory, and the same advantages apply as in sampling fish via ChesMMAP. Fewer striped bass are collected per typical year on NEAMAP vs. ChesMMAP, however, as all may be sampled, we anticipate a similar number of striped bass will be sampled by these methods.

In addition to the scientific sampling platforms described above, we also intend to engage the fishing community in collection of striped bass samples. To this end, we will attend striped bass fishing tournaments from Fall 2011- Spring 2012. We will target major tournaments fishing primarily in VA coastal waters and within Chesapeake Bay, including but not limited to the following:

- American Striper Association (ASA) Fall Tournament/Million Dollar Rockfish Challenge (Virginia Beach, VA)
- Mid-Atlantic Rockfish Shootout (Virginia Beach, VA)
- Annual Virginia Beach Rockfish Frostbite Challenge (Virginia Beach, VA)
- Maryland Saltwater Sportfishermen's Association (MSSA) Spring and Fall Tournaments (MD)
- CCA Green Top Tournament (Deltaville, VA)

We will collect scale samples from tournament-caught fish, which will allow microsatellite analysis (DNA extracted from scale samples) as well as aging of collected fish. Fishing tournaments are ideal for sample collections in this case, as large, migratory fish are preferentially targeted. In all cases, we will ask for contact information from anglers, and will send them a report on the age and origin of their catch when this data is generated. In this way, we will provide information of interest to anglers for minimal inconvenience, and will have the opportunity to provide outreach regarding ongoing striped bass research. Our goal will be for approximately one quarter of our samples to be derived from this activity.

Ultimately, we believe this type of research will have direct applicability to ongoing management of striped bass, and that regular or periodic monitoring of coastal stock composition may be useful to managers. If this is to take place, it would ideally involve participation of the fishing community. To this end, we will target approximately one quarter of our study samples to be collected independently by anglers. We will contact anglers via public outreach at tournaments and Coastal Conservation Association-sponsored events and distribute a limited number of sampling packets, including detailed instructions, a scale collection envelope, and a postage-paid mailer for return of scales to ODU. Sampling of fish will require only nonlethal collection of scales, and therefore will not be subject to additional permitting outside of normal seasonal and size regulations. As with the other sampling methods, we will use scales for microsatellite analysis and age determination, and anglers returning samples will receive information on the age and population of origin of their fish. This sampling method will provide useful scientific information for the study, and will also give us practical information on the

logistics of angler-based sampling, public interest in the work, and ability to reliably extract DNA from angler-collected samples.

DNA will be extracted from dried scale samples by proteinase K/chelex extraction [19]. Fourteen microsatellite loci will be PCR-amplified and screened for genetic variability using an ABI 3130xl Genetic Analyzer (Applied Biosystems, Forest City, CA). All 14 loci have previously been successfully and consistently amplified from scale samples in our previous work. The size of individual alleles, in base pairs, will be assessed with Genemarker software (SoftGenetics, State College, PA). Assignment of samples to population of origin will be performed with Structure software [20]. Assignment testing will be performed using baseline data generated by Drs. Gauthier and Carlsson in previous work [21]. This baseline data was generated using 50 young-of-year (YOY) striped bass from 11 sites along the Atlantic coast, including Hudson River (2), Delaware River (1), Chesapeake Bay (5), Albemarle Sound (2), and South Carolina (1), and provides sufficient resolution for (at minimum) resolution between Hudson River, Delaware River/Chesapeake Bay/North Carolina complex, and South Carolina stocks. Additional distinctions may be made at lower stringency levels (e.g. Chesapeake Bay vs. North Carolina), as appropriate. Age will be determined using dorsal scales by modification of previous methods [22].

Project personnel and responsibilities. Dr. David Gauthier will be the principal investigator on this project. Dr. Gauthier will perform technical and fiscal oversight of the project, including mentoring of a doctoral student (Brandon Rowan) who will coordinate and perform sample collection, processing and data analysis. Dr. Gauthier will oversee all sample collections, public outreach, molecular techniques and analysis of data generated by these techniques. All samples will be processed in Dr. Gauthier's laboratory at ODU. Dr. Carlsson is currently at University College Cork in Ireland, and maintains adjunct Assistant Professor status at Duke University. Dr. Carlsson specializes in population genetics of finfishes and shellfishes, and was the principal investigator on the NOAA/Saltonstall-Kennedy funded grant that established the panel of microsatellites to be used here. Dr. Carlsson will provide additional expertise on population genetics, genotyping, and statistical analyses, and will participate in production of final products, including reports, publications, presentations to fisheries managers and the scientific community. Drs Gauthier and Carlsson will jointly oversee the progress of the doctoral student in this project.

Regular conference calls via Skype will be performed between Dr. Gauthier, Dr. Carlsson, and Mr. Rowan to discuss progress performance and details.

V. Location:

Sample collections for these studies will be performed aboard the ChesMMAP and NEAMAP surveys during their normal schedules. The ChesMMAP survey ranges from the Susquehanna flats in the northern Chesapeake Bay to the Bay mouth, and NEAMAP ranges from Cape Hatteras, NC to Cape Cod, MA. Participation in fishing tournaments will take place in Virginia and Maryland, as appropriate. All sample preparation and processing will be performed in-house at Old Dominion University Department of Biological Sciences (Norfolk, VA).

VI. Estimated Cost and Justification:

	Sponsor	**Match**
Salaries	$ 17,666	$ 0
Fringe Benefits	$ 1,681	$ 0
Student stipend	$ 20,000	$ 0
Student tuition	$ 5,667	$ 0
Supplies	$ 20,000	$ 0
Travel	$ 2,000	$ 0
Indirect Costs	$ 15,337	$ 15,337
TOTALS	**$ 82,351**	**$ 15,337**

Salary (Gauthier, Carlsson): We request salary support for Drs. Gauthier and Carlsson for this work. The roles of these investigators in this project are described in the previous section. Faculty salary for the Principal Investigator, Dr. David Gauthier, is based on a 9-month performance period. Amounts charged are calculated as follows: salary/9 = rate per month. Rate per month x number of months in semester x percent effort in semester = charge per period. Dr. Gauthier's salary at the start of this project will be $61,000 and he will devote approximately 1.5 months of summer effort to this project. Dr. Carlsson requests $7,500 for activities related to this scope of work. This equates to 150 hours over the duration of the project at a $50/hr consulting rate.

Fringe Benefits: The fringe benefits applicable to the Principal Investigator's summer salary include FICA, worker's compensation and unemployment insurance premiums. FICA, worker's compensation and unemployment insurance premiums have been budgeted for the summer salary of the Graduate Research Assistant.

Student stipend/tuition: This project will support a doctoral-level student (Mr. Brandon Rowan) who will perform all laboratory tasks associated with the work. The project will also serve as a major portion of Mr. Rowan's doctoral dissertation research. We seek funds to support Mr. Rowan for the duration of the project. Graduate Research Assistant (GRA) wages are based on a 7.5 month performance period, during which the GRA may devote up to 50-percent effort to research or sponsored programs. A GRA may devote 50% academic year effort and 100% summer effort to the project each year. Specific wage rates are determined by the academic departments, and they are based on the level of the student (masters or doctoral student) and on the number of years of experience the individual has had on research and sponsored projects. The wage rate for the GRA on this project is $20,000.

Supplies: We request a supply budget to cover microsatellite-based genotyping of striped bass (n=700). The cost per locus is $2.00 including allowance for re-runs of problematic samples. At 14 loci per fish and 700 fish, this totals $19,600. We further request $400 for costs associated with printing and postage for angler-collected samples.

Travel: We request $1000 for travel to local fishing tournaments to collect samples. We also seek $1000 to partially defray costs associated with presentation of our results at a national meeting (i.e. AFS annual meeting).

Tuition Remission: Tuition remission of $5,667 is included in the project budget. This amount covers 15 credit hours and all semester fees for the GRA. (based on In-State credit hour rates)

Indirect costs: Our ONR negotiated agreement dated July 22, 2009 authorizes an on-campus indirect cost rate of 50% of modified total direct costs effective July 1, 2009 until amended. However, for this proposal recoverable indirect costs are capped at 25%, in accordance with sponsor policy.

Mandatory cost share: This proposal requires cost-share of up to 10% of total project cost. In accordance with sponsor guidelines, we will apply the unrecoverable portion (25%) of our federally negotiated indirect cost rate to cost-share.

Literature Cited

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